User Manual for

IMBA Professional Plus

(Version 4.0)

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Prepared by

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Origins of IMBA Professional Plus



IMBA Professional Plus has been developed by the UK's Health Protection Agency - Radiation Protection Division (HPA-RPD), in association with ACJ & Associates, Inc., USA. The software is based on the IMBA Expert[™] series of customized Windows® bioassay and internal dosimetry software applications (www.imbaexpert.com). These software packages provide user-friendly interfaces with the UK National Radiological Protection Board's (NRPB's) proprietary suite of Integrated Modules for Bioassay Analysis (IMBA). They automatically apply the NRPB's extensively quality-assured IMBA code modules to estimate single or multiple intakes of various radionuclides, and to calculate the resulting doses from measurements of activity in the body and/or excreta. The IMBA code modules implement all of the International Commission on Radiological Protection's (ICRP's) currently recommended respiratory tract, GI-tract, tissue dosimetry, biokinetic and bioassay models for the selected radionuclides, for the ICRP68 Reference Worker.





Note: IMBA Professional Plus is fully compatable with data files generated by the IMBA Expert^M and IMBA Professional Series of software products (*i.e.*, all IMBA-based software applications distributed previously).

Authors and Acknowledgements





Dr. Alan Birchall (<u>NRPB</u>, UK) designed the user interface, wrote the IMBA Expert[™]/Professional Plus code, and managed the NRPB software development team.

Dr. Tony James (<u>ACJ & Associates, Inc.</u>) was responsible for technical and contractual liaison with the U.S. and Canadian sponsors of the initial IMBA Expert[™] projects (USDOE-Edition, OCAS-Edition and CANDU-Edition), overall design and development of these projects, software testing, quality assurance, and documentation.

Dr. James Marsh (NRPB, UK) managed the development of new and/or improved organ retention and excretion functions, software testing and quality assurance, and helped with code development.

Ms. Denise Dorrian, Ms. Katie Davis, Tony Smith and David King (NRPB, UK) carried out the development of organ retention and excretion functions and the software "benchmark" testing.

Dr. Alan Phipps and Mrs. Tracy Smith (NRPB, UK) ran the NRPB's **PLEIADES** code to benchmark IMBA Expert[™]/Professional Plus's calculations of doses and excretion rates.

Dr. Naomi Jarvis (US Consultant) developed the extensions of NRPB's **IMBA Suite** needed for IMBA Expert[™]/Professional Plus to perform their specialized calculations.

Tony Riddell (Westlakes Research Institute, UK) and Mark Peace (British Nuclear Fuels Limited, UK) authored the **IMBA** code module **"BNFL.FIT"** that implements the maximum likelihood fitting method.

Dr. Matthew Puncher and Ms. Frances Smith (NRPB, UK) were responsible for developing

tools and Active-X controls used by IMBA Expert[™]/Professional Plus, and also for validating parts of the code.

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IMBA Professional Plus - Base Unit



IMBA Professional Plus (Version 4.0) is a compilation of features and capabilities developed for <u>IMBA Expert[™] USDOE-Edition</u>, <u>IMBA Expert[™] CANDU-Edition</u>, and <u>IMBA Expert[™] OCAS-Edition</u>, with new features developed by <u>HPA-RPD</u>. The IMBA Professional Plus - Base Unit includes the capability to:

- 1. assess an intake from bioassay measurement data
- 2. calculate bioassay quantities at different times from a specific intake
- 3. calculate equivalent organ doses and effective dose from a single intake.

The base unit is the core of IMBA Professional Plus and enables the user to perform basic internal dosimetry calculations (*e.g.*, calculating doses from a specified intake, estimating an intake from bioassay measurements and calculating bioassay quantities from a given intake). It implements the latest ICRP biokinetic models. Output is both tabular and graphical and special tools enable data transfer between Windows[™] applications. For standard calculations, all of the ICRP default values can be selected from built in databases at the touch of a button. For more detailed calculations, the user can enter individual parameter values. Calculations are performed 6-10 times faster than in the previous software (IMBA Expert[™]/Professional Series). The product has been extensively quality assured and comes with complete documentation.

The IMBA Professional Plus - Base Unit (Version 4.0.8) includes the following 75 radionuclides (listed alphabetically by radiolement):

- actinium (^{227,228}Ac);
- **americium** (^{241,243}Am);
- antimony (^{124,125}Sb);
- **barium** (¹⁴⁰Ba);
- caesium (^{134,137}Cs);
- californium (²⁵²Cf);
- carbon (¹⁴C) as particulate or as gaseous or vapor forms of carbon;
- cerium (^{141,144}Ce);
- chromium (⁵¹Cr);
- cobalt (^{57,58,60}Co);
- curium (^{242,243,244} Cm);
- europium (^{152,154,155,156}Eu);
- hafnium (¹⁸¹Hf);
- hydrogen [tritium] (³H) with biokinetic models for tritiated water (HTO) and organically bound tritium (OBT) - as particulate or as gaseous or vapor forms of tritium;
- iodine (^{125,129,131,133,134,135}I) as particulate or as gaseous or vapor forms of iodine;
- iron (^{55,59}Fe);
- lanthanum (¹⁴⁰La);
- manganese (⁵⁴Mn);
- **neptunium** (^{237,239}Np);
- nickel (⁶³Ni);
- **niobium** (^{94,95}Nb);
- phosphorus (^{32,33}P);
- plutonium (^{238,239,240,241,242}Pu);
- promethium (¹⁴⁷Pm);
- protactinium (²³¹Pa);
- **polonium** (²¹⁰Po);
- **radium** (^{224,226,228} Ra) assuming same biokinetic model for parent and radioactive progeny note that ICRP68 assumes independent kinetics for the progeny;
- ruthenium (^{103,106}Ru);
- silver (^{110m}Ag);
- sodium (^{22,24}Na);
- **strontium** (^{85,89,90}Sr);
- sulphur (³⁵S) as particulate, for both inorganic and organically incorporated sulfur -

a version update will include gaseous and vapor forms of sulphur;

- **terbium** (¹⁶⁰Tb);
- **thorium** (^{228,230,232} Th) assuming same biokinetic model for parent and radioactive progeny note that ICRP68 assumes independent kinetics for the progeny;
- tin (¹¹³Sn);
- **uranium** (^{234,235,236,238}U) assuming same biokinetic model for parent and radioactive progeny note that ICRP68 assumes independent kinetics for the progeny;
- **yttrium** (⁹⁰Y);
- **zinc** (⁶⁵Zn);
- **zirconium** (⁹⁵Zr).

The IMBA Professional Plus - Base Unit enables you to do the following:

- Assess an intake from either inhalation, ingestion, injection, or a transdermal wound.
- Calculate **bioassay quantities** as a function of time implemented quantities are:
 - 1. Whole Body
 - 2. Lungs
 - 3. Urine
 - 4. Faeces
 - 5. Blood
 - 6. Thyroid
 - 7. Liver
 - 8. User Defined.

The IMBA Professional Plus - Base Unit includes the following basic features:

- Calculate the best estimate of the **amount of intake** from a single **exposure event** (**intake regime**), based on the user-specified intake scenario.
- Analyse any of the above types of bioassay measurement for a given indicator radionuclide.
- Save all assumptions, parameter values and results to a single, nameable data file which can be read in to any version of IMBA Expert[™]/Professional Series/Professional Plus, running on any compatible PC computer system.
- Specify the date and time-of-day of each bioassay measurement.
- Track time as either date + hh:mm or fractional d.
- Specify the collection period for each urine and faecal sample (in fraction of a day).
- Import/export bioassay data between IMBA Expert[™]/Professional Series/Professional Plus and a Windows® spreadsheet.
- Exclude unreliable data points from the fitting process but not from the data record and mark these as such in the associated graph of the data.
- Apply the maximum likelihood fitting method to deal with:
 - 1. data recorded as "less than the limit of detection" (< LOD);
 - 2. explicit error on each data point;
 - 3. lognormal or normal error distributions;

- 4. up to 200 data points (for each bioassay quantity).
- Obtain the **best estimate** of the amount of intake repeating the calculation with the same assumptions and data yields an identical result.
- Calculate the **committed equivalent dose to each organ or tissue -** and the **effective dose -** from an **indicator radionuclide**.
- Toggle between ICRP60/68, ICRP26, or 10 CFR 835 tissue weighting factors and remainder tissue rules.
- Create a comprehensive **report file** containing administrative details, all case parameter assumptions, and the calculated results.
- Define all **absorption parameters** and **aerosol characteristics** or select the absorption parameters from a built-in **database** of ICRP-recommended values.
- Define **bioassay retention functions** or select these from a **database** of ICRP-recommended values.
- Enter user specified particle transport rates (in the respiratory tract) or use ICRP defaults and perform calculations for both Reference Worker (light activity) and heavy activity.
- Apply **built-in ICRP biokinetic models** for each radioelement or specify **user-defined models**.
- Display **bioassay data** (with **error bars** and the **fitted bioassay function**) graphically **on-screen** in multiple windows.
- Interchangeably display tables of bioassay data and predicted bioassay quantities with graphs of the same quantities.
- Use built-in, highly flexible, graphical and spreadsheet tools to facilitate setting up your graphs and data entry.
- Copy data to-and-from spreadsheets and other Windows® applications.
- Copy data to-and-from an ASCII file.
- The ability to deal with **chelated intakes** by marking and excluding "treatment enhanced" excretion data from the intake assessment.
- Apply the **built-in** *ICRP Publication 38* radiation database and view complete decay chains and nuclear data on-screen.
- Toggle between **pCi** and **Bq** activity units.
- Calculate **bioassay quantities** over specified time intervals for design of future monitoring programs.
- Save and reload all assumed parameter values and calculated results for a particular case study in a comprehensive parameter file.

The IMBA Professional Plus - Base Unit is accompanied by the following documentation:

- User's Manual (internal interactive HTML and hard-copy report).
- Appendix A Technical Basis (internal interactive HTML and PDF file).
- Appendix B Bioassay Quality Assurance (PDF file).
- Appendix C Dose Quality Assurance (PDF file).
- Appendix D Example Bioassay Cases (PDF file).

The IMBA Professional Plus - Base Unit is intended for the user who does not require all of the advanced features provided as modular "Add Ons." For the more advanced user, the various <u>Add Ons</u> provide additional, highly specialised, fully-integrated features, which greatly enhance the software's functionality.

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Additional Functionality in IPP "Add-Ons"



The following Add-On modules increase the functionality of the IMBA Professional Plus (IPP) - Base Unit:

- Add-On 1 <u>Multiple Intake Regimes</u>.
- Add-On 2 Multiple Bioassay Types.
- Add-On 3 <u>Associated Radionuclides</u>.
- Add-On 4 Uranium Mixtures.
- Add-On 5 <u>Uptake from a Wound</u>.
- Add-On 6 <u>Errors on Intake</u>.
- Add-On 7 <u>Bayes Implementation</u>.
- Add-On 8 <u>Tritium Tool</u>.
- Add-On 9 <u>Dose Calculations for Causation</u>.
- Add-On 10 Ingrowth of Americium-241.
- Add-On 11 Statistics Package.

Selected Add-On modules can be provided with the initial IMBA Professional Plus - Base Unit installational, or can be added later by downloading *via* the HPA-RPD <u>IMBA Professional</u> <u>Plus</u> web site.

Add-On 1: Multiple Intake Regimes

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Description

An intake regime defines both the mode of intake (inhalation of an aerosol or vapours, ingestion, injection, wound, *etc*) and the time of intake (*e.g.*, an acute intake on a certain date, or a chronic intake between two dates). This Add-On enables you to deal with up to 10 separate intake regimes simultaneously. Thus, when calculating doses or predicting bioassay quantities, the software automatically includes the contribution from each intake. It is also possible to assign different model parameter values separately to each intake regime. This option also works during intake estimation, and so up to 10 intakes can be fitted to the measurement data simultaneously.

How is it implemented?

This Add-On is implemented seamlessly on the <u>Main screen</u>. You select the number of intake regimes, and each intake regime (IR) can be set up independently by selecting the appropriate tab.

Intake Regimes Clear All Intake Regimes IR 1 IR 2 IR 3	Enter Number of In	take Regimes (1-10)
Route Inhalation Ingestion Injection Wound	Mode Acute Start Date	C Chronic
C Vapour		Edit Complex Regime

In the <u>Bioassay screen</u>, the single intake on the left hand side of the screen is replaced by the chosen number of intakes. For <u>dose calculations</u>, the dose to each organ is calculated separately for each intake regime. The total dose (from all intake regimes) is also given.

- For an example bioassay case analysis involving multiple intakes see <u>Case of Multiple</u> <u>Intakes</u>.
- Return to List of Add-Ons.

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Add-On 2: Multiple Bioassay Types

Description

The base unit will deal with 8 different bioassay quantities (whole body, lung, urinary and faecal excretion, blood, thyroid, liver and user defined). However, only one type of data set can be used at any one time. This Add-on enables the user to fit the intake to different bioassay types simultaneously. This Add-on also works with Add-On 1 (Multiple Intake Regimes) to enable multiple intakes to be fitted to multiple bioassay data types simultaneously.

How is it implemented?

This Add-On integrates seamlessly into the <u>Bioassay screen</u> of the base module. When assessing intakes from bioassay measurements, you simply select which type of bioassay data to use by checking the appropriate boxes.

Intakes to Bioassay	Bioassay to Intake
	Select which data to use
	I Lungs
	🔽 Urine
Display Statistics	Feces
	🖂 Blood
Bayesian Analysis Tool	Thyroid
	Liver
Start Calculation	User Defined

- For an example bioassay case analysis involving multiple intakes see <u>Case of Multiple</u> <u>Bioassay Quantities</u>.
- Return to List of Add-Ons.

Add-On 3: Associated Radionuclides



Description

The base unit performs dose calculations on the selected radionuclide (known in IMBA Professional Plus as the indicator nuclide). In some situations, many different radionuclides are bound together in a particle matrix (e.g., fission products). This Add-on enables you to specify up to 30 additional associated radionuclides, defining the amount of each with respect to the indicator radionuclide. Subsequent dose calculations will include the components from all of the associated radionuclides. In the dose calculations, it is assumed that the absorption rates (and f1 values) of each <u>associated radionuclide</u> are identical to that

of the indicator radionuclide. *How is it implemented?*

With this Add-On, you can specify up to 30 additional radionuclides from the main screen. The abundance of each associated radionuclide (the percentage of activity relative to the Indicator Nuclide) is entered by selecting the appropriate tab.

Co-60 Pu-241 Am-241 Co-131	
Select Radionuclide	Abundance 10 %
Delste Radionuclide	Half Life: 1.324E+C3 d

- For an example of a dose calculation involving associated radionuclides see <u>Doses from</u> <u>Associated Radionuclides</u>.
- Return to List of Add-Ons.

Add-On 4: Uranium Mixtures



Description

This Add-On enables you to specify a mixture of uranium isotopes (U-234, U-235, U-236 and U-238) for dose and bioassay calculations. You can choose default values for enriched, depleted, or natural uranium, or specify the mixtures directly. The specific activity of the resulting mixture is automatically calculated. The Add-On also allows you to specify the intakes in terms of mass (mg).

How is it implemented?

You select 'Uranium-mixture' from the drop down list of uranium isotopes in the periodic table. When this is selected, a button labelled 'Specify U mixture' appears on the Main screen. This brings up a new form enabling you to specify the isotopic composition.



Details of uranium n Help	nixture	
Isotopic Abundance U-234 48.86 U-235 2.28 U-236 0 U-238 48.86	% C User Defined % C Depleted % C Natural % C Low-Enriched % C High Enriched	Select by Activity Mass Clear
Resulting Specific Activ 2.5270E+01 6.8296E+02	ity Bq/mg pCi/mg	Allow Units
	OK. Cancel	

After exiting this screen, the uranium isotopes are automatically included as associated radionuclides with the selected <u>abundances</u>. In this case, the 'indicator' radionuclide is the complete uranium isotope mixture.

Note: The 'Uranium Mixture' Add-On does not require the 'Associated Radionuclides' Add-On to be installed. However, the latter module is needed to include associated radionuclides for all Indicator Nuclides other than the uranium
ISOTOPIC MIXTURE

- For an example of a bioassay analysis and dose calculation involving a uranium mixture see <u>Case of Uranium Isotopic Mixture</u>.
- Return to List of Add-Ons.

Add-On 5: Uptake from a Wound



Description

The Base Unit allows intakes via inhalation (aerosols and vapours), ingestion or direct injection. This Add-on enables you to deal with intakes from a wound site, i.e., transdermal intake. A generic wound model is specified by the user. This functionality is integrated automatically with all of the calculations (dosimetry, bioassay and intake fitting). It is planned to include default parameter values from the forthcoming NCRP wound model (when

these are available).

How is it implemented?

With this Add-On, you can select 'Wound' as a route of intake (from the Main screen). The 'Wound' button in the 'Model Parameters' panel is enabled, and the retention function can be entered as a sum of exponential terms.

💐 Generic Wound Model	
Wound Model	
A diagram of the NCRP wound following its pu	model will be placed here iblication
Ret(t) = a(1) exp[-lam(1) t] + a	(2) exp[-lam(2) t] +
Select	Wound Retention
User Defined Mode	i ali) lamli
- NCBP Defaulte	1
Wesk	3
<u>vcav</u>	5
Moderate	
Simon	Clear
200.9	
Avid	
	<u>D</u> K <u>C</u> ancel
Not Specified	
	1

- For an example of a bioassay analysis and dose calculation involving a intake via a wound see <u>Case of Wound Uptake</u>.
- Return to List of Add-Ons.

Add-On 6: Errors on Intake



Description

In cases where an intake is being estimated from bioassay data, and all of the data are assumed to be normally distributed with a specified standard deviation, then this Add-On will propagate the errors to calculate their contribution to the error in the estimate of intake. The error propagation is based on the Least Squares method.

How is it implemented?

You must first select Advanced Fitting Options from the Main screen (Advanced | Advanced Options | Fitting Tab), or from the Bioassay screen (Advanced | Advanced Fitting Options) and select Least Squares as the method of fitting.

After calculating the Intake, the Error value will be displayed automatically below the intake value - on the left side of the Bioassay screen.

🐴 Advanced Options 📃 🗆 🔀	INTAKE
These options should be used with extreme care	IR1 9.805E+03 B
Dose Fitting Bioassay Misc	+/- 9.782E+02 E
Select Fitting Method © Least Squares Maximum Likelihood © Bayesian	
<u>D</u> K <u>C</u> ancel	

- For an example involving the estimation of errors on calculated values of intake see <u>Case Evaluating Errors on Intake</u>.
- See Technical Basis of Least Squares Fitting.
- Return to List of Add-Ons.

Add-On 7: Bayes Implementation



Description

The Base Unit uses a fitting method based on the Maximum Likelihood Method to estimate

intakes from measurement data. This Add-On enables you to use a <u>Bayesian approach</u> to estimate an intake. Thus, prior knowledge about the intake (either from other measurements such as air sampling, or from hypothetical judgements) can be used in conjunction with the bioassay measurement data to obtain the probability distribution of intake. You can choose from a variety of 'prior' intake distributions, and both graphical and statistical displays are provided. This Add-On works in conjunction with the <u>Multiple Intake</u> <u>Regimes</u> Add-On to enable the probability distributions of several different intakes (each with their own prior) to be estimated simultaneously.

How is it implemented?

From the Bioassay screen menu, select 'Advanced | Fitting Options' and click the Bayesian option. A new button called Bayesian Analysis Tool will appear in the Bioassay screen. Pressing this button will call up the Bayesian Analysis Tool and enable you to calculate probability distributions of intake under different prior assumptions.

The prior distribution selected in this screen will also be used in any further fitting processes.

- For an example involving Bayesian analysis of intake see <u>Case Implementing Bayesian</u> <u>Analysis</u>.
 - See Technical Basis of Bayesian Analysis.
- Return to List of Add-Ons.

Add-On 8: Tritium Tool



- For an example using the tritium tool see <u>Case Implementing Tritium Tool</u>.
- Return to List of Add-Ons.

Add-On 9: Dose Calculations for Causation



• For an example calculation of equivalent doses received each year by a specified tissue (for use in the determination of cancer causation likelihood) see <u>Dose Calculations for</u> <u>Causation</u>.

Return to <u>List of Add-Ons</u>.

Add-On 10: In-growth of Americium-241

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 - For an example intake and dose calculation using external measurements of 241Am

activity as an indicator of plutonium activity in the lungs see Case of Am-241 In-growth.

• Return to List of Add-Ons.

Add-On 11: Statistics Package



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- For an example using the statistics package to evaluate an intake see <u>Case Using Statistics</u> <u>Package</u>.
- Return to List of Add-Ons.

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Additional Functionality in IPP "Add-Ons"



The following Add-On modules increase the functionality of the IMBA Professional Plus (IPP) - Base Unit:

- Add-On 1 <u>Multiple Intake Regimes</u>.
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- Add-On 5 <u>Uptake from a Wound</u>.
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- Add-On 7 <u>Bayes Implementation</u>.
- Add-On 8 <u>Tritium Tool</u>.
- Add-On 9 <u>Dose Calculations for Causation</u>.
- Add-On 10 Ingrowth of Americium-241.
- Add-On 11 Statistics Package.

Selected Add-On modules can be provided with the initial IMBA Professional Plus - Base Unit installational, or can be added later by downloading *via* the HPA-RPD <u>IMBA Professional</u> <u>Plus</u> web site.

Add-On 1: Multiple Intake Regimes

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Description

An intake regime defines both the mode of intake (inhalation of an aerosol or vapours, ingestion, injection, wound, *etc*) and the time of intake (*e.g.*, an acute intake on a certain date, or a chronic intake between two dates). This Add-On enables you to deal with up to 10 separate intake regimes simultaneously. Thus, when calculating doses or predicting bioassay quantities, the software automatically includes the contribution from each intake. It is also possible to assign different model parameter values separately to each intake regime. This option also works during intake estimation, and so up to 10 intakes can be fitted to the measurement data simultaneously.

How is it implemented?

This Add-On is implemented seamlessly on the <u>Main screen</u>. You select the number of intake regimes, and each intake regime (IR) can be set up independently by selecting the appropriate tab.

Intake Regimes Clear All Intake Regimes IR 1 IR 2 IR 3	Enter Number of In	take Regimes (1-10)
Route Inhalation Ingestion Injection Wound	Mode Acute Start Date	C Chronic
C Vapour		Edit Complex Regime

In the <u>Bioassay screen</u>, the single intake on the left hand side of the screen is replaced by the chosen number of intakes. For <u>dose calculations</u>, the dose to each organ is calculated separately for each intake regime. The total dose (from all intake regimes) is also given.

- For an example bioassay case analysis involving multiple intakes see <u>Case of Multiple</u> <u>Intakes</u>.
- Return to List of Add-Ons.

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Add-On 2: Multiple Bioassay Types

Description

The base unit will deal with 8 different bioassay quantities (whole body, lung, urinary and faecal excretion, blood, thyroid, liver and user defined). However, only one type of data set can be used at any one time. This Add-on enables the user to fit the intake to different bioassay types simultaneously. This Add-on also works with Add-On 1 (Multiple Intake Regimes) to enable multiple intakes to be fitted to multiple bioassay data types simultaneously.

How is it implemented?

This Add-On integrates seamlessly into the <u>Bioassay screen</u> of the base module. When assessing intakes from bioassay measurements, you simply select which type of bioassay data to use by checking the appropriate boxes.

Intakes to Bioassay	Bioassay to Intake
	Select which data to use
	I Lungs
	🔽 Urine
Display Statistics	Feces
	🖂 Blood
Bayesian Analysis Tool	Thyroid
	Liver
Start Calculation	User Defined

- For an example bioassay case analysis involving multiple intakes see <u>Case of Multiple</u> <u>Bioassay Quantities</u>.
- Return to List of Add-Ons.

Add-On 3: Associated Radionuclides



Description

The base unit performs dose calculations on the selected radionuclide (known in IMBA Professional Plus as the indicator nuclide). In some situations, many different radionuclides are bound together in a particle matrix (e.g., fission products). This Add-on enables you to specify up to 30 additional associated radionuclides, defining the amount of each with respect to the indicator radionuclide. Subsequent dose calculations will include the components from all of the associated radionuclides. In the dose calculations, it is assumed that the absorption rates (and f1 values) of each <u>associated radionuclide</u> are identical to that

of the indicator radionuclide. *How is it implemented?*

With this Add-On, you can specify up to 30 additional radionuclides from the main screen. The abundance of each associated radionuclide (the percentage of activity relative to the Indicator Nuclide) is entered by selecting the appropriate tab.

Co-60 Pu-241 Am-241 Co-131	
Select Radionuclide	Abundance 10 %
Delste Radionuclide	Half Life: 1.324E+C3 d

- For an example of a dose calculation involving associated radionuclides see <u>Doses from</u> <u>Associated Radionuclides</u>.
- Return to List of Add-Ons.

Add-On 4: Uranium Mixtures



Description

This Add-On enables you to specify a mixture of uranium isotopes (U-234, U-235, U-236 and U-238) for dose and bioassay calculations. You can choose default values for enriched, depleted, or natural uranium, or specify the mixtures directly. The specific activity of the resulting mixture is automatically calculated. The Add-On also allows you to specify the intakes in terms of mass (mg).

How is it implemented?

You select 'Uranium-mixture' from the drop down list of uranium isotopes in the periodic table. When this is selected, a button labelled 'Specify U mixture' appears on the Main screen. This brings up a new form enabling you to specify the isotopic composition.



Details of uranium n Help	nixture	
Isotopic Abundance U-234 48.86 U-235 2.28 U-236 0 U-238 48.86	% C User Defined % C Depleted % C Natural % C Low-Enriched % C High Enriched	Select by Activity Mass Clear
Resulting Specific Activ 2.5270E+01 6.8296E+02	ity Bq/mg pCi/mg	Allow Units
	OK. Cancel	

After exiting this screen, the uranium isotopes are automatically included as associated radionuclides with the selected <u>abundances</u>. In this case, the 'indicator' radionuclide is the complete uranium isotope mixture.

Note: The 'Uranium Mixture' Add-On does not require the 'Associated Radionuclides' Add-On to be installed. However, the latter module is needed to include associated radionuclides for all Indicator Nuclides other than the uranium
ISOTOPIC MIXTURE

- For an example of a bioassay analysis and dose calculation involving a uranium mixture see <u>Case of Uranium Isotopic Mixture</u>.
- Return to List of Add-Ons.

Add-On 5: Uptake from a Wound



Description

The Base Unit allows intakes via inhalation (aerosols and vapours), ingestion or direct injection. This Add-on enables you to deal with intakes from a wound site, i.e., transdermal intake. A generic wound model is specified by the user. This functionality is integrated automatically with all of the calculations (dosimetry, bioassay and intake fitting). It is planned to include default parameter values from the forthcoming NCRP wound model (when

these are available).

How is it implemented?

With this Add-On, you can select 'Wound' as a route of intake (from the Main screen). The 'Wound' button in the 'Model Parameters' panel is enabled, and the retention function can be entered as a sum of exponential terms.

💐 Generic Wound Model							
Wound Model							
A diagram of the NCRP wound following its pu	model will be placed here ublication						
Ret(t) = a(1) exp[-lam(1) t] + a	(2) exp[-lam(2) t] +						
Select	Wound Retention						
User Defined Mode	i ali lamli						
- NCBP Defaults	1						
West	3						
<u> </u>	5						
Moderate							
Strong	Clear						
Avid							
	<u>D</u> K <u>C</u> ancel						
Not Specified							

- For an example of a bioassay analysis and dose calculation involving a intake via a wound see <u>Case of Wound Uptake</u>.
- Return to List of Add-Ons.

Add-On 6: Errors on Intake



Description

In cases where an intake is being estimated from bioassay data, and all of the data are assumed to be normally distributed with a specified standard deviation, then this Add-On will propagate the errors to calculate their contribution to the error in the estimate of intake. The error propagation is based on the Least Squares method.

How is it implemented?

You must first select Advanced Fitting Options from the Main screen (Advanced | Advanced Options | Fitting Tab), or from the Bioassay screen (Advanced | Advanced Fitting Options) and select Least Squares as the method of fitting.

After calculating the Intake, the Error value will be displayed automatically below the intake value - on the left side of the Bioassay screen.

🐴 Advanced Options 📃 🗆 🔀	INTAKE
These options should be used with extreme care	IR1 9.805E+03 E
Dose Fitting Bioassay Misc	+/- 9.782E+02 E
Select Fitting Method © Least Squares © Maximum Likelihood © Bayesian	
<u>Q</u> K <u>C</u> ancel	

- For an example involving the estimation of errors on calculated values of intake see <u>Case Evaluating Errors on Intake</u>.
- See Technical Basis of Least Squares Fitting.
- Return to List of Add-Ons.

Add-On 7: Bayes Implementation



Description

The Base Unit uses a fitting method based on the Maximum Likelihood Method to estimate

intakes from measurement data. This Add-On enables you to use a <u>Bayesian approach</u> to estimate an intake. Thus, prior knowledge about the intake (either from other measurements such as air sampling, or from hypothetical judgements) can be used in conjunction with the bioassay measurement data to obtain the probability distribution of intake. You can choose from a variety of 'prior' intake distributions, and both graphical and statistical displays are provided. This Add-On works in conjunction with the <u>Multiple Intake</u> <u>Regimes</u> Add-On to enable the probability distributions of several different intakes (each with their own prior) to be estimated simultaneously.

How is it implemented?

From the Bioassay screen menu, select 'Advanced | Fitting Options' and click the Bayesian option. A new button called Bayesian Analysis Tool will appear in the Bioassay screen. Pressing this button will call up the Bayesian Analysis Tool and enable you to calculate probability distributions of intake under different prior assumptions.

The prior distribution selected in this screen will also be used in any further fitting processes.

- For an example involving Bayesian analysis of intake see <u>Case Implementing Bayesian</u> <u>Analysis</u>.
 - See Technical Basis of Bayesian Analysis.
- Return to List of Add-Ons.

Add-On 8: Tritium Tool



- For an example using the tritium tool see <u>Case Implementing Tritium Tool</u>.
- Return to List of Add-Ons.

Add-On 9: Dose Calculations for Causation



• For an example calculation of equivalent doses received each year by a specified tissue (for use in the determination of cancer causation likelihood) see <u>Dose Calculations for</u> <u>Causation</u>.

Return to <u>List of Add-Ons</u>.

Add-On 10: In-growth of Americium-241

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- _
 - For an example intake and dose calculation using external measurements of 241Am

activity as an indicator of plutonium activity in the lungs see Case of Am-241 In-growth.

• Return to List of Add-Ons.

Add-On 11: Statistics Package



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- .
- For an example using the statistics package to evaluate an intake see <u>Case Using Statistics</u> <u>Package</u>.
- Return to List of Add-Ons.

"What's This?" - Visual Tour

This **tour** will **guide** you through the layout and operation of IMBA Professional Plus' three working screens, and the tools provided for data entry, export, and visualization:

- 1. <u>Main Screen</u> (Opening Screen).
- 2. Bioassay Calculations Screen.
 - <u>Table Tool</u> (for data entry, editing, export)
 - Graph Tool (for data visualization)
- 3. Dose Calculations Screen.

Visual Tour of Main Screen



IMBA Professional Plus

- Just three, easy-to-navigate, tightly-integrated work screens!

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htte ween	IMBA	Professional Plus		
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Radionuclide Database (ICRP Publication 38)



Respiratory Tract and Gut Models



Clear









Tip: If you needed to scroll to see the right-edge of those images - or if you see only part of the "pop-ups" on the right of the "Feature Tour" below try **enlarging** the viewing panel by **dragging the left border** over the "Contents | Index | Search" panel!

Feature Tour:

Click on a **HOT ZONE** in the figure below - for a "pop-up" description of the function of that part of the screen (and/or control).

C)



Note: Except for the "greyed out" items, ALL of the features shown in Figure 2.5 (below) are fully functional in IMBA Professional (Full Edition) Version 3.0. The pop-ups indicate which of these functions are "Star" features - and therefore not available in the basic Lite-Edition. See also <u>Additional</u> <u>Functionality in "Star" and "Professional" Editions</u>.

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Figure 2.5. What's in the Main Screen?

Visual Tour of Bioassay Calculations Screen



Tip: If you needed to scroll to see the right-edge of this image - or if you see only part of the "pop-ups" on the right of the "Feature Tour" below try **enlarging** the viewing panel by **dragging the left border** over the "Contents | Index | Search" panel!

Feature Tour:

Click on a **HOT ZONE** below (in either figure) - for a "pop-up" description of the function of that part of the screen (and/or control):

- Figure 2.7: Screen in default "Bioassay to Intake" mode.
- Figure 2.8: Screen in selectable "Intakes to Bioassay" mode.



Note: The "multiple intake" function shown in Figures 2.7 and 2.8 (below), and the ability to analyse several bioassay quantities simultaneously, are "Star" features - and therefore not available in the basic Lite-Edition. See also <u>Additional Functionality in "Star" and "Professional" Editions</u>.



Figure 2.7. Bioassay Calculations screen in default "Bioassay to Intakes" mode.



Figure 2.8. Bioassay Calculations screen with "Intakes to Bioassay" mode selected.

Visual Tour of the Table Tool


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<u>Tip:</u> If you needed to scroll to see the right-edge of this image - or if you see only part of the "pop-ups" on the right of the "Feature Tour" below try <u>enlarging</u> the viewing panel by <u>dragging the left border</u> over the "Contents | Index | Search" panel!

Feature Tour:

Click on a <u>HOT ZONE</u> in the figure below - for a "pop-up" description of the function of that part of the screen (and/or control).

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Visual Tour of the Graph Tool





<u>Tip:</u> If you needed to scroll to see the right-edge of this image - or if you see only part of the "pop-ups" on the right of the "Feature Tour" below try <u>enlarging</u> the viewing panel by <u>dragging the left border</u> over the "Contents | Index | Search" panel!

Feature Tour:

Click on a <u>HOT ZONE</u> in the figure below - for a "pop-up" description of the function of that part of the screen (and/or control).



Visual Tour of Dose Screen

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Tip: If you needed to scroll to see the right-edge of this image - or if you see only part of the "pop-ups" on the right of the "Feature Tour" below try <u>enlarging</u> the viewing panel by <u>dragging the left border</u> over the "Contents | Index | Search" panel!

Feature Tour:

Click on a <u>HOT ZONE</u> in the figure below - for a "pop-up" description of the function of that part of the screen (and/or control).

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Figure 2.14. What's in the Dose Calculations screen?

Main Screen (Opening Screen)

The MainScreen (openingscreen)appearswhenyouclick the IMBAProfessional Plus icon - which runsIMBA.exe.This screen is shown in Figure 2.1.

IMBA Professional Plus

- Just three, easy-to-navigate, tiç	ghtly-integrated wor	k screens!	
Ry Main Screen Bie Edit Baraneters Calculations Tools Advanced Help			
Cpen Save New Quick Save Load Load Report Help		Apr 05	
IMBA F	Professional Plus	Age ()	
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Figure 2.1. The Main Screen (opening screen).

The screen is divided into these functional parts - from the top:

- Menu Bar;
- Tool Bar;
- Parameter File Bar.

Top main panel:

- Intake Scenario subdivided into;
 - 1. Intake Regimes (IR) sub-panel left side
 - 2. Units sub-panel center

3. Radionuclide(s) and Intake - by IR - right side.

Bottom main panel:

Model Parameters and Calculations;

Bottom row:

• Status Bar.

Visual Tour

• Click here for a Visual Tour of the Main Screen and its various functions.

Main Menus

The **Menu Bar**, shown at the top-left of the main window, gives the following options.

- File menu.
- Edit menu.
- <u>Parameters</u> menu.
- <u>Calculations</u> menu.
- Tools menu.
- <u>Advanced</u> menu.
- Help menu.

File Menu

🍣 Main Screen 👘		
File Edit Parameters	Calculations Tools Advanc	ed Help
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Save	ened	
Save As		
Quick Save Quick Load		IMBA
Create a Report	ario — — — — — — — — — — — — — — — — — — —	
Exit	es	



The File options are as follows:

- New Re-load (and reset) *IMBA Professional* for a new case study with a blank parameter file.
- **Open** Open any parameter file **"*.ix"** from the Folder C:\JABASOFT\IMBAEXUS\USERDATA (Figure 3.3), or browse to another Folder.
- Save Save the current parameter set to the same "*.ix" filename.
- Save As Allows you to define a new name for the "*.ix" file (appearance of dialog box is identical to Figure 3.3, but with **Save** button).

- **Quick Save** Save the current set of parameter values (and calculated results) to the default parameter file "**parameters.ix**" in the Folder C:\JABASOFT\IMBAEXUS.
- **Quick Load** Re-load the parameter values (and calculated results) from the default parameter file "**parameters.ix**" in the Folder C:\JABASOFT\IMBAEXUS.
- Create a Report Open the "Report" window. This will guide you through the steps needed to generate and save a Case Report.
- Exit Unload and Exit IMBA Professional.

Open		?×
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History Desktop My Documents	Development interesting.ix IXUS- I Mi99 - Pu.ix IXUS-II PH_UO2_urine_JT.ix USTUR Case 0269 Single Intake.ix Case 060501F.ix Test 2 - Urine.ix IAEA Case 4 - 90Sr.ix Test Case 1.ix IAEA Case 7 - 239Pu.ix USTUR0259.ix IAEA#7 - 238Pu - Data.ix USTUR0425urine1.ix iaeacase3M.ix Single Students	
My Computer	File name: IMBA Professional Files (*.ix) Files of type: IMBA Professional Files (*.ix) Open as read-only	oen ncel

Figure 3.3. The Open parameter file dialog box.

Edit Menu



Figure 3.4. Drop-down Edit list box.

The **Edit** options are as follows:

- Data Open the Bioassay Calculations screen in the "Bioassay Quantity" to "Intake" mode. This enables you to enter (or edit) Bioassay Data and/or perform Intake calculations.
- **Parameter File** *Open* the named **Parameter File** in MS NotePad. If no name has been specified, a blank MS Notepad file will be opened.
- **Preferences** *Choose* to play the "theme tune" at start-up or keep the default setting (silence).





Figure 3.5. Start-up preference.

Parameters Menu

00



Figure 3.6. Drop-down Parameters list box.

The **Parameters** options are as follows:

- **Particle Transport** *Open* the Particle Transport Model window. This enables you to *load* the values of **mechanical transport rates** recommended in *ICRP Publication* 66 for the <u>respiratory tract model</u> or define your own parameter values.
- Absorption Open the Absorption Model window. This enables you to *load* the default values of absorption rates recommended in *ICRP Publication 66* for the respiratory tract model or define your own parameter values.
- **Deposition** *Open* the Deposition Model window. This enables you to select the default values of **aerosol size characteristics** recommended in *ICRP Publication 66* for the **respiratory tract model** (occupational exposure) or define your own parameter values.
- **GI-Tract** *Open* the **GI** Tract Model window. This enables you to *select* the default values of **transport rates between compartments of the** <u>**GI tract**</u> recommended in *ICRP Publication 30* or define your own parameter values.
- **Bioassay** Open the Bioassay Model window. This enables you to select the **bioassay** function for each <u>bioassay quantity</u> either the function currently recommended by ICRP, or you can define your own function.
- **Biokinetics** *Open* the Biokinetic Model window. This enables you to *select* the **retention function** for each source organ or tissue either the function currently recommended by

ICRP, or you can define your own function.

- Vapour (Star-Plus Module) Open the Gases and Vapours Model window. This will enable you to *select* the default values recommended in *ICRP Publication 68* to represent occupational exposure to gases or vapours or define your own parameter values.
- Wound (Star-Plus Module) Open the NCRP Wound Model window. This will enable you to *select* the wound retention function by default retention type, or you can define your own function.

Calculations Menu



🌇 M	ain Sc	reen			
File	Edit	Param	neters	Calculations	Too
C É	2			Bioassay	
Ope	n	Save	New	Dose	
					_

Figure 3.7. Drop-down Calculations list box.

The Calculations options are:

- **Bioassay** *Open* the Bioassay Calculations screen in the "**Bioassay Quantity**" to "**Intake**" mode. This enables you to enter (or edit) **Bioassay Data** and/or perform <u>Intake</u> calculations.
- Dose Open the Dose Calculations screen. This enables you to:
 - 1. select radiation weighting factors;
 - 2. select tissue weighting factors;
 - 3. *calculate* doses from the selected Indicator Radionuclide;
 - 4. calculate doses from any selected Associated Radionuclides.

Tools Menu

🌇 Má	ain So	reen								
File	Edit	Parame	ters	Calculation	ns [Tools	Advan	ced	Help	
C î	×		Γ			Cal	culator			
Oper	r n	Save	New	Quick Sav	ve	Not	tePad			
Ver 3.0 No file opened				Loa	ad ICRP [Defau	ults			
]		Loa	ad 10-CF	R-83	5 Defaults	

Figure 3.8. Drop-down Tools list box.

The **Tools** options are:

- Calculator Open the standard Microsoft® Calculator window (Figure 3.9).
- Notepad Open an "Untitled" Microsoft® NotePad File window.
- Load ICRP Defaults Open automatically (in sequence):

- the F1 Values for *** window where "***" is the pre-selected radionuclide so you can *select* the appropriate value of the <u>gut uptake fraction</u> (f1) for the preselected radionuclide;
- 2. the Bioassay Model window this confirms that all currently recommended ICRP **bioassay functions** AND all other currently recommended ICRP models for the pre-selected radionuclide have been loaded.
- Load 10-CFR-835 Defaults Open automatically (in sequence):
 - the F1 Values for *** window where "***" is the pre-selected radionuclide so you can *select* the appropriate value of the **gut uptake fraction** (f1) for the pre-selected radionuclide;
 - the Bioassay Model window this confirms that all currently recommended ICRP bioassay functions and organ/tissue retention functions for the pre-selected radionuclide have been loaded - BUT the loaded tissue weighting factors and remainder tissue rules are those prescribed in the 10-CFR-835 Regulation (applicable in the U.S.).

🕅 Calci	ulator									_ 🗆 🗡
<u>E</u> dit <u>V</u> iew <u>H</u> elp										
										0.
C Hex C Dec C Oct C Bin C Degrees C Radians C Grads									ls	
🗖 Inv		Нур				Backsp	ace	CE		С
Sta	F-E	(1	MC	7	8	9	1	Mod	And
Ave	dms	Exp	In	MB	4	5	6	×	Or	Xor
Sum	sin	х^у	log	MS	1	2	3	•	Lsh	Not
S	cos	х^З	nl	M+	0	+/-		+	=	Int
Dat	tan	x^2	1/x	pi	A	В	С	D	E	F

Figure 3.9. Standard Microsoft® Calculator.

Advanced Menu

🂐 Mair	n Sa	reen				
File E	Edit	Param	neters	Calculations	Tools	Advanced Help
- r 2			∩			👖 🗹 Apply Model Params to All IRs
Open		Save	New	Quick Save		Lo Enable Complex Intake Regimes
Ver 3.0		No file o	pened			Enable DOS preview
				ļ	J	 Advanced Dosimetry Options

Figure 3.10. Drop-down Advanced list box.



The Advanced options are:

- Apply Model Parameters to All IRs the DEFAULT option (ticked). This applies a single set of selected model parameters to ALL Intake Regimes. Disable (untick) this default if you want to specify model parameters individually (and independently) for every intake regime.
- Enable **Complex Intake Regimes** this will enable you to define specific patterns of intake over periods of time.
- Enable DOS preview this is a "debugging" tool, used by the software's developers to examine the integrity of DOS input files produced by IMBA Professional in order to run the IMBA code modules.
- Advanced Dosimetry Options Opt to Exclude <u>nuclear recoil energy</u> from the <u>SEEs</u> for alpha emissions. For all Professional Series versions, the "default" is to **Include** nuclear recoil energy.

Advanced Dosimetry Options	<u>_ X</u>
These options should be used with extreme care	
Dose Fitting Bioassay Misc	
- Nuclear Recoil Energy-	
 Include 	
C Exclude	
Dose Calculation Optimisation The dose calculation for is already optimised for both speed and accuracy	
<u>O</u> K <u>C</u> ancel	

Figure 3.11. Tabs to select Advanced Dosimetry Options.

Help Menu



🍕 Main S	creen				
File Edit	Parameters	Calculations	Tools	Advanced	Help
Ê		•		RP CFR	Documentation
Open	Save New	Quick Save	Loa	id Load	About IMBA Professional
Ver 3.0	No file opened				Conditions of Use
		Help Mode			
مان ر	lit h				Quick Start

Figure 3.12. Drop-down Help list box.

The Help options are:

- Documentation Show (this) User Manual and Technical Basis documentation.
- About IMBA Professional Show Authorship and Copyright Notice (Figure 3.13).

🐴 About IMBA Professional		
IMBA Professional Full Edition	**	
by Alan Birchall		Ver 3.0.63
Other Authors		
Apr 2003		
	and	nrpb
Warning: this computer program is protected by copyright law and international treaties.	<u>S</u> ystem Info	ОК

Figure 3.13. Authorship and Copyright Notice.

- Conditions of Use Show End-User License Agreement ("EULA") for the IMBA Professional Series.
- Help Mode Switch operation of IMBA Professional from "Run" mode to special "Mouseover Help" mode. In this special mode, a "?" appears next to your mouse pointer. When you move this over a screen control region, a brief message appears to explain the function of the control - see Figure 3.14 for the message that appears in *Help Mode* when your mouse pointer is over the **Tool Bar**. To exit *Help Mode* - and go back to the "Run" mode, you simply "un-tick" (disable) the *Help Mode* option (see Figure 3.15).

💐 M	🏘 Main Screen										
File	Edit	Parameters	Calculations	Tools	Advanced	Help					
[c	[These buttons enable you to perform common tasks with a single click C										
Ver .	_										

Figure 3.14. Help Mode message describing the function of the Tool Bar.

🍕 M	ain Sc	reen				
File	Edit	Parameters	Calculations	Tools	Advanced	Help
(Documentation			
C Ver	- ,		J			About IMBA Professional Conditions of Use
	Juli	<i>au</i> ∕∏ift				 ✓ Help Mode Quick Start

Figure 3.15. Re-click the Help Mode option to remove the tick (disable Help Mode).

• **Quick Start** - **Opens** the scrollable *Quick Start* window (Figure 3.16). This contains a condensed description of the layout and operation of IMBA Professional - to help you (as an experienced internal dosimetrist) get started more directly with using the software.

🗠 Quick Start								
Quick Start								
This quick outline guide is intended for those already experienced in using internal dosimetry software. It will introduce you to the layout and operation of the IMBA Professional Series software, and list the easy steps involved in:								
 Estimating one or more intakes of an indicator radionuclide from bioassay data. Calculating the resulting committed organ doses and effective dose. Calculating doses from associated radionuclides. Predicting bioassay quantities as a function of time. 								
See Help Documentation for a full description of What IMBA Professional Series Does and for the full HTML Help User Manual and Technical Basis.								
<u>Overall Program Design</u>								
All calculations in IMBA Professional Series are performed from just three main screens:								
the <i>Main Screen</i> (startup screen);								
 the <i>Bioassay Calculations</i> screen, and; 								
the Dose Calculations screen.								
The Main Screen								
This is divided into three parts:								
• the top part of the screen handles the <i>Intake Scenario</i> (<i>Number</i> of <i>Intake Regimes</i> and their <i>Individual Characteristics</i>), selection of the <i>Indicator Radionuclide</i> (and any								
<u>Q</u> K <u>Print</u>								

Figure 3.16. Scrollable Quick Start Help window.

Tool Buttons



The **Tool Bar**, shown at the top-left of the *Main Screen*, just below the **Menu Bar**, contains **Tool Buttons** to let you perform common tasks with a **single click**. The tool buttons change appearance as the mouse pointer is passed over them.



Open a **Parameter File "*.ix"** from the directory C:\JABASOFT\IMBAEXUS\USERDATA - or browse to another folder.





Save the current parameter set to the **"*.ix"** Filename shown in the **"Parameter File"** box (top-right-corner of Main Screen). If no Filename is shown, the <u>Save</u> button opens the Save As dialog box (Figure 3.17).



New - clear all parameter values and case data and open a blank parameter file. This warning message will appear - to prevent you from accidentally losing unsaved data! If you click "**Yes**," the "**Parameter File**" box will display "**No file opened**."

Warning		×
You will lose all data if th	ey have not beer	n saved
Do you wish to continu	e?	
Yes	No	



Quick Save the current parameter set (and all case data) to the Folder**filename** [C:]\JABASOFT\IMBAEXUS**parameters.ix**.

Quick Load the parameter file [C:]

\JABASOFT\IMBAEXUS**parameters.ix**. If you installed IMBA Professional (**IMBA.exe**) on a different drive, the **parameters.ix** file will automatically be saved to and reloaded from your installation drive.



Load ICRP Defaults - **Quick-load** ALL ICRP-recommended models with minimum interaction from

you. <u>Clicking</u> the <u>button</u> will <u>Open</u> automatically (in sequence):
(1) the *F1 Values for **** window - where "***" is the pre-selected radionuclide - so you can <u>select</u> the appropriate value of the <u>gut uptake</u> <u>fraction</u> (f1) for the pre-selected radionuclide;

(2) the *Bioassay Model* window - to <u>confirm</u> that all currently recommended ICRP bioassay functions AND all other currently recommended ICRP models for the pre-selected radionuclide have been loaded.

Load 10-CFR-835 Defaults - Quick-load ALL ICRP-recommended models with 10-CFR-835 prescribed tissue weighting factors. <u>Clicking</u> the <u>button</u> will <u>Open</u> automatically (in sequence): (1) the *F1 Values for* *** window - where "***" is the pre-selected



radionuclide - so you can <u>select</u> the appropriate value of the **gut uptake** fraction (f1) for the pre-selected radionuclide;

(2) the *Bioassay Model* window - to <u>confirm</u> that all currently recommended ICRP bioassay functions and organ/tissue retention functions for the pre-selected radionuclide have been loaded - AND the loaded tissue weighting factors and remainder tissue rules are those prescribed in the 10-CFR-835 Regulation.



Report - **Open** the *Report* window to create a case report. This will be saved in Folder**filename**

C:\JABASOFT\IMBAEXUS\UserData**Default.RPT** (or in the equivalent folder on your installation drive). Alternatively, you can **browse** to save your **Report** in any other **folder** and/or **filename** of your choice.



 Help - $\underline{\textit{View}}$ a scrollable summary of available Help Options (Figure 3.18).



Figure 3.17. Save As dialog box.



Figure 3.18. Summary of available Help Options.

Parameter File Bar



Figure 3.19. Parameter File bar.

- This shows the **Folder** where the current **Parameter File** ("*.ix") was last saved and its filename.
- The box to the left shows the Version Number of this software (Ver. 3.0).





Main Status Bar

All IRs	Absorption: Not Specified	Part Tran: Not Specified	GI-Tract: Not Specified	f1=		Biokinetics: Not
---------	---------------------------	--------------------------	-------------------------	-----	--	------------------

Figure 3.20. New Status Bar - appearance for New (blank) Parameter File.

The Main Status Bar is on the bottom row of the Main Screen. When

you select a **New** (blank) **Parameter File**, the **Main Status Bar** appears as shown in Figure 3.20. The items listed are:

- All IRs (Star Feature Only) indicates that all specified model parameters will apply to *ALL* Intake Regimes (the default setting).
- Absorption respiratory tract <u>absorption</u> parameters initially Not Specified.
- Part Tran respiratory tract particle transport parameters initially Not Specified.
- GI-Tract gastrointestinal tract model parameters initially Not Specified.
- f1 gut absorption fraction initially Blank.
- Biokinetics biokinetic model parameters initially Not Specified.
- **Deposition** respiratory tract deposition model parameters initially Not Specified.
- **AMAD** <u>activity median aerodynamic diameter</u> (and other aerosol size parameters) initially *Not Specified*.
- Wound (Star-Plus Module Only) wound model parameters initially Not Specified.

Figure 3.21 shows the **Main Status Bar** for a **Parameter File** in which all of the above items have been specified (except for the **Wound** model parameters). In this example, the **"All IRs"** label has been replaced with the **"IR 1"** label. This denotes that the parameter settings displayed on the **Main Status Bar** apply to **Intake Regime #1**. Up to **10 IRs** can be specified independently - and their parameter settings can each be displayed (one **IR** at-a-time) on the **Main Status Bar**.

IR 1	Absorption: Type M	Part Tran: ICRP Defaults	GI-Tract: ICRP Defaults	f1=0.0005		Biokinetics: ICRP Pu
------	--------------------	--------------------------	-------------------------	-----------	--	----------------------

Figure 3.21. Working Status Bar - appearance for Working (in-use) Parameter File.

Intake Scenario Panel

🕰 Main Screen					
Ele Edit Parameters Calculation	ons <u>T</u> ools <u>A</u> dvanced <u>H</u> elp)			
Open Save New	Quick Save Load	Load Report	Felp		
Ver 4.0 Add-Ons: 10	No file opened				
Tit کندندهن		IM	BA P	Professional	Plus
Intake Scenario					
Intake Regimes Clear All Intake Regimes IB 1 Route © Inhalation © Ingestion	Enter Number of Inta Mode	ke Regimes (1-10)	1	Units Specify Time As O Date Time (d) since 1/1/1980 #	Intake (IR 1) 0 Bq Associated Radione
C Injection C Wound C Vapour	Start Time (d)	0 Edit Complex Reg	#	Bq C dpm C pCi C mg Dose Sv C rem C mSv C mrem	
				200	

Figure 3.22. Intake Scenario panel.

The Intake Scenario panel holds the sub-panels for specifying:

- Intake Regimes left side;
- Units center;
- Intake Amounts/Radionuclides right side.

Intake Regimes and Units



∣Intake Scenario-			
Clear All Intake Regimes	Units Specify Time As Date		
Route Inhalation Ingestion Injection	Mode Acute Start Time(d)	C Chronic	since 01/01/1980 # Intake © Bq C dpm
O Wound O Vapor		Edit Complex Regime	OpCi Omg Dose ⊙Sv Orem OmSv Omrem

Figure 3.23. Intake Regimes sub-panel with adjacent Units sub-panel.

Figure 3.23 shows the **Intake Regimes** sub-panel, together with the adjacent **Units** sub-panel, as they appear when IMBA Professional Plus is run for the first time - or when a "**New**" (blank) parameter file is opened. The functions of these two sub-panels are closely coupled.

1. Intake Regimes Sub-panel

By default, the **Number of Intake Regimes** (Intakes) is set to "1". A single index card is therefore displayed - with the **Tab** label "IR 1." You can <u>select</u> up to **10**_intake regimes (IRs). Use the selection arrows (Star Feature Only) on the Enter Number of Intake Regimes (1-10) to increase the number of IRs - or simply <u>highlight</u> and type the required number of IRs directly in this box.

For each IR, you can select:

- the Route of intake (from Inhalation, Ingestion, Injection, or Wound);
- the Mode of intake (from <u>Acute</u> or <u>Chronic</u>);
- the Start Time (d) of intake.

With the **Units** of **Time** at the default setting of "**Time** (d) since," <u>Selecting</u> the **Chronic Mode** automatically displays an additional dialog box - the **End Time** (d) box - for you to specify the end of the period of chronic intake (Figure 3.24).

In both the **Start Time (d)** and **End Time (d)** boxes, you enter the time value in **integer** or **decimal-fraction** days, relative to the <u>reference</u> "**Time (d) since**" value. For example, with the "**Time (d) since**" time-of-day set at 07:00:

- 0, 5 start time is the zeroth day (at 7:00 AM), end time is the fifth day (at 7:00 AM);
- 0.4375, 6.75 <u>start time</u> is the zeroth day (at 5:30 PM), <u>end time</u> is the sixth day (at 1:00 AM).

∣Intake Scenario-				
Clear All Intake Regimes	Units Specify Ti O Date O Time (o	me As		
Route Inhalation Ingestion Vound Vapor	Mode C Acute Start Time(d) End Time(d)	Chronic CHronic (0.4375 # 6.75 # Edit Complex Regime	since 01/04/20 ○ Bq ○ pCi Oose ○ Sv ○ mSv	00 07:0[dpm mg rem mrem

Figure 3.24. The End Time (d) dialog box appears when you select the Chronic intake Mode - for the displayed IR only.

Note: IMBA Professional automatically detects the "Country Setting" of your computer - and automatically displays all dates in your correct "Date Convention." However, to ensure global "transportability" of data files, the Parameter.ix file stores all dates in the U.S. date convention, <u>i.e.</u>, as MM/DD/YYYY.

Tip: Take care when using two-digits to specify the year (YY). By convention, "00 - 29" is automatically interpreted by Windows**â** as "2000 - 2029" - and "30 - 99" as "1930 - 1999." If in any doubt, it is safest to use four-digits to specify the year (YYYY). If you want to specify 2030, then you MUST enter "2030!"

2. Reference Date and Time



Figure 3.25. The reference "Time (d) since" value.

For all calculations of <u>bioassay quantities</u> (as a function of time), and to plot graphs, IMBA Professional uses a single, common timescale. The starting point of this timescale is defined by the **Date (and Time-of-Day)** entered in the "**Time (d) since**" dialog box. The "pre-loaded" default starting value is 1/1/1980 (January 1_{st}, 1980) - see Figure 3.23 at the top of this page.



Note: For every IR, IMBA Professional automatically tracks **Time** values relative to the single **Reference Date (and Time)** that is displayed in the **Units** sub-panel - in the "**Time (d) since**" dialog box.

Key Tip: As the first step in entering your data in IMBA Professional, <u>change</u> the default value in the "**Time (d) since**" dialog box to a Date/Time-of-Day that is appropriate for your data. For example: (1) the starting date and time of the first intake that you want to analyse, or (2) the start of employment - for a complex case involving multiple intakes over an extended period of years.

3. Units Sub-panel to Specify Time (d) or Date

This is used to switch the **Unit** in which **Time** is displayed. Under the heading "**Specify Time As**," you can <u>select</u>:

- Date to display Start and End times as Date + hh:mm:ss, or;
- Time (d) since the default setting, to display Start and End times as decimalfraction days.

Figure 3.26 shows how the Figure 3.24 display changes when you switch to the **Date** option.

Intake Scenario−			
Intake Regimes Clear All Intake Regimes IR 1	Units Specify Time As Date		
Route Inhalation Ingestion Nigestion Wound Vecore	Mode C Acute Start Date End Date	Chronic 01/04/2000 17:30:00 # 08/04/2000 01:00:00 #	© nine (u) since 01/04/2000 07:0(
		Edit Complex Regime	⊙Sv Crem OmSv Omrem

Figure 3.26. The Start Date (and time-of-day) and End Date (and time-ofday) appear automatically (in the Chronic intake Mode) when you select Date under "Specify Time As."

- Note: In the example shown in Figures 3.24 and 3.26, the Reference Date (and Time) is 01/04/00 07:00 AM (April 1_{st}, 2000 at 07:00 - in U.K./European time convention). The Start Time (d) for IR1 is "0.4375" so the Start Date of the Chronic intake is set automatically as April 1st, 2000 at 17:30 (by adding "0.4375 d' to the reference date and time). Similarly, the End Date is set automatically by adding "6.75 d" to the Reference Date (and Time).

Note: the selected "**Specify Time As**" setting will be applied automatically throughout IMBA Professional - in all three **Screens (Main Screen, Bioassay Calculations** and **Dose Calculations**).

Tip: at any time during your use of IMBA Professional (except when a calculation is underway), you can return to the **Main Screen** (and the **Units** sub-panel) - to switch the **Unit** for ALL displayed **Time** values. This has NO effect on the calculated results. It simply enables you to match the **Time** display to the time-unit convention used in your data files - or to your own preference for direct data entry.

4. Drop-down Calendars

	Route • Inhalation	Mode C Acute C Chronic					© Time (d) since 01/04/2000 07:0(#					
	C Ingestion C Injection C Wound	Start Date		01/04/2000 17:30:00						Intake — ⓒ Bq ⓒ pCi	O dpm O mg	
	C Vapor	End Date	<u>Mon</u> 27 3 10	Tue 28 4 11	<u>Wed</u> 29 5 12	Thu 30 6 13	Fri 31 7 14	Sat 1 8 15	Sun 2 9 16)ose ● Sv ○ mSv	O rem O mrem	
N	lodel Paramete	rs——	17 24 1	18 25 2	19 26 3	20 27 4	21 28 5	22 29 6	23 30 7		> <	

Figure 3.27. Drop-down Windowsâ Calendar for date selection.

As an alternative to <u>typing</u> in the full **Date** directly in the dialog box, <u>clicking</u> the "#" sign to the right of each of IMBA Professional's **Date** dialog boxes brings up the Windows â **Calendar** tool. Use your mouse pointer to select the required **day** in the displayed month - if necssary, use the Calendar's <u>arrow buttons</u> to **SCrOII** backwards or forwards through the months (and years). <u>Click</u> on the required **Date** to load this into the associated dialog box (e.g., as **DD:MM:YYYY for U.K./European date settings**). The Calendar will close automatically.

Once you have registered the correct **Date** in the dialog box, you can move your mouse pointer to the **right** of the displayed **Date**, <u>click</u>, <u>type</u> a "**space**," and then <u>type</u> in any specific "**time-of-day**." If you don't add the time-of-day, IMBA Professional interprets this as 00:00 AM (midnight).



Tip: If the **Calendar** is not already set on your desired **Year** when first opened, it is usually quicker to overtype the **YYYY** value shown in the associated dialog box - before using the **Calendar** to find the required day or month.

Tip: To close the **Calendar** without changing the previously displayed **Date** in the dialog box, <u>re-click</u> the "#" sign next to the dialog box.

Specifying Several Intake Regimes (Star Feature)

00

_ Intake Scenario-				
Intake Regimes Clear All Intake Regimes IR 1 IR 2 IR 3 Route C Inhalation Injection Wound Vapour	Enter Number of Intake Re IR 4 IR 5 IR 6 IR 7 Mode • Acute Start Date 0170	egimes (1-10) 10 + IR 8 IR 9 IR 10 Chronic 4/2000 07:00:00 #	Units Specify Time As Date Time (d) since 01/04/2000 07:0(Intake Bq O dpm O pCi O mg Dose Sv O rem O mSv O mren	Associa
Model Paramete	rs IR 5 IR 6 IR 7 IR 8 Vapor Wound bsorption GI-Tract	IR 9 IR 10 Bioassay Biokinetics	Close	Calcu
IR 5 Absorption: Not Spec	cified Part Tran: Not Specified G	al-Tract: Not Specified f1=		Biokinetics: Not 9

Figure 3.28. Specifying the 5th (IR 5) of 10 Intake Regimes - as an Ingestion.

Figure 3.28 shows how to set up IMBA Professional to assess **multiple intakes** - a total of **10** intakes in this case. The **Intake Regimes** sub-panel displays one intake at-a-time. The fifth intake (**IR 5**) is shown here. This is an **Ingestion**. In this case, IMBA Professional is set up to define independently the model parameters for **IR 5**, as indicated in the **Status Bar** (bottom row left).

The set-up steps are:

- 1. Enter Number of Intake Regimes (1-10) select 10.
- 2. Select the Advanced menu (from the Main Screen menu bar).
- 3. De-select (un-check) the default "Apply Model Params to All IRs" option this enables the model parameters to be set up independently for all IRs.
- 4. Select the index Tab for IR 5.
- 5. Select "Ingestion" as the **Route** of intake.
- 6. Select the appropriate Units under "Specify Time As" in this case "Date."
- 7. Select the Start Date of the intake.

In **Step 4**, as the index **Tab** for **IR 5** is selected, the label of the **Intake** dialog box (top-right-corner of Figure 3.28) changes automatically to "**Intake (IR 5)**." This enables you to specify a (hypothetical) **intake amount** for the selected **intake regime (IR 5)**.

In **Step 5**, as soon as "**Ingestion**" is selected, the **Model Parameters** display for **IR 5** changes - to highlight the "**Ingestion**" button in red. This flags that it is necessary for you to define the **Ingestion** model parameters (as described under <u>Model Parameters Subpanel</u>). Whichever "**Route** of intake" option you select, IMBA Professional will red-flag in the **Model Parameters** sub-panel the associated **models** (parameters) that still need to be **defined** before any calculations can be performed.

Activity Units of Intake



Units Specify Time As © Date
🔿 Time (d)
since
01/04/2000 07:0(
- Intake
⊙ Bq C dpm
O pCi O mg

Figure 3.29. Specifying the activity Units of Intake.

You can select to work in:

- the International (SI) unit of activity Bq (bequerel);
- the Traditional units of activity dpm (disintegrations per minute), pCi (pico-curie).

The "**mg**" unit is not currently available. This is reserved for a **Star-Plus Function**, where it may be provided to specify measurements of **mass**, e.g., phosphorescence measurements of uranium-in-urine.



-

Units of Dose





Figure 3.30. Specifying the Units of Dose.

From the **Units** sub-panel, you can **select** the **Unit** of **Dose** to be:

- International (SI) either Sv (sievert) or mSv;
- Traditional either rem or mrem.



Note: All doses (<u>equivalent</u> or <u>effective</u>) calculated by IMBA Professional Plus are 50-y committed doses.

Intake Amounts/Radionuclides Subpanel

Intake (IR 1) 0 Bq/d	Indicator Nuclide Select Radionuclide Number of Associated Radionuclides:	
Associated Radio	Halt Life: Unknown d	
	None Selected	

Figure 3.31. Specifying the Indicator Nuclide and Intake amount.

Figure 3.31 shows the sub-panel for specifying **intake amounts** and **radionuclides**, as it appears when IMBA_Professional is run for the first time - or when a "New" (blank) parameter file is opened. Notice that the small panel labeled "Intake (IR 1)" is <u>highlighted</u> in red - as is the "Select Radionuclide" <u>button</u>. This warns that neither an intake amount nor an Indicator Nuclide has been defined.



Selecting the Indicator Nuclide

Sel Sel	ect th	e requ	uired r	adion	uclide											_	
Н			Isoto	ре	[Hydro	gen-3 (organio	c) 💌]							He
Li	Be											В	С	N	0	F	Ne
Na	Mg											Al	Si	Ρ	S	CI	Ar
К	Ca	Sc	Ti	\vee	Cr	Mn	Fe	Co	Ni	Cu	Zn	Ga	Ge	As	Se	Br	Kr
RЬ	Sr	Y	Zr	NЬ	Мо	Tc	Ru	Rh	Pd	Ag	Cd	In	Sn	Sb	Те	T	Xe
Cs	Ba	La	Hf	Ta	\mathbb{W}	Re	Os	Ir	Pt	Au	Hg	ΤI	РЬ	Bi	Po	At	Rn
Fr	Ra	Ac	Ce	Pr	Nd	Pm	Sm	Eu	Gd	ТЬ	Dy	Но	Er	Tm	Yb	Lu	1
			Th	Pa	U	Np	Pu	Am	Cm	Bk	Cf	Es	Fm	Md	No	Lr	1
.oad C	Complet	te															_
				Ī		(<u>0</u> K		<u>C</u> a	ancel					<u> </u>)ecay	

Figure 3.32. Selecting the Indicator Nuclide from the periodic table of the elements.

The **Indicator Nuclide** is selected from the periodic table of the elements (Figure 3.32). To display this, <u>click</u> the "Select Radionuclide" <u>button</u> (top right-corner of Main Screen). To <u>select</u> a specific radionuclide:

- 1. <u>Click</u> the required element this puts the first **isotope** available for that element in the **Isotope** dialog box.
- 2. <u>Click</u> the "down" arrow on the **I sotope** dialog box this displays all the available isotopes for that element.
- 3. <u>Highlight</u> and <u>click</u> your required **isotope** from the drop-down list this puts your isotope in the dialog box (Figure 3.33).
- <u>Click</u> the "OK" <u>button</u> in the "Select the required radionuclide" window to confirm your choice - and load your chosen radionuclide as the Indicator Nuclide.



Note: When you open the "**Select the required radionuclide**", you will see the (blue) progress bar move in the lower-left corner of the window. This indicates "**Load Complete**", <u>i.e.</u>, that your IMBA Professional Series software has "**loaded**" all of your available radionuclides. Only the IMBA Professional (Full Version) includes all <u>75 radionuclides</u>. The more basic versions will automatically display fewer elements (for radioelement selection) than those shown in Figure 3.32.

🍂 Se	lect th	e requ	uired r	adionu	uclide											_		
н			Isoto	pe	Į	Uraniu	Uranium-234											
Li	Be					Uraniu Uraniu Uraniu	Jranium-234 Jranium-235 B C N O F Jranium-236											
Na	Mg					Uraniu	anium-238 Al Si P S							S	CI	Ar		
K	Ca	Sc	Ti	\vee	Cr	Mn	Fe	Co	Ni	Cu	Zn	Ga	Ge	As	Se	Br	Kr	
Rb	Sr	Y	Zr	NЬ	Мо	Тс	Ru	Rh	Pd	Ag	Cd	In	Sn	SЬ	Те	T	Xe	
Cs	Ba	La	Hf	Ta	W	Re	Os	Ir	Pt	Au	Hg	TI	РЬ	Bi	Po	At	Rn	
Fr	Ra	Ac	Ce	Pr	Nd	Pm	Sm	Eu	Gd	ТЬ	Dy	Ho	Er	Tm	YЪ	Lu	1	
			Th	Pa	U	Np	Pu	Am	Cm	Bk	Cf	Es	Fm	Md	No	Lr		
Load	Comple	te															_	
				Ĩ			<u>0</u> K		<u>C</u> a	ancel					D	ecay		

Figure 3.33. Selecting Uranium-238 from the Isotope drop-down list.

<u>Clicking</u> "OK" closes the "**Select the required radionuclide**" window - and displays the radionuclide in the **Indicator Nuclide** window (top-right-corner of the **Main Screen**), as shown in Figure 3.34. Once a radionuclide has been selected the red <u>highlight</u> on the "**Select Radionuclide**" <u>button</u> disappears.



Figure 3.34. The selected radionuclide displayed in the Indicator Nuclide window.

List of Available Radionuclides (Full Version)

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The radionuclides implemented in IMBA Professional (Full Version) are:

- actinium (227,228Ac);
- americium (241,243Am);
- antimony (124,125Sb);
- barium (140Ba);
- caesium (134,137Cs);
- californium (252Cf);
- **carbon** (14C) as particulate a <u>version update</u> will include gaseous and vapour forms of carbon;
- cerium (141,144Ce);
- chromium (51Cr);
- cobalt (57,58,60Co);
- curium (242,243,244Cm);
- europium (152,154,155,156Eu);
- hafnium (181 Hf);
- hydrogen [tritium] (3H) as particulate, with biokinetic models for tritiated water (HTO) and organically bound tritium (OBT) - a <u>version update</u> will include gaseous and vapour forms of tritium;
- iodine (125,129,131,133,134,1351);
- iron (55,59Fe);
- lanthanum (140La);
- manganese (54Mn);
- neptunium (237,239Np);
- nickel (63Ni);
- niobium (94,95 Nb);
- phosphorus (32,33P);
- plutonium (238,239,240,241,242Pu);
- polonium (210Po);
- promethium (147Pm);
- protactinium (231Pa);
- **radium** (224,226,228Ra) assuming same biokinetic model for parent and radioactive progeny note that <u>ICRP68</u> assumes independent kinetics for the progeny;
- ruthenium (103,106Ru);
- silver (110mAg);
- **sodium** (22,24 Na);
- strontium (85,89,90Sr);
- **sulphur** (35S) as particulate, for both inorganic and organically incorporated sulfur a <u>version update</u> will include gaseous and vapour forms of sulphur;
- terbium (160Tb);
- **thorium** (228,230,232Th) assuming same biokinetic model for parent and radioactive progeny note that <u>ICRP68</u> assumes independent kinetics for the progeny;
- tin (113Sn);
- uranium (234,235,236,238U) assuming same biokinetic model for parent and radioactive

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progeny - note that ICRP68 assumes independent kinetics for the progeny;

- yttrium (90Y);
- **zinc** (65Zn);
- zirconium (95Zr).

Displaying the Decay Series

Fr Ra Ac	Ce	Pr	Nd	Pm	Sm	Eu	Gd	ТЬ	Dy	Ho	Er	Tm	Yb	Lu
	Th	Pa	U	Np	Pu	Am	Cm	Bk	Cf	Es	Fm	Md	No	Lr
Load Complete					<u>0</u> K		<u>C</u> ar	ncel					D	ecay

Figure 3.35. "Decay" button (bottom-right-corner of "Select the required radionuclide" window).

To display the complete decay chain of your selected radionuclide, you click the "Decay" button in the "Select the required radionuclide" window (Figure 3.35). The "Decay chain of **-***" window will open (where "**-***") is the selected radionuclide. Figure 3.36 shows the "Decay chain of U-238" window as it first appears (partial view).



Figure 3.36. "Decay chain of Pu-239" window - partial view.

For a long decay chain (such as that of 238U), you can view the whole chain by hitting the Windowsâ "maximize" button (center of the three-button cluster, top-right-corner of Figure 3.36). The complete decay chain will then be "re-sized" to fit your whole screen (Figure 3.37).



Figure 3.37. Maximized view of the whole "Decay chain of U-238" window.

To exit this window, click the Windowsâ "**Exit**" button ("**X**" - in the top-right-corner). This will return you to the **Main Screen** - leaving the "**Select the required radionuclide**" still open. Click this window's own "**X**" button to close it.

Displaying the ICRP38 Radiation Data

At

4

85



β4

ß

234

ß

Pa

2.8E-01d

α

91

234

234

230

226

U

8.9E+07 d

92

234

Τĥ

2.4E+01d

230 Th

90

90 2.8E+07 d

Figure 3.38. Clicking on a radionuclide for more information.

226 Ra

88 5.8E+05 d

In the "Decay Chain" window, you can display the ICRP Publication 38 radiation data for each radionuclide - by *clicking* on the radionuclide (Figure 3.38). *Highlight* either the "Properties" or "Particle Energies" option and click to display the respective radiation data.

📲 Decay chain of U-238
Decay chain of U-238 Units of halfilife. O Hours Days Years Click on a radionuclide for more information. Image: Click on a radionuclide for more information Image: Click on a radionuclide for more information Image: Click on a radionuclide for more information At Rn Radionuclide for more information Image: Click on a radionuclide for more information Image: Click on a radionuclide for more information At Rn Radionuclide for more information Image: Click on a radionuclide for more information Image: Click on a radionuclide for more information At Rn Radionuclide for more information Image: Click on a radionuclide for more information Image: Click on a radionuclide for more information Halflife (d) 1.631E+12 Image: Click on a radionuclide only has one daughter Image: Click on a radionuclide for more information Image: Click on a radionuclide for more information Branching n/a Image: Click on a radionuclide for more information Image: Click on a radionuclide for more information Branching n/a Image: Click on a radionuclide for more information Image: Click on a radionuclide for more information Branching n/a Image: Click on a radionuclide for more information Image: Click on a radionuclide for more information Branching

Figure 3.39. Displaying the Decay Information for Uranium -238.

Figure 3.39 shows the "**Decay Information**" window that appears when you *click* the "**Properties**" *option* for 238U. You can pre-select the displayed "**Units of halflife**" (hours, days, or years) in the "**Decay chain**" window. Figure 3.40 shows the "**Energies of decay products**" window that appears when you *click* the "**Particle Energies**" *option* in the "**Decay chain of U-238**" window (Figure 3.38).
Intake (IR 1)

Ο

Bq

Associated Radionuclides

Select Radionuclide

Delete Radionuclide

A	pha		Beta	Ele	etron	P	ositron	Ph	ioton
Energy	Yield	Energy	Yield	Energy	Yield	Energy	Yield	Energy	Yield
4.04E+00	2.29E-03			2.91E-02	2.80E-03			4.96E-02	6.97E-0
4.15E+00	2.29E-01			2.99E-02	8.75E-02			1.30E-02	2.96E-0
4.20E+00	7.68E-01			3.33E-02	7.67E-02			1.61E-02	4.47E-0
				4.55E-02	4.55E-02			1.91E-02	1.02E-0
				4.96E-02	1.68E-02			1.45E-02	9.22E-0
				1.01E-02	4.45E-02			1.11E-02	1.41E-0
				1.35E-02	3.05E-02				
				1.61E-02	5.17E-03				
				3.67E-03	2.33E-01				

U-238

d

0

Half Life: Unknown

%

d

Abundance

Figure 3.40. Displaying the Energies of decay products for Uranium -238.

Selecting Associated Radionuclides (Star Function)

Number of Associated Radionuclides: Half Life: 163100000000

Indicator Nuclide

Select Radionuclide

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cards" (Figure 3.41). You can then use the "**Select Radionuclide**" *button* to *select* each associated radionuclide from the periodic table of elements - as you did for the **Indicator Nuclide**. You also need to **define** the "**Abundance**" (%) for each associated radionuclide - relative to the activity of the **Indicator Nuclide** in the **Intake**. Figure 3.42 shows **two** additional radionuclides (239Pu and 241Am) set up to be associated with a hypothetical (**1 Bq) Intake** of the indicator nuclide (238U). The "**Delete Radionuclide**" *button* removes the indexed associated radionuclide.

Intake (IR 1)	Indicator Nuclide Select Radionuclide				
	Number of Associated Radionuclides: 2 Half Life: 163100000000 d				
Associated Radionuclides					
Select Radionuc	ide Abundance 1.3 %				
Delete Radionuc	ide Half Life: 157800 d				

Figure 3.42. Adding 239Pu and 241Am as Associated Radionuclides.



Setting Hypothetical Intake Amounts

Intake (IR 1)	Indicator Nuclide
10 Bq	Select Radionuclide Cs-137
	Number of Associated Radionuclides: 4 Half Life: 10950 d
Associated Radio	onuclides
Sr-90 Pu-238 Pu-23	9 U-234
_	
Select Radionuc	ide Abundance 0.52 %
Delete Radionuc	iide Half Life: 8784000 d

Figure 3.43. Setting a hypothetical amount for Intake (IR 1).

To project **bioassay quantities** and/or **doses** for hypothetical amounts of intake, you can enter an assumed value of intake directly into IMBA Professional - for each **Intake Regime** (**IR**). You do this in the **Intake** (**IR** #) dialog box (Figure 3.43). If you have more than one **IR**, then *select* each **IR** in turn (from the "**Intake Regimes**" index **Tabs**). Once you have entered a value in the **Intake** (**IR** #) dialog box, and the program "focus" has left the box, the red *highlight* will be removed automatically for that **Intake** (**IR** #). This indicates that the entered intake amount has been stored in memory. However, it will NOT be saved to the **Parameter File** for your case study until "**Save**" is pressed.



Model Parameters Sub-panel



Figure 3.44. Model Parameters sub-panel at start-up - for a New (blank) parameter file.

Figure 3.44 shows **Model Parameters** sub-panel as it appears when IMBA Professional is run for the first time, or when a **New** (blank) **parameter file** is loaded. The following "**Model**" buttons are *highlighted* in red:

- Deposition
- Particle Transport
- <u>Absorption</u>
- <u>GI-Tract</u>

These *buttons* are *highlighted* because, by default, "**Inhalation**" is selected as the **Route** of intake - and it is necessary for you to *select* the **parameters** for ALL FOUR of these **models** BEFORE you can carry out any calculation. Neither the **Bioassay** nor **Biokinetics** model buttons are *highlighted* at this stage. These WILL be *highlighted* later, when you are preparing to carry out specific **Calculations** (as described later).



Tip: If you attempt to run a calculation without defining the required model parameters, IMBA Professional will display an appropriate WARNING message.

If you select "**Ingestion**" as the **Route** of intake, the **Model Parameters** sub-panel will change automatically to that shown in Figure 3.45. In this case, the only full **model** required for calculations is the <u>GI-Tract</u> model. However, you will also need to specify the <u>gut uptake fraction</u> (<u>f1</u>), which is part of the "**Absorption**" model. In this case, the **absorption parameters** for the <u>respiratory tract model</u> are NOT required.

Model Parameters							
These Model Parameters Apply to All IRs							
Respiratory Tract]					
Deposition	Vapor	Wound	Bioassay				
Particle Transport	Absorption	GI-Tract	Biokinetics				

Figure 3.45. Model Parameters sub-panel for "Ingestion" as the Route of intake.

If you *select* "**Injection**" as the **Route** of intake, none of the models *highlighted* above are required, and so none are *highlighted* (Figure 3.46).



Figure 3.46. Model Parameters sub-panel for "Injection" as the Route of intake.

Deposition Parameters

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📲 Deposition Mo	odel	
Extrathoracic Ainways (ET1 & ET2) Conducting Airways (BB & bb) Deep Lung - (Al)		Exposure
		<u>O</u> K <u>C</u> ancel

Figure 3.47. Deposition Parameters window.

Clicking the "**Deposition**" *button* in the **Model Parameters** sub-panel (**Respiratory Tract** section) displays the **Deposition Parameters** window (Figure 3.47). This is used to define:

- the exposed worker's Ventilation Rate classification Light work or Heavy work;
- the radioactive Aerosol Parameters.

IMBA Professional enables you to <u>select</u> either of two *options* to define the values of the parameters that will be substituted in the <u>ICRP Publication 66 model</u> to evaluate the deposition of activity in each region of the respiratory tract for each **Intake Regime (IR)**:

- User Defined;
- LOAD ICRP DEFAULTS.

Figure 3.48 shows the parameter values that are used when you **LOAD ICRP DEFAULTS** - by *clicking* the "**LOAD ICRP DEFAULTS**" *button*, followed by the "**OK**" *button*.

Exposure							
. 💽 Light Worker 🕜 Heavy Worker							
Aerosol Parameters							
0	• AMAD • AMTD	5	μm				
	Sigma-G	2.4977233					
	Density	3	g/ml				
	Shape factor	1.5					
Select							
User Defined							
ICRP Defaults							

Figure 3.48. Selection of ICRP Defaults for Deposition Parameters.

The following default parameter values (as recommended in ICRP Publication 66) are loaded:

- Standard worker average ventilation rate 1.2 m3 h-1.
- AMAD 5 µm.
- Sigma-G (<u>sg</u>) 2.4977233.
- [Particle] Density (r) 3 g cm-3.
- [Particle] Shape Factor (SF) 1.5.

The **Status Bar** automatically indicates the selection of the **ICRP Defaults** for the **Deposition Parameters** (Figure 3.49).

All IRs	Absorption: Not Specified	Part Tran: Not Specified	GI-Tract: Not Specified	f1=		Biokinetics: Not 9
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Figure 3.49. Selection of ICRP Defaults is automatically indicated on the Status Bar.

 Note: As an alternative to the Light worker, you can select Heavy worker. This will evaluate the deposition of activity in each region of the respiratory tract according to the recommendations in *ICRP Publication 66* for representing heavy work (average ventilation rate of 1.688 m 3 h-1).
Warning: If you select Heavy worker (instead of the <u>ICRP68 Reference</u>. Worker classification of the Light worker), your "non-standard" selection will NOT be indicated on the Status Bar. However, your selection of Heavy worker WILL automatically be recorded in the Parameter File for your case study.

IMBA Professional also enables you to enter specific values of the **Aerosol Parameters**, that may better characterize an intake by inhalation that the default values recommended in *ICRP Publication 66*. To do this, you *select* the "**User Defined**" option (Figure 3.50).

– Exposur	e							
	Light Worke	r 🔿 Heavy	Worker					
Aerosol Parameters								
6	AMAD AMTD	10	μm					
	Sigma-G	2.5						
	Density	10	g/ml					
	Shape factor	1.5						
-Select-								
	<u>U</u> se	r Defined						
LOAD ICRP DEFAULTS								
User Defined								

Figure 3.50. Selection of User Defined values for Deposition Parameters.

In the example shown in Figure 3.50, the following values of Aerosol Parameters have been defined:

- AMAD 10 µm.
- Sigma-G (<u>sg</u>) 2.5.
- [Particle] **Density** (r) 10 g cm-3.
- [Particle] Shape Factor (SF) 1.5.

For these "non-ICRP-default" values, the **Status Bar** automatically indicates the selection of "**User Defined**" **Deposition**, and also shows the selected value of **AMAD** (Figure 3.51).

All IRs Absorption: Not Specified Part Tran: Not S	Specified GI-Tract: Not Specified f1=	Biokinetics: Not
----------------------------------------------------	---------------------------------------	------------------

Figure 3.51. Selection of User Defined aerosol parameter values is automatically indicated on the Status Bar.

To represent sub-micron aerosols, IMBA Professional enables you to define the aerosol AMTD (Figure 3.52). In this case, the **Status Bar** will show the defined value of the **AMTD**.

Exposur	e						
C Light Worker C Heavy Worker							
Aerosol Parameters							
6) AMAD 8 AMTD	0.15	μm				
	Sigma-G	2.0					
	Density	10	g/ml				
	Shape factor	1.5					
Select							
	<u>U</u> se	r Defined					
LOAD ICRP DEFAULTS							
User Defined							

Figure 3.52. Characterizing a sub-micron aerosol by its AMTD.



Key Tip: If you are assessing a case with multiple **Intakes** by **Inhalation (Star Feature)**, you can define different **Aerosol Parameter** values (and choose either **Light worker** or **Heavy Worker**) independently for EACH **Intake Regime (IR)**.

Vapour Parameters

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The *ICRP Publication 66* model for **gases and** <u>vapours</u> will be implemented as a **Star-Plus Module**.

Particle Transport Parameters



Figure 3.53. Particle Transport Model window.

Clicking the "**Particle Transport**" *button* in the **Model Parameters** sub-panel (**Respiratory Tract** section) displays the **Particle Transport** window (Figure 3.53). *Clicking* the "**LOAD ICRP DEFAULTS**" *button*, followed by the "**OK**" *button*, automatically loads all of the parameter values recommended in ICRP Publication 66 to represent **Particle Transport** in the respiratory tract of the Reference Worker (Figure 3.54).

Rate Constants (/d)	
All to bb1 0.02 Extrathoracic	
Al2 to bb1 0.001	
AI3 to bb1 0.0001	
Al3 ro LNTH 0.00002 LNET ETseq ETseq	T2
bb1 to BB1 2	
bb2 to BB1 0.03 Thoracia	
bbseq to LNTH 0.01	
BB1 to ET2 10 BBseq BBseq BB2 B	B1
BB2 to ET2 0.03	
BBseq to LNTH 0.01 LNTH description bbseq bb2 bb2 bb2	ob1
ET2 to GI 100	
ET seq to LNET 0.001	
	<u> </u>
BReed/BB 0.007 User Defined	
bbseq/ bb 0.007	
ICRP Defaults	<u>C</u> ancel
Clear	

Figure 3.54. Particle Transport Model window loaded with parameter values recommended in *ICRP Publication 66* (**ICRP DEFAULTS**).

Notice that the **ICRP-default** parameter values shown in the **Particle Transport Model** are "greyed-out." These CANNOT be changed. If you wish to define different values, *click* the "**User Defined**" *button*. The **Particle Transport Model** window will then change to that shown in Figure 3.55. This enables you to change the value of ANY **Rate Constant**.



Figure 3.55. Particle Transport Model window in its "User Defined" mode.

In the "User Defined" mode, all of the initially loaded parameter values are those recommended in ICRP Publication 66. In this mode, you can change as many values as you wish. However, if you change ANY of the ICRP-recommended values, this will be "flagged" automatically in the Status Bar as "Part Tran: User Defined" (Figure 3.56).

All IRs	Absorption: Not Specified	Part Tran: User Defined	GI-Tract: Not Specified	f1=		Biokinetics: Not S
---------	---------------------------	-------------------------	-------------------------	-----	--	--------------------

Figure 3.56. Selection of **User Defined** particle transport parameter values is automatically indicated on the **Status Bar**.





Warning: You MUST enter values of particle transport **Rate Constants** in the **Unit** "d-1," *i.e.*, "**per day**."

Tip: Technical Basis section gives an example in which changing the value of the rate constant of particle transport from **AI3** to **LNTH** (for an individual case) improved the prediction of tissue analysis data (James et al., 2003).

Absorption Parameters



IMBA Professional provides two methods of defining the values of <u>absorption</u> parameters for substitution in the *ICRP Publication 66* respiratory tract absorption model - and the associated value of the <u>gut uptake fraction</u> (f<u>1</u>).

- <u>Select ICRP-recommended "default" values</u> using a built-in **data library** compiled from *ICRP Publication* sources;
- <u>Define your own values</u> utilizing experimental or other data that is "**specific**" to the material involved in the intake.

Selecting ICRP Default Absorption Parameters





Figure 3.57. Absorption Model window.

Clicking the "Absorption" *button* in the Model Parameters sub-panel (Respiratory Tract section) displays the Absorption window (Figure 3.57). This window is used to define BOTH:

- the gut absorption fraction (f1), and;
- the absorption characteristics for material in the respiratory tract.

Clicking the "Help" button in this window provides you with information taken from ICRP documents which gives BOTH default absorption rates and $f\underline{1}$ values for different chemical forms of the Indicator Nuclide. Figure 3.58 shows the F1 values for Am window.

🍂 F1 v	F1 values and absorption Types for Americium					
	Abs.	f1	ICRP	Chemical Form		
+	F	0.0005	71			
	М	0.0005	71			
	S	0.0005	71			
	М	0.0005	68	All compounds		
	Ing	0.0005	68	All compounds		
Note: only	Note: only the absorption parameters are entered. NOT the default AMAD.					

Figure 3.58. F1 values window - for Help in selecting the value of f1.



You can *select* BOTH the **Absorption Type** and its associated value of f_1 from the **F1** values window - by *clicking* on any **cell** in the desired **row**, and then *clicking* the "**OK**" *button*. This will load BOTH the selected f_1 value (into the "**f1**" dialog box in the **Absorption Model** window) and the **Absorption Type** - and you will be returned to the **Absorption Model** window.

<u>Tip:</u> If you need to define your own value of <u>f</u>1, then you can do this directly in the <u>Absorption Model</u> window - by typing your specific <u>f</u>1 value in the "<u>f1</u>" dialog box.

<u>Tip:</u> You can also define the value of $\underline{f_1}$ in the <u>GI Tract</u> <u>Model</u> window. BOTH the <u>Absorption Model</u> window and the <u>GI</u> <u>Tract Model</u> window display the currently loaded value of $\underline{f_1}$ - and this can be modified in EITHER window.

In Figure 3.59, **Absorption Type** "**M**" is selected. *Clicking* the "**OK**" *button* loads the value "**5.00E-04**" (taken from ICRP Publication 71) into the "**f1**" dialog box in the **Absorption Model** window. It also loads the selected ICRP Publication 66 **Absorption Type** ("**M**"), as shown in Figure 3.59. The **Status Bar** will also be updated automatically (Figure 3.60).



71 recommended f1 value for Type M (Americium) loaded.

All IRs	Absorption: Type M	Part Tran: User Defined	GI-Tract: Not Specified	f1=0.0005	Biokinetics: Not Specifi
					r

Figure 3.60. The selected Type M absorption behavior and the f1 value is automatically indicated on the Status Bar.

You can switch the selection of ICRP Default Absorption Type in the "Absorption Model" window - by clicking another "Type" button. For example, Figure 3.61 shows the changed parameter values that are displayed when you *click* the "Type S" button.

_	_	
		\sim
_		\sim

Initial dissolution Transformation Final dissolution	rate: Sp 1.0000E-01 rate: Spt 1.0000E+02 Fraction to bound state: Fb rate: St 1.0000E-04 Uptake rate from bound state: Sb	
f1 0.0005	Select Type E Type M Type S	Help
Clea <u>r</u>	Type S	<u>O</u> K <u>C</u> ancel

Figure 3.61. Absorption Model window after selecting "Type S" absorption behavior.

% "******	Warning: Selecting a different respiratory tract Absorption Type does NOT automatically select an appropriate value of the <u>gut absorption fraction</u> (f <u>1</u>). This is YOUR responsibility! The previously-loaded value of f <u>1</u> will remain in the "f1" dialog box until you Clear and/or replace this with a new value.
×	Tip: It is a good idea to go back and <i>click</i> the "Help" button again - to check out the ICRP-recommended value of f <u>1</u> that is appropriate for your newly selected respiratory tract Absorption Type .
93 🚞	Note: Remember that selecting an ICRP default from the " Help " button loads BOTH the Absorption Type and f <u>1</u> value, whereas selecting the Absorption Type by <i>clicking</i> a " Type " <i>button</i> will load ONLY the Absorption Type .

Defining Your Own Absorption Parameters





Figure 3.62. Absorption Model window for User Defined parameter option.

Click the "**User Defined**" button in the **Absorption Model** window to define your own specific values for the respiratory tract **Absorption Parameters** (Figure 3.62). You can then type your required values for the absorption rate constants directly into the respective dialog boxes. These dialog boxes are:

- the Initial dissolution rate: Sp (in d-1);
- the [particle] Transformation rate: Spt (in d-1);
- the Final dissolution rate: St (in d-1);
- the Fraction to bound state: Fb;
- the Uptake rate from bound state: Sb.

The ICRP Publication 66 respiratory tract absorption model, and these special absorption terms, are described in the **Technical Basis** (<u>Model of Material Absorption</u> section).



Key Tip: Throughout IMBA Professional, dialog boxes in which you can type a value directly are indicated by a *white* background. A "*greyed*" box indicates a value that CANNOT be changed (in the current window setting).

Figure 3.63 shows a hypothetical example of absorption rates that might be entered for an extremely insoluble material, *i.e.*, a material that dissolves and is absorbed **more**

slowly than the ICRP default **Type S**. Also in this hypothetical example, it is assumed that **5%** of the radionuclide activity that is **dissolved** (from the particles) is "**bound**" temporarily to respiratory tract tissues - to be released into the blood at the rate of **10-3 d**-1. The hypothetical values of the absorption parameters are:

- **s**p = 10<u>-2</u> d<u>-1</u>;
- **s**_{pt} = 100 d<u>-1</u>;
- st = 10<u>-5</u> d<u>-1</u>;
- $\mathbf{f}_b = 0.05;$
- $s_b = 10 3 d_{-1}$.



Figure 3.63. Entering your own (non-default) values of Absorption Rates.

	Warning: The Unit in which Absorption Rates are expressed in IMBA
23	Professional is ALWAYS "d-1," <i>i.e.</i> , "per day." You MUST enter your values in
	 the same Unit (" d -1").

IMBA Professional implements both representations of particle dissolution and absorption of material from the respiratory tract that were recommended in <u>ICRP Publication 66</u>:

- the "Standard Representation" as shown in Figure 3.62;
- the "Alternative Representation."

Figure 3.64 shows the **Alternative Representation** of the hypothetical particle dissolution, radionuclide binding, and absorption characteristics listed above (for comparison with the **Standard Representation** shown in Figure 3.63). IMBA Professional automatically calculates the mathematical transformation between these two representations. As described in the **Technical Basis** (Model of Material Absorption section), these two representations of the dissolution and absorption processes give identical results.

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Figure 3.64. Automatically calculated **Alternative Representation** of the particle dissolution, material binding and absorption characteristics shown in Figure 3.63.

The alternative dissolution and absorption parameters are:

- Fraction dissolved rapidly, fr = 9.9890 ' 10-5;
- Rapid rate, sr = 100.01 d-1;
- Slow rate, ss = 10<u>-5</u> d<u>-1;</u>
- Fraction to bound state, fb = 5 ´ 10<u>-2</u>;
- Uptake rate from bound state, sb = 10<u>-3</u> d<u>-1</u>.

Both representations of the particle dissolution and material absorption processes have their practical uses. The **Standard Representation** is helpful when a physical process (such as particle fragmentation) leads to the gradual transformation of deposited particles into a more soluble form, *i.e.*, in cases where the overall absorption rate *increases* with time - see **Technical Basis** for an example of this. The **Alternative Representation** is useful for the more general situation, where the overall absorption rate *decreases* with time. For example, *in vitro* solubility studies are usually interpreted in terms of "fast" and "slow" dissolution fractions, with their associated dissolution rates. Such results can be substituted directly in the **Alternative Representation** (Figure 3.64)._

Wound Model

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The NCRP model for wound retention and systemic uptake will be implemented when this is available (as a **Star-Plus Module**).

GI Tract Retention Parameters



Figure 3.65. The <u>ICRP Publication 30 GI Tract Model</u> with ICRP Default parameter values loaded.

If, for a particular Intake Regime (IR) you have selected either Inhalation or Ingestion, then the "GI-Tract" <u>button</u> in the "Model Parameters" sub-panel is <u>enabled</u> automatically). <u>Click</u> the "GI-Tract" <u>button</u> to display the GI Tract Model window. <u>Click</u> the "LOAD ICRP DEFAULTS" <u>button</u> in this window to load the ICRP-recommended parameter values (Figure 3.65).

In Figure 3.65, the " $f\underline{1}$ " dialog box is displaying the value of "**0.0005**" for the <u>gut absorption</u> <u>fraction</u> (f1). If you had selected the f1 value earlier, <u>e.g.</u>, in the **F1 Values** window and/or the **Absorption Model** window (see <u>Selecting ICRP Default Parameters</u>), then the same f1 value would have been loaded automatically in the " $f\underline{1}$ " dialog box. If, however, you had loaded a **New** (blank) **Parameter File**, and proceeded directly to set up the parameters for an **Ingestion** intake, the " $f\underline{1}$ " dialog box would have appeared empty. In either case, you can type a new value of f1 directly into the " $f\underline{1}$ " dialog box (Figure 3.65).

To "look up" an appropriate ICRP-default value of f1, <u>click</u> the "Help" button in the GI Tract

Model window. This will **<u>open</u>** the **F1 Values** window for the currently selected **Indicator Nuclide** (Figure 3.66) - from which you can <u>**select**</u> your f**1** value.

<mark>%2 ''''''''''</mark>	Note: The f1 "Help" <u>button</u> only appears in the GI Tract Model window IF you have selected "Ingestion" as the Route of intake.
⁹³	Note: In the f1 "Help" window, <u>indicate</u> a row displaying your desired f1 value, and then <u>click</u> "OK." ONLY the displayed f1 value will be loaded . The associated respiratory tract absorption type (Abs. Type) is NOT loaded - since this is irrelevant for the intake by Ingestion .

Bioassay Parameters

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Figure 3.68. The Bioassay Model window.

Click the "**Bioassay**" button in the "**Model Parameters**" sub-panel to display the Bioassay Model (Figure 3.68). If you have previously selected the Indicator Nuclide, this window enables you to select (or define) all of the required bioassay functions. Click the down arrow on the **Bioassay Function** list box to see the drop-down list of bioassay options (Figure 3.69).

Bioassay Model			
File Edit Function			
Ka(1)	Whole body Whole body Lungs Urine Feces Blood Thyroid Liver User Defined	ent Ka(9)	Ka(10)

Figure 3.69. List Bioassay options.

Highlight and click your required bioassay option. In this example, selection of **urine** changes the **Bioassay Model** window to that shown in Figure 3.70.

💐 Bioassay Mode	:I					
<u>File</u> <u>Edit</u> Function						
- Bioassay Functio	n	Urine				
				······		
		Trar	nsfer Compa	artment		
	Ka(1)/Lam((1) Ka(2)/La	am(2)	Ka	^{a(9)} /Lam(9)	Ka(10) /Lam(10)
Dummy Compartme	ents Comp 1	Comp 2		Comp	9 Com	np 10
	Lam(1)	Lam(2)			Lam(9)	Lam(10)
			Excretion			
Bioassay Function Lam(i)	Lam(i)		┌ Select	E	lood half time (к) 🔽
1 2 3				<u>U</u> ser D	efined Mode	
<u>4</u> 5				<u>L</u> OAD ICF	RP DEFAULTS	
6 7 8				Not S	pecified	
<u>3</u> 10				<u>0</u> K	<u>_</u> a	ancel
WHOLE BODY LL	JNGS URINE	FECES	BLOOD	THYROID	LIVER	USER DEFINED

Figure 3.70. Selecting Urine in the Bioassay Model window.

Notice that the "URINE" indicator button is now "raised." As yet, however, the **Bioassay** Function is Not Specified. You have two options to specify this:

- User Defined Mode;
- LOAD ICRP DEFAULTS.
- 1. "LOAD ICRP DEFAULTS" Option

If you click the LOAD ICRP DEFAULTS button, the window will display the parameters of

the selected **Bioassay Function** (Figure 3.71). In this case, the function is for **plutonium** in **urine**. This was fitted to the ICRP Publication 67 plutonium biokinetic model's predictions of plutonium excretion in urine after injection of unit activity into the blood (see **Technical Basis** section, <u>Fitted Excretion Functions</u>).



Figure 3.71. Loading the parameters of the Bioassay Function for Pu-in-urine.

Notice that the label "**Std Pu Model**" is now shown under the "**URINE**" indicator button, and also under the "*L***OAD ICRP DEFAULTS**" button. If you then go back to the **Bioassay Function** drop-down list, select "**Feces**," and click the "*L***OAD ICRP DEFAULTS**" button again - then the displayed parameters will change to those shown in Figure 3.72.

	Bioas: a("	say Function 1) 8.84930696308	66E-07			E	lood half time	(K) 0.0000001
	i 1 2 3 4 5 6 7 8 9 10	a(i) 8.849E-07 5.804E-02 9.054E-03 -9.471E-02 4.281E-06 2.757E-02 3.216E-05 5.278E-06 -1.649E-06 8.919E-07	Lam(i) 9.354E+00 1.744E+00 3.535E-01 1.370E+00 2.881E-04 9.186E-01 1.841E-03 3.691E-05 1.593E-02 4.581E-08		Select	User Do LOAD ICF Std P	efined Mode PDEFAULTS 'U Model	ancel
Wł	IOLE	BODY LUNGS	URINE Std Pu Model	FECES Std Pu Model	BLOOD	THYROID	LIVER	USER DEFINED

Figure 3.72. Adding the parameters of the Bioassay Function for Pu-in-faeces.

Notice that BOTH the "URINE" and "FECES" indicator buttons are now labeled "Std Pu Model." If you try to load a "Thyroid" Bioassay Function (for plutonium), then the Not Specified label shown in Figure 3.73 will be displayed. <u>IMBA Professional</u> "knows" that the thyroid is not included specifically in the ICRP Publication 67 biokinetic model for plutonium, and therefore does NOT have a Bioassay Function.

Bioassay Fun a(1)	ction	Lam(i)		Select-	E	lood half time	(K) 0
2					<u>U</u> ser D	efined Mode	
4 5					LOAD ICF	P DEFAULT:	;
6 7 8					Not S	pecified	
9 10					<u>0</u> K	<u>[</u>	ancel
WHOLE BODY	LUNGS	URINE	FECES	BLOOD	THYROID	LIVER	
		Std Pu Model	Std Pu Model				1.

Figure 3.73. Label displayed if you try to load an "ICRP" Bioassay Function for Pu-in-thyroid.

Similarly, if you try to load a **Bioassay Function** for the **Lungs**, then **IMBA Professional** reminds you that "**No systemic model is required for the lungs**" (Figure 3.74) - since **lung retention** is calculated automatically (using the ICRP Publication 66 respiratory tract model).

Bioassay Model	
Eile Edit Function	
Lungs	
No systemic model is	required for the lung
- Bioassay Function	
	Blood half time (K)
	Select
	LOAD ICRP DEFAULTS
	Not Cresified
	пот Specified
	OK Const
WHOLE BODY LUNGS URINE FECES	BLOOD THYROID LIVER USER DEFINED
Std Pu Model Std Pu Model	

Figure 3.74. Message displayed if you try to load a Bioassay Function for the Lungs.

The selected **Bioassay Functions** are NOT indicated in the **Status Bar** (Figure 3.75). However, they ARE recorded in the **Parameter File** for your case study.



Figure 3.75. The Status Bar does NOT indicate the selected Bioassay Functions.

2. "User Defined Mode"

🍕 Bioassay Mo	odel						<u>- 0 ×</u>
<u>File</u> <u>E</u> dit Functio	on						
– Bioassay Fun	iction		User Define	d	_		
		Ka(1)	Trar Ka(2)	isfer Comp	partment	a(9)	Ka(10)
Systemic Retention		omp 1	Comp 2		Comp	9 Comp	10 Lam(10)
				Excretion			
Bioassay Func	tion	1 (2)		Calaat	E	3lood half time (K)	0
1 a(I) 1 2 3 4 5		Lam(i)		Select	LOAD ICF	efined Mode	
6 7 8 9					User	Defined	
10					<u>0</u> K	Cano	el
WHOLE BODY	LUNGS	URINE Std Pu Model	FECES Std Pu Model	BLOOD	THYROID	LIVER	ISER DEFINED

Figure 3.76. The Bioassay Model window in the "User Defined Mode."

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IMBA Professional also enables you to define and use your own **Bioassay Function** - see discussion in the **Technical Basis** on how this should be done. You can set up an additional function (to represent an additional **Bioassay Quantity**, e.g., "**SKELETON**") under the eighth **Bioassay Function** indicator button (labeled "**USER DEFINED**"). You can also define and load your own **Bioassay Function** (in place of the "**ICRP DEFAULT**") for any of the seven **Bioassay Quantities** that are specified in **IMBA Professional**.

Warning: If you substitute a different Bioassay Function for any Bioassay

Quantity in <u>IMBA Professional</u>, then any Dose Calculations that you perform with ICRP-recommended "Default" Biokinetic Models may be INCONSISTENT with your bioassay analyses. For Dose Calculations, <u>IMBA</u> <u>Professional</u> solves all Biokinetic Models simultaneously, and so altering the Biokinetic Model for a major organ of uptake will affect the amount of radionuclide taken up by other organs - see discussion in Technical Basis.

3. "Quick-Loading" All ICRP-Default Bioassay Functions

As an alternative to defining and loading each **Bioassay Function** separately, **IMBA Professional** enables you to "Quick-Load" the bioassay functions for ALL ICRPrecommended **Bioassay Models** in one operation - see "One-step Loading of All Model Parameters."

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- -

Biokinetic Parameters

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Figure 3.77. The Biokinetic Model window.

Click the "**Biokinetics**" button in the "**Model Parameters**" sub-panel to open the Biokinetic Model window (Figure 3.77). If you have previously selected the Indicator Nuclide, this window enables you to "*L*OAD ICRP DEFAULTS," i.e., select all of the required source region (source organ or tissue) retention functions.

Warning: If you have NOT previously selected the Indicator Nuclide, then the LOAD ICRP DEFAULTS button will be "greyed out" - and you will NOT be able

to use this to load an "ICRP" model for a selected "Source Organ."

1. "LOAD ICRP DEFAULTS" option



Figure 3.78. Loading the ICRP Default Biokinetic Models for americium.

Clicking the LOAD ICRP DEFAULTS button automatically loads the <u>fitted retention functions</u> that represent the complete set of ICRP-default **Biokinetic Models** - for your selected **Indicator Nuclide**. The **Source Organs** involved are automatically highlighted in the **Biokinetic**

Model window (Figure 3.78). You can examine the **retention function** loaded for any highlighted **Source Organ** by clicking its indicator button. For example, Figure 3.79 shows the retention function loaded for "**Liver**" - which represents liver uptake and retention of americium according to the ICRP Publication 67 **Biokinetic Model**.



Figure 3.79. The retention function for americium in liver.

When the "Liver" retention function is displayed in the **Biokinetic Model** window, the "Liver" indicator button is shown "depressed." Selecting another **Source Organ** will "release" the "Liver" indicator button, "depress" the button for the newly selected **Source Organ**, and display its retention function.

All IRs	Absorption: Type M	Part Tran: ICRP Defaults	GI-Tract: ICRP Defaults	f1=0.0005	Biokinetics: ICRP Am

Figure 3.80. The Status Bar indicates that the ICRP Am Model for "Biokinetics" has been loaded.

The fact that the **complete** ICRP-default biokinetic model has been loaded is indicated automatically in the **Status Bar** (Figure 3.80).

2. "User Defined Mode"

You can select the "User Defined Mode" to replace one or more retention functions with your own parameter values. The **Biokinetic Model** window displaying the "ICRP" retention function for americium in "Liver" (Figure 3.79) changes to that shown in Figure 3.81 when you click the "User Defined Mode" button.

C Orga	an retention function	1	Select
Lam	(1) 33.675427037	9936	User Defined Mode
i	a(i)	Lam(i)	LOAD ICRP DEFAULTS
1 2 3 4 5 6	-3.400E-01 -1.587E-01 3.767E-01 4.156E-02 1.121E-01 -3.176E-02	3.368E+01 9.589E-01 1.046E-03 3.007E-05 2.952E-04 1.457E-02	User Defined
7 8 9 10			<u>D</u> K <u>C</u> ancel

Figure 3.81. The "User Defined Mode" for re-defining the retention function for americium in liver.

In this mode, the parameter values representing the ICRP-default **Biokinetic Model** are initially retained, but the "**Organ retention function**" display becomes a dialog box (with a white background). You can now select the parameter that you want to change, and type your new value into the dialog box [see Figure 3.81, where the parameter "Lam(1)" has been selected]. Your new **retention function** can have up to **ten** exponential terms (see **Technical Basis**). Once you have selected the *User Defined Mode*, the **Status Bar** will indicate this (Figure 3.82) - even if you make no change to an "ICRP-default" parameter value.

C C

All IRs	Absorption: Type M	Part Tran: ICRP Defaults	GI-Tract: ICRP Defaults	f1=0.0005		Biokinetics: User Defi
---------	--------------------	--------------------------	-------------------------	-----------	--	------------------------

Figure 3.82. The Status Bar indicates that the User Defined Mode for "Biokinetics" has been selected.

×	Tip: You can re-load ALL of the "ICRP-default" parameter values by re- clicking the "LOAD ICRP DEFAULTS" button. This will re-set the Status Bar indicator - to confirm that ALL ICRP DEFAULT Biokinetic Model parameter values have been re-loaded.
92	Warning: If you substitute a different Source Organ retention function for any "ICRP-default" Bioassay Model in <u>IMBA Professional</u> , then the Dose Calculations that you perform may NOT be valid for ALL Source/Target Organ combinations. <u>IMBA Professional</u> solves all Biokinetic Models simultaneously, and so altering the Biokinetic Model for a major organ of uptake will affect the amount of radionuclide taken up by other source organs - see discussion in Technical Basis.

One-step Loading of All Model Parameters

1. ICRP-recommended Parameters

es h	lain S	creen							
<u>F</u> ile	<u>E</u> dit	<u>P</u> arameters	<u>Calculations</u>	<u>T</u> ools	Advanced	<u>H</u> elp			
	P en	Save	New	0 Quick S	ave	ICRP DEFS Load	CFR DEFS		P Help
Ver 3	3.0	No file ope	ened			Loa	ad all ICRP de	rault parameters	
Jult Suff						IM	BA P	rofes	sional

Figure 3.83. The "ICRP DEFS Load" tool button.

If you move your mouse pointer over the "ICRP DEFS Load" button in the Tool Bar, the "ICRP DEFS" symbol will change color - to yellow (Figure 3.83). Clicking the button will then display the "F1 values" window for the selected radioelement (Figure 3.84).

💐 F1 va	F1 values and absorption Types for Americium							
	Abs.	f1	ICRP	Chemical Form				
	F	0.0005	71					
+	M	0.0005	71					
	S	0.0005	71					
	м	0.0005	68	All compounds				
	Ing	0.0005	68	All compounds				
Note: only the absorption parameters are entered. NOT the default AMAD.								

Figure 3.84. The "F1 values for Am" window for selecting both the Absorption Type and \underline{f}_1 value for americium.

Select the **row** with your required combination of ICRP-default **Absorption Type** and <u>**f**</u> value - and _{click} "**OK**." This will close the "**F1** values" window. If you now click on the **Bioassay Model** button (**Main Screen**), the **Bioassay Model** window will appear as shown in Figure 3.85.
🂐 Bioassay Mo	del						_ 🗆 ×	1
<u>File</u> <u>E</u> dit Functio	n							
– Bioassay Fund	otion		User Define	d	•			
			Trar	isfer Compa	artment			
		Ka(1)	Ka(2)		ĸ	a(9)	Ka(10)	
Systemic Retentior		omp 1	Comp 2		Comp	9 Com	p 10	
		Lam(1)	🛛 🕂 Lam(2)		- -	Lam(9)	Lam(10)	
		*		Excretion				
Bioassay Functi Lam(i)	on	Lam(i)		Select		Blood half time (f	<) 10	
1 2 3					<u>U</u> ser D	efined Mode		
5					LOAD IC	RP DEFAULTS		
6 7 8					Not S	Specified		
10					<u>0</u> K	<u>C</u> a	ncel	
WHOLE BODY	LUNGS	URINE	FECES	BLOOD	THYROID	LIVER	USER DEFINED	1
Std Am Model		Std Am Model	Std Am Model			Std Am Model		1

Figure 3.85. The Bioassay Model window confirming that ALL ICRP-default parameters have been loaded.

Note that the indicators on the bottom row of the **Bioassay Model** window record that the "**Std Am Model**" (in this example) has been loaded. These indicators specify the **WHOLE BODY**, **URINE** and **FAECES**, which are the only "standard" Bioassay Quantities used for americium. Clicking "OK" closes this window - and returns you to the **Main Screen**.

The **Status Bar** (Figure 3.86) records that the following **ICRP-default** parameter values have been loaded (by your click of the "**ICRP DEFS Load**" button):

• Absorption Type - "M" was selected;

- Particle Transport;
- GI -Tract;
- **<u>f</u>1** "0.0005" was selected along with the **Type M** absorption;
- Biokinetics "Am" was selected (the Indicator Nuclide);
- Deposition the respiratory tract model;
- **AMAD** "5" μm.

The "Wound" model was NOT specified. This is NOT an "ICRP default."

All IRs Absorption: Type M Part Tran: ICRP Defaults GI-Tract: ICRP Defaults f1=0.0005 Biokinetics: ICRP Am

Figure 3.86. The Status Bar indicating that ALL ICRP-Default parameter values have been loaded (for Type M americium).

Note: Using the "**ICRP DEFS Load**" tool also loads ICRP-default parameter values for **Dose Calculation**, i.e., the ICRP Publication 60/68 radiation weighting factors, tissue weighting factors, and remainder tissue rules (see the **Technical Basis**, <u>ICRP's Dosimetric Quantities</u>).

2. 10-CFR-835 Prescribed Parameters

🍂 Main	Screen										
<u>F</u> ile <u>E</u> di	<u>P</u> arameters	<u>Calculations</u>	<u>T</u> ools	Advanced	<u>H</u> elp						
Open	Save	New	回 Quick S	ave	ICRP DEFS Load	EFI DEF Loa		REP Report	Help		
Ver 3.0	No file op	ened					Load II	CHP mod	el parameters	with 10 L	<u>FR 835 WTs</u>
	nit Stit				IM	BA	Pr	ofe	ssior	nal	Full E

Figure 3.87. The "CFR DEFS Load" tool button.

If you **move** your mouse pointer over the "CFR DEFS Load" button in the Tool Bar, the "CFR DEFS" symbol will change color - to purple (Figure 3.87). Clicking the button will then display the "F1 values" window (as shown in Figure 3.84, above) - from which you can again select the row with your required combination of <u>ICRP-DEFAULT</u> Absorption Type and <u>f</u>1 value. When you then click "OK", <u>IMBA Professional</u> will load ALL of the <u>ICRP-DEFAULT</u> Biokinetic Model AND Bioassay Model parameters. <u>However</u>, the loaded radiation weighting factors (wR), tissue weighting factors (wT), and remainder tissue rules will be those prescribed by the 10-CFR-835 Regulation (as currently used in the U.S).

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Setting Up Different Models for Each Intake Regime

By **default**, IMBA Professional stores and applies a **single set of parameter values** for each **Model**, *i.e.*, the last-loaded set of parameter values for those of the following models that you have defined:

- 1. **Deposition** model;
- 2. Particle Transport model;
- 3. Absorption model;
- 4. Wound model;
- 5. GI-Tract model;
- 6. Biokinetic models;
- 7. Bioassay models.

In IMBA Professional, you can define up to **10 Intake Regimes (IRs)**, each of which can be selected from **Inhalation**, **Ingestion**, **Injection** (or, in future, **Wound**). Calculations for each of these four different **Routes** of intake use a different combination of **Models**, as follows (by **Model #**):

- Inhalation model ## 1, 2, 3, 5, 6 and 7;
- Ingestion model ## 5, 6 and 7;
- Injection model ## 6 and 7;
- Wound model ## 4, 6 and 7.

Therefore, in the *default* mode where each of the seven types of model can have only ONE defined set of parameters, the **Model Parameters** sub-panel and **Status Bar** are displayed as shown in Figure 3.88.

_ Moo	del Parameters—			
Thes	e Model Parameters Apply to A	ll IRs		
B	espiratory Tract			1
	Deposition Vapor	Wou	and Bioa	ssay
	Particle Transport Absorption	GI-TI	ract Bioki	netics
All IRs	Absorption: Type M Part Tra	an: ICRP Defaults	GI-Tract: ICRP De	efaults f1=0.00

Figure 3.88. The Model Parameters sub-panel and Status Bar in the "These Model Parameters Apply to All IRs" mode.

In this *default* mode, if several of the **IRs** are by **Inhalation**, then for example you can define only a single set of **Aerosol Parameters** (**Ventilation Rate**, **AMAD**, <u>Sg</u>, <u>r</u> and **SF** - in **model #1**), or **Absorption Parameters** (**Absorption Type** and <u>f1</u> value - in **model #3**). This would limit you to analyzing simultaneously multiple intakes of only the same type of material (with the same aerosol characteristics).

IMBA Professional overcomes this limitation by enabling you to define *independently* ALL model parameters for **each IR**. To do this, you first *de-select* (*un-tick*) the "**Apply Model Params to All IRs**" *option* in the **Advanced** menu (Figure 3.89).

🂐 Main	Screen					
<u>F</u> ile <u>E</u> d	it <u>P</u> arameters	<u>Calculations</u>	<u>T</u> ools	Advanced	<u>H</u> elp	
Open	Save	New	回 Quick S	 Apply Mo Enable C Enable D 	odel Params to All IRs Complex Intake Regimes ODS preview	EP port
Ver 3.0	No file ope	ened		Advance		

Figure 3.89. De-selecting "Apply Model Params to ALL IRs" in Advanced menu.

The **Model Parameters** sub-panel will then change to display multiple **Index Tabs** - one for *each* **IR**. You can then set up specific parameter values for each individual **IR** #. *Click* on the **IR** # *tab index* - to display all of its associated model *options* (Figure 3.90). The parameter values for every model specified in the **Model Parameters** sub-panel will now be applied ONLY for the *indexed* **IR** # (i.e., **IR# 5** in the example shown in Figure 3.90).



💐 Mai	n Screen						
<u>F</u> ile <u>E</u>	dit <u>P</u> arameters	<u>Calculations</u>	<u>T</u> ools	<u>A</u> dvance	d <u>H</u> elp		
Open	Save	New	回 Quick S	ave	ICRP DEF5 Load	CFR DEFS Load	REP Report
Ver 3.0	No file ope	ened					
2	میں کی م				IM	BA P	rofe
	ake Scena ake Regime ear All Intake Reg 3 1 1 IR 2 1 Route C Inhalation C Ingestion C Injection C Wound	UTIO es ajimes R 3 IR 4 Moo (©	Enter Nu IR 5 de Acute Sta	umber of Ir IR 6) art Date	ntake Regim IR 7) IR (28/11/20	es (1-10) 11 8 1 IR 9 1 C Chronic 000 14:30	IR 10
	C Vapour						

Figure 3.90. Display mode for setting up model parameters independently for each IR.

Key Tip: This *multi-dimensional-model* capability is useful not just for analyzing several known intake events (of *different* materials). It can also be used to "*fit*" an *unknown* value of a critical parameter for a single intake, *e.g.*, the aerosol AMAD or solubility type. IMBA Professional can be set up for several simultaneous instances of the same intake event, assuming various hypothetical parameter values for each instance. IMBA Professional can then automatically determine which set of parameter values is most likely, based on the bioassay data.

Saving All Model Parameters



Figure 3.91. The "Quick Save" *tool button* for Saving All Model Parameters (and calculated results).

At any time while you are using **IMBA Professional** to set up (or change) parameter values or model options, you can **Save** a complete record of the current status (including all selected model options and parameter values, together with the most recently calculated results). You can do this in any of the following ways.

1. Using the "Quick Save" Tool Button

Clicking the "Quick Save" tool button (Figure 3.91) saves all parameter values and results to the default Parameter File named "parameters.ix." This is located in the folder "[Install Drive:]\JABASOFT\IMBAEXUS\," where [Install Drive:] is the disk drive (root directory) on which you installed IMBA Professional. If you accepted the default installation option, this will be [C:].

***** **	Warning: "Quick Save" will over-write any existing "parameters.ix" file - so this facility should be used only as a temporary file , <i>e.g.</i> , to save your work periodically as you proceed through setting up a complex case study.
**************************************	Note: The "Quick Save" <i>tool button</i> only appears on the Main Screen. However, you can return to the Main Screen from either of the Calculations screens - at any time except when IMBA Professional is performing a calculation.

2. Using the "Save" Option

Clicking the "**Save**" *tool button* (Figure 3.93) saves all parameter values and results to the **Parameter File** named (with its location) in the parameter file box. However, if you are working with a "**New**" (and un-named) parameter file, then you will be prompted for the **File** <u>name</u> for your saved parameter file (Figure 3.92). The default location in which your file will be saved is **[Install Drive:]\JABASOFT\IMBAEXUS\USERDATA**. You can **browse** to save the file in any other folder.

****	Warning: IMBA Professional will automatically enter the last-used parameter file name (for the current session) in the " Save As " dialog box. If you do NOT want to over-write that file, be sure to change the file name BEFORE <i>clicking</i> <u>S</u> _{ave} .
🧏 📰	Note: Selecting "File Save" from the Menu Bar performs exactly the same function as the "Save" tool button.
⁷²	Note: The "Save" tool button also appears on the Bioassay Calculations and Dose Calculations screens. The File Save menu option is available in both the Main Screen and Dose Calculations Screen

3. Using the "File | Save As" Option

The "Save As" window, and "File <u>n</u>ame" *dialog box* (Figure 3.92) always appear when you select "File | Save As" from the Menu Bar (in the Main Screen).

Save As		? ×
Savejn:	🔄 USERDATA 💽 🔶 🖆 🖪	
History Desktop My Documents My Computer	Development interesting.ix IXUS- I Mi99 - Pu.ix IXUS-II PH_UO2_urine_JT.ix USTUR Case 0269 Single Intake.ix Case 060501F.ix Test 2 - Urine.ix IAEA Case 4 - 905r.ix Test Case 1.ix IAEA Case 7 - 239Pu.ix USTUR0259.ix IAEA#7 - 238Pu - Data.ix USTUR0425urine1.ix	Save
Mu Network P	Save as type: IMBA Professional Files (*.ix)	Cancel
		1.

Figure 3.92. The "Save As" dialog box opened automatically by the "Save" tool button when no Parameter File name has been specified.

-

Example Parameter File



The parameter file named "Mi99 - Associated Nuclides.ix" that was put in your /JABASOFT/IMBAEXUS/USERDATA directory when you installed IMBA **Professional**. This is an example (partly hypothetical) of a case that involves:

- the Indicator Nuclide 239Pu;
- two Associated Radionuclides (239Pu and 241Am);
- three Intake Regimes.

Click "<u>Mi99 - Associated Radionuclides.ix</u>" to view the content of this file.

Note: This file is **VERY long**. It contains **ALL** the information entered about this case - plus the calculated results. Many of the saved values are **ZERO** or **"*"**. These represent **"null**" values, *e.g.*, non-defined values for the remaining **seven** available **Intake Regimes** (**IR4 - IR10**) not used in this

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Mi99_Associated_Radionuclides.ix

UNITS			
Date			
Bq			
6/9/194	5		
UNITS2			
Sv			
INTAKE	REGIMES	5	
1			
3			
1,	1,	0,	0
1,	1,	9464,	0
1,	1,	9956,	0
1,	1,	0,	0
1,	1,	О,	0
1,	1,	О,	0
1,	1,	О,	0
1,	1,	0,	0
1,	1,	0,	0
1,	1,	0,	0
RADION	UCLIDE		
Pu-238			
Pu			
ASSOCI	ATED RAI	DIONUCLID	ES
2			
2			
Pu-239			
3.5			
Am-241			
0.8			
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ASSOCIATED RADIONUCLIDES 2
Pu
8784000
Am
157800
INTAKES
498.13
530.34
135.27
0
0
0
0
0
0
0
ADVANCED
no
no
BIOASSAY QUANTITIES
IBQ
table
graph
clear
9337
10067
200
LIN
2
2
-1
DATA
Whole body
2
* * * * * * * * * * * * *
Lungs
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2 * * * * * * * * * * * * Urine 201 9337 , 1.0000E+00 , 2.8681E-04 , 8315 , 1.0000E+00 , 1.0000E-03 , Real , 9.0000E-04, NORM, 3.089352447E-04, 9340.7, 1.0000E+00, 2.8674E-04, 8405, 1.0000E+00, 1.8000E-03, Real, 9.0000E-04, NORM, 3.0684808E-04, * 9344.3 , 1.0000E+00 , 2.8667E-04 , 8497 , 1.0000E+00 , 3.0000E-04 , Real , 9.0000E-04, NORM, 3.047509527E-04, 9348 , 1.0000E+00 , 2.8659E-04 , 8588 , 1.0000E+00 , 4.8000E-03 , Real , 2.0000E-03, NORM, 3.026986571E-04, 9351.7 , 1.0000E+00 , 2.8652E-04 , 8685 , 1.0000E+00 , 0.0000E+00 , Real , 9.0000E-04 , NORM , 3.005417542E-04 , * 9355.3 , 1.0000E+00 , 2.8644E-04 , 8958 , 1.0000E+00 , 0.0000E+00 , Real , 9.0000E-04, NORM, 2.946389137E-04, 9359, 1.0000E+00, 2.8637E-04, 9049, 1.0000E+00, 0.0000E+00, Real, 9.0000E-04, NORM, 2.927260945E-04, 9362.7 , 1.0000E+00 , 2.8630E-04 , 9140 , 1.0000E+00 , 5.0000E-04 , Real , 9.0000E-04, NORM, 2.908332005E-04, 9366.3 , 1.0000E+00 , 2.8623E-04 , 9238 , 1.0000E+00 , 5.0000E-04 , Real , 9.0000E-04, NORM, 2.888207553E-04, * 9370 , 1.0000E+00 , 2.8615E-04 , 9413 , 1.0000E+00 , 1.2000E-03 , Real , 7.0000E-04, NORM, 2.852939949E-04, 9373.7, 1.0000E+00, 2.8608E-04, 9516, 1.0000E+00, 4.1000E-03, Real, 7.0000E-04, NORM, 4.748030001E-03, * 9377.4 , 1.0000E+00 , 2.8600E-04 , 9601 , 1.0000E+00 , 2.2000E-03 , Real , 5.0000E-04, NORM, 3.482088721E-03, * 9381, 1.0000E+00, 2.8593E-04, 9963, 1.0000E+00, 1.2900E-02, Real, 1.6000E-03, NORM, 1.653366556E-02, 9384.7 , 1.0000E+00 , 2.8586E-04 , 10044 , 1.0000E+00 , 7.5000E-03 , Real , 1.1000E-03, NORM, 4.031108966E-03, 9388.4 , 1.0000E+00 , 2.8578E-04 , 10141 , 1.0000E+00 , 2.0000E-03 , Real , 4.0000E-04 , NORM , 3.051661442E-03 , 9392, 1.0000E+00, 2.8571E-04, 10245, 1.0000E+00, 3.0000E-03, Real, 6.0000E-04, NORM, 2.709333359E-03, * 9395.7 , 1.0000E+00 , 2.8564E-04 , 10327 , 1.0000E+00 , 2.7000E-03 , Real , 5.0000E-05, NORM, 2.559842362E-03, * 9399.4 , 1.0000E+00 , 2.8556E-04 , 10422 , 1.0000E+00 , 3.1000E-03 , Real , 6.0000E-04, NORM, 2.429309066E-03, 9403 , 1.0000E+00 , 2.8549E-04 , 10512 , 1.0000E+00 , 1.1000E-03 , Real , 4.0000E-04, NORM, 2.324279706E-03, * 9406.7 , 1.0000E+00 , 2.8542E-04 , 10600 , 1.0000E+00 , 3.8000E-03 , Real , 7.0000E-04 , NORM , 2.231645322E-03 , 9410.4 , 1.0000E+00 , 2.8534E-04 , 10691 , 1.0000E+00 , 2.1000E-03 , Real , 5.0000E-04, NORM, 2.143644365E-03, * 9414 , 1.0000E+00 , 2.8527E-04 , 10784 , 1.0000E+00 , 1.5000E-03 , Real , 4.0000E-04, NORM, 2.060503916E-03, *

1.0000E+00 , 2.8520E-04 , 10873 , 1.0000E+00 , 2.0000E-03 , Real , 94177 4.0000E-04 , NORM , 1.986686833E-03 , 9421.4 , 1.0000E+00 , 2.8512E-04 , 10964 , 1.0000E+00 , 1.1000E-03 , Real , 4.0000E-04, NORM, 1.916358067E-03, * 9425, 1.0000E+00, 2.8505E-04, 11059, 1.0000E+00, 8.0000E-04, Real, 4.0000E-04, NORM, 1.848100598E-03, 9428.7 , 1.0000E+00 , 2.8498E-04 , 11143 , 1.0000E+00 , 1.0000E-03 , Real , 4.0000E-04, NORM, 1.791663094E-03, * 9432.4 , 1.0000E+00 , 2.8491E-04 , 11239 , 1.0000E+00 , 1.2000E-03 , Real , 4.0000E-04, NORM, 1.731462914E-03, * 9436 , 1.0000E+00 , 2.8484E-04 , 11346 , 1.0000E+00 , 1.4000E-03 , Real , 4.0000E-04, NORM, 1.669218578E-03, 9439.7 , 1.0000E+00 , 2.8476E-04 , 11418 , 1.0000E+00 , 1.4000E-03 , Real , 4.0000E-04, NORM, 1.630015035E-03, * 9443.4 , 1.0000E+00 , 2.8469E-04 , 11505 , 1.0000E+00 , 5.0000E-04 , Real , 4.0000E-04 , NORM , 1.585337421E-03 , * 9447.1 , 1.0000E+00 , 2.8462E-04 , 11703 , 1.0000E+00 , 1.0000E-03 , Real , 4.0000E-04 , NORM , 1.493329802E-03 , 9450.7 , 1.0000E+00 , 2.8454E-04 , 11786 , 1.0000E+00 , 4.0000E-04 , Real , 4.0000E-04 , NORM , 1.458421214E-03 , * 9454.4 , 1.0000E+00 , 2.8447E-04 , 12137 , 1.0000E+00 , 2.2000E-03 , Real , 5.0000E-04, NORM, 1.330735485E-03, 9458.1 , 1.0000E+00 , 2.8440E-04 , 12186 , 1.0000E+00 , 3.0000E-04 , Real , 4.0000E-04 , NORM , 1.315174705E-03 , 9461.7 , 1.0000E+00 , 2.8433E-04 , 12276 , 1.0000E+00 , 9.0000E-04 , Real , 4.0000E-04, NORM, 1.287796628E-03, * 9465.4 , 1.0000E+00 , 1.0384E-01 , 12368 , 1.0000E+00 , 4.0000E-04 , Real , 4.0000E-04 , NORM , 1.261406319E-03 , * 9469.1 , 1.0000E+00 , 2.0448E-02 , 12406 , 1.0000E+00 , 1.6000E-03 , Real , 4.0000E-04 , NORM , 1.250908863E-03 , * 9472.7 , 1.0000E+00 , 9.9146E-03 , * , * , * , * , * , * , * , * 9476.4 , 1.0000E+00 , 6.9547E-03 , * , * , * , * , * , * , * 9480.1 , 1.0000E+00 , 6.0610E-03 , * , * , * , * , * , 9483.7 , 1.0000E+00 , 5.7315E-03 , * , * , * , * , * , * , * 9487.4 , 1.0000E+00 , 5.5496E-03 , * , * , * , * , * , * 9491.1 , 1.0000E+00 , 5.4154E-03 , * , * , * , * , * , * , * , * 9494.7, 1.0000E+00, 5.3014E-03, *, *, *, *, * , * , * 9498.4 , 1.0000E+00 , 5.1929E-03 , * ,* ,* ,* ,* ,* ,* ,* ,* ,* 9502.1, 1.0000E+00, 5.0905E-03, *,*,*,*,*,*,*,* 9505.7, 1.0000E+00, 4.9958E-03, *,*,*,*,*,*,*,* 9509.4 , 1.0000E+00 , 4.9031E-03 , * , * , * , * , * , * , * , * 9513.1, 1.0000E+00, 4.8146E-03, *, *, *, *, *, * 9516.7 , 1.0000E+00 , 4.7323E-03 , * , * , * , * , * , * , * , * , * 9520.4 , 1.0000E+00 , 4.6514E-03 , * , * , * , * , * , * , * 9524.1 , 1.0000E+00 , 4.5740E-03 , * , * , * , * , * , * , * , * , * 9527.8 , 1.0000E+00 , 4.4998E-03 , * , * , * , * , *

9531.4 ,	1.0000E+00 ,	4.4306E-03 ,	*	* '	* ,	*	, * ,	*	* '	, * ,	
9535.1 ,	1.0000E+00 ,	4.3622E-03,	*	, * ,	* ,	*	, * ,	*	, * ,	, * ,	
9538.8 ,	1.0000E+00 ,	4.2965E-03,	*	, * ,	* ,	*	, * ,	*	, * ,	, * ,	
9542.4 ,	1.0000E+00,	4.2350E-03,	*	, * ,	* ,	*	, * ,	*	, * '	, * ,	
9546.1 ,	1.0000E+00,	4.1742E-03,	*	, * ,	* ,	*	, * ,	*	, * ,	*	
9549.8 ,	1.0000E+00,	4.1157E-03,	*	, * ,	* ,	*	, * ,	*	, * ,	, * ,	
9553.4 ,	1.0000E+00,	4.0607E-03,	*	, * ,	* ,	*	, * ,	*	, * '	, * ,	
9557.1 ,	1.0000E+00,	4.0062E-03,	*	, * ,	* ,	*	, * ,	*	, * '	, * ,	
9560.8 ,	1.0000E+00,	3.9537E-03,	*	, * ,	* ,	*	, * ,	*	, *	, *	
9564.4 ,	1.0000E+00,	3.9043E-03,	*	, * ,	* ,	*	, * ,	*	, * ,	, * ,	
9568.1 ,	1.0000E+00,	3.8551E-03,	*	, * ,	* ,	*	*	*	, * ,	, * ,	
9571.8 ,	1.0000E+00,	3.8077E-03,	*	, * ,	* ,	*	, * ,	*	, * ,	, * ,	
9575.4 ,	1.0000E+00 ,	3.7630E-03,	*	, * ,	* ,	*	, * ,	*	*	, * ,	
9579.1,	1.0000E+00 ,	3.7185E-03,	*	, * ,	* ,	*	, * ,	*	*	, * ,	
9582.8 ,	1.0000E+00,	3.6755E-03,	*	, * ,	* ,	*	, * ,	*	*	*	
9586.4 ,	1.0000E+00,	3.6349E-03,	*	, * ,	* ,	*	*	*	, * ,	, * ,	
9590.1 ,	1.0000E+00,	3.5944E-03,	*	, * ,	* ,	*	, * ,	*	, * ,	, * ,	
9593.8,	1.0000E+00 ,	3.5551E-03,	*	, * ,	* ,	*	, * ,	*	*	, * ,	
9597.5,	1.0000E+00,	3.5171E-03,	*	, * ,	* ,	*	, * ,	*	*	*	
9601.1 ,	1.0000E+00,	3.4811E-03,	*	, * ,	* ,	*	, * ,	*	, * '	*	
9604.8 ,	1.0000E+00,	3.4452E-03,	*	, * ,	* ,	*	*	*	, * ,	, * ,	
9608.5 ,	1.0000E+00,	3.4103E-03,	*	, * ,	* ,	*	, * ,	*	, * ,	, * ,	
9612.1 ,	1.0000E+00 ,	3.3773E-03,	*	, * ,	* ,	*	, * ,	*	*	, * ,	
9615.8,	1.0000E+00,	3.3443E-03,	*	, * ,	* ,	*	, * ,	*	, * '	*	
9619.5 ,	1.0000E+00,	3.3123E-03,	*	, * ,	* ,	*	, * ,	*	, * '	*	
9623.1 ,	1.0000E+00,	3.2819E-03,	*	, * ,	* ,	*	*	*	, * ,	, * ,	
9626.8 ,	1.0000E+00,	3.2515E-03,	*	, * ,	* ,	*	*	*	, * ,	, * ,	
9630.5 ,	1.0000E+00,	3.2220E-03,	*	, * ,	* ,	*	, * ,	*	*	*	
9634.1 ,	1.0000E+00,	3.1939E-03,	*	, * ,	* ,	*	*	*	, * ,	, * ,	
9637.8 ,	1.0000E+00,	3.1658E-03,	*	, * ,	* ,	*	, * ,	*	, *	, *	
9641.5 ,	1.0000E+00,	3.1384E-03,	*	, * ,	* ,	*	, * ,	*	, * '	, *	
9645.1 ,	1.0000E+00,	3.1125E-03,	*	, * ,	* ,	*	, * ,	*	, * ,	*	
9648.8 ,	1.0000E+00,	3.0865E-03,	*	, * ,	* ,	*	, * ,	*	, *	, *	
9652.5 ,	1.0000E+00,	3.0611E-03,	*	, * ,	* ,	*	, * ,	*	, *	, *	
9656.1 ,	1.0000E+00,	3.0370E-03,	*	, * ,	* ,	*	, * ,	*	, * '	, * ,	
9659.8 ,	1.0000E+00,	3.0128E-03,	*	, * ,	* ,	*	, * ,	*	, * '	, * ,	
9663.5 ,	1.0000E+00,	2.9892E-03,	*	, * ,	* ,	*	, * ,	*	, * ,	, * ,	
9667.2 ,	1.0000E+00,	2.9661E-03,	*	, * ,	* ,	*	, * ,	*	, *	, *	
9670.8 ,	1.0000E+00,	2.9442E-03,	*	* ,	* ,	*	, * ,	*	, * ,	, *	
9674.5 ,	1.0000E+00,	2.9222E-03,	*	* ,	* ,	*	, * ,	*	, * ,	, *	
9678.2 ,	1.0000E+00,	2.9007E-03,	*	, * ,	* ,	*	, * ,	*	, * ,	, * ,	
9681.8,	1.0000E+00,	2.8802E-03,	*	, * ,	* ,	*	, * ,	*	, * '	, *	

9685.5,	1.0000E+00 ,	2.8597E-03,	*	, * ,	*	*	*	*	*	, * ,
9689.2 ,	1.0000E+00 ,	2.8396E-03,	*	, * , ,	*	*	, *	*	, *	, * ,
9692.8 ,	1.0000E+00 ,	2.8205E-03,	*	, * ,	*	*	, *	*	*	, * ,
9696.5 ,	1.0000E+00 ,	2.8012E-03,	*	, * ,	*	*	*	*	*	, *
9700.2 ,	1.0000E+00 ,	2.7824E-03,	*	, * ,	*	*	*	*	*	, *
9703.8 ,	1.0000E+00 ,	2.7644E-03,	*	, * ,	*	*	*	*	*	, *
9707.5 ,	1.0000E+00 ,	2.7464E-03,	*	, * ,	*	*	*	*	*	, *
9711.2,	1.0000E+00 ,	2.7287E-03,	*	, *	*	*	*	*	*	, * ,
9714.8,	1.0000E+00 ,	2.7119E-03,	*	, * ,	*	*	*	*	*	, *
9718.5 ,	1.0000E+00 ,	2.6949E-03,	*	, * ,	*	*	*	*	*	, *
9722.2 ,	1.0000E+00 ,	2.6782E-03,	*	, * ,	*	*	*	*	*	, *
9725.8,	1.0000E+00 ,	2.6624E-03,	*	, * ,	*	*	*	*	*	, *
9729.5 ,	1.0000E+00 ,	2.6464E-03,	*	, *	*	*	, *	*	*	*
9733.2,	1.0000E+00 ,	2.6307E-03,	*	, *	*	*	*	*	, *	, * ,
9736.8,	1.0000E+00 ,	2.6158E-03,	*	, *	*	*	*	*	, *	, * ,
9740.5 ,	1.0000E+00 ,	2.6007E-03,	*	, *	*	*	*	*	, *	, * ,
9744.2 ,	1.0000E+00 ,	2.5860E-03,	*	, *	*	*	, *	*	*	*
9747.9,	1.0000E+00,	2.5715E-03,	*	*	*	*	*	*	*	*
9751.5,	1.0000E+00 ,	2.5576E-03,	*	, * ,	*	*	*	*	*	, * ,
9755.2 ,	1.0000E+00,	2.5437E-03,	*	*	*	*	*	*	*	*
9758.9 ,	1.0000E+00 ,	2.5300E-03,	*	, * ,	*	*	, *	*	, *	, * ,
9762.5 ,	1.0000E+00 ,	2.5168E-03,	*	, * ,	*	*	*	*	*	, * ,
9766.2 ,	1.0000E+00 ,	2.5036E-03,	*	, *	*	*	, *	*	, *	, * ,
9769.9 ,	1.0000E+00 ,	2.4906E-03,	*	, * ,	*	*	*	*	*	, * ,
9773.5 ,	1.0000E+00 ,	2.4782E-03,	*	, *	*	*	, *	*	*	*
9777.2 ,	1.0000E+00 ,	2.4657E-03,	*	, *	*	*	, *	*	*	*
9780.9 ,	1.0000E+00 ,	2.4534E-03,	*	, * ,	*	*	*	*	*	, * ,
9784.5,	1.0000E+00 ,	2.4416E-03,	*	, *	*	*	, *	*	, *	, * ,
9788.2,	1.0000E+00 ,	2.4297E-03,	*	, * ,	*	*	, *	*	, *	, * ,
9791.9 ,	1.0000E+00 ,	2.4180E-03,	*	, *	*	*	, *	*	*	*
9795.5,	1.0000E+00 ,	2.4068E-03,	*	, * ,	*	*	*	*	*	, * ,
9799.2 ,	1.0000E+00 ,	2.3955E-03,	*	, *	*	*	, *	*	*	*
9802.9 ,	1.0000E+00 ,	2.3844E-03,	*	*	*	*	*	*	*	*
9806.5 ,	1.0000E+00 ,	2.3737E-03,	*	*	*	*	*	*	*	*
9810.2,	1.0000E+00 ,	2.3629E-03,	*	, * ,	*	*	*	*	*	, * ,
9813.9,	1.0000E+00 ,	2.3524E-03,	*	*	*	*	*	*	*	*
9817.6,	1.0000E+00 ,	2.3420E-03,	*	*	*	*	*	*	*	, * ,
9821.2,	1.0000E+00 ,	2.3320E-03,	*	*	*	*	*	*	*	, * ,
9824.9,	1.0000E+00 ,	2.3218E-03,	*	*	*	*	*	*	*	, * ,
9828.6,	1.0000E+00 ,	2.3119E-03,	*	*	*	*	*	*	*	, * ,
9832.2,	1.0000E+00 ,	2.3024E-03,	*	, * ,	*	*	*	*	*	, * ,
9835.9,	1.0000E+00,	2.2927E-03,	*	*	*	*	*	*	*	*

9839.6, 1.0000E+00, 2.2832E-03,	,	*	, *	,	*	, *	,	*	1	*	, *	; ,	*	
9843.2 , 1.0000E+00 , 2.2741E-03 ,	,	*	, *	,	*	, *	,	*	,	*	, *	۰ ۱	*	
9846.9 , 1.0000E+00 , 2.2649E-03 ,	,	*	, *	,	*	, *	,	*	,	*	, *	۰ ۱	*	
9850.6 , 1.0000E+00 , 2.2558E-03 ,	,	*	, *	,	*	, *	,	*	,	*	, *	۰ ۱	*	
9854.2, 1.0000E+00, 2.2471E-03,	,	*	, *	,	*	, *	,	*	,	*	, *	۰ ۱	*	
9857.9, 1.0000E+00, 2.2383E-03,	,	*	, *	,	*	, *	,	*	,	*	, *	۰ ۱	*	
9861.6 , 1.0000E+00 , 2.2296E-03 ,	,	*	, *	,	*	, *	,	*	,	*	, *	۰ ۱	*	
9865.2 , 1.0000E+00 , 2.2213E-03 ,	,	*	, *	,	*	, *	,	*	,	*	, *	۰ ۱	*	
9868.9, 1.0000E+00, 2.2128E-03,	,	*	, *	,	*	, *	,	*	,	*	, *	۰ ۱	*	
9872.6 , 1.0000E+00 , 2.2045E-03 ,	,	*	, *	,	*	, *	,	*	,	*	, *	۰ ۱	*	
9876.2, 1.0000E+00, 2.1964E-03,	,	*	, *	,	*	, *	,	*	,	*	, *	۰ ۱	*	
9879.9, 1.0000E+00, 2.1884E-03,	,	*	, *	,	*	, *	,	*	,	*	, *	۰ ۱	*	
9883.6 , 1.0000E+00 , 2.1803E-03 ,	,	*	, *	,	*	, *	,	*	,	*	, *	۰ ۱	*	
9887.3 , 1.0000E+00 , 2.1725E-03 ,	,	*	, *	,	*	, *	,	*	,	*	, *	۰ ۱	*	
9890.9 , 1.0000E+00 , 2.1649E-03 ,	,	*	, *	,	*	, *	,	*	,	*	, *	۰ ۱	*	
9894.6 , 1.0000E+00 , 2.1572E-03 ,	,	*	, *	,	*	, *	,	*	,	*	, *	۰ ۱	*	
9898.3, 1.0000E+00, 2.1496E-03,	,	*	, *	,	*	, *	,	*	,	*	, *	۰ ۱	*	
9901.9 , 1.0000E+00 , 2.1423E-03 ,	,	*	, *	,	*	, *	,	*	,	*	, *	۰ ۱	*	
9905.6, 1.0000E+00, 2.1349E-03,	,	*	, *	,	*	, *	,	*	,	*	, *	۰ ۱	*	
9909.3 , 1.0000E+00 , 2.1277E-03 ,	,	*	, *	,	*	, *	,	*	,	*	, *	۰ ۱	*	
9912.9 , 1.0000E+00 , 2.1207E-03 ,	,	*	, *	,	*	, *	,	*	,	*	, *	۰ ۱	*	
9916.6 , 1.0000E+00 , 2.1135E-03 ,	,	*	, *	,	*	, *	,	*	,	*	, *	۰ ۱	*	
9920.3 , 1.0000E+00 , 2.1065E-03 ,	,	*	, *	,	*	, *	,	*	,	*	, *	· ,	*	
9923.9, 1.0000E+00, 2.0998E-03,	,	*	, *	,	*	, *	,	*	,	*	, *	۰ ۱	*	
9927.6, 1.0000E+00, 2.0929E-03,	,	*	, *	,	*	, *	,	*	,	*	, *	۰ ۱	*	
9931.3 , 1.0000E+00 , 2.0862E-03 ,	,	*	, *	,	*	, *	,	*	,	*	, *	÷	*	
9934.9 , 1.0000E+00 , 2.0797E-03 ,	,	*	, *	,	*	, *	,	*	,	*	, *	۰ ۱	*	
9938.6, 1.0000E+00, 2.0730E-03,	,	*	, *	,	*	, *	,	*	,	*	, *	۰ ۱	*	
9942.3 , 1.0000E+00 , 2.0665E-03 ,	,	*	, *	,	*	, *	,	*	,	*	, *	÷	*	
9945.9, 1.0000E+00, 2.0603E-03,	,	*	, *	,	*	, *	,	*	,	*	, *	۰ ۱	*	
9949.6, 1.0000E+00, 2.0539E-03,	,	*	, *	,	*	, *	,	*	,	*	, *	۰ ۱	*	
9953.3 , 1.0000E+00 , 2.0476E-03 ,	,	*	, *	,	*	, *	,	*	,	*	, *	۰ ۱	*	
9956.9, 1.0000E+00, 2.6302E-02,	,	*	, *	,	*	, *	,	*	,	*	, *	۰ ۱	*	
9960.6 , 1.0000E+00 , 1.8373E-02 ,	,	*	, *	,	*	, *	,	*	,	*	, *	۰ ۱	*	
9964.3 , 1.0000E+00 , 1.5694E-02 ,	,	*	, *	,	*	, *	,	*	,	*	, *	÷	*	
9968 , 1.0000E+00 , 1.3637E-02 ,	*	,	*	, *	ı	*	, *	,	*	,	*	, *		
9971.6 , 1.0000E+00 , 1.2015E-02 ,	,	*	, *	,	*	, *	,	*	ı	*	, *	· ,	*	
9975.3 , 1.0000E+00 , 1.0656E-02 ,	,	*	, *	,	*	, *	,	*	ı	*	, *	· ,	*	
9979 , 1.0000E+00 , 9.5457E-03 ,	*	,	*	*	ı	*	, *	,	*	1	*	, *		
9982.6 , 1.0000E+00 , 8.6574E-03 ,	,	*	, *	,	*	, *	1	*	ı	*	, *	۰ ۱	*	
9986.3 , 1.0000E+00 , 7.9026E-03 ,	,	*	, *	,	*	, *	1	*	ı	*	, *	۰ ۱	*	
9990, 1.0000E+00, 7.2771E-03,	*	,	*	*	,	*	, *	,	*	,	*	, *		

```
9993.6, 1.0000E+00, 6.7689E-03, *,*,*,*,*
                                                , *
9997.3, 1.0000E+00, 6.3302E-03, *, *, *
                                          , *
                                             , *
                                                 , *
10001, 1.0000E+00, 5.9603E-03, *,*
                                      , *
10005, 1.0000E+00, 5.6234E-03, *,*
                                      , *
10008, 1.0000E+00, 5.4059E-03, *,*
                                      , *
10012 , 1.0000E+00 , 5.1547E-03 , * , *
                                      , *
                                          , *
                                                , *
10016 , 1.0000E+00 , 4.9399E-03 , * , *
                                      , *
10019 , 1.0000E+00 , 4.7986E-03 , * , *
                                      , *
                                          , *
                                                , *
10023 , 1.0000E+00 , 4.6322E-03 , * , * , *
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                                                , *
                                             , *
                                         , *
                                             , *
10027 , 1.0000E+00 , 4.4868E-03 , * ,*
                                      , *
                                                , *
10030, 1.0000E+00, 4.3893E-03, *,*
10034 , 1.0000E+00 , 4.2724E-03 , * ,*
10038, 1.0000E+00, 4.1681E-03, *,*
10041 , 1.0000E+00 , 4.0969E-03 ,
                                * *
10045 , 1.0000E+00 , 4.0102E-03 , * ,*
10049, 1.0000E+00, 3.9314E-03, *,*
10052 , 1.0000E+00 , 3.8768E-03 , * , *
                                      , *
10056, 1.0000E+00, 3.8095E-03, *, *, *
                                         , *
                                             , *
                                                , *
10060, 1.0000E+00, 3.7473E-03, *, *
                                      , *
                                         , *
                                             , *
                                                , *
10063 , 1.0000E+00 , 3.7037E-03 , * , * , * , *
                                             , *
                                                , *
10067, 1.0000E+00, 3.6494E-03, *, *, *, *
                                            , *
                                                , *
Feces
2
* * * * * * * * * * *
Blood
2
* * * * * * * * * *
Thyroid
2
* * * * * * * * * *
Liver
2
* * * * * * * *
User Defined
2
* * * * * * * * * * * *
PARAMETERS BIOASSAY
TAB 1
7
BQ 0
Std Pu Model
0.0000001
```

```
5
-0.0013931 , 7.82562
0.0975364 , 0.000303686
0.0435031 , 0.00218295
0.816737 , 0.0000212165
0.0436166 , 0.299214
BQ 1
Not Specified
0
0
BQ 2
Std Pu Model
0.0000001
7
-0.0139864109 , 12
0.00480886 , 0.355332
0.000012634 \ , \ 0.0000248355
0.00897385 , 1.26205
0.000139833 , 0.014097
0.0000414124 , 0.000864541
0.0000098215 , 0.000211543
BQ 3
Std Pu Model
0.0000001
10
0.00000987605 , 9.00225
0.0580447 , 1.74433
0.00905385 , 0.35351
-0.0947113 , 1.37032
0.00000428085 , 0.000288176
0.0275708 , 0.918619
0.0000321603 , 0.00184051
0.0000052992 , 0.0000368268
-0.00000164911 , 0.0159327
0.00000871155 \ , \ 0.000000422684
BQ 4
Not Specified
0
0
BQ 5
Not Specified
```

```
0
```

```
0
BQ 6
Not Specified
0
0
BQ 7
Not Specified
0
0
TAB 2
7
BQ 0
Std Pu Model
0.0000001
5
-0.0013931 , 7.82562
0.0975364 , 0.000303686
0.0435031 , 0.00218295
0.816737 , 0.0000212165
0.0436166 , 0.299214
BQ 1
Not Specified
0
0
BQ 2
Std Pu Model
0.000001
7
-0.0139864109 , 12
0.00480886 , 0.355332
0.000012634 , 0.0000248355
0.00897385 , 1.26205
0.000139833 , 0.014097
0.0000414124 , 0.000864541
0.0000098215 , 0.000211543
BQ 3
Std Pu Model
0.0000001
10
0.00000987605 , 9.00225
0.0580447 , 1.74433
0.00905385 , 0.35351
```

```
-0.0947113 , 1.37032
0.00000428085 , 0.000288176
0.0275708 , 0.918619
0.0000321603 , 0.00184051
0.0000052992 \ , \ 0.0000368268
-0.00000164911 , 0.0159327
0.00000871155 , 0.000000422684
BQ 4
Not Specified
0
0
BQ 5
Not Specified
0
0
BQ 6
Not Specified
0
0
BQ 7
Not Specified
0
0
TAB 3
7
BQ 0
Std Pu Model
0.0000001
5
-0.0013931 , 7.82562
0.0975364 , 0.000303686
0.0435031 \ , \ 0.00218295
0.816737 , 0.0000212165
0.0436166 , 0.299214
BQ 1
Not Specified
0
0
BQ 2
Std Pu Model
0.0000001
7
```

```
-0.0139864109 , 12
0.00480886 , 0.355332
0.000012634 , 0.0000248355
0.00897385 , 1.26205
0.000139833 , 0.014097
0.0000414124 , 0.000864541
0.0000098215 , 0.000211543
BQ 3
Std Pu Model
0.0000001
10
0.00000987605 , 9.00225
0.0580447 , 1.74433
0.00905385 , 0.35351
-0.0947113 , 1.37032
0.0000428085 , 0.000288176
0.0275708 , 0.918619
0.0000321603 , 0.00184051
0.0000052992 , 0.0000368268
-0.00000164911 , 0.0159327
0.00000871155 , 0.000000422684
BQ 4
Not Specified
0
0
BQ 5
Not Specified
0
0
BQ 6
Not Specified
0
0
BQ 7
Not Specified
0
0
TAB 4
7
BQ 0
Std Pu Model
0.0000001
```

```
5
-0.0013931 , 7.82562
0.0975364 , 0.000303686
0.0435031 , 0.00218295
0.816737 , 0.0000212165
0.0436166 , 0.299214
BQ 1
Not Specified
0
0
BQ 2
Std Pu Model
0.0000001
7
-0.0139864109 , 12
0.00480886 , 0.355332
0.000012634 \ , \ 0.0000248355
0.00897385 , 1.26205
0.000139833 , 0.014097
0.0000414124 , 0.000864541
0.0000098215 , 0.000211543
BQ 3
Std Pu Model
0.0000001
10
0.00000987605 , 9.00225
0.0580447 , 1.74433
0.00905385 , 0.35351
-0.0947113 , 1.37032
0.00000428085 , 0.000288176
0.0275708 , 0.918619
0.0000321603 , 0.00184051
0.0000052992 , 0.0000368268
-0.00000164911 , 0.0159327
0.00000871155 \ , \ 0.000000422684
BQ 4
Not Specified
0
0
BQ 5
Not Specified
```

```
0
```

```
0
BQ 6
Not Specified
0
0
BQ 7
Not Specified
0
0
TAB 5
7
BQ 0
Std Pu Model
0.0000001
5
-0.0013931 , 7.82562
0.0975364 , 0.000303686
0.0435031 , 0.00218295
0.816737 , 0.0000212165
0.0436166 , 0.299214
BQ 1
Not Specified
0
0
BQ 2
Std Pu Model
0.000001
7
-0.0139864109 , 12
0.00480886 , 0.355332
0.000012634 , 0.0000248355
0.00897385 , 1.26205
0.000139833 , 0.014097
0.0000414124 , 0.000864541
0.0000098215 , 0.000211543
BQ 3
Std Pu Model
0.0000001
10
0.00000987605 , 9.00225
0.0580447 , 1.74433
0.00905385 , 0.35351
```

```
-0.0947113 , 1.37032
0.00000428085 , 0.000288176
0.0275708 , 0.918619
0.0000321603 , 0.00184051
0.0000052992 \ , \ 0.0000368268
-0.00000164911 , 0.0159327
0.00000871155 , 0.000000422684
BQ 4
Not Specified
0
0
BQ 5
Not Specified
0
0
BQ 6
Not Specified
0
0
BQ 7
Not Specified
0
0
TAB 6
7
BQ 0
Std Pu Model
0.0000001
5
-0.0013931 , 7.82562
0.0975364 , 0.000303686
0.0435031 \ , \ 0.00218295
0.816737 , 0.0000212165
0.0436166 , 0.299214
BQ 1
Not Specified
0
0
BQ 2
Std Pu Model
0.0000001
7
```

```
-0.0139864109 , 12
0.00480886 , 0.355332
0.000012634 , 0.0000248355
0.00897385 , 1.26205
0.000139833 , 0.014097
0.0000414124 , 0.000864541
0.0000098215 , 0.000211543
BQ 3
Std Pu Model
0.0000001
10
0.00000987605 , 9.00225
0.0580447 , 1.74433
0.00905385 , 0.35351
-0.0947113 , 1.37032
0.00000428085 , 0.000288176
0.0275708 , 0.918619
0.0000321603 , 0.00184051
0.0000052992 , 0.0000368268
-0.00000164911 , 0.0159327
0.00000871155 , 0.000000422684
BQ 4
Not Specified
0
0
BQ 5
Not Specified
0
0
BQ 6
Not Specified
0
0
BQ 7
Not Specified
0
0
TAB 7
7
BQ 0
Std Pu Model
0.0000001
```

```
5
-0.0013931 , 7.82562
0.0975364 , 0.000303686
0.0435031 , 0.00218295
0.816737 , 0.0000212165
0.0436166 , 0.299214
BQ 1
Not Specified
0
0
BQ 2
Std Pu Model
0.0000001
7
-0.0139864109 , 12
0.00480886 , 0.355332
0.000012634 \ , \ 0.0000248355
0.00897385 , 1.26205
0.000139833 , 0.014097
0.0000414124 , 0.000864541
0.0000098215 , 0.000211543
BQ 3
Std Pu Model
0.0000001
10
0.00000987605 , 9.00225
0.0580447 , 1.74433
0.00905385 , 0.35351
-0.0947113 , 1.37032
0.00000428085 , 0.000288176
0.0275708 , 0.918619
0.0000321603 , 0.00184051
0.0000052992 , 0.0000368268
-0.00000164911 , 0.0159327
0.00000871155 \ , \ 0.000000422684
BQ 4
Not Specified
0
0
BQ 5
Not Specified
```

```
0
```

```
0
BQ 6
Not Specified
0
0
BQ 7
Not Specified
0
0
TAB 8
7
BQ 0
Std Pu Model
0.0000001
5
-0.0013931 , 7.82562
0.0975364 , 0.000303686
0.0435031 , 0.00218295
0.816737 , 0.0000212165
0.0436166 , 0.299214
BQ 1
Not Specified
0
0
BQ 2
Std Pu Model
0.000001
7
-0.0139864109 , 12
0.00480886 , 0.355332
0.000012634 , 0.0000248355
0.00897385 , 1.26205
0.000139833 , 0.014097
0.0000414124 , 0.000864541
0.0000098215 , 0.000211543
BQ 3
Std Pu Model
0.0000001
10
0.00000987605 , 9.00225
0.0580447 , 1.74433
0.00905385 , 0.35351
```

```
-0.0947113 , 1.37032
0.00000428085 , 0.000288176
0.0275708 , 0.918619
0.0000321603 , 0.00184051
0.0000052992 \ , \ 0.0000368268
-0.00000164911 , 0.0159327
0.00000871155 , 0.000000422684
BQ 4
Not Specified
0
0
BQ 5
Not Specified
0
0
BQ 6
Not Specified
0
0
BQ 7
Not Specified
0
0
TAB 9
7
BQ 0
Std Pu Model
0.0000001
5
-0.0013931 , 7.82562
0.0975364 , 0.000303686
0.0435031 \ , \ 0.00218295
0.816737 , 0.0000212165
0.0436166 , 0.299214
BQ 1
Not Specified
0
0
BQ 2
Std Pu Model
0.0000001
7
```

```
-0.0139864109 , 12
0.00480886 , 0.355332
0.000012634 , 0.0000248355
0.00897385 , 1.26205
0.000139833 , 0.014097
0.0000414124 , 0.000864541
0.0000098215 , 0.000211543
BQ 3
Std Pu Model
0.0000001
10
0.00000987605 , 9.00225
0.0580447 , 1.74433
0.00905385 , 0.35351
-0.0947113 , 1.37032
0.00000428085 , 0.000288176
0.0275708 , 0.918619
0.0000321603 , 0.00184051
0.0000052992 , 0.0000368268
-0.00000164911 , 0.0159327
0.00000871155 , 0.000000422684
BQ 4
Not Specified
0
0
BQ 5
Not Specified
0
0
BQ 6
Not Specified
0
0
BQ 7
Not Specified
0
0
TAB 10
7
BQ 0
Std Pu Model
0.0000001
```

```
5
-0.0013931 , 7.82562
0.0975364 , 0.000303686
0.0435031 , 0.00218295
0.816737 , 0.0000212165
0.0436166 , 0.299214
BQ 1
Not Specified
0
0
BQ 2
Std Pu Model
0.0000001
7
-0.0139864109 , 12
0.00480886 , 0.355332
0.000012634 \ , \ 0.0000248355
0.00897385 , 1.26205
0.000139833 , 0.014097
0.0000414124 , 0.000864541
0.0000098215 , 0.000211543
BQ 3
Std Pu Model
0.0000001
10
0.00000987605 , 9.00225
0.0580447 , 1.74433
0.00905385 , 0.35351
-0.0947113 , 1.37032
0.00000428085 , 0.000288176
0.0275708 , 0.918619
0.0000321603 , 0.00184051
0.0000052992 , 0.0000368268
-0.00000164911 , 0.0159327
0.00000871155 \ , \ 0.000000422684
BQ 4
Not Specified
0
0
BQ 5
Not Specified
```

```
0
```

0
BQ 6
Not Specified
0
0
BQ 7
Not Specified
0
0
PARAMETERS PARTICLE TRANSPORT
ICRP Defaults
0.02
0.001
0.0001
0.00002
2
0.03
0.01
10
0.03
0.01
100
0.001
1
0.0005
0.007
0.007
0.6
0.1
ICRP Defaults
0.02
0.001
0.0001
0.00002
2
0.03
0.01
10
0.03
0.01
100
0.001

1
0.0005
0.007
0.007
0.6
0.1
ICRP Defaults
0.02
0.001
0.0001
0.00002
2
0.03
0.01
10
0.03
0.01
100
0.001
1
0.0005
0.007
0.007
0.6
0.1
ICRP Defaults
0.02
0.001
0.0001
0.00002
2
0.03
0.01
10
0.03
0.01
100
0.001
1
0.0005
0.007
0.007

0.6
0.1
ICRP Defaults
0.02
0.001
0.0001
0.00002
2
0.03
0.01
10
0.03
0.01
100
0.001
1
0.0005
0.007
0.007
0.6
0.1
ICRP Defaults
0.02
0.001
0.0001
0.00002
2
0.03
0.01
10
0.03
0.01
100
0.001
1
0.0005
0.007
0.007 0.007
0.007 0.007 0.6
0.007 0.007 0.6 0.1
0.007 0.007 0.6 0.1 ICRP Defaults

0.001
0.0001
0.00002
2
0.03
0.01
10
0.03
0.01
100
0.001
1
0.0005
0.007
0.007
0.6
0.1
ICRP Defaults
0.02
0.001
0.0001
0.00002
2
0.03
0.01
10
0.03
0.01
100
0.001
1
0.0005
0.007
0.007
0.6
0.1
ICRP Defaults
0.02
0.001
0.0001
0.00002

2

0.03
0.01
10
0.03
0.01
100
0.001
1
0.0005
0.007
0.007
0.6
0.1
ICRP Defaults
0.02
0.001
0.0001
0.00002
2
0.03
0.01
10
0.03
0.01
100
0.001
1
0.0005
0.007
0.007
0.6
0.1
PARAMETERS ABSORPTION
Туре М
Normal
0.099955
100
0.005
0
0
Туре М

Normal

0.099955
100
0.005
0
0
User Defined
Normal
0.09955
100
0.05
0
0
Туре М
Normal
0.099955
100
0.005
0
0
Туре М
Normal
0.099955
100
0.005
0
0
Туре М
Normal
0.099955
100
0.005
0
0
Туре М
Normal
0.099955
100
0.005
0
0
Туре М
Normal

0.099955
100
0.005
0
0
Туре М
Normal
0.099955
100
0.005
0
0
Туре М
Normal
0.099955
100
0.005
0
0
PARAMETERS GI-Tract
ICRP Defaults
24
6
1.8
1
0.0005
ICRP Defaults
24
6
1.8
1
0.0005
ICRP Defaults
24
6
1.8
1
0.0005
ICRP Defaults
24
6
1

```
0.0005
ICRP Defaults
24
6
1.8
1
0.0005
PARAMETERS ORGAN RETENTIONS
TAB 1
1
ICRP Pu Model
```

```
0
ADRENALS
0
BLADDER
7
-0.001165681225 , 1.19987E+01
0.000011659 , 1.41314E-02
0.00000343345 , 8.71154E-04
0.000401149 , 3.55543E-01
0.000747544 , 1.26294E+00
0.00000835345 , 2.18047E-04
0.00000106043 , 2.50778E-05
BRAIN
0
BREAST
0
G. BLADD
0
HEART CT.
0
HEART WL.
0
KIDNEYS
7
-0.004866002 , 1.26127E+00
-0.0104525 , 3.55064E-01
0.00372916 , 1.40094E-03
0.000290264 , 1.24857E-04
0.000458568 , 4.25213E-04
0.0103148 , 1.39221E-02
0.00052571 , 2.16919E-05
LIVER
5
-0.085449 , 1.34673E+00
-0.21266 , 3.76109E-01
0.239998 , 2.68343E-05
0.295656 , 1.85293E-04
-0.237545 , 3.35067E-04
MUSCLE
0
OVARIES
5
```

```
-0.0000286439 , 1.41065E+00
0.000852949 , 1.84121E-04
0.000080518 , 2.14761E-05
-0.000824848 , 1.98367E-04
-0.0000799751 , 3.89897E-01
PANCREAS
0
TESTES
5
-0.000092753 , 1.41093E+00
0.00101186 , 1.71104E-04
0.000258506 , 2.12454E-05
-0.000918511 , 2.11593E-04
-0.000259102 , 3.89940E-01
THYROID
0
R.B.M.
6
-0.0198474483 , 7.82506E-03
0.0000386163 , 1.25541E+00
0.0122563 , 3.49469E-04
0.00414815 , 1.81476E-05
0.000289932 , 3.52552E-01
0.00311445 , 8.15105E-05
BONE
0
CORT VOL
6
-0.24714990438 , 8.53426E-05
0.00000209448 , 1.26224E+00
-0.000033387 , 6.87895E-03
0.0237225 , 2.94142E-04
0.223443 , 2.73988E-05
0.0000156969 , 3.55388E-01
CORT SURF
4
-0.056006 , 1.35921E+00
-0.120006 , 2.81695E-04
-0.142614 , 3.78615E-01
0.318626 , 2.89246E-05
TRAB VOL
7
```

```
0.0000190871 , 1.25850E+00
-0.133532 , 7.76870E-04
-0.000002501 , 7.76870E-04
-0.000203435 , 9.47279E-03
0.101421 , 3.00063E-04
0.0321533 , 2.74300E-05
0.000142298 , 3.53682E-01
TRAB SURF
6
-0.0961547 , 1.26486E+00
-0.204196 , 3.56094E-01
0.173469 , 7.02621E-04
0.0588142 , 2.62987E-05
0.0101238 , 6.13083E-03
0.0579437 , 2.48708E-04
STOMACH
0
S.I.
9
0.000002319452 , 5.95605E+00
-0.00000258125 , 1.30481E+00
-0.00000145591 , 5.94293E+00
0.00000204386 , 1.42473E-03
0.00000374311 , 2.30152E-03
0.00000378586 , 2.30125E-04
-0.00000161905 , 3.72082E-01
-0.00000331261 , 3.63339E-01
0.000000483812 , 2.53754E-05
U.L.I.
9
-0.018145365303 , 1.80353E+00
0.00330195 , 3.55146E-01
0.000017873 , 1.90398E-03
-0.00000119168 , 8.87723E-03
0.000000107983 , 8.80750E-03
0.0148205 , 1.25865E+00
0.000002311 , 3.69827E-04
0.00000151967 , 1.02814E-05
0.00000229533 , 6.21726E-05
L.L.I.
8
0.04111566638 , 1.79498E+00
```

```
-0.6345 , 1.16251E+00
0.583868 , 1.13111E+00
0.0000178572 , 1.77880E-03
0.00000439178 , 2.42701E-04
0.00000567754 , 2.56698E-05
0.00947443 , 3.57888E-01
0.0000139771 , 1.77924E-03
ST. WALL
0
SKIN
0
SPLEEN
0
SOFT TISS
7
2.45320282 , 1.34274E+00
0.00845648 , 3.66703E-03
2.01555 , 1.83172E-05
-2.80238 , 1.33343E+00
0.0848507 , 8.41887E-04
0.20465 , 3.51307E-01
-1.96433 , 1.94455E-05
WB
0
BLOOD
5
0.627495442 , 1.26199E+00
0.372409 , 3.55291E-01
0.000166134 , 2.78392E-04
0.000219279 , 2.67517E-05
-0.000289855 , 7.10001E-03
TAB 2
1
ICRP Pu Model
0
ADRENALS
0
BLADDER
7
-0.001165681225 , 1.19987E+01
0.000011659 , 1.41314E-02
0.00000343345 , 8.71154E-04
```

```
0.000401149 , 3.55543E-01
0.000747544 , 1.26294E+00
0.00000835345 , 2.18047E-04
0.00000106043 , 2.50778E-05
BRAIN
0
BREAST
0
G. BLADD
0
HEART CT.
0
HEART WL.
0
KIDNEYS
7
-0.004866002 , 1.26127E+00
-0.0104525 , 3.55064E-01
0.00372916 , 1.40094E-03
0.000290264 , 1.24857E-04
0.000458568 , 4.25213E-04
0.0103148 , 1.39221E-02
0.00052571 , 2.16919E-05
LIVER
5
-0.085449 , 1.34673E+00
-0.21266 , 3.76109E-01
0.239998 , 2.68343E-05
0.295656 , 1.85293E-04
-0.237545 , 3.35067E-04
MUSCLE
0
OVARIES
5
-0.0000286439 , 1.41065E+00
0.000852949 , 1.84121E-04
0.000080518 , 2.14761E-05
-0.000824848 , 1.98367E-04
-0.0000799751 , 3.89897E-01
PANCREAS
0
TESTES
```

```
5
-0.000092753 , 1.41093E+00
0.00101186 , 1.71104E-04
0.000258506 , 2.12454E-05
-0.000918511 , 2.11593E-04
-0.000259102 , 3.89940E-01
THYROID
0
R.B.M.
6
-0.0198474483 , 7.82506E-03
0.0000386163 , 1.25541E+00
0.0122563 , 3.49469E-04
0.00414815 , 1.81476E-05
0.000289932 , 3.52552E-01
0.00311445 , 8.15105E-05
BONE
0
CORT VOL
6
-0.24714990438 , 8.53426E-05
0.00000209448 , 1.26224E+00
-0.000033387 , 6.87895E-03
0.0237225 , 2.94142E-04
0.223443 , 2.73988E-05
0.0000156969 , 3.55388E-01
CORT SURF
4
-0.056006 , 1.35921E+00
-0.120006 , 2.81695E-04
-0.142614 , 3.78615E-01
0.318626 , 2.89246E-05
TRAB VOL
7
0.0000190871 , 1.25850E+00
-0.133532 , 7.76870E-04
-0.000002501 , 7.76870E-04
-0.000203435 , 9.47279E-03
0.101421 , 3.00063E-04
0.0321533 , 2.74300E-05
0.000142298 , 3.53682E-01
TRAB SURF
```

```
6
-0.0961547 , 1.26486E+00
-0.204196 , 3.56094E-01
0.173469 , 7.02621E-04
0.0588142 , 2.62987E-05
0.0101238 , 6.13083E-03
0.0579437 , 2.48708E-04
STOMACH
0
S.I.
9
0.000002319452 , 5.95605E+00
-0.00000258125 , 1.30481E+00
-0.00000145591 , 5.94293E+00
0.00000204386 , 1.42473E-03
0.00000374311 , 2.30152E-03
0.00000378586 , 2.30125E-04
-0.00000161905 , 3.72082E-01
-0.00000331261 , 3.63339E-01
0.00000483812 , 2.53754E-05
U.L.I.
9
-0.018145365303 , 1.80353E+00
0.00330195 , 3.55146E-01
0.000017873 , 1.90398E-03
-0.00000119168 , 8.87723E-03
0.00000107983 , 8.80750E-03
0.0148205 , 1.25865E+00
0.000002311 , 3.69827E-04
0.00000151967 , 1.02814E-05
0.00000229533 , 6.21726E-05
L.L.I.
8
0.04111566638 , 1.79498E+00
-0.6345 , 1.16251E+00
0.583868 , 1.13111E+00
0.0000178572 , 1.77880E-03
0.00000439178 , 2.42701E-04
0.00000567754 , 2.56698E-05
0.00947443 , 3.57888E-01
0.0000139771 , 1.77924E-03
ST. WALL
```

```
0
SKIN
0
SPLEEN
0
SOFT TISS
7
2.45320282 , 1.34274E+00
0.00845648 , 3.66703E-03
2.01555 , 1.83172E-05
-2.80238 , 1.33343E+00
0.0848507 , 8.41887E-04
0.20465 , 3.51307E-01
-1.96433 , 1.94455E-05
WB
0
BLOOD
5
0.627495442 , 1.26199E+00
0.372409 , 3.55291E-01
0.000166134 , 2.78392E-04
0.000219279 , 2.67517E-05
-0.000289855 , 7.10001E-03
TAB 3
1
ICRP Pu Model
0
ADRENALS
0
BLADDER
7
-0.001165681225 , 1.19987E+01
0.000011659 , 1.41314E-02
0.00000343345 , 8.71154E-04
0.000401149 , 3.55543E-01
0.000747544 , 1.26294E+00
0.00000835345 , 2.18047E-04
0.00000106043 , 2.50778E-05
BRAIN
0
BREAST
0
```

```
G. BLADD
0
HEART CT.
0
HEART WL.
0
KIDNEYS
7
-0.004866002 , 1.26127E+00
-0.0104525 , 3.55064E-01
0.00372916 , 1.40094E-03
0.000290264 , 1.24857E-04
0.000458568 , 4.25213E-04
0.0103148 , 1.39221E-02
0.00052571 , 2.16919E-05
LIVER
5
-0.085449 , 1.34673E+00
-0.21266 , 3.76109E-01
0.239998 , 2.68343E-05
0.295656 , 1.85293E-04
-0.237545 , 3.35067E-04
MUSCLE
0
OVARIES
5
-0.0000286439 , 1.41065E+00
0.000852949 , 1.84121E-04
0.000080518 , 2.14761E-05
-0.000824848 , 1.98367E-04
-0.0000799751 , 3.89897E-01
PANCREAS
0
TESTES
5
-0.000092753 , 1.41093E+00
0.00101186 , 1.71104E-04
0.000258506 , 2.12454E-05
-0.000918511 , 2.11593E-04
-0.000259102 , 3.89940E-01
THYROID
0
```

```
R.B.M.
6
-0.0198474483 , 7.82506E-03
0.0000386163 , 1.25541E+00
0.0122563 , 3.49469E-04
0.00414815 , 1.81476E-05
0.000289932 , 3.52552E-01
0.00311445 , 8.15105E-05
BONE
0
CORT VOL
6
-0.24714990438 , 8.53426E-05
0.00000209448 , 1.26224E+00
-0.000033387 , 6.87895E-03
0.0237225 , 2.94142E-04
0.223443 , 2.73988E-05
0.0000156969 , 3.55388E-01
CORT SURF
4
-0.056006 , 1.35921E+00
-0.120006 , 2.81695E-04
-0.142614 , 3.78615E-01
0.318626 , 2.89246E-05
TRAB VOL
7
0.0000190871 , 1.25850E+00
-0.133532 , 7.76870E-04
-0.000002501 , 7.76870E-04
-0.000203435 , 9.47279E-03
0.101421 , 3.00063E-04
0.0321533 , 2.74300E-05
0.000142298 , 3.53682E-01
TRAB SURF
6
-0.0961547 , 1.26486E+00
-0.204196 , 3.56094E-01
0.173469 , 7.02621E-04
0.0588142 , 2.62987E-05
0.0101238 , 6.13083E-03
0.0579437 , 2.48708E-04
STOMACH
```

```
0
S.I.
9
0.000002319452 , 5.95605E+00
-0.00000258125 , 1.30481E+00
-0.00000145591 , 5.94293E+00
0.00000204386 , 1.42473E-03
0.00000374311 , 2.30152E-03
0.00000378586 , 2.30125E-04
-0.00000161905 , 3.72082E-01
-0.00000331261 , 3.63339E-01
0.00000483812 , 2.53754E-05
U.L.I.
9
-0.018145365303 , 1.80353E+00
0.00330195 , 3.55146E-01
0.000017873 , 1.90398E-03
-0.00000119168 , 8.87723E-03
0.00000107983 , 8.80750E-03
0.0148205 , 1.25865E+00
0.000002311 , 3.69827E-04
0.00000151967 , 1.02814E-05
0.00000229533 , 6.21726E-05
L.L.I.
8
0.04111566638 , 1.79498E+00
-0.6345 , 1.16251E+00
0.583868 , 1.13111E+00
0.0000178572 , 1.77880E-03
0.00000439178 , 2.42701E-04
0.00000567754 , 2.56698E-05
0.00947443 , 3.57888E-01
0.0000139771 , 1.77924E-03
ST. WALL
0
SKIN
0
SPLEEN
0
SOFT TISS
7
2.45320282 , 1.34274E+00
```

```
0.00845648 , 3.66703E-03
2.01555 , 1.83172E-05
-2.80238 , 1.33343E+00
0.0848507 , 8.41887E-04
0.20465 , 3.51307E-01
-1.96433 , 1.94455E-05
WB
0
BLOOD
5
0.627495442 , 1.26199E+00
0.372409 , 3.55291E-01
0.000166134 , 2.78392E-04
0.000219279 , 2.67517E-05
-0.000289855 , 7.10001E-03
TAB 4
1
ICRP Pu Model
0
ADRENALS
0
BLADDER
7
-0.001165681225 , 1.19987E+01
0.000011659 , 1.41314E-02
0.00000343345 , 8.71154E-04
0.000401149 , 3.55543E-01
0.000747544 , 1.26294E+00
0.00000835345 , 2.18047E-04
0.00000106043 , 2.50778E-05
BRAIN
0
BREAST
0
G. BLADD
0
HEART CT.
0
HEART WL.
0
KIDNEYS
7
```

```
-0.004866002 , 1.26127E+00
-0.0104525 , 3.55064E-01
0.00372916 , 1.40094E-03
0.000290264 , 1.24857E-04
0.000458568 , 4.25213E-04
0.0103148 , 1.39221E-02
0.00052571 , 2.16919E-05
LIVER
5
-0.085449 , 1.34673E+00
-0.21266 , 3.76109E-01
0.239998 , 2.68343E-05
0.295656 , 1.85293E-04
-0.237545 , 3.35067E-04
MUSCLE
0
OVARIES
5
-0.0000286439 , 1.41065E+00
0.000852949 , 1.84121E-04
0.000080518 , 2.14761E-05
-0.000824848 , 1.98367E-04
-0.0000799751 , 3.89897E-01
PANCREAS
0
TESTES
5
-0.000092753 , 1.41093E+00
0.00101186 , 1.71104E-04
0.000258506 , 2.12454E-05
-0.000918511 , 2.11593E-04
-0.000259102 , 3.89940E-01
THYROID
0
R.B.M.
6
-0.0198474483 , 7.82506E-03
0.0000386163 , 1.25541E+00
0.0122563 , 3.49469E-04
0.00414815 , 1.81476E-05
0.000289932 , 3.52552E-01
0.00311445 , 8.15105E-05
```

```
BONE
0
CORT VOL
6
-0.24714990438 , 8.53426E-05
0.00000209448 , 1.26224E+00
-0.000033387 , 6.87895E-03
0.0237225 , 2.94142E-04
0.223443 , 2.73988E-05
0.0000156969 , 3.55388E-01
CORT SURF
4
-0.056006 , 1.35921E+00
-0.120006 , 2.81695E-04
-0.142614 , 3.78615E-01
0.318626 , 2.89246E-05
TRAB VOL
7
0.0000190871 , 1.25850E+00
-0.133532 , 7.76870E-04
-0.000002501 , 7.76870E-04
-0.000203435 , 9.47279E-03
0.101421 , 3.00063E-04
0.0321533 , 2.74300E-05
0.000142298 , 3.53682E-01
TRAB SURF
6
-0.0961547 , 1.26486E+00
-0.204196 , 3.56094E-01
0.173469 , 7.02621E-04
0.0588142 , 2.62987E-05
0.0101238 , 6.13083E-03
0.0579437 , 2.48708E-04
STOMACH
0
S.I.
9
0.000002319452 , 5.95605E+00
-0.00000258125 , 1.30481E+00
-0.00000145591 , 5.94293E+00
0.00000204386 , 1.42473E-03
0.00000374311 , 2.30152E-03
```

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0.00000378586 , 2.30125E-04
-0.00000161905 , 3.72082E-01
-0.00000331261 , 3.63339E-01
0.000000483812 , 2.53754E-05
U.L.I.
9
-0.018145365303 , 1.80353E+00
0.00330195 , 3.55146E-01
0.000017873 , 1.90398E-03
-0.00000119168 , 8.87723E-03
0.00000107983 , 8.80750E-03
0.0148205 , 1.25865E+00
0.000002311 , 3.69827E-04
0.00000151967 , 1.02814E-05
0.00000229533 , 6.21726E-05
L.L.I.
8
0.04111566638 , 1.79498E+00
-0.6345 , 1.16251E+00
0.583868 , 1.13111E+00
0.0000178572 , 1.77880E-03
0.00000439178 , 2.42701E-04
0.00000567754 , 2.56698E-05
0.00947443 , 3.57888E-01
0.0000139771 , 1.77924E-03
ST. WALL
0
SKIN
0
SPLEEN
0
SOFT TISS
7
2.45320282 , 1.34274E+00
0.00845648 , 3.66703E-03
2.01555 , 1.83172E-05
-2.80238 , 1.33343E+00
0.0848507 , 8.41887E-04
0.20465 , 3.51307E-01
-1.96433 , 1.94455E-05
WB
0
```

```
BLOOD
5
0.627495442 , 1.26199E+00
0.372409 , 3.55291E-01
0.000166134 , 2.78392E-04
0.000219279 , 2.67517E-05
-0.000289855 , 7.10001E-03
TAB 5
1
ICRP Pu Model
0
ADRENALS
0
BLADDER
7
-0.001165681225 , 1.19987E+01
0.000011659 , 1.41314E-02
0.00000343345 , 8.71154E-04
0.000401149 , 3.55543E-01
0.000747544 , 1.26294E+00
0.00000835345 , 2.18047E-04
0.00000106043 , 2.50778E-05
BRAIN
0
BREAST
0
G. BLADD
0
HEART CT.
0
HEART WL.
0
KIDNEYS
7
-0.004866002 , 1.26127E+00
-0.0104525 , 3.55064E-01
0.00372916 , 1.40094E-03
0.000290264 , 1.24857E-04
0.000458568 , 4.25213E-04
0.0103148 , 1.39221E-02
0.00052571 , 2.16919E-05
LIVER
```

```
5
-0.085449 , 1.34673E+00
-0.21266 , 3.76109E-01
0.239998 , 2.68343E-05
0.295656 , 1.85293E-04
-0.237545 , 3.35067E-04
MUSCLE
0
OVARIES
5
-0.0000286439 , 1.41065E+00
0.000852949 , 1.84121E-04
0.000080518 , 2.14761E-05
-0.000824848 , 1.98367E-04
-0.0000799751 , 3.89897E-01
PANCREAS
0
TESTES
5
-0.000092753 , 1.41093E+00
0.00101186 , 1.71104E-04
0.000258506 , 2.12454E-05
-0.000918511 , 2.11593E-04
-0.000259102 , 3.89940E-01
THYROID
0
R.B.M.
6
-0.0198474483 , 7.82506E-03
0.0000386163 , 1.25541E+00
0.0122563 , 3.49469E-04
0.00414815 , 1.81476E-05
0.000289932 , 3.52552E-01
0.00311445 , 8.15105E-05
BONE
0
CORT VOL
6
-0.24714990438 , 8.53426E-05
0.00000209448 , 1.26224E+00
-0.000033387 , 6.87895E-03
0.0237225 , 2.94142E-04
```

```
0.223443 , 2.73988E-05
0.0000156969 , 3.55388E-01
CORT SURF
4
-0.056006 , 1.35921E+00
-0.120006 , 2.81695E-04
-0.142614 , 3.78615E-01
0.318626 , 2.89246E-05
TRAB VOL
7
0.0000190871 , 1.25850E+00
-0.133532 , 7.76870E-04
-0.000002501 , 7.76870E-04
-0.000203435 , 9.47279E-03
0.101421 , 3.00063E-04
0.0321533 , 2.74300E-05
0.000142298 , 3.53682E-01
TRAB SURF
6
-0.0961547 , 1.26486E+00
-0.204196 , 3.56094E-01
0.173469 , 7.02621E-04
0.0588142 , 2.62987E-05
0.0101238 , 6.13083E-03
0.0579437 , 2.48708E-04
STOMACH
0
S.I.
9
0.000002319452 , 5.95605E+00
-0.00000258125 , 1.30481E+00
-0.00000145591 , 5.94293E+00
0.00000204386 , 1.42473E-03
0.00000374311 , 2.30152E-03
0.00000378586 , 2.30125E-04
-0.00000161905 , 3.72082E-01
-0.00000331261 , 3.63339E-01
0.000000483812 , 2.53754E-05
U.L.I.
9
-0.018145365303 , 1.80353E+00
0.00330195 , 3.55146E-01
```

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0.000017873 , 1.90398E-03
-0.00000119168 , 8.87723E-03
0.00000107983 , 8.80750E-03
0.0148205 , 1.25865E+00
0.000002311 , 3.69827E-04
0.00000151967 , 1.02814E-05
0.00000229533 , 6.21726E-05
L.L.I.
8
0.04111566638 , 1.79498E+00
-0.6345 , 1.16251E+00
0.583868 , 1.13111E+00
0.0000178572 , 1.77880E-03
0.00000439178 , 2.42701E-04
0.00000567754 , 2.56698E-05
0.00947443 , 3.57888E-01
0.0000139771 , 1.77924E-03
ST. WALL
0
SKIN
0
SPLEEN
0
SOFT TISS
7
2.45320282 , 1.34274E+00
0.00845648 , 3.66703E-03
2.01555 , 1.83172E-05
-2.80238 , 1.33343E+00
0.0848507 , 8.41887E-04
0.20465 , 3.51307E-01
-1.96433 , 1.94455E-05
WB
0
BLOOD
5
0.627495442 , 1.26199E+00
0.372409 , 3.55291E-01
0.000166134 , 2.78392E-04
0.000219279 , 2.67517E-05
-0.000289855 , 7.10001E-03
TAB 6
```

```
1
ICRP Pu Model
0
ADRENALS
0
BLADDER
7
-0.001165681225 , 1.19987E+01
0.000011659 , 1.41314E-02
0.00000343345 , 8.71154E-04
0.000401149 , 3.55543E-01
0.000747544 , 1.26294E+00
0.00000835345 , 2.18047E-04
0.00000106043 , 2.50778E-05
BRAIN
0
BREAST
0
G. BLADD
0
HEART CT.
0
HEART WL.
0
KIDNEYS
7
-0.004866002 , 1.26127E+00
-0.0104525 , 3.55064E-01
0.00372916 , 1.40094E-03
0.000290264 , 1.24857E-04
0.000458568 , 4.25213E-04
0.0103148 , 1.39221E-02
0.00052571 , 2.16919E-05
LIVER
5
-0.085449 , 1.34673E+00
-0.21266 , 3.76109E-01
0.239998 , 2.68343E-05
0.295656 , 1.85293E-04
-0.237545 , 3.35067E-04
MUSCLE
0
```

```
OVARIES
5
-0.0000286439 , 1.41065E+00
0.000852949 , 1.84121E-04
0.000080518 , 2.14761E-05
-0.000824848 , 1.98367E-04
-0.0000799751 , 3.89897E-01
PANCREAS
0
TESTES
5
-0.000092753 , 1.41093E+00
0.00101186 , 1.71104E-04
0.000258506 , 2.12454E-05
-0.000918511 , 2.11593E-04
-0.000259102 , 3.89940E-01
THYROID
0
R.B.M.
6
-0.0198474483 , 7.82506E-03
0.0000386163 , 1.25541E+00
0.0122563 , 3.49469E-04
0.00414815 , 1.81476E-05
0.000289932 , 3.52552E-01
0.00311445 , 8.15105E-05
BONE
0
CORT VOL
6
-0.24714990438 , 8.53426E-05
0.00000209448 , 1.26224E+00
-0.000033387 , 6.87895E-03
0.0237225 , 2.94142E-04
0.223443 , 2.73988E-05
0.0000156969 , 3.55388E-01
CORT SURF
4
-0.056006 , 1.35921E+00
-0.120006 , 2.81695E-04
-0.142614 , 3.78615E-01
0.318626 , 2.89246E-05
```

```
TRAB VOL
7
0.0000190871 , 1.25850E+00
-0.133532 , 7.76870E-04
-0.000002501 , 7.76870E-04
-0.000203435 , 9.47279E-03
0.101421 , 3.00063E-04
0.0321533 , 2.74300E-05
0.000142298 , 3.53682E-01
TRAB SURF
6
-0.0961547 , 1.26486E+00
-0.204196 , 3.56094E-01
0.173469 , 7.02621E-04
0.0588142 , 2.62987E-05
0.0101238 , 6.13083E-03
0.0579437 , 2.48708E-04
STOMACH
0
S.I.
9
0.000002319452 , 5.95605E+00
-0.00000258125 , 1.30481E+00
-0.00000145591 , 5.94293E+00
0.00000204386 , 1.42473E-03
0.00000374311 , 2.30152E-03
0.00000378586 , 2.30125E-04
-0.00000161905 , 3.72082E-01
-0.00000331261 , 3.63339E-01
0.00000483812 , 2.53754E-05
U.L.I.
9
-0.018145365303 , 1.80353E+00
0.00330195 , 3.55146E-01
0.000017873 , 1.90398E-03
-0.00000119168 , 8.87723E-03
0.00000107983 , 8.80750E-03
0.0148205 , 1.25865E+00
0.000002311 , 3.69827E-04
0.00000151967 , 1.02814E-05
0.00000229533 , 6.21726E-05
L.L.I.
```

```
8
0.04111566638 , 1.79498E+00
-0.6345 , 1.16251E+00
0.583868 , 1.13111E+00
0.0000178572 , 1.77880E-03
0.00000439178 , 2.42701E-04
0.00000567754 , 2.56698E-05
0.00947443 , 3.57888E-01
0.0000139771 , 1.77924E-03
ST. WALL
0
SKIN
0
SPLEEN
0
SOFT TISS
7
2.45320282 , 1.34274E+00
0.00845648 , 3.66703E-03
2.01555 , 1.83172E-05
-2.80238 , 1.33343E+00
0.0848507 , 8.41887E-04
0.20465 , 3.51307E-01
-1.96433 , 1.94455E-05
WB
0
BLOOD
5
0.627495442 , 1.26199E+00
0.372409 , 3.55291E-01
0.000166134 , 2.78392E-04
0.000219279 , 2.67517E-05
-0.000289855 , 7.10001E-03
TAB 7
1
ICRP Pu Model
0
ADRENALS
0
BLADDER
7
-0.001165681225 , 1.19987E+01
```

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0.000011659 , 1.41314E-02
0.00000343345 , 8.71154E-04
0.000401149 , 3.55543E-01
0.000747544 , 1.26294E+00
0.00000835345 , 2.18047E-04
0.00000106043 , 2.50778E-05
BRAIN
0
BREAST
0
G. BLADD
0
HEART CT.
0
HEART WL.
0
KIDNEYS
7
-0.004866002 , 1.26127E+00
-0.0104525 , 3.55064E-01
0.00372916 , 1.40094E-03
0.000290264 , 1.24857E-04
0.000458568 , 4.25213E-04
0.0103148 , 1.39221E-02
0.00052571 , 2.16919E-05
LIVER
5
-0.085449 , 1.34673E+00
-0.21266 , 3.76109E-01
0.239998 , 2.68343E-05
0.295656 , 1.85293E-04
-0.237545 , 3.35067E-04
MUSCLE
0
OVARIES
5
-0.0000286439 , 1.41065E+00
0.000852949 , 1.84121E-04
0.000080518 , 2.14761E-05
-0.000824848 , 1.98367E-04
-0.0000799751 , 3.89897E-01
PANCREAS
```

```
0
TESTES
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0.00101186 , 1.71104E-04
0.000258506 , 2.12454E-05
-0.000918511 , 2.11593E-04
-0.000259102 , 3.89940E-01
THYROID
0
R.B.M.
6
-0.0198474483 , 7.82506E-03
0.0000386163 , 1.25541E+00
0.0122563 , 3.49469E-04
0.00414815 , 1.81476E-05
0.000289932 , 3.52552E-01
0.00311445 , 8.15105E-05
BONE
0
CORT VOL
6
-0.24714990438 , 8.53426E-05
0.00000209448 , 1.26224E+00
-0.000033387 , 6.87895E-03
0.0237225 , 2.94142E-04
0.223443 , 2.73988E-05
0.0000156969 , 3.55388E-01
CORT SURF
4
-0.056006 , 1.35921E+00
-0.120006 , 2.81695E-04
-0.142614 , 3.78615E-01
0.318626 , 2.89246E-05
TRAB VOL
7
0.0000190871 , 1.25850E+00
-0.133532 , 7.76870E-04
-0.000002501 , 7.76870E-04
-0.000203435 , 9.47279E-03
0.101421 , 3.00063E-04
0.0321533 , 2.74300E-05
```

```
0.000142298 , 3.53682E-01
TRAB SURF
6
-0.0961547 , 1.26486E+00
-0.204196 , 3.56094E-01
0.173469 , 7.02621E-04
0.0588142 , 2.62987E-05
0.0101238 , 6.13083E-03
0.0579437 , 2.48708E-04
STOMACH
0
S.I.
9
0.000002319452 , 5.95605E+00
-0.00000258125 , 1.30481E+00
-0.00000145591 , 5.94293E+00
0.00000204386 , 1.42473E-03
0.00000374311 , 2.30152E-03
0.00000378586 , 2.30125E-04
-0.00000161905 , 3.72082E-01
-0.00000331261 , 3.63339E-01
0.00000483812 , 2.53754E-05
U.L.I.
9
-0.018145365303 , 1.80353E+00
0.00330195 , 3.55146E-01
0.000017873 , 1.90398E-03
-0.00000119168 , 8.87723E-03
0.000000107983 , 8.80750E-03
0.0148205 , 1.25865E+00
0.000002311 , 3.69827E-04
0.00000151967 , 1.02814E-05
0.00000229533 , 6.21726E-05
L.L.I.
8
0.04111566638 , 1.79498E+00
-0.6345 , 1.16251E+00
0.583868 , 1.13111E+00
0.0000178572 , 1.77880E-03
0.00000439178 , 2.42701E-04
0.00000567754 , 2.56698E-05
0.00947443 , 3.57888E-01
```

```
0.0000139771 , 1.77924E-03
ST. WALL
0
SKIN
0
SPLEEN
0
SOFT TISS
7
2.45320282 , 1.34274E+00
0.00845648 , 3.66703E-03
2.01555 , 1.83172E-05
-2.80238 , 1.33343E+00
0.0848507 , 8.41887E-04
0.20465 , 3.51307E-01
-1.96433 , 1.94455E-05
WΒ
0
BLOOD
5
0.627495442 , 1.26199E+00
0.372409 , 3.55291E-01
0.000166134 , 2.78392E-04
0.000219279 , 2.67517E-05
-0.000289855 , 7.10001E-03
TAB 8
1
ICRP Pu Model
0
ADRENALS
0
BLADDER
7
-0.001165681225 , 1.19987E+01
0.000011659 , 1.41314E-02
0.00000343345 , 8.71154E-04
0.000401149 , 3.55543E-01
0.000747544 , 1.26294E+00
0.00000835345 , 2.18047E-04
0.00000106043 , 2.50778E-05
BRAIN
0
```

```
BREAST
0
G. BLADD
0
HEART CT.
0
HEART WL.
0
KIDNEYS
7
-0.004866002 , 1.26127E+00
-0.0104525 , 3.55064E-01
0.00372916 , 1.40094E-03
0.000290264 , 1.24857E-04
0.000458568 , 4.25213E-04
0.0103148 , 1.39221E-02
0.00052571 , 2.16919E-05
LIVER
5
-0.085449 , 1.34673E+00
-0.21266 , 3.76109E-01
0.239998 , 2.68343E-05
0.295656 , 1.85293E-04
-0.237545 , 3.35067E-04
MUSCLE
0
OVARIES
5
-0.0000286439 , 1.41065E+00
0.000852949 , 1.84121E-04
0.000080518 , 2.14761E-05
-0.000824848 , 1.98367E-04
-0.0000799751 , 3.89897E-01
PANCREAS
0
TESTES
5
-0.000092753 , 1.41093E+00
0.00101186 , 1.71104E-04
0.000258506 , 2.12454E-05
-0.000918511 , 2.11593E-04
-0.000259102 , 3.89940E-01
```

```
THYROID
0
R.B.M.
6
-0.0198474483 , 7.82506E-03
0.0000386163 , 1.25541E+00
0.0122563 , 3.49469E-04
0.00414815 , 1.81476E-05
0.000289932 , 3.52552E-01
0.00311445 , 8.15105E-05
BONE
0
CORT VOL
6
-0.24714990438 , 8.53426E-05
0.00000209448 , 1.26224E+00
-0.000033387 , 6.87895E-03
0.0237225 , 2.94142E-04
0.223443 , 2.73988E-05
0.0000156969 , 3.55388E-01
CORT SURF
4
-0.056006 , 1.35921E+00
-0.120006 , 2.81695E-04
-0.142614 , 3.78615E-01
0.318626 , 2.89246E-05
TRAB VOL
7
0.0000190871 , 1.25850E+00
-0.133532 , 7.76870E-04
-0.000002501 , 7.76870E-04
-0.000203435 , 9.47279E-03
0.101421 , 3.00063E-04
0.0321533 , 2.74300E-05
0.000142298 , 3.53682E-01
TRAB SURF
6
-0.0961547 , 1.26486E+00
-0.204196 , 3.56094E-01
0.173469 , 7.02621E-04
0.0588142 , 2.62987E-05
0.0101238 , 6.13083E-03
```

```
0.0579437 , 2.48708E-04
STOMACH
0
S.I.
9
0.000002319452 , 5.95605E+00
-0.00000258125 , 1.30481E+00
-0.00000145591 , 5.94293E+00
0.00000204386 , 1.42473E-03
0.00000374311 , 2.30152E-03
0.00000378586 , 2.30125E-04
-0.00000161905 , 3.72082E-01
-0.00000331261 , 3.63339E-01
0.000000483812 , 2.53754E-05
U.L.I.
9
-0.018145365303 , 1.80353E+00
0.00330195 , 3.55146E-01
0.000017873 , 1.90398E-03
-0.00000119168 , 8.87723E-03
0.00000107983 , 8.80750E-03
0.0148205 , 1.25865E+00
0.000002311 , 3.69827E-04
0.00000151967 , 1.02814E-05
0.00000229533 , 6.21726E-05
L.L.I.
8
0.04111566638 , 1.79498E+00
-0.6345 , 1.16251E+00
0.583868 , 1.13111E+00
0.0000178572 , 1.77880E-03
0.00000439178 , 2.42701E-04
0.00000567754 , 2.56698E-05
0.00947443 , 3.57888E-01
0.0000139771 , 1.77924E-03
ST. WALL
0
SKIN
0
SPLEEN
0
SOFT TISS
```

```
7
2.45320282 , 1.34274E+00
0.00845648 , 3.66703E-03
2.01555 , 1.83172E-05
-2.80238 , 1.33343E+00
0.0848507 , 8.41887E-04
0.20465 , 3.51307E-01
-1.96433 , 1.94455E-05
WB
0
BLOOD
5
0.627495442 , 1.26199E+00
0.372409 , 3.55291E-01
0.000166134 , 2.78392E-04
0.000219279 , 2.67517E-05
-0.000289855 , 7.10001E-03
TAB 9
1
ICRP Pu Model
0
ADRENALS
0
BLADDER
7
-0.001165681225 , 1.19987E+01
0.000011659 , 1.41314E-02
0.00000343345 , 8.71154E-04
0.000401149 , 3.55543E-01
0.000747544 , 1.26294E+00
0.00000835345 , 2.18047E-04
0.00000106043 , 2.50778E-05
BRAIN
0
BREAST
0
G. BLADD
0
HEART CT.
0
HEART WL.
0
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KIDNEYS
7
-0.004866002 , 1.26127E+00
-0.0104525 , 3.55064E-01
0.00372916 , 1.40094E-03
0.000290264 , 1.24857E-04
0.000458568 , 4.25213E-04
0.0103148 , 1.39221E-02
0.00052571 , 2.16919E-05
LIVER
5
-0.085449 , 1.34673E+00
-0.21266 , 3.76109E-01
0.239998 , 2.68343E-05
0.295656 , 1.85293E-04
-0.237545 , 3.35067E-04
MUSCLE
0
OVARIES
5
-0.0000286439 , 1.41065E+00
0.000852949 , 1.84121E-04
0.000080518 , 2.14761E-05
-0.000824848 , 1.98367E-04
-0.0000799751 , 3.89897E-01
PANCREAS
0
TESTES
5
-0.000092753 , 1.41093E+00
0.00101186 , 1.71104E-04
0.000258506 , 2.12454E-05
-0.000918511 , 2.11593E-04
-0.000259102 , 3.89940E-01
THYROID
0
R.B.M.
6
-0.0198474483 , 7.82506E-03
0.0000386163 , 1.25541E+00
0.0122563 , 3.49469E-04
0.00414815 , 1.81476E-05
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0.000289932 , 3.52552E-01
0.00311445 , 8.15105E-05
BONE
0
CORT VOL
6
-0.24714990438 , 8.53426E-05
0.00000209448 , 1.26224E+00
-0.000033387 , 6.87895E-03
0.0237225 , 2.94142E-04
0.223443 , 2.73988E-05
0.0000156969 , 3.55388E-01
CORT SURF
4
-0.056006 , 1.35921E+00
-0.120006 , 2.81695E-04
-0.142614 , 3.78615E-01
0.318626 , 2.89246E-05
TRAB VOL
7
0.0000190871 , 1.25850E+00
-0.133532 , 7.76870E-04
-0.000002501 , 7.76870E-04
-0.000203435 , 9.47279E-03
0.101421 , 3.00063E-04
0.0321533 , 2.74300E-05
0.000142298 , 3.53682E-01
TRAB SURF
6
-0.0961547 , 1.26486E+00
-0.204196 , 3.56094E-01
0.173469 , 7.02621E-04
0.0588142 , 2.62987E-05
0.0101238 , 6.13083E-03
0.0579437 , 2.48708E-04
STOMACH
0
S.I.
9
0.000002319452 , 5.95605E+00
-0.00000258125 , 1.30481E+00
-0.00000145591 , 5.94293E+00
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0.00000204386 , 1.42473E-03
0.00000374311 , 2.30152E-03
0.00000378586 , 2.30125E-04
-0.00000161905 , 3.72082E-01
-0.00000331261 , 3.63339E-01
0.000000483812 , 2.53754E-05
U.L.I.
9
-0.018145365303 , 1.80353E+00
0.00330195 , 3.55146E-01
0.000017873 , 1.90398E-03
-0.00000119168 , 8.87723E-03
0.000000107983 , 8.80750E-03
0.0148205 , 1.25865E+00
0.000002311 , 3.69827E-04
0.00000151967 , 1.02814E-05
0.00000229533 , 6.21726E-05
L.L.I.
8
0.04111566638 , 1.79498E+00
-0.6345 , 1.16251E+00
0.583868 , 1.13111E+00
0.0000178572 , 1.77880E-03
0.00000439178 , 2.42701E-04
0.00000567754 , 2.56698E-05
0.00947443 , 3.57888E-01
0.0000139771 , 1.77924E-03
ST. WALL
0
SKIN
0
SPLEEN
0
SOFT TISS
7
2.45320282 , 1.34274E+00
0.00845648 , 3.66703E-03
2.01555 , 1.83172E-05
-2.80238 , 1.33343E+00
0.0848507 , 8.41887E-04
0.20465 , 3.51307E-01
-1.96433 , 1.94455E-05
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WB
0
BLOOD
5
0.627495442 \ , \ 1.26199E\!+\!00
0.372409 , 3.55291E-01
0.000166134 , 2.78392E-04
0.000219279 , 2.67517E-05
-0.000289855 , 7.10001E-03
TAB 10
1
ICRP Pu Model
0
ADRENALS
0
BLADDER
7
-0.001165681225 , 1.19987E+01
0.000011659 , 1.41314E-02
0.00000343345 , 8.71154E-04
0.000401149 , 3.55543E-01
0.000747544 , 1.26294E+00
0.00000835345 , 2.18047E-04
0.00000106043 , 2.50778E-05
BRAIN
0
BREAST
0
G. BLADD
0
HEART CT.
0
HEART WL.
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KIDNEYS
7
-0.004866002 , 1.26127E+00
-0.0104525 , 3.55064E-01
0.00372916 , 1.40094E-03
0.000290264 , 1.24857E-04
0.000458568 , 4.25213E-04
0.0103148 , 1.39221E-02
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0.00052571 , 2.16919E-05
LIVER
5
-0.085449 , 1.34673E+00
-0.21266 , 3.76109E-01
0.239998 , 2.68343E-05
0.295656 , 1.85293E-04
-0.237545 , 3.35067E-04
MUSCLE
0
OVARIES
5
-0.0000286439 , 1.41065E+00
0.000852949 , 1.84121E-04
0.000080518 , 2.14761E-05
-0.000824848 , 1.98367E-04
-0.0000799751 , 3.89897E-01
PANCREAS
0
TESTES
5
-0.000092753 , 1.41093E+00
0.00101186 , 1.71104E-04
0.000258506 , 2.12454E-05
-0.000918511 , 2.11593E-04
-0.000259102 , 3.89940E-01
THYROID
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R.B.M.
6
-0.0198474483 , 7.82506E-03
0.0000386163 , 1.25541E+00
0.0122563 , 3.49469E-04
0.00414815 , 1.81476E-05
0.000289932 , 3.52552E-01
0.00311445 , 8.15105E-05
BONE
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CORT VOL
6
-0.24714990438 , 8.53426E-05
0.00000209448 , 1.26224E+00
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-0.000033387 , 6.87895E-03
0.0237225 , 2.94142E-04
0.223443 , 2.73988E-05
0.0000156969 , 3.55388E-01
CORT SURF
4
-0.056006 , 1.35921E+00
-0.120006 , 2.81695E-04
-0.142614 , 3.78615E-01
0.318626 , 2.89246E-05
TRAB VOL
7
0.0000190871 , 1.25850E+00
-0.133532 , 7.76870E-04
-0.000002501 , 7.76870E-04
-0.000203435 , 9.47279E-03
0.101421 , 3.00063E-04
0.0321533 , 2.74300E-05
0.000142298 , 3.53682E-01
TRAB SURF
6
-0.0961547 , 1.26486E+00
-0.204196 , 3.56094E-01
0.173469 , 7.02621E-04
0.0588142 , 2.62987E-05
0.0101238 , 6.13083E-03
0.0579437 , 2.48708E-04
STOMACH
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S.I.
9
0.000002319452 , 5.95605E+00
-0.00000258125 , 1.30481E+00
-0.00000145591 , 5.94293E+00
0.00000204386 , 1.42473E-03
0.00000374311 , 2.30152E-03
0.00000378586 , 2.30125E-04
-0.00000161905 , 3.72082E-01
-0.00000331261 , 3.63339E-01
0.00000483812 , 2.53754E-05
U.L.I.
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9

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-0.018145365303 , 1.80353E+00
0.00330195 , 3.55146E-01
0.000017873 , 1.90398E-03
-0.00000119168 , 8.87723E-03
0.00000107983 , 8.80750E-03
0.0148205 , 1.25865E+00
0.000002311 , 3.69827E-04
0.00000151967 , 1.02814E-05
0.00000229533 , 6.21726E-05
L.L.I.
8
0.04111566638 , 1.79498E+00
-0.6345 , 1.16251E+00
0.583868 , 1.13111E+00
0.0000178572 , 1.77880E-03
0.00000439178 , 2.42701E-04
0.00000567754 , 2.56698E-05
0.00947443 , 3.57888E-01
0.0000139771 , 1.77924E-03
ST. WALL
0
SKIN
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SPLEEN
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SOFT TISS
7
2.45320282 , 1.34274E+00
0.00845648 , 3.66703E-03
2.01555 , 1.83172E-05
-2.80238 , 1.33343E+00
0.0848507 , 8.41887E-04
0.20465 , 3.51307E-01
-1.96433 , 1.94455E-05
WB
0
BLOOD
5
0.627495442 , 1.26199E+00
0.372409 , 3.55291E-01
0.000166134 , 2.78392E-04
0.000219279 , 2.67517E-05
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```
-0.000289855 , 7.10001E-03
PARAMETERS DEPOSITION
ICRP Defaults
light
AMAD
5
2.4977233
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ICRP Defaults
light
AMAD
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ICRP Defaults
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AMAD
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ICRP Defaults
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AMAD
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ICRP Defaults
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AMAD
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ICRP Defaults
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AMAD
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ICRP Defaults
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PARAMETERS WOUND
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FITTING BIOASSAY QUANTITY

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DOSE-Values2

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7.8681E-04, 4.6102E-04, 2.4008E-04, 1.4879E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 007.8682E-04, 4.6103E-04, 2.4009E-04, 1.4879E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00 7.8679E-04, 4.6101E-04, 2.4008E-04, 1.4879E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00 7.8678E-04, 4.6100E-04, 2.4007E-04, 1.4879E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 007.8686E-04, 4.6105E-04, 2.4010E-04, 1.4880E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00 7.8678E-04, 4.6100E-04, 2.4007E-04, 1.4879E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00 1.9582E-03, 1.5582E-03, 8.2708E-04, 4.3435E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00 9.5343E-02, 6.3226E-02, 3.2979E-02, 1.9155E-01, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00 7.8679E-04, 4.6101E-04, 2.4008E-04, 1.4879E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00 5.9328E-03, 3.8495E-03, 2.0046E-03, 1.1787E-02, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00 7.8679E-04, 4.6101E-04, 2.4008E-04, 1.4879E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 006.0467E-03, 3.9233E-03, 2.0430E-03, 1.2013E-02, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00 7.8678E-04, 4.6100E-04, 2.4007E-04, 1.4879E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 002.2335E-02, 1.7237E-02, 9.1197E-03, 4.8692E-02, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 004.5125E-01, 2.8715E-01, 1.4968E-01, 8.8808E-01, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00 7.8704E-04, 4.6129E-04, 2.4010E-04, 1.4884E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 007.8745E-04, 4.6172E-04, 2.4013E-04, 1.4893E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00 7.9089E-04, 4.6536E-04, 2.4046E-04, 1.4967E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00 7.9884E-04, 4.7379E-04, 2.4119E-04, 1.5138E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00 7.8678E-04, 4.6100E-04, 2.4007E-04, 1.4879E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00 7.8678E-04, 4.6100E-04, 2.4007E-04, 1.4879E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 007.8678E-04, 4.6100E-04, 2.4007E-04, 1.4879E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 007.8678E-04, 4.6100E-04, 2.4007E-04, 1.4879E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00

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0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00 0.0000E + 00,0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00 0.0000E + 00, 0.0000E + 00,0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00 2.3603E-05, 1.3830E-05, 7.2021E-06, 4.4636E-05, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00 2.6802E-03, 2.0684E-03, 1.0944E-03, 5.8430E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 001.3538E-02, 8.6145E-03, 4.4904E-03, 2.6642E-02, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 000.0000E + 00, 0.0000E + 00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00 0.0000E + 00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00 4.7453E-05, 2.7922E-05, 1.4428E-05, 8.9803E-05, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 004.7930E-05, 2.8427E-05, 1.4471E-05, 9.0829E-05, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00 0.0000E + 00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00 0.0000E + 00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00 0.0000E + 00, 0.0000E+00, 0.0000E + 00,0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00 0.0000E + 00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00 4.5347E-04, 4.6020E-04, 1.8078E-05, 9.3175E-04, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00 1.4074E-03, 1.4532E-03, 2.3174E-04, 3.0923E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00 0.0000E + 00, 0.0000E + 00,0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00 0.0000E + 00, 0.0000E + 00, 0.0000E + 00,0.0000E + 00, 0.0000E+00, 0.0000E + 00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00 0.0000E + 00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00 0.0000E + 00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00 0.0000E + 00, 0.0000E+00, 0.0000E + 00,0.0000E + 00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00 0.0000E + 00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00 0.0000E + 00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00 0.0000E+00, 0.0000E + 00,0.0000E+00, 0.0000E+00, 0.0000E + 00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00 0.0000E + 00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00

1.5117E-03, 9.8083E-04, 5.1075E-04, 3.0033E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00

0.0000E+00, 0.0000E+00

0.0000E+00, 0.0000E+00

2.5665E-02, 1.7604E-02, 8.4458E-03, 5.1715E-02, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00

Intake Regime 1: Remainder organs are: Liver; ET; Kidneys; L.L.I.; U.L.I.; Intake Regime 2: Remainder organs are: Liver; ET; Kidneys; L.L.I.; U.L.I.; Intake Regime 3: Remainder organs are: Liver; Kidneys; ET; L.L.I.; U.L.I.; Intake Regime 4: Remainder organs are: Liver; ET; Kidneys; L.L.I.; U.L.I.; Intake Regime 4: Remainder organs are: Liver; ET; Kidneys; L.L.I.; U.L.I.;

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5.5989E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00	1.2586E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	6.8575E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,
5.5992E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00	1.2573E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	6.8565E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00,	0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,
5.5989E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00	1.2578E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	6.8567E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E +00, 0.0000E +00, 0.0000E +00, 0.0000E +00, 0.0000E +00,
5.5988E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00	1.2573E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	6.8561E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00,	0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E +00, 0.0000E +00, 0.0000E +00, 0.0000E +00, 0.0000E +00,
5.5992E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00	1.2589E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	6.8580E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,
5.5989E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00	1.2577E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	6.8566E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00,	0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,
1.5542E-02, 0.0000E+00, 0.0000E+00,	5.1660E-03, 0.0000E+00, 0.0000E+00,	2.0708E-02, 0.0000E+00, 0.0000E+00,	0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E+00, 0.0000E+00, 0.0000E+00,

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0.0000E+00, 0.0000E+00, 0.0000E+00	0.0000E+00, 0.0000E+00,	0.0000E+00, 0.0000E+00,	0.0000E+00, 0.0000E+00,	0.0000E+00, 0.0000E+00,	0.0000E+00, 0.0000E+00,
7.1500E-01, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00	6.1955E-02, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	7.7696E-01, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00,	0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00,	0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00,
5.5989E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00	1.2576E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	6.8565E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00,	0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,
4.4120E-02, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00	1.7212E-02, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	6.1333E-02, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,
5.5989E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00	1.2580E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	6.8569E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00,
4.4968E-02, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00	1.7079E-02, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	6.2047E-02, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00,	0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00,	0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00,
5.5988E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00	1.2574E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	6.8562E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00,	0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00,
1.7652E-01, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00	3.3699E-02, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	2.1022E-01, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00,	0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,
3.3229E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00	8.6368E-01, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	4.1866E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00,	0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,
5.6007E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	1.2579E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	6.8586E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00,	0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00,

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5.6036E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00	1.2588E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	6.8624E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00,	0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00,
5.6278E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00	1.2650E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	6.8928E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00,	0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00,	0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00,
5.6840E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00	1.2793E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	6.9633E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00,	0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00,	0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00,
5.5988E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00	1.2572E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	6.8560E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00,
5.5988E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00	1.2574E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	6.8562E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00,	0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00,
5.5988E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00	1.2574E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	6.8562E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00,	0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00,
5.5988E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00	1.2574E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	6.8562E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00,	0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00,	0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00,
5.3100E-02, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00	1.2518E-02, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	6.5618E-02, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E +00, 0.0000E +00, 0.0000E +00, 0.0000E +00, 0.0000E +00,	0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00,
7.9434E-02, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00	2.0640E-02, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	1.0007E-01, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00,
5.6521E-03,	1.2712E-03,	6.9233E-03,	0.0000E+00,	0.0000E+00,	0.0000E+00,

0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00	0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00,	0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00,	0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00,	0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00,	0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,
1.0996E-02, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00	2.5451E-02, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	3.6448E-02, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00,	0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00,	0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,
5.3187E-02, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00	1.2516E-02, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	6.5703E-02, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E +00, 0.0000E +00, 0.0000E +00, 0.0000E +00, 0.0000E +00,	0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,
7.6799E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00	1.7644E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	9.4443E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E +00, 0.0000E +00, 0.0000E +00, 0.0000E +00, 0.0000E +00,	0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,
1.9189E-01, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00	5.4115E-02, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	2.4600E-01, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00,	0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,
1.8679E-02, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00	6.4367E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	2.5116E-02, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00,	0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,
9.6533E-02, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00	2.2878E-02, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	1.1941E-01, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00,	0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,
3.6682E-02, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00	8.8178E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	4.5500E-02, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00,	0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,
1.5334E-02, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00	3.6242E-03, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	1.8958E-02, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00,	0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,
5.5988E-03, 0.0000E+00, 0.0000E+00,	1.2574E-03, 0.0000E+00, 0.0000E+00,	6.8562E-03, 0.0000E+00, 0.0000E+00,	0.0000E + 00, 0.0000E + 00, 0.0000E + 00,	0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E+00, 0.0000E+00, 0.0000E+00,

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4.4968E-02, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00	1.7212E-02, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	6.2180E-02, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00,	0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,
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0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00	0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00,	0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00,	0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00,
0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00	0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00,	0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00,	0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00, 0.0000E+00,	0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00, 0.0000E + 00,
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END OF COMMENTS

Calculations Sub-panel

Calculatio	ons		
	Bioassay Calc	ulations	
	Dose Calcu	lations	

Figure 3.93. The Calculations Sub-panel.

This sub-panel provides the only **portal** between the **Main Screen** and the two "Calculations" screens:

- Bioassay Calculations **Click** this **button** to open the *Bioassay Calculations* screen (set up the **bioassay calculations**, estimate the amount(s) of **Intake(s)**, and/or predict **Bioassay Quantities**);
- <u>Dose Calculations</u> **Click** this **button** to open the *Dose Calculations* screen (set up the **dose calculations** and calculate **Doses**).

Bioassay Calculations Screen



The *Bioassay Calculations Screen* (Figure 4.1) opens when you *click* the "Bioassay Calculations" *button* (on the Main Screen).

The screen works as follows:

- You select the direction of the CALCULATION in the center of the screen. This can be from BIOASSAY QUANTITY to INTAKE(S) - the default setting, or from INTAKE(S) to BIOASSAY QUANTITY.
- 2. The **calculated** (or **hypothetical**) values of INTAKE(S) are displayed on the **left**.
- 3. The **predicted** and/or **measured** values of the BIOASSAY QUANTITY are displayed on the **right**.



Figure 4.1. The Bioassay Calculations screen.

The screen is divided into these functional parts - from the top:

- Menu Bar.
- Short-cut Icon.

Main panel:

- 1. Intake sub-panel left side
- 2. Calculation sub-panel center
- 3. Bioassay Quantity sub-panel right side.

Bottom left corner panel:

• Progress Indicator.

Bioassay Menus

The **Menu Bar**, shown at the top of the **Bioassay Calculations** window, gives the following options:

- File menu.
- Advanced menu.
- <u>Tools</u> menu.
- Help menu.

Bioassay File Menu

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Figure 4.2. Drop-down bioassay File list box.

Click File | Print to send a screen dump of the displayed Bioassay Calculations screen to your Windows® printer - *e.g.* Figure 4.3.





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File Advanced	Tools Help			
Save Quick	3 Save		Bioassay Calcula	ations
INTA	\KE	CALCU	JLATION	BIOAS
INTA IB 1 1.282E+00 Progress Indice Deposition Collating Times Bioassay Calces Current		CALCU Intakes to Bioassay Specify Times (d) [Col 1] Start Time(d) 1 Stop Time(d) 6500 Specify Collection Periods [Col 2] Calculate Bioassay Quantity [Col 3]	JLATION Bioassay to Intake Number of Times (1-200) 100 ÷ C Linear Send to all open windows C 1-2-5 mode Send> 3 Start Calculation	BIOAS: Graph C Table C Hide U Specified Time (d) Collectic period (c 1.000E+00 1.000 1.092733547E+00 1.000 1.194066606E+00 1.000 1.304796638E+00 1.000 1.425795059E+00 1.000 1.425795059E+00 1.000 1.558014093E+00 1.000 1.558014093E+00 1.000 1.959327699E+00 1.000 1.000 C Graph C Table C Hide U 1.0E+00 1.0E+00 1.0E+00 1.0E+00 1.0E+00 1.0E+00 1.0E+00 1.0E+00 1.0E+00 1.0E+00 1.0E+00 1.0E+00 1.0E+00 C Graph C Table C Hide U
			ŪK	
Pu-238	Pu Model	Max Likelihood fit		

Figure 4.3. Printed screen dump of Bioassay Calculations screen.

Figure 4.3 shows the printed image of the **Bioassay Calculations** screen with the example parameter file "**USTUR0259.ix**" loaded.

Bioassay Advanced Menu



🐴 Bioassay Calculations					
File	Advanced	Tools	Help		
E	Fitting O	ptions	Ľ		
Bioassay Options					

Figure 4.4. Advanced menu options for Bioassay Calculations -

The "Advanced" menu enables you to select from the following Advanced Dosimetry Options:

• Fitting - select from "Least Squares", "Maximum Likelihood" (the default), or "Bayesian" fitting methods (Figure 4.5). • Bioassay - enable (Figure 4.6) the special feature to calculate ingrowth of Am-241 activity in the lungs from an intake of plutonium isotopes (containing a known fraction of 241 Pu activity).

💐 Advanced Dosimetry Options	
These options should be used with extreme care	
Dose Fitting Bioassay Misc Select Fitting Method C Least Squares Maximum Likelihood C Bayesian	
<u>O</u> K <u>C</u> ancel	

Figure 4.5. Selecting Fitting options in the Advanced Dosimetry Options window.
00

Dose Fitting Bioassay Misc Ingrowth of indicator radionuclide Ingrowth of Am-241 from Pu-241
Dose Fitting Bioassay Misc Ingrowth of indicator radionuclide Ingrowth of Am-241 from Pu-241 Allow ingrowth of Am-241 from Pu-241
Ingrowth of indicator radionuclide Allow ingrowth of Am-241 from Pu-241
<u> </u>

Figure 4.6. **Enabling the** Bioassay option **to measure ingrowth of** 241 Am **activity** (from 241 Pu).

Bioassay Tools Menu



Figure 4.7. Drop-down Bioassay Tools list box.

The Bioassay Tools options are:

- **Table Tools** Enable you to open the <u>Table Tool</u> (spreadsheet-like facility) to enter and/or edit bioassay data, sample time (or date), and sample duration (for urine and feces), for any **one** of the three **Bioassay Quantity** windows (see Figure 4.8).
- **Graph Tools** Enable you to open the <u>Graph Tool</u> (graph editing facility) to specify how you want a graph to be displayed (ranges of the x- and y-axes, linear or logarithmic plots) for any **one** of the three **Bioassay Quantity** windows (see Figure 4.9).
- Change Units to Date toggle instantly between Time Units of Date or Time (d) throughout the program (all three screens) see Figure 4.10.

ions Help

💐 Bioassay Calculations							
File Adv	anced	Tools	Help				
	Гі	Tab	ole Tools	Þ	Window 1		
	U-	Gra	ph Tools	+	Window 2		
Jave	Quic	Cha	ange Units to	Date	Window 3		
	INT	AKE				CA	

Figure 4.8. Drop-down list of Bioassay Quantity windows for using Table Tools.

🍂 Bi	🐴 Bioassay Calculations							
File	Adva	anced	Tools	Help				
		Г	Tab	ole Tools	÷	·		
		U Outie	Gra	ph Tools	•		Window 1	
00	ive	Quic	Cha	ange Units to	o Date		Window 2	
INTAKE							Window 3	P/

Figure 4.9. Drop-down list of Bioassay Quantity windows for using Graph Tools.

🗳 Bi	💐 Bioassay Calculations					
File	Adva	inced	Tools	Help		
		Г	Tab	ole Tools	•	
Court Ouis		Graph Tools		→		
00	sve .	Quic	Cha	ange Units to	o Date	
INTAKE						

Figure 4.10. Toggle control to change the Time Units.

Selecting "Change Units to Date" will switch the Time Unit shown in all Bioassay Quantity tables to Date (+hh:mm) - calendar Date plus twodigit Hour and Minute values (Figure 4.11).

BIOASSAY QUANTITY						
O Graph ⊙ Table ⊂ Hide Urine 💌 tool						
Specified Date (+hh:mm)	Collection period (d)	Calculated Rate(Bq/d)	Measurement Date (+hh:mm]	^		
01/01/1971	1.000E+00	2.8681E-04	15/03/1968			
04/01/1971 16:48:00	1.000E+00	2.8674E-04	13/06/1968			
08/01/1971 07:12:00	1.000E+00	2.8667E-04	13/09/1968			
12/01/1971	1.000E+00	2.8659E-04	13/12/1968			
15/01/1971 16:48:00	1.000E+00	2.8652E-04	20/03/1969			
19/01/1971 07:12:00	1.000E+00	2.8644E-04	18/12/1969			
23/01/1971	1.000E+00	2.8637E-04	19/03/1970			
26/01/1971 16:49:00	1 000F±00	2.8635.04	18/06/1970	-		

Figure 4.11. Displaying when samples were taken as a **Date (+hh:mm)** as the alternative to the default display of **Time (d)**.

The label of the *Change Time Units* control will switch automatically once you make a change (Figure 4.12) - so that you can easily toggle back to the original *Time/Date* unit.



Figure 4.12. "*Change Units*" label switches automatically to enable toggling between *Time* and *Date*.

Bioassay Help Menu

Bioassay Calculations File Advanced Tools Help

 Image: Decumentation

 Save
 Quick Save

 About IMBA Expert

 Conditions of Use

 Help Mode

 Quick Start

Figure 4.13. Drop-down Bioassay Help list box.

The **Help** features available from the **Help Menu** in the **Bioassay Calculations** screen are the same as those available from the **Main Screen** (Figures 3.13 through 3.16). So, while setting up **Bioassay Calculations**, you do NOT have to return to the **Main Screen** to access the **Help** features.

Data Housekeeping

The Bioassay Calculations screen is designed to:

- 1. Make it easy for you to <u>Save</u> your entered data at any stage of data entry.
- Make it easy for you to <u>Exit</u> and return to the Main Screen (to revise Model Parameters and/or Intake Regimes) without losing any of your bioassay data.

Bioassay Save Icons

💐 Bioassay Calculations 👘					
File Advar	Advanced Tools Help				
Fa Save	[Quicl	回 k Save			

Figure 4.11. Bioassay Save icon.





Clicking the "Save" icon in the Bioassay Calculations screen saves all of the displayed values in the current Parameter File ("*.ix"). You can do this at any time (except when *IMBA Professional* is performing a calculation), for example, at several points while entering a long series of bioassay data. When you exit the Bioassay Calculations screen (to return to the Main Screen), the Parameter File is automatically updated with all of the displayed data.

Clicking the "Quick Save" icon (Figure 4.12) saves all of the displayed values (and all other parameter values) in the default Parameter File (named "Parameters.ix").

💐 Bioassay Calculations 👘						
File	Advar	nced	Tools	Help		
S	ave	[Quicl	□ < Save			

Figure 4.12. Bioassay Quick Save icon.

Closing the Bioassay Calculations Screen

rogress Indica	tor		
eposition			
Collating Times			
Bioassay Calcs			
Current Operation		Calculation Complet	e
			<u>0</u> K

Figure 4.13. The "OK" button for closing and exiting the Bioassay Calculations screen.

You can return to the **Main Screen** at any time (except when *IMBA Professional* is performing a bioassay calculation) by clicking the "OK" button (bottom-left panel of the **Bioassay Calculations** screen - see Figure 4.13).



Performing Bioassay Calculations

All bioassay calculations are *run* from the **CALCULATION** panel - top-center of the **Bioassay Calculations** screen. The calculation can go in either direction:

- 1. From **right** to **left** <u>Bioassay Quantity (Measurements) to estimated Intake(s)</u> as indicated by a **blue** arrow (Figure 4.14).
- From left to right value(s) of <u>Intake(s) to predicted Bioassay Quantity</u> as indicated by a green arrow (Figure 4.15).

The **arrow** colour indicates whether the bioassay data shown in a **Bioassay Quantity Table** are **measured** or **predicted** values, *i.e.*:

- 1. **Measured** bioassay values are always displayed on a **blue** background.
- 2. **Predicted** bioassay values are always displayed on a **green** background.

The same colour coding is used for a Bioassay Quantity Graph, *i.e.*:

- 1. Blue lines are used to join the values of a Bioassay Quantity that are fitted to the measured data.
- 2. Green lines join the predicted values of a Bioassay Quantity.

You can *toggle* the bioassay calculation in either direction, simply by *clicking* the **coloured arrow** (to reverse its direction) - or by *selecting* the required **index tab** ("**Intakes to Bioassay**" or "**Bioassay to Intake**").



CALCULATION				
Intakes to Bioassay	Bioassay to Intake			
	Select which data to use			
	🗖 Whole body			
	🗖 Lungs			
	🔽 Urine			
	Feces			
	Elood			
	Thyroid			
	Liver			
Start Calculation	🗖 User Defined			

Figure 4.14. Bioassay calculation set as "Bioassay to Intake" and indicated by a blue arrow.

e
00 1
o all /s

Figure 4.15. Bioassay calculation set as "Intakes to Bioassay" and indicated by a green arrow.

From Bioassay Measurements to Intake(s)



For a single intake (and a single set of bioassay data), provided that the time of the intake and the aerosol and absorption characteristics of the material are known, then calculation of the most likely amount of intake is simple and straightforward.

However, for multiple intakes (**Star Feature**) without precise knowledge of the times and nature of the intakes, estimating the intake amounts must be done by **iteration**. In general, this will involve:

- **Defining** a hypothetical set of parameter values to provide an **initial estimate** of the intake amounts.
- **Examining** the "goodness-of-fit" of the corresponding predicted bioassay quantity to the measured bioassay data.
- Refining the assumed values of unknown parameters (within realistic bounds).
- *Calculating* the resulting new estimates of the intake amounts.
- **Re-examining** the resulting "goodness-of-fit" of the predicted bioassay quantity.
- **Repeating** this iterative process until an adequate fit to the measured bioassay data is obtained (with justifiable parameter values).

IMBA Professional provides the computational tools needed to facilitate the iterative "fitting" process, while allowing you to control this by exercising your own judgment. You can switch very easily between estimating the intake amounts and graphically comparing the predicted and measured values, as you proceed through the iterative process of refining the assumed parameter values.

The following sections of the User Manual give step-by-step examples (with real data) of:

- 1. estimating a **single intake** at a known time and for known material characteristics;
- 2. estimating **three separate intakes** (**Star Feature**) with uncertain times of intake and material characteristics.
- 3. estimating an intake using multiple bioassay quantities (Star Feature).

These examples will introduce you to the main "built-in" features and functions of IMBA Professional that are provided for **bioassay analysis**. Or, you can "browse" through the Visual Tour of all features and functions available for bioassay calculations.

- **Example** of simple estimation of single intake.
- Example of iterative estimation of multiple intakes (Star Feature).
- Example of estimating intake using multiple bioassay quantities (Star Feature).
- Visual Tour of the Bioassay Calculations screen and its functions.

From Intake(s) to Bioassay Quantity

Calculation of the amount of a **Bioassay Quantity** as a function of the **Time** variable is used to:

- plan a Bioassay Program by calculating the expected amount at prescribed time points;
- provide **fine time-resolution** in the **predicted bioassay quantity** for graphical comparison with the measured data as an integral part of the **fitting procedure for estimating Intake(s)**.

The application of the "Intakes to Bioassay" calculation to the fitting procedure is illustrated in Figure 4.16. See also:

- the Example of a Single Intake Estimation;
- the Example of a Multiple (Iterative) Intake Estimation (Star Feature).
- the Example of Multiple Bioassay Quantities (Star Feature).

Bioassay Calculations File Advanced Tools Help	5		
		Bioassay Calcula	ations
INTAKES	CALC	ULATION	BIOASSAY QUANTITY
IR 1 4.981E+02 Bq			C Graph © Table C Hide Urine tool Snanibard Date (Althoum) Collection Calculated Measurement Date
IFI 2 5.303E+02 Bq IFI 3 1.353E+02 Bq	Intakes to Bioassay Specily Dates (Col 1)	Bioassay to Intake Number of Dates (1-200)	01/01/1971 1.000E+00 2.96974E 04 15/03/1969 04/01/1971 07:12:00 1.000E+00 2.96974E 04 13/06/1968 08/01/1971 07:12:00 1.000E+00 2.96574E 04 13/09/1968 12/01/1971 1.000E+00 2.9659E 04 13/09/1969 15/01/1971 16:48 00 1.000E+00 2.9655E 04 20/03/1969
	Start Date 01/01/1971 Stop Date 31/12/1972	C Logarithmic C Logarithmic C 1-25 mode C 1-	19/01/19/1 07:12:00 1:000E+00 2:8644E-04 18/12/1969 23/01/1971 1:000E+00 2:8637E-04 19/03/1970 C Gradh C Table C Hide Urine tool
	Specify Collection Periods (Col 2 1 Calculate Bioassay Quantity (Col	Send → 3) Start Calculation	2.50E-00 2.28E-02 1.75E-02 1.75E-02 1.28E-02 1.00E-02 7.50E-03 5.00E-03 0.00E+00 8315 8724 9133 9542 9051 1036110770111791158811997 12406
Progress Indicator Deposition Collating Times Bioassay Calcs Current Dependion	Calculation Comp	olete	C Greph C Tetre C Hide
		<u>D</u> K	

Figure 4.16. "INTAKES" sub-panel displays Intake amounts for up to 10 Intake Regimes (IRs).

Am-241 As Indicator Of Plu-241

Intake (IR 1)	Indicator Nuclide
0 Bq	Select Radionuclide Am-241
	Number of Associated Radionuclides: 3 Half Life: 1.578E+05 d
Associated Radion	ıclides
Select Radionucli	de Abundance 250 %
Delete Radionucli	de Half Life: 5.256E+03 d

Figure 4.17. Combination of 241Am as the Indicator Nuclide and 241Pu as an Associated Radionuclide

00



Important: The Abundance of each Associated Radionuclide is defined as the fraction of the activity of the Indicator Nuclide. In the current version of IMBA Professional Plus you can define the Abundance separately for each individual intake (at the time of each intake). Alternatively, you can define a single Abundance (or set of isotopic ratios) to apply at t = 0, in common for all intakes – see Figure 4.18.

- In cases where inhalation of relatively insoluble forms of plutonium has occurred, and the inhaled plutonium contains a significant amount of 241Pu, higher sensitivity for lung counting can often be achieved by measuring the activity of the 241Am progeny (59.5 keV and 35.7% abundance g-ray) rather than the low-energy and low-abundance L X-rays emitted by 239Pu (and 238Pu). For particulate material retained in the respiratory tract, it is reasonable to assume that the absorption of 241Am (from the particle matrix) will occur at the same rate(s) as that of the plutonium isotopes. Thus, the 241Am activity measured in the lungs should be a good indicator of the parent 241Pu activity, and thus the total retained plutonium activity. However, account must be taken of the 14-y decay half-life of 241Pu, and the subsequent in-growth of the 241Am activity in the lungs can be used to calculate the total lung retention of a defined mixture of plutonium isotopes.
- In order to activate this special tool, it is first necessary to define 241Am as the Indicator Nuclide and 241Pu as an Associated Radionuclide (Figure 4.22). The tool can be activated (Figure 4.23) from EITHER the Main Screen ("Advanced | Advanced Dosimetry Options" menu) OR the Bioassay Calculations Screen ("Advanced | Bioassay Options" menu).

Advanced Dosimetry Options	3
These options should be used with extreme care	
Dose Fitting Bioassay Misc Ingrowth of indicator radionuclide Image: Weight of the second se	
<u>Q</u> K <u>C</u> ancel	
Figure 4.18. Bioassay option to track	"in-growth

Nuclide for 241 Pu in the lungs.

'in-growth" of 241 Am as the Indicator

For a worked example of how to use this "241Am ingrowth" tool, see "Example Cases -Bioassay: Case of Am-241 In-growth".



Using the Table Tool for Data Entry

Note: This topic is part of **both** the **single intake** and **multiple intakes** examples. For brevity, only the **single intake** data are illustrated.

💐 Table Too	l : Whole body D	ata							
<u>File Edit Bio</u>	assay <u>M</u> easureme	nt <u>H</u> elp							
Specified	Time (d)	N/A	Calculated Value(Bg)	Measurement	Time (d)	N/A	Measuremen Value(Bg)	Data Type	Measuremen E Error [
1									
KEY									
	Bioassay Prediction	\$							
	Measurement Data		No Rows :	1 Apply.					
	Measurement Fit O	utput							

Figure 7.1. Table Tool before data entry - with "Whole body" as the Bioassay Quantity.

The **Table Tool** shows all of the data columns (without you having to scroll left and right). When you open this [from a **Bioassay Quantity (BQ)** window], the **Table Tool** will display the same number of rows as the **BQ** window. When opened with a New (blank) Parameter File, the **default single row** is displayed. Your first task is to open up enough rows to hold all of the **measured bioassay data** that you want to analyse. In the whole-body measurement example for 60Co (Single Intake example), there are **8** values of whole -body activity. So, in that case:

- <u>Ensure</u> that you are opening the **Table Tool** from a **Bioassay Quantity** window that is set to show a Table of "**Whole body**" data.
- Enter "8" in the "Number of Rows" dialog box (bottom panel, left-of-center) see Figure 7.2.
- <u>Click</u> the "Apply" <u>button</u> to the right of the dialog box.

BŞ 1	able Too	I: Whole body [Data						
Eile	<u>E</u> dit <u>B</u> io	bassay <u>M</u> easureme	nt <u>H</u> elp	Calculated			Measuremen		Measuremen
	Specified	l Time (d)	N/A	Value(Bq)	Measurement Time (d)	N/A	Value(Bq)	Data Type	Error
2]						
3									
4									
6									
7									
8									
KE	Y								
		Bioassay Prediction	ns	No Decore					
		Measurement Data	1 . Amerika	No Hows :	8 Accly				
		Measurement Fit O	utput						

Table 7.2. Table Tool with 8 rows opened.

The data to be entered (in the columns with blue background shown in Figure 7.2) are:

- 1. Measurement date (plus optional hh:mm).
- 2. N/A column <u>leave</u> this blank a "Collection period" is Not Applicable for whole-body activity.
- 3. Measurement value (Bq).
- 4. Data Type (< LOD, Real or Excluded).
- 5. Measurement Error value of the measurement error.
- 6. Error Distribution type of error distribution (NORM or LOGNORM).



You have three options for entering the measured bioassay data:

- 1. <u>Type</u> this in manually (cell by cell or block of cells).
- 2. <u>Copy</u> a block of data into the **Table Tool** from a Windows ® application using the Windows ® clipboard.
- 3. <u>Read</u> the data into the **Table Tool** from an external file.

Data validation

Data validation is first performed automatically in the **Table Tool** after the "**OK**" button is <u>clicked</u>. While validation is being performed, the mouse pointer displays an hourglass icon. For large data sets, a status bar is displayed (Figure 7.3). The validation tests performed are:

- 1. Data in columns is assumed to be part of a continuous set of data and scrutinised by the validation procedure from the first (top) cell until an empty cell is encountered.
- 2. Any cell data encountered after an empty cell is ignored by the validation process.
- 3. The validation routine will halt at the first cell encountered in the data grid that contains invalid data. A message box is displayed, and the offending cell is <u>highlighted</u>.

The criteria for invalid data are:

- 1. Non-numerical data in cells expected to contain numerical input.
- 2. Data that cannot be converted to a valid date/time value in cells expected to contain date/time.
- 3. Columns for "**Collection Period**" are validated only for urinary or faecal bioassay quantities.

If the data validation is successful, the mouse pointer icon reverts to the default, and the **Table Tool** form is hidden.



Figure 7.3. Data Validation.



Tip: The "**validation**" feature, whereby IMBA Professional ignores all data entered below an "**empty**" cell, allows you to enter additional information relating to a dataset (but not part of the analysis) - below the data set.

A second, more rigorous, validation is performed automatically before any calculation, to ensure that all data values are sensible.

Select one of these options to:

- Proceed to Step #8 in the single intake example ("Graphing the Data Single Intake");
- <u>Proceed</u> to Step #10 in the multiple intake example ("Graphing the Data -Multiple Intakes").

Or∶

- <u>Return</u> to the **case description** and list of steps for the **single intake** example.
- <u>Return</u> to the **case description** and list of steps for the **multiple intakes** example.

For a comprehensive **catalog** of the features and functions of the **Table Tool**, see <u>Visual Tour</u> of the Table Tool.

Manual Data Entry



Data Columns ## 1 and 3

In this example, the bioassay data to be analysed are comprised of **8** paired values of **Measurement date** and **Whole-body activity (Bq)** - see **Table 1** in Example of Single Intake Estimation. Each pair of values can be typed directly into the **first** and **third** column, respectively, of the **measurement data table** (Figure 7.4).

<u>F</u> ile	<u>E</u> dit <u>B</u> ioassay <u>M</u> easureme	nt <u>H</u> elp				
	Specified Date (+hh:mm)	Collection period (d)	Calculated Rate(Bq/d)	Measurement Date (+hh:mm]	Collection period (d)	Measurer Rate(Bg/
1				25/2/88		2
2				1/3/88		1
3				11/3/88		1
- 4				28/3/88		
5				16/5/88		
6				11/8/88		
- 7				29/11/90		
8				19/2/92		

7.4. Typing paired values of **Measurement date** and **Measurement value** into the **Table Tool**.



Tip: All common keyboard and mouse functions, e.g., Backspace, arrow keys, highlight, Delete, ^C (Copy), ^V (Paste), will work during manual data entry.

If you now click "**OK**" (bottom right-corner of the **Table Tool**) to return to the **Bioassay Quantity** window - and scroll to the right - you will see the values that you have entered displayed in the table (Figure 7.5).

BIOASSAY QUANTITY									
O Graph ⊙ Table O Hide Whole body 🔽 🚺									
Measurement Date (+hh:mm]	N/A	Measuremen Value(Bq)	Data Type	Measuremen 📥 Error					
25/02/1988		2.720E+03							
01/03/1988		1.150E+03							
11/03/1988		1.010E+03							
28/03/1988		7.900E+02							
16/05/1988		4.820E+02							
11/08/1988		3.580E+02							
29/11/1990		7.800E+01							
19/02/1992		3 5005 +01		_					
				<u> </u>					

Figure 7.5. Values entered in the Table Tool are automatically displayed in the corresponding Bioassay Quantity window.

Data Column #2

- In this example, the **Bioassay Quantity** is "**Whole body**", so **Data Column #2** is not applicable ("**N/A**"). In this case, the *IMBA Professional* data validation procedure automatically ignores any entries in this column.
- If, however, the Bioassay Quantity is an excretion rate (urinary or faecal), it is necessary to enter the "Collection Period" for each sample (Measurement Value). The Table Tool then provides a short-cut for entering repetitive values, e.g., the common collection period of "1 d". You simply highlight the whole column of cells, and type "1" - Figure 7.6.

	Specified Time (d)	Collection period (d)	Calculated Rate(pCi/d)	Measurement Time (d)	Collection period (d)	Measuremen Rate(pCi/d)	Data Type	Measure Error
1				2.000E+00	1	4.000E-03	<lod< td=""><td>1.800</td></lod<>	1.800
2				3.000E+00	1	4.000E-03 <	<lod< td=""><td>1.800</td></lod<>	1.800
3				4.000E+00	1	4.000E-03 <	<lod< td=""><td>1.800</td></lod<>	1.800
4				7.600E+01	1	4.000E-03 <	<lod< td=""><td>1.800</td></lod<>	1.800
5				1.230E+02	1	1.600E-01 F	Real	1.800
6				1.500E+02	1	7.000E-02 F	Real	1.800
7				1.860E+02	1	7.000E-02 F	Real	1.800
8				2.090E+02	1	1.000E-01 F	Real	1.800
9				2.640E+02	1	1.600E-01 F	Real	1.800
10				2.830E+02	1	1.800E-01 F	Real	1.800
11				2.930E+02	1	2.000E-01 F	Real	1.800
12				3.280E+02	1	3.100E-01 F	Real	1.800
13				3.590E+02	1	2.300E-01 F	Real	1.800
14				3.870E+02	1	2.600E-01 F	Real	1.800
15				4.150E+02	1	2.000E-01	Real	1.800
16				5.060E+02	1	3.700E-01 F	Real	1.800
17				5.930E+02	1	2.300E-01 F	Real	1.800
18				6.850E+02	1	2.400E-01 F	Real	1.800
19				7.760E+02	1	2.400E-01 F	Real	1.800
20				8.700E+02	1	3.300E-01	Real	1.800
21				9.640E+02	1	3.100E-01 F	Real	1.800
22				1.048E+03	1	3.500E-01 F	Real	1.800
23				1.143E+03	1	3.700E-01 F	Real	1.800
24				1.231E+03	1	5.800E-01 F	Real	1.800
25				1.293E+03	1	2.100E-01	Real	1.800
26				1.481E+03	1	4.300E-01 F	Real	1.800
27				1.668E+03	1	4.100E-01 F	Real	1.800
28				1.847E+03	1	4.400E-01 F	Real	1.800
29				2.027E+03	1	3.500E-01 F	Real	1.800
30				2.123E+03	1	1.600E-01	Real	1.800
31				2.212E+03	1	2.100E-01 F	Real	1.800
32				2.212E+03	1	1.600E-01 F	Real	1.800
33				2.575E+03	1	2.200E-01	Real	1.800
34				2.689E+03	1	2.800E-01	Real	1.800
ord				2.881E+03	1	1.200E-01	Real	1.800
35				3.100E+03	1	2.800E-01 F	Real	1.800





<u>Tip:</u> Highlight the <u>whole</u> data column with a single click - by rightclicking the column <u>heading</u> - "<u>Collection Period (d)</u>" in this case.

Data Column #4

- In this example, all **8** measured values are "**Real**" data, i.e., **finite** measured values. Therefore, "**Real**" must be entered in all cells of the fourth data column. *IMBA Professional* provides a further **short-cut** for doing this in the **Table Tool** (Figure 7.7):
- highlight the whole of the fourth data column;
- right-click on any highlighted cell the drop-down menu will automatically appear (Figure 7.7);
- select "Real" from the drop-down menu.

File	Edit Bioassay Meas	urement Help				
	Specified Date (+hh:)	nm) N/A	Calculated Value(Bq)	Measurement Date [+hh:mm]	N/A	Measurer Value(Bg
1				25/02/1988 00:00:00		2.720E
2				01/03/1988 00:00:00		1.150E
3				11/03/1988 00:00:00		1.010E
- 4				28/03/1988 00:00:00		7.900E
5				16/05/1988 00:00:00		4.820E
6				08/11/1988 00:00:00		3.580E
- 7				29/11/1990 00:00:00		7.800E
8				19/02/1992 00:00:00		3.500E

Figure 7.7. Drop-down menu for entering the "Data Type."

This will enter "Real" in all of the highlighted cells (Figure 7.8).

Measurement Date (+hh:mm]	N/A	Measuremen Value(Bq)	Data Type	Measuremen Error	Error Distribution
25/02/1988 00:00:00		2.720E+03	Real		
01/03/1988 00:00:00		1.150E+03	Real		
11/03/1988 00:00:00		1.010E+03	Real		
28/03/1988 00:00:00		7.900E+02	Real		
16/05/1988 00:00:00		4.820E+02	Real		
08/11/1988 00:00:00		3.580E+02	Real		
29/11/1990 00:00:00		7.800E+01	Real		
19/02/1992 00:00:00		3.500E+01	Real		

Figure 7.8. Entering the "Data Type" in all cells of data column #4.

Data Column # 5

- In this example, there are **no explicit measurement** errors. However, in order to apply the **Maximum Likelihood Method** to "**fit**" the data, an explicit **error**
 - weighting MUST be defined for every data point. Again, *IMBA Professional* provides a **short-cut** for doing this in the **Table Tool**. This gives you the option of applying:
- a Uniform Absolute error;
- a Uniform Relative error;
- a Square Root error.

In this example, the measured values vary over a large range (from 2720 Bq to 35 Bq). For accurate dosimetry, it is as important to "fit" the small values, as it is to fit the initial high values. In this case, it is reasonable to apply a **Uniform Relative** error to all data points. To do this you simply:

- highlight the whole of the fifth data column;
- right-click on any highlighted cell;

• select "Generate Errors" - Figure 7.9.

- 1 -	Table Tool : Whole body D	ata				
File	Edit Bioassay Measureme	nt Help				
	Specified Date (+hh:mm)	N/A	Calculated Value(Bq)	Measurement Date (+hh:mm]	N/A	Measuren Value(Bq)
1				25/02/1988 00:00:00		2.720E
2				01/03/1988 00:00:00		1.150E
3				11/03/1988 00:00:00		1.010E
4				28/03/1988 00:00:00		7.900E
5				16/05/1988 00:00:00		4.820E
6				11/08/1988 00:00:00		3.580E
- 7				29/11/1990 00:00:00		7.800E
8				19/02/1992 00:00:00		3.500E

Figure 7.9. Drop-down menu to "Generate Errors."

Measurement Date (+hh:mm]	N/A	Measuremen Value(Bq)	Data Type	Measuremen Error	Error Distribution	Theoretical Value(Bq)
25/02/1988 00:00:00		2.720E+03	Real			
01/03/1988 00:00:00		1.150E+03	Real			
11/03/1988 00:00:00		1.010E+03	Real			
28/03/1988 00:00:00		7.900E+02	Real			
16/05/1988 00:00:00		4.820E+02	Real		Generate	Errors
11/08/1988 00:00:00		3.580E+02	Real		C. Huller	and days and the second
29/11/1990 00:00:00		7.800E+01	Real		C Uniform Ac	isolute U
19/02/1992 00:00:00		3.500E+01	Real		• Uniform Re	ciative _, Can
					С <u>S</u> quare Ro К 0.1	ot
						10 - 2PV -

Figure 7.10. The "Generate Errors" window.

In the "generate Errors" window:

- "Uniform Relative" error is set by default or select alternative;
- "Apply to all" measurement values is set by default or un-check to apply to a selected range of measurement values;
- the value of the "Error Constant" ("K") must be entered.
- For a **Uniform Relative** error, the chosen value of "K" (when applied to ALL measurement values) has no effect on the fitted value since all data points are given a proportional error-weighting. "K" can be any **non-zero** value. The value "**0.1**" is a convenient **default**. (Figure 7.10).
- When you click the "**OK**" button to apply your selected value of "**K**" you will be warned that "**This will overwrite the measurement errors**" and you will be given an opportunity to change your mind (Figure 7.11).



Figure 7.11. Warning message before overwriting measurement errors.

Data Column #6

The final data column defines the type of **Error Distribution** for each error value. This is either:

- NORM normal (Gaussian), or;
- LOGNORM lognormal.

To enter the type of **Error Distribution** for all **8** error values (Figure 7.12):

- highlight all of the cells in data column #6 this will automatically display the Error Distribution menu;
- select "NORM" to specify a Normal error distribution for all errors.

Measurement Date [+hh:mm]	N/A	Measuremen Value(Bq)	Data Type	Measuremen Error	Error Distribution	Theoretical Value(Bq)
25/02/1988 00:00:00		2.720E+03	Real	2.720E+02		
01/03/1988 00:00:00		1.150E+03	Real	1.150E+02		
11/03/1988 00:00:00		1.010E+03	Real	1.010E+02		
28/03/1988 00:00:00		7.900E+02	Real	7.900E+01		
16/05/1988 00:00:00		4.820E+02	Real	4.820E+01	NURN	1
11/08/1988 00:00:00		3.580E+02	Real	3.580E+01	LOGN	ORM
29/11/1990 00:00:00		7.800E+01	Real	7.800E+00	Cut	
19/02/1992 00:00:00		3.500E+01	Real	3.500E+00	Copri	
					Paste	
					Insert	Measurement Ro
					Delete	Measurement F
					Delete	: Cell Contents
					File Im	port

Figure 7.12. Selecting a Normal distribution for each error value.

"**NORM**", signifying a "**Normal**" distribution of errors, will then be entered automatically in all highlighted cells of data column #6 (Figure 7.13).

Measurement Date [+hh:mm]	N/A	Measuremen Value(Bq)	Data Type	Measuremen Error	Error Distribution	The Val
25/02/1988 00:00:00		2.720E+03	Real	2.720E+02	NORM	
01/03/1988 00:00:00		1.150E+03	Real	1.150E+02	NORM	
11/03/1988 00:00:00		1.010E+03	Real	1.010E+02	NORM	
28/03/1988 00:00:00		7.900E+02	Real	7.900E+01	NORM	
16/05/1988 00:00:00		4.820E+02	Real	4.820E+01	NORM	
11/08/1988 00:00:00		3.580E+02	Real	3.580E+01	NORM	
29/11/1990 00:00:00		7.800E+01	Real	7.800E+00	NORM	
19/02/1992 00:00:00		3.500E+01	Real	3.500E+00	NORM	

Figure 7.13. Completed measurement data in Table Tool.

Completed data table in Bioassay Quantity window

Figure 7.14 shows the resulting completed **table of measurement data**, as it appears in the corresponding **Bioassay Quantity** window.

	BIOASSAY QUANTITY									
) // hole body									
🔿 Graph	 Table 	⊖ Hide	Whole body			tool				
Calculated Value(Bq)	Measuremer (+hh:mm]	nt Date	N/A	Measuremen Value(Bq)	Data Type	Measuremen Error	Error Distribution			
		2/25/1988		2.720E+03	Real	2.720E+02	NORM			
		3/1/1988		1.150E+03	Real	1.150E+02	NORM			
		3/11/1988		1.010E+03	Real	1.010E+02	NORM			
		3/28/1988		7.900E+02	Real	7.900E+01	NORM			
		5/16/1988		4.820E+02	Real	4.820E+01	NORM			
		8/11/1988		3.580E+02	Real	3.580E+01	NORM			
		11/29/1990		7.800E+01	Real	7.800E+00	NORM			
		2/19/1992		3.500E+01	Real	3.500E+00	NORM			
•							Þ			

Figure 7.14. Completed Bioassay Quantity table of data.



Example of Single Intake

This completes Step #7 in the single intake example - using manual data entry:

- Proceed to the next step plot a Graph of your data.
- <u>Return</u> to the **case description** and list of steps.
- Check out how to enter data using the Windows® Clipboard.

Example of Multiple Intake

This completes Step #9 in the multiple intake example - using manual data entry:

- Proceed to the next step plot a Graph of your data.
- Return to the case description and list of steps.
- Check out how to enter data using the Windows® Clipboard.

Using the Clipboard



You can very easily *enter* your bioassay measurement data into the **Table Tool** using the Windows® clipboard:

 highlight the required column(s) of data in your source Windows® application (Figure 7.15);

- 2. *copy* the highlighted block of data;
- 3. open the Table Tool for the appropriate bioassay quantity;
- click on destination cell for the copied data block this will automatically show the "Paste" menu (Figure 7.16);
- 5. paste the block of data.

🔀 м	icrosoft Excel - I	AEA Co-60					
	<u>File E</u> dit <u>V</u> iew	Insert Form	mat <u>T</u> ools	<u>D</u> ata <u>W</u> ind	low		
D	2 🖬 🔒 🖏 🎒	🗟 💖 🐰	🖻 🛍 • 🝼	K) + (21 +	۹.		
Arial		• 10 • B	IU 🗄	≣ ≣ ඕ	\$		
2							
	A3	• ;	£ 2/25/19	88			
	A	В	С	D			
1	60Co Single Int	take - IAEA	Annex IV				
2							
3	25-Feb-88	2720					
4	1-Mar-88	1150					
5	11-Mar-88	1010					
6	28-Mar-88	790					
7	16-May-88	482					
8	11-Aug-88	358					
9	29-Nov-90	78					
10	19-Feb-92	35					
11							
12							
13							
14							

Figure 7.15. Highlighting a block of data in Microsoft Excel spreadsheet for copying to the Windows® clipboard.

E 1	able Tool : Whole body	Data						
File	Edit Bioassay Measurem	ent Help						
	Specified Time (d)	N/A	Calculated Value(Bq)	Measurement T	ime (d)	N/A	Me. Val	asuremen ue(Bq)
1					Cut Copy Paste Insert M Delete N	easurement Measuremen	Row t Row	
					Delete (Cell Contents	;	
					File Imp	ort		

7.16. Clicking on the **destination** cell in the **Table Tool** shows the "Paste" menu.

To *paste* the block of data from the Windows® clipboard to the destination cell in the **Table Tool**, you can use:

- the "Paste" button on a Microsoft Office-type keyboard;
- **^V** (control paste);
- "Paste" in the drop-down menu (Figure 7.16).

You will see the following **Warning** notice (Figure 7.17). If you click "**Yes**", the **Table Tool** will *open* a sufficient number of rows (below your insertion level) to accommodate your pasted data (Figure 7.18).

Table To	ol : Whole body Data 🛛 🕅
?	There are currently not enough rows available, below the currently selected row, to display the data on the clipboard ! Do you want the Table Tool to increase the number of rows automatically ?
	Yes No

Figure 7.17. Warning notice.

es 1	📲 Table Tool : Whole body Data								
File	File Edit Bioassay Measurement Help								
	Specified Time (d)	N/A	Calculated Value(Bq)	Measurement Time (d)	N/A	Measuremen Value(Bq)			
1				25-Feb-88	2720				
2				1-Mar-88	1150				
3				11-Mar-88	1010				
4				28-Mar-88	790				
5				16-May-88	482				
6				11-Aug-88	358				
- 7				29-Nov-90	78				
8				19-Feb-92	35				

Figure 7.18. Block of data *pasted* into the destination cell (top-left) of the Table Tool.

Notice in Figure 7.18 above, that the **measurement values** were pasted into the next column to the right of "**Measurement Date (+hh:mm)**." In this case, they need to be *moved* (manually) to the correct "**Measurement Value (Bq)**" column:

- click on the "N/A" (incorrect) column heading to highlight the whole column of data to be moved;
- *right-click* on any highlighted cell the "**Cut/Copy**" menu will appear (Figure 7.19);
- click "Cut" this will put the column of data into the clipboard;
- *click* the "**Measurement Value (Bq)**" column heading this will *highlight* all of the "target" cells in this column;
- right-click on any target cell the "Paste" menu will automatically appear (Figure 7.20);
- click "Paste".

- 1 -	Table Tool : Whole body D	ata				
File	Edit Bioassay Measuremer	nt Help				
	Specified Date (+hh:mm)	N/A	Calculated Value(Bq)	Measurement Date (+hh:mm]	N/A	Measuremen Value(Bq)
1				25/02/1988 00:00:00	2.720E	+03
2				01/03/1988 00:00:00	1.150E	+03
3				11/03/1988 00:00:00	1.010E	+03
- 4				28/03/1988 00:00:00	7.900E	+02
5				16/05/1988 00:00:00	4.82	Cut
6				11/08/1988 00:00:00	3.58	Cut
- 7				29/11/1990 00:00:00	7.80	Сору
8				19/02/1992 00:00:00	3.50	Paste
						Insert Measurement
						Delete Measuremen
						Delete Cell Contents
						File Import

Figure 7.19. Moving a column of data in the Table Tool.

	Specified Date (+hh:mm)	N/A	Calculated Value(Bq)	Measurement Date (+hh:mm]	N/A	Measuremen Value(Bg)
1				25/02/1988 00:00:00		
2				01/03/1988 00:00:00		
3				11/03/1988 00:00:00		
- 4				28/03/1988 00:00:00		
5				16/05/1988 00:00:00		
6				11/08/1988 00:00:00		
- 7				29/11/1990 00:00:00		
8				19/02/1992 00:00:00		
						[





Key Tip: The drop-down menu that appears when you *right-click* anywhere in the **Table Tool** is "**context sensitive**" - *i.e.*, it automatically shows you only those options that are applicable to the *clicked* cell.

Completing the remaining data columns (## 2, 4, 5 and 6)

Enter the data required for the **remaining four columns** (blue background) using the **tools** already described to facilitate <u>manual data entry</u>. These columns are:

- Collection Period (d) this is not applicable (N/A) for Whole Body as the bioassay quantity.
- **Data Type** either < LOD, Real or Imaginary.
- Measurement Error value of the error for each measurement.
- Error Distribution either Normal or Lognormal.

00

Example of Single Intake

This completes **Step #7** in the **single intake** example - entering data *via* the **Windows® clipboard**:

- <u>Proceed</u> to the next step plot a <u>graph</u> of your data.
- <u>Return</u> to the case description and list of steps.
- Check out how import an <u>external data file</u>.

Example of Multiple Intakes

This completes **Step #9** in the **multiple intake** example - entering data *via* the **Windows® clipboard**:

- <u>Proceed</u> to the next step plot a <u>graph</u> of your data.
- <u>Return</u> to the case description and list of steps.
- Check out how import an external data file.

Importing a Data File

<i>ब्य</i> ा.	AEA C	0-60 - N	otepad				
Eile	<u>E</u> dit	F <u>o</u> rmat	Help				
2/2 3/1 3/2 5/1 8/1 11/ 2/1	5/88 /88 8/88 6/88 1/88 29/9 9/92	N/A N/A N/A N/A 0 N/A	2720 1150 1010 790 482 358 N/A 35	Real Real Real Real Real 78 Real	272 115 101 79 48.2 35.8 Real 3.5	NORM NORM NORM NORM 7.8 NORM	NORM

Figure 7.21. Tab delimited text file ("IAEA Co-60.txt") holding measurement data.

You can import data directly into the **Table Tool** from an **ASCII text file** with the following types of delimiter:

- comma separated values;
- tab delimited values;

- **space** delimited values;
- your own definition of the delimiter.

To import your data:

- right-click on the destination cell for your imported text file data (Figure 7.22) the "File Import" menu will appear;
- click "File Import".

8	Table Tool : Whole body D	ata					
File	Edit Bioassay Measureme	nt Help					
	Specified Date (+hh:mm)	N/A	Calculated Value(Bq)	Mea (+hh	surement Date :mm]	N/A	Measuremen Value(Bq)
1					Cut	, 	
2					Сору		
3					Paste	-	
4							
5					Insert Measurement R	ow 📘	
6					👘 Delete Measurement F	low	
- 7							
8					Delete Cell Contents		
					Elle Jacobia		
					File Import		

Figure 7.22. "File Import" menu.

The message shown in Figure 7.23 will appear - to remind you to check that you are importing the file into the correct location in the Table.

Table Tool : Whole body Data 🛛 🕅								
?	Imported data will be displayed in the cells below and to the right of the currently selected cell (Row: 1 Column: 4 - highlighted).							
	Do you want to continue with the import process ?							
	<u>Y</u> es <u>N</u> o							

Figure 7.23. Notice to confirm the target location in the data table.

Click "Yes" to open the "ASCII file import wizard" (Figure 7.24). Use the wizard to:

- browse to the ASCII text file containing your measurement data;
- view the data file Figure 7.25;
- select the appropriate type of data delimitation "Tab delimited" in this example.

ASCII file import wizard	×
The ASCII import wizard helps you import data from a text file into IMBA-Expert US-DOE.	
Text file C:\JabaSoft\IMBAEXUS\USERDATA\IAEA Co-60.txt	
⊻iew	
Select type of text file	
Comma separated C Tab delimited C Space delimited	
O Other delimeter	
<back next=""> Cancel</back>	

Figure 7.24. ASCII file import wizard for browsing to the data text file containing measurement data.

al 🛃	EA C	o-60 - N	lotepad						
<u>F</u> ile	<u>E</u> dit	F <u>o</u> rmat	<u>H</u> elp						
2/2 3/1, 3/1 3/28 5/10 8/11 11/2 2/19	5/88 /88 L/88 3/88 5/88 L/88 L/88 29/9 9/92	N/A N/A N/A N/A N/A N/A	2720 1150 1010 790 482 358 N/A 35	Real Real Real Real Real 78 Real	272 115 101 79 48.2 35.8 Real 3.5	NORM NORM NORM NORM NORM 7.8 NORM	NORM		

Figure 7.25. Text data file viewed in the ASCII file import wizard.

Clicking "Next" in the ASCII file import wizard enables you to *select* (by *highlighting*) the data that you wish to import into the Table Tool (Figure 7.26). *Click* the "Select All" *button* to select all of the whole ASCII text file. Once you have selected the data that you want to import into the Table Tool, *click* "Next" (Figure 7.26).

R.	ASCII file import wizard						×
	Please select	the data that	you wish to in	nport			
		A	В	C	D	E 🔺	1
	1	2/25/88	N/A	2720	Real	27	1
	2	3/1/88	N/A	1150	Real	11	
	3	3/11/88	N/A	1010	Real	10	
	4	3/28/88	N/A	790	Real	7	
	5	5/16/88	N/A	482	Real	48.	
	6	8/11/88	N/A	358	Real	35.	
	•	11/20/00	NI AA	70	Deel		
	Select All						
	<back cancel<="" td=""></back>						

Figure 7.26. Selecting the data in the ASCII text file to import into the Table Tool.

Click "Next". You will be given an opportunity to change your mind about pasting the selected data - which will overwrite any existing data in the target cells of the **Table Tool** (Figure 7.27).

ASCII file import wizard	×
Click the Finish button to complete the import.	
The data that you have selected will be pasted into the table tool after you have pressed Finish.	
< <u>B</u> ack <u>Einish</u> <u>C</u> ancel	

Figure 7.27. Reminder that you are about to paste data into the Table Tool.

Click "Fir	Click "Finish" to proceed with your data import (Figure 7.28) - or "Cancel" this.					
ASCII file	import wizard 🔀					
?	The area of the Table Tool you want to import data into already contains data. Do you want to overwrite it ?					
	Yes <u>N</u> o					

Figure 7.28. Warning that you are about to overwrite existing data in the target cells.

To *complete* the importation of your selected data, *click* "Yes". This will automatically write your **imported data** to the target cells of the **Table Tool**, starting in the first row of the first measurement data column (blue background), as shown in Figure 7.29.

🙀 Table Tool : 🗰 Whole body Data					
<u>E</u> dit <u>B</u> ioassay <u>M</u> easuremer	nt <u>H</u> elp				
Specified Date (+hh:mm)	N/A	Calculated Value(Bq)	Measurement Date (+hh:mm]	N/A	Measuremen Value(Bq)
			2/25/88	N/A	2720
			3/1/88	N/A	1150
			3/11/88	N/A	1010
			3/28/88	N/A	790
			5/16/88	N/A	482
			8/11/88	N/A	358
			11/29/90	N/A	78
			2/19/92	N/A	35
	able Tool : Whole body D Edit Bioassay Measuremer Specified Date (+hh:mm)	able Tool : Whole body Data Edit Bioassay Measurement Help Specified Date (+hh:mm) N/A	Whole body Data Edit Bioassay Measurement Help Specified Date (+hh:mm) N/A Calculated Value(Bq) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hi:mm) Ima	able Tool : Whole body Data Edit Bioassay Measurement Help Specified Date (+hh:mm) N/A Calculated Value(Bq) Measurement Date (+hh:mm) Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) Image: Specified Date	able Tool : Whole body Data Edit Bioassay Measurement Help Specified Date (+hh:mm) N/A Calculated Value(Bq) Measurement Date (+hh:mm) N/A Image: Specified Date (+hh:mm) N/A Calculated Value(Bq) Measurement Date (+hh:mm) N/A Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) N/A N/A Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) N/A Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) N/A Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) N/A Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) N/A Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) N/A Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) N/A Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) N/A Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) N/A Image: Specified Date (+hh:mm) Image: Specified Date (+hh:mm) N/A Image: Specified Date (+hi:mm) Image: Specified Date (+hi:mm) N/A Image: Specified Date (+hi:mm

Figure 7.29. Data successfully imported into the Table Tool.

If there are **not enough rows open** in the **Table Tool** to hold your data, you will be **warned** (Figure 7.30).

ASCII file	import wizard			
?	There are currently not enough rows available in the Table Tool, below the currently selected row, to display the imported data !			
	Do you want the import wizard to increase the number of rows automatically ?			
	<u>Yes</u> <u>N</u> o			

Figure 7.30. Warning message if there are too few rows opened in the Table Tool to receive imported data.

In this case, *click* "Yes" to automatically *add* the required number of new rows to the table - and *import* the *highlighted* data from the **external file**.

BIOASSAY QUANTITY						
⊂Graph ⊙Table ⊂ H	O Graph					
Measurement Date (+hh:mm]	N/A	Measuremen Value(Bq)	Data Type	Measuremen 📥 Error		
25/02/1988	N/A	2.720E+03	Real	2.720E+02		
03/01/1988	N/A	1.150E+03	Real	1.150E+02		
03/11/1988	N/A	1.010E+03	Real	1.010E+02		
28/03/1988	N/A	7.900E+02	Real	7.900E+01		
16/05/1988	N/A	4.820E+02	Real	4.820E+01		
08/11/1988	N/A	3.580E+02	Real	3.580E+01		
29/11/1990	N/A	7.800E+01	Real	7.800E+00		
19/02/1992	N7A	3 5005 ±01	Raal	3 5005 +00		

Figure 7.31. Imported data as it appears in the Bioassay Quantity window.



Important: IMBA Professional automatically **converts all dates** in the imported file to **your international setting**. In the example above, the dates in the imported text file were in the "U.S." convention. These were automatically converted to the "European" convention when the data was written to the Bioassay Quantity window (Figure 7.31).

Example of Single Intake

This completes **Step #7** in the **single intake** example - **importing** data from an **external ASCII text file**:

- <u>Proceed</u> to the next step plot a <u>graph</u> of your data.
- <u>Return</u> to the case description and list of steps.

Example of Multiple Intakes

This completes **Step #9** in the **multiple intake** example - **importing** data from an **external ASCII text file**:

- Proceed to the next step plot a graph of your data.
 - <u>Return</u> to the case description and list of steps.

Graph Tool for Viewing the Data and Fit

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Note: This topic is part of BOTH the **single intake** and **multiple intakes** examples. For brevity, only the **multiple intakes** data are illustrated.



Figure 8.1. Selecting Axes Automatically in the Graph Tool.

In the "**Tools**" sub-panel, *click* **Select Axes Automatically** (Figure 8.1). This will set up the range of the X- and Y-axes to include **all of the data points**.

To *plot* the data points with their error bars (as in Figure 8.2):

- select "Outline Circle" for the Shape of the data symbol ("Plot" sub-panel);
- check the "Plot" box;
- check the "Error Bars" box.

As you *check* each *box*, the respective symbol is plotted automatically (Figure 8.2).

- In the example shown (Figure 8.2), the following "User" selections have been made for the Y-axis:
- Scientific scale;
- "1" decimal place;

• "3" intervals.

You can also **select** the **scale** of the **X-axis**, the appearance of **plotted symbols**, and the "Line Style" of the plotted "Fit" and "Bioassay Predictions."



Figure 8.2. Plotting the data points and error bars.

Tip: Before you leave the Graph Tool, *check* the "Plot" box under the heading "Fit." This will automatically plot the fit to the data (in both the Graph Tool and the linked Bioassay Quantity window) - when you *calculate* the maximum likelihood estimate of the Intake amount(s).

Click the "*O*K" *button* (right-side panel) to close the **Graph Tool** - and return to the **Bioassay Quantity** windows. The **graph** of the **data and error bars** will then be displayed in the opened **graph window** (Figure 8.3).

🖸 🙆

BIOASSAY QUANTITY								
🔿 Graph 💿	Table	Он	lide	Urine		•		tool
Measurement (+hh:mm]	Date		Collec period	:tion I (d)	Measuremen Rate(Bq/d)	Data Typ	эе	Measuremen A
	15/03/	/1968	1.00)0E+00	1.000E-03	Real		9.000E-04
	13/06/	/1968	1.00)0E+00	1.800E-03	Real		9.000E-04
	13/09/	/1968	1.00)0E+00	3.000E-04	Real		9.000E-04
	13/12/	/1968	1.00)0E+00	4.800E-03	Real		2.000E-03
	20/03/	/1969	1.00)0E+00	0.000E+00	Real		9.000E-04
	18/12/	/1969	1.00)0E+00	0.000E+00	Real		9.000E-04
	19/03/	/1970	1.00)0E+00	0.000E+00	Real		9.000E-04
•	18706.	/1970	1 00)UE <u>*</u> UU	5 000F-04	Real		9 000F.04
🖲 Graph 🔿	Table	Он	lide	Urine		•	C	tool
0.0150				ſ				
0.0100 -				Ţ	T			
0.0050 -	ł		 3	₽	r " _æ æ _æ æ_æ_	Ø	70.	₽ m
0.0000 831	5 8724	913	<u>∲</u> ⊈ 3 954	12 995	1 10361 1077	0 11179		<u>90 70</u> 38 11997 12406

Figure 8.3. Graph of Whole body data and error bars displayed in Bioassay Quantity window.

This completes **Step #8** in the **single intake** example:

- Proceed to the Intake Calculation (Step #9);
- Return to the case description and list of steps for the single intake example.

This completes **Step #10** in the **multiple intakes** example:

- <u>Proceed</u> to the Multiple Intakes Calculation (Step #11);
- <u>Return</u> to the **case description** and list of steps for the **multiple intakes** example.

For a Visual Tour of the Graph Tool, see Visual Tour of Bioassay Screen: Graph Tool.

Maximizing and Exporting the Graph



Figure 8.4. Maximised view of the Graph.

Clicking <u>View</u> <u>Maximise</u> (from the <u>View</u> menu, top-left corner of the Graph Tool window) maximises the graph plot so that you can view this in finer detail, as shown in Figure 8.4.



Tip #1: Use the **Ctrl/Alt/Print Scrn** keys (together) to send the "maximized" image of the graph to the Windows ® clipboard. You can then **paste** this image directly into another Windows® application file, *e.g.*, a **report** being prepared in a word processor.

Tip #2: If you wish to "crop" the graph image to show only the plot itself (and not the background parts of the key etc.), you must currently use a separate "graphics" application to do this. The "Copy Graph" feature will be included in a future version – to enable you to export just the graph plot.

Dose Calculations Screen

The **Dose Calculations** screen (Figure 5.1) opens when you *click* the **"Dose Calculations"** *button* (on the **Main Screen**).

Dose Calculations						Ê.	
File Iools Advanced Help							
Save Quick Save		Γ	Dose Ca	lculatio	ons		
INTAKE		CALCULA	TION				DC
		ſ	>		€ Equiv	Eff	Indicato
IR 1 0.000E+00 Bq					Target Organs	Equivalent Dose (Sv) IR(1)	Equivalent Dose (Sv) Total
	Calculations	WR WT			Adrenals	0.00E+00	0.00E+0
					Urinary Bladder Brain	0.00E+00	0.00E+0
		Select			Breast	0.00E+00	0.00E+0
		(1) Dava from Indiantes No		- 1	Gall Bladder	0.00E+00	0.00E+0
		(1) Dose from Indicator No	iciide:		Heart Wall Kidneus	0.00E+00	0.00E+0
		(2) Droop from Associated	🛛 odiosus Islas		IT I		
		(z) obse normanio saled	neuprucides			Eff	Associated F
		(3) Drose in each Calenda	i Yesr	- II			
		(0) 0 000 11 0 001 0 000100		·			
	П		Effective Dose (Sv)				
			0.00E+00				
		00					
Progress Indicator						Eff	Calendar 1
(1)							
(2)							
(3)							
Current							
Uperation							
				<u>o</u> k			
WR	- Not Specified	WT=Not Specified	Model				

Figure 5.1. The Dose Calculations screen.

The screen is divided into these functional parts:

- <u>Menu Bar</u>.
- Intake sub-panel.
- Calculation sub-panel.
- Calculation Progress Indicator.
- Dose Results windows.

Dose Calculations Menus



💐 Dose Calculations					
<u>F</u> ile	<u>T</u> ools	Advanced	Help		
S	ave				
S	ave	Quick Save			

Figure 5.2. Dose Calculations Menus.

These are:

- the File menu to Save all parameter values to a Parameter File;
- the <u>Tools</u> menu to open the "Equivalent Doses to Selected Organ Calculated in Each Calendar Year" window;
- the Advanced menu to open "Advanced Dosimetry Options";
- the <u>Help</u> menu giving access to the full range of <u>Help</u> facilities.

Dose Calculation Tools



📑 D	Section 2012 Calculations						
<u>F</u> ile	<u>T</u> ools	Advanced	Help				
E	Organ Doses received each year						
Sa	ave	Quick Save					

Figure 5.3. Tool to open "Equivalent Doses to Selected Organ Calculated in Each Calendar Year" window.

Clicking on "**Organ Doses received in each year**" opens the "**Equivalent Doses to Selected Organ Calculated in Each Calendar Year**" window (Figure 5.4). This option (developed for <u>IMBA Expert™ OCAS-Edition</u>) is provided in IMBA Professional Plus, Add-On 9, <u>Dose Calculation For Causation</u>. It will enable you to calculate equivalent doses received by a specified organ over a prescribed time period, as used to calculate cancer causation probability - see the OCAS-IREP web page (<u>http://www.cdc.gov/niosh/ocas/ocasirep.html#irep</u>).



Figure 5.4. Window used to calculated equivalent doses received by a specified organ in each year.

Advanced Dose Calculations Menu

💐 Dose Calculations						
<u>F</u> ile	<u>T</u> ools	Advanced	Help .			
		Advance	ed Dosimetry Options			
Save		Quick Save				

Figure 5.5. Tool to open the "Advanced Dosimetry Options" window.

The "Advanced Dosimetry Options" window gives the following options:

- Exclude nuclear recoil energy from the <u>SEEs</u> for alpha emissions.
- Use Bayesian Analysis in the bioassay fitting procedure.
- Use measurements of <u>Am-241 activity to evaluate Pu-241</u> content.
- <u>Miscellaneous special functions</u> reserved for the future.
Nuclear Recoil Energy in SEE



Advanced Dosimetry Options	
These options should be used with extreme care	
Dose Fitting Bioassay Misc	
Nuclear Recoil Energy © Include © Exclude	
Dose Calculation Optimisation The dose calculation for is already optimised for both speed and accuracy	
<u>O</u> k <u>C</u> ancel	

Figure 5.6. Advanced Dosimetry Options window showing option to Exclude nuclear recoil energy from the SEEs for alpha emissions.

In the basic software version (*IMBA Professional* <u>Lite-Edition</u>), nuclear recoil energy is (by default) **included** in the SEEs for alpha emissions.

Special Fitting Procedure



Select to apply the "Least Squares", "Maximum Likelihood" (the default), or "Bayesian" fitting method (Figure 5.7) in the calculation of intake(s). This option is also available from the <u>Bioassay Calculations</u> screen (Advanced Menu).



Figure 5.7. "Fitting" Options window.

Special Bioassay Procedure



This will enable measurements of 241**Am**, e.g., in the lungs, to be used as an indicator of 241**Pu** activity (Figure 5.8), by automatically accounting for 241**Am** in-growth over time. The option is made available <u>automatically</u> when the **Indicator Nuclide** is defined as 241**Am**, <u>AND</u> 241**Pu** is included in the list of **Associated Radionuclides**. See <u>Case Of Am-241 In-growth</u> as an example.

Advanced Dosimetry Options	
These estimates about the sound with estimate and	
i nese options should be used with extreme care	
Dose Fitting Bioassay Misc	_
Allow ingrowth of Am-241 from Pu-241	
<u>O</u> k <u>C</u> ancel	

Figure 5.8. Future Special Bioassay feature.

()

•

Specify Intakes In Mass Units (mg)

Advanced Dosimetry Options	- 🗆 🛛
These options should be used with extreme care	
Dore Filting Bioarray Miac	_
Specific Activity Allow inlakes to be specified in mg (Main Screen) Enter Specific Activity Bg/mg	
DK Earcel	

Figure 5.9. "Miscellaneous" Option - Use of "Mass" as the Unit of Intake.

When *checked*, this option allows **Intakes** to be specified in terms of **Mass** rather than **Activity**, with the associated **Specific Activity**. If you don't define the specific activity, you will be prompted to do this (figure 5.10).

IMBA Expert Help
In order to enable units of mg (on the main screen) you must specify a value for the Specific Activity
COK

Figure 5.10. Prompt to define Specific Activity in order to use Mass as the Unit of Intake.

Checking this option automatically highlights and enables the "**mg**" *Unit of Intake* in the "**Units**" panel of the **Main Screen** (Figure 5.11).



Figure 5.11. "mg" Unit of Intake enabled.

For an example of the use of "**Mass**" as the **Unit of Intake**, see Example Bioassay Cases - "<u>Case of Uranium Isotopic Mixture</u>".

Intake Sub-Panel - Dose Calculations

💐 Dose Calculations
<u>File Tools Advanced</u> Help
Save Quick Save
INTAKE
IR 1 2.998E+02 Bq
IR 2 1.534E+02 Bq
IR 3 1.169E+02 Bq

Figure 5.12. Intake sub-panel.

The **Intake** sub-panel shown in Figure 5.12 is displaying the calculated amounts of three intakes (IR1, IR2 and IR3). These values are the result of the <u>Example of Estimating Multiple</u> <u>Intakes</u> using the <u>Miller et al. (1999)</u> data. You can also enter hypothetical values of intake, or values from other sources, directly in the **Intake** dialog boxes.

Dose Calculations Sub-Panel



00

CALCULATION		
WR WT		
Select		
(1) Dose from Indicator Nuclide:		
(3) Dose in each Calendar Year		
Effective Dose (Sv)		
	CALCULATION CALCULATION WB WT Select (1) Dose from Indicator Nuclide: (2) Dose from Associated Radionuclides (3) Dose in each Calendar Year Effective Dose (Sv) Calculate Calculate Calculate Calculate	

Figure 5.13. Dose Calculation sub-panel at start-up.

Figure 5.13 shows the **Dose Calculation** sub-panel as it appears for a **New** case (blank **Parameter File**). Note the red flags above the "**WR**" and "**WT**" tabs, signifying that neither the **Radiation Weighting Factors** nor the **Tissue Weighting Factors** to be used in the dose calculation have yet been defined. Also, no **Indicator Nuclide** has yet been defined - signified by the absence of a named radionuclide in the "**(1) Dose from Indicator Nuclide**" label.

Dose from Associated Radionuclides

Returning to the <u>Miller et al. (1999</u>) example case, let's assume that each intake of <u>238</u>Pu was associated with two additional radionuclides, <u>239</u>Pu and <u>241</u>Am. Let's hypothesize that the <u>239</u>Pu activity concentration in the inhaled material was 15% of the indicator <u>238</u>Pu value, and the <u>241</u>Am activity concentration 5%. These values are set up in the **Associated Radionuclides** sub-panel of the **Main Screen**, as shown in Figure 5.14.

ull Edition	n nrpb			
Intake (IR 1) 299.83 Bq	Indicator Nuclide Select Radionuclide Pu-238 Number of Associated Radionuclides: 2 Half Life: 32030 d			
Associated Radionuclides Pu-239 Am-241				
Select Radionuc	slide Abundance <mark>5</mark> % Slide Half Life: 157800 d			

Figure 5.14. Example of two Associated Radionuclides, with 238Pu as the Indicator Nuclide.

For this example, the **Dose Calculation** sub-panel will appear as shown in Figure 5.15. Note that a second checkbox is now activated - for "(2) **Dose from Associated Radionuclides**".

CALCULATION			
Calculation	s wr		
	- Select		
	(1) Dose from Indicator Nuclide: Pu-238	•	
	(2) Dose from Associated Radionuclides		
	(3) Dose in each Calendar Year		
	Effective Dose (Sv)		
	Calculate 0.00E+00		

Figure 5.15. Dose Calculation sub-panel for case with Associated Radionuclides.

Defining the Radiation Weighting



Factor

CALCULATION				
Calculations WR WT				
This option allows you to specify the radiation weighting factors that will be used in the calculation of equivalent dose.				
Alpha 20 ICRP Defaults				
Beta 1 User Defined				
Gamma 1				
ICRP Defaults				

Figure 5.16. Selection of ICRP-recommended Radiation Weighting Factors.

Click the "**WR**" *tab* and *click* the "**ICRP Defaults**" *button* to load the ICRP-recommended values for the <u>Radiation Weighting Factors</u>. You can also define your own (**User Defined**) value for Alpha, Beta and/or Gamma radiation.

Selecting the Tissue Weighting Factors





Figure 5.17. Selection of ICRP60/68 Tissue Weighting Factors and Remainder Tissue Rules.

Click the "WT" *tab* to *select* or *edit* the **Tissue Weighting Factors** and **Remainder Tissue Rules** to be used for the calculation of **Effective Dose** (Figure 5.17). In this example, the values recommended in ICRP 60/68 have been selected. *Click* the "**Edit Tissue Weighting Factors**" button to view these selected (and loaded) values (Figure 5.18).

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🍕 Tissue Weig	hting Fa	ctors				
Target Organ	WT	Remainder	Target Organ	WT	Remainder	
, ,		,		,		
Adrenals			Skin	0.01		ICRP 60/68 CRP 26/30 10 C
Urinary Bladder	0.05		Spleen			
Brain		$\overline{\mathbf{v}}$	Thymus			ICRP 68 Defaults User Defined
Breast	0.05		Uterus			
Gall Bladder			ET			Bules
Heart Wall			Lung	0.12		
Kidneys			+Colon	0.12		 Apply splitting rule to the remain Selected list) which receives the
Liver	0.05		ET1			equivalent dose.
Muscle			ET2	<u> </u>		Always apply splitting rule to
*Ovaries			LN(ET)			C Do NOT apply the splitting rule
Pancreas			BBsec			
*Testes		Г	BBbas			
Thyroid	0.05	Г	ьр		Г	
R.B.M.	0.12	Г	AI			
Bone Surface	0.01	Г	LN(TH)			
Stomach	0.12	Г	Esophagus	0.05	Г	
S.I.		$\overline{\vee}$	*Gonads	0.2		ICRP 68
U.L.I.		Г	Spare			
L.L.I.			Remainder	0.05		
* Gonads dose is t	he higher	of Testes and	l Ovaries doses			+ Colon dose is the mass weighted average of L

Figure 5.18. The Tissue Weighting Factors window.

In this window, you can also *opt* to use the values of **Tissue Weighting Factor** and **Remainder Tissue Rules** required in <u>10 CFR 835</u> (for use in the U.S.), or those recommended in <u>ICRP26/30</u>, on which the **10 CFR 835** values are based.

Dose Calculation Progress Indicator

To *calculate* (and display) the resulting doses, *check* the required calculation(s), and *click* the "Calculate" *button*. If you have forgotten to *specify* the **Biokinetic Model** for the **Indicator Nuclide**, you will see the **Warning Notice** shown in Figure 5.19. Once you have *selected* the **Biokinetic Model**, the dose calculation will proceed automatically.

IMBA-X Help	×
The biokinetic model for intake regime 1 has not been specified. the 'Biokinetics' button (under model parameters, bottom right)	You need to specify this by going to the main screen and hitting
Do you want to do this now?	
	No

Figure 5.19. Warning Notice to select a Biokinetic Model for the Indicator Nuclide.

Note: For all **Associated Radionuclides**, IMBA Professional automatically selects the **currently recommended ICRP biokinetic model**.

The **Progress Indicator** (Figure 5.20) displays which part of the calculation is currently being performed, and when the final dose calculations are complete. All calculations are sequenced and performed automatically. In the example shown in Figure 5.20, IMBA **Professional** is calculating the numbers of radioactive disintegrations in each source organ resulting from the third intake (**IR3**) - for the **Associated Radionuclides** - the second *checked* calculation.

INTAKE	CALCULATION
IR 1 2.998E+02 Bq	
IR 2 1.534E+02 Bq	Calculations WR WT
IR 3 1.169E+02 Bq	Select
	(1) Dose from Indicator Nuclide: Pu-238
	(2) Dose from Associated Radionuclides 🔽
	(3) Dose in each Calendar Year 🗖
	Effective Dose (Sv)
Progress Indicator	
(1)	
(2)	
(3)	
Current Operation	Calculating Disintegrations (IR 3)

Figure 5.20. Progress Indicator shows what calculation is currently being performed.

Dose Results Windows



Figure 5.21. Displayed results of a completed **Dose Calculation** set to show **Equivalent Doses** in the "**Dose**" windows.

Figure 5.21 shows the results for **Equivalent Dose** displayed in two windows:

- Indicator Radionuclide window for each separate Intake Regime (IR), together with the Total Equivalent Dose from all intake regimes to each Target Organ;
- Associated Radionuclide window for each Associated Radionuclide, together with the Total Equivalent Dose from all associated radionuclides to each Target Organ.

You can *toggle* the "**Equiv/Eff**" selector for either window to switch the display instantly between **Equivalent Dose** and **Effective Dose**. Figure 5.22 shows both window displays switched to **Effective Dose**.

DOSE								
O Equiv 🤇	C Equiv C Eff Indicator Nuclide tool							
Target Organs	Cont. to Eff Dose (Sv) IR(1)	Cont. to Eff Dose (Sv) IR(2)	Cont. to Eff Dose (Sv) IR(3)	Effective Dose (Sv) Total				
Adrenals	0.00E+00	0.00E+00	0.00E+00	0.00E+00				
Urinary Bladder	5.05E-05	2.58E-05	1.97E-05	9.59E-05				
Brain	0.00E+00	0.00E+00	0.00E+00	0.00E+00				
Breast	5.05E-05	2.58E-05	1.97E-05	9.59E-05				
Gall Bladder	0.00E+00	0.00E+00	0.00E+00	0.00E+00				
Heart Wall	0.00E+00	0.00E+00	0.00E+00	0.00E+00				
Kidnevs	0 00F+00	0 00F +00	0 00F +00	0 00F +00	▼ ►			
C Equiv 🖸	Eff [Associated Ra	dionuclides	to	ol			
Target Organs	Eff Dose from Pu-239 (Sv)	Eff Dose from Am-241 (S∨)	Eff Dose from ALL AR's (S∨)					
Adrenals	0.00E+00	0.00E+00	0.00E+00					
Urinary Bladder	1.62E-05	5.70E-06	2.19E-05					
Brain	0.00E+00	0.00E+00	0.00E+00					
Breast	1.62E-05	5.70E-06	2.19E-05					
Gall Bladder	0.00E+00	0.00E+00	0.00E+00					
Heart Wall	0.00E+00	0.00E+00	0.00E+00					
Kidnevs ◀	1 0 00F+00	0 00F +00	0 00F +00		▼ ►			

Figure 5.22. Displayed results of a completed **Dose Calculation** set to show **Effective Doses** in the "**Dose**" windows.



Note: During a calculation, the dialog box labeled "**Effective Dose (Sv)**" in Figure 5.21 displays first the **Effective Dose** calculated for the **Indicator Nuclide** - as soon as this result is available. Once the calculations are completed for the **Associated Radionuclide(s)**, the total **Effective Dose** from the latter is automatically **added** to that from the **Indicator Nuclide**, and the result (overall total) is displayed in the dialog box.__

Example Dose Calculation

Note: This example illustrates the calculation of doses for the multiple intakes case (Miller et al., 1999) described earlier.

Clicking the "Dose Calculations" button in the Main Screen, opens the Dose Calculations screen (Figure 5.23). The Indicator Nuclide defined in the Main Screen is automatically shown in the "Dose from indicator radionuclide" label - under the "Calculations" tab in this example "Pu-238." Also, the previously estimated amounts of each intake (in this example IR1, IR2 and IR3) are also displayed automatically under "INTAKE."

Section 24 Calculations					
<u>File T</u> ools <u>A</u> dvanced Help					
Save Quick Save				ose Ca	alculati
INTAKE		CA	LCULAT	ION	
		_		>	
IR 2 1.534E+02 Bq	Calculations	WR	WT		
IR 3 1.169E+02 Bq	Г	Select			
		(1) Dose from	Indicator Nuclid	le: Pu-238	V
		(2) Dose from	Associated Rad	lionuclides	
		(3) Dose in ea	ach Calendar Ye	ar	
		<u>C</u> alculate	Effec	ctive Dose (Sv)	

Figure 5.23. Checking the "Dose from indicator radionuclide (Pu-238)" dialog box in the Dose Calculations screen.

BEFORE calculating any doses, you need to select the values of Radiation Weighting Factor (w_R) to be used. This is done by *clicking* the "WR" *tab* in the "CALCULATION" subpanel. If the values of w_R have NOT already been specified, the "WR" tab will appear as in Figure 5.24.

CALCULATION							
Calculations WR WT							
This option allows you to specify the radiation weighting factors that will be used in the calculation of equivalent dose.							
Alpha 0 ICRP Defaults Beta 0 User Defined Gamma 0							
Not Specified							



Click the "ICRP Defaults" button, to load the ICRP-recommended (as also prescribed by 10-CFR-835) values of w_R :

CALCULATION							
Calculations WR WT							
This option allows you to specify the radiation weighting factors that will be used in the calculation of equivalent dose.							
Alpha 20 [ICRP Defaults] Beta 1 User Defined							
Gamma 1							
ICRP Defaults							

Figure 5.25. Loading the ICRP Default values of radiation weighting factor.

Click the "**WT**" *tab* to *select* (or confirm the previous selection of) the **ICRP60/68** tissue weighting factors (w_{τ}) - see Figure 5.26.



Figure 5.26. Selection of ICRP60/68 tissue weighting factors.

Click the "Edit Tissue Weighting

Factors" *button* to *select* and/or *confirm* the **ICRP60/68** values of tissue weighting factors and the remainder tissue rules (Figure 5.27). *Click* the "**OK**" *button* to *return* to the **Dose Calculations** screen.

🍕 Tissue Weig	jhting Fa	ictors				
Target Organ	WT	Remainder	Target Organ	WT	Remainder	
, ,)		1		
Adrenals			Skin	0.01		ICRP 60/68 ICRP 26/30 10 C
Urinary Bladder	0.05	Г	Spleen			· · · · · · · · · · · · · · · · · · ·
Brain			Thymus			ICRP 68 Defaults User Defined
Breast	0.05		Uterus			<u></u>
Gall Bladder			ET			Bules
Heart Wall		Г	Lung	0.12	Г	
Kidneys		V	+Colon	0.12	Г	 Apply splitting rule to the remain Selected list) which receives the
Liver	0.05	Г	ET1		Г	equivalent dose.
Muscle		V	ET2		Г	Always apply splitting rule to
*Ovaries		Г	LN(ET)		Г	C Do NOT apply the splitting rule
Pancreas			BBsec		Г	
*Testes		Г	BBbas		Г	
Thyroid	0.05	Г	ЬЬ		Г	
R.B.M.	0.12	Г	Al		Г	
Bone Surface	0.01	Г	LN(TH)		Г	
Stomach	0.12	Г	Esophagus	0.05	Г	
S.I.		$\overline{\mathbf{V}}$	*Gonads	0.2	Г	ICRP 68
U.L.I.		Г	Spare		Г	ОК
L.L.I.		Г	Remainder	0.05		
* Gonads dose is	the higher	of Testes and	l Ovaries doses			+ Colon dose is the mass weighted average of L

Figure 5.27. Selection of **ICRP60/68** values for the tissue weighting factors and **ICRP60/68** remainder tissue rules.

Calculation of Equivalent Doses

To *calculate* the equivalent doses received by **all** target tissues (from **each of the 3 intakes**):

- *click* the "Calculations" *tab*;
- click the "Calculate" button.

The **calculated doses** will be displayed in the "**DOSE**" table for the **Indicator Radionuclide** (Figure 5.28). Use the *scroll bar* (right-side) to *view* the **equivalent doses** calculated for the additional **Target Organs**.

00

🔍 Dose Calo	culations								
File Iools &	Advanced	Help							
Save Q	ick Save				Dose	Calcula	tions		
IN	TAKE		CA	LCULA	TION				DC
		,	_				@ Equity	CEff	Indicato
			_				to Science .	Envirolant	Envirolant
IR 1 2.9988	E+O2 Bq		γ	r Y	_		Target Organs	Dose (Sv) IR(1)	Dose (Sv) IR(2)
IB 2 1.5348	E+02 Bq	Calculations	WR	WT			Adrenals	1.01E-03	5.16E-0
1.0010							Urinary Bladder	1.01E-03	5.16E-0
IR 3 1.1696	E+02 Bq		Calact				Breast	1.01E-03	5.16E-0
			Select				Gall Bladder	1.01E-03	5.16E-(
			(1) Dose from	Indicator Nu	iclide: Pu-238	ম	Heart Wall	1.01E-03	5.16E-0
							Kidneus	2.51E-03	1.28E-0
			(2) Dose from	Associated	Radionuclides	E			
			,-,			_	C Equiv 6	Eff	Associated F
			(3) Dose in e	ach Calendar	Year		Target Organs	Eff Dose from Pu-239 (Sv)	Eff Dose fro Am-241 (Sv)
							Adrenals	0.00E+00	0.00E+0
				E	ffective Dose (Sv)	Urinary Bladder	0.00E+00	0.00E+0
			<u>C</u> alculate	l r	3.41E-02		Brain	0.00E+00	0.00E+0
					0.412 02		Gall Bladder	0.00E+00	0.00E+0
							Heart Wall	0.00E+00	0.00E+(
							Kidneys	0.00F+00	0.00E+0
- Program	Indicator	0	00						
riogressi								Eff	Calendar 1
(1)									
(2)	Г								
(3)	Г								
Current Operation	In	ake Regime 1: Applying Spl	tting Rule to Bon	ne Surface. T	his is already a r	named			
						<u>0</u> K			
Pu-238		WR=ICRP Defaults	WT=ICRP 68		Pu Model				

Figure 5.28. Calculated values of Equivalent Dose (for the Indicator Radionuclide).

Display of Effective Doses

IMBA Professional Plus calculates (and **stores**) ALL doses of interest (including the **effective dose resulting from each intake**) in one step. Therefore, it is not necessary to carry out a further calculation to **display the effective doses**. Simply *click* the "**Eff**" *option* to *switch* the display to Effective Dose (Figure 5.29).

00

Dose Calculations				
File Iools Advanced Help				
Save Quick Save	Dose Calculation	ons		
INTAKE	CALCULATION			DC
		C Equiv (• Eff [Indicato
IR 1 2.998E+02 Bq		Target Organs	Cont. to Eff Dose (Sv) IR(1)	Cont. to Eff Dose (Sv) IR(2)
IB 2 1.534E+02 Bg	Calculations WR WT	LN(TH)	0.00E+00	0.00E+0
1.0012-02		Esophagus	5.05E-05	2.58E-0
IR 3 1.169E+02 Bq		Gonads	1.55E-03	7.93E-0
	Select	Spare	0.00E+00	0.00E+0
		Remainder	5.12E-05	2.62E-0
	[1] Dose from Indicator Nuclide: Pu-238	TOTAL	1.79E-02	9.18E-0
	(2) Dose from Associated Radionuclides	C Equiv @	'Eff ∫	Associated F
	(3) Dose in each Calendar Year	Target Organs	Eff Dose from Pu-239 (Sv)	Eff Dose fro Am-241 (Sv)
		Adrenals	0.00E+00	0.00E+0
	Effective Dose (Sv)	Urinary Bladder	0.00E+00	0.00E+0
	Calculate	Brain	0.00E+00	0.00E+0
	3.41E-02	Breast	0.00E+00	0.00E+0
		Gall Bladder	0.00E+00	0.00E+0
		Heart Wall	0.00E+00	0.00E+0
	0.00	Kidneus	0.00E+00	0.00E+0

Figure 5.29. Displaying the **TOTAL Effective Dose** resulting from each intake (and the contributions from each target organ).

The values of **Effective Dose** that are calculated to result from **each separate intake** (in the **multiple intakes** example case) are:

- EIR1 = 17.9 mSv (1.8 rem);
- EIR2 = 9.2 mSv (0.9 rem);
- EIR3 = 7.0 mSv (0.7 rem).

The TOTAL Effective Dose (from all Intakes) is calculated to be 34.1 mSv (3.4 rem).



Tip: It is instructive to repeat the above calculation for the "initial" and each subsequent estimate of the intake amounts (see <u>Optimizing the Intake Estimation</u>), together with their respective assumed **Model Parameters**. This will indicate the **range of uncertainty** in the calculated **Effective Dose** that results solely from the **intake estimation process**. Try this for yourself - it is quick and easy! Uncertainties in the biokinetic models (and dose-weighting factors) will, of course, contribute **additional uncertainty** to the **Effective Dose**.

Tip: Also try repeating the example dose calculation after selecting 10 CFR 835 tissue weighting factors and remainder tissue rules.

Calculating Doses from Associated Radionuclides (Using Add-On 3)



Doses from <u>Associated Radionuclides</u> are calculated at the same time as those from the **Indicator Nuclide** - see <u>Dose Results Windows</u>. In fact, setting up the dose calculation for **Associated Radionuclides** is even simpler than setting up the **Indicator Radionuclide** dose calculation:

- 1. Select each Associated Radionuclide from the Periodic Table of the Elements (in the Main Screen).
- Define the Abundance (in %) of each Associated Radionuclide relative to the activity of the Indicator Nuclide - this is assumed to be the same for all Intake Regimes.
- 3. Check the "Dose from Associated Radionuclides" box in the "Calculations" sub-panel (Dose Calculations screen).
- 4. Click the "Calculate" button.

IMBA Professional Plus will automatically load the recommended **ICRP Biokinetic Model** for each **Associated Radionuclide** (to calculate the number of disintegrations in each Source Organ) and then use the recommended **ICRP SEE Data File** to calculate the resulting doses to Target Organs. See also the **Technical Basis** section on Treatment of Associated Radionuclides.

Example Cases - Bioassay & Dosimetry



The following case examples (taken from real cases) illustrate the main features provided in IMBA Professional Plus (Version 4.0) for estimating intake(s) from bioassay data (and calculating the resulting doses):

- Calculation of a single intake performed by Base Unit.
- Calculation of <u>multiple</u> intakes requires Add-On 1.
- Calculation using multiple bioassay data sets requires Add-On 2.
- Calculations for associated radionuclides require Add-On 3.
- Calculations with uranium isotopic mixtures require Add-On 4.
- Calculations involving an intake via a wound see <u>Case of Wound Uptake</u> requires Add-On 5.
- Calculations involving the estimation of errors on calculated values of intake see <u>Case</u> <u>Evaluating Errors on Intake</u> - requires Add-On 6.
- Calculation involving Bayesian analysis of intake see <u>Case Using Bayesian Analysis</u> requires Add-On 7.
- Calculation involving <u>Case Implementing Tritium Tool</u> requires Add-On 8.
- Calculation of equivalent doses received each year by a specified tissue (for use in the determination of cancer causation likelihood) see <u>Dose Calculations for Causation</u> requires Add-On 9.
- Calculation using external measurements of ²⁴¹Am activity as an indicator of plutonium activity in the lungs see <u>Case of Am-241 In-growth</u> requires Add-On 10.
- Calculation using the statistics package to evaluate an intake see <u>Case Using Statistics</u> <u>Package</u> - requires Add-On 11.

Note: All but the first of these example cases require one or more IMBA Professional Plus "Add-On" modules.

Example Case of Single Intake -Requires Only Base Unit

This example is one of the study cases taken from <u>IAEA (1999)</u> - see their Annex IV Case 3. The data are whole-body activity measurements of <u>60</u>Co commencing 1 day after an accidental inhalation of a cobalt metal and/or oxide aerosol. All external body surface contamination was removed by shower -bathing. A profile scan indicated dominant lung deposition. The accident occurred on February 24<u>th</u>, 1988. The whole-body activity measurements are given in Table 4.1.

 Table 4.1.
 60Co whole-body measurement results.

Measurement date	Whole-body activity (Bq)
February 25, 1988	2720
March 1, 1988	1150
March 11, 1988	1010

March 28, 1988790May 16, 1988482August 11, 1988358November 29, 199078February 19, 199235

• <u>View</u> list of steps for estimating a single intake.

Steps in Calculation of Single Intake

The following steps (in the listed order) are recommended for calculating the amount of a single intake (by inhalation) from a set of whole-body measurements - where the time of the intake is known, and the aerosol and absorption parameters of the inhaled material can be specified with reasonable confidence. The additional steps required for a more complicated assessment (involving multiple intakes with unknown parameters) are described separately.

- 1. <u>Select</u> the <u>Indicator Nuclide</u> in the <u>Main Screen</u>.
- 2. Define the Reference Date in the Main Screen.
- 3. <u>Select</u> the <u>Reference Activity Units</u> in the <u>Main Screen</u>.
- 4. <u>Select</u> the <u>Bioassay Model</u> and other required <u>Model Parameters</u> in the <u>Main Screen</u>.
- 5. Define the Intake Regime (IR1) in the Main Screen.
- <u>Select</u> in the <u>Bioassay Calculations</u> screen the <u>Bioassay Quantity</u> as "<u>Whole body</u>" (for display in the top <u>Bioassay Quantity</u> window).
- 7. Enter the bioassay data using the <u>data entry</u> "tool" in the <u>Bioassay Quantity</u> window.
- 8. <u>Graph</u> the bioassay data using the <u>graph set up</u> "tool" in <u>Bioassay Quantity</u> window.
- 9. Select which bioassay data to use ("Whole body") and click "Start Calculation."
- 10. Improve the data fit using the Graph of the Bioassay Quantity.

• Follow a more complex example involving the calculation of <u>multiple intakes</u> with <u>unknown</u> <u>intake parameters</u> (Star Function). This example demonstrates an <u>iterative</u> <u>optimization</u> of the <u>Model Parameters</u>.

Indicator Nuclide for Single Intake

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Intake (IR 1) 0 Bq	Indicator Nuclide Co-60 Select Radionuclide 0 Number of Associated Radionuclides: 0 Half Life: 1924 d
Associated Radio	onuclides
	None Selected

Figure 4.17. Selecting the Indicator Nuclide (60Co).

<u>Select</u> the Indicator Nuclide (60Co in this example case) from the top-right-corner of the Main Screen (Figure 4.17). IMBA Professional will then be able to select automatically the bioassay model(s) appropriate for cobalt, and automatically take into account the radioactive half-life 60Co.



This completes Step #1 of the single intake example:

- <u>Proceed</u> to the next step.
- <u>Return</u> to the case description and list of steps.

Reference Date for Single Intake

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<u>IMBA Professional</u> keeps track of the Intake and all bioassay measurements on a common timescale. All events are timed with respect to a single Reference Date (and time-of-day, if necessary). The Reference Date is defined in the Main Screen (Figure 4.18). The IMBA System must always have a reference date - even if you are working entirely in the Time (d) mode. The default value (January 1 st, 1980) is loaded at start-up.

Intake Scenario Intake Regimes Clear All Intake Regimes	Enter Number of Ir	ntake Regimes (1-10) 👖 🛓	1	- Units	ime As	Intaka 0
Route C Inhalation C Ingestion	Mode	C Chronic		intake -	aj 180 #	Associ
C Injection	Start Time(d)	0 #		⊙ Bq ⊙ pCi	O dpm O mg	
		Edit Complex Regime		⊙ Sv ⊙ mSv	O rem O mrem	

Figure 4.18. Default "since" date loaded at start-up.

In this example case, the intake occurred on February $24\underline{th}$, 1988, and so this is the appropriate value for the Reference Date. The date of the intake is entered directly in the "Time (d) since" dialog box (Figure 4.19). The source data did not give the time-of-day. If no value for the hh:mm (time-of-day) of the intake is entered, IMBA Professional assigns this as 00:00 (midnight).



Figure 4.19. Entering the Reference Date.

Since in this example, the bioassay measurements are tabulated with their collection Date, it is convenient at this point to switch the "Specify Time As" Units to "Date" (Figure 4.20). This switch from "Time" to "Date" will be passed automatically to the Bioassay Calculations screen and data tables.

Enter Number of I	Specify Time As		
Mode • Acute	C Chronic	Time (d) since 24/02/1988	
Start Date	24/02/1988 #	Intake ⊙ Bq O dpm ⊙ pCi O mg	
	Edit Complex Regime	Dose ⊙Sv Orem OmSv Omrem	

Figure 4.20. Switching the Units of Time to Date.

Notice that the "Start Time (d)" value of " $\underline{0}$ " (Figure 4.20) has now automatically switched to display the "Start Date" as "24/02/1988" - the value entered as the Reference Date before the switch of time units.

Key Tip: Always set the Reference Date for each case study - in the "Time (d) since" dialog box ("Units" sub-panel in the Main Screen).

This completes Step #2 of the single intake example:

- Proceed to the next step.
- <u>Return</u> to the case description and list of steps.

Reference Activity Units for Single Intake

In <u>IMBA Professional</u>, the estimated Intake has the same Unit of activity as the measured (or predicted) bioassay quantity. As with the Unit of Time, the Unit of Activity is selected in the Main Screen (Figure 4.21).

For this example case, the whole-body activity results are tabulated as Bq. Therefore, the required Unit of Activity is "Bq."



Figure 4.21. Selecting the Unit of activity (Intake and Bioassay Quantity) as "Bq."

Warning: IMBA Professional works with the primary bioassay quantity - which for urinary or faecal excretion is the average excretion rate over a prescribed collection period (and not the amount of activity in each sample). So, urinary and fecal bioassay measurements must ALWAYS be entered as the amount of activity in the sample (in the selected unit) divided by the collection period (in d)._

This completes Step #3 of the single intake example:

- Proceed to the next step.
- <u>Return</u> to the case description and list of steps.

Select Required Model Parameters for Single Intake

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Before you can carry out any calculations with <u>IMBA Professional</u>, you MUST define all of the necessary Model Parameters. It is most efficient to do this while you are still in the Main Screen - although (if you forget to do this) it is very easy and quick to switch backwards and forwards between the Bioassay Calculations screen and the Main Screen (with a single <u>click</u>).

To estimate an Intake (by inhalation) from a measured Bioassay Quantity, you must all define the following Model Parameters -as indicated by the "red" buttons in Figure 4.22:

- Bioassay model.
- Deposition model.
- Particle Transport model.
- Absorption model.
- GI-Tract model.

If you omit defining any of these models, then <u>IMBA Professional</u> will prompt you for each missing model definition before proceeding with a calculation.



Figure 4.22. Bioassay button for selecting the Bioassay Model.

Bioassay model (for example of single 60Co intake)

For the Bioassay model, select the "Standard Co Model" for whole-body retention (Figure 4.23):

- <u>select</u> "Whole body" as the Bioassay Function this will already have been defined if you had previously selected Whole body in the Bioassay Quantity window (Bioassay Calculations screen);
- <u>click</u> the "LOAD ICRP DEFAULTS" button;
- <u>click</u> "OK".

Bioassay Mode	1					
- Bloassay Functio	n	Whole body		-		
				_		
		Trans	fer Comp	artment		
	Ka(1)	Ka(2)		Ka	a(9)	Ka(10)
Systemic Retention	Comp 1	Comp 2		Comp	9 Cor	np 10
	Lam(1)	Lam(2)			Lam(9)	Lam(10)
		E	Excretion			
Bioassay Function a(1) 0.33973 i a(i) 1 3.397E-01	1388888591 Lam(i) 1.155E-01		Select	E	3lood half time	(K) 0.0000001
2 1.012E-01 3 1.001E-01 4 -3.019E-01 5 2.865E-01	1.155E-02 8.664E-04 1.386E+00 1.800E+00			User D	efined Mode	
6 5.301E-01 7 -5.564E-02 8 9	1.000E+00 1.200E+01			Std C	o Model	
10				<u>0</u> K	Ē	ancel
WHOLE BODY LL Std Co Model	JNGS URINE	FECES	BLOOD	THYROID	LIVER	USER DEFINED

Figure 4.23. Standard Co Model for Whole body selected as the Bioassay Model.

<u>Deposition model</u> (for example of single <u>60</u>Co intake)

For the Deposition model, select the "Light worker" (Figure 4.24):

- <u>click</u> the "LOAD ICRP DEFAULTS" button;
- click "OK".

🖏 Deposition Model	
Extrathoracic Ainways (ET1 & ET2) Conducting Airways (BB & bb) Deep Lung (A)	Exposure C Light Worker C Heavy Worker Aerosol Parameters Aerosol Parameters AMAD 5 μm Sigma-G 2.4977233 Density 3 g/ml Shape factor 1.5
Clear	Select User Defined User Defaults ICRP Defaults

Figure 4.24. Selecting the Deposition Model for a Light worker.

Particle transport model (for example of single <u>60</u>Co intake)

For the Particle Transport model (Figure 4.25):
<u>click</u> the "LOAD ICRP DEFAULTS" button;
<u>click</u> "OK".

💐 Particle Tra	nsport Model	
Rate Constants	(/d)	
Al1 to bb1	0.02	
AI2 to bb1	0.001	
AI3 to bb1	0.0001	
AI3 to LNTH	0.00002	LNET ETseq ET2
bb1 to BB1	2	
bb2 to BB1	0.03	Thoracio
bbseq to LNTH	0.01	
BB1 to ET2	10	BBseq BB2 BB1
BB2 to ET2	0.03	
BBseq to LNTH	0.01	LNTH bbseq bb2 bb1
ET2 to GI	100	
ETseq to LNET	0.001	
ET1 Out	1	
FTseq/FT2	0.0005	- Select
BBseg/BB	0.0005	User Defined
bbseq/bb	0.007	
AI2/AI	0.007	
	0.1	ICRP Defaults <u>OK</u> <u>Cancel</u>
AI3/AI	0.1	
	Clea <u>r</u>	

Figure 4.25. Selecting the ICRP Default Particle Transport Model.

Absorption model (for example of single <u>60</u>Co intake)

For the Absorption model, select the Type M ICRP Default model (Figure 4.26) see Cobalt Biokinetic Model (Technical Basis Section):

- <u>click</u> the "Type M" button;
 <u>click</u> "OK".



_

To_select_an appropriate (ICRP-recommended) value of f¹:

- click the "Help" button (Figure 4.26);
- select the "Abs.: M" row (Figure 4.27);
- click <u>"OK"</u>.

🗠 F1 v	values and	d absorpti	on Types	s for Cobalt		
	Abs.	f1	ICRP	Chemical Form		
	F	0.1	71			
	M	0.1	71			
	S	0.01	71			
+	M) 0.1	68	Unspecified compounds		
	S	0.05	68	Oxides, hydroxides, halides and nitrates		
	Ing	0.1	68	Unspecified compounds		
	Ing	0.05	68	Oxides, hydroxides and inorganic compounds		
Note: on	Note: only the absorption parameters are entered. NOT the default AMAD.					

Figure 4.27. Selecting the ICRP-recommended value of \underline{f}^1 .

<u>GI-Tract model</u> (for example of single <u>60</u>Co intake)

For the GI-Tract model, select LOAD ICRP DEFAULTS (Figure 4.28):

- <u>click</u> the "LOAD ICRP DEFAULTS" button;
- <u>click</u> "OK".



Figure 4.28. Selecting the ICRP Default GI - Tract Model.

This completes the definition of ALL Model Parameters required to calculate the Intake of <u>60</u>Co in the <u>IAEA (1999)</u> example case.

Key Tip: You can short-cut the process of loading each of the above Model Parameters individually by clicking the "ICRP Defs LOAD" tool button. You will then be prompted to choose the Absorption Model and value of \underline{f}^1 .

This completes Step #4 of the single intake example:

- Proceed to the next step.
- <u>Return</u> to the case description and list of steps.

Select Intake Regime (IR1)



By default, IMBA Professional sets up a **Single Intake Regime (IR1)** - as an **Acute Inhalation** (Figure 4.29). At this point no value of the **Intake** has been set (or calculated).

⊢Intake Scenario	
Intake Regimes Clear All Intake Regimes Enter Number of Intake Regimes (1-10)	Units Specify Time As O Date O Lime (0
Route Mode Chronic	Since 24/02/1988 # Associated Radionuclides
C Ingestion C Injection Start Date 24/02/1988 # C Wound	C pCi C mg

Figure 4.29. IR1 defined (by default) as Acute Inhalation.

This completes Step #5 in the single intake example:

- <u>Proceed</u> to the next step.
- <u>Return</u> to the case description and list of steps.

Select Whole Body Activity as Bioassay Quantity

0	٢

BIOASSAY QUANTITY							
C Graph	Whole body Item tool Whole body rement Date Lungs m] Urine m] Feces Blood Thyroid Liver User Defined Value						
⊂ Graph ⊂ Table ⊙ Hide							

Figure 4.30. Drop-down Bioassay Quantity list box.

The previous steps were carried out in the **Main Screen**. You select the **Bioassay Quantity** in the **Bioassay Calculations** screen. From the **Main Screen** you:

- <u>Click</u> the "Bioassay Calculations" button (bottom-right-corner of the Main Screen) to open the Bioassay Calculations screen.
- In the top **Bioassay Quantity** window (set as "**Table**" by default), <u>select</u> "**Whole body**" from the drop-down list box (Figure 4.30).

This "<u>opens</u>" the first **Bioassay Quantity** window to **display** in that window a **Table** containing both **measured** whole-body activity data (on a **blue background**) and **predicted** whole-body activity data (on a **green background**).



This completes Step #6 in the single intake example:

- Proceed to the next step.
- Return to the case description and list of steps.

Enter Measurement Data



<u>IMBA Professional</u> provides a "**Table Tool**" in the form of an expanded data table with various editing and automated data entry functions.

Opening the Table Tool

Once you have selected the **bioassay quantity** for display in the **Bioassay Quantity** window, the "**tool**" button (in the top-right-corner) is activated - see Figure 4.31. Click this "**tool**" button to open the <u>Table Tool</u>. This will enable you to enter (and/or edit) the **whole-body activity** data.

BIOASSAY QUANTITY				
🔿 Graph 💿 Table	O Hide	Whole body	-	tool

Figure 4.31. Bioassay Quantity window set to hold "Whole body" data - with active "tool" button.

- See <u>Using the Table Tool</u> (Step #7 in the single intake example):
- <u>Return</u> to the case description and list of steps.

Graphing the Data



<u>IMBA Professional</u> provides a "**Graph Tool**" in the form of an expanded graphical display with full facilities for setting up the type of graph (linear or logarithmic), ordinate and abscissa scales, etc.

Opening the Graph Tool

Select "**Graph**" and "**Whole body**" for display in the second **Bioassay Quantity** window (Figure 4.32). Then click the "**tool**" button to open the <u>Graph Tool</u>.

BIOASSAY QUANTITY											
O Graph	• T	able	Он	lide	Whole	body		•		tool	
Measurem (+hh:mm]	nent D	ate		N/A		Measureme Value(Bq)	n I	Data Type	Mea Erro	asuremen or	-
	2	5/02/	1988			2.720E+0)3 I	Real	2.	720E+02	
	0	1/03/	1988			1.150E+0	I3	Real	1.	150E+02	
	1	1/03/	1988			1.010E+0	I3	Real	1.	010E+02	
	2	8/03/	1988			7.900E+0	12	Real	7.	900E+01	
	1	6/05/	1988			4.820E+0	12	Real	4.	820E+01	
	0	8/11/	1988			3.580E+0	12	Real	3.	580E+01	
	2	9/11/	1990			7.800E+0	11	Real	7.	800E+00	
	1	9/02/	1992			3 5005 ±0	11	Rasi	5	500F ±00	<u> </u>
•										<u> </u>	
🖲 Graph	O L	able	Он	lide	Whole	body				tool	
400					Whole	body					
90]					Lungs						
80 -					Feces						
70 -					Blood						
50 1					Thyroid	ł					
40 -					Liver						
30 -					User D	efined	_				
20 -											
101											
Ő	1	0	20	30	40	50 60)	70 8)	90 10	0

Figure 4.32. Opening a Graph window for the Whole body bioassay quantity.

Warning: You CANNOT open the **Graph Tool** until you have entered (or read in from a file) a value of "**Measurement Error**" - for every tabulated "**Measurement Value**". If you attempt to do this, you will be prompted to complete the data entry._

• See Graph Tool for Viewing Data and Fit (Step #8 in the single intake example):

• <u>Return</u> to the case description and list of steps.

Selecting Bioassay Data to Use - and Calculating Intake

Before you can calculate the amount of Intake, you MUST first Select which data to use. In the "CALCULATION" sub-panel (Bioassay to Intake - Figure 4.33):

• check the Whole body box.

If you forget to do this, you will be prompted.

To calculate the maximum likelihood estimate of the Intake amount:

• click the "Start Calculation" button (Figure 4.33).

This will:

- display automatically the Intake amount for the single Intake Regime (IR1);
- plot automatically the corresponding **fit** to the **data points** (see Figure 4.33) provided that the "**Plot Fit**" box was checked in the **Graph Tool**.



In this example, with the selected values of Model Parameters , the calculated Intake amount is $10,341 \ Bq$.

INTAKE	CALCU	ATION	BIOASSAY
IR 1 1.034E+04 Bq	Intakes to Bioassay	Bioassay to Intake Select which data to use Whole body Lungs Urine Feces Blood Thyroid Liver User Defined	Graph © Table © Hide Whole B Measurement Date N/A (+hh:mm) 25/02/1988 01/03/1988 11/03/1988 11/03/1988 16/05/1988 16/05/1988 11/08/1988 29/11/1990 19/02/1992 Image: Straph © Table © Hide Whole B 3000 1000 100 100
Progress Indicator	000		

Figure 4.33. Calculated Intake amount with corresponding best fit to the data.

You will see from the **Table** and **Figure** displayed in the **Bioassay Quantity** windows (Figure 4.33) that the **fit** to data points is generally poorer that the assumed measurement errors. This fit can be improved quite readily, by <u>reviewing</u>, and if necessary making <u>reasonable changes</u> to, one or more of the assumed **Model Parameters** (see <u>Improving the Data Fit</u>).

Improving the Data Fit



In this example case (single intake of <u>60Co</u> by inhalation), the **fit** to the data is <u>clearly</u> <u>improved</u> by varying the assumed aerosol <u>Activity Median Aerodynamic Diameter (AMAD)</u> from the <u>5-µm default value</u> recommended by **ICRP** - to an **AMAD of 1** µm (with <u>sg</u> = **2.47**). The resulting **improved data fit** (at least to the earliest 6 data points) is shown in Figure 4.34. The corresponding (better) estimate of the **Intake** amount is **9,805 Bq**.



Figure 4.34. Improved data fit obtained by changing the value of aerosol AMAD.

Tip: As a useful exercise, try varying other **Model Parameters** (within reasonable ranges) to examine their effect on the **data fit**.

This completes the single intake example:

- <u>Return</u> to the case description and list of steps.
- Follow a <u>more complex example</u> involving the calculation of <u>multiple intakes</u> with **unknown intake parameters**. This example demonstrates an **iterative optimization** of the **Model Parameters**.

Example Case of Multiple Intakes -Requires Add-On 1

This example is taken from <u>Miller et al. (1999)</u> - see their Appendix 2. The data are urinary excretion measurements of <u>238</u>Pu in 37 samples taken from March 15<u>th</u>, 1968 through May 28<u>th</u>, 1979. The worker concerned had several intakes (by inhalation) of mixed <u>239</u>Pu/<u>238</u>Pu:

- 1. In the mid-1950s and assumed for analysis purposes to have occurred on June 9th, 1945.
- 2. On May 8<u>th</u>, 1971.
- At some unknown time between the routine sampling dates of September 22nd, 1971 and September 18th, 1972.

In their analysis, Miller et al. assigned the date of the third intake as March 21 st, 1972 (midway between the prior- and post-intake sample dates). No information about the physical properties of the <u>239</u>Pu/<u>238</u>Pu material (or aerosol) was presented. The published urinalysis results are given in Table 2.
Table 2.238Pu urinalysis results.

Collection date	Excretion rate (mBq d <u>-1</u>) \pm 1
March 15, 1968	1 <u>±</u> 0.9
June 13, 1968	1.8 <u>±</u> 0.9
September 13, 1968	0.3 <u>±</u> 0.9
December 13, 1968	4.8 <u>±</u> 2
March 20, 1969	0 <u>±</u> 0.9
December 18, 1969	0 <u>±</u> 0.9
March 19, 1970	0 <u>±</u> 0.9
June 18, 1970	0.5 <u>±</u> 0.9
September 24, 1970	0.5 <u>±</u> 0.9
March 18, 1971	1.2 <u>±</u> 0.7
June 29, 1971	4.1 <u>±</u> 0.7
September 22, 1971	2.2 <u>±</u> 0.5
September 18, 1972	12.9 <u>±</u> 1.6
December 8, 1972	7.5 <u>±</u> 1.1
March 15, 1973	2 <u>±</u> 0.4
June 27, 1973	3 <u>+</u> 0.6
September 17, 1973	2.7 <u>±</u> 0.5
December 21, 1973	3.1 <u>±</u> 0.6
March 21, 1974	1.1 <u>±</u> 0.4
June 17, 1974	3.8 <u>±</u> 0.7
September 16, 1974	2.1 <u>+</u> 0.5
December 18, 1974	1.5 <u>±</u> 0.4
March 17, 1975	2 <u>±</u> 0.4
June 16, 1975	1.1 <u>±</u> 0.4
September 19, 1975	0.8 <u>±</u> 0.4
December 12, 1975	1 <u>+</u> 0.4
March 17, 1976	1.2 <u>±</u> 0.4
July 2, 1976	1.4 <u>±</u> 0.4
September 12, 1976	1.4 ± 0.4
December 8, 1976	0.5 <u>±</u> 0.4
June 24, 1977	1 <u>+</u> 0.4
September 15, 1977	0.4 ± 0.4
September 1, 1978	2.2 <u>±</u> 0.5
October 20, 1978	0.3 ± 0.4
January 18, 1979	0.9 ± 0.4
April 20, 1979	0.4 <u>+</u> 0.4
May 28, 1979	1.6 <u>±</u> 0.4

• <u>View</u> list of steps for estimating multiple intakes.

Steps in Multiple Intake Calculation - Steps Initial Estimates

The following steps (in the listed order) are recommended for making an **initial estimate** of the amounts of the three separate intakes in this example.

- 1. Select the Indicator Nuclide in the Main Screen.
- 2. Define the <u>Reference Date</u> in the Main Screen.
- 3. Select the <u>Reference Activity Units</u> in the Main Screen.
- 4. Select the Common Model Parameters to be used for all IRs in the Main Screen.
- 5. Select the Number of Intake Regimes (IRs) back in the Main Screen.
- 6. Select the option for Independent Model Parameters for all IRs in the Main Screen.
- 7. Define the <u>Date of Each Intake</u> in the **Main Screen**.
- 8. Select in the **Bioassay Calculations Screen** the <u>Bioassay Quantity</u> as "**Urine**" (for display in the top **Bioassay Quantity** window).
- 9. Enter the bioassay data using the <u>data entry</u> "tool" in the **Bioassay Quantity** window.

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- 10. Graph the bioassay data using the graph set up "tool" in Bioassay Quantity window.
- 11. Select which bioassay data to use ("Urine") in the CALCULATION sub-panel.
- 12. Click the "Start Calculation" button.

When you have completed these steps - and made your initial estimate of the amounts of each intake - you will start the **iterative** process of **refining** these estimates by comparing the **predicted** urinary excretion rates with the **measured** values.



Indicator Nuclide for Multiple Intakes

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Figure 4.35. Selecting the Indicator Nuclide (238Pu).

<u>Select</u> the Indicator Nuclide (<u>238</u>Pu in the example case) from the top-right-corner of the Main Screen (Figure 4.35). IMBA Professional will then be able to select automatically the bioassay model(s) appropriate for plutonium, and automatically take into account the radioactive half-life of <u>238</u>Pu.



Tip: In this example case, we are using bioassay data to calculate intake (s). Therefore, it is NOT necessary to enter a (hypothetical) value in the displayed "Intake (IR 1)" dialog box. IMBA Professional will automatically display the calculated values of Intake(s) in their respective dialog boxes.

This completes Step #1 of the multiple intakes example:

- Proceed to the next step.
- Return to the case description and list of steps.

Reference Date for Multiple Intakes

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Important: This is a KEY parameter - especially for cases where more than one intake is being analyzed. It also determines the origin of the time scale for all graphs.

IMBA Professional keeps track of all Intakes and bioassay measurements on a common timescale. All events are timed with respect to a single Reference Date (and time-of-day, if necessary). The Reference Date is defined in the Main Screen (Figure 4.36). The IMBA System must always have a reference date - even if you are working

entirely in the Time (d) mode - so a default value (January 1st, 1980) is loaded at start-up.

Clear All Intake Regimes Enter Number of Intake Regimes (1-10)						
Mode Acute Start Time(d)	Chronic Chronic Edit Complex Regime					
	Enter Number of Ir Mode Acute Start Time(d)					

Figure 4.36. Default "since" date loaded at start-up.

In the example case, the earliest date of interest is June 9<u>th</u>, 1945, and so this is the appropriate value for the Reference Date. This is entered directly in the "Time (d) since" dialog box (Figure 4.37).

C Date	
 Time (d) since 	
09/06/45 #	

Figure 4.37. Entering the Reference Date.

Since in this example, the bioassay measurements are tabulated with their collection Date, it is necessary at this point to switch the "Specify Time As" Units to "Date" (Figure 4.38). This switch from "Time" to "Date" will be passed automatically to the Bioassay Calculations screen and data tables.

Intake Regimes Clear All Intake Regimes IB 1	Enter Number of I	ntake Regimes (1-10) 👖 💌	Specify Time As © Date
Route Inhalation Ingestion Injection Vound	Mode Acute Start Date	C Chronic 09/06/1945 #	orince 09/06/1945 Intake O Bq O dpm C pCi O mg
C Vapor		Edit Complex Regime	Dose

Figure 4.38. Switching the Units of Time to Date.

Notice that the "Start Time (d)" value of "0" (Figure 4.38) has now automatically switched to display the "Start Date" as "9/6/1945" - the value entered as the Reference Date before the switch of time units.



This completes Step #2 of the multiple intakes example:

- <u>Proceed</u> to the next step.
- <u>Return</u> to the case description and list of steps.
- -
- _

Reference Activity Units for Multiple Intakes

```
In IMBA Professional, the estimated Intake has the same Unit of activity as the measured (or predicted) bioassay quantity. As with the Unit of Time, the Unit of Activity is selected in the Main Screen (Figure 4.39).
```

For the example case, the urinalysis results are tabulated as mBq d<u>-1</u>. Therefore, the required Unit of Activity is "Bq."



Figure 4.39. Selecting the Unit of activity (Intake and Bioassay Quantity) as "Bq."



This completes Step #3 in the multiple intakes example:

- <u>Proceed</u> to the next step.
- Return to the case description and list of steps.

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Select the Common Model Parameters for All IRs

Before you can carry out any calculations with IMBA Professional, you MUST define all of the necessary Model Parameters. It is most efficient to do this while you are still in the Main Screen - although (if you forget to do this) it is very easy and quick to switch backwards and forwards between the Bioassay Calculations screen and the Main Screen (with a single click).

Key Tip: You can "pre-set" ALL model parameters to "ICRP Default" values - with a single click of the "ICRP DEFS Load" button.

Load Then, as you open additional Intake Regimes (IRs), the "Default" models will be loaded automatically - so that you won't have to carry out all of the individual steps listed below (for each IR). In general, it is much quicker to load (first) ALL ICRP Default model parameter values (for ALL IRs) - and then change only the relatively few parameters values that are specific to your case.

To estimate an Intake (by inhalation) from a measured Bioassay Quantity, you must all define the following Model Parameters - as indicated by the "red" buttons in Figure 4.40:

- Bioassay model.
- Deposition model.
- Particle Transport model.

ICRP DEFS

- Absorption model.
- GI-Tract model.

If you omit defining any of these models, then IMBA Professional will prompt you for each missing model definition before proceeding with a calculation.



Figure 4.40. Bioassay button for selecting the Bioassay Model.

Bioassay model (for example of multiple 238Pu intake)

For the Bioassay model, select the "Standard Pu Model" for urinary excretion (Figure 4.41):

 select "Urine" as the Bioassay Function - this will already have been defined if you had previously selected Urine in the Bioassay Quantity window (Bioassay Calculations screen);

- click **the** "LOAD ICRP DEFAULTS" button;
- click "<u>O</u>K."

Bioassay a(1)	Function -0.0139864109]		B	lood half time (I	K) 0.0000001	
i a(1 -1 2 4. 3 1. 4 8. 5 1. 6 4. 7 9. 8 9 10	i) .399E-02 809E-03 263E-05 974E-03 398E-04 141E-05 822E-06	Lam(i) 1.200E+01 3.553E-01 2.484E-05 1.262E+00 1.408E-02 8.645E-04 2.115E-04		- Select	User Do LOAD ICF Std P	efined Mode PDEFAULTS UMOdel	ncel	
WHOLE BO	DY LUNGS	URINE Std Pu Model	FECES	BLOOD	THYROID	LIVER		[]. [].

Figure 4.41. Standard Pu Model for Urine selected as the Bioassay Model.

Deposition model (for example of multiple 238Pu intake)

For the Deposition model, select the "Standard worker" (Figure 4.42):

- click **the** "LOAD ICRP DEFAULTS" button;
- click "OK."

- Exposur	e						
	Light Worke	ef C Heavy	Worker				
Aerosol Parameters							
6	amad Amtd	5	μm				
	Sigma-G	2.4977233					
	Density	3	g/ml				
	Shape factor	1.5					
Select							
<u>U</u> ser Defined							
LOAD ICRP DEFAULTS							
ICRP Defaults							

Figure 4.42. Selecting the Deposition Model for a Light worker.

Particle transport model

For the Particle Transport model (Figure 4.43):

- click the "LOAD ICRP DEFAULTS" button;
 click "OK."

💐 Particle Tra	nsport Model	
Rate Constants	(/d)	
Al1 to bb1	0.02	Extrathoracic
AI2 to bb1	0.001	
AI3 to bb1	0.0001	
AI3 to LNTH	0.00002	LNET ETseq ET2
bb1 to BB1	2	
bb2 to BB1	0.03	Thereasie
bbseq to LNTH	0.01	
BB1 to ET2	10	BBseq BB2 BB1
BB2 to ET2	0.03	
BBseq to LNTH	0.01	LNTH bbseq bb2 bb1
ET2 to GI	100	
ETseq to LNET	0.001	
ET1 Out	1	
FTeed/FT2	0.0005	- Select
BBeeg/BB	0.0005	<u>U</u> ser Defined
bbseq/bb	0.007	
AI2/AI	0.007	
	0.1	ICRP Defaults <u>OK</u> <u>Cancel</u>
AI3/AI	0.1	
	Clea <u>r</u>	

Figure 4.43. Selecting the ICRP Default Particle Transport Model.

<u>Absorption model</u> (for example of multiple <u>238</u>Pu intake)

For the Absorption model, select the Type M ICRP Default model (Figure 4.44) - see Plutonium Biokinetic Model (Technical Basis section):

- click **the** "Type <u>M</u>" button;
- click "OK."

.....

	Initial dissolution ra Transformation rate Final dissolution rate	te: Sp 1.0000E+01 e: Spt 9.0000E+01 e: St 5.0000E-03	Fraction to bound state: Fb Uptake rate from bound state: Sb		
f1	Clear	Select 	Type S	Help OK Cano	el

Figure 4.44. Selecting the Type M Absorption Model.

To select an appropriate (ICRP-recommended) value of f1:

- click the "Help" button (Figure 4.44);
- select the "Abs.: M" row (Figure 4.45);
- click "OK."

💐 F1 🕯	F1 values and absorption Types for Plutonium						
	Abs.	f1	ICRP	Chemical Form			
	F	0.0005	71				
	м	0.0005	71				
	S	0.00001	71				
+	M	0.0005	68	Unspecified compounds			
	S	0.00001	68	Insoluble oxides			
	Ing	0.0005	68	Unspecified compounds			
	Ing	0.0001	68	Nitrates			
	Ing	0.00001	68	Insoluble oxides			
Note: on	ote: only the absorption parameters are entered. NOT the default AMAD.						

Figure 4.45. Selecting the ICRP-recommended value of <u>f1</u>.

GI-Tract model

For the GI-Tract model, select LOAD ICRP DEFAULTS (Figure 4.46):

- click the "LOAD ICRP DEFAULTS" button;
- click "<u>O</u>K."



Figure 4.46. Selecting the ICRP Default GI-Tract Model.

This completes the definition of ALL Model Parameters required to calculate the (3) Intakes of <u>238</u>Pu in the <u>Miller at al. (1999) example case.</u>



This completes Step #4 in the multiple intakes example:

- Proceed to the next step.
- Return to the case description and list of steps.

Setting Up Multiple Intake Regimes (IRs)

Intake Scenario-		
Intake Regimes —		
Clear All Intake Regimes	Enter Number of I	ntake Regimes (1-10) 🛛 🛨
IR 1 IR 2 IR 3		
Route Inhalation	Mode	C Chronic
C Wound	Start Date	09/06/1945 #
		Edit Complex Regime

Figure 4.47. Selecting <u>3</u> separate Intake Regimes (IRs).

In the "Intake Scenario" panel ("Intake Regimes" sub-panel) simply enter the required number of individual (separate) intake events in the dialog box.

This completes Step #5 in the multiple intakes example:

- Proceed to the next step.
- <u>Return</u> to the case description and list of steps.

Select Independent Model Parameters

🂐 Main So	creen					
<u>F</u> ile <u>E</u> dit	<u>P</u> arameters	<u>Calculations</u>	<u>T</u> ools	Advanced	<u>H</u> elp	
0oen	Sava	New		Apply Mo Enable C	odel Params to All IRs Complex Intake Regimes	
Ver 3.0	No file ope	ened	QUICK 5	Enable D Advance	00S preview ed Dosimetry Options	

Figure 4.48. Un-checking "Apply Model Params to All IRs" in the "Advanced" menu.

By default, IMBA Professional applies all of the defined Model Parameters to All Intake Regimes (IRs). If you want to specify independently ANY parameter value (e.g., in the Deposition or Absorption models) for ANY individual IR, you MUST first un-check the default condition in the "Advanced" menu (Figure 4.48).

Note: When you have selected more than <u>1</u> Intake Regime - AND you have <u>un-checked</u> the default "Apply Model Params to All IRs", the appropriate number of tabs will appear automatically in the "Model Parameters" sub-panel (Figure

4.49). You can then proceed to set up (or modify) ANY model parameter for ANY individual IR#.



Figure 4.49. Individual IR# tabs for setting up Model Parameters specific to each IR.

This completes Step #6 in the multiple intakes example:

- <u>Proceed</u> to the next step.
- Return to the case description and list of steps.

Defining the Date of Each Intake

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Intake Regimes		
Clear All Intake Regimes	Enter Number of I	Intake Regimes (1-10) 📔 🖵
IR1 IR2 IR3		
Route	Mode	
Inhalation	 Acute 	C Chronic
C Ingestion	<u> </u>	
C Injection	Start Date	08/05/1971 #
C Wound		
C Vapour		
-		

Figure 4.50. Setting the Date of IR 2 as May 8th, 1971.

Once you have specified independent model parameters **for** all IRs, **you simply** <u>click</u> **on each** IR # <u>tab</u> **displayed in the** "Intake Regimes" **sub-panel to** <u>specify</u> **the** intake parameter values **for that** IR # **(Figure 4.50)**.

For the initial estimate of the amounts of each (acute) Intake:

- enter the "Start Date" of IR 2 as May 8th, 1971;
- enter the estimated "Start Date" of IR 3 as March 21st, 1972.

Note: In this example, all <u>3</u> of the intakes are assumed to be "acute." You can, of course, specify "chronic" for ANY intake, as appropriate.

This completes Step #7 in the multiple intakes example:

- Proceed to the next step.
- Return to the case description and list of steps.

Selecting the Bioassay Quantity

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BIOASSAY QUANTITY					
⊂ Graph ⊙ Table ⊂ H	ide	Urine 💌	tool		
Specified Date (+hh:mm)	Collec	Whole body Lungs Urine Feces Blood Thyroid Liver User Defined	rement Date m]	Co pe	
•				▶	

Figure 4.51. Drop-down Bioassay Quantity list box.

The previous steps were carried out in the Main Screen. You select the Bioassay Quantity in the Bioassay Calculations screen. From the Main Screen you:

- Click the "Bioassay Calculations" button (bottom-right-corner of the Main Screen)
 to open the Bioassay Calculations screen.
- Select the "Bioassay to Intake" direction for the CALCULATION (indicated by a blue arrow) if you loaded a "new" (blank) Parameter File, this calculation mode will have been selected already (by default).
- Select in the top Bioassay Quantity window (set as "Table" by default) -"Urine" from the drop-down list box (Figure 4.51).

This "opens" the first Bioassay Quantity window to display in that window a Table containing both measured urinary excretion data (on a blue background) and predicted urinary excretion data (on a green background).



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This completes Step #8 in the multiple intakes example:

- <u>Proceed</u> to the next step.
- Return to the case description and list of steps.

Data Entry - Multiple Intake Example

<u>IMBA Professional provides a "</u>Table Tool" in the form of an expanded data table with various editing and automated data entry functions.

Opening the Table Tool

The Table Tool shows all of the data columns (without you having to scroll). When you open this [from a Bioassay Quantity (BQ) window], the Table Tool will display the same number of rows as the BQ window. Initially, only a default single row is displayed. Your first task is to open up enough rows to hold all of the measured bioassay data that you want to analyze - in this example, 37 values of daily urinary excretion:

- <u>Enter "37" in the "Number of Rows" dialog box (bottom panel, left-of-center see Figure 4.52).</u>
- <u>Click the "Apply" button to the right of the dialog box.</u>



Tip: The number of data rows shown in the Table Tool depends on your screen resolution setting. The minimum recommended screen resolution (1024 X 768) shows 36 rows - as in Figure 4.52.

- 1	l able I oo	: 01	ne Data					
<u>F</u> ile	e <u>E</u> dit <u>B</u> ioassay <u>M</u> easurement <u>H</u> elp							
	Specified	Date	(+hh:mm)	Collection period (d)	Calculated Rate(Bq/d)	Measurement Date (+hh:mm]	Collection period (d)	Measuremen Rate(Bq/d)
1								
2								
3								
4								
5								
6								
- 7								
8								
9								
10								
11								
12								
13								
14								
15								
16								
17								
18								
19								
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22								
23								
- 24								
25								
26								
27								
28								
29								
30								
31								
32								
33								
34								
35								
36								
_ K	EY —							
		Bioass Measu	ay Prediction urement Data	\$	No Rows :	37 🕂 Apply		
		Measu	arement Fit Ut	itput				

Table 4.52. Table Tool with 37 rows opened.

Note: The "Using the Table Tool" link below will take you to the pages describing Step #7 in the single intake example. For your convenience, those pages also have a forward "navigation" path to the next step in this "multiple intake" example - or you can use the Help Contents list to navigate.

- See Using the Table Tool (Step #9 in the multiple intakes example), or:
- Return to the case description and list of steps.

ordinate and abscissa scales, etc.

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Graphing the Data - Multiple Intakes

<u>IMBA Professional</u> provides a "Graph Tool" in the form of an expanded graphical display with full facilities for setting up the type of graph (linear or logarithmic),

Opening the Graph Tool

<u>Select</u> "Urine" and "Graph" for display in the second Bioassay Quantity window (Figure 4.53). Then <u>click</u> the "tool" <u>button</u> to <u>open</u> the <u>Graph Tool</u>.



Figure 4.53. Opening a Graph window for the Urine bioassay quantity.

See <u>Graph Tool for Viewing Data and Fit</u> (Step #10 in the multiple intakes example):
<u>Return</u> to the case description and list of steps.

Calculating the Intake Amounts



Before you can <u>calculate</u> the amounts of each of the three Intakes, you MUST first Select which data to use. In the "CALCULATION" sub-panel (Bioassay to Intake - Figure 4.54):

• <u>check</u> the Urine <u>box</u>.

If you forget to do this, you will be prompted.

Save Quick Save		Bioassay Calcula
INTAKES	CALCU	LATION
IR 1 0.000E+00 Bq		
IR 2 0.000E+00 Bq	Intakes to Bioassay	Bioassay to Intake
IR 3 0.000E+00 Bq	Start Calculation	Select which data to use Whole body Lungs Urine Feces Blood Thyroid Liver User Defined



To calculate the maximum likelihood estimate of the Intake amounts:

• <u>click</u> the "Start Calculation" <u>button</u> (Figure 4.55).

This will:

- <u>display</u> automatically the Intake amounts for all three Intake Regimes (IR1, IR2 and IR3);
- <u>plot</u> automatically the corresponding fit to the data points (see Figure 4.55) provided that the "Plot Fit" <u>box</u> was <u>checked</u> in the Graph Tool.

Save Quick Save		Bioassay Calcula	ations
INTAKES	CALCU	LATION	
IR 1 9.051E-01 Bq			C Graph Measurem
IR 2 3.986E+02 Bq	Intakes to Bioassay	Bioassay to Intake	[+hh:mm]
IR 3 3.811E+02 Bq	Start Calculation	Select which data to use Whole body Lungs Urine Feces Blood Thyroid Liver User Defined	 ✓ Graph 0.014 0.012 0.010 0.008 0.006 0.004 0.004 0.004
	000		0.002
Progress Indicator			C Graph
Figure 4.55. Calculated In assumed Type M absorpti	takes with corresponding b on behavior).	est fit to the data (for	

In this example, with the selected values of Model Parameters, the calculated Intakes are:

- IR1 = 0.91 Bq;
- IR2 = 398.6 Bq;
- IR3 = 381.1 Bq.

Figure 4.55 shows that the resulting fit to data points is poor, especially:

- 1. in not representing the well defined "peak" (from IR3) in the measured urine data (with its subsequent rapid decay) at 9,963 d;
- 2. in predicting "zero" urinary excretion (from IR1 = 0) prior to the second intake (from IR2) on May 8th, 1971 (at 9,464 d).

To improve the "fit" to the measured urinary excretion data, it is necessary to <u>review</u>, and <u>modify</u> appropriately, the assumed Model Parameters for each Intake Regime.

For example, since the absorption behavior of the inhaled material is unknown, it is reasonable to change this (for all 3 IRs), and see the effect on the data fit. Changing the absorption behavior for All IRs to "Type S" - with the associated value of $\underline{f1} = 0.00001$ - and recalculating the intake amounts, gives the result shown in Figure 4.56.

Save Quick Save		Bioassay Calcula	ations
INTAKES	CALCU	LATION	
IR 1 8.424E+03 Bq			C Graph Measurem
IR 2 6.501E+03 Bq	Intakes to Bioassay	Bioassay to Intake	(+hh:mm]
IR 3 <u>5.246E-04</u> Bq	Start Calculation	Select which data to use Whole body Lungs Urine Feces Blood Thyroid Liver User Defined	Graph 0.014 0.012 0.010 0.008 0.006 0.004 0.002 0.000 8
Progress Indicator			
Deposition			C Graph

Figure 4.56. Calculated Intakes with corresponding best fit to the data for assumed Type S absorption behaviour.

Clearly, the assumption of Type S absorption behavior gives a worse overall fit to the measured urine data than Type M (Figure 4.55). Type S behavior does predict a step-wise increase in urinary excretion at 9,464 d (from IR2), and also the presence of finite excretion prior to that date (from IR1). However:

- 1. it CANNOT fit the observed sharp increase in the excretion rate following IR3;
- 2. NOR the observed sharp drops in the excretion rate following both IR2 and IR3.

Note that changing the assumed absorption behaviour also changes significantly the "best estimates" of the intake amounts to:

- IR1 = 8,424 Bq;
- IR2 = 6,501 Bq;
- IR3 = 0.0005 Bq.

Optimising the Fit to the Data

Although the assumption of Type M absorption behavior in this example gave a much better fit (figure 4.55) to the measured data than Type S, the fit was still not good. To improve this, <u>IMBA Professional</u> provides a further powerfull tool for optimising the data fit - the "Intakes to Bioassay" option in the "CALCULATIONS" sub-panel. This enables you to predict the bioassay quantity with sufficient time-resolution to examine in detail the fit achieved for rapidly changing data (significant observed "peaks" in the data). The optimisation procedure is

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decribed (for this example of multiple intakes) in Optimising the Intake Estimation.

This completes Step #11 in the multiple intakes example (obtaining the Initial Estimate of Multiple Intakes):

- Proceed to Optimising the Intake Estimation.
- <u>Return</u> to the case description and list of steps.

Optimizing the Intake Estimation

The first step in optimizing an intake estimation is to switch the "CALCULATION" mode from "Bioassay to Intake" (blue arrow) to "Intakes to Bioassay" (green arrow) - as shown in Figure 4.57.

💐 Bioassay Calculations		
<u>File A</u> dvanced <u>T</u> ools Help		
Save Quick Save	Bioassay Calcula	ations
INTAKES	CALCULATION	
IR 1 9.051E-01 Bq		C Graph Specified [
IR 2 3.986E+02 Bq	Intakes to Bioassay Bioassay to Intake	<u> </u>
IR 3 3.811E+02 Bq	Number of Dates (1-200) Specify Dates [Col 1] Start Date 01/01/1971 Calculate Bioassay Quantity [Col 3] Start Calculation	04/0 08/0 12/0 15/0 19/0 23/0 26/0 ▼ 6 Graph 0.014 0.012 0.010 0.008 0.006 0.004 0.002 0.000 83
Figure 4.57. Setting u	up a series of times at which to predict the bioassay quanti	ty.

In the multiple intakes example, the measured urinary excretion data exhibited significant "peaks" in 1971 and 1972. However, these bioassay data were taken at "routine" sampling intervals - and NOT in response to intake events (known or suspected). As a result, much of the early urinary excretion of relatively soluble plutonium would have been missed. The "Intakes to Bioassay" option enables this predicted early excretion to be examined on the same graph plot as the measured data.

For this example (Figure 4.57):

- select 200 as the Number of Dates (1-200);
 - select Linear for the time series;
 - specify the Start Date as "1/1/71";
 - specify the Stop Date as "31/12/72";
- click the "Send to all open windows ®" button;
- enter "1" in the "Specify Collection Periods [Col 2]" dialog box;
 - click the "Send ®" button.

This will automatically:

- 1. open 200 rows (green background) in the Bioassay Quantity table;
- 2. enter [in Column 1] the 200 values of date/time (at linear intervals);
- 3. enter "1" for the Collection Period [Column 2] for each of the 200 sample times.

To calculate the predicted amount of urinary excretion for all 200 (hypothetical) samples for the displayed "initial" estimates of the intake amounts - and to display the results in Column 3 of the table:

• click the "Start Calculation" button.

The predicted values are shown in Figure 4.58.

💐 Bioassay Calculations			
<u>File Advanced T</u> ools Help			
Save Quick Save		Bioassay Calcula	tions
INTAKES	CALCU	LATION	
IR 1 9.051E-01 Bq		\rightarrow	C Graph
IR 2 3.986E+02 Bq	Intakes to Bioassay	Bioassay to Intake	
IR 3 3.811E+02 Bq	Specify Dates [Col 1] Start Date 01/01/1971 Stop Date 31/12/72 Specify Collection Periods [Col 2]-	Number of Dates (1-200) 200 C Linear Send to all open windows 1-2-5 mode Send>	04/0 08/0 12/0 15/0 19/0 23/0 26/0 • Graph 0.014 0.012
Concernation in the factor	Calculate Bioassay Quantity (Col 3	Start Calculation	0.010 0.008 0.006 0.004 0.002 0.000 8:
Progress indicator			
Collating Times			U uraph
Current Operation	Calculation Compl	ete	
Figure 4.58. Predicted	bioassay quantity displayed i	<u>D</u> K	DW.



Plotting the predicted bioassay quantity

This is done in the Graph Tool (Figure 4.59):

- <u>click the "Select Axes Automatically" button ("Tools" sub-panel):</u>
 <u>check the "Plot" dialog box under "Bioassay Predictions" ("Plot" sub-panel).</u>

The predicted values of the bioassay quantity will automatically be added to the graph of the data (as a green curve).



Figure 4.60. Curve of predicted bioassay quantity displayed in Bioassay Quantity window.

Tip: Use the higher resolution provided by the Graph Tool for critical comparisons of predicted curves with the measured values.

Examine closely the Graph Tool plot (Figure 4.59), and you will see that:

- 1. <u>the predicted early urinary excretion for the known intake time (IR2) is</u> <u>substantially higher than the next measured value (at 9,516 d);</u>
- 2. the next two data points (at 9,516 and 9,601 d) are reasonably-well predicted.
- 3. the values of the two highest measured values (following IR3) are NOT predicted.

<u>Clearly, from the predicted rapid fall-off in urinary excretion, the actual date of intake for IR3 must have been much closer to 18/9/1972 (9,963 d), the date of the next urine sample, than the "mid-interval" date (21/3/1972) assumed initially for IR3.</u>

To test this interpretation:

- in the Main Screen, change the assumed "Start Date" for IR3 to "11/9/72";
- <u>back in the Bioassay Calculations screen</u>, "Bioassay to Intakes" option (blue arrow), click the "Start Calculation" button.

Figure 4.61. Calculating new intake amounts for a different assumed date of intake for IR3.

With the revised date of intake for IR3, the calculated Intakes are:

• <u>IR3 = 367.7 Bq.</u>



Figure 4.62 shows the enlarged plot in the Graph Tool.



To plot the corresponding predicted bioassay quantity curve simply:

switch to the "Intakes to Bioassay" option (green arrow);
 click the "Start Calculation" button.

The new predicted curve will be displayed automatically in the Bioassay Quantity window. Open the Graph Tool (Figure 4.63) to examine this.



Figure 4.63. Predicted rapid changes in urinary excretion from IR2 and IR3.

Comparison of the predicted (green curve) early urinary excretion following IR3 with the measured fall-off (between the samples at 9,963 d and 10.044 d) suggests that the actual fall-off in urinary excretion is substantially slower than predicted (by the assumed Type M absorption behavior). To test this interpretation, the assumed absorption rate for IR3 can be changed, and the effect on the fitted intake amounts and predicted urinary excretion curve can be examined, as follows:

- Un-check "Apply Model Params to All IRs" in the "Advanced" menu (Main Screen). This will enable you to vary the absorption rate for IR3 independently of IR1 and IR2.
- Increase the "Final dissolution rate, St" for IR3 from 5 X 10-3 d-1 to 5 X 10-2 d-1.
- For consistency with an increased absorption rate, decrease the aerosol AMAD to 0.5 µm.
 Back in the Bioassay Calculations screen, "Bioassay to Intakes" option (blue

The result is shown in Figure 4.64.

arrow), click the "Start Calculation" button.

INTAKES	CALCU	LATION	
IR 1 2.998E+02 Bq			C Graph
IR 2 1.534E+02 Bq IR 3 1.169E+02 Bq Progress Indicator	Intakes to Bioassay	Bioassay to Intake Select which data to use Whole body Lungs Vinne Feces Blood Thyroid Liver User Defined	Specified 04/0 08/0 12/0 15/0 23/0 ▼ 26/0 ▼ 0.014 0.014 0.012 0.010 0.008 0.006 0.004 0.002 0.000 8:
Figure 4.64. Calculating	<u>g new intake amounts for an ir</u>	ncreased absorption rate for I	<u>R3.</u>

Note: Improving the data fit for IR3 enables the maximum likelihood method to fit simultaneously a finite intake amount for IR1.

With the revised absorption rate for IR3, the calculated Intakes are:

- <u>IR1 = 299.8 Bq;</u>
- IR2 = 153.4 Bq;
- <u>IR3 = 116.9 Bq.</u>

Figure 4.65 shows the enlarged plot in the Graph Tool.



Figure 4.65. Improved data fit by refining the assumed absorption rate for IR3.

 Warning: The "solution" of the Miller et al. (1999) case illustrated in Figure 4.65 is NOT intended to be definitive - merely "illustrative" of the procedures available in IMBA Professional for estimating multiple intakes. Inclusion of additional information about the nature of the three intakes considered here could well lead to a different set of estimates for the intake amounts.
 Important: The decision on when the "parameter optimization" procedure has found an "acceptable" solution, will, of course, be determined by your Regulatory Guidance [e.g., in the U.S. by the DOE Standard for Internal Dosimetry (DOE-STD-1121-98)]. Your intake-fitting procedure should include the evaluation and consideration of the resulting committed doses. IMBA Professional enables you to evaluate these doses very easily (by switching to the Dose Calculations screen) after each stage of the intake-fitting procedure.

This completes the multiple intakes example:

- Return to the case description and list of steps.
- Proceed to the example dose calculation.

Example Case of Multiple Bioassay Quantities - Requires Add-On 2

file://C:\Documents%20and%20Settings\Administrator\Local%20Settings\Temp\~hh... 15/10/2005

This example is taken from <u>IAEA (1999)</u> - see Case #4 in their Appendix 2. A person (green activist) penetrated through barriers into an area of "low-level waste" in an abandoned sand mine. He found a barrel with a "radioactive substances" label, took out a tin labelled "ISOMET <u>90</u>Sr", opened the tin and found white powder. After a few days, the person started to "worry" - and sought out a measurement with a "dose-rate meter." This indicated serious external contamination. The high reading persisted after the person showered - indicating substantial internal contamination. Surface contamination was found in his home - and on various personal belongings.

The following bioassay monitoring was performed:

- Whole body activity 15 measurements from approximately 5 days after the intake, over a 21-month period (see Table 4.3).
- Urine sampling 9 measurements from approximately 5 days after the intake, over a 9-month period (see Table 4.4)
- Faecal sampling 6 measurements from approximately 6 days after the intake, over a 10-day period (see Table 4.5).

No "error" values were reported.

Measurement date	Activity (kBq)	Measurement date	Activity (kBq)
November 29, 1990	692	December 12, 1990	215
November 30, 1990	400.5	May 27, 1991	118.5
December 3, 1990	292	June 5, 1991	135
December 4, 1990	272	July 4, 1991	110.5
December 5, 1990	256.5	August 8, 1991	102.5
December 6, 1990	261.5	June 2, 1992	96
December 7, 1990	248	August 11, 1992	79
December 10, 1990	218		

 Table 4.3.
 90 Sr/90 Y whole body activity measurements.

 Table 4.4.
 90Sr urine activity measurements.

Sample date	Collection period (h)	Daily excretion rate (kBq d <u>-1</u>)
November 29, 1990	19	56.60
December 1, 1990	-	55.28
	19	14.46

December 3, 1990		
December 4, 1990	19	10.81
December 6, 1990	18	9.80
December 9, 1990	19	5.91
December 11, 1990	24	4.44
July 3, 1991	24	0.47
August 7, 1991	24	0.20

Table 4.5.	90Sr faecal	activity	measurements
10010 1101	<u></u> e		mouour onnonto

Sample date	Collection period (h)	Daily excretion rate (kBq d <u>-1</u>)
December 1, 1990	-	8.54
December 3, 1990	-	2.56
December 4, 1990	-	10.52
December 6, 1990	-	0.36
December 9, 1990	-	0.12
December 11, 1990	-	2.3

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No information was available on:

- the particle size of the powder;
- the chemical form of the powder;
- the nature of the intake (i.e., whether by inhalation or ingestion).

This case can be solved (rapidly) with the following steps:

- assume appropriate <u>errors</u>;
- 2. assume ICRP-recommended bioassay models;
 - 3. test hypothetical intake scenarios;
 - evaluate the <u>likely intake;</u>
 - 5. evaluate **the** <u>likely dose</u>.

Error Assumptions - Multiple Bioassay Quantities



No information on the magnitude of measurement errors is available in this <u>example</u> <u>case</u>. However, in order to give an appropriate "weight" to each set of bioassay measurements, it is important to assign a realistic error value for each type of data. Let's assume the following:

• Whole body activity measurements - Relative error with K = 0.2 - Normal error

distribution.

- Urinary excretion rate measurements Lognormal error distribution with sg = 1.8.
- Faecal excretion rate measurements Lognormal error distribution with sg = 4.0.



Note: These assumed errors are meant to reflect the fact that Whole Body measurements (of 90Sr/90Y) are reasonably precise, whereas the Urinary Excretion Rate is subject to substantial biological variability, and the Faecal Excretion Rate to even greater biological variability.

The resulting tables of input data, completed in the Table Tool, are shown in Figures 4.68 through 4.70, for Whole Body, Urine and Faeces, respectively.

es -	Table Tool : Whole body D	ata				
File	Edit Bioassay Measuremen	nt Help				
	Specified Date (+hh:mm)	N/A	Calculated Value(Bq)	Measurement Date (+hh:mm]	N/A	Measuremen Value(Bq)
1				29/11/1990 00:00:00		6.92000E+05
2				30/11/1990 00:00:00		4.00500E+05
3				03/12/1990 00:00:00		2.92000E+05
4				04/12/1990 00:00:00		2.72000E+05
5				05/12/1990 00:00:00		2.56500E+05
6				06/12/1990 00:00:00		2.61500E+05
- 7				07/12/1990 00:00:00		2.48000E+05
8				10/12/1990 00:00:00		2.18000E+05
9				12/12/1990 00:00:00		2.15000E+05
10				27/05/1991 00:00:00		1.18500E+05
11				05/06/1991 00:00:00		1.35000E+05
12				04/07/1991 00:00:00		1.10500E+05
13				08/08/1991 00:00:00		1.02500E+05
14				02/06/1992 00:00:00		9.6000E+04
15				11/08/1992 00:00:00		7.9000E+04

Figure 4.68. Whole body data and assumed errors for IAEA Case #4.

es -	Table Tool : Urine Data					
File	Edit Bioassay Measuremen	nt Help				
	Specified Date (+hh:mm)	Collection period (d)	Calculated Rate(Bq/d)	Measurement Date (+hh:mm]	Collection period (d)	Measuremen Rate(Bq/d)
1				29/11/1990 00:00:00	7.920E-01	5.6600E+04
2				01/12/1990 00:00:00	1.000E+00	5.5280E+04
3				03/12/1990 00:00:00	7.920E-01	1.4460E+04
4				04/12/1990 00:00:00	7.920E-01	1.0810E+04
5				06/12/1990 00:00:00	7.500E-01	9.800E+03
6				09/12/1990 00:00:00	7.920E-01	5.910E+03
- 7				11/12/1990 00:00:00	1.000E+00	4.440E+03
8				03/07/1991 00:00:00	1.000E+00	4.700E+02
9				07/08/1991 00:00:00	1.000E+00	2.000E+02

Figure 4.69. Urine data and assumed errors for IAEA Case #4.

es 1	Table Tool : Feces Data					
File	Edit Bioassay Measuren	nent Help				
	Specified Date (+hh:mm)	Collection period (d)	Calculated Rate(Bq/d)	Measurement Date (+hh:mm]	Collection period (d)	Measuremen Rate(Bq/d)
1				01/12/1990 00:00:00	1.000E+00	8.540E+03
2				03/12/1990 00:00:00	1.000E+00	2.560E+03
3				04/12/1990 00:00:00	1.000E+00	1.0520E+04
- 4				06/12/1990 00:00:00	1.000E+00	3.600E+02
5				09/12/1990 00:00:00	1.000E+00	1.200E+02
6				11/12/1990 00:00:00	1.000E+00	2.300E+03

Figure 4.70. Faecal data and assumed errors for IAEA Case #4.

This completes Step #1 in the multiple bioassay quantities example (assuming
reasonable <u>Error Values</u>):
 Proceed to Select Reference Bioassay Models.

• Return to the case description and list of steps.

Select Reference Bioassay Models -Multiple Bioassay Quantities



Once you have defined the Indicator Nuclide (90Sr), and also the Bioassay Quantities (in the Bioassay Quantity windows), you can specify use of ICRP's currently recommended Bioassay Models in one quick step - by clicking the "ICRP DEFS Load" icon (Figure 4.71).

🖼 М	lain S	creen					
File	Edit	Parameters	Calculations	Tools	Advan	ced Help	
C Op) Den	Save	New	回 Quick S	ave 🕇	ICRP DEFS Load	CFR DEFS Load
Ver 3	.0	C:\JabaSo	oft\IMBAEXUS	USERD)ATA\IA	EA Case 4 -	90Sr.ix

Figure 4.71. The "ICRP DEFS Load" icon for specifying use of all ICRP default models.

You will be prompted to select an "f1 Value" and "Absorption Type" for the <u>90</u>Sr material (Figure 4.72). Select type "M".

F 0.3 71 M 0.1 71 S 0.01 71 F 0.3 68 Unspecified compounds S 0.01 68 Strontium titanate (SrTiO3) Ing 0.3 68 Unspecified compounds Ing 0.01 68 Strontium titanate (SrTiO3)	Abs.	f1	ICRP	Chemical Form
M 0.1 71 S 0.01 71 F 0.3 68 Unspecified compounds S 0.01 68 Strontium titanate (SrTiO3) Ing 0.3 68 Unspecified compounds Ing 0.3 68 Unspecified compounds	F	0.3	71	
S 0.01 71 F 0.3 68 Unspecified compounds S 0.01 68 Strontium titanate (SrTiO3) Ing 0.3 68 Unspecified compounds Ing 0.01 68 Strontium titanate (SrTiO3)	M	0.1	71	
F 0.3 68 Unspecified compounds S 0.01 68 Strontium titanate (SrTi03) Ing 0.3 68 Unspecified compounds Ing 0.01 68 Strontium titanate (SrTi03)	S	0.01	71	
S 0.01 68 Strontium titanate (SrTiD3) Ing 0.3 68 Unspecified compounds Ing 0.01 68 Strontium titanate (SrTiD3)	F	0.3	68	Unspecified compounds
Ing 0.3 68 Unspecified compounds Ing 0.01 68 Strontium titanate (SrTiO3)	S	0.01	68	Strontium titanate (SrTiD3)
Ing 0.01 68 Strontium titanate (SrTiO3)	Ing	0.3	68	Unspecified compounds
	Ing	0.01	68	Strontium titanate (SrTiO3)

Figure 4.72. Selecting the f1 value and absorption type for Strontium.

If you then click the "Bioassay" button in the "Model Parameters" panel (Main Screen) you will see that the "Std Sr Model" bioassay models have been loaded for Whole body, Urine and Faeces (Figure 4.73).



Figure 4.73. Confirming that the "Std Sr Model" has been loaded for Whole Body, Urine and Faeces.

This completes Step #2 in the multiple bioassay quantities example (loading Standard ICRP Bioassay Models for Strontium):

Proceed to Hypothetical Intake Scenarios.

<u>Return</u> to the case description and list of steps.

Hypothetical Intake Scenarios -Multiple Bioassay Quantities



The nature of the intake was unknown in this case (<u>IAEA Case #4</u>) - so let's try to get <u>IMBA Professional</u> to indicate the most likely type of intake! To do this we simply have to set up several hypothetical intake scenarios to occur simultaneously - and let <u>IMBA Professional</u> use the bioassay data (whole body, urine and faeces) simultaneously to "choose" the most likely scenario.

> Important Note: The availability of <u>3</u> independent sets of bioassay data plus the ability to analyse these data simultaneously - makes it possible to apply IMBA Professional in this manner to determine the relative "weight" of several hypothetical intake scenarios - when the actual conditions of intake are unknown. This method is not likely to work if you have data on just one bioassay quantity!

In this example case, we don't know whether the intake occurred by inhalation or ingestion, or by a combination of both. We also know nothing about the chemical form of the material, or the particle size distribution of any airborne material. ICRP's recommendations concerning potential chemical forms of strontium are displayed in the "F1 values and absorption Types for Strontium" window (Figure 4.74).

F 0.3 71 M 0.1 71 S 0.01 71 F 0.3 68 Unspecified compounds S 0.01 68 Strontium titanate (SrTiO3) Ing 0.3 68 Unspecified compounds Ing 0.3 68 Unspecified compounds		
M 0.1 71 S 0.01 71 F 0.3 68 Unspecified compounds S 0.01 68 Strontium titanate (SrTi03) Ing 0.3 68 Unspecified compounds Ing 0.01 68 Strontium titanate (SrTi03)	0.3 71	F
S 0.01 71 F 0.3 68 Unspecified compounds S 0.01 68 Strontium titanate (SrTi03) Ing 0.3 68 Unspecified compounds Ing 0.01 68 Strontium titanate (SrTi03)	0.1 71	м
F 0.3 68 Unspecified compounds S 0.01 68 Strontium titanate (SrTiO3) Ing 0.3 68 Unspecified compounds Ing 0.01 68 Strontium titanate (SrTiO3)	0.01 71	S
S 0.01 68 Strontium titanate (SrTiO3) Ing 0.3 68 Unspecified compounds Ing 0.01 68 Strontium titanate (SrTiO3)	0.3 68	F
Ing 0.3 68 Unspecified compounds Ing 0.01 68 Strontium titanate (SrTiO3)	0.01 68	S
Ing 0.01 68 Strontium titanate (SrTiO3)	g 0.3 68	Ing
	g 0.01 68	Ing

Figure 4.74. ICRP's currently recommended "default" values for Strontium gut uptake fraction and absorption Type.

Let's try setting up <u>4</u> hypothetical (but possible) intake scenarios, and seeing if <u>IMBA Professional</u> can distinguish between them, as follows:

- IR1 Ingestion with f1 = 0.1.
- IR2 Inhalation ICRP default aerosol Type "F" absorption (f1 = 0.3).
- IR3 Inhalation ICRP default aerosol Type "M" absorption (f1 = 0.1).
- IR4 Inhalation ICRP default aerosol Type "S" absorption (f1 = 0.01).

To do this (most easily):

- select <u>4</u> Intake Regimes;
- click "ICRP DEFS Load";
- un-check "Apply Model Parameters to All IRs" in the "Advanced" menu;
- set each IR in turn, as listed above.

Figure 4.75 shows the resulting Main Screen set to indicate the Model Parameters for IR1 (the hypothetical Ingestion).

	ore set to "	24/11/90)".	п пурот	hetic	al (acu	ite) intake is	
File Edit Parameters Calcu	ulations Tools Adva	nced Help						
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_Intake Scenario-								
Intake Regimes Clear All Intake Regimes IR 1 IR 2 IR 3 Route C Inhalation G Ingestion C Injection	Enter Number	of Intake Regin (24/11/1	nes (1-10) 4		Inits Specify Ti O Date O Time (tince 24/11/19 Intake O Bq	me As d) 90	Intake (IR 1) 1 Bq Associated Ra Y-90	Indicator No Select Rai Number of Ass Half Life: 10 adionuclides
C Wound C Vapour		Edit D	omplex Regime		C pCi Dose ⊙ Sv C mSv	C mg C rem C mrem	Select Radio	onuclide
				-C	~		<u> </u>	
[Model Paramete	ers						Calculation	\$
IR 1 IR 2 IR 3 IR Respiratory Tract Deposition	4 Vapor	Wound	Bioassay		*	X	,	Bioassay C
					~	`		Dose Ca

Figure 4.75. First hypothetical intake regime (IR1) set up as "Ingestion" with $f_{\underline{1}} = 0.1$.

To calculate the most likely amounts of intake from each IR (in the Bioassay Calculations Screen):

- check Whole body, Urine and Faeces (in the Bioassay to Intake mode);
- click "Start Calculation".

Figure 4.76 shows the result.

💐 Bioassay Calc	ulations						
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Save Quick S] Bave		Bi	oassay Calcul	ations		
INTAK	(ES	CAL	CULA	ΓΙΟΝ		BI	OASSA
		/			C Grach G	Table C I	lide Whole
IR 1 5.275E+06	Bq				Measurement	Date	N/A
IR 2 5.828E+05	Bq	Intakes to Bioassay	Í	Bioassay to Intake		29/11/1990	
						30/11/1990	
IR 3 5.494E+04	Bq		<u>ح</u>	elect which data to use		03/12/1990	
IB 4 0 0005 .00	Ba			Vhole body		04/12/1990	
**** [0.000E+00	bq					05/12/1990	
				Lungs		07/12/1990	
				🔽 Urine		10/12/1990	
				Feces			
				E Blood	C Graph 📀	Table 🔿 H	lide Urine
				E Thursda	Measurement	t Date	Collection
				I hyroid	(+hh:mm]		period (d)
				Liver		29/11/1990	7.920E-01
		Start Calculation		User Defined		03/12/1990	7.920E+00
						04/12/1990	7.920E-01
						06/12/1990	7.500E-01
		000			1	09/12/1990	7.920E-01
-						11/12/1990	1.000E+00
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Deposition					C Graph 🖸	Table 🔿 His	de Feces
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Connect						03/12/1990	1.000E+00
Operation						04/12/1990	1.000E+00
						06/12/1990	1.000E+00
				[11/12/1990	1.000E+00
				DK		111201000	1.0002.100
				Constant and a second s	•		
Sr-90	Sr Model	Max Likelihood fit					

Figure 4.76. Calculated amounts of 4 hypothetical intakes.

The resulting total estimated intake is about 5.91 MBq, of which:

- IR1 is assigned about 89%;
- IR2 is assigned about 10%;
- IR3 is assigned about 1%;
- IR4 is assigned 0%.

Figure 4.77 shows the resulting overall "fits" to all 3 sets of bioassay data.



Figure 4.77. Overall fits to the bioassay data given by a combination of 4 hypothetical acute intakes.

From the above, we can conclude that:

- the overall fits to all 3 sets of bioassay data are reasonably consistent with the assumed error distributions;
- inhalation intake of both Types "S" and "M" material can be neglected in comparison with that of Type "F" and that by ingestion.

We now need to refine our hypothetical intake scenario(s) accordingly (see Step #4).

This completes Step #3 in the multiple bioassay quantities example (trying Hypothetical Intake Scenarios):

- Proceed to Refining the Intake Assessment.
- Return to the case description and list of steps.
- -
Refining the Intake Assessment -Multiple Bioassay Quantities



From the initial evaluation of hypothetical intake scenarios, it was clear that the actual intake comprised primarily of:

ingestion, and/or;

• inhalation of Type "F" material.

In this case, we can proceed to test hypothetical combinations of ingestion (with $f_1 = 0.3$) and inhalation (Type "F" with various assumed values of the AMAD), as follows:

- IR1 Ingestion with $f_1 = 0.3$.
- IR2 Inhalation Type "F" absorption with AMAD = 5 μ m (ICRP default aerosol);
 - IR3 Inhalation Type "F" absorption with AMAD = 20 $\mu m;$
 - IR4 Inhalation Type "F" absorption with AMAD = 100 μ m.

Figure 4.78 shows the result.

Bioassay Calculations			
Eile Advanced Iools Help			
Save Quick Save	Γ	Bioassay Calcul	ations
INTAKES	CALCU	LATION	BIOASSAY
IR 1 2.480E+06 Bq			Graph C Table C Hide Whole be
IR 2 1.162E+01 Bq IR 3 6.333E+00 Bq IR 4 7.491E+03 Bq	Intakes to Bioassay	Bioassay to Intake Select which data to use Whole body Lungs Unine Feces Blood Thyroid Liver User Defined	1.0E+05 5.0E+04 0 100 200 30 Graph O Table O Hide Urine 1.0E+05 1.0E+04 1.0E+04 1.0E+03
Progress Indicator	000		1.0E+02 E 1.0E+01 0 50 100
Collating Times Bioassay Calcs			1.0E+05
Current Operation	Calculation Compl	ete <u>o</u> ĸ	1.0E+03 1.0E+02 1.0E+01 0 2 4 6 8
Sr-90 Sr Model	Max Likelihood fit		

Figure 4.78. Intake amounts calculated for 4 hypothetical (simultaneous) intake scenarios.

The "best estimates" of each type of intake are:

- IR1 Ingestion 2.480 MBq;
- IR2 Inhalation 5 µm AMAD 11.62 Bq;
- IR3 Inhalation 20 µm AMAD 6.333 Bq;
- IR4 Inhalation 100 µm AMAD 7.491 kBq.

Clearly, the bioassay data (in conjunction with ICRP's current respiratory tract model and biokinetic model for strontium) indicate intake predominantly by ingestion. Figures 4.79 through 4.81 show the fits obtained, for the whole body, urine and faecal data, respectively.



Figure 4.79. Graph Tool plot of whole body data.



Figure 4.80. Graph Tool plot of urine data.



Figure 4.81. Graph Tool plot of faecal data.

Except for the additional retention in the nose and tracheobronchial region, inhalation of very large particles has a similar effect to ingesting these particles - since most of the inhaled activity not cleared from the nares (by nose blowing) is swallowed. If we had assumed that ALL of the intake had occurred by inhalation of a 100- μ m-AMAD aerosol, the resulting "fit" to the bioassay data would have been as shown in Figure 4.82. In this case, the estimated intake would have been 4.438 MBq.



Figure 4.82. "Best Fit" to the bioassay data obtained when the intake is assumed to be by ingestion.

By eye, it is impossible to distinguish between the "fit" shown in Figure 4.82 (assuming intake by inhalation of large particles) from that shown in Figure 4.78 (assuming predominant intake by ingestion). However, in terms of "numerical likelihood," <u>IMBA Professional</u> found the fit in Figure 4.78 (ingestion) substantially "better." However, for radiological protection purposes, it is prudent to consider which intake route would give the higher effective dose - see Step #5.



This completes Step #4 in the multiple bioassay quantities example (Refining the Intake Assessment):

- Proceed to Evaluating the Dose.
- Return to the case description and list of steps.

Evaluating the Dose - Multiple Bioassay Quantities



As the final step in this example, we will calculate the doses resulting from the two "hypothetical" intake scenarios that we found to be most consistent with the bioassay data:

- 1. Ingestion of 2.486 MBq of material with an f1 of 0.3.
- Inhalation of 4.438 MBq of a 100-µm-AMAD aerosol of Type "F" material.

Figures 4.83 and 4.84, respectively, give the resulting values of effective dose.



Section Calculations										
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Save Quick Save	Dose Calculations									
INTAKE	CALCULATION			DC						
		C Equiv (Elf	Indicato						
IR 1 2.486E+06 Bq		Target Organs	Cont. to Eff Dose (Sv) IR(1)	Effective Dose (Sv) Total						
	Calculations WR WT	LN(TH)	0.00E+00	0.00E+0						
		Esophagus	8.23E-05	8.23E-0						
		Gonads	3.29E-04	3.29E-0						
	Select	Spare	0.00E+00	0.00E+0						
		Remainder	8.35E-05	8.35E-0						
	(1) Dose from Indicator Nuclide: Sr-90	TOTAL	6.86E-02	6.86E-0						
		T								
	(2) Dose from Associated Radionuclides 🔽	C Equiv G	Eff	Associated F						
	(3) Dose in each Galendar Year	Target Organs	Eff Dose from Y-90 (Sv)	Eff Dose fro ALL AR's (Sv)						
		LN(TH)	0.00E+00	0.00E+0						
	Effective Dose (Sv)	Esophagus	4.86E-06	4.86E-0						
	Calculate	Gonads	1.94E-05	1.94E-0						
	7.42E-02	Spare	0.00E+00	0.00E+0						
		Remainder	9.54E-06	9.54E-0						
		TOTAL	5.64E-03	5.64E-0						
	000									

Figure 4.83. Effective doses calculated for ingestion of 90Sr/90Y powder.

Dose Calculations											
File Tools Advanced Help											
Save Quick Save	Dose Calculations										
INTAKE	CALCULATION	DC									
		C Equiv (• Eff	Indicato							
IR 1 4.438E+06 Bq		Target Organs	Cont. to Eff Dose (Sv) IR(1)	Effective Dose (Sv) Total							
	Calculations WR WT	LN(TH)	0.00E+00	0.00E+0							
		Esophagus	8.24E-05	8.24E-0							
		Gonads	3.30E-04	3.30E-(
	Select	Spare	0.00E+00	0.00E+0							
		Remainder	8.29E-05	8.29E-0							
	[1] Dose from Indicator Nuclide: Sr-90	TOTAL	6.65E-02	6.65E-0							
	(2) Dose from Associated Radionuclides 🔽	C Equiv G	Eff	Associated F							
	(3) Dose in each Calendar Year	Target Organs	Eff Dose from Y-90 (Sv)	Eff Dose fro ALL AR's (Sv)							
		LN(TH)	0.00E+00	0.00E+0							
	Effective Dose (Sv)	Esophagus	5.03E-06	5.03E-0							
	Calculate	Gonads	2.01E-05	2.01E-(
	6.85E-02	Spare	0.00E+00	0.00E+0							
		Remainder	6.25E-06	6.25E-0							
		TOTAL	1.96E-03	1.96E-0							
	000										
D 17.											

Figure 4.84. Effective doses calculated for inhalation of 90Sr/90Y aerosol (100-µm-AMAD, Type "F").

 Table 4.6.
 Comparison of effective doses calculated by assuming intake by ingestion or inhalation.

	Effective Dose	Effective Dose	Total Effective Dose
Route of Intake	from <u>90</u> Sr (mSv)	from <u>90</u> Y (mSv)	(mSv)
Ingestion	68.6	5.64	74.2
Inhalation	66.5	1.96	68.5

Clearly, in this case, we can conclude that:

- the total effective dose is about 75 mSv;
- it makes little difference if the actual intake occurred by ingestion or inhalation.

. Insulation	Note: The Associated Radionuclide (90Y) is included in the dose calculations.
<u> </u>	The ICRP-recommended biokinetic models are assumed for both 90Sr and 90Y.
	and also the ICRP68 radiation and tissue weighting factors.

This completes the final step in the multiple bioassay quantities example (Evaluating the Dose):

<u>Return to the case description and list of steps.</u>

Case of Uranium Isotopic Mixture -Requires Add-On 4



Details of the (real) case

- A release of uranium feed material at a uranium fuel fabrication plant was indicated by an installed continuous air monitor.
- The material released was sintered LEU of known isotopic composition, in the form of highly insoluble oxide.
- Earlier studies of airborne contamination in this area of the workplace indicated an aerosol AMAD of 5.9 $\mu m.$
- Both urine and fecal bioassay was carried out for the worker concerned, commencing immediately.

Isotopic composition (by Activity)

- **234**U 83.6%.
- **235**U 3.05%.
- **238**U 13.4%.

Urine bioassay data

- The first urine sample was obtained from the worker concerned at 30 minutes after the incident.
- Ten further (contiguous) samples were collected over the following 3 days.
- The results were reported as total uranium mass (µg) per collection period, together with the associated uncertainty (measurement error) and the total volume of urine collected.

Fecal bioassay data

- The first fecal sample was obtained from the worker concerned at 3 hours after the incident.
- Four further (contiguous) samples were collected over the following 3 days.
- The results were reported as total uranium activity (pCi) per collection period, together with the associated uncertainty (measurement error).

Case Analysis

Follow these steps to analyze this case:

- Set up Uranium Mixture.
- Enter Uranium-in-Urine Data (in mg/d).
- Enter Uranium-in-Feces Data (in mg/d).
- Initial Joint Analysis of Urine/Fecal Data.
- Correct for Dietary Uranium Intake.
- Optimize Intake Model Parameters.
- Calculate Committed Doses.

See also:

- Published Data on "Background" Uranium-in-Urine.
- Overall Case Summary



Note: This case demonstrates how to use <u>IMBA Professional</u> <u>Plus</u>to_detect_the_(assumed)_constant background contributions to urinary and fecal excretion rates made by an individual's dietary intake of uranium.

Set up Uranium Mixture



-	📲 Select the required radionuclide																	
H Isotope Uranium-Mixture									Не									
	Li	Be				Uraniu Uraniu Uraniu	um-Mixtu um-234 um-225	ure					В	С	N	0	F	Ne
	Na	Mg				Uraniu Uraniu Uraniu	um-236 um-238						AL	Si	Ρ	S	CI	Ar
	К	Ca	Sc	Ti	\vee	Cr	Mn	Fe	Co	Ni	Cu	Zn	Ga	Ge	As	Se	Br	Kr
	RЬ	Sr	Y	Zr	NЬ	Мо	Tc	Ru	Rh	Pd	Ag	Cd	In	Sn	Sb	Те	Ι	Xe
	Cs	Ba	La	Hf	Ta	W	Re	Os	l r	Pt	Au	Hg	ΤI	РЬ	Bi	Po	At	Rn
	Fr	Ra	Ac	Ce	Pr	Nd	Pm	Sm	Eu	Gd	ТЬ	Dy	Но	Er	Tm	Yb	Lu	
				Th	Pa	U	Np	Pu	Am	Cm	Bk	Cf	Es	Fm	Md	No	Lr	
Lo	Load Complete																	
	<u>D</u> Ecay																	

Figure 4.92. Selecting Uranium - Mixture as the Indicator Nuclide.

Intake (IR 1)	Indicator Nuclide	
0 Bq	Select Radionuclide	U-mix
Specify U mixture	Number of Associated Radionuclides: Half Life: 1.000E+09 d	
Associated Radion	uclides	
	None Selected	

Figure 4.93. "Specify U mixture" button.

🖻 Details o	f uranium mixture		
Help			
- Isotopic U-234 U-235 U-236	Abundance 83.6 3.05 0	% Select % Iser Defined % O Depleted % Natural % Low-Enriched	Select by C Activity Mass Clear
U-238	13.4	% C High Enriched	
Resulting	9 Specific Activity 8.9611E+01 2.4219E+03	Bq/mg pCi/mg	Allow Units
	<u> </u>	Cancel	

Figure 4.94. User Defined details of uranium mixture with resulting specific activity.

Warning	X					
Abundances do not add up to 100% Do you still wish to leave this form?						
<u>Y</u> es <u>N</u> o						

Figure 4.95. Warning notice.

- Units	
- Specifu Time As-	Intake (IR 1) Indicator Nuclide
C Date	0 mg Select Radionuclide U-mix
 Time (d) since 1/1/1980 # 	Number of Associated Radionuclides: 4 Specify U mixture Half Life:
	Associated Radionuclides
ntake	U-234 U-235 U-236 U-238
⊂ Bq ⊂ dpm	
⊂ pCi ⊙ mg	
Dose C Sv C rem	Select Radionuclide Abundance 83.6 %
C mSv 💿 mrem	Delete Radionuclide Half Life: 8.924E+07 d

Figure 4.96. Selected U-mix showing Associated Radionuclides and "mg" Intake Unit.

To define the isotopic composition and measurement unit for the uranium mixture:

- 1. <u>Select</u> "Uranium Mixture" as the Indicator Nuclide (Figure 4.92).
- 2. <u>Click</u> the "Specify U mixture" button (Figure 4.93).
- 3. <u>Enter</u> the Isotopic Abundance values (% by Activity in this case), <u>check</u> the Allow Units "mg" box (Figure 4.94), and <u>click</u> "OK".
- 4. You will be warned if your Abundance values don't add up to 100% (Figure 4.95) ignore the warning for this example.
- 5. Select "mg" in the "Units" panel (Figure 4.96) since, in this example, most of the measurements (urinary excretion rates) are reported in "mg/d".



This completes the 1st Step in the uranium isotopic mixture example:

- Proceed to Enter Urine Data.
- Return to the case description and list of steps.

Enter Uranium-in-Urine Data (in mg/d)



Figure 4.97 shows the urine bioassay data as entered in a NotePad® text file, ready for importing into the <u>Table Tool</u> of <u>IMBA Professional Plus</u>. <u>Note that:</u>

- These are <u>real</u> data.
- The dates have been changed (by subtracting from the reported values a constant number of yy:mm:hh) in order to preserve confidentiality.
- The third column of values (the actual <u>bioassay quantity</u>) is the calculated daily uranium <u>excretion rate</u> - in μg d-1.
- We have assumed a <u>lognormal</u> error distribution, with a <u>sg</u>of <u>1.8</u>. This is a more realistic representation of the data variability than the reported <u>measurement</u> uncertainties. The measurement uncertainties do NOT represent the sytematic (biological) variability in urinary excretion which is substantially greater.

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<u>F</u> ile <u>E</u> dit F <u>o</u> rmat <u>V</u> iew <u>H</u> elp					
3/10/1995 12:30:00 AM 3/10/1995 5:30:00 AM 3/10/1995 12:15:00 PM 3/10/1995 11:05:00 PM 3/11/1995 6:10:00 AM 3/11/1995 4:20:00 PM 3/11/1995 4:30:00 PM 3/11/1995 8:50:00 PM 3/11/1995 10:50:00 PM 3/12/1995 2:30:00 AM 3/12/1995 4:30:00 PM	2.080E-02 2.080E-01 2.810E-01 4.510E-01 2.950E-01 4.240E-01 6.940E-03 1.670E-01 8.330E-02 1.670E-01 5.830E-01	1.830E-02 5.640E-04 3.770E-04 1.510E-04 1.380E-04 1.070E-04 2.620E-03 2.180E-04 3.430E-04 2.180E-04 7.890E-05	Real Real Real Real Real Real Real Real	1.8 1.8 1.8 1.8 1.8 1.8 1.8 1.8 1.8 1.8 1.8 1.8 1.8 1.8 1.8	LOGNORM LOGNORM LOGNORM LOGNORM LOGNORM LOGNORM LOGNORM LOGNORM LOGNORM

Figure 4.97. Uranium-in-urine bioassay data set.



This completes the 2<u>nd</u> Step in the uranium isotopic mixture example:

- Proceed to Enter Fecal Data.
- <u>Return</u> to the case description and list of steps.

Enter Uranium-in-Feces Data (in mg/d)

Figure 4.98 shows the fecal bioassay data as entered in a NotePad® text file, ready for importing into the Table Tool of IMBA Professional Plus. Note that:

- Again, these are <u>real</u> data.
- Again, the dates have been changed (by subtracting from the reported values the same number of yy:mm:hh as for the urine data) in order to preserve confidentiality.
- The third column of values (the actual bioassay quantity) is the calculated daily uranium excretion rate in µg d-1. These values are calculated from the reported values of excretion rate in terms of pCi d-1, using the displayed (calculated) specific activity of the mixture (2,421.9 pCi/mg see Figure 4.94).

•

• We have assumed a <u>lognormal</u> error distribution, with a <u>sq</u> of <u>3.0</u>, c.f., <u>sq</u> = <u>1.8</u> for the urine data. This is a more realistic representation of the variability in fecal excretion rate than the reported <u>measurement</u> uncertainties. The raw measurement uncertainties drastically underestimate the sytematic (biological) variability in fecal excretion.

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<u>File E</u> dit F <u>o</u> rmat <u>V</u> iew <u>H</u> elp				
3/10/1995 3:00:00 AM 3/10/1995 4:30:00 PM 3/10/1995 6:35:00 PM 3/11/1995 4:30:00 PM 3/12/1995 4:30:00 PM	1.250E-01 5.630E-01 8.680E-02 9.130E-01 1.000E+00	1.220E-01 2.500E-01 1.140E+00 2.170E-02 1.090E-02	Real Real Real Real Real	3.000E+00 3.000E+00 3.000E+00 3.000E+00 3.000E+00

Figure 4.98. Uranium-in-feces bioassay data set.



Tip: The reported (normal) measurement errors are given in the data file "IU_FECES_2.txt" - which is included in the [Install Drv]:\JABASOFT\IMBAEXUS\UserData1\Demo\ folder at installation. It is instructive to re-analyze this case using these reported_errors instead of the (realistic) lognormal errors.

This completes the 3rd Step in the uranium isotopic mixture example:

- <u>Proceed</u> to Initial Joint Analysis of Urine/Fecal Data.
- <u>Return</u> to the case description and list of steps.

Initial Joint Analysis of Urine/Fecal Data

file://C:\Documents%20and%20Settings\Administrator\Local%20Settings\Temp\~hh... 15/10/2005

👒 Bioassay Calculations			
Eile <u>A</u> dvanced <u>T</u> ools Help			
Save Quick Save Tribium		Bioassay Calc	ulations
INTAKE	CALCULATIO	N	BIOASSAY QUA
IR1 2.055E+00 mg			C Graph C Table C Hide Unine Measurement Date Collection Measurem
	Intakes to Bioassay	Bioassay to Intake	[+hh:mm] period (d) Rate(mg/c 3/10/1995 12:30:00 AM 2:080E-02 1:830E-
	Bayesian Analysis Start Calculation	Select which data to use Whole body Lungs Unine Feces Blood Thyroid Liver User Defined	3/10/1995 5:30:00 AM 2:080E-01 5:640E- 3/10/1995 12:15:00 PM 2:810E-01 3:770E- 3/10/1995 11:05:00 PM 4:510E-01 1:510E- 3/11/1995 4:20:00 PM 4:2950E-01 1:380E- 3/11/1995 4:20:00 PM 4:2950E-01 1:380E- 3/11/1995 4:20:00 PM 6:940E-03 2:620E- 3/11/1995 8:50:00 PM 1:670E-01 2:180E- 3/11/1995 8:50:00 PM 8:330E-02 3:430E- 3/11/1995 10:50:00 PM 8:330E-02 3:430E- € € 6 Graph C Table C Hide Unine
- Progress Indicator	000		0.0 0.5 1.0
Deposition			Graph C Table ⊂ Hide Feces
Collating Times			5.000 °L
Bioassay Calcs			1.000
Current Operation	Calculation Complet	e	0.100
		<u></u> K	
U-mix	Max Likelihood fit		

<u>4.99.</u> Initial data "fit" for assumed acute inhalation of Type 'S' uranium at t = 0.

Figure 4.99 shows the initial result of analysing jointly the measured urinary and fecal excretion rates, under the following assumptions:

- <u>Acute inhalation</u>, at <u>t = 0</u>.
- <u>Aerosol characteristics</u> <u>AMAD/MMAD</u> = 5.9 μm, sg = 2.5, particle density (r) = 10 g cm-3, particle shape factor (SF) = 1.5.
- Absorption characteristics Type 'S'.
- Mechanical transport parameters (respiratory tract) ICRP66 Default.
- <u>GI-Tract transport parameters</u> <u>ICRP66 Default</u>.
- <u>Gut uptake fraction</u> (<u>f1</u>) 0.002 (<u>ICRP68</u> highly insoluble uranium compounds: UO<u>2</u>, U<u>3</u>O<u>8</u>).
- Two reported uranium-in-urine outlier values have been excluded from the "fit":
 - the <u>first value</u> (from the sample collected 30 minutes after the intake) is assumed to result from <u>sample contamination</u>. the rate of excretion of uranium in urine following an acute intake requires several hours to "<u>build up</u>"
 it does NOT decrease over this period.
 - the <u>seventh value</u> (from the sample collected at about 1.8 d after the intake) is also assumed to result from <u>sample contamination</u>.

00

Initial findings from plotted data fits

The resulting initial data fits (Figure 4.99) show clearly that:

- After peaking at about 0.2 day after the intake, the <u>predicted</u> urinary excretion rate <u>falls</u> <u>off more rapidly</u> than the measured values.
- After the first day, the observed urinary excretion rates are relatively constant.
- The predicted fecal excretion rate <u>peaks at approximately the same time</u> after intake as the measured values.
- Over the period of the first fecal sample (about 0 0.1 d after intake), the predicted fecal excretion rate is more than <u>an order of magnitude lower</u> than the measured rate.
- After the measured "peak" in fecal excretion of uranium (during the first day), the <u>measured</u> excretion rate is about an order of magnitude <u>lower</u> than that <u>predicted</u>.

The above observations suggest that BOTH the measured urinary AND fecal excretion rates are strongly influenced by a relatively high "background" excretion of uranium. Since, in this case, continuous workplace air monitoring did NOT indicate the presence of chronic airborne contamination, in order to "fit" the observed excretion values, it is necessary to consider another <u>relatively constant</u> source of intake. The obvious candidate is <u>dietary intake</u>.

This completes the 4<u>th</u> Step in the uranium isotopic mixture example:

- Proceed to Correct for Dietary Uranium Intake.
- <u>Return</u> to the case description and list of steps.

Correct for Dietary Uranium Intake

👒 Bioassay Cal	culations			
Elle <u>A</u> dvanced]	ools Help			
Save Quick S	ave Tritium		Bioassay Calcu	llations
INTA	KES	CALCULA	TION	BIOASSAY QUA
		- /	1	
IR1 3.568E-01	mg	<		Measurement Date Collection Measurem
IR2 8.120E-03	3 mg/d	Intakes to Bioassay	Bioassay to Intake	3/10/1995 12:30:00 AM 2.080E-02 1.830E-
jo. 1202.0.		Bayesian Analysis Start Calculation	Select which data to use Whole body Lungs Vinne Feces Blood Thyroid Liver User Defined	3/10/1995 5:30:00 AM 2:080E-01 5:640E 3/10/1995 12:15:00 PM 2:810E-01 3:770E 3/10/1995 11:05:00 PM 4:510E-01 1:510E 3/11/1995 6:00:00 AM 2:950E-01 1:380E 3/11/1995 4:20:00 PM 6:940E-03 2:620E 3/11/1995 8:50:00 PM 1:670E-01 2:180E 3/11/1995 8:50:00 PM 1:670E-01 2:180E 3/11/1995 10:50:00 PM 8:330E-02 3:430E C Graph C Table C Hide Unive 5:0E-02 1:0E-02 1:0E-03
				1.0E-04
- Program la fa	alor			1.0E-05 + 0.5 1.0
Deposition				C Such C Table C Mide Factor
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bioassay Calca				1.000
Current Operation		Calculation Com	plete	0.100
			<u>o</u> k	
U-mix		Max Likelihood fit		

Figure 4.100. Data "fit" for assumed combination of acute inhalation with <u>background chronic ingestion</u>.

Figure 4.100 shows the result of analysing jointly the measured urinary and fecal excretion rates, under the assumption that a single acute inhalation of Type 'S' uranium (Figure 4.99) is superimposed on a long-term (uniform chronic) intake of uranium in the diet. The chronic intake is defined by:

• A uniform chronic ingestion of uranium with a <u>gut uptake fraction</u>, <u>f1 = 0.02</u>, <u>i.e.</u>, an "unknown" form of uranium - commencing 20 y prior to the inhalation intake - and continuing beyond the bioassay monitoring period.

Findings from plotted data fits

The resulting data fits (Figure 4.100) show clearly that:

- The assumption of chronic "background" intake (by ingestion) significantly improves the "fit" to the urinary excretion data.
- The "peak" values of fecal excretion rate (within a day of the inhalation intake) are substantially "under-predicted" and the fecal excretion rates measured over the following 2 days are substantially "over-predicted."

These observations indicate that the chronic mass intake rate must have been substantially higher than the value (of about 8 μ g/d) fitted on the assumption of 'moderate' absorption (corresponding to the assumed <u>f1</u> value of 0.02). In fact, the data shows that the early fecal excretion rates were about an order of magnitude <u>higher</u> than the fitted rates - without significantly influencing urinary excretion. This can only happen if the chronically ingested material has a substantially lower value of <u>f1</u> than we assumed here, <u>i.e.</u>, the dietary uranium is <u>significantly less readily absorbed</u>. So, we can expect to improve the data "fit" by <u>finding</u> more appropriate parameter values, <u>i.e.</u>, by <u>optimizing the intake model</u>.

This completes the 5th Step in the uranium isotopic mixture example:

- Proceed to Optimize Intake Model Parameters.
- <u>Return</u> to the case description and list of steps.

Optimize Intake Model Parameters

In reality, the "background" dietary intake would have been "<u>natural</u>" uranium, and not "<u>LEU</u>" - as assumed in the <u>previous analysis</u>. Therefore a different conversion factor to <u>mass</u> should have been applied to the "baseline" fecal excretion rates (measured and reported as "pCi/d"). The "background" uranium mass excretion rates should be higher by a factor of about <u>3.55</u> - in the ratio of the specific activities of <u>LEU:U-Nat</u> (approximately <u>2,422:683</u>). Accordingly, before "optimizing" the data "fit", the "input" uranium mass excretion rates representing the "baseline" uranium excretion should be adjusted - as shown in Figure 4.101.

🖡 Untitled - Notepad				
<u>File E</u> dit F <u>o</u> rmat <u>V</u> iew <u>H</u> elp				
3/10/1995 3:00:00 AM 3/10/1995 3:00:00 AM 3/10/1995 4:30:00 PM 3/10/1995 6:35:00 PM 3/11/1995 4:30:00 PM 3/12/1995 4:30:00 PM 3/11/1995 4:30:00 PM 3/12/1995 4:30:00 PM	1.250E-01 1.250E-01 5.630E-01 8.680E-02 9.130E-01 1.000E+00 9.130E-01 1.000E+00	1.220E-01 4.330E-01 2.500E-01 1.140E+00 2.170E-02 1.090E-02 7.700E-02 3.870E-02	Excluded Real 3.0 Real 3.0 Real 3.0 Excluded Excluded Real 3.0 Real 3.0	3.000E+ 00E+00 00E+00 3.000E+ 3.000E+ 00E+00 00E+00

<u>Figure 4.101.</u> Adjusting the 1<u>st</u>, 4<u>th</u> and 5<u>th</u> values of uranium mass excretion rates for the specific activity of <u>natural uranium</u>.

👒 Bioassay Calculations			
Elle <u>A</u> dvanced <u>I</u> ools Help			
Save Quick Save Triti]] ium	Bioassay Calculat	ions
INTAKES	CALCULATI	DN	BIOASSAY QUA
IR1 7.143E-01 mg	-		C Graph Table C Hide Unine Measurement Date Collection Measurement
IR2 7.918E-02 mg/d	Intakes to Bioassay	Bioassay to Intake	[+hit:mm] penod (d) [Hate(mg/k 3/10/1995 12:30:00 AM 2:080E-02 1:830E-
	Bayesian Analysis Start Calculation	Select which data to use Whole body Lungs Vine Feces Blood Thyroid Liver User Defined	3/10/1995 5:30:00 AM 2:080E-01 5:640E- 3/10/1995 12:15:00 PM 2:810E-01 3:770E- 3/10/1995 11:05:00 PM 4:510E-01 1:510E- 3/11/1995 6:10:00 AM 2:950E-01 1:380E- 3/11/1995 6:00 00 PM 4:240E-01 1:070E- 3/11/1995 8:50:00 PM 1:670E-01 2:180E- 3/11/1995 8:50:00 PM 1:670E-01 2:180E- 3/11/1995 10:50:00 PM 8:330E-02 3:430E- C Graph C Table C Hide Unine
	000		1.0E-05
Progress Indicator			0.0 0.5 1.0
Deposition			Graph ⊂ Table ⊂ Hide Feces Fecees Feces Feces Fecees Fecees Fecees Fe
Collating Times			5.000 F T
Bioassay Calcs			1.000
Current Operation	Calculation Comple	te	0.100
		<u>O</u> K	
U-mix	Max Likelihood fit		

Figure 4.102. Data "fit" obtained by "optimizing" intake and GI-tract model parameter values - with adjusted "baseline" fecal uranium mass excretion rates.

Figure 4.102 shows the result of "optimizing" the data "fit" - by using the adjusted "baseline" fecal uranium mass excretion rates (Figure 4.101) and manually varying the model parameters. The changes made to the model parameters were as follows:

- 1. Reducing the <u>f1</u> value for the acute inhalation (<u>IR1</u>) to <u>0.0002</u> (from the "default" value of 0.002).
- 2. Reducing the <u>f1</u> value for the "background" chronic dietary intake (IR2) to <u>0.002</u> (from the "default" value of 0.02).
- Doubling the rate of transport through the <u>SI</u> to <u>12</u> <u>d-1</u> (from the "default" value of 6 d-1).
- Doubling the rate of transport through the ULI to <u>3.6</u> <u>d-1</u>(from the "default" value of 1.8 d-1).
- Doubling the rate of transport through the <u>LLI</u> to <u>2</u> <u>d-1</u>(from the "default" value of 1 d-1).
- The first change reflects the high-fired (ceramic) nature of the airborne particles.
- The second change is necessary to improve the "fit" the adjusted "baseline"

fecal excretion rate, i.e., after the "bolus" of inhaled LEU material has been excreted.

• The third, fourth and fifth changes (see Figure 4.103) improve the "fit" to the observed "peak" in fecal excretion within the first day, and also predict a substantial reduction in fecal excretion over the following two days - down towards the adjusted "baseline" rates.



Figure 4.103. "User Defined" values of rate constants in the GI Tract model.

Important Note: The interpretation of the data developed here in this example case is not intended to be "definitive." It has NOT been reviewed by USDOE nor any other Regulatory Authority. It is intended merely to illustrate the flexibility and power provided in IMBA Professional Plus - which_enables YOU to "test" the effects of reasonable "hypotheses" about the conditions of intake and other "model" parameters. You are invited to investigate this example further - in order to draw your own conclusions!

This completes the 6<u>th</u> Step in the uranium isotopic mixture example:

• <u>Proceed</u> to Committed Doses from U-Mixture.

• <u>Return</u> to the case description and list of steps.

Committed Doses from U-Mixture



Our "optimized" estimates (Figure 4.102) of the components of uranium intake (by mass) in this example are:

- Acute inhalation of LEU (0.714 mg) at 0:00 AM on March 10th, 1995.
- Chronic dietary intake (natural uranium) of $\underline{79.2 \ \mu g \ d-1}$ (assumed here to have started at 0:00 AM on March 10th, 1975).

As for all dose calculations, for this "<u>Uranium Mixture</u>" case, you calculate the resulting committed doses by <u>clicking</u> the "Dose Calculations" button in the Main Screen (Figure 4.104) - to open the "Dose Calculations" screen. In this case, we are only interested in the "occupational" dose from the acute intake of LEU (<u>IR1</u>).

🍕 Main Screen						
Elle Edit Parameters Calculat	tions <u>T</u> ools <u>A</u> dvance	d <u>H</u> elp				
Open Save New	Quick Save	ICRP CFR DEFS DEFS Load Load	Report Help			
Ver 3.1 C: \JABASOFT \IMB	AEXUSVUSERDATAVU	SDOE-IIVU_Case_2.ix				
Intake Scenario	Enter Number	r of Intake Regimes (1-10		Units Specify Time As (* Date (* Time (d) since 3/10/1995 #	S-Edition	Indicator Nuclie Select Radior Number of Associat Half Life: 1.0006 Inuclides
C Injection	Start Da	ste 3/10/1995		⊂ Bq ⊂ dpm		
C Wound		1		⊂ pCi ⊙ mg		
C Vapor		Edit Comp	vlex Regime	Dose ⊂Sv Crem ⊂mSv ©rmrem	Select Radion Delete Radion	uclide
Model Parameters	;				Calculations-	
IB1 IB2 Bestitatory Tract			1	0045		
Deposition	Vapor	Wound	Bioassay	Office of Compensation Analysis and Support		Bioassay Calc
Particle Transport	Absorption	GI-Tract	Biokinetics	Close		Dose Calcu
IR 1 Absorption: Type S Pa	art Trans ICRP Defaults	GI-Tract: User Defined	f1=0.0002	Biokinetics: Not Specified	Deposition: User Defined	AMAD: 5.9 µm Wour

Figure 4.104. "Dose Calculations" button for calculating committed doses for a Uranium Mixture (treated as Associated Radionuclides).

For this example, we have:

- <u>Checked</u> "<u>mrem</u>" as the dose unit (Figure 4.104).
- <u>Reduced</u> the number of intake regimes to ONE (<u>IR1</u>) also shown in Figure 4.104.
- <u>Selected</u> the "<u>ICRP Default</u>" values of <u>radiation weighting factor</u> (wR) in the "<u>Dose</u> <u>Calculations</u>" screen.
- <u>Selected</u> the "<u>10CFR835 Default</u>" values of <u>tissue weighting factor</u> (<u>wT</u>).
- Checked the "Dose from Associated Radionuclides" box .
- <u>Checked</u> the "<u>Dose Committed in Each Calendar Year</u>" box.
- Selected the "<u>Speed</u>" calculation option from the <u>Advanced | Advanced Dosimetry</u> <u>Options | Dose menu (Figure 4.105 - see also Appendix A: Effect of Merging SEEs</u>).
- <u>Clicked</u> the "<u>Calculate</u>" button.

dvanced Dosimetry Options	
These options should be used with extreme	e care
Dose Fitting Bioassay Misc	
Nuclear Recoil Energy Include C Exclude	
Dose Calculation Optimisation	
Speed C Accuracy	
<u>O</u> K <u>C</u> ancel	1
<u>4.105.</u> Selecting the "Speed" option -	to "merge" the initial shor

Note: In this case (and in all "practical" cases) you should use the "Speed" option to calculate doses from intakes of 235U and 238U. This option "merges" the disintegrations of the initial short-lived progeny of these uranium isotopes - and represents more closely the actual situation - where these short-lived progeny are taken into the body in radioactive equilibrium with the parent uranium isotope. The "Accuracy" option assumes that ONLY the parent uranium isotopes are taken into the body - which is the case ONLY for ICRP-published "dose coefficients" (see <u>Appendix C: Dose Quality</u> <u>Assurance</u> for discussion). Not only will the "Accuracy" option give the wrong answers, but the dose calculation will take a lot longer to complete - because of the wasted time spent calculating progeny in-growth!

The resulting calculated doses are shown in Figure 4.106.

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👒 Dose Calculations									
Elle <u>A</u> dvanced <u>T</u> ools !	Help								
Save Quick Save			Dos	e Calc	ulatio	ns			
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	Calcul	Select (1) Dose from India	wT		г				
		(2) Dose from Asso (3) Dose in each D	ociated Radionuclides Calendar Year		K K	C Equiv	Eff Eff Dose from U-234	Associate Eff Dose from U-235	d Rac Eff Di U-238
		Calculate	Effective Do	se (mrem)		bb Al LN(TH) Esophagus Gonads Spare Remainder TOTAL	(mrem) 0.00E+00 0.00E+00 0.00E+00 9.05E+00 9.05E+00 0.00E+00 0.00E+00 5.07E+01	(mrem) 0.00E+00 0.00E+00 0.00E+00 0.00E+00 3.11E-04 0.00E+00 0.00E+00 1.66E+00	(mren 0. 0. 0. 0. 0. 0. 0. 0.
- Programs Indicator		000			_	< 11			
(1)					_			Annual C	timmo
(2)					Π	Year	Eff Dose from U-234 (mrem)	Eff Dose from U-235 (mrem)	Eff Di U-236 (mren
(3) Current Operation						1995 TOTAL	5.07E+01 5.07E+01	1.66E+00 1.66E+00	0.
				0	к	<			
U-mix	WR=ICRP Defaults	WT= 10 CFR 835	Not Specified						

Figure 4.106. Calculated total effective dose together with the year in which it was committed.

Figure 4.106 shows that:

• The committed effective dose from the estimated acute intake of LEU (<u>IR1 = 0.714 mg</u>) is <u>59.1 mrem</u>.

This completes the Last Analytical Step in the uranium isotopic mixture example:

- Proceed to Published Data on "Background" U-in-Urine.
- <u>Return</u> to the case description and list of steps.

Published Data on Background U-in-

Urine

In this case, the average of the measured (background) uranium mass excretion rates in urine was $0.19 \mu g/d$, with a standard deviation of $0.11 \mu g/d$ - see the 6th and 8th through 11th values in the data tabulation (Figure 4.97). The reported ranges of the "background" urinary excretion rate for dietary uranium are:

- 0.01 0.05 µg/d (Karpas et al 1996).
- 0.005 0.5 μg/d (Dang et al 1992).
- 0.035 0.085 µg/d (CDC 2001) U.S. Population.



In their 2004 Information

Paper (http://www.deploymentlink.osd.mil/du_library/lab_assessment/lab_assessment_s02.ht the Department of Defence assumed a "typical" background excretion rate (for dietary uranium in urine) of $0.05 \mu g/d$. The value of $0.19 \mu g/d$, that we have associated in this example with background excretion of dietary uranium is therefore about four-fold higher than the DoD's estimate of the typical value for a member of the U.S. population, i.e., it is double the upper bound value reported by CDC (2001). Therefore, the "background" urinary excretion of uranium in urine measured in this example case may well include a substantial component from past "occupational" uranium exposure.

- <u>Proceed</u> to Uranium Example Case Summary.
- Return to the case description and list of steps.

Uranium Example Case Summary

In summary, it is instructive to compare the estimates of committed effective dose obatined at each stage of the analysis for this case.

Assuming single acute inhalation intake of Type 'S' LEU

• Joint analysis of the measured urinary and fecal uranium mass excretion rates (without correction for "background" excretion) gave an estimated LEU intake of 2.055 mg - with a corresponding committed effective dose of 170 mrem.

Assuming acute inhalation of Type 'S' LEU - together with chronic dietary intake ($\underline{f1}$ value of 0.02)

• Joint analysis of the measured urinary and fecal uranium mass excretion rates gave an estimated (acute) LEU intake of <u>0.357 mg</u> - with a corresponding committed effective dose of <u>29.6 mrem</u>.

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"Optimizing" the model parameters

• Joint analysis of the measured urinary and (adjusted) fecal uranium mass excretion rates gave an estimated (acute) LEU intake of 0.714 mg - with a corresponding committed effective dose of 59.1 mrem.

·•••••	Note #1: Least squares analysis only of the measured urinary uranium mass excretion rates (including the two "outlying" dta points) together with the reported normal (counting) errors - as is the common practice
	- gave an estimated LEU intake (assuming acute inhalation of Type 'S' uranium) of 0.575 mg (\pm 0.246 mg standard error). The corresponding
	estimate of committed effective dose is $\frac{47.6}{2}$
	mrem (± 20.4 mrem standard error). In this case, reasonable
	agreement with the value of <u>59.1 mrem</u> derived by more exhaustive
	analysis is fortuitous.
To Imperiately	Note #2: The value of 0.575 mg acute LEU intake obtained using
22 ==	the least squares fitting method in IMBA Professional Plus is identical to the
	value given by the software package IMBA-URAN (for the same model
	assumptions). As expected, the identical value is also obtained using
	the maximum likelihood fitting method (in IMBA Professional Plus).

Case of Wound Uptake - Requires Add-On 5

In this case, a laboratory worker received an accidental needle-puncture wound (on the thumb) while performing iodinations. The total amount of 1251 used in the procedure was about 2 mCi, but only a small fraction of this was still in the syringe at the time of the incident. A thyroid measurement was made within a few hours, and followed up with 4 further measurements over the next 34-d period. 'Background' thyroid measurements were available both prior to the incident, and at 75 and 138 d afterwards. After washing the wound, the estimated (retained) activity was about 300 nCi. At 4 d after the incident, the 1251 activity at the wound site had fallen to about 3.5% of the original measurement. At 7 d, the 1251 activity at the wound site remained at about 3.5% of the original measurement. At 13 d, the 1251 activity at the wound site had fallen to about 3.5% of the original measurement.

The thyroid measurements are given in Table D.19.

Table D.19. 125 I activity measured in the thyroid.

Approximate time relative to puncture-wound (d)	Thyroid activity ± standard error (pCi)
-177	<u>5,000 ± 2,000</u>
-151	2,000 ± 3,000
0.1	<u> 6,000 ± 2,000 </u>
4	14,000 ± 3,000

Example Cases - Bioassay & Dosimetry

7	<u>10,000 ± 3,000</u>
13	<u> </u>
34	<u> 16,000 ± 3,000</u>
75	<u> </u>
138	9,000 ± 2,000

Figure D.147 shows the data values as entered (from the date + time information) in the Table Tool of IMBA Professional Plus.

Table Tool : Thyroid D	lētā							
le Edit Bioassay Measures	nent Help							
Specified Time (d)	N/A	Calculated Value(pCi)	Heasurement Time (d)	N/A	Measurement Value(pCi)	Data Type	Measurement	Error Distribution
1			-1.769166667E+02		5.000E+03	Real	2.000E+03	NORM
2			-1.509166667E+02		2.000E+03	Real	3.000E+03	NORM
3			8.303333333E-02		6.000E+03	Real	2.000E+03	NORM
4			4.063333333E+00	1	1.4000E+04	Real	3.000E+03	NORM
5			7.083333333E+00	Ê.	1.0000E+04	Real	3.000E+03	NORM
6			1.308333333E+01		1.5000E+04	Real	3.000E+03	NORM
7			3.408333333E+01		1.6000E+04	Real	3.000E+03	NORM
8			7.508333333E+01		3.000E+03	Real	3.000E+03	NORM
9			1.380833333E+02		9.000E+03	Real	2.000E+03	NORM
10								

Figure D.147. Input data on thyroid uptake of 125 with assumed error distribution.

In this example, we will:

- Set up a <u>"Wound" intake scenario</u>.
- <u>Test "default" assumed value(s)</u> for the uptake rate(s) from the wound to blood.
- Derive the most likely absorption rate(s) from the wound to blood.
- Calculate the <u>Bayesian "Posterior Probability Distribution"</u> of the intake amount.

Setting Up Wound Intake



The necessary steps (carried out in the Main Screen) are:

- 1. Set the <u>Reference Date</u>, i.e., the <u>Date</u> and <u>Time</u> of the incident.
 - 2. Select the Indicator Nuclide, i.e., Iodine-125.
- 3. Select the "<u>Wound</u>" radio button to define the <u>Intake Scenario</u> in the "<u>Model</u> <u>Parameters</u>" panel (Figure D.148).

Selecting "<u>Wound</u>" as the <u>Intake Scenario</u> will automatically activate the "<u>Wound</u>" model button (displayed in <u>pink</u> in Figure D.148).

Main Screen			
Ide Eat Calculations I cols Advanced Help Image: Copen Save Image: Copen Imag			Mar 2004
IMBA Expe	ert™ USDO	E Phase I	nrpb
Intake Scenario			
	Onits Specily Time As C Date F Time (d) since Data (d)	Intake (IR 1) 0 Bo	Indicator Nuclide Select Radonuclide Number of Associated Radonuclides: Hall Life: Unknown
Inholation Injection Injection Injection Vapor Vapor Edit Complex Repres	Intake P Bq C dpm C pG C mo Doze P Sv C mem C mSv C mem	Associated Radio	None Selected
Model Parameters	000	Calculations-	
These Model Parameters Apply to All IPs Respiratory Tract Decosition Viscor Viscor Risentar Risentar			Bioestay Calculations
Particle Absorption GillTract Biokinetics	Close		Dese Calculations
III Absorption: Not Specified Part Tran: Not Specified Gi-Tract: Not Specified I1+	Biokinetics: Not Sp	ecilied Deposition: Not Spec	ified N/A Wound Not Specified

Figure D.148. Main Screen with activated button to define the "Wound" model.

Click the "<u>Wound</u>" model button to open the <u>'Generic Wound Model'</u> window (Figure D.149).

Seneric Wound Model	
- Wound Model	
A diagram of the NCRIP woun following its	d model will be placed here publication
Ret(t) = a(1) exp[-lam(1) t] + a	a(2) exp[-lam(2) t] +
Lizer Defined Mode	i a(i) lan(i)
NCRP Defaults	2
<u>W</u> eak	3 4 E
Moderate	÷
Storg	Cleag
Evid	
Not Specified	QK Cancel

Figure D.149. The 'Generic Wound Model' window.

At this time (March, 2004), the National Council on Radiological Protection (NCRP) has not

yet recommended specific parameter values to represent retention of different types of material in a sub-cutaneous wound. Therefore, IMBA Professional Plus has incorporated a "<u>generic</u>" form of "<u>wound model</u>", in which retention is represented by the sum of a series of exponentially decaying terms (Figure D.149). You can define up to five exponential terms in the "<u>User Defined Mode</u>" by clicking the so-named button (Figure D.150).

ct	Wound Retention
User Delined Mode	i a(i) lan(i)
NCRP Defaults	2
<u>Wesk</u>	3 4
Hadavan	5
Downers	
Storg	Clear
jorid	

Figure D.150. User Defined Mode for entering a "Wound Retention" function.

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For all compounds of iodine, ICRP Publication 68 (ICRP 1994b) recommended Type <u>'F'</u> to represent absorption from the respiratory tract (at a characteristic rate of 100 d<u>-1</u>), with a GI-tract absorption fraction of 1. Therefore, as a first "guess", it is reasonable to assume very rapid uptake of the <u>1251</u> "iodination" compound from the puncture-wound involved in this incident. We can represent this simply by entering the following values for the retention parameters (as shown in Figure D.151):

- <u>a(1)</u> = 1;
- <u>lam(1)</u> = 100 d<u>-1</u>.

elect		Wound Ret	ention	
1	User Defined Mode	i a	0	lam(i)
NCRE	Defaults	1 1		100
Ţ	<u>W</u> eak	3 4 5		
	Moderate	0		
1	Storg			Clear
E	Asid			
Ę.	Avid		- 1	

Figure D.151. Setting the rate constant for retention in a wound as 100 d-1.

In the next section, we will test how well this assumed rapid eleimination rate from the wound site "fits" the measured time-course of <u>1251</u> uptake and retention in the thyroid.

- Proceed to the next step in this example case.
- Return to the case description.

Test Default Absorption Rates



Figure D.152. Thyroid uptake and retention predicted for 'rapid' release of 125 from the wound site to the blood.

The assumed uptake rate of 100 d-1 accounts well for the observed rapid initial uptake of <u>125</u>I by the thyroid, but not for the apparent "retention" of <u>125</u>I in the thyroid up to 34 d after the incident. The calculated total value of the <u>c2</u> statistic (as shown in the Table Tool – Figure D.153) is <u>32.2</u>. This is substantially higher than the "expected" value (= 9), which is equal to the number of data points.

Heasurement Time (d)	N/A	Measurement Value(pCi)	Data Type	Measurement Error	Error Distribution	Theoretical Value(pCi)	Chi-Square
-1.769166667E+0	2	5.000E+03	Real	2.000E+03	NORM	0.000E+00	6.250E+0
-1.509166667E+0	2	2.000E+03	Real	3.000E+03	NORM	0.000E+00	4.44Æ-0
8.333333333E-0	2	6.000E+03	Real	2.000E+03	NORM	3.2291E+03	1.920E+0
4.083333333E+0	D	1.4000E+04	Real	3.000E+03	NORM	1.6273E+04	5.741E-0
7.083333333E+0	D	1.0000E+04	Real	3.000E+03	NORM	1.5341E+04	3.169E+0
1.308333333E+0	1	1.5000E+04	Real	3.000E+03	NORM	1.3664E+04	1.984E-0
3.408333333E+0	1	1.6000E+04	Real	3.000E+03	NORM	9.2471E+03	5.067E+0
7.508333333E+0	1	3.000E+03	Real	3.000E+03	NORM	4.4183E+03	2.235E-0
1 380833333E+0	2	9.000E+03	Real	2.000E+03	NORM	1.434E+03	1.431E+0

Figure D.153. Calculated Chi-Square values for an assumed uptake rate of 100 d-1.

However, as shown in Figure D.153, the first 2 data points (primarily the 1st point) contribute a large fraction of the total <u>c2</u>, and these points are clearly NOT related to the incident (at time t = 0). Thus, the appropriate value of <u>c2</u> to consider is that related to the 7 data points obtained "post-incident". This value is <u>25.5</u>.

We can conclude that the assumption of an uptake rate of 100 d<u>-1</u> from the wound site is NOT supported by the bioassay (thyroid) data. In the next section, we let IMBA Professional Plus itself "select" the most likely absorption behavior.

<u>Proceed</u> to the next step in this example case.
 <u>Return</u> to the <u>case description</u>.

Most Likely Wound Uptake Rate(s)

00

IMBA Professional Plus allows up to 10 intakes to be analyzed simultaneously. In this case, and many others for which critical <u>intake scenario</u> parameter values are UNKNOWN, this facility for simultaneous analysis provides a direct means of "fitting" the unknown parameter values. This is done by choosing an appropriately broad <u>range</u> of <u>hypothetical</u> values, and letting IMBA Professional Plus "<u>rank</u>" these values according to the <u>amount of intake</u> that it calculates for each. In this example, both the observed thyroid "retention" and the measured retention of contamination on the worker <u>'s hand</u> suggest that a significant component of the absorption occurs slowly.

In this example, in order to examine the degree of "slow uptake", we have set up 6 simultaneous acute <u>'wound'</u> intakes at time t = 0. The <u>'hypothetical'</u> rates tested are:

- IR1 = 100 d<u>-1</u>;
- IR2 = 0.2 d<u>-1</u>;
- IR3 = 0.1 d<u>-1;</u>
- IR4 = 0.05 d<u>-1</u>;
- IR5 = 0.02 d<u>-1</u>;
- $IR6 = 0.01 \text{ d}_{-1}$.

Figure D.154. shows the resulting amounts of intake calculated using the maximum likelihood method for each of these 6 intake scenarios, and the resulting overall 'fit' to the observed thyroid retention. The corresponding calculated values of <u>c2</u> are shown in Figure D.155 (as displayed in the <u>Table Tool</u>).

Save Quát Save Tritum	CALCULAT	Bioassay Calcula	tions					
INTAKES	CALCULAT	ION						
			E	IOASS	AY QUAN	TITY		
IR1 4.694E+04 pCi	\langle		Graph @ Table	C Hide	Thyroid Calculated	·	tool	
IR2 0.000E+00 pC IR3 0.000E+00 pC IR4 0.000E+00 pC IR5 0.000E+00 pC IR6 1.179E+05 pC	Intakes to Bioassay Basesian Analysis Tad Start Calculation	Bioassay to Intake Select which data to use Uhine Fungs Fulime Feces Blood Thyroid Liver User Defined	1.775833335 1.72198575 1.72198575 1.616743424 1.616743424 1.616743424 1.554324424 1.551306615 1.55126374 1.5512637 1.5512637 1.5512637 1.5512637 1.5512637 1.5512637 1.5512637 1.5512637 1.5512637 1.5512637 1.5512637 1.5512637 1.5512637 1.5512637 1.5512637 1.551263 1.551263 1.551263 1.551263 1.551263 1.551263 1.551263 1.551263 1.551263 1.551263 1.551263 1.551263 1.551263 1.551263 1.551263 1.551263 1.551263 1.551263 1.551263 1.55126 1.55126 1.55126 1.55126 1.55126 1.5512 1.551 1.551 1.551 1.551 1.551 1.551 1.551 1.551 1.551 1.551 1.551 1.551 1.551 1.551 1.551 1.551 1.551 1.551 1.551 1.551 1.551 1.551 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55 1.55	+02 +02 +02 +02 +02 +02 +02 +02 +02 +02	Value(pc) 0.000E+00 0.000E+00 0.000E+00 0.000E+00 0.000E+00 0.000E+00 0.000E+00 0.000E+00 0.000E+00 Thyroid und Case - Thyro	1.7031606676 +0 1.5031606676 +0 8.000300056 +0 4.000300056 +0 7.000300058 +0 0.340603003058 +0 0.340603030328 +0 1.0000303038 +0 1.0000303038 +0 1.0000303038 +0 1.0000303038 +0 1.000030308 +0 1.000030308 +0 1.000030308 +0 1.000030308 +0 1.000030308 +0 1.000030308 +0 1.000030308 +0 1.000030308 +0 1.00005000 +0 1.000050000 +0 1.000050000 +0 1.000050000 +0 1.0000500000000000000000000000000000000	2 2 2 2 0 0 0 1 1 1 1 2 2 2 0 0 0 1 1 1 1	

Figure D.154. Data 'fit' obtained with 6 hypothetical absorption rates.

Measurement	Time (d)	N/A	Measurement Value(pCi)	Data Type	Measurement Error	Error Distribution	Theoretical Value(pCi)	Chi-Square
	1.769166667E +02		5.000E+03	Excluded	2.000E+03	NORM	0.000E+00	0.000E+0
	1 509166667E -02		2.000E+03	Excluded	3.000E+03	NORM	0.000E+00	0.000E+0
	8.33333333330E-02		6.000E+03	Real	2.000E+03	NORM	2.596E+03	2.914E+0
	4.083333333E+00		1.4000E+04	Real	3.000E+03	NORM	1.4230E+04	5.866E-0
	7.08333333E+00		1.0000E+04	Real	3.000E+03	NORM	1.4330E+04	2.083E+0
	1.308333333E +01		1.5000E+04	Real	3.000E+03	NORM	1.4375E+04	4.339E-0
	3.408333333E +01		1.6000E+04	Real	3.000E+03	NORM	1.3368E+04	7.698E-0
	7.508333333E+01		3.000E+03	Real	3.000E+03	NORM	9.3907E+03	4.538E+0
	1.380833333E +02		9.000E+03	Real	2.000E+03	NORM	4.2767E+03	5.577E+0

Figure D.155. Calculated values of <u>c2</u> for 6 hypothetical absorption rates.

The calculated intake amounts are:

- IR1 = 46,940 pCi;
- IR2 = 0 pCi;
- IR3 = 0 pCi;
- IR4 = 0 pCi;
- IR5 = 0 pCi;
- IR6 = 117,900 pCi.

In other words, IMBA Professional Plus calculated a total intake of 164,840 pCi, with 28.5% of this assigned an absorption rate of 100 d<u>-1</u> and 71.5% the slowest assumed absorption rate of 0.01 d<u>-1</u>. The total <u>c2</u> is now reduced to <u>17.1</u>. This is significantly lower than the previous value (obtained for 100% absorption at a rate of 100 d<u>-1</u>), but it is still significantly higher than the "expected" value (for the 7 residual data points).

However, the largest <u>c2</u> contribution (of 5.6) is made by the data point obtained at 138 d after the incident. We can examine the effect of treating this point as an "outlier" by marking it as "<u>excluded</u>" in the <u>Table Tool</u> (as we did for the first 2 data points <u>–</u> prior to the incident). The effect of excluding the last data point from the <u>'fit</u>' is shown in Figure D.156.



Figure D.156. Data 'fit' obtained by excluding the data point at 138 d.

Treating the data point at 138 d as an "outlier" clearly improved the 'fit' of predicted thyroid retention of <u>125</u>I to the remaining 6 measured values. The resulting values of <u>c2</u> are shown in Figure D.157 (from the <u>Table Tool</u>).

Measurement Time (d)	N/A	Measurement Value(pCi)	Data Type	Measurement Error	Error Distribution	Theoretical Value(pCi)	Chi-Square
-1.769166667E +02		5.000E+03	Excluded	2.000E+03	NORM	0.000E+00	0.000E+0
-1.509166667E +02		2.000E+03	Excluded	3.000E+03	NORM	0.000E+00	0.000E+0
8.33333333E-02		6.000E+03	Real	2.000E+03	NORM	2.1808E+03	3.647E+0
4.083333333E+00		1.4000E+04	Real	3.000E+03	NORM	1.3114E+04	8.730E-0
7.083333333E+00		1.0000E+04	Real	3.000E+03	NORM	1.3784E+04	1.591E+0
1.308333333E+01		1.5000E+04	Real	3.000E+03	NORM	1.4369E+04	4.419E-0
3.408333333E+01		1.6000E+04	Real	3.000E+03	NORM	1.2555E+04	1.319E+0
7.508333333E+01		3.000E+03	Real	3.000E+03	NORM	6.7252E+03	1.542E+0
1 360633333E+02		9.000€+03	Excluded	2.000E+03	NORM	2.2242E+03	0.000E+0

Figure D.157. Calculated values of <u>c2</u> after excluding the data point at 138 d.

The The total <u>c2</u> is now reduced to <u>8.2</u>, which is a substantially more likely value (for 6 residual data points).

Notice also (from Figure D.156) that the intake amounts assigned to each of the 6 hypothetical absorption rates have now changed substantially. The new values are:

- IR1 = 39,520 pCi;
- IR2 = 0.0064 pCi;
- IR3 = 0.018 pCi;
- IR4 = 45,080 pCi;
- IR5 = 0 pCi;
- IR6 = 0 pCi.

In other words, neglecting both IR2 and IR3, IMBA Professional Plus calculated a significantly smaller total intake of 84,600 pCi, with 46.7% of this assigned an absorption rate of 100 d_{\pm} 1 and 53.3% assigned an absorption rate of 0.05 d_{\pm}. The corresponding 'retention function' is:

$$R_{\text{Arrest}}(t) = 0.467 \exp(-100t) + 0.533 \exp(-0.05t) \dots (D.1).$$

This function can now be entered directly in the '<u>Generic Wound Model</u>' window to define the most likely absorption behavior for the single acute intake in this case (Figure D.158).

ect		Wound	Wound Retention			
Uper (Defined Mode	E	40	[an(i)		
NCRP Defaults		1	0.467	100		
	<u>W</u> eak	34				
	loderate	3				
	Stong		_	Clear		
	évid					

Figure D.158. Derived absorption behavior of <u>125</u>I needle-puncture wound.

In the next section, we use the integrated Bayesian Analysis 'tool' to calculate the posterior probability distribution of intake for this case.

<u>Proceed</u> to the next step in this example case.
 <u>Return</u> to the <u>case description</u>.

Bayesian Probability of Wound Intake

Having entered the derived retention function [in the form of Equation (D.1)], we can now use <u>Bayesian Inference</u> to calculate the posterior probability distribution of intake and its associated statistics. This is done in the Bioassay Calculations screen, by first selecting the 'Bayesian' radio button from the Advance | Fitting Options | Fitting menu. Clicking the 'Start Calculation' button then gives the result (calculated intake amount and resulting data 'fit') shown in Figure D.159. As expected, the calculated (mean) intake value (85,220 pCi) is close to the total intake value obtained earlier (84,600 pCi) using the maximum likelihood method (with non-rounded parameter values). The resulting 'fit' to the bioassay data is shown in Figure D.160.



Figure D.159. Calculated mean value of the intake distribution_using the <u>'Bayesian'</u> fitting option.



Figure D.160. Dat <u>'fit'</u> obtained with derived wound retention function.

In the <u>'</u>Bayesian Analysis Tool' (Figure D.161), we will select a <u>'</u>Uniform' prior probability distribution of intake, over the range 1 pCi to 1,000,000 pCi (1 μ Ci).



Figure D.161. Selecting a 'Uniform' prior in the 'Bayesian Analysis Tool'.

The calculated 'Log-Likelihood Function' is shown in Figure D.162.




The resulting calculated 'posterior' probability distribution for the intake amount is shown in Figure D.163.



Figure D.163. Calculated posterior probability distribution for the amount of intake.

The calculated <u>'statistics'</u> of the posterior probability distribution are shown in Figure D.164.

X-min 1 No Intervals 10 X-max 1000000	Y-min 0.00E+00 No Intervals 10 Y-max 2.45E-01
☐ Show Gridines	Show Gridines Clog 📀 lin
No Dec Plcs 0 C Numerical	No Dec Plcs 2 C Numerical
Statistics	
Median 9.52715+04 Mode 9.52	25E +0.4 95% CL 6 6929E +0.4 1 0526E +08

Figure D.164. Calculated 'statistics' of the posterior probability distribution.

The calculated <u>'</u>statistics' of the posterior probability distribution of intake amount are:

- Median value = 85,271 pCi;
- Modal (most likely) value = 85,225 pCi;
 - Mean value = 85,200 pCi;
- Standard Deviation = 9,077 pCi, i.e., 10.7% of the Mean;
 - 95% Confidence Interval = 66,939 pCi <u>-</u> 105,260 pCi.

Case Using the Least Squares Fitting Method - Requires Add-On 6

To illustrate the use of the <u>least squares</u> fitting method for evaluating the error on an estimated intake, we will re-analyze the first example case (<u>IAEA 1999</u>) - which is stored in the parameter file "<u>[Install Drv]:\\JABASOFT\IMBAEXUS\USERDATA\Demo\IAEA</u> <u>Case 3 - 60Co.ix</u>". This case involved an accidental inhalation of a cobalt metal and/or oxide aerosol - with whole body measurements of <u>60</u>Co starting at 1 d after the intake. The data were given in <u>Table 4.1</u>.



To use the <u>least squares</u> fitting method, you <u>select</u> this option in the Bioassay Calculations screen (Figures 4.145 and 4.146) - and <u>click</u> "OK".

Bioassay Calculations
File Advanced Tools Help
Fitting Options
Bioassay Options
Tium
INTAKE

Figure 4.145. Opening the "Fitting Options" menu.

👒 Bioassay Calculations				
File Advanced Tools Help				
Save Quick Save Tritium		Bioassay Cal	culations	
INTAKE	CALC	ULATION		BIOASSAY QUA
IR1 9 805F+03 Bg	_		⊂ Graph ⊙ Ta	able C Hide Whole body
	Intaken to Bio	Advanced Desimetry Options	Specified Date (a)	Value(Bq)
Progress Indicator Deposition Collating Times Bioassay Calcs	Specily Dates [Col 1]- Start Date 2/25 Stop Date 2/19 Specily Collection Perix Calculate Bioassay Que	These options should be u Dose Fitting Bioass Select Fitting Method • Least Squares • Maximum Likelihood • Bayesian	sed with extreme care y Misc Cancel	3.3342E 2.6838E 2.0321E 1.540E 1.2784E 1.1632E 1.1011E 1.0269E 9.3997E Hide Whole body 10 ide

Figure 4.146. Selecting the "Least Squares" Fitting option.

Back in the Bioassay Calculations screen, you then <u>click</u> the <u>Blue</u> arrow - to <u>re-calculate</u> the amount of Intake (IR1) from the tabulated bioassay data. The result is shown in Figure 4.147.

👒 Bioassay Calculations			
Elle <u>A</u> dvanced <u>T</u> ools Help			
Save Quick Save Tribium		Bioassay Calcula	tions
INTAKE	CALCULATI	ON	BIOASSAY QUA
IR1 9.805E+03 Bq			C Graph
+/- 9.782E+02 Bq	Intakes to Bioassay	Bioassay to Intake	2/25/1988
	Bayesian Analysis Start Calculation	Select which data to use Whole body Lungs Unine Feces Blood Thyroid Liver User Defined	2/25/1988 11:12:44 AM 2/26/1988 3:39:45 AM 2/27/1988 3:47:53 AM 2/27/1988 3:12:32 PM 3/1/1988 7:09:47 PM 3/4/1988 11:23:21 PM 3/9/1988 11:23:21 PM 3/16/1988 11:33 PM 3/16/1988 11:18:36 AM C Graph C Table C Hide Whole body 1000
<u> </u>	000		
Progress Indicator			
Deposition			C Graph C Table C Hide
Collating Times			
Bioassay Calcs			
Current Operation	Calculation Comple	te	
Co-60	Least Squares fit	<u>o</u> ĸ	

Figure 4.147. Result of least squares fitting for "IAEA Case 3 - 60Co".

As expected, the calculated value of IR1 is 9,805 Bq - the <u>same value</u> as calculated by the <u>maximum likelihood</u> method. However, the <u>least squares</u> method also calculates the <u>standard error</u> on this estimated intake - in this case \pm 978.2 Bq.



To further illustrate the application of the <u>least squares</u> fitting method, we can use this to "fit" the <u>241</u>Am chest-counting data from the <u>HAN-1 case</u>. Figure 4.148 shows the result - for the "optimized" set of <u>HRTM model parameters</u>. The <u>least</u> <u>squares</u> method calculates an intake of <u>9,875 pCi (\pm 114.2 pCi standard error) - c.f.</u>, the same value (<u>9,875 pCi</u>) obtained with <u>maximum likelihood fitting</u>.

👒 Bioassay Calculations			
Eile <u>A</u> dvanced <u>T</u> ools Help			
Save Quick Save Tribium		Bioassay Calculat	ions
INTAKE	CALCULATIO	DN	BIOASSAY QUA
IR1 9.875E+03 pCi			Graph C Table C Hide Lungs HAN-1 Case: Arn-241 B
+/- 1.141E+02 pCi	Intakes to Bioassay	Bioassay to Intake	4000 -
		Select which data to use	≩ 2500 - t 2000 -
		Whole body	9 1500 9 1000
		✓ Lungs	₹ 500-
		Urine Urine	0 500 1000 1500 2000 2500 3000 35
		Feces	
		E Blood	C Graph C Table C Hide LL2008
	Bayesian Analysis	Thyroid	Measurement Time (d) N/A Measurem Value(pCi)
		Liver	5.000E-01 1.300E+ 1.500E+00 1.200E+
		User Defined	3.000E+00 1.350E+
	Start Calculation	1 000 00000	7.000E+00 1.300E+
			2.050E+01 1.250E+
			3.500E+01 1.200E+
6	000		4.850E+01 1.200E+
			5.550E+01 1.300E+
Progress Indicator			1.160E+02 1.300E+

Figure 4.148. Least squares "fit" of the bioassay data in the HAN-1 case.

It is also of interest to re-analyze the HAN-1 case using the <u>least squares</u> method - with the (inappropriate) assumption of all <u>ICRP Default</u> HRTM parameter values and Type 'S' absorption behavior (Figure 4.149).

Bio	assay Calcula	ations
CALCULATION		BIOASSAY QUA
Intakes to Bioassay	Bioassay to Intake elect which data to use Whole body Lungs Urine Feces	© Graph C Table C Hide Lungs HAN-1 Case: Am-241 B 4000 5000 5000 5000 0 500 1000 1500 2000 2500 3000 35 Time since in C Graph © Table C Hide Lungs
Bayesian Analysis Start Calculation	Thyroid Liver User Defined	Measurement Time (d) N/A Measurem Value(pCi) 5.000E-01 1.300E 1.500E+00 1.200E 3.000E+00 1.300E 2.050E+01 1.200E 3.500E+01 1.200E 4.850E+01 1.200E 6.950E+01 1.200E 1.165E+02 1.300E
	Bio CALCULATION	Intakes to Bioassay Bioassay to Intake Intakes to Bioassay Bioassay to Intake Select which data to use Whole body Lungs Unine Bayesian Analysis Diass Statt Calculation User Defined

Figure 4.149. Using the least squares method to analyze the HAN-1 case with ICRP default

parameter values.

Again, the <u>least squares</u> method calculates the same (to the fourth significant figure) value for the intake amount (44,550 pCi) as the <u>maximum likelihood method</u> - with a calculated standard error of \pm 4,800 pCi - <u>c.f.</u>, 44,560 pCi.

Cautionary Note: The standard error calculated by the least squares method is a numerical statistic only. It DOES NOT measure the "goodness of fit" of the <u>underlying model assumptions</u>. Hence, the <u>relative</u> standard error is the same for the "fits" shown in Figures 4.148 and 4.149 - whereas, in Figure 4.149, the "model" clearly DOES NOT "fit" the data! The overall "goodness of fit" of the model is measured by the <u>c2</u>-sum statistic.

Case Using Bayesian Analysis -Requires Add-On 7



To illustrate the use of the <u>Bayesian inference</u> in the fitting procedure, we will again re-analyze the first example case (<u>IAEA 1999</u>) - stored in the parameter file "<u>[Install</u> <u>Drv]:\JABASOFT\IMBAEXUS\USERDATA\Demo\IAEA Case 3 - 60Co - Bayes.ix</u>". This case involved an accidental inhalation of a cobalt metal and/or oxide aerosol - with whole body measurements of 60Co starting at 1 d after the intake. The data were given in <u>Table 4.1</u>.

An introduction to Bayesian inference, and a description of how this is implemented in IMBA Professional Plus, is given in the section of Appendix A: Technical Basis entitled "Using Bayesian Inference". That description includes the types of Bayesian Prior probability distribution that are available in this version of the software.

To use the "<u>Bayesian</u>" <u>Fitting</u> option, you must first <u>select</u> this - from the <u>Bioassay</u> <u>Calculation</u> screen's <u>Advanced | Fitting Options</u> menu (Figure 4.150).

👒 Bioassay Calculations	
File Advanced Tools Help	
Save Quick Save Tribium	Bioassay Calculations
INTAKE	CALCULATION BIOASSAY QU
IR1 9.805E+03 Bq	C Graph Table C Hide Whole be Measurement Date N/A Measurement Date N/A Value
	Intakes to Bioa Select Fitting Method Select Fitting Method
	C Least Squares C Maximum Likelihood Bayesian Start Calcul
Progress Indicator Deposition Collating Times Bioassay Calcs	10
Current Operation	

Figure 4.150. Selecting the "Bayesian" Fitting option.

This will <u>activate</u> the "<u>Bayesian Analysis</u>" button in the <u>Bioassay Calculations</u> screen (Figure 4.151).

Bioassay Calculations			
Elle Advanced Iools Help			
Save Quick Save Tritium		Bioassay Calculati	ons
INTAKE	CALCULATIO	ON	
IR1 9.805E+03 Bq			C Graph (* Measurement Da
	Intakes to Bioassay	Bioassay to Intake	(+nr.mi)
	Bayesian Analysis Start Calculation	Select which data to use Whole body Lungs Urine Feces Blood Thyroid Liver User Defined	Graph C 4000 1000 100
Figure 4.151. "Bayes	<u>ian Analysis</u> " button a	ctivated.	

<u>Clicking</u> the "<u>Bayesian Analysis</u>" button opens a new screen - the <u>Bayesian Analysis</u> tool (Figure 4.152).



Figure 4.152. <u>Bayesian Analysis</u> screen as it appears for a "<u>New</u>" case - with no bioassay data loaded.

Tip: Figure 4.152 shows the "default" settings of the Bayesian Analysis tool - for the type of prior (defaulted to "Uniform"), the X- and Yaxis ranges, and for display of the "Log Likelihood Function"). Other types of prior are selected using radio buttons (bottom-left-corner). The other types of function ("Prior Distribution" or "Probability of Intake") are also selected using radio buttons (top-right-corner).

If you have previously calculated the amount of intake (<u>e.g.</u>, using the <u>maximum</u> <u>likelihood</u> or <u>least squares</u> method), the <u>X-axis</u> in the <u>Bayesian Analysis</u> tool will "<u>auto-range</u>" accordingly - when the tool is opened (Figure 4.153).

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Figure 4.153. "Auto-ranging" of X-axis when the intake amount (IR1) has already been calculated.

Note: The Y-axes also "<u>auto-ranges</u>" when you calculate the other types of probability distribution. However, the X-axis DOES NOT. You have to <u>choose</u> the appropriate X-axis range - to include the whole calculated distribution.

In this section of the <u>User Manual</u>, we will show how each type of "<u>Prior Distribution</u>" affects the calculated "<u>Log Likelihood Function</u>" and the posterior probability distribution of intake ("<u>Probability of Intake</u>") in the "<u>IAEA Case 3</u>" 60Co whole body monitoring example - as follows:

• <u>Uniform prior</u>.

*3*0

- Inverse prior.
- Gaussian prior.
- Lognormal prior
- 'Alpha' prior.

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Probability Distribution of Intake Assuming a Uniform Prior



👒 Bayesian Analysis		
File		
	Bayesian Analysis	
INTAKE	GRAPH	
ID1 Francisco Da	Prior Distribution for Intake Regime 1	Select Gra
IR1 9.805E+03 Bd	2.00E-06	G Prior
	1.855-06 -	, e ritor
	1.70E-06 -	C Log L Func
	1.555-06 -	C Prob
	<u> 국</u> 1.40E-06 -	
	<u> </u>	- Calculation
	2 1.10E-06 -	Carcarano
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	8.005.07 -	[Be] Calc
	6.00E.07	Up
	0 2000 4000 6000 8000 10000 12000 14000 16000 18000 20000	
	Intake (Bq)	A
<	000	-
IR1	X-axis	
Select Prior Probability Distribution	X-min 0 No Intervals 10 Y-min 5,	00E-07 No.
Uniform	Parameter Values X-max 20000 Y-max 2	00E-06
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(Inverse	Format	
C Gaussian	To 1000000 No Dec Plcs O C Scientific No Dec Plc	s 2
C Lognormal	Cancel	
	Statistics	
C Alpha	Median Mode 952	tul
	Qk Mean SD	Calc

Figure 4.154. "Prior Distribution" calculated (and displayed) over a suitable X-axis range.

Figure 4.154 shows the starting point for Bayesian Analysis of the bioassay data in "IAEA Case 3" - the calculation (and display) of the "Prior Distribution". In this case, we have selected "Uniform" as the "Prior Probability Distribution" type - and clicked the "AUTO CALC" button (middle-right-side of the Bayesian Analysis tool).

Cautonary Note: Before you can use the Bayesian Analysis tool to calculate (and display) the posterior probability distribution of intake, after selecting your prior distribution, you must FIRST calculate the median value of the intake distribution. You do this back in the Bioassay Calculations screen by clicking the "Start Calculations" button (just as you do for maximum likelihood or least squares fitting).

To calculate (and display) the <u>Log Likelihood Function</u>, you simply click its radio button - and click "AUTO CALC" again. The calculated Log Likelihood Function is shown in Figure 4.155.



Figure 4.155. Calculated Log Likelihood Function.

Tip: Notice here that the Y-axis has "auto-ranged" - but the X-axis range has retained its initial setting.
 Note: The Log Likelihood Function, P(m|1), is independent of the prior. It is the logarithm of the Likelihood Function, i.e., the logarithm of the likelihood of observing ALL of the measured values (m) expressed as a function of intake (1). This depends only on the measurements and the bioassay function.

To calculate the posterior probability distribution, i.e., the "Probability of Intake", you simply click its radio button - and then click "AUTO CALC" again. The result is shown in Figure 4.156.



Figure 4.156. Calculated Probability of Intake - for a uniform prior.

To calculate the statistical parameters of this distribution, you simply click the "Calculate Statistics" button (bottom-right-corner of the Bayesian Analysis tool). The results are automatically displayed (Figure 4.157).



Figure 4.157. Calculating and displaying the statistical parameters of the posterior probability distribution of intake.

In this example, the statistical parameters of the intake distribution are:

- Median: 9,805.0 Bq.
- Mean: 9,805.1 Bq.
- Mode: 9,805.3 Bq.
- Standard Deviation: 358.53 Bq.
- 95% Confidence Interval: 9,091 10,519 Bq.

⁸	Note #1: This distribution is very close to normal (symmetrical).
22 *****	Note #2: As expected, the calculated median of the posterior probability distribution of intake ($9,805$ Bq) is IDENTICAL to the mean value calculated by <u>least squares</u> - but the standard deviation of the intake distribution (358.5 Bq) is NOT the same as the standard error of the intake calculated by least squares (978.2 Bq).

Probability Distribution of Intake Assuming an Inverse Prior



Figure 4.158. Inverse prior - plotted on Log-Log axes.

The <u>Inverse</u> prior probability distribution is shown in Figure 4.158. With this prior, the calculated <u>median</u> value of the intake distribution is 9,793 Bq (<u>c.f.</u>, 9,805 Bq for the <u>uniform</u> prior). The calculated Log Likelihood Function (which is independent of the prior) was shown in <u>Figure 4.155</u> (for the <u>uniform</u> prior).

The calculated posterior probability distribution of intake is shown in Figure 4.159, together with the calculated statistical parameters of this distribution.



Figure 4.159. Posterior probability distribution of intake calculated for the inverse prior.

In this example, the statistical parameters of the intake distribution are:

- Median: 9,792.0 Bq.
- Mean: 9,791.9 Bq.
- Mode: 9,791.7 Bq.
- Standard Deviation: 358.78 Bq.
- 95% Confidence Interval: 9,078 10,506 Bq.

Note: This posterior distribution is very close to <u>normal</u> (symmetrical) - as was the case for the <u>uniform</u> prior. However, the distribution has been <u>shifted</u> (very slightly) to <u>lower</u> values of the median, mean and mode.

Probability Distribution of Intake



Assuming a Gaussian Prior



Figure 4.160. Example of a Gaussian prior.

A <u>Gaussian</u> prior probability distribution is shown in Figure 4.160. The <u>median</u> (= mean) of this distribution is 2,000 Bq, and the standard deviation 1,500 Bq. With this prior, the calculated <u>median</u> value of the intake distribution is 9,383 Bq (c.f., 9,805 Bq for the <u>uniform</u> prior). The calculated Log Likelihood Function (which is independent of the prior) was shown in Figure 4.155 (for the <u>uniform</u> prior).

The calculated posterior probability distribution of intake is shown in Figure 4.161, together with the calculated statistical parameters of this distribution.



Figure 4.161. Posterior probability distribution of intake calculated for a Gaussian prior.

In this example, the statistical parameters of the intake distribution are:

- Median: 9,383.3 Bq.
- Mean: 9,383.2 Bq.
- Mode: 9,382.9 Bq.
- Standard Deviation: 348.71 Bq.
- 95% Confidence Interval: 8,688 10,076 Bq.

Note: Again, this posterior distribution is very close to <u>normal</u> (symmetrical) as was the case for the <u>uniform</u> prior. However, in this example, the distribution has been <u>shifted</u> to <u>lower</u> values of the median, mean and mode. The amount of "shift" depends on BOTH the assumed <u>median</u> (<u>= mean</u>) value AND the <u>standard deviation</u> of the <u>Gaussian</u> prior.

Probability Distribution of Intake Assuming a Lognormal Prior





Figure 4.162. Example of a Lognormal prior.

A Lognormal prior probability distribution is shown in Figure 4.162. The median (<u>1 mean</u>) of this distribution is <u>2,000 Bq</u>, and the geometric standard deviation is <u>3</u>. With this prior, the calculated median value of the intake distribution is 9,775 Bq (<u>c.f.</u>, 9,805 Bq for the <u>uniform</u> prior). The calculated Log Likelihood Function (which is independent of the prior) was shown in Figure 4.155 (for the <u>uniform</u> prior).

The calculated posterior probability distribution of intake is shown in Figure 4.163, together with the calculated statistical parameters of this distribution.



Figure 4.163. Posterior probability distribution of intake calculated for a Lognormal prior.

In this example, the statistical parameters of the intake distribution are:

- Median: 9,774.7 Bq.
- Mean: 9,774.6 Bq.
- Mode: 9,774.3 Bq.
- Standard Deviation: 358.89 Bq.
- 95% Confidence Interval: 9,062 10,489 Bq.

Note: Again, this posterior distribution is very close to <u>normal</u> (symmetrical) as was the case for the <u>uniform</u> prior. However, in this example, the distribution has been <u>shifted</u> to <u>marginally lower</u> values of the median, mean and mode. The amount of "shift" depends on BOTH the assumed <u>median</u> (<u>1 mean</u>) value AND the geometric <u>standard deviation</u> of the <u>Lognormal</u> prior.

Probability Distribution of Intake Assuming an 'Alpha' Prior





Figure 4.164. Example of an 'Alpha' prior.

An '<u>Alpha'</u> prior probability distribution is shown in Figure 4.164. This example is defined by an 'Alpha' value of 0.001, and an 'Imax' value of 100,000. The calculated <u>median</u> of this distribution is 50.79 Bq, with a very large <u>standard deviation</u> of <u>4,737.2 Bq</u>. With this prior, the calculated <u>median</u> value of the intake distribution is 9,805 Bq - which is identical to the value for the <u>uniform</u> prior. The calculated Log Likelihood Function (which is independent of the prior) was shown in Figure 4.155 (for the <u>uniform</u> prior).

The calculated posterior probability distribution of intake is shown in Figure 4.165, together with the calculated statistical parameters of this distribution.



Figure 4.165. Posterior probability distribution of intake calculated for an 'Alpha' prior.

In this example, the statistical parameters of the intake distribution are:

- Median: 9,792.0 Bq.
- Mean: 9,791.9 Bq.
- Mode: 9,791.7 Bq.
- Standard Deviation: 358.78 Bq.
- 95% Confidence Interval: 9,078 10,507 Bq.

Note: Again, this posterior distribution is very close to <u>normal</u> (symmetrical) as was the case for the <u>uniform</u> prior. However, in this example, the distribution has been <u>shifted</u> to <u>marginally lower</u> values of the median, mean and mode.

Case ImplementingTritium Tool -Requires Add-On 8



Example Cases - Bioassay & Dosimetry

This case is an example of routine tritium urinalysis (for exposure to tritium vapor - HTO) carried out over a 553-d period on a weekly sampling schedule. The case is taken from the European IDEAS project (Case #22) -

see http://hikwww2.fzk.de/hs/strahlenschutz/IDEAS/default.htm.

The urinalysis data (ready for importing into <u>IMBA Professional Plus</u>) is provide in the <u>ACSII</u> text file "Case_22_Tritium.txt" - - which is included in the [Install

Drv]:\JABASOFT\IMBAEXUS\USERDATA\Demo\ folder at installation. The first part of this file is shown in Figure 4.107.

Case_22_Trit	ium.txt - Notepad			
<u>File E</u> dit F <u>o</u> rmat	⊻iew <u>H</u> elp			
Case_22_Trit Eile Edit Format 7.000E+00 1.400E+01 2.100E+01 2.100E+01 2.800E+01 3.500E+01 3.500E+01 4.200E+01 5.600E+01 4.200E+01 5.600E+01 7.000E+01 5.600E+01 7.700E+01 8.400E+01 1.050E+02 1.120E+02 1.120E+02 1.120E+02 1.300E+02 1.400E+02 1.400E+02 1.610E+02 1.610E+02 1.610E+02 1.680E+02 1.820E+02 1.960E+02 1.890E+02 1.960E+02 2.100E+02 1.310E+02 1.890E+02 2.310E+02 2.380E+02 2.380E+02 2.380E+02 2.590E+02 2.730E+02 2.730E+02 2.800E+02 2.800E+02	<u>View Help</u> 4. 98750E- 2. 83500E- 6. 95625E- 5. 74875E- 1. 26000E- 1. 12875E- 9. 4500E+ 4. 7250E+ 8. 6625E+ 8. 4000E+ 3. 6750E+ 2. 6250E+ 7. 0875E+ 3. 6750E+ 3. 9375E+ 3. 9375E+ 5. 2500E+ 3. 9375E+ 5. 2500E+ 3. 9375E+ 5. 2500E+ 3. 9375E+ 1. 0500E+ 3. 9375E+ 1. 0500E+ 3. 9375E+ 1. 0500E+ 3. 9375E+ 1. 0500E+ 1. 050E+ 1. 050E+	+05 Real +05 Real +05 Real +05 Real +05 Real 04 Real	1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00	LOGNORM LOGNORM LOGNORM LOGNORM LOGNORM LOGNORM LOGNORM LOGNORM LOGNORM LOGNORM LOGNORM LOGNORM LOGNORM LOGNORM LOGNORM LOGNORM LOGNORM LOGNORM LOGNORM LOGNORM LOGNORM LOGNORM LOGNORM LOGNORM LOGNORM LOGNORM LOGNORM LOGNORM
2.800E+02 2.870E+02 2.940E+02 3.010E+02 3.080E+02 3.150E+02	1.07625E 1.023750 3.67500E 5.53875E 2.33625E 3.415125	+US Real E+06 Real +05 Real +05 Real +05 Real	1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00	LOGNORM LOGNORM LOGNORM LOGNORM LOGNORM
3.220E+02 3.360E+02 3.430E+02	8.32125E 3.04500E 2.52000E	+05 Real +05 Real +05 Real +05 Real	1.800E+00 1.800E+00 1.800E+00 1.800E+00	LOGNORM LOGNORM LOGNORM
2				

Figure 4.107. ASCII text file of input data for tritium urinalysis case.

In this example, we will:

- Use the whole dataset to <u>determine individual intake events</u> and the resulting effective doses. This is the way that <u>IMBA Professional Plus is used for most radionuclides</u>.
- Use the special routine tritium urinalysis 'tool' to calculate intakes and resulting doses automatically from sub-sets of urinalysis data.
- -

• Compare doses estimated by these two different methods.

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Determine Individual Tritium Intakes and Resulting Doses

This is done in IMBA Professional Plus by:

- Setting up the required "HTO" models.
- Identifying and "fitting" discrete intake events.
- Calculating doses from HTO intakes.

You can also use IMBA Professional Plus to:

• Calculate doses committed over several monitoring periods.

This feature is used in this example to provide "benchmark" values of committed dose - in order to "test" the values of dose calculated <u>directly</u> (from the HTO urinalysis data) using the <u>routine tritium urinalysis "tool"</u>.

Setting up the HTO Models

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Figure 4.108 shows the Main Screen of IMBA Professional Plus as set up to analyze the input data. The setup steps are:

- <u>Select</u> "H(i) -3" as the Indicator Nuclide <u>i.e.</u>, inorganic tritium (HTO).
- Specify "Time (d) since" (the Start Date) as 9/25/1986.
- Select "10"_Intake Regimes.
- Define All Intake Regimes as "Injection" ICRP treats inhalation of HTO as injection see Appendix A: Assumed Metabolism of Tritiated Water.
- <u>Click</u> the "Load ICRP DEFS" button this loads the "Std H(i)" bioassay model (Figure 4.109) defining retention of HTO in the "<u>bioassay quantity</u>" (Whole Body) and also the "ICRP Default H(i)" biokinetic model (Figure 4.110) defining HTO retention in the blood, bladder and whole body (WB) - for dosimetry.

🌇 Main Screen	
Elle Edit Parameters Calculations Tools Advanced Help Open Save New Quick Save Load Load Report Help Ver 3.1 C:\JABASOFT\IMBAEXUS\USERDATA\USDOE-II\Case22 - HTO - MP.ix C C C C C	
IMBA Expe	rt™ USDOE Phase II
Intake Scenario	
Intake Regimes Enter Number of Intake Regimes (1-10) 10 • IR1 IR2 IR3 IR4 IR5 IR6 IR7 IR8 IR9 IR 10 Route	Units Intake (IR 10) Indicator Nuclid C Date [13648 Bq/d Select Radion Since Syl25/1986 # Intake Number of Associate Syl25/1986 # Associated Radionuclides Associated Radionuclides Intake © pCi mg None Select Dose None Select None Select
Model Parameters These Model Parameters Apply to All IRs Respiratory Tract Deposition Vapor Wound Bioassay Particle Absorption Transport Absorption	Close Calculations
All IRs Absorption: Type F Part Tran: ICRP Defaults GI-Tract: ICRP Defaults f1=1	Biokinetics: ICRP H(i) Model Deposition: ICRP Defaults N/A V

Figure 4.108. <u>Main Screen</u> setup for analysis of 10 discrete intakes of inorganic tritium vapor (HTO).

👒 Bioassay Model		
File Edit Function		
Bioassay Function	Whole body	×
Ka(1) Systemic Retention	Transfer Compe Ka(2) omp 2	Comp 9 Comp 10
Bioassay Function Lam(1)	Lam(2) Excretion	Lam(9) Lam(10) Blood half time (K) 0.0000001
i a(i) Lam(i) 1 -2.506E-02 2.773E+00 2 9.949E-01 6.931E-02 3 3.019E-02 1.733E-02 4 5 6 7 8 9	Select	User Defined Mode
WHOLE BODY LUNGS URINE	FECES BLOOD	QK Cancel THYROID LIVER USER DEFINED
Figure 4.109. ICRP's " <u>St</u>	andard H(i) M	<u>odel</u> " for HTO bioassay (V

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💀 Biokinetic Model.										
Elle Edit Function										
So	Source Organs									
	ADRENALS	BLADDER	BRAIN	BREAST	G. BLADD	HEART CT.				
	HEART WL.	KIDNEYS	LIVER	MUSCLE	OVARIES	PANCREAS				
	TESTES	THYROID	R.B.M.	BONE	CORT VOL	CORT SURF				
	TRAB VOL	TRAB SURF	STOMACH	\$.I.	U.L.I.	LLI.				
	ST. WALL	SKIN	SPLEEN	SOFT TISS	WB	BLOOD				
_	Transfer Compartment Ka(1) Ka(2) Ka(9) Ka(10)									
Or Re	Organ Retention Comp 1 Comp 2 Comp 9 Comp 10 Lam(1) Lam(2) Lam(9) Lam(10)									
			Exc	retion						
_ Org	pan retention functi	ion		Select						
	a(1) -1.02506047	7411708			User Defined Ma	ode				
Ī	ali	Lam(i)			LOAD ICRP DEFAULTS					
1	-1.025E+00	2.773E+00			-					
43	3.019E-02	1.733E-02				odol				
4					ICKP H(I) M	odei				
6										
7										
9	1			[
1	0				<u>o</u> k					

Figure 4.110. Default "ICRP H(i) Model" for HTO biokinetics.

- Proceed to the next step in this example case.
- Return to the case description.

Fitting Discrete HTO Intake Events



Figure 4.111. Routine tritium urinalysis data together with 'fit' obtained by assuming 10 separate intake events.

Figure 4.111 shows the result of an analysis of the variation of whole body retention of HTO at the time of each weekly urine sample carried out for the <u>IDEAS Project</u> (personal communication, Dr. M. Puncher, NRPB). Note that: the whole body retention is calculated on the assumption that the concentration of HTO in all body tissues is in equilibrium with, <u>i.e.</u>, equal to, that in urine. IMBA Professional Plus allows up to <u>10</u> discrete intakes to be defined. In this case, it was necessary to use <u>all 10</u> in order to "fit" the major temporal features of the bioassay data.

The "fitting" process is not as complicated as it might appear to be. Since HTO is eliminated rather rapidly from the body (97% with an assumed 10-d half-time, with 3% retained with a 40-d half-time - see <u>Appendix A: Assumed Metabolism of Tritiated</u> Water), there is relatively little "carry over" of HTO through to monitoring periods several weeks into the future. The "fitting" process is therefore carried out <u>iteratively</u> - starting with the earliest monitoring results. Once a reasonable "fit" is obtained to the first "temporal pattern" of HTO retention - by postulating either an "acute" intake at an assumed time - or "chronic" intake over an assumed time-range (and leaving all "future" intakes <u>undefined</u>) - you can repeat this process for the second "temporal pattern". In order to "fit" both patterns, you will probably have to refine your assumptions (somewhat) about the timing of the first intake

event.

Note: It is only necessary for you to "guess" the temporal parameters of each postulated intake. IMBA Professional Plus <u>automatically</u> calculates the resulting value(s) of the intake amount(s) (in the bioassay data to intakes mode of the Bioassay Calculations screen) - to give the "most likely" fit to the data. This is a surprisingly quick process - once you get the hang of it!

Figure 4.112 shows this "solution" of the progressive "fitting" task.

🗣 Bioassay Calculations					
Eile <u>A</u> dvanced <u>I</u> ools Help					
Save Quick Save Tritium		Bioassay Calcula	ations		
INTAKES	CALCULATIO	N		BIOASS	AY QUA
IR1 8.481E+04 Bq/d			⊂ Graph ⊙ Ta	able C Hide	Whole body Measurem
IR2 4.016E+03 Bq/d	Intakes to Bioassay	Bioassay to Intake	7	000E+00	1.98750E+
IR3 6.271E+03 Bq/d		Select which data to use	1. 2' 2'	400E+01 100E+01 800E+01	2.83500E+ 3.95625E+ 3.74875E+
IR4 2.523E+06 Bq		Vhole body	30	500E+01 200E+01	1.26000E+ 1.12875E+
IR5 3.571E+06 Bq		Lungs	40	900E+01 600E+01	9.4500E+ 4.7250E+
100 1000		Urine Urine	6.	300E+01	8.6625E+
100 6.181E+04 04/0		Feces	G Gunh C L	ubla C Hida	Whole body
IR7 1.287E+06 Bq/d		F Blood	S PEACE -	IDEAS (case 22 Routi
IR8 5.646E+03 Bq/d	Bayesian Analysis	Thyroid	1 a F		
IR9 1.399E+05 Bg		Liver	⊕ 1.0E+06 ≩	5	
1040	Start Calculation	User Defined	1.0E+05	II ITT	-4-4
1.365E+04 Bq/d			e Bod		19
	000		→ ¹ / ₂ 1.0E+04 + 5.3E+03 +		¥ -
Progress Indicator			7.0	61.6 116.2 4	70.8 225.4 2 Time (c
Deposition			C Graph C Ta	able (🖲 Hide	
Collating Times					
Bioassay Calcs					
Current Operation					
		Ωĸ			
		L			
H-3 M	fax Likelihood fit				

Figure 4.112. Calculated intakes (IR1 through IR10) for tritium urinalysis case.

The "best estimates" of the 10 discrete intakes that gave rise to the observed HTO retention pattern are:

Table 4.6. Discrete intake calculated from the tritium urinalysis data.

Example Cases - Bioassay & Dosimetry

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Intake regime	Assumed timing	Intake amount/rate (Bq/Bq d <u>-1</u>)
IR1 - chronic	0 - 20 d	84,810 Bq/d
IR2 - chronic	40 - 150 d	4,016 Bq/d
IR3 - chronic	170 - 280 d	6,271 Bq/d
IR4 - acute	280 d	2,530,000 Bq
IR5 - acute	310 d	3,571,000 Bq
IR6 - chronic	340 - 357 d	61,810 Bq/d
IR7 - chronic	413 - 425 d	1,287,000 Bq/d
IR8 - chronic	390 - 440 d	5,646 Bq/d
IR9 - acute	500 d	139,900 Bq
IR10 - chronic	502 - 530 d	13,650 Bq/d



Tip: Try this fitting process <u>yourself</u> - from "scratch" - using the raw input data (by importing the text file [Install Drv]:\JABASOFT\IMBAEXUS\UserData1 \Demo\Case_22_Tritium.txt **into the** <u>Table Tool</u>). The "solution" above is saved in the parameter file "Case22 - HTO - MP.ix" (in the same folder).

- Proceed to the next step in this example case.
- Return to the case description.

Calculating Doses from HTO Intakes

file://C:\Documents%20and%20Settings\Administrator\Local%20Settings\Temp\~hh... 15/10/2005

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Target Organs	Cont. to Elf Dose (Sv) IR(1)	Cont. to Elf Dose (Sv) IR(2)	Cont. to Elf Dose (Sv) IR(3)	Cont. to Elf Dose (Sv) IR(4)	Cont. to Elf Dose (Sv) IR(5)	Cont. to Elf Dose (Sv) IR(6)	Cont. to Elf Dose (Sv) IR(7)	Cont. to Elf Dose (Sv) IR(8)	Cont. to E (Sv) IR(9)
Adrenals	0.00E+00	(
Urinary Bladder	1.55E-06	4.04E-07	6.30E-07	2.30E-06	3.26E-06	9.60E-07	1.41E-05	2.58E-07	
Brain	0.00E+00	(
Breast	1.55E-06	4.04E-07	6.30E-07	2.30E-06	3.26E-06	9.60E-07	1.41E-05	2.58E-07	
Gall Bladder	0.00E+00	(
Heart Wall	0.00E+00	(
Kidneys	0.00E+00	(
Liver	1.55E-06	4.04E-07	6.30E-07	2.30E-06	3.26E-06	9.60E-07	1.41E-05	2.58E-07	
Muscle	0.00E+00	(
Ovaries	0.00E+00	(
Pancreas	0.00E+00	(
Testes	0.00E+00	(
Thyroid	1.55E-06	4.04E-07	6.30E-07	2.30E-06	3.26E-06	9.60E-07	1.41E-05	2.58E-07	
R.B.M.	3.72E-06	9.69E-07	1.51E-06	5.53E-06	7.83E-06	2.30E-06	3.39E-05	6.19E-07	
Bone Surface	3.10E-07	8.07E-08	1.26E-07	4.61E-07	6.52E-07	1.92E-07	2.82E-06	5.16E-08	
Stomach	3.72E-06	9.69E-07	1.51E-06	5.53E-06	7.83E-06	2.30E-06	3.39E-05	6.19E-07	
S.I.	0.00E+00	(
U.L.I.	0.00E+00	(
L.L.I.	0.00E+00	(
Skin	3.10E-07	8.07E-08	1.26E-07	4.61E-07	6.52E-07	1.92E-07	2.82E-06	5.16E-08	
Spleen	0.00E+00	(
Thymus	0.00E+00	(
Uterus	0.00E+00	(
ET	0.00E+00	(
Lung	3.72E-06	9.69E-07	1.51E-06	5.53E-06	7.83E-06	2.30E-06	3.39E-05	6.19E-07	
Colon	3.72E-06	9.69E-07	1.51E-06	5.53E-06	7.83E-06	2.30E-06	3.39E-05	6.19E-07	
ET1	0.00E+00	(
ET2	0.00E+00	(
LN(ET)	0.00E+00	(
BBsec	0.00E+00	(
BBbas	0.00E+00	(
bb	0.00E+00	(
Al	0.00E+00	(
LN(TH)	0.00E+00	(
Esophagus	1.55E-06	4.04E-07	6.30E-07	2.30E-06	3.26E-06	9.60E-07	1.41E-05	2.58E-07	
Gonads	6.20E-06	1.61E-06	2.52E-06	9.22E-06	1.30E-05	3.84E-06	5.64E-05	1.03E-06	
Spare	0.00E+00	(
Remainder	1.55E-06	4.04E-07	6.30E-07	2.30E-06	3.26E-06	9.60E-07	1.41E-05	2.58E-07	
TOTAL	3.10E-05	8.07E-06	1.26E-05	4.61E-05	6.52E-05	1.92E-05	2.82E-04	5.16E-06	

Figure 4.113. Contributions to total effective dose from each HTO intake.

The contributions to the overall committed effective dose made by each of the 10 intakes (Figure 4.113) is calculated simply in the <u>Dose Calculations</u> screen, in this example (Figure 4.114) by:

- <u>Selecting</u> the "<u>ICRP Default</u>" radiation weighting factors (<u>wR</u>).
- <u>Selecting</u> the "<u>ICRP68</u>" tissue weighting factors (wT).

👒 Dose Calculations								
Elle <u>A</u> dvanced <u>T</u> ools	Help							
Save Quick Save			Dose (Calculatio	ns			
INTAKE		CALCULA	TION				DOS	Е
					C Equiv	I Eff Cont. to Eff	Indie Cont. to Eff	cator N
IR1 8.481E+04	Bq/d				Target Organs	Dose (Sv) IR(1)	Dose (Sv) IR(2)	Dose IR(3)
IR2 4.016E+03 E	Bq/d Calcula	tions WH	WI		Al	0.00E+00	0.00E+00	0.
IR3 6.271E+03	Bq/d	Select			Esophagus Gonads	0.00E+00 1.55E-06 6.20E-06	0.00E+00 4.04E-07 1.61E-06	6
IR4 2.523E+06	Bq	(1) Dose from India	cator Nuclide: H(i)-3	V	Spare Remainder	0.00E+00 1.55E-06	0.00E+00 4.04E-07	0.
IR5 3.571E+06	Bq		visited Deduceration	_	TOTAL	3.10E-05	8.07E-06	1
IR6 6.181E+04 F	Bq/d				(€ Equiv (C Eff	Associat	ed Rac
IR7 1.287E+06	Bq/d	(3) Annual Commit	ted Doses					
IR8 5.646E+03	Bq/d		Effective Dava (C					
IR9 1.399E+05	Bq	Calculate	4.79E-04	1				
IR10 1.365E+04	Bq/d							
		000						
Progress Indicator		000					- Annual (X
(1)							Annual	Johnme
(2)								
(3)								
Current Operation	Intake Regime 1: Applying S splitting rule will not apply. Ec	plitting Rule to Esophagus. T quivalent Dose to remainder i	his is already a named organ s 3.10E-05. Mass weighted r	so the emainder				
				<u>O</u> K				
н-з	WR=ICRP Defaults	WT=ICRP 68	ICRP H(i) Model					

Figure 4.114. Calculating and displaying both the contributions to effective dose from each HTO intake and the effective doses committed each year.



- <u>Proceed</u> to the next step in this example case.
- <u>Return</u> to the case description.

Dose Committed During HTO Monitoring Periods



The next section (<u>Using the Routine Tritium Urinalysis "Tool"</u>), describes how to calculate committed doses <u>directly</u> from the tritium urinalysis data - without having first to determine

(by manual fitting) the amounts of each discrete tritium intake. The urinalysis "tool" analyses up to <u>10 sequential urinalysis results</u> - and calculates automatically the <u>total</u> <u>effective dose</u> committed over this <u>whole monitoring period</u>.

In this example, we can use the special feature provided in <u>IMBA Professional Plus</u> to calculate the <u>Annual Committed Doses</u> resulting from a series of intakes - to generate "benchmark" values of dose for comparison with the results obtained using the <u>Urinalysis</u> <u>"Tool"</u>. The "Tool" analyses a sequence of up to <u>10 routine monitoring results</u>. In this example, the first 10 monitoring results covered the period from day "<u>0</u>" to day "<u>70</u>" (Figure <u>4.107</u>). In this example, we can calculate the total dose committed over just this initial 70-day period, by simply:

- <u>Changing</u> the "<u>Start Date</u>" (in the <u>Main Screen</u>) to [<u>December 31</u>st, <u>1986</u> 70 d] = <u>October 22nd</u>, <u>1986</u>.
- <u>Re-calculating</u> the "<u>Annual Committed Doses</u>".

Figure 4.115 shows the resulting values of committed effective dose for the years 1986, 1987 and 1988. The value displayed for 1986 ($33.3 \mu Sv$) corresponds to the effective dose committed during the first 70-d monitoring period.

Annual Committed Doses tool									
Year	Eff Dose from H(i)-3 (IN) (Sv)	Effective Dose (Sv) Total							
1986	3.33E-05	3.33E-05							
1987	4.36E-04	4.36E-04							
1988	9.95E-06	9.95E-06							
TOTAL	4.79E-04	4.79E-04							
						>			

Figure 4.115. Annual committed doses in 1986, 1987 and 1988.

Tip: The effective dose committed during the first 70-d period of monitoring can also be calculated easily from the tabulated values of effective dose resulting from each discrete intake (Figure 4.113) together with the tabulated duration of each intake (Table 4.6). The required value is the sum of 31.0 μ Sv (from IR1) and 30/110 $\stackrel{<}{}$ 8.1 μ Sv (from IR2) = 33.2 μ Sv (rounded). You can extract the dose committed during any other monitoring period in the same way.

This completes the Determine Individual Tritium Intakes example:

- Proceed to Using the Routine Tritium Analysis 'Tool'.
- Return to the case description.

Using the Tritium Routine Monitoring

'Tool'

The **Tritium Routine Monitoring Tool** works independently of the standard "**Bioassay Data to Intake**" calculation mode (for determining the occurrence and amounts of discrete tritium intakes) that was described in the <u>previous section</u>. Here we will describe how you set up and use the Tritium Routine Monitoring Tool from "scratch" to calculate intakes and committed doses automatically from the **bioassay data**, in this case the whole body retention of HTO at a series of time-points that is derived from the urinalysis samples. See:

• <u>Setting up the Tritium Tool</u>.

Setting up the Tritium Tool

After clicking the "**New**" button - or opening <u>IMBA Professional Plus</u> from its desktop icon - you first:

- <u>Select</u> "<u>H(i)-3</u>" "inorganic tritium (HTO)" as the <u>Indicator Nuclide</u>.
- Click the "ICRP DEFS Load" button.
- Click the "Bioassay Calculations" button.
- <u>Select</u> "<u>Whole Body</u>" as the bioassay data to use.
- <u>Click</u> the "<u>H3 Tritium</u>" button top-left-corner of the <u>Bioassay Calculations</u> screen.

This will open the "Tritium Routine Monitoring Tool" window (Figure 4.116).

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S Bi	oassay Calc											
File /	Advanced To	ools He	lp									
			H			Bi	bassay Cal	culation	IS			
Sav	e Quick Sa		Tritium			ATION	-			DIOACCA	N OU	
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IR1	0.000E+00	Bq	R Trit	ium Routine Mo	nitoring Tool							
			File To	ols Help								
			Chem	ical Form	Intakes							
			(€ in C or	nganic H (HTO) ganic H (HCT)	Number of I	ntake Regimes	IRs) to use in the calculation	on 1 🗄	Intake assumpt	ion Single acute al C Constant chror	t midpoint of nic througho	pe ut
			Speci	fy the monitoring	period correspon	ding to each	measurement					
				Monitoring Peri	ods		Measurement Data (Whole Body)			1	In
				Start (day)	End (day)	Time (day)	Value (Bq)				
			IR1								IR1	0.
			IR 2								IR 2	
			IR 3								IR 3	
			IR 4								IR4	-
			IB 6							Cala Intelace	IB6	H
			IR 7							Calc Intakes	IR 7	h
			IR 8								IR 8	F
			IR 9								IR 9	
- P	ogress Indical	or	IR 1)							IR 10	Γ
D	eposition		-	Def	ault Monitoring Perio	ds	Edit Meas	surement Data				
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B	inaesau Calco		<u> </u>							J	- 1	
	carry carr									<u>K</u>		
0	urrent peration											
							Q	к				
H-3				Max Likelihood fit								

Figure 4.116. Opening the Tritium Routine Monitoring Tool.



You can use the Tritium Routine Monitoring Tool in two different ways:

- 1. To work on bioassay data already "loaded" in the Table Tool.
- 2. To work on bioassay data imported directly from an external ASCII text file.

The Tritium Routine Monitoring Tool is designed to simplify both ways of working, as

00

follows:

- Using <u>"pre-loaded" bioassay data</u> from the Table Tool.
- Using the "Import Wizard".

Loading Tritium Data Already in the Table Tool

🍕 Bi	oassay Calci	ulation	\$						
File	Advanced To	ols Hel	p						
			H		[Bioassay Ca	lculations		
Sav	Ne Quick Sav		ritium					DIOACC	
	INTAK	ES			CALCULAT			BIOASS	AT GUA
				-			C Graph		Whole body
IR1	8.481E+04	Bq/	Triti	um Routine Mor	vitoring Tool				
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in2	4.016E+03	bф	Chemie	al Form	Intakes				
IR3	6.271E+03	— Bq/	(inc	namic H (HTO)			and the second second	G Sincle acute	at michoriet of na
			Cora	anic H (HCT)	Number of Intake F	Regimes (IRs) to use in the calcul	ation 10 📩 Intake a	C Constant ch	onic throughout
IR4	2.523E+06	Bq		,					
IR5	3 571E+06	— Ba	Specif	the monitoring	period corresponding	to each measurement			
	10.0112100			Monitoring Peri	ods	Measurement Data	(Whole Body)		In
IR6	6.181E+04	Bq/		Start (day)	End (day)	Time (day)	Value (Bo)	~	
107		- 8-1	IB 1	Start (aby)	2.10 (00))	7.000	E+00 4.98750E+05		IB1 0
in/	1.287E+06	вф⁄	IB 2			1.4006	E+01 2.83500E+05		IB2 4
IRS	5.646E+03	— Bq/	IR 3				E+01 6.95625E+05		IR 3 6
	1		IR4				E+01 5.74875E+05		> IR 4 2
IR9	1.399E+05	Bq	IR 5			3.5006			IR 5 3.
IP10	L COTT OF	- Pal	IR 6			4.2006		Calc Intakes	IR 6 6.
init	1.365E+04	bψ	IR 7				E+01 9.4500E+04		- IR7 1.
_			IR 8				E+01 4.7250E+04		IR 8 5.
_			IR 9				2+01 8.6625E+04		IR 9 1.
E P	togress Indicato	ж	IR 10				0.40002+04	×	IR 10 1.
D	eposition			Defa	ault Monitoring Periods	Edit M	easurement Data		
	alatina Timor	1		Cle	ar Monitoring Periods		This launches the Ta	able Tool	
	lolating Times		L				[mondamentes and re		
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0	peration								
							<u>o</u> k		
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11-5				Nov Levelnood III.					

Figure 4.117. Opening the Tritium Routine Monitoring Tool with "Whole Body" data already in the Table Tool - from "Case22 - HTO - MP.ix".

If you open the Tritium Routine Monitoring Tool when the Table Tool already contains bioassay data, in this case "Whole Body" data, the first 10 rows of "Time (day)" and "Value (Bq)" data will be displayed automatically in the tritium tool (Figure 4.117) - under the heading "Measurement Data (whole Body)". The tritium tool will also display the last-calculated values of intake amounts (<u>IR1</u> through <u>IR10</u>) - under the heading "Intake (Bq)".
The Tritium Routine Monitoring Tool analyzes the bioassay data a maximum of 10 rows (i.e., 10 data points) at a time. Therefore, you need to select up to 10 rows of data from the Table Tool - exclude all other rows. Figure 4.118 shows how you do this for rows 11 and below - by highlighting the corresponding "Real" entries in the "Data Type" column, right-clicking anywhere in the highlighted column, and clicking "Excluded".

et 1	Table Tool: Whole body Da	ta							
File	Edit Bioassay Measurement	Help	0.1.1.1.1						
	Specified Time (d)	N/A	Value(Bg)	Measurement Time (d)	N/A	Value(Bo)	Data Type	Error	Dis
4	1.488442211E+01			2.800E+01		5.74875E+05	Real	1.800E+00	LOC
5	1.751256281E+01			3.500E+01		1.26000E+05	Real	1.800E+00	LOC
6	2.014070352E+01			4.200E+01		1.12875E+05	Real	1.800E+00	LOC
7	2.276884422E+01			4.900E+01		9.4500E+04	Real	1.800E+00	LOC
8	2.539698492E+01			5.600E+01		4.7250E+04	Real	1.800E+00	LOC
- 9	2.802512563E+01			6.300E+01		8.6625E+04	Real	1.800E+00	LOC
10	3.065326633E+01			7.000E+01		8.4000E+04	Real	1.800E+00	LOC
11	3.328140704E+01			7.700E+01		3.6750E+04	Real	1.900E+00	1.00
12	3.590954774E+01			8.400E+01		2.6250E+04	Real Re	al	
13	3.853768844E+01			1.050E+02		7.0875E+04	Real <	00	
14	4.116582915E+01			1.120E+02	2	3.6750E+04	Real Ex	duded	
15	4.379396985E+01			1.190E+02	2	5.2500E+04	Real		
16	4.642211055E+01			1.260E+02		3.9375E+04	Real	t	
17	4.905025126E+01			1.330E+02		3.9375E+04	Real Co	ру	
18	5.167839196E+01			1.400E+02		5.5125E+04	Real Pa:	,te	
19	5.430653266E+01			1.540E+02	2	5.250E+03	Real Tex	ert Maaci versect i	0 com
20	5.693467337E+01			1.610E+02	2	3.4125E+04	Real	ert Measurennert P	David
21	5.956281407E+01			1.680E+02		7.875E+03	Real	ece measurement	KOW
22	6.219095477E+01			1.750E+02		1.0500E+04	Real De	ete Cell Contents	
23	6.481909548E+01			1.820E+02		5.2500E+04	Real		
24	6.744723618E+01			1.890E+02	2	4.7250E+04	Real	Import	
25	7.007537688E+01			1.960E+02		3.9375E+04	Real	1.800E+00	LOC
26	7.270351759E+01			2.020E+02		1.05000E+05	Real	1.800E+00	100
27	7.533165829E+01			2.100E+02		8.4000E+04	Real	1.800E+00	LOC
28	7.795979899E+01			2.310E+02		5.5125E+04	Real	1.800E+00	LOC
29	8.05879397E+01			2.380E+02		3.1500E+04	Real	1.800E+00	LOC
30	8.32160904E+01			2.590E+02		1.05000E+05	Real	1.800E+00	LOC
31	8.584422111E+01			2.730E+02		9.9750E+04	Real	1.800E+00	LOC
32	8.847236181E+01			2.800E+02		1.07625E+05	Real	1.800E+00	LOC
33	9.110050251E+01			2.870E+02		1.023750E+06	Real	1.800E+00	LOC
34	9.372864322E+01			2.940E+02		3.67500E+05	Real	1.800E+00	LOC
35	9.635678392E+01			3.010E+02		5.53875E+05	Real	1.800E+00	LOC
36	9.898492462E+01			3.080E+02		2.33625E+05	Real	1.800E+00	LOC
37	1.016130653E+02			3.150E+02		3.415125E+06	Real	1.800E+00	LOC
38	1.04241206E+02			3.220E+02		8.32125E+05	Real	1.800E+00	LOC
39	1.068693467E+02			3.360E+02		3.04500E+05	Real	1.800E+00	LOC
40	1.094974874E+02			3.430E+02		2.52000E+05	Real	1.800E+00	LOC
41	1.121256281E+02			3.500E+02		2.94000E+05	Real	1.800E+00	LOC
42	1.147537688E+02			3.570E+02		4.41000E+05	Real	1.800E+00	LOC
43	1.173819095E+02			3.780E+02		1.54875E+05	Real	1.800E+00	LOC
44	1.200100503E+02			3.850E+02		6.3000E+04	Real	1.800E+00	LOC
N	Bioassay Predictions Measurement Data Measurement Fit Outpu	No Re	ws: 200	Apply					

Figure 4.118. Excluding all data in rows 11 and below in the Table Tool.

This will change the color of all data entries in row 11 and below to <u>red</u>, and also change the color of the corresponding data points plotted in the Bioassay Quantity graph (Figure 4.119).

📲 Bioassay Co	alculations										
File Advanced	Tools Help										
Save Quick	Save Tribum			Bioas	say	Calc	ulatic	ons			
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								Measurer	nent Time (d	() N/A	Measur
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ber of Intake Regi	mes (IRs) to use in th	e calculation	10 🕂 Intake assump	tion Single acute at	midpoint of	of period			1.400	E+01	2.83500
-				C Constant chron	ic through	out period			2.100	E+01	3.95625
									2.800	E+01	5.74875
esponding to e	ach measurement	t		1					3.500	E+01	1.25000
	Measuremen	nt Data fWhole	Bodyl			Intake fi	Bal		4.200	E+01	9.4500
							~		5.600	E+01	4.7250
d (day)	Time (day)	Val	ue (Bq) 🔷						6.300	E+01	8.6625
			4.98750E+05		IR 1	8.4805E 4	-04	<			
			2.83500E+05		IR 2	4.0164E4	-03	Graph	C. Table	C Hid	whole bo
			6.95625E+05		IR 3	6.2706E	-03			IDE	AS Case 22 Rr
			5.74875E+05		. IR 4	2.5225E4	-06	5.8E	⁻⁰⁶ E	1012	NO 0436 22110
			1.26000E+05		IR 5	3.5710E4	-06	2	E F		
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			8.6625E+04		IB 9	1.39855	-05	8	F		
			8.4000E+04		IR 10	1.3648E4	-04	€ 1.0E	•04 [4	
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				<u>0</u> K		Can	cel				
KURACEART A											

Figure 4.119. Excluding the 11<u>th</u> and all further data points from analysis by the tritium tool.

The next step is to "Specify the monitoring period corresponding to each measurement". If the sampling intervals are contiguous, the associated monitoring periods can be specified automatically - by simply clicking the "Default Monitoring Periods" button (as in Figure 4.120).

💐 Triti	um Routine Monitorin	g Tool				×
<u>Ele I</u> oo	ls Help					
Chemic	al Form	ntakes				
inor Corg	ganic H (HTO) anic H (HCT)	Number of Intake Regimes (I	Rs) to use in the calculation	10 📩 Intake assum	ption [©] Single acute at midpoi [©] Constant chronic through	nt of period aghout period
Specify	the monitoring period	corresponding to each r	neasurement Measurement Data (W)	vole Rodu)		Intake (Bo)
	Start (day)	End (day)	Time (day)	Value (Bq)		make (ed)
IB 1	0	7.000E+00	7.000E+00	4.98750E+05	IB	1 8.4805E+04
IR 2	7.000E+00	1.400E+01		2.83500E+05	IR	2 4.0164E+03
IR 3	1.400E+01	2.100E+01		6.95625E+05	IR IR	3 6.2706E+03
IR 4	2.100E+01	2.800E+01	2.800E+01	5.74875E+05		4 2.5225E+06
IR 5	2.800E+01	3.500E+01		1.26000E+05		5 3.5710E+06
IR 6	3.500E+01	4.200E+01	4.200E+01	1.12875E+05	Calc Intakes IR	6.1808E+04
IR 7	4.200E+01	4.900E+01	4.900E+01	9.4500E+04	IR	7 1.2868E+06
IR 8	4.900E+01	5.600E+01		4.7250E+04	IR	8 5.6463E+03
IR 9	5.600E+01	6.300E+01		8.6625E+04	IR	9 1.3985E+05
IR 10	6.300E+01	7.000E+01		8.4000E+04	IR	10 1.3648E+04
	Default Mon	toring Periods	Edit Measur	ement Data		
	Clear Monit	oring Periods				
					Ωĸ	Cancel

Figure 4.120. Specifying the monitoring periods automatically.

If the monitoring periods are not in fact all contiguous, you can edit any "Start (day)" value directly in the Tritium Routine Monitoring Tool table. Also, clicking the "Edit Measurement Data" button (Figure 4.120) will return you to the Table Tool - so that you can edit any of the "input" bioassay data values. The functioning of the Tritium Routine Monitoring Tool is fully integrated with that of the Table Tool.



<u>This completes the step of loading a sub-set of the bioassay data into the Tritium Routine</u> Monitoring Tool - directly from the Table Tool.

• Proceed to Using the Tritium 'Tool' to Calculate Intakes Automatically.

Loading Tritium Data with the Import Wizard

<u>Clicking</u> the "<u>Edit Measurement Data</u>" button in the <u>Tritium Routine Monitoring Tool</u> opens the <u>Table Tool</u>. You can then <u>import</u> the required bioassay data (Figure 4.117A).

- Y	Table To	0(: W	note body D	ata							
File	Edit Bio	assay	Measurement	Help							
	Specified	dTime	(d)	N/A	Calculated Value(Bq)	Measurement Tir	ne (d)	N/A	Measurement Value(Bq)	Data Type	Measurement Err Error Dis
1							Cut	-			
							Сору				
							Paste		-		
							Insert Me	sasurement Row			
							Delete M	easurement Row	-		
							Delete Ci	ell Contents	_		
							File Impo	rt			
- 11	EV.										
K		Disast	w Dradiations								
	H	Measu	rement Data	N	Rows: 1	Acoly					
	H	Measu	rement Fit Outp	ut	p.	•					

Figure 4.117A. Blank Table Tool ready to import a file of whole body bioassay data.

In the <u>Table Tool</u>, <u>right-click</u> on the empty cell under the "<u>Measurement Time (d)</u>" heading (Figure 4.117A). From the drop-down menu, select "<u>File Import</u>" (as in Figure 4.117A). This will open the "ASCII file import wizard" (Figure 4.118A).

📲 ASCII file import wizard 🛛 🔀
The ASCII file import wizard helps you to import data directly from a text file
Text file C:\JABASOFT\IMBAEXUS\USERDATA\Demo\Case_2
[<u>V</u> iew]
Select type of text file
C Comma separated
C Other delimiter
< <u>B</u> ack <u>N</u> ext> <u>C</u> ancel

Figure 4.118A. The ASCII file import wizard.

In the ASCII file import wizard, browse to the folder [Install

<u>Drv]:\\JABASOFT\IMBAEXUS\UserData1\Demo\</u> and <u>select</u> the file "<u>Case_22_Tritium.txt</u>" data file, and <u>click View</u> (Figure 4.118A). This will open the file in NotePad® (Figure 4.119A).

Case_22_Tritium.t	xt - Notepad				
Eile Edit Format View	Help				
7.000E+00 1.400E+01 2.100E+01 3.500E+01 4.200E+01 5.600E+01 5.600E+01 7.000E+01 7.700E+01 8.400E+01 1.050E+02 1.120E+02 1.260E+02	4.98750E+05 2.83500E+05 6.95625E+05 5.74875E+05 1.26000E+05 1.12875E+05 9.4500E+04 4.7250E+04 8.6625E+04 8.4000E+04 3.6750E+04 2.6250E+04 3.6750E+04 3.6750E+04 5.2500E+04 5.2500E+04	Real Real Real Real Real Real Real Real	1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00 1.800E+00	LOGNORM LOGNORM LOGNORM LOGNORM LOGNORM LOGNORM LOGNORM LOGNORM LOGNORM LOGNORM LOGNORM LOGNORM LOGNORM LOGNORM	-
Figure 4.119A.	First part of the	"Case	22 Tritium	.txt" data file -	viewed in NotePad®.

This file is "tab delimited" - and so you need to <u>click</u> the "<u>Tab delimited</u>" button (Figure 4.118A) before <u>clicking Next</u>. The whole file will then be imported (into rows and columns) in the ASCII file import wizard (Figure 4.120A).

	ASCII file	import wiz	ard				×
	Please select	the data that	you wish to in	nport			
		С	D	E	F	~	
	7	9.4500E+04	Real	1.800E+00	LOGNORM		
	8	4.7250E+04	Real	1.800E+00	LOGNORM		
	9	8.6625E+04	Real	1.800E+00	LOGNORM		
	10	8.4000E+04	Real	1.800E+00	LOGNORM		
	11	3.6750E+04	Real	1.800E+00	LOGNORM		
	12	2.6250E+04	Real	1.800E+00	LOGNORM	~	
	40 K	2 00755 04		1 0005 00	1000000		
						<u>S</u> elect All	
_	< <u>B</u> ack	<u>N</u>	ext>			<u>C</u> ancel	

Figure 4.120A. Selecting the first 10 rows of data.

The <u>Tritium Routine Monitoring Tool</u> analyzes the bioassay data a <u>maximum</u> of 10 rows (<u>i.e.</u>, 10 data points) at a time. Therefore, you should highlight just 10 rows of data in the import wizard - before clicking the <u>Next</u> button. The highlighted 10 rows are then automatically loaded into the <u>Table Tool</u> (Figure 4.121).

5	Table Tool : Whole body Dat	a							
Ele	Edit Bioassay Measurement	<u>t</u> elp							
	Specified Time (d)	N/A	Calculated Value(Bq)	Measurement Time (d)	N/A	Measurement Value(Bq)	Data Type	Measurement Error	Em Dis
1				7.000E+00		4.98750E+05	Real	1.800E+00	LOC
2				1.400E+01		2.83500E+05	Real	1.800E+00	LOC
3				2.100E+01		6.95625E+05	Real	1.800E+00	LOC
4				2.800E+01		5.74875E+05	Real	1.800E+00	LOG
5				3.500E+01		1.26000E+05	Real	1.800E+00	LOG
6				4.200E+01		1.12875E+05	Real	1.800E+00	LOC
7				4.900E+01		9.4500E+04	Real	1.800E+00	LOC
8				5.600E+01		4.7250E+04	Real	1.800E+00	LOC
9				6.300E+01		8.6625E+04	Real	1.800E+00	LOG
10				7.000E+01		8.4000E+04	Real	1.800E+00	LOG

Figure 4.121. 10 rows of bioassay (whole body) data imported into the Table Tool.

<u>Clicking</u> "<u>OK</u>" in the <u>Table Tool</u> returns you to the <u>Bioassay Calculations</u> screen - with the <u>Tritium Routine Monitoring Tool</u> window still open. However, the imported data is now visible (automatically) in this window (figure 4.122).

mical Form inorganic H (HTO)	Intakes Number of Intake Be	cimes (IBs) to use in the calculation 11	Intake assumption	Single acute at midpo	int of period
organic H (HCT)		2 () is an error of the second s		Constant chronic thro	ughout period
cify the monitoring	period corresponding to	each measurement			
Monitoring Per	iods	Measurement Data (Whole I	Body)		Intake (Bq)
Start (day)	End (day)	Time (day) Valu	e (Bq)		
		7.000E+00	4.98750E+05	IB	1 1.0000E+00
2			2.83500E+05	IB	2 0.0000E+00
			6.95625E+05	, IB	3 0.0000E+00
		2.800E+01	5.74875E+05		4 0.0000E+00
		3.500E+01	1.26000E+05		5 0.0000E+00
		4.200E+01	1.12875E+05		6 0.0000E+00
		4.900E+01	9.4500E+04	Laic Intakes	7 0.0000E+00
			4.7250E+04	IB	8 0.0000E+00
		6.300E+01	8.6625E+04	IB	9 0.0000E+00
0		7.000E+01	8.4000E+04	IR	10 0.0000E+00
De	ault Monitoring Periods	Edit Measuremen	Data		
a	ear Monitoring Periods				

The next step is to "<u>Specify the monitoring period corresponding to each measurement</u>". If the sampling intervals are <u>contiguous</u>, the associated monitoring periods can be specified automatically - by simply <u>clicking</u> the "<u>Default Monitoring Periods</u>" button (as in Figure 4.123).

Elle <u>T</u> ool	s Help					
Chemic	al Form	ntakes				
€ inor C orga	ganic H (HTO) N vnic H (HCT)	lumber of Intake Regimes (I	Rs) to use in the calculation	10 🕂 Intake assumpt	ion 🏵 Single acute at mid	point of period roughout period
Specify	the monitoring period of Monitoring Periods	corresponding to each	measurement Measurement Data (W	hole Body)]	Intake (Bq)
	Start (day)	End (day)	Time (day)	Value (Bg)		
IR1	0	7.000E+00		4.98750E+05	1	R1 1.0000E+00
IR 2	7.000E+00	1.400E+01		2.83500E+05	1	R 2 0.0000E+00
IR 3	1.400E+01	2.100E+01		6.95625E+05		R 3 0.0000E+00
IR 4	2.100E+01	2.800E+01		5.74875E+05		R 4 0.0000E+00
IR 5	2.800E+01	3.500E+01	3.500E+01	1.25000E+05		R 5 0.0000E+00
IR 6	3.500E+01	4.200E+01	4.200E+01	0.45005+00	Calc Intakes	R 6 0.0000E+00
IR7	4.2000+01	4.500E+01		A 7250E +04		R 7 0.0000E+00
IK 8	5.600E+01	6 300E+01		8.6625E+04		R 8 0.0000E+00
IR 10	6.300E+01	7.000E+01	7.000E+01	8.4000E+04		R 10 0.0000E+00
	Default Monit	toring Periods	Edit Measu	rement Data		
	Clear Monito	oring Periods				
						1

Figure 4.123. Specifying the monitoring periods automatically.

If the monitoring periods are not in fact all contiguous, you can edit any "Start (day)" value directly in the <u>Tritium Routine Monitoring Tool</u> table. Also, <u>clicking</u> the "<u>Edit Measurement</u> <u>Data</u>" button (Figure 4.123) will return you to the <u>Table Tool</u> - so that you can <u>edit</u> any of the

"input" bioassay data values. The functioning of the <u>Tritium Routine Monitoring Tool</u> is integrated with that of the <u>Table Tool</u>.

22 III	<u>Warning:</u> By default, the <u>Tritium Routine Monitoring Tool</u> assumes a " <u>Start</u> (day)" value of " $\underline{0}$ " - since the actual value is not included in the imported data. If " $\underline{0}$ " is incorrect, you will have to <u>enter</u> the appropriate value yourself.
	This is generally the " <u>End (day)</u> " of previous (most recent) set of monitoring
	data.

This completes the step of loading the bioassay data into the <u>Tritium Routine Monitoring</u> <u>Tool</u> - using the <u>Import Wizard</u>.

• <u>Proceed</u> to Using the Tritium 'Tool' to Calculate Intakes Automatically.

Automated "Fitting" of Tritium Intakes



Once you have loaded a series of up to 10 bioassay results (<u>i.e.</u>, 10 rows in the <u>Measurement</u> <u>Data</u> table) and defined all of the associated <u>Monitoring Periods</u> (as in Figure 4.123), you can use the <u>Tritium Routine Monitoring Tool</u> to calculate automatically a set of discrete <u>Intakes</u> that "fit" the measured bioassay values. In order to do this, you must first assume a value of the "time" of occurrence of each intake. The <u>Tritium Routine Monitoring</u> <u>Tool</u> provides two standard (commonly made) assumptions - that are applied automatically to all potential intakes:

- <u>Single Acute</u> intake at the <u>mid-point</u> of each monitoring period set by default.
- <u>Constant Chronic</u> intake <u>throughout</u> each monitoring period.

For the default setting (<u>Single Acute</u>), the <u>Tritium Routine Monitoring Tool</u> automatically calculates_the <u>time</u> value corresponding to each sample mid-point. For the "<u>Constant</u> <u>Chronic</u>" option, the pre-calculated "<u>Start (day)</u>" and "<u>End (day)</u>" values are used to calculate the associated Intake values. In order to "fit" the monitoring data (bioassay values), the <u>Tritium Routine Monitoring Tool</u> uses the <u>maximum likelihood method</u> (as extended to <u>multiple intakes</u> in <u>IMBA Professional Plus</u>) to find the <u>most likely</u> value of the <u>hypothetical intake</u> during each sampling period.

Important Note #1: In effect, this method in which a limited sequence of monitoring results (maximum of 10) is analyzed does not correct the earliest monitoring results for "carry over" of tritium activity from previous intakes. Thus, the first "calculated" intake amount will always <u>over-estimate</u> the actual intake during this monitoring period - by the amount of "carry over". However this effect will become <u>smaller</u> for each subsequent intake calculation, <u>i.e.</u>, later intakes will be calculated more accurately.
 Important Note #2: This methodology leads to a somewhat <u>conservative</u> estimate of the <u>effective dose</u> committed over the whole monitoring period - although, <u>usually not a serious over-estimate</u> if the whole monitoring period is greater than a month.

Example Cases - Bioassay & Dosimetry

Figure 4.124 shows the calculated values of intake (IR1 through IR10) that result for the first 10 bioassay measurements (values of whole body activity) in <u>this example</u>. In this case, we have assumed (by default) that each potential intake would have occurred at the mid-point of each sampling period.

mical For	-	takas				
micarro		NdKUS				
inorganic H organic H ((HTO) (HCT)	lumber of Intake Regimes	(IRs) to use in the calculation	10 - Intake assumptio	 Single acute at midpoint Constant chronic through 	of period hout period
cify the r	nonitoring period	corresponding to each	measurement			
Moni	toring Periods		Measurement Data (Whe	ole Body)		Intake (Bq)
Star	(day)	End (day)	Time (day)	/alue (Bq)		
1	0.000E+00	7.000E+0	7.000E+00	4.98750E+05	IB 1	5.8407E+05
2	7.000E+00	1.400E+0	1.400E+01	2.83500E+05	IR 2	0.0000E+00
3	1.400E+01	2.100E+0	2.100E+01	6.95625E+05	N IR 3	4.2797E+05
4	2.100E+01	2.800E+0	2.800E+01	5.74875E+05	IR 4	0.0000E+00
5	2.800E+01	3.500E+0	3.500E+01	1.26000E+05	IR 5	0.0000E+00
6	3.500E+01	4.200E+0	4.200E+01	1.12875E+05	Calc Intakes IR 6	0.0000E+00
7	4.200E+01	4.900E+0	4.900E+01	9.4500E+04	IR 7	0.0000E+00
8	4.900E+01	5.600E+0	5.600E+01	4.7250E+04	IR 8	0.0000E+00
9	5.600E+01	6.300E+0	6.300E+01	8.6625E+04	IR 9	5.8375E+04
10	6.300E+01	7.000E+0	7.000E+01	8.4000E+04	IR 1	3.3435E+04
	Default Moni	toring Periods	Edit Measure	ment Data		
	Clear Monit	oring Periods				

Figure 4.124. Result of clicking the "<u>Calc Intakes ...</u>" button in the <u>Tritium Routine Monitoring</u> <u>Tool</u>.

<u>Note:</u> For this set of 10 bioassay values, the <u>Tritium Routine Monitoring</u> <u>Tool</u> calculated 4 finite values of intake (for <u>IR1</u>, <u>IR3</u>, <u>IR9</u> and <u>IR10</u>). All other potential intakes were calculated to be <u>zero</u>._

<u>Clicking</u> the "<u>OK</u>" button in the <u>Tritium Routine Monitoring Tool returns</u> you to the <u>Bioassay</u> <u>Calculations</u> screen (Figure 4.125).

🍕 Bio	oassay Calo	culatio	ins													
Ele é	<u>A</u> dvanced <u>I</u>	ools H	ielp													
Save	e Quick Sa	ave	Tritium			Γ	Bioa	ssay	/ Calo	culati	ons					
	INTA	KES			CALCU	JLATI	ON						В	IOAS	SA	Y QUA
															-	
IB1	E 0415-00	B	a		[ヨン	>			C Graph	۲	Table	C Hide	, I	Whole body
	J.041E+00	_	-		Las Is Dissas		r –	Diamo	. In Latel a		Specifier	d Time	(d)	N/A		Value(Bq)
IR2	0.000E+00	B	q	Inta	kes to Bioassa	y		Bioassa	ay to Intake				1.000E	+00		0.000E+
IR3	4.280E+05	. в	q				Marchand		70	<u> </u>			3.000E	+00		0.000E+
	14.2002.100		-				Number of	limes (1-2	00) [13				4.000E	+00		5.75060E+
IR4	0.000E+00	B	q	- Specify Ti	mes (d) [Col 1]								5.000E	+00		5.05300E+
IDE			-	Start Tin	ne (d) 1		@ Line	sar	Send to	al			7.000E	+00		1.72240E+
ing	10.000E+00) 0	4				C Log	arithmic	open				9.000E	+00		1.41380E+ 1.12560E+
IR6	0.000E+00	B	q	Stop Tin	ne (d) 70		C 1-2	5 mode	>	°	< 11		0.0002			
IB7	0.000E+00	B	9	C	Realize Deda & R	5.1.00					Graph	0	Table	C Hide	. [//hole body
	10.0002.000			- Specity Lo	pliection Periods (l			-			7E+	05 2	T		. 0	
IRS	0.000E+00	B	9				_	Ser	nd>			E			\land	<u> </u>
IR9	5.838E+04	н В	q	Calculate	Bioassay Quantity	[Col 3]						ŀ	11	\forall		
		_					[Start C	alculation			F		1		
IR10	3.344E+04	t B	٩				-				1E+	05 ÷				
-				-	$\sim \sim$	<u> </u>				_		Ē				
_										_	SE+	04 	ż	14	21	28
P	ogress Indica	tor														
De	eposition									[C Graph	C	Table	 Hide 	Γ	
Co	ollating Times					шп				Ĩ						
Bi	oassay Calcs									Ĩ						
0.	uttent			0			•									
Ōŗ	peration			Ca	alculation (Comple	ete									
									08	.						
										`						
						_					1					
H-3			1	Max Likelihood fit												

<u>Figure 4.125.</u> The amount of intake calculated to have given rise to each successive bioassay measurement is displayed automatically in the <u>Bioassay Calculations</u> screen.

Tip: If you set up a <u>Graph</u> window for the <u>Bioassay Quantity</u> (Figure 4.125), you can view (automatically) the result of the fitting process - in this example, the fitted whole body retention as a function of time together with the input "point estimates" represented by the measured (bioassay) values.
 Note: The fitted whole body retention shown in Figure 4.125 results from assuming that each of the 4 fitted intakes occurred at the mid-point of the corresponding sampling interval. The effect of the alternative assumption (that each intake occurred continuously over the corresponding sampling interval) is described in the topic "<u>Effect of Assumed HTO Intake Pattern</u>".

<u>Clicking</u> "<u>OK</u>" in the <u>Bioassay Calculations</u> screen then returns you to the Main Screen (Figure 4.126).

略 Main S	icreen											
Ele Edit	Parameters Cal	culations <u>T</u> ools <u>A</u>	dvanced Help	_		_						
Open	Save N	ew Quick Save	Load	Load	Report	Help						
Ver 3.2	C:\JABASOFT	JMBAEXUS/USERD	ATA\Demo\Ca	se22 · HTO ·	JA.ix							
نانی	nft Stift			II	MBA	Exp	ber	t™	oc	AS	-Edition	
Intake	e Scenario											
Fintak	ar All Intake Regim ar All Intake Regim I IR 2 IR Route C Inhalation C Ingestion C Ingestion C Ingestion C Wound	es Enter 3 IR 4 IR 5 Mode (* Acute	Number of Intal	e Regimes (IR 7 1R) (66.5	1-10) 1 8 1 IR 9 ° Cheonic	10 × 10 × 10 × 10 × 10 × 10 × 10 × 10 × 10 × 10 ×	Un Si c si i I	its pecify Ti Date Time (nce /1/1980 /1/1980 /1/1980	me As d) C dpm C mg	#	Intake (IR 10)	Indicator Nuclid Select Radior Number of Associat Half Life: 4.5088
	C Vapor						-D.	ose Sv mSv	C rem C mren	n		None Select
Mode	el Paramet	ers —								-	Calculations	
These	Model Parameters spiratory Tract Deposition	Apply to All IRs	Wour	nd	Bioassay		Offic	ce of C lysis a	Compens nd Supp	Sation		Bioassay Calc
	Particle Transport	Absorption	GI-Tra	ect	Bickinetic	:			Close			Dose Calcu
All IR:	Absorption: Not Sp	ecified Part Tran: N	ot Specified G	I-Tract: Not \$	Specified (1	-	-	Bi	okinetics: 10	CRP H(i)	Model Deposition: Not Sp	ecified N/A

Figure 4.126. Main Screen after returning from the Tritium Routine Monitoring Tool.

Note: The calculated intake values (and the assumed times and durations of the intakes) are automatically displayed in the <u>Main Screen</u> - so that you can proceed directly to the <u>Dose Calculation</u>.

This completes the step of calculating automatically the associated <u>Tritium Intakes</u>:

• Proceed to Using the Tritium 'Tool' to Calculate Doses Automatically.

Automated Tritium Dose Calculation

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<u>Clicking</u> the <u>Dose Calculations</u> button in the <u>Main Screen</u> opens the <u>Dose Calculations</u> screen (Figure 4.127). Then, to calculate the resulting values of effective dose, you simply <u>click</u> the "<u>Calculate</u>" button. The results for the whole tritium monitoring period (<u>0 to 70 d</u>) are shown

in Figure 4.127.

Dose Calculations								
Elle <u>A</u> dvanced <u>T</u> ools	Help					_		
Save Quick Save			Dose (Calculation	IS			
INTAKE		CALCULA	ATION				DOS	E
			\equiv >		(* Equiv	C Ell	Indi	cator N
IR1 5.841E+05	Bq				Target Organs	Equivalent Dose (Sv) IR(1)	Equivalent Dose (Sv) IR(2)	Equiv Dose IR(3)
102	Calcul	ations WR	WT		BBbas	1.07E-05	0.00E+00	7
0.000E+00	pq				bb	1.07E-05	0.00E+00	7
IB3 4 2005 - 05	Ra				AI INITHI	1.07E-05	0.00E+00	
4.2006 +00		Select			Esophagus	1.07E-05	0.00E+00	7
IB4 0.000E+00	Bq				Gonads	1.07E-05	0.00E+00	7
10.0000-000		(1) Dose from Ind	icator Nuclide: H(i)-3		Spare	0.00E+00	0.00E+00	0.
IR5 0.000E+00	Bq				Remainder	1.07E-05	0.00E+00	7
IR6 0.000E+00	Bq	(2) Dose from Ass	ociated Radionuclides		(* Equiv (Ēff	Associal	ed Rac
		(2) Dava in each (Colondos Veres	_				
IR7 0.000E+00	Bq	(3) Dose in each	Lalendar i ear	, •				
IR8 0.000E+00	Bq							
IR9 5 0005 .04	Ba	·	Effective Dose (Sv	0				
10 D.838E+04	94	Calculate	2.025.05					
IR10 3.344F+04	Ba							
Income of								
		000						
Progress Indicator							Annual	Commit
(1)						Eff Dose from	Effective	
(2)					Year	H(i)-3 (IN) (Sv)	Dose (Sv) Total	
(3)					1986	2.02E-05	2.02E-05	
Current Operation	Intake Regime 1: Applying 9 splitting rule will not apply. E	plitting Rule to Esophagus. 1 quivalent Dose to remainder	This is already a named organ is 1.07E-05. Mass weighted r	n so the emainder	TUTAL	2.022-05	2.026-05	
				QK				
H-3	WR=ICRP Defaults	WT=ICRP 68	ICRP H(i) Model					

Figure 4.127. Calculating and displaying the resulting committed effective dose.

In this case, the total committed effective dose is $20.2 \ \mu Sv$.

Repeating this whole process for subsequent sets of 10 tritium monitoring results - by importing rows of data 10-at-a-time from the ASCII text file "<u>Case_22_Tritium.txt</u>" - gives the calculated values of committed effective dose shown in Table 4.7.



Table 4.7. Total com	mitted effective dose calcu	llated for each monitoring period.
	Total Committed Effective	_
Monitoring period (d)	<u>Dose (µSv)</u>	
#1: 0 - 70	20.2	_

Example Cases - Bioassay & Dosimetry

#2: 70 - 161		4.6	
#3: 161 - 259		8.7	
#4: 259 - 343		57.6	
#5: 343 - 427		179	
#6: 427 - 518		43.6	
#7: 518 - 553		3.5	
<u>Total: 0 - 553</u>	<u>317</u>		



<u>Note:</u> These calculated values assume that intakes occurred at the mid-point of the corresponding sampling interval. The total committed effective dose (317 μ Sv) is <u>substantially lower</u> than the value (479 μ Sv) <u>calculated earlier</u> - by manually "fitting" discrete intake events to the whole bioassay data set.

This completes the step of calculating doses automatically - assuming that all intakes occurred at the <u>mid-point</u> of the corresponding sampling interval:

• <u>Proceed</u> to Effect of Assumed HTO Intake Pattern.

Effect of Assumed HTO Intake Pattern



Instead of using the default assumption that all intakes occur at the <u>mid-point</u> of the corresponding sampling period, the <u>Tritium Routine Monitoring Tool</u> gives you the option of assuming that all intakes occur continuously (<u>i.e.</u>, are uniform chronic) over the corresponding sampling interval. Figure 4.128 shows the effect of making the <u>uniform</u> <u>chronic</u> assumption on the intakes calculated for the first set of monitoring data (from 0 to 70d).

🐴 Bioassay Calculations			
Ele Advanced Iools Help			
Save Quick Save Tribium		Bioassay Calculati	ons
INTAKES	CALCULAT	ION	BIOASSAY QUA
IP1 Fears at Pald		=>	⊂ Graph ← Table ← Hide Whole body
111 8.272E+04 040			Specified Time (d) N/A Calculater Value(Bq)
IR2 0.000E+00 Bq/d	Intakes to Bioassay	Bioassay to Intake	1.000E+00 8.1281E+ 2.000E+00 1.57840E+
IR3 6.063E+04 Bq/d		Number of Times (1-200)	3.000E+00 2.29420E+ 4.000E+00 2.96320E+
IR4 0.000E+00 Bq/d	Specify Times (d) [Col 1]		5.000E+00 3.58850E+ 6.000E+00 \$17290E+
IB5 0.0005.00 Bo/d	Start Time (d)	Linear Send to all	7.000E+00 1.71920E+
10000E+00 04-0	Step Time (d)	C Logarithmic open windows	9.000E+00 1.41720E+ 9.000E+00 1.12930E+
IR6 0.000E+00 Bq/d	Sub time (u) //	C 1-2-5 mode	
IR7 0.000E+00 Bq/d	Specify Collection Periods [Col 2]		(• Graph C Table C Hide White body
IR8 0.000E+00 Bq/d		Send>	
IR9 8.284E+03 Bq/d	Calculate Bioassay Quantity [Col 3]		
IP10 A 2005 CO. Rold		Start Calculation	-/ I
14.733E+U3 04/0			1E+05
	000		5E+04 - , , , , , , ,
Progress Indicator			0 7 14 21 28
Deposition			C Graph C Table @ Hide
Collating Times			
Bioassay Calcs			
Current			
		<u>D</u> K	
H-3	fax Likelihood fit		

<u>Figure 4.128.</u> The amount of intake calculated to have given rise to each successive bioassay measurement on the assumption of constant chronic intake over the corresponding sampling interval.

The resulting values of committed effective dose calculated for all 7 monitoring periods in this example (assuming constant chronic intake over the corresponding sampling interval) are shown in Table 4.8.

Table 4.8. Total committed effective doses calculated for each monitoring period.

<u>Total Committed Effective</u>
Dose (µSv)
20.0
4.5
8.3
57.0
177
43.1
3.4
13

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<u>Note:</u> These calculated values are very close to (<u>marginally lower</u> than) the values calculated by assuming that the intakes occurred at the mid-point of the corresponding sampling interval. The total committed effective dose is (313 μ Sv) - to be compared with (317 μ Sv) for the "mid-point" assumption (<u>Table 4.7</u>).

This completes the step of calculating doses automatically - assuming that all intakes occurred <u>continuously</u> over the corresponding sampling interval:

• <u>Proceed</u> to a comparison of Automated vs Manual HTO Analysis.

Automated vs Manual HTO Analysis

In this section we:

- Test the repeatability of the manual "fitting" procedure.
- Examine the effect of using < 10 sampling intervals in the "automated" procedure.
- Compare the "goodness of fit" of the "manual" and "automated" procedures.

1. Repeatability of "Manual" Fitting

The parameter file "<u>Case22 - HTO - JA.ix</u>" contains a solution to this example case that was obtained (by ACJ & Associates, Inc.) independently of the "<u>Case22 - HTO - MP.ix</u>" solution. This independent solution is shown in Figure 4.129.



Figure 4.129. A second solution of the tritium routine monitoring example case.

Table 4.8 shows the 10 discrete intakes fitted to the bioassay data - $\underline{c.f.}$, the results of the earlier solution (<u>Table 4.6</u>).

Table 4.8.	Discrete intake calculated from the tritium urinalysis data.
------------	--------------------------------------------------------------

Intake regime	Assumed timing	Intake amount/rate (Bq/Bq_d-1)
IR1 - chronic	0 - 20 d	51,330 Bq/d
IR2 - chronic	40 - 155 d	1,860 Bq/d
IR3 - chronic	180 - 280 d	5,495 Bq/d
IR4 - acute	280 d	1,354,000 Bq
IR5 - acute	310 d	1,940,000 Bq
IR6 - chronic	340 - 357 d	61,810 Bg/d
IR7 - chronic	400 - 440 d	5.837 Ba/d
IR8 - acute	418 d	4.977.000 Ba
IR9 - acute	500 d	213,700 Bq
IR10 - chronic	520 - 550 d	1,654 Bq/d

Comparison of the values in Table 4.8 with those in <u>Table 4.6</u> shows substantial differences. However, it is more difficult to detect (by eye) substantial differences (biasses?) in the graphical displays of the corresponding data fits - Figure 4.129 vs <u>Figure 4.111</u>, respectively.

Figure 4.130 shows the committed effective doses calculated from the estimates of intake given in Table 4.8.

👒 Dose Calculations	;									
Elle <u>A</u> dvanced <u>T</u> ools	Help									
Save Quick Save)ose (Calculat	tion	s		
INTAKE		(CALCUL	ATION						DOSE
					>		[C Equiv	€ Eff	Indicator N
IR1 5.133E+04	Bq/d							Target Organs	Cont. to Eff Dose (Sv) IR(1)	Cont. to Eff Cont. Dose (Sv) Dose IR(2) IR(3)
IR2 1.860E+03	Bq/d Cal	culations	WR	WT			_	bb Al	0.00E+00 0.00E+00	0.00E+00 0. 0.00E+00 0.
IR3 5.495E+03	Bq/d	⊢ Se	elect					LN(TH) Esophagus Gonads	0.00E+00 9.38E-07 3.75E-06	0.00E+00 0. 1.95E-07 5 7.82E-07 2
IR4 1.354E+06	Bq		(1) Dose from Inc	dicator Nuclide: I	4(i)-3	•		Spare Remainder	0.00E+00 9.38E-07 1.99E-05	0.00E+00 0. 1.95E-07 5 3.91E-06 1
IR5 1.940E+06	Bq		(2) Dose from As	sociated Radior		Г		C Enix	C 54	
IR6 1.916E+04	89/0	C Eff							Associated had	
IR7 5.837E+03	89/8		(o) Announ Comm	and boats		,*				
1P0 4.977E+06	Pa			Effe	ctive Dose (S	v]				
IP10 10.000	Paid		Calculate	1.9	Æ-04					
INTO 1.654E+03	ρψu									
		0	00				_			
Progress Indicator							i r			Annual Commit
(1)									Eff Dose from	Effective
(2)								Year	H(i)-3 (IN) (Sv)	Dose (Sv) Total
(3)								1986	1.98E-05	1.98E-05
Current						^		1987	1.74E-04 5.24E-06	1.74E-04 5.24E-06
Uperation	Intake Regime 1: Apply splitting rule will not app	ing Splitting Rul ly. Equivalent D	le to Esophagus.) ose to remainde	This is already a ris 1.88E-05. Ma	named organ ss weighted r	n so the remainder		TOTAL	1.99E-04	1.99E-04
						<u>D</u> K		< 111		
н-з	WR=ICRP Defaults	WT=ICR	IP 68	ICRP H(i) Mo	del					

Figure 4.130. Dose calculated from the second solution of the tritium routine monitoring example case.

ĨШ 8	<u>Note #1:</u> The total committed effective dose calculated in this second solution (199 μ Sv) is less than half the value (479 μ Sv) calculated in the earlier solution.
Name 1	<u>Note #2:</u> However, the <u>average</u> of the two independent estimates of total committed effective dose is <u>339 µSv</u> (<u>± 198 µSv</u> standard deviation). This is within <u>8%</u> of the <u>average</u> value (<u>315 µSv</u>) obtained using the " <u>automated</u> " fitting procedure!

2. Effect of using Fewer Sampling Intervals in the "Automated" Procedure

In order to examine the effect of using fewer sampling intervals in the automated analysis, we repeated the <u>Automated Tritium Intake Estimation</u> (and <u>Dose Calculation</u>) using 13 sets of 5 measured values (rows of data) - instead of 6 sets of 10 values plus a residual set of 5 values. The resulting calculated doses are shown in Table 4.9. They are to be compared with those shown in <u>Table 4.7</u> (where the monitoring period was divided into seven parts). In both cases, it was assumed that intakes occurred at the <u>mid-point</u> of the corresponding sampling interval.

	Total Committed Effective
Monitoring period (d)	<u>Dose (µSv)</u>
#1: 0 - 35	19.9
#2: 35 - 70	4.7
#3: 70 - 119	3.6
#4: 119 - 161	1 9
#5: 161 - 196	19
#6: 196 - 259	7 4
#7: 259 - 301	25.5
#8: 301 - 343	40.9
#9: 343 - 392	11.3
#10: 392 - 427	168
#11: 427 - 476	37.7
#12: 476 - 259	8.2
#13: 518 - 518	3.5
<u> Total: 0 - 553</u>	<u>334</u>

Table 4.9. Total committed effective dose calculated for each monitoring period.

Note #1: The total committed effective dose (<u>334 μ Sv</u>) shown in Table 4.9 is <u>higher</u> (by 5%) than the value (<u>317 μ Sv</u>) obtained earlier - when we analyzed larger sets (<u>6 ´ 10 + 1 ´ 5</u>) of bioassay data.

Note #2: This observation is consistent with our earlier Important Note that the analysis of a small series of tritium sample values tends to <u>over-estimate</u> the total intake (and thus dose). If previous intake has occurred (within a month-or-so), the value of intake calculated for the first sampling interval of a new set will ALWAYS over-estimate the actual intake value (assuming no bias in the "time of intake" model, since there will always be some "carry-over" of tritium activity from the previous intake. The amount of this "un-corrected" carry-over decreases with each subsequent sample. Therefore, the more sample values included in the set, the <u>smaller</u> the resulting <u>over-estimate</u> for the set as a <u>whole</u>. It follows that the earlier analysis (using the maximum number of sample values in each set) should have given a less biassed estimate of total intake (and committed dose) than this analysis carried out with only 5 sample values in each set.

3. "Goodness of Fit" Comparison between "Automated" and "Manual" Procedures

Table 4.10 summarizes the estimates of effective dose committed over the whole (553-d) monitoring period - comparing the results of both manual fitting exercises and both "automated" fits. The table also shows the total value of **c**2_calculated in each case by comparing the "predicted" and "observed" values of the bioassay quantity.

Case Analysis: Intake Assumption	Estimated Effective Dose c2-sum			
Manual (Whole Dataset):				
MP	479	56.9		
JA	199	55.7		
<u>Automated (6 10 + 1 5):</u>				
"Mid-point"	317	25.2		
"Continuous"	313	25.2		
Automated (13 5):				
"Mid-point"	334	24.4		
"Continuous"	331	24.4		

Table 4.10.	Comparison of estimated total committed doses and the associated c2	<u>2</u> -
sum_statistic.		

The points to note from Table 4.10 are:

- The "Manual" analyses (of the whole dataset) differed only <u>marginally</u> in their "goodness of fit" <u>i.e.</u>, the respective **c2**-sum_statistics were 56.9 and 55.7 (for 10 intakes fitted to 65 data points) and yet the resulting estimates of total committed dose differed by a <u>large</u> factor (2.4).
- The "Automated" analyses can (and do) fit a larger number of discrete intakes to the dataset as a whole thus there are fewer "degrees of freedom" with the result that the c2_values are substantially smaller.
- With these example data (from routine weekly monitoring), the assumed time of occurrence of intake ("mid-point" or "continuous") makes very little difference (less than 2%) to the calculated values of committed dose and no overall difference to the c2 statistic.
- The (5% lower) value of total committed dose calculated using bioassay values 10-at-atime (the maximum number) is likely to be <u>more accurate</u> (less biassed) than value obtained by analyzing bioassay values 5-at-a-time.

Note: This topic should be studied further using Monte Carlo methods to simulate complex tritium intake patterns - and the resulting variability in the bioassay sample values. The applicability and performance of the "Tritium Tool" provided here should thus be examined further.

Dose Calculations for Causation -Requires Add-On 9



Health

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Note: The case example below is taken from IMBA Expert[™] OCAS-Edition. It relates specifically to the application of calculated annual tissue doses rotection in that software to the U.S. Department of Labor's compensation program for former workers at atomic weapons sites. The implementation of annual dose calculations in IMBA Professional Plus is modified from that in IMBA Expert[™] OCAS-Edition. This decsriptive material will be updated in due course by the U.K. Health Protection Agency - Radiation Protection Division (HPA-RPD), as appropriate specifically to the IMBA Professional Plus implementation.

IMBA Expert[™] OCAS-Edition was designed specifically to meet NIOSH's requirements under the Energy Employees' Occupational Illness Compensation Program Act (EEOICPA). In particular, the software is customized to do the following:

- 1. Provide all of the capabilities of the IMBA Expert[™] USDOE-Edition (Phase 11) software for analyzing bioassay data and estimating the most likely intake(s) of radionuclides, as described in previous sections of this User Manual. The software is designed to provide the means for initial input of bioassay data via the built-in Table Tool - for each individual claimant whose internal exposure is to be assessed.
- 2. <u>Calculate equivalent doses received by specified target organs and tissues in each</u> Calendar Year - from the start of a claimant's qualifying occupational exposure through to the date(s) of diagnosis of the claimant's gualifying cancers.
- 3. Import claimant-specific information in a standardized format from the 'Initiation file' (*.ini) generated by Oak Ridge Associated Universities Inc.'s (ORAU's) Energy Employees Ocupational Illness Compensation Program Dose Reconstruction Project.
- 4. Interface with the Interactive RadioEpidemiological Program (NIOSH-IREP) for calculation of the probability distribution of cancer causation.

Important Note: IMBA Professional Plus was designed to function best in the above listed order - for each internal dose assessment, *i.e.*, (1) carry out the bioassay data analysis and assessment of intake(s), then (2) 'merge' the calculated annual equivalent doses with the externally generated claimant case data (in the form of a standard Initiation file - '*.ini') - in order to (3) produce a complete case report suitable for <u>direct</u> input into 'FeedIREP'.

Dose Calculations for NIOSH-IREP

We will use here the example bioassay data analysis for the IAEA (1999) whole -body activity measurements of 60Co (Annex IV Case 3) to illustrate the calculation of annual equivalent doses to designated target organs in relation to a hypthetical diagnosis of cancer. Figure 9.1 shows the Main Screen of IMBA Expert[™] OCAS-Edition after opening the file [Install Drv]:\\JABASOFT\IMBAEXUS\UserData1\Demo\IAEA Case 3 - 60Co.ix.



Important Note: NIOSH-IREP_requires calculated annual equivalent doses to be experessed in <u>centi-Sv</u> (<u>cSv</u>), <u>i.e.</u>, in the traditional dose unit '<u>rem</u>'. Therefore, it is IMPORTANT to ensure that you have <u>selected</u> 'rem' as the dose unit (in the Main Screen) - as shown in Figure 9.1.

In this example case, the most likely intake was calculated to be 9,805 Bq - by inhalation of a 1- μ m AMAD aerosol of 'Type M' <u>60</u>Co on February <u>24th</u>, <u>1988</u>. To calculate the annual equivalent doses received by all target organs or tissues:

• <u>click the "Dose Calculations" button - to open the Dose Calculations screen.</u>

file://C:\Documents%20and%20Settings\Administrator\Local%20Settings\Temp\~hh...

• <u>click the "ORG DOSE Calendar" button - to open the 'Equivalent Dose to selected organ</u> received in each calendar year' window (Figure 9.2).

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Figure 9.2. Opening the 'Equivalent Dose to selected organ received in each calendar year' window.





of the software will enable annual doses for a time-span of up to 70 y to be calculated (in a single step).

Note #4: The selected '<u>tissue weighting factors</u>' - shown in the 'Status Bar' (Figure 9.2) do NOT affect the calculated values of <u>equivalent dose</u>. These apply ONLY to the calculation of <u>effective dose</u>.

Proceed to "Example Annual Dose Calculation".

Example Annual Dose Calculation

We will assume for this example (<u>IAEA Case 3 - 60Co.ix</u>):

- that the (hypothetical) claimant data file defines the diagnosed cancer as "<u>Cancer1=Stomach (151)</u>";
- that the (hypothetical) claimant data file defines the '<u>Date of Diagnosis</u>' as "<u>Cancer1DiagnosisDate=02/25/1997</u>".

The corresponding data values in the <u>'Equivalent Dose to selected organ received in each</u> calendar year' are shown in Figure 9.3.

			STOMACH	_
Calendar Year	Start Date	End Date	Equivalent Dose (rem)	
1988	01/01/1988	01/01/1989	0.000E+00	-
1989	01/01/1989	01/01/1990	0.000E+00	
1990	01/01/1990	01/01/1991	0.000E+00	
1991	01/01/1991	01/01/1992	0.000E+00	
1992	01/01/1992	01/01/1993	0.000E+00	
1993	01/01/1993	01/01/1994	0.000E+00	
1994	01/01/1994	01/01/1995	0.000E+00	
1995	01/01/1995	01/01/1996	0.000E+00	
1996	01/01/1996	01/01/1997	0.000E+00	
1997	01/01/1997	2/25/1997	0.000E+00	
End Year	1388 -		Stomach Split doses into components	
	Apply		2 /25/1997 Export Results	
			To Cipboard	
Progress Indica	ator		ToElle]

Figure 9.3. Settings of 'Equivalent Dose to selected organ received in each calendar year' window for hypothetical case of stomach cancer.

To calculate the total annual equivalent doses, you simply click the 'Start Calculation' button. The resulting values are shown (in 'rem') in Figure 9.4.

			STOMACH	
Calendar Year	Start Date	End Date	Equiva	alent Dose (rem)
1988	01/01/1988	01/01/1989		2.645E-03
1989	01/01/1989	01/01/1990		7.170E-04
1990	01/01/1990	01/01/1991		3.313E-04
1991	01/01/1991	01/01/1992		1.984E-04
1992	01/01/1992	01/01/1993		1.256E-04
1993	01/01/1993	01/01/1994		7.987E-05
1994	01/01/1994	01/01/1995		5.102E-05
1995	01/01/1995	01/01/1996		3.260E-05
1996	01/01/1996	01/01/1997		2.088E-05
1997	01/01/1997	2/25/1997		2.404E-06
EndYear	1997		Stomach	Components
	Apply		2 /25/1997	Start Calculation
				ToCipboard
Promess Indic	ator			To <u>F</u> ile

Figure 9.4. Total annual equivalent doses displayed for the stomach wall.

To 'split' the annual equivalent doses into separate alpha, beta, and gamma components, you simply check the 'Split doses into components' box before clicking the 'Start Calculation' button. The resulting 'split' values are shown (in 'rem') in Figure 9.5.

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			STON	ACH			
Calendar Year	Start Date	End Date	Alpha Dose (rem)	Beta Dose (rem)	e Gamma Dose Gamma Dose (rem) (rem) <30keV 30-250keV		Gamma Dose (rem) >250keV
1988	01/01/1988	01/01/1989	0.000E+00	8.803E-05	4.450E-10	0.000E+00	2.557E-03
1989	01/01/1989	01/01/1990	0.000E+00	4.493E-05	3.012E-10	0.000E+00	6.720E-04
1990	01/01/1990	01/01/1991	0.000E+00	2.858E-05	1.912E-10	0.000E+00	3.028E-04
1991	01/01/1991	01/01/1992	0.000E+00	1.826E-05	1.221E-10	0.000E+00	1.802E-04
1992	01/01/1992	01/01/1993	0.000E+00	1.169E-05	7.818E-11	0.000E+00	1.140E-04
1993	01/01/1993	01/01/1994	0.000E+00	7.446E-06	4.979E-11	0.000E+00	7.242E-05
1994	01/01/1994	01/01/1995	0.000E+00	4.758E-06	3.182E-11	0.000E+00	4.626E-05
1995	01/01/1995	01/01/1996	0.000E+00	3.041E-06	2.034E-11	0.000E+00	2.956E-05
1996	01/01/1996	01/01/1997	0.000E+00	1.948E-06	1.302E-11	0.000E+00	1.893E-05
1997	01/01/1997	2/25/1997	0.000E+00	2.242E-07	1.500E-12	0.000E+00	2.180E-06
End Year	1997		Stomach	•	K	 Split doses in components 	WR
△pply Date of Diagnosis Start Calculation 2 /25/1997 ▼						ion	
						To <u>C</u> lipboar	в
Progress Indicator To Ele							

Figure 9.5. 'Split' components of annual equivalent doses displayed for the stomach wall.

Important Note: The values of radiation weighting factor used by IMBA Expert[™] OCAS-Edition to calculate the annual equivalent dose are shown by clicking the 'WR' button (Figure 9.5). These 'standard' values (Figure 9.6) are those currently required by NIOSH-OCAS - and MUST NOT be changed. The <u>NIOSH-IREP program</u> automatically applies the required pre-defined 'weighting' distributions (as multipliers) to evaluate the corresponding uncertainty distributions of equivalent dose.

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🖻 Radiatio	on Weighting 🔳 🗖 🔀						
These weighting factors will be used for the calculation of equivalent doses to each target organ when the 'Split Doses into Components' option is checked. These weights apply to compensation calculations only.							
Enter WR:	3						
20	Alpha						
1	Beta						
1	Gamma (< 30 MeV)						
1	Gamma (30-250 MeV)						
1	Gamma (>250 MeV)						
<u>k</u>	Cancel						

Figure 9.6. Standard values of radiation weighting factor used to calculate 'split' annual equivalent doses.

ore impaired	Important Note: IMBA Expert [™] OCAS-Edition (Version 3.2) calculates annual
22 ===	equivalent doses ONLY for the Indicator Nuclide. Annual doses from
	any Associated Radionuclide(s), must be calculated separately for the
	corresponding intake amount(s) - and intake regimes -
	and <u>summed</u> (year-by-year) before entry into the <u>NIOSH-IREP program</u> .

- <u>See 'Summing Annual Doses from Multiple Radionuclides' by exporting results to a</u> <u>spreadsheet via the Windows clipboard.</u>
- Proceed to "How to Use the '*.ini' File".

Summing Annual Doses Calculated for Associated Radionuclides

Equivalent I	Dose to selec	ted organ re	eceived in e	ach calenda	r year		Ē
			STON	ACH			
Calendar Year	Start Date	End Date	Alpha Dose (rem)	Beta Dose (rem)	Gamma Dose (rem) <30keV	Gamma Dose (rem) 30-250keV	Gamma Dose (rem) >250keV
1988	01/01/1988	01/01/1989	0.000E+00	8.803E-05	4.450E-10	0.000E+00	2.557E-03
1989	01/01/1989	01/01/1990	0.000E+00	4.493E-05	3.012E-10	0.000E+00	6.720E-04
1990	01/01/1990	01/01/1991	0.000E+00	2.858E-05	1.912E-10	0.000E+00	3.028E-04
1991	01/01/1991	01/01/1992	0.000E+00	1.826E-05	1.221E-10	0.000E+00	1.802E-04
1992	01/01/1992	01/01/1993	0.000E+00	1.169E-05	7.818E-11	0.000E+00	1.140E-04
1993	01/01/1993	01/01/1994	0.000E+00	7.446E-06	4.979E-11	0.000E+00	7.242E-05
1994	01/01/1994	01/01/1995	0.000E+00	4.758E-06	3.182E-11	0.000E+00	4.626E-05
1995	01/01/1995	01/01/1996	0.000E+00	3.041E-06	2.034E-11	0.000E+00	2.956E-05
1996	01/01/1996	01/01/1997	0.000E+00	1.948E-06	1.302E-11	0.000E+00	1.893E-05
1997	01/01/1997	2/25/1997	0.000E+00	2.242E-07	1.500E-12	0.000E+00	2.180E-06
Start Year End Year	1988		Stomach	-	R	Split doses in components	WR
△pply Date of Diagnosis Start Calculation 2 /25/1997 ▼ To _lipboard							
Progress Indicator To File							
			<u>O</u> K	Ça	ncel		

Figure 9.7. The 'Export Results - To <u>Clipboard' button</u>.

<u>Clicking</u> the Export Results - To <u>Clipboard'</u> button (Figure 9.7) <u>copies</u> the displayed table of calculated annual equivalent doses to the Windows® clipboard. These data can then be pasted into any Windows® spreadsheet (or database) application - as in Figure 9.8.

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	🛅 🔄 🖄 🖾 🏷 🖉 🖳 📭 Y Reply with Changes End Review									
	F22 ▼ fx									
	A	В	С	D	E	F	G	Н		
1	Equivalent	Doses calo	culated to: S	STOMACH						
2	1988	1/1/1988	1/1/1989	0.00E+00	8.80E-05	4.45E-10	0.00E+00	2.56E-03		
3	1989	1/1/1989	1/1/1990	0.00E+00	4.49E-05	3.01E-10	0.00E+00	6.72E-04		
4	1990	1/1/1990	1/1/1991	0.00E+00	2.86E-05	1.91E-10	0.00E+00	3.03E-04		
5	1991	1/1/1991	1/1/1992	0.00E+00	1.83E-05	1.22E-10	0.00E+00	1.80E-04		
6	1992	1/1/1992	1/1/1993	0.00E+00	1.17E-05	7.82E-11	0.00E+00	1.14E-04		
7	1993	1/1/1993	1/1/1994	0.00E+00	7.45E-06	4.98E-11	0.00E+00	7.24E-05		
8	1994	1/1/1994	1/1/1995	0.00E+00	4.76E-06	3.18E-11	0.00E+00	4.63E-05		
9	1995	1/1/1995	1/1/1996	0.00E+00	3.04E-06	2.03E-11	0.00E+00	2.96E-05		
10	1996	1/1/1996	1/1/1997	0.00E+00	1.95E-06	1.30E-11	0.00E+00	1.89E-05		
11	1997	1/1/1997	2/25/1997	0.00E+00	2.24E-07	1.50E-12	0.00E+00	2.18E-06		
12										
13										
14										
15										

Figure 9.8. Calculated 'split' annual equivalent doses imported into a spreadsheet.

The Windows® spreadsheet (or database) application can be used to <u>add</u> the annual doses calculated (separately) for ALL <u>Associated Radionuclides</u>. The resulting total annual equivalent doses can then be copied and pasted directly into the <u>NIOSH-IREP input file</u> - by-passing part of the function of '<u>FeedIREP</u>'.

As an alternative to copying the calculated results directly to a Windows ® spreadsheet (or database) application (using the Windows® clipboard), you can export the calculated data table to an ASCII (*.txt) file.

- Proceed to "Exporting to an ASCII Data File".
- Proceed to "How to Incorporate the '*.ini' File Data".

Exporting to an ASCII Data File

👒 Dose Calo	culations											
File Advance	d Tools Hel	þ										
		DRG DOSE				Dos	e Calo	ulatio	ns			
Save Qu		alendar		💐 Equivalent (ose to selec	ted organ r	eceived in e	ach calenda			1	×
IN	TAKE											
							STON	ACH				N COL N
IP1 Page	Pa			Calendar Year	Start Date	End Date	Alpha Dose (rem)	Beta Dose (rem)	Gamma Dose (rem) <30keV	Gamma Dose (rem) 30-250keV	Gamma Dose (rem) >250keV	
9.805	5E+03 04		-	1988	01/01/1988	01/01/1989	0.000E+00	8.803E-05	4.450E-10	0.000E+00	2.557E-03	
			Calcu	1989	01/01/1989	01/01/1990	0.000E+00	4.493E-05	3.012E-10	0.000E+00	6.720E-04	
				1990	01/01/1990	01/01/1991	0.000E+00	2.858E-05	1.912E-10	0.000E+00	3.028E-04	
				1991	01/01/1991	01/01/1992	0.000E+00	1.826E-05	1.221E-10	0.000E+00	1.802E-04	
				1992	01/01/1992	01/01/1993	0.000E+00	1.169E-05	7.818E-11	0.000E+00	1.140E-04	
				1993	01/01/1993	01/01/1994	0.000E+00	7.446E-06	4.979E-11	0.000E+00	7.242E-05	
				1994	01/01/1994	01/01/1995	0.000E+00	4.758E-06	3.182E-11	0.000E+00	4.626E-05	
				1995	01/01/1995	01/01/1996	0.000E+00	3.041E-06	2.034E-11	0.000E+00	2.9568-05	
				1995	Export	wizard					2.1005-06	
				1557							2.1002-00	
					How do y	ou want to expo	it the data ?					Rac
					G Lui	not to owned the	12A as at stel	The second of the				
				Select Calenda		ant to export the	data to an ASU	an (*.ox) text in		.		
				Charles View	0.1%	ant to export the		Ison Elikoel spre	adsmoet (*.xis) nie	· -		
				Start Year	© I w	ant to export the	data to an Imb	a Expert (*.rpt) I	ile for FeedIREP	in	to	
										\$	-	
				End Year	< <u>B</u> ack	. <u> </u>	lext>		<u> </u>	ancel	WR	
						_	Date of Diagno	sis				
					Apply		-			Start Calcula	tion	
			_				2 /25/199	7 👻	Expo	rt Results		
Progress	Indicator							_				
m										To <u>C</u> lipboar	rd 🛛	
										To Edu	_	
(2)				Progress Indica	ator					TOTIC		
(3)												
Current	. [1			
							<u>o</u> k	<u>C</u> a	ncel			
								<u>о</u> к				
Co-60	V	VR=ICRP Def	aults	WT= 10 CFR 835	ICRE	^o Co Model			,			
				1								

Figure 9.9. Opening the 'Export Wizard'.

IMBA Professional Plus **provides an 'Export Wizard' (Figure 9.10) that is opened in the 'Equivalent Dose to selected** organ received in each calendar year' window. This enables the calculated annual doses to be exported to:

- an ASCII (*.txt) file, or;
- an IMBA Expert (*.rpt) file for 'FeedIREP'.

Exporting to an ASCII (*.txt) File

With the 'I want to export the data to an ASCII (*.txt) text file' option checked (the default), <u>clicking</u> the '<u>Next</u>' button opens 'Please specify the name and location of the ASCII file you want to create' <u>browse</u> option in the ' Export Wizard' (Figure 9.10).



Figure 9.10. Specifying the name and location of the ASCII (*.txt) output text file.

You simply <u>browse</u> to the folder where you want to store the output (*.txt), and <u>name</u> the file. <u>Clicking</u> the '<u>Next</u>' button enables you to <u>select</u> the type of <u>text delimiter</u> that you want to use (Figure 9.11).

💐 Export wizard	1			
Please select the te C Comma separate C Other delimiter	xt delimiter you wa ed 🕞 Tab	nt to use : o delimited	C Spa	ce delimited
< <u>B</u> ack	<u>F</u> inish			<u>C</u> ancel

Figure 9.11. Selection of a 'Tab delimited' output (*.txt) file.

In this example we have selected a 'Tab delimited' output file. <u>Clicking</u> the '<u>Finish</u>' button completes the data export process. Successful export of the data will be confirmed (Figure 9.12), and <u>clicking</u> the 'View File ...' button will <u>display</u> the resulting (*.txt) file (Figure 9.13) in NotePad®.

🐴 Export wizard	
The export process has been completed successfully !	
View File	
(<u>o</u> k

Figure 9.12. Confirmation of successful data export to a (*.txt) file.

00

Edic Format View Help Equivalent Doses calculated to: STOMACH Calendar Year Start Date End Date Alpha Dose (rem) Beta Dose (rem) Beta Dose (rem) Gamma Dose (rem) 1988 01/01/1988 01/01/1989 01/01/1989 01/01/1989 0.000E+00 1989 01/01/1989 01/01/1980	🗖 IAEA	Case 3	- 60Co	- Outpu	t Text File.txt -	Notepad					[×
Equivalent Doses calculated to: STOMACH Calendar Year Start Date End Date Alpha Dose (rem) Beta Dose (rem) Gamma Dose (rem) 1988 01/01/1988 01/01/1989 0.000E+00 8.803E-05 4.450E-10 0.000E+00 1989 01/01/1989 01/01/1990 0.000E+00 4.493E-05 3.012E-10 0.000E+00	Ele Ed	it Forma	at ⊻jew	Help									
1990 01/01/1990 01/01/1991 0.000E+00 2.858E-05 1.912E-10 0.000E+00 1991 01/01/1991 01/01/1992 0.000E+00 1.826E-05 1.221E-10 0.000E+00 1 1992 01/01/1992 0.000E+00 1.826E-05 1.221E-10 0.000E+00 1 1993 01/01/1993 01/01/1994 0.000E+00 7.446E-06 4.979E-11 0.000E+00 1 1994 01/01/1994 0.000E+00 7.446E-06 3.182E-11 0.000E+00 1 1995 01/01/1995 0.000E+00 4.758E-06 3.182E-11 0.000E+00 1 1995 01/01/1995 0.000E+00 3.041E-06 2.034E-11 0.000E+00 1 1995 01/01/1997 0.000E+00 1.948E-06 1.302E-11 0.000E+00 1 1996 01/01/1997 0.000E+00 2.242E-07 1.500E-12 0.000E+00 1 1997 01/01/1997 2/25/1997 0.000E+00 2.242E-07 1.500E-12 0.000E+00 1	Equiva Calent 1988 1989 1991 1991 1993 1994 1995 1996 1997	alent dar Ye 01/ 01/ 01/ 01/ 01/ 01/ 01/ 01/	Doses ar S 01/198 01/198 01/199 01/199 01/199 01/199 01/199 01/199 01/199	calcul tart D 9 0 1 2 3 4 5 6 6 7	ated to: STO ate End 01/01/1989 01/01/1990 01/01/1991 01/01/1993 01/01/1994 01/01/1994 01/01/1995 01/01/1997 2/25/1997	MACH Date 0.000E+ 0.000E+ 0.000E+ 0.000E+ 0.000E+ 0.000E+ 0.000E+ 0.000E+ 0.000E+	Alpha 00 00 00 00 00 00 00 00 00 00	Dose (rem) 8.803E-05 2.858E-05 1.826E-05 7.446E-06 4.758E-06 3.041E-06 1.948E-06 2.242E-07	Beta Dose 4.450E-10 3.012E-10 1.912E-10 7.818E-11 4.979E-11 3.182E-11 2.034E-11 1.302E-11 1.500E-12	(rem)	Gamma Dose 0.000E+00 0.000E+00 0.000E+00 0.000E+00 0.000E+00 0.000E+00 0.000E+00 0.000E+00 0.000E+00 0.000E+00	(rem)	~

-igure 9.13. Resulting (^.txt) file displayed in NotePad®.

Note: The exported (*.txt) file contains only the results of the last -performed calculation of annual equivalent doses. You will have to <u>add</u> other information, such as the identity of the <u>indicator nuclide</u>, or other case details. IMBA Professional Plus **can** add **such case information automatically - in a file format that can be** fed directly **to** 'FeedIREP' - see "Input '*.ini' File" and "Incorporating the '*.ini' File Data".

The Input '*.ini' File - and How to Use It

Example Cases - Bioassay & Dosimetry

```
; IMBA/IREP COnfiguration File
: Introductory Header
; This configuration file is used by the IMBA and FeedIREP programs
to provide
; case header information which will be used to populate selected
fields in
; the applications, and set defaults for various controls within
the programs,
; such as check buttons.
; NOTICE: The information contained in this file is protected by
; Privacy Act 5 USC Section 552a; disclosure to any third party
without
; the written consent of the individual to whom the information
pertains
; is strictly prohibited.
[Claimant Information]
NIOSHID=999999
FirstName=John
MiddleName=C.
LastName=Smith
SSN=111-22-3333
DOB=02/25/1950
Gender=M
DOLOffice=DE
SmokingHistory=Never Smoked
Ethnicity=White-Non-Hispanic
Cancerl=Stomach (151)
CancerlDiagnosisDate=02/25/1997
CancerlRank=1
[General Details]
AdministrativeDetails=T
SoftwareVersion=T
ParameterFilename=T
[Input Information]
IndicatorRadionuclide=T
AssociatedRadionuclide=F
IntakeRegimes=T
ModelParameters=T
MeasurementData=T
RadiationWeightingFactors=F
TissueWeightingFactors=F
[Results of Calculations]
Intakes=T
BioassayResults=T
[Indicator Radionuclide]
EquivalentDoses=F
EffectiveDoses=F
[Associated Radionuclides]
EquivalentDoses=F
EffectiveDoses=F
[Calendar Year Doses]
EquivalentDoses=T
```

Figure 9.14. Standard 'Case Configuration File' (*.INI) used to import Case Information into IMBA Professional Plus

The detailed specification of the data fields in the 'Case Configuration File' (*.ini) is Proprietary to Oak Ridge Associated Universities, Inc. and MJW Corporation Inc. This specification was incorporated into IMBA Professional Plus, to enable the software to import all of the claimant-specific information in the precise form needed to pass through to the <u>NIOSH-IREP</u> program.

Figure 9.14 shows the general layout of the '*.INI' file. We describe here how to import this file into IMBA Professional Plus.



• Proceed to "Incorporating the '*.ini' File Data".

Incorporating the '*.ini' File Data

💐 Equivalent Dose to selected organ received in each calendar year × STOMACH Gamma Dose Gamma Dose Gamma Dose Alpha Dose Beta Dose Calendar Year Start Date End Date (rem) <30keV (rem) 30-250keV [rem] (rem) >250keV 1988 01/01/1988 01/01/1989 0.000E+00 8.803E-05 4.450E-10 0.000E+00 2.557E-03 1989 01/01/1989 01/01/1990 0.000E+00 4.493E-05 3.012E-10 0.000E+00 6.720E-04 1990 01/01/1990 01/01/1991 0.000E+00 2.858E-05 1.912E-10 0.000E+00 3.028E-04 1991 01/01/1991 01/01/1992 0.000E+00 1.826E-05 1.221E-10 0.000E+00 1.802E-04 1992 01/01/1992 01/01/1993 0.000E+00 1.169E-05 7.818E-11 0.000E+00 1.140E-04 1993 01/01/1993 01/01/1994 0.000E+00 7.446E-06 4.979E-11 0.000E+00 7.242E-05 1994 01/01/1994 01/01/1995 0.000E+00 4.758E-06 3.182E-11 0.000E+00 4.626E-05 1995 01/01/1995 01/01/1996 0.000E+00 3.041E-06 2.034E-11 0.000E+00 2.9568-05 1996 1.893E-05 💐 Export wizard 1997 2.180E-06 How do you want to export the data ? C I want to export the data to an ASCII (".txt) text. file Select Calend C I want to export the data to a Microsoft Excel spreadsheet (*.xis) file Start Year (*) I want to export the data to an Imba Expert (*.rpt) file for FeedIREP End Yea WR Next> Cancel Date of Diagnosis Start Calculation Apply 2 /25/1997 Ŧ Export Results To Clipboard To File Progress Indicator 0K Cancel

Figure 9.15. Using the 'Export Wizard' to export data directly to a (*.rpt) file - formatted for 'FeedIREP'.

The '<u>Export Wizard</u>' enables you to export calculated annual equivalent doses to a (<u>*.rpt</u>) file that is formatted for <u>direct</u> input into '<u>FeedIREP</u>' (Figure 9.15). This method of exporting the calculated results has two advantages:

- 1. Personal information about the claimant (from the approved <u>standard</u> format Initiation file '*.ini') is <u>automatically</u> combined with the calculated doses in the output (*.rpt) file.
- 2. ALL details of the intake and dose assessment that you have performed can also

be automatically included (and thus recorded) in the (*.rpt) file.

<u>Checking</u> the 'I want to export the data to an IMBA Expert (*.rpt) file for FeedIREP' and <u>clicking</u> the '<u>N</u>ext ' button (Figure 9.15) opens the Export Wizard's 'Browse' dialog box (Figure 9.16). Use this to find, and load, the required Initiation file (*.ini). In this example, we are using the file "C:\JABASOFT\IMBAEXUS\UserData1\11122333_Co60.ini".

💐 Export wizard								
Please supply the Initialization file (*.ini) for this claimant:								
C:\JABASOFT\IMBAEXUS\UserData1\Demo\11122333_Co60.ini								
(Note: The .rpt file will be created with the same name and location as the .ini file)								
< <u>B</u> ack <u>N</u> ext>	<u>C</u> ancel							

Figure 9.16. Browsing to locate the Initiation file (*.ini).



Once you have located the '*.ini' file, <u>clicking</u> '<u>N</u>ext' in the 'Export Wizard' will ask you "How do you want to configure the *.rpt file?" (Figure 9.17). The <u>default</u> option is "Automatically" - and this is RECOMMENDED for compatibility with 'FeedIREP'.

🐴 Export wizard							
How do you want to configure the *.rpt file ?							
 Automatically - Use the default layout specified by the .ini file (RECOMMENDED). 							
Manually - Let me review the layout specified by the .ini file.							
-							
< <u>B</u> ack <u> </u>	<u>C</u> ancel						

Figure 9.17. Default option for "Automatically" configuring the '*.rpt' file.

<u>Clicking</u> '<u>F</u>inish' will complete the export process. The resulting '*.rpt' file can be <u>viewed</u> by clicking the 'View File ...' button (Figure 9.18.).



Figure 9.18. Confirmation of successful export of a '*.rpt' file.



Standard-format Output to 'FeedIREP'

bit122332_Co60.rpt - Notepad bit Edit Format Yow teb Report Generated by INBA Expert OCAS-Edition on 3/24/2004 report Generated by INBA Expert OCAS-Edition of Generated by Information of Generated by Inform

Figure 9.19. '<u>11122333_Co60.rpt</u>' file produced for the example case - as viwed in NotePad®.

The complete '<u>11122333 Co60.rpt</u>' file listing is:

```
Report Generated by IMBA Expert OCAS-Edition on 3/24/2004
Report Filename is C:\JABASOFT\IMBAEXUS\UserData1\Demo\11122333_Co60.rpt
ADMINISTRATIVE DETAILS
NAME: John C. Smith
Date of Birth: 02/25/1950
Employee ID:
Employee SSN: 111-22-3333
Sex: Male
Case ID: 999999
File Name Prefix:
Case Flag:
Description of Case:
Date of Assessment:
Additional Comments:
SOFTWARE VERSION
* * * * * * * * * * * * * * * *
IMBA Expert OCAS-Edition
Issued in Feb 2004
Version number 3.2.00
PARAMETER FILENAME
* * * * * * * * * * * * * * * * * *
All of the parameter values used in this assessment are stored in the following file
C:\JABASOFT\IMBAEXUS\IMBA1\C:\JABASOFT\IMBAEXUS\USERDATA\Demo\IAEA Case 3 -
60Co.ix
INDICATOR RADIONUCLIDE
Radionuclide: Co-60
Halflife: 1924 (d)
INTAKE REGIMES
* * * * * * * * * * * * *
There is only one intake regime
Intake 1 : acute inhalation on day 0
MODEL PARAMETERS
* * * * * * * * * * * * * * * *
The following model parameters are different for each intake regimes
INTAKE REGIME 1
Aerosol/deposition parameters were: User Defined
AMAD = 1 \mu m
GSD = 2.47
```
Density = 3g/cc Shape Factor = 1.5 Worker Type = light Absorption to blood was: Type M Fr= 9.99549977498875E-02 Sr=100 Ss = 0.005Fb=0Sb=0Particle transport parameters were ICRP Defaults AI1 to bb1 = 0.02 $\begin{array}{rrrr} AI2 & to & bb1 &= 0.001 \\ AI3 & to & bb1 &= 0.0001 \\ \end{array}$ <u>AI3 to LNTH = 0.00002</u> <u>bb1 to BB1 = 2</u> <u>bb2 to BB1 = 0.03</u> bbseq to LNTH = 0.01 BB1 to ET2 = 10 BB2 to ET2 = 0.03 BBseq to LNTH = 0.01ET2 tO GI = 100ETseq to LNET = 0.001ET1 out 1

 $\frac{\text{Initial deposition partitioning}}{\text{ETseq/ET2} = 0.0005}$ $\frac{\text{BBseq/BB} = 0.007}{\text{bbseq/bb} = 0.007}$ $\frac{\text{A12/A1} = 0.6}{\text{A13/A1} = 0.1}$

GI-tract parameters were ICRP DefaultsStomach (ST)= 24Small intestine (SI)= 6Upper Large Intestine (ULI)= 1.8Lower Large Intestine (LLI)= 1Absorption to Blood (f1)= 0.1

Biokinetic model parameters were ICRP Co Model Organ/tissue retention functions were as follows:

LIVER

 a(i),
 lam(i)

 -5.2817600000000E-02,
 1.3862900000000E+00

 3.27273000000000E-02,
 1.15525000000000E-01

 1.0084000000000E-02,
 1.15525000000000E-02

 1.0006300000000E-02,
 8.6643400000000E-04

 Fraction to urine
 8.5714300000000E-01

<u>SOFT TISS</u>

a(i), lam(i) -4.7535760000000E-01, 1.3862900000000E+00 2.9454500000000E-01, 1.15525000000000E-01 9.0756300000000E-02, 1.15525000000000E-02 9.0056300000000E-02, 8.6643400000000E-04 Fraction to urine 8.57143000000000E-01

BLOOD

<u>a(i), lam(i)</u> <u>1.00000000000000E+00, 1.3862900000000E+00</u> <u>Fraction to urine 8.57143000000000E-01</u>

Bioassay function for Whole body was Std Co Model a(i), lam(i) 5.301073120979730E-01, 1.00000000000000E+00

<u>3.3973100000000E-01, 1.15525000000000E-01</u> <u>-3.0193600000000E-01, 1.38629000000000E+00</u> <u>2.8646200000000E-01, 1.800000000000E+00</u> <u>1.0118600000000E-01, 1.15525000000000E+00</u> <u>1.0008800000000E-01, 8.66434000000000E-04</u> <u>-5.5639200000000E-02, 1.200000000000E+01</u> Blood retention: 1.0000E-07

_ Bioassay function for Urine was Std Co Model

<u>a(i), lam(i)</u>

-6.676703004002170E-01, 1.200000000000000E+01 6.3387500000000E-01, 1.3862900000000E+00 3.2721900000000E-02, 1.15525000000000E-01 9.99494000000000E-04, 1.15525000000000E-02 7.43176000000000E-05, 8.66434000000000E-04 Blood retention: 1.0000E-07

Bioassay function for Feces was Std Co Model a(i), lam(i) -1.052446700679250E+00, 1.3862900000000E+00

5.3010700000000E-01, 1.0000000000000E+00 5.1563200000000E-01, 1.800000000000E+00 6.5254100000000E-03, 1.1552500000000E-01 1.6945400000000E-04, 1.15525000000000E-02 1.2402100000000E-05, 8.66434000000000E-04 Blood retention: 1.0000E-07

- 2
- _

MEASUREMENT DATA

Whole body data

1. , ,	2720 ,	Real,	272 ,	NORM,	3334.2
6. , ,	1150 ,	Real,	115 ,	NORM ,	<u>1195.9</u>
16. ,	, 1010	, Real	, 101	, NORM	, 1007.7
33. ,	, 790 ,	Real,	79,	NORM ,	<u>828.3</u>
82. ,	, 482 ,	Real,	48.2	, NORM	<u>, 555.59</u>
<u>169. ,</u>	, 358	, Real	, 35.8	, NORM	<u>, 338.12</u>
1009.	, 78	, Real	, 7.8	, NORM	<u>, 37.122</u>
1456.	, 35	, Real	, 3.5	, NORM	<u>, 20.779</u>

During the fitting procedure, the following data were used:

<u>3.15825231481358</u> ,	<u>, 1540</u>
4.63370370370467 ,	<u>, 1278.4</u>
<u>6.79846064814774</u> ,	<u>, 1169.2</u>
<u>9.97454861110964</u> ,	<u>, 1101.1</u>
14.6344097222209 ,	, 1026.9
21.4712499999987 ,	, 939.97
31.5021064814828 ,	, 841.05
46.2191319444428 ,	<u>, 731.49</u>
<u>67.8115972222222 ,</u>	<u>, 614.57</u>
99.4915393518531 ,	, 495.85
145.971585648149 ,	, 380.5
214.165983796298 ,	, 272.57
<u>314.219155092593</u> ,	, 178.78
<u>461.014768518518 ,</u>	, 108.29
676.389756944445 ,	, 63.956
992.382731481484 ,	, 38
<u>1456 , , 20.779</u>	

-

-

INTAKES

-

-

~ ~ ~ ~ ~ ~ ~ ~		~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~		~ ~ ~ ~ ~ ~ ~ ~	~ ~ ~ ~ ~ ~ /		~ ~ ~ ~ ~	~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~	~ ^ ^
year,	alpha,	beta,	gam	ma1,	gamm	ia2,	gamm	<u>a3,</u>	
1988,	0.000E+0	0, 8.80	3E-07,	4.450E	-12,	0.000E+	00,	2.557E-05,	
<u>1989, </u>	0.000E+0	0, 4.49	<u>3E-07,</u>	<u>3.012E</u>	-12,	<u>0.000E+</u>	00,	<u>6.720E-06,</u>	
<u>1990,</u>	0.000E+0	0, 2.85	8E-07,	1.912E	-12,	0.000E+	00,	<u>3.028E-06,</u>	
<u>1991,</u>	0.000E+0	0, 1.82	6E-07,	1.221E	-12,	0.000E+	00,	<u>1.802E-06,</u>	
<u>1992, </u>	0.000E+0	<u>)0, 1.16</u>	<u>9E-07,</u>	7.818E	<u>-13,</u>	0.000E+	00,	<u>1.140E-06,</u>	
<u>1993, </u>	0.000E+0	<u>)0, 7.44</u>	<u>6E-08,</u>	4.979E	<u>-13,</u>	0.000E+	00,	<u>7.242E-07,</u>	
<u>1994, </u>	0.000E+0	<u>)0, 4.75</u>	8E-08,	<u>3.182E</u>	-13,	0.000E+	00,	<u>4.626E-07,</u>	
<u>1995,</u>	0.000E+0	0, 3.04	1E-08,	2.034E	-13,	0.000E+	00,	2.956E-07,	
<u>1996,</u>	0.000E+0	<u>)0, 1.94</u>	<u>8E-08,</u>	1.302E	<u>-13,</u>	0.000E+	00,	<u>1.893E-07,</u>	
1997.	0.000E+0	0, 2.24	2E-09,	1.500E	-14.	0.000E+	00,	2.180E-08.	

Note(A): The calendar dose in 1997 is that received up to 2/25/1997 because this is when the cancer was diagnosed. Note(B): The additional energy from the nucleus caused by alpha recoil has

been included where necessary

Note(C): These calculations have been optimised for accuracy

Note(D): gamma1 = 30 keV, gamma2 = 30-250 keV, gamma3 = >250keV

-



<u>Note:</u> Consult the approved operating procedure documentation for ORAU's Energy Employees Occupational Illness Compensation Program Dose Reconstruction Project for instructions on how to use '<u>FeedIREP</u>' to read the '<u>*.rpt</u>' file formatted by IMBA Professional Plus - **and also the** '<u>User's Guide</u>' **to** <u>run</u> NIOSH-IREP.

Case of ²⁴¹Am In-growth - Requires Add-On 10



This case involved an acute inhalation of high-fired plutonium oxide. It is of particular interest because about 94% of the plutonium activity was 241 Pu (at the time of the inhalation), with a substantial. The 241 Am progeny of 241 Pu was present in the inhaled material - with about 0.9% of the total plutonium activity. However, this amount of 241 Am "contamination" enabled the retention of material in the lungs to be measured relatively accurately - over many years.

The case was first reported in the literature by <u>Bihl et al (1988)</u>, with a longer-term "follow-up" reported by <u>Carbaugh et al (1991)</u>. These authors concluded that this case demonstrated very unusual respiratory tract clearance behavior, both in terms of low "solubility" of the plutonium particles (evidenced by an undetectable excretion rate in urine), and the virtual absence of particle clearance from the respiratory tract. In fact, Bihl et al coined the term "Super Class Y" to describe the unusually low solubility, and, rather than decreasing over time, the <u>241</u>Am activity in the lungs actually built up - by a factor of about 2 - over 12 years.

Very recently (January 28th, 2004), Gene Carbaugh has published an updated slide presentation on this case - entitled 'The Plutonium Reality Show: "Super Class Y vs. Class W and Class Y" - A Contest of Bioassay and Internal Dosimetry' - available at <u>http://bidug.pnl.gov/references/Carbaugh_PNNL_%20Plutonium_%20Reality_%</u> <u>20Show_s.pdf</u>. We have taken an exploratory look at this case (HAN-1) here since IMBA Professional Plus is always ready for a challenge!

The raw data (provided in an Excel spreadsheet by Gene Carbaugh) include:

- Measured <u>isotopic composition</u> of the inhaled material (% by atom) from mass spectrometry.
- Measured <u>241Am-in-lung activity</u> in vivo from the first through 6,639<u>th</u> day (18-y follow-up).
- Measured <u>241Am-in-liver activity</u> in-vivo measurable from about 6,000 d.
- Measured <u>241Am-in-skeleton activity</u> in-vivo also measurable from about 6,000 d.
- Measured <u>239/240Pu excretion rate in urine</u> measurable from about 1,800 d onwards.

See Input Data for Am-241 in Lung Case.

Input Data - ²⁴¹Am in Lung Case



1. Isotopic Composition

Table 4.11. Isotopic composition of plutonium oxide material inhaled in HAN-1.

% by Number of
Radionuclide% By Activity

Example Cases - Bioassay & Dosimetry

<u>241Am</u>	0.25	0.56
<u>238</u> Pu	0.065	0.71
<u>239</u> Pu	86.4	3.46
<u>240</u> Pu	11.6	1.71
<u>241Pu</u>	<u>1.4</u>	<u>93.6</u>
<u>242</u> Pu	0.24	6 <u> </u>

Clearly, from Table 4.11:

- <u>239/240</u>Pu dominates by number of atoms.
- <u>241</u>Pu dominates by activity.
- <u>241</u>Am is a minor "contaminant" of the plutonium particle "matrix" in terms of both number of atoms (mass) and activity.

2. 241Am in the Lungs

A total of <u>259</u> in vivo measurements of <u>241</u>Am activity in the lungs. This exceeds the capacity (<u>200</u>) for any single Bioassay Quantity provided in IMBA Professional Plus. Therefore, we "reduced" the data set in a manner that would not introduce bias into the fitting procedure - by averaging each successive pair of measurement date and value. The last (odd-numbered) data point was discarded. Table 4.12. gives the reduced data set.

Table 4.12. Reduced data set_of 241 A	Am activity in the lungs.
---------------------------------------	---------------------------

Mid-point	
Date/Time	Activity (pCi)
5/23/78 12:00 PM	1300
5/24/78 12:00 PM	1200
5/26/78 12:00 AM	1350
5/30/78 12:00 AM	1300
6/12/78 12:00 PM	1250
6/27/78 12:00 AM	1200
7/10/78 12:00 PM	1200
7/31/78 12:00 PM	1300
9/16/78 12:00 PM	1300
10/11/78 12:00 AM	1500
11/3/78 12:00 AM	1450
2/13/79 12:00 PM	1250
3/14/79 12:00 AM	1450
4/13/79 12:00 AM	1500
5/10/79 12:00 PM	1550
6/29/79 12:00 AM	1700

8/13/79 12:00 PM	1600
10/12/79 12:00 AM	1600
11/30/79 12:00 AM	1600
1/25/80 12:00 AM	1600
3/14/80 12:00 AM	1700
4/11/80 12:00 AM	1950
6/13/80 12:00 AM	1750
9/29/80 12:00 PM	1950
1/2/81 12:00 AM	1850
3/16/81 12:00 PM	1700
5/15/81 12:00 AM	1700
6/26/81 12:00 AM	1800
9/23/81 12:00 AM	1650
1/20/82 12:00 AM	1550
4/26/82 12:00 PM	1500
8/13/82 12:00 AM	1750
12/13/82 12:00 PM	1750
3/28/83 12:00 PM	1950
7/11/83 12:00 PM	1900
9/12/83 12:00 PM	2250
1/13/84 12:00 AM	2650
2/24/84 12:00 AM	2800
5/28/84 12:00 PM	3000
7/27/84 12:00 AM	2550
10/12/84 12:00 AM	2150
11/14/84 12:00 PM	2400
3/11/85 12:00 PM	2500
5/2/85 12:00 AM	2350
5/2/85 12:00 AM	2450
5/2/85 12:00 AM	2300
7/12/85 12:00 AM	2100
9/13/85 12:00 AM	2450
11/25/85 12:00 PM	2500
3/28/86 12:00 AM	2350
5/16/86 12:00 AM	2450

6/27/86 12:00 AM	2375
8/11/86 12:00 PM	2515
10/6/86 12:00 PM	2350
10/17/86 12:00 AM	2445
12/19/86 12:00 AM	2300
2/13/87 12:00 AM	2480
3/27/87 12:00 AM	2600
6/7/87 12:00 AM	2630
8/13/87 12:00 PM	2315
11/12/87 12:00 AM	2975
11/25/87 12:00 AM	2725
3/14/88 12:00 PM	2500
7/11/88 12:00 PM	2335
9/12/88 12:00 PM	2275
10/24/88 12:00 PM	2335
10/24/88 12:00 PM	2335
12/23/88 12:00 AM	2240
2/10/89 12:00 AM	2445
3/10/89 12:00 AM	2060
4/10/89 12:00 PM	2510
5/26/89 12:00 AM	2740
8/4/89 12:00 AM	3375
8/25/89 12:00 AM	2510
10/27/89 12:00 AM	2310
1/26/90 12:00 AM	2840
3/26/90 12:00 PM	2635
5/11/90 12:00 AM	2695
6/11/90 12:00 PM	3130
7/30/90 12:00 PM	2825
9/28/90 12:00 AM	2585
11/12/90 12:00 PM	2760
12/14/90 12:00 AM	2895
1/11/91 12:00 AM	2880
2/8/91 12:00 AM	2530
3/11/91 12:00 PM	2395

4/29/91 12:00 PM	2595
6/14/91 12:00 AM	2695
7/8/91 12:00 PM	2725
8/30/91 12:00 AM	2345
9/27/91 12:00 AM	3160
10/25/91 12:00 AM	2735
11/22/91 12:00 AM	2490
12/27/91 12:00 AM	1965
1/31/92 12:00 AM	3585
3/27/92 12:00 AM	3395
4/24/92 12:00 AM	3090
5/29/92 12:00 AM	3465
7/31/92 12:00 AM	3300
8/28/92 12:00 AM	3355
9/28/92 12:00 PM	2940
11/9/92 12:00 PM	3225
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3/12/93 12:00 AM	2810
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7/5/93 12:00 PM	2855
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10/8/93 12:00 AM	3160
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1/12/94 12:00 PM	3160
2/11/94 12:00 AM	3335
4/1/94 12:00 AM	2985
6/10/94 12:00 AM	3480
7/22/94 12:00 AM	3610
9/29/94 12:00 AM	3630
10/13/94 12:00 AM	3630
11/16/94 12:00 AM	3680

Page 1	70	of 1	85
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12/30/94 12:00 AM	3505
1/27/95 12:00 AM	3390
2/24/95 12:00 AM	3290
4/21/95 12:00 AM	3410
5/19/95 12:00 AM	3145
6/30/95 12:00 AM	2565
9/22/95 12:00 AM	4010
11/3/95 12:00 AM	3390
4/26/96 12:00 AM	3670

3. 241Am in the Liver

Table 4.13.	In vivo measurements of	of <u>241</u>A r	m activity	in the	liver.
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Date Measurement	ofMeasured 241Am Activity (nCi)	<u>Minimum Detectable</u> Activity (nCi)
9/29/1994	0.2	0.05
1/27/1995	0.3	0.05
8/25/1995	0.2	0.05
11/17/1995	0.3	0.06
5/31/1996	0.2	0.05
7/26/1996	0.0	<u>0.06</u>

The activity of 241 Am in the liver was measurable (in vivo) from September, 1994 onwards (see Table 4.13). To represent these data we have averaged all 6 measured values, and taken this average value (and its standard deviation) to represent the amount of 241 Am in the liver on September 20th, 1995 (the average of the measurement dates). The resulting "point" estimate is 0.21 ± 0.09 nCi.

4. 241Am in the Skeleton

-

Table 4.14. In vivo measurements of 241 Am activity in the skeleton.

Date Measurement	ofMeasured 241 Am	Minimum Detectable Activity (nCi)
7/29/1994		
12/6/100/	0.0	0.2
12/0/1994	0.4	0.2
5/19/1995	0.2	0.2
3/22/1996	0.2	<u>0.2</u>

The activity of <u>241</u>Am in the skeleton, as measured (<u>in vivo</u>) over a similar period to that measured in the liver, is shown in Table 4.14. To represent these data we have averaged the 4 measured values, and taken this average (and its standard deviation) to represent the

amount of <u>241</u>Am in the skeleton on April 11<u>th</u>, 1995 (the average of the measurement dates). The resulting "point" estimate is <u>0.20 \pm 0.18 nCi</u>.

5. 239Pu in Urine

The rate of excretion of <u>239</u>Pu in urine was measurable (by ICP mass spectrometry) from 1983 onwards. The calculated activity excretion rates (simulated 24-h urine samples) are shown in Table 4.15.

Table 4.15. Measured urinary excretion rate of 239 Pu.

Date	ofMeasured I	Excretion Rate Estimated Error
Measurement	<u>(pCi d-1)</u>	<u>(pCi d-1)</u>
4/20/1983	0.0071	0.0038
12/21/1983	0.0081	0.0041
9/20/1984	0.0090	0.0025
7/11/1985	0.0207	0.0043
7/9/1986	0.0062	0.0021
7/8/1987	0.0017	0.0019
7/12/1988	0.0031	0.0018
7/13/1989	0.0065	0.0035
8/21/1990	0.0059	0.0041
7/11/1991	0.0153	0.0058
7/22/1992	0.0131	0.0034
7/14/1993	0.0194	0.0039
7/20/1994	0.0071	0.0025
7/18/1995	0.0181	0.0038
7/10/1996	0.0179	0.0037

 <u>Proceed</u> to <u>Analysis of 241</u>Am Retention in the Lungs - Using ICRP Default HRTM Parameter Values.

Analysis of ²⁴¹Am-in-lung Data using ICRP Defaults





Figure 4.131. Comparison of 241 Am-in-lung data with ICRP30 Class 'Y' prediction (from Carbaugh 2004).

Figure 4.131 shows Gene Carbaugh's updated summary of the <u>241</u>Am-in-lung data from the HAN-1 case, compared with the temporal behavior "predicted" by the ICRP Publication 30 (ICRP79) lung model - for Class 'Y' plutonium. Beyond 6,000 d, the measured <u>241</u>Am retention is about 30-fold greater than predicted.

We have analyzed these data using IMBA Professional Plus - with the current ICRP "default" assumption of Type 'S' absorption characteristics (Figure 4.132). The "fit" is better than for Class 'Y' - but still very bad. Figure 4.132 also compares the "predicted" build-up of <u>241</u>Am activity in the <u>Liver</u> and <u>Skeleton</u> with the in vivo measurements.

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			2.050E+01 1.250E+
			4.950E+01 1.200E+
			6.950E+01 1.300E+
			1.165E+02 1.300E+
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Figure 4.132. Most likely "fit" to HAN-1 241 Am-in-lung data assuming ICRP default HRTM parameter values (Type 'S').

Note: The predicted monotonic decrease of <u>241</u>Am activity in the lung includes the calculated "in-growth" of <u>241</u>Am activity into that of the parent <u>241</u>Pu.

In this example, IMBA Professional Plus automatically calculated the "in-growth" of 241 Am activity in the respiratory tract that resulted from the decay of 241 Pu. However, in order to do this, it was first necessary to define the <u>Isotopic</u> Composition of the inhaled plutonium material. This was done by treating all of the isotopes of plutonium that are present in the particle matrix as <u>Associated</u> Radionuclides of 241 Am (the Indicator Nuclide) - see Figure 4.133.

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Figure 4.133. Setting up plutonium isotopes as Associated Radionuclides.

Figure 4.133 shows the 5 associated plutonium isotopes -

<u>238</u>Pu, <u>239</u>Pu, <u>240</u>Pu, 241<u>Pu</u> and <u>242</u>Pu. <u>Note that</u> the "Abundance" of 241<u>Pu</u> is very high (16,813% - relative to the <u>241</u>Am activity).

The calculated amount of 241 Am intake was 41,691 pCi - on the assumption that the inhaled plutonium oxide (particle matrix) had Type 'S' absorption behavior. The relative abundance of 239 Pu was 621% (Table 4.11). Therefore, the associated intake of 239 Pu would have been 258,900 pCi (258.9 nCi).

We can test this estimate of the $239\underline{Pu}$ intake by comparing the predicted excretion rate in urine with that actually measured (<u>Table 4.15</u>). To do this, however, we have to set up a second "case" in IMBA Professional Plus - with $239\underline{Pu}$ as the <u>Indicator</u> <u>Nuclide</u>, and the amount of intake set at <u>258,900 pCi</u>. The resulting "predicted" urinary excretion rate is shown in Figure 4.134.

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Figure 4.134. Urinary excretion rate and lung retention predicted for Type 'S' plutonium.

The urinary excretion rate for inhaled Type 'S' plutonium is predicted to decrease after about 1,000 d (Figure 4.134). However, the trend in the measured values (from about 1,800 through 6,700 d) is for the actual urinary excretion rate to increase with time. Again, therefore, the "fit" to the observed temporal behavior of urinary excretion (of 239Pu) is not good.

Summary of Observed Departures from ICRP-Default Behavior

The following observations are NOT consistent with the predictions (for a particle matrix consisting of Type 'S' plutonium):

- The the measured 241<u>Am</u> activity in the lungs remained essentially constant over the first 70 d (Figure 4.135) - whereas Type 'S' absorption together with ICRP's recommended mechanical transport rates from the <u>alveolar-interstitial</u> (AI) region predicted a marked decrease of activity over this initial period (Figure 4.135). Note that the effect of "in-growth" of <u>241</u>Am activity as a result of <u>241</u>Pu decay over this period is negligible.
- 2. Over the long term (18 y) the 241<u>Am</u> activity in the lungs was observed

to increase markedly - whereas, for Type 'S' plutonium it should have decreased approximately 10-fold (Figure 4.132).



Figure 4.135. Comparison of predicted and measured early changes in 241 Am activity in the lungs.

From the above, it appears that BOTH the absorption characteristics of the plutonium particle matrix AND the mechanical elimination rate of particles deposited in the "deep lung" of this individual worker differ substantially from the standard ICRP default values.

Note: ICRP has recommended that <u>Default</u> parameter values should be used <u>in</u> the absence of better (specific) information. This case is a prime example of significant departure in parameterized characteristics from the available defaults.

• Proceed to Optimizing the HRTM Parameter Values to Fit the HAN-1 Data.

Optimizing HRTM Parameter Values to Fit HAN-1 Data



In order to obtain a credible "fit" to ALL of the HAN-1 data, we found it necessay to vary the following parameter values:

 In the HRTM Mechanical Transport Model (Figure 4.136) - the <u>rates of transport</u> to the bronchioles (compartments bb<u>1</u>) from BOTH compartments AI<u>1</u> and AI<u>2</u> (of the alveolarinterstitial region).

- 2. In the HRTM Particle Absorption Model (Figure 4.137) the "slow" absorption rate.
- 3. In the HRTM Particle Deposition Model (Figure 4.138) the aerosol AMAD.



Figure 4.136. User Defined values of the Rate Constants "AI1 to bb1" and "AI2 to bb2" - from their default values of "0.02 d-1" and "0.001 d-1", respectively.

These changes to the transport rates out of compartments **AI** and **AI** are equivalent to <u>eliminating</u> the "fast" and "intermediate" phases of mechanical particle clearance from the AI region. In other words, ALL of the material deposited in the AI region is cleared "slowly" - at the ICRP-recommended rate for "slow" clearance. Such clearance behavior has been observed previously in some individuals (<u>ICRP 1994a</u>) - and is not uncommon in cigarette smokers.



Figure 4.137. User Defined value of the "Slow" absorption rate ($S_{\underline{S}}$) - from the default value of 0.0001 d-1 for Type 'S'.

This changed "slow" absorption rate (Ss) represents a <u>five-fold reduction</u> from the Type 'S' default values (0.0001 d-1).

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Seposition Model	
Extrathoracic Airways (ET, & ET2) Conducting Airways (BB & bb) Deep Lung (A)	Exposure C Light Worker C Heavy Worker Aerosol Parameters Aerosol Parameters Aerosol Parameters AMAD AMAD AMAD C AMAD 0.5 µm Sigma-G 2.4977233 Density 3 g/ml Shape factor 1.5
Clear	Select User Defined UOAD ICRP DEFAULTS User Defined
	<u>Q</u> K <u>C</u> ancel

Figure 4.138. User Defined value of the aerosol AMAD (0.5 µm).

• Examine the Resulting "Fit" to the HAN-1 Data.



Tip #1: The parameter files "HAN-1_Am-241.ix" and "HAN-1_Pu-239.ix", for 241Am and 239Pu as the Indicator Nuclide, respectively, have been set up with these modified parameter values - together with the HAN-1 "test" data. Tip #1: It is informative to try varying these parameter values - so as to understand the effect of each one on the overall "fit" to these data. You will find that the "approriate" range of parameter values is reasonably tightly defined.

Improved Representation of HAN-1 Data

Figure 4.139 shows the resulting improved "fit" to the measured build-up of 241Am activity in the lungs. Furthermore, Figure 4.140 shows that the very much improved "fit" to the observed early "constancy" of the 241Am activity in the lungs.



Figure 4.139. Improved "fit" to the measured build-up of 241Am activity in the lungs.



Figure 4.140. Resulting "fit" to the constant 241Am activity in the lungs maesured over the first 70 d.

You will have noted (from Figure 4.139) that we have excluded from this "fit" the

last "block" of data (from about 5,000 d onwards). There is clearly a "discontinuity" in the measured values at about 5,000 d. By excluding these data, we have obtained a better overall "fit".

<u>Tip:</u> See for yourself how <u>inclusion/exclusion</u> of the last "block" of data affects the overall "fit". You will find that the effect is not unduly critical!

Figure 4.141 includes the "predicted" build-up of 241Am activity in the Liver and Skeleton.

👒 Bioassay Calculations				
Elle Advanced Tools Help				
Save Quick Save Tritium		Bioassay Calcula	tions	
INTAKE	CALCULA	TION		BIOASSAY QUA
IR1 3.875E+03 pCi	Intakes to Bioassay Specily Times (d) [Col 1] Start Time (d) Top Time (d) Top Time (d) Top Time (d) Specily Collection Periods [Col 2] Calculate Bioassay Quantity [Col 3]	Bioassay to Intake Number of Times (1-200)	 Graph C I 4500 4000 3500 3500 3500 3000 422500 500 500	able C Hide Lungs HAN-1 Case: Am-241 B HAN-1 Case: Am-241 B 100 1000 1500 2000 2500 3000 35 Time since in Table C Hide Liver HAN-1 Case: Am-241 B
	000	-		700 1400 2100 2800 35 Time since in
Deposition			Graph C T	able C Hide User Defined
Collating Times Bioassay Calcs			400 350 - 것 300 -	HAN-1 Case: Am-241 Bu
Current Operation	Calculation Comp	olete	250 - 200 - 150 - 150 -	
		ŪK	\$ 50- 0	0 1000 1500 2000 2500 3000 35 Time since in
Am-241	fax Likelihood fit			

Figure 4.141. Improved overall "fit" to the HAN-1 data obtained by modifying parameter values in the HRTM.

Important Note: The calculated build-up of 241 Am activity in the Liver and Skeleton does NOT include "in-growth" from 241 Pu that is also taken up by these organs. IMBA Professional Plus calculates such_"in-growth" ONLY for the lungs - where it is assumed that 241 Am formed from decay of 241 Pu in the particle matrix remains with the



Figure 4.142 shows the resulting "fit" to the 239Pu excretion rate in urine. this is a substantially more "credible" representation of the measured values than the initial "prediction" - based on ICRP default parametr values (Figure 4.134).

🖳 Bioassay Calculations				
Elle Advanced Tools Help				
Save Quick Save Tritium		Bioassay Calcu	lations	
INTAKE	CALCULAT	ION		BIOASSAY QUA
IR1 6.132E+04 pCi	Intakes to Binassau	Bipassay to Intake	Graph 🕫	Table C Hide Unine ime (d) Collection Measurem period (d) Measurem 1.7845.000 - 1.0005.000 - 7.1005
	Specify Times (d) [Col 1]	Number of Times (1-200)	3	1.734E+03 1.000E+00 7.100E 2.039E+03 1.000E+00 8.100E+ 2.313E+03 1.000E+00 9.000E+ 2.607E+03 1.000E+00 9.000E+ 2.970E+03 1.000E+00 0.200E+ 2.924E+03 1.000E+00 1.200E
	Start Time (d) 0 Stop Time (d) 7000	Image: C C Linear Send to all open windows C 1-2-5 mode >		3.334E+03 1.000E+00 1.700E 3.704E+03 1.000E+00 3.100E 4.070E+03 1.000E+00 5.900E 4.474E+03 1.000E+00 5.900E
	Specify Collection Periods [Col 2]	Send> Start Calculation		HAN-1 Case: PU-239 E
Progress Indicator	000		0.001	700 1400 2100 2800 38 Time since in
Deposition Collating Times Bioassay Calcs Current Operation		<u>D</u> K	Graph 8000 7000 00 5000 5000 3000 5000 5000 0 5000 1000 0 0 0 0 0 0 0 0 0 0 0 0	Table C Hide Lungs HAN-1 Case: Pu-239 500 1000 1500 2000 2500 3000 36 Time since in
Pu-239 M	fax Likelihood fit			

Figure 4.142. Predicted 239Pu urinary excretion rate and lung retention.

<u>Note:</u> As with the other example cases "solved" in this <u>User Manual</u>, the
 "solutions" offered are NOT intended to be scientifically definitive. They are

C)

presented ONLY to demonstrate the scope and flexibility of the <u>IMBA</u> <u>Professional Plus</u>. More thorough review of the specific health physics information relating to each case may well indicate revised modeling assumptions.

• <u>Proceed</u> to Compare Doses Calculated using ICRP Default and Optimized Parameter Values.

Dose Calculation for HAN-1 Case

We can use EITHER the "HAN-1_Pu-239.ix" OR the "HAN-1_Am-241.ix" parameter file to calculate the resulting committed effective doses - so we will use BOTH - with the <u>10CFR835</u> tissue weighting factors.

Solutions Calculations						
Elle <u>A</u> dvanced <u>T</u> ools <u>H</u> elp						
Save Quick Save	Dose Ca	alculation	s			
INTAKE	CALCULATION				DOS	E
			C Equiv	€ Eff	Indic	ator N
IR1 6.132E+04 pCi			Target Organs	Cont. to Eff Dose (rem) IR(1)	Effective Dose (rem) Total	
	Calculations WR WT		bb Al	0.00E+00 0.00E+00	0.00E+00	-
			LNITHI	0.00E+00	0.00E+00	
			Esophagus	0.00E+00	0.00E+00	
	Select		Gonads	1.68E-01	1.68E-01	
			Spare	0.00E+00	0.00E+00	
	 Dose from Indicator Nuclide: Pu-239 		Remainder	0.00E+00	0.00E+00	
			TOTAL	1.51E+01	1.51E+01	
	(2) Dose from Associated Radionuclides		C Equiv	€ Eff	Associate	ed B er
	(3) Annual Committed Doses	Г	Target Organs	Eff Dose from Pu-238 (rem)	Eff Dose from Pu-240 (rem)	Eff Di Pu-24 (rem)
			bb	0.00E+00	0.00E+00	0.
			Al	0.00E+00	0.00E+00	0.
	Effective Dose (rem)		LN(TH)	0.00E+00	0.00E+00	0.
	Calculate 3.49E+01		Esophagus	0.00E+00	0.00E+00	0.
	0.452 401		Gonads	2.94E-02	8.29E-02	1
			Spare	0.00E+00	0.00E+00	0.
			Hemander	0.00E+00	0.00E+00	U.
	000		TOTAL	2.300 +00	7.47E+00	0.
Progress Indicator					Annual (`ommit
(1)					1	
(2)						
(3)						
Current Operation Intake Regime 1 Intake Regime(T	: Remainder organs are: Liver; ET; Kidneys; LiLit; U.Lit; otal]: Remainder organs are: Liver; ET; Kidneys; LiLit; U.Lit;					
		<u>о</u> к				
Pu-239 WR=ICRP Del	aults WT = 10 CFR 835 ICRP Pu Model					

Figure 4.143. Effective doses calculated using <u>239</u>Pu as the Indicator Nuclide.

Solutions Calculations							
Elle <u>A</u> dvanced <u>I</u> ools <u>H</u> elp							
Save Quick Save		Dose	Calculatio	ns			
INTAKE	CALC	CULATION				DOS	E
				C Equiv	€ Eff	Indic	ator N
IR1 9.875E+03 pCi				Target Organs	Cont. to Eff Dose (rem) IR(1)	Effective Dose (rem) Total	
	Calculations WR	WT		bb	0.00E+00	0.00E+00	
				Al	0.00E+00	0.00E+00	
				Econhague	0.00E+00	0.00E+00	_
	Select			Gonads	4.42E-02	4.42E-02	_
				Spare	0.00E+00	0.00E+00	
	(1) Dose	from Indicator Nuclide: Am-241		Remainder	0.00E+00	0.00E+00	
				TOTAL	2.52E+00	2.52E+00	
	(2) Dava	from Associated Devices and the	-				
	(2) Dose	from Associated Hadionucides	10	C Equiv	€ Eff	Associate	ed Rac
	(3) Annua	al Committed Doses		Target Organs	Eff Dose from Pu-238 (rem)	Eff Dose from Pu-239 (rem)	Eff Di Pu-24 (rem)
				bb	0.00E+00	0.00E+00	0.
		Effective Doce ((mai	Al	0.00E+00	0.00E+00	0.
		Ellective Dose (remj	LN(TH)	0.00E+00	0.00E+00	0.
	Calo	ulate 3.49E+01		Esophagus	2.955.02	1.00E+00	U.
				Spare	0.00E+02	0.00E+00	0
				Bemainder	0.00E+00	0.00E+00	0
				TOTAL	2.96E+00	1.51E+01	7.
	-000)		< (2)			
Progress Indicator						Annual C	timmo:
(1)						1	
(2)							
(3)							
Current Operation Intake Regime Intake Regime	1: Remainder organs are: ET; Liv Fotal): Remainder organs are: ET	ver; Kidneys; L.L.I.; Heart Wall; F; Liver; Kidneys; L.L.I.; Heart Wall;	~				
			<u>Q</u> K				
Am-241 WR= ICRP De	faults WT = 10 CFR 835	ICRP Am Model					

Figure 4.144. Effective doses calculated using <u>241</u>Am as the Indicator Nuclide.

As expected, the calculated total effective dose is the same - irrespective of whether specific radionuclides are defined as the Indicator Nuclide or as an Associated Radionuclide. Table 4.16 summarizes the contributions to total effective dose made by each of the 6 radionuclides involved in this example - for both of the above calculations - and the fraction of effective dose contributed by radionuclide retention in the lungs. For comparison, the Table also shows the calculated effective dose that would result from the initial assumption of Type 'S' plutonium - and all ICRP default parameter values.

<u>Contribution</u> from:	Optimized Parameter Values - with 239Pu as the Indicator Nuclide	Optimized Parameter Values - with 241Am as the Indicator Nuclide	<u>ICRP Default</u> <u>Parameter Values</u> - <u>Type 'S' Plutonium</u>
<u>238Pu</u>	2.95	2.96	<u>3.05</u>
<u>239Pu</u>	<u>15.1</u>	<u>15.1</u>	<u>14.9</u>

Table 4.16. Contributions to effective dose (in rem and %).

Example Cases - Bioassay & Dosimetry

<u>240Pu</u>	<u>7.47</u>	7.48	7.30
<u>241Pu</u>	6.82	6.82	<u>3.93</u>
<u>242Pu</u>	0.00256	0.00252	0.00247
<u>241Am</u>	2.52	2.52	2.44
Total from All Nuclides	<u>34.9 (100%)</u>	<u>34.9 (100%)</u>	<u>31.5 (100%)</u>
<u>Total from</u> Lungs	<u>27.7 (79%)</u>	<u>27.7 (79%)</u>	<u>10.9 (39%)</u>

Note #1: You will have noticed that the quantity "effective dose" is remarkably "robust" (at least, for highly insoluble plutonium). In this case, the changes that we had to make to the HRTM "input" parameter values - in order to "fit" the bioassay data - changed the total effective dose only marginally from that calculated using standard ICRP default parameter values. Using "case specific" parameter values increased the calculated effective dose by just 11%!
Note #2: However, use of "case specific" HRTM parameter values DOES have a substantial effect on the distribution of effective dose between the Lungs and other body organs. The lung dose is calculated to increase by

Case Using Statistics Package -Requires Add-On 11

a factor of about 2.5 (154%).





Note: The "Statistics Package" (Add-On 11) was developed especially for IMBA Professional Plus. HPA-RPD will add the documentation for this package here - when this is available.

Case of ²⁴¹Am In-growth - Requires Add-On 10



This case involved an acute inhalation of high-fired plutonium oxide. It is of particular interest because about 94% of the plutonium activity was ²⁴¹Pu (at the time of the inhalation), with a substantial . The ²⁴¹Am progeny of ²⁴¹Pu was present in the inhaled material - with about 0.9% of the total plutonium activity. However, this amount of ²⁴¹Am "contamination" enabled the retention of material in the lungs to be measured relatively accurately - over many years.

The case was first reported in the literature by <u>Bihl et al (1988)</u>, with a longer-term "followup" reported by <u>Carbaugh et al (1991)</u>. These authors concluded that this case demonstrated very unusual respiratory tract clearance behavior, both in terms of low "solubility" of the plutonium particles (evidenced by an undetectable excretion rate in urine), and the virtual absence of particle clearance from the respiratory tract. In fact, Bihl et al coined the term "Super Class Y" to describe the unusually low solubility, and, rather than decreasing over time, the ²⁴¹Am activity in the lungs actually built up - by a factor of about 2 - over 12 years.

Very recently (January 28th, 2004), Gene Carbaugh has published an updated slide presentation on this case - entitled 'The Plutonium Reality Show: "Super Class Y vs. Class W and Class Y" - A Contest of Bioassay and Internal Dosimetry' - available at <u>http://bidug.pnl.gov/references/Carbaugh_PNNL_%20Plutonium_%20Reality_%</u> <u>20Show_s.pdf</u>. We have taken an exploratory look at this case (HAN-1) here - since IMBA Professional Plus is always ready for a challenge!

The raw data (provided in an Excel spreadsheet by Gene Carbaugh) include:

- Measured <u>isotopic composition</u> of the inhaled material (% by atom) from mass spectrometry.
- Measured <u>241Am-in-lung activity</u> in vivo from the first through 6,639th day (18-y follow-up).
- Measured <u>241Am-in-liver activity</u> in-vivo measurable from about 6,000 d.
- Measured <u>241Am-in-skeleton activity</u> *in-vivo* also measurable from about 6,000 d.
- Measured <u>239/240Pu excretion rate in urine</u> measurable from about 1,800 d onwards.

See Input Data for Am-241 in Lung Case.

Input Data - ²⁴¹Am in Lung Case



1. Isotopic Composition

Table 4.11.Isotopic composition of plutonium oxide material inhaled in HAN-1.% by Number of
Radionuclide% By Activity

Case of Am-241 In-growth

241Am ²³⁸ Pu	<u>0.25</u> 0.065	<u>0.56</u> 0.71
²³⁹ Pu	86.4	3.46
²⁴⁰ Pu	11.6	1.71
<u>241Pu</u>	<u>1.4</u>	<u>93.6</u>
²⁴² Pu	0.24	6 <u>10⁻⁴</u>

Clearly, from Table 4.11:

- ^{239/240}Pu dominates by number of atoms.
- ²⁴¹Pu dominates by activity.
- ²⁴¹Am is a minor "contaminant" of the plutonium particle "matrix" in terms of both number of atoms (mass) and activity.

2. 241Am in the Lungs

A total of <u>259</u> *in vivo* measurements of ²⁴¹Am activity in the lungs. This exceeds the capacity (200) for any single Bioassay Quantity provided in IMBA Professional Plus. Therefore, we "reduced" the data set in a manner that would not introduce bias into the fitting procedure - by averaging each successive pair of measurement date and value. The last (odd-numbered) data point was discarded. Table 4.12. gives the reduced data set.

Table 4.12. Reduced data set_of ²⁴¹Am activity in the lungs.

Mid-point Date/Time	Activity (pCi)
5/23/78 12:00 PM	1300
5/24/78 12:00 PM	1200
5/26/78 12:00 AM	1350
5/30/78 12:00 AM	1300
6/12/78 12:00 PM	1250
6/27/78 12:00 AM	1200
7/10/78 12:00 PM	1200
7/31/78 12:00 PM	1300
9/16/78 12:00 PM	1300
10/11/78 12:00 AM	1500
11/3/78 12:00 AM	1450
2/13/79 12:00 PM	1250
3/14/79 12:00 AM	1450
4/13/79 12:00 AM	1500
5/10/79 12:00 PM	1550
6/29/79 12:00 AM	1700
8/13/79 12:00 PM	1600
10/12/79 12:00 AM	1600
11/30/79 12:00 AM	1600
1/25/80 12:00 AM	1600
3/14/80 12:00 AM	1700
4/11/80 12:00 AM	1950
6/13/80 12:00 AM	1750
9/29/80 12:00 PM	1950
1/2/81 12:00 AM	1850
3/16/81 12:00 PM	1700
5/15/81 12:00 AM	1700
6/26/81 12:00 AM	1800
9/23/81 12:00 AM	1650

4/26/82 12:00 PM 1500 8/13/82 12:00 PM 1750 3/28/83 12:00 PM 1950 7/11/83 12:00 PM 1900 9/12/83 12:00 PM 2250 1/13/84 12:00 AM 2650 2/24/84 12:00 AM 2800 5/28/84 12:00 AM 250 1/13/84 12:00 AM 250 1/11/85 12:00 AM 250 1/11/85 12:00 AM 2400 3/11/85 12:00 AM 2300 5/2/85 12:00 AM 2300 7/12/85 12:00 AM 2450 5/2/85 12:00 AM 2300 7/12/85 12:00 AM 2450 5/2/85 12:00 AM 2350 5/16/86 12:00 AM 2350 5/16/86 12:00 AM 2350 5/16/86 12:00 AM 2350 10/17/86 12:00 AM 2445 12/19/86 12:00 AM 2450 6/27/87 12:00 AM 2300 2/13/87 12:00 AM 2450 6/7/87 12:00 AM 2450 6/7/87 12:00 AM 2355 10/24/88 12:00 PM 2355 11/25/87 12:00 AM 2355 9/12/88 12:00 PM <td< th=""><th>1/20/82 12·00 AM</th><th>1550</th></td<>	1/20/82 12·00 AM	1550
8/13/82 12:00 AM 1750 12/13/82 12:00 PM 1750 3/28/83 12:00 PM 1950 7/11/83 12:00 PM 2250 1/13/84 12:00 AM 2650 2/24/84 12:00 AM 2800 5/28/84 12:00 PM 3000 7/27/84 12:00 AM 2550 10/12/84 12:00 AM 2500 11/14/84 12:00 PM 2400 3/11/85 12:00 AM 2300 5/28/5 12:00 AM 2300 7/12/85 12:00 AM 2450 5/2/85 12:00 AM 2450 5/2/85 12:00 AM 2450 11/2/85 12:00 AM 2450 5/16/86 12:00 AM 2350 5/16/86 12:00 AM 2350 5/16/86 12:00 AM 2350 10/17/86 12:00 AM 2445 12/19/86 12:00 AM 2460 2/13/87 12:00 AM 2460 6/7/87 12:00 AM 2450 6/7/87 12:00 AM 2350 10/17/86 12:00 PM 2355 11/287 12:00 AM 2445 11/12/87 12:00 AM 2450 6/7/87 12:00 AM 2450 7/11/88 12:00 PM	4/26/82 12:00 PM	1500
12/13/82 12:00 PM 1750 3/28/83 12:00 PM 1950 7/11/83 12:00 PM 1900 9/12/83 12:00 PM 2250 1/13/84 12:00 AM 2650 2/24/84 12:00 AM 2800 5/28/84 12:00 AM 2500 10/12/84 12:00 AM 2150 11/14/84 12:00 PM 2400 3/11/85 12:00 AM 2300 5/2/85 12:00 AM 2300 5/2/85 12:00 AM 2450 5/2/85 12:00 AM 2450 5/2/85 12:00 AM 2300 7/12/85 12:00 AM 2450 11/25/85 12:00 AM 2450 5/2/85 12:00 AM 2350 5/16/86 12:00 AM 2350 5/16/86 12:00 AM 2350 10/17/86 12:00 AM 2450 12/19/86 12:00 AM 2350 10/17/86 12:00 AM 2460 3/27/87 12:00 AM 2460 3/27/87 12:00 AM 2600 6/7/87 12:00 AM 2600 6/7/87 12:00 AM 2355 11/12/87 12:00 AM 2355 11/12/87 12:00 AM 2355 11/12/87 12:00 AM	8/13/82 12:00 AM	1750
3/28/83 12:00 PM 1950 7/11/83 12:00 PM 1900 9/12/83 12:00 PM 2250 1/13/84 12:00 AM 2650 2/24/84 12:00 AM 2800 5/28/84 12:00 AM 2500 10/12/84 12:00 AM 2150 11/14/84 12:00 PM 2500 5/2/85 12:00 AM 2300 5/2/85 12:00 AM 2300 7/12/85 12:00 AM 2400 3/185 12:00 AM 2300 7/12/85 12:00 AM 2450 5/2/85 12:00 AM 2450 5/2/85 12:00 AM 2350 5/16/86 12:00 AM 2350 5/16/86 12:00 AM 2350 10/17/86 12:00 AM 2350 10/17/86 12:00 AM 2445 12/19/86 12:00 AM 2450 6/7/87 12:00 AM 2600 6/7/87 12:00 AM 2600 6/7/87 12:00 AM 2600 7/11/88 12:00 PM	12/13/82 12:00 PM	1750
3/20/03 12:00 PM 1900 9/12/83 12:00 PM 2250 1/13/84 12:00 AM 2650 2/24/84 12:00 AM 2800 5/28/84 12:00 AM 250 10/12/84 12:00 AM 2150 11/14/84 12:00 AM 2150 5/2/85 12:00 AM 2400 3/11/85 12:00 AM 2350 5/2/85 12:00 AM 2400 3/11/85 12:00 AM 2450 5/2/85 12:00 AM 2450 5/2/85 12:00 AM 2450 5/2/85 12:00 AM 2450 5/2/85 12:00 AM 2350 5/16/86 12:00 AM 2350 5/16/86 12:00 AM 2350 6/27/86 12:00 AM 2450 10/17/86 12:00 AM 2450 10/17/86 12:00 AM 2400 2/13/87 12:00 AM 2400 3/27/87 12:00 AM 2600 6/7/87 12:00 AM 2335 11/12/87 12:00 AM	3/28/83 12:00 PM	1050
7/17/0312:00 PM15:009/12/8312:00 PM22501/13/8412:00 AM26502/24/8412:00 PM30007/27/8412:00 AM215010/12/8412:00 AM215011/14/8412:00 PM24003/11/8512:00 PM25005/2/8512:00 AM23505/2/8512:00 AM24505/2/8512:00 AM24009/13/8512:00 AM245011/25/8512:00 AM24505/2/8512:00 AM23505/16/8612:00 AM23505/16/8612:00 AM23506/27/8612:00 AM245010/17/8612:00 AM24506/27/8712:00 AM24503/27/8712:00 AM24603/27/8712:00 AM24803/27/8712:00 AM26006/77/8712:00 AM26308/13/8712:00 AM27253/14/8812:00 PM23359/12/8812:00 PM23359/12/8812:00 PM233510/24/8812:00 PM233510/24/8812:00 PM233510/24/8812:00 PM233510/24/8912:00 AM24453/10/8912:00 AM24453/10/8912:00 AM24453/10/8912:00 AM245010/24/8812:00 PM235510/24/8912:00 AM24505/26/8912:00 AM2510<	7/11/83 12:00 PM	1000
3/12/03 12:00 PM 2230 1/13/84 12:00 AM 2650 2/24/84 12:00 AM 2800 5/28/84 12:00 PM 3000 7/27/84 12:00 AM 2150 10/12/84 12:00 PM 2400 3/11/85 12:00 PM 2500 5/2/85 12:00 AM 2350 5/2/85 12:00 AM 2450 5/2/85 12:00 AM 2450 5/2/85 12:00 AM 2450 5/2/85 12:00 AM 2450 9/13/85 12:00 AM 2450 11/25/85 12:00 AM 2450 6/27/86 12:00 AM 2350 5/16/86 12:00 AM 2350 10/17/86 12:00 AM 2350 10/17/86 12:00 AM 2445 12/19/86 12:00 AM 2460 6/7/87 12:00 AM 2460 6/7/87 12:00 AM 2600 6/7/87 12:00 AM 2600 6/7/87 12:00 AM 2725 3/14/88 12:00 PM 2335 9/12/88 12:00 PM 2335 9/12/88 12:00 PM 2335 9/12/88 12:00 PM 2335 10/24/88 12:00 PM 2335 10/24/88 12:00 PM <	0/12/02 12:00 PM	2250
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5/19/95 12:00 AM	3145
6/30/95 12:00 AM	2565
9/22/95 12:00 AM	4010
11/3/95 12:00 AM	3390
4/26/96 12:00 AM	3670

3. 241Am in the Liver

Table 4.13.	In vivo measurement	s of ²⁴¹ Am activity in the liver.
Date of	Measured 241 Am	Minimum Detectable
Measurement	<u>Activity (nCi)</u>	<u>Activity (nCi)</u>
9/29/1994	0.2	0.05
1/27/1995	0.3	0.05
8/25/1995	0.2	0.05
11/17/1995	0.3	0.06

5/31/1996	0.2	0.05
7/26/1996	0.0	0.06

The activity of ²⁴¹Am in the liver was measurable (in vivo) from September, 1994 onwards (see Table 4.13). To represent these data we have averaged all 6 measured values, and taken this average value (and its standard deviation) to represent the amount of ²⁴¹Am in the liver on September 20th, 1995 (the average of the measurement dates). The resulting "point" estimate is 0.21 ± 0.09 nCi.

4. 241Am in the Skeleton

Table 4.14. Ir	<i>vivo</i> measurements	of ²⁴¹ Am activity in the skeleton.
Date of	Measured 241 Am	Minimum Detectable
Measurement	<u>Activity (nCi)</u>	Activity (nCi)
7/29/1994	0.0	0.2
12/6/1994	0.4	0.2
5/19/1995	0.2	0.2
3/22/1996	0.2	0.2

The activity of ²⁴¹Am in the skeleton, as measured (in vivo) over a similar period to that measured in the liver, is shown in Table 4.14. To represent these data we have averaged the 4 measured values, and taken this average (and its standard deviation) to represent the amount of 241 Am in the skeleton on April 11th, 1995 (the average of the measurement dates). The resulting "point" estimate is 0.20 ± 0.18 nCi.

5. 239Pu in Urine

The rate of excretion of ²³⁹Pu in urine was measurable (by ICP mass spectrometry) from 1983 onwards. The calculated activity excretion rates (simulated 24-h urine samples) are shown in Table 4.15.

Table 4.15. Measured urinary excretion rate of ²³⁹ Pu.					
Date of	Measured Excretion Rate	<u>Estimated Error</u>			
<u>Measurement</u>	<u>(pCi d-1)</u>	<u>(pCi d-1)</u>			
4/20/1983	0.0071	0.0038			
12/21/1983	0.0081	0.0041			
9/20/1984	0.0090	0.0025			
7/11/1985	0.0207	0.0043			
7/9/1986	0.0062	0.0021			
7/8/1987	0.0017	0.0019			
7/12/1988	0.0031	0.0018			
7/13/1989	0.0065	0.0035			
8/21/1990	0.0059	0.0041			
7/11/1991	0.0153	0.0058			
7/22/1992	0.0131	0.0034			
7/14/1993	0.0194	0.0039			
7/20/1994	0.0071	0.0025			
7/18/1995	0.0181	0.0038			
7/10/1996	0.0179	0.0037			

 <u>Proceed</u> to <u>Analysis of 241</u> Am Retention in the Lungs - Using ICRP Default HRTM Parameter Values.

Analysis of ²⁴¹Am-in-lung Data using ICRP Defaults



Figure 4.131. Comparison of ²⁴¹Am-in-lung data with ICRP30 Class 'Y' prediction (from Carbaugh 2004).

Figure 4.131 shows Gene Carbaugh's updated summary of the ²⁴¹Am-in-lung data from the HAN-1 case, compared with the temporal behavior "predicted" by the ICRP Publication 30 (ICRP79) lung model - for Class 'Y' plutonium. Beyond 6,000 d, the measured ²⁴¹Am retention is about 30-fold *greater* than predicted.

We have analyzed these data using IMBA Professional Plus - with the current ICRP "default" assumption of Type 'S' absorption characteristics (Figure 4.132). The "fit" is better than for Class 'Y' - but still *very bad*. Figure 4.132 also compares the "predicted" build-up of ²⁴¹Am activity in the <u>Liver</u> and <u>Skeleton</u> with the *in vivo* measurements.



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Am-241		Max Likelihood fit									

Figure 4.132. Most likely "fit" to HAN-1 ²⁴¹Am-in-lung data assuming ICRP default HRTM parameter values (Type 'S').

<u>Note:</u> The predicted monotonic decrease of ²⁴¹Am activity in the lung includes the calculated "in-growth" of ²⁴¹Am activity into that of the parent ²⁴¹Pu.

In this example, IMBA Professional Plus automatically calculated the "in-growth" of ²⁴¹Am activity in the respiratory tract that resulted from the decay of ²⁴¹Pu. However, in order to do this, it was first necessary to *define* the <u>Isotopic Composition</u> of the inhaled plutonium material. This was done by treating all of the isotopes of plutonium that are present in the particle matrix as <u>Associated Radionuclides</u> of ²⁴¹Am (the <u>Indicator Nuclide</u>) - see Figure 4.133.

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Figure 4.133. Setting up plutonium isotopes as Associated Radionuclides.

Figure 4.133 shows the 5 associated plutonium isotopes -

²³⁸Pu, ²³⁹Pu, ²⁴⁰Pu, <u>241Pu</u> and ²⁴²Pu. <u>Note that</u> the "Abundance" of <u>241Pu</u> is very high (16,813% - relative to the ²⁴¹Am activity).

The calculated amount of <u>241Am</u> intake was <u>41,691 pCi</u> - on the assumption that the inhaled plutonium oxide (particle matrix) had Type 'S' absorption behavior. The relative abundance of <u>239Pu</u> was <u>621%</u> (<u>Table 4.11</u>). Therefore, the associated intake of <u>239Pu</u> would have been <u>258,900 pCi</u> (<u>258.9 nCi</u>).

We can test this estimate of the <u>239Pu</u> intake by comparing the predicted excretion rate in urine with that actually measured (<u>Table 4.15</u>). To do this, however, we have to set up a second "case" in IMBA Professional Plus - with <u>239Pu</u> as the <u>Indicator Nuclide</u>, and the amount of intake set at <u>258,900 pCi</u>. The resulting "predicted" urinary excretion rate is shown in Figure 4.134.

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Figure 4.134. Urinary excretion rate and lung retention predicted for Type 'S' plutonium.

The urinary excretion rate for inhaled Type 'S' plutonium is predicted to *decrease* after about 1,000 d (Figure 4.134). However, the trend in the measured values (from about 1,800 through 6,700 d) is for the actual urinary excretion rate to *increase* with time. Again, therefore, the "fit" to the observed temporal behavior of urinary excretion (of 239 Pu) is *not good*.

Summary of Observed Departures from ICRP-Default Behavior

The following observations are NOT consistent with the predictions (for a particle matrix consisting of Type 'S' plutonium):

- The the measured <u>241Am</u> activity in the lungs remained essentially constant over the first 70 d (Figure 4.135) - whereas Type 'S' absorption together with ICRP's recommended mechanical transport rates from the <u>alveolar-interstitial</u> (AI) region predicted a marked *decrease* of activity over this initial period (Figure 4.135). Note that the effect of "in-growth" of ²⁴¹Am activity as a result of ²⁴¹Pu decay over this period is *negligible*.
- 2. Over the long term (18 y) the <u>241 Am</u> activity in the lungs was observed to *increase* markedly whereas, for Type 'S' plutonium it should

have decreased approximately 10-fold (Figure 4.132).



Figure 4.135. Comparison of predicted and measured early changes in ²⁴¹Am activity in the lungs.

From the above, it appears that BOTH the *absorption characteristics* of the plutonium particle matrix AND the *mechanical elimination rate* of particles deposited in the "deep lung" of this *individual worker* differ substantially from the standard ICRP <u>default</u> values.

Note: ICRP has recommended that <u>Default</u> parameter values should be used <u>in</u> the absence of better (specific) information. This case is a prime example of significant departure in parameterized characteristics from the available defaults.

• Proceed to Optimizing the HRTM Parameter Values to Fit the HAN-1 Data.

Optimizing HRTM Parameter Values to Fit HAN-1 Data



In order to obtain a credible "fit" to ALL of the *HAN-1* data, we found it necessay to vary the following parameter values:

- 1. In the *HRTM Mechanical Transport Model* (Figure 4.136) the <u>rates of transport</u> to the bronchioles (compartments bb¹) from BOTH compartments Al¹ and Al² (of the alveolar-interstitial region).
- 2. In the HRTM Particle Absorption Model (Figure 4.137) the "slow" absorption rate.



3. In the HRTM Particle Deposition Model (Figure 4.138) - the aerosol AMAD.

Figure 4.136. User Defined values of the Rate Constants "AI1 to bb1" and "AI2 to bb2" - from their default values of "0.02 d-1" and "0.001 d-1", respectively.

These changes to the transport rates out of compartments AI¹ and AI² are equivalent to <u>eliminating</u> the "fast" and "intermediate" phases of mechanical particle clearance from the AI region. In other words, ALL of the material deposited in the AI region is cleared "slowly" - at the ICRP-recommended rate for "slow" clearance. Such clearance behavior has been observed previously in some individuals (<u>ICRP 1994a</u>) - and is not uncommon in cigarette smokers.



Figure 4.137. User Defined value of the "*Slow*" absorption rate (S^s) - from the default value of 0.0001 d-1 for Type 'S'.

This changed "slow" absorption rate (S^s) represents a <u>five-fold reduction</u> from the Type 'S' default values (0.0001 d-1).
00

🖏 Deposition Model	
Extrathoracic Ainways (ET, & ET2) Conducting Ainways (BB & bb) Deep Lung (A)	Exposure C Light Worker C Heavy Worker Aerosol Parameters AMAD AMAD AMTD Sigma-G Density 3 g/ml Shape factor 1.5
Clear	Select User Defined UOAD ICRP DEFAULTS User Defined User Defined

Figure 4.138. User Defined value of the aerosol AMAD (0.5 µm).

• Examine the Resulting "Fit" to the HAN-1 Data.

Tip #1: The parameter files "*HAN-1_Am-241.ix*" and "*HAN-1_Pu-239.ix*", for 241Am and 239Pu as the *Indicator Nuclide*, respectively, have been set up with these modified parameter values - together with the *HAN-1* "test" data. *Tip #1:* It is informative to try varying these parameter values - so as to understand the effect of each one on the overall "fit" to these data. You will find that the "approriate" range of parameter values is reasonably tightly defined.

Improved Representation of HAN-1 Data

Figure 4.139 shows the resulting improved "fit" to the measured build-up of 241Am activity in the lungs. Furthermore, Figure 4.140 shows that the very much improved "fit" to the observed early "constancy" of the 241Am activity in the lungs.



Figure 4.139. Improved "fit" to the measured ^{build-up} of 241Am activity in the lungs.



Figure 4.140. Resulting "fit" to the constant 241Am activity in the lungs maesured over the first 70 d.

You will have noted (from Figure 4.139) that we have <u>excluded</u> from this "fit" the last "block" of data (from about 5,000 d onwards). There is clearly a "discontinuity" in the measured values at about 5,000 d. By excluding these data, we have obtained a better overall "fit".

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^{Tip:} See for yourself how <u>inclusion/exclusion</u> of the last "block" of data affects the overall "fit". You will find that the effect is not unduly critical!

Figure 4.141 includes the "predicted" build-up of 241Am activity in the *Liver* and *Skeleton*.

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	000			700 1400 2100 2800 35
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		<u>D</u> K	\$ 100- \$ 50- 0 5	500 1000 1500 2000 2500 3000 35 Time since in
Am-241	fax Likelihood fit			

Figure 4.141. Improved overall "fit" to the HAN-1 data obtained by modifying parameter values in the HRTM.

Important Note: The calculated build-up of 241Am activity in the Liver and Skeleton does NOT include "in-growth" from 241Pu that is also taken up by these organs. IMBA Professional Plus calculates such_"in-growth" ONLY for the lungs - where it is assumed that 241Am formed from decay of 241 Pu in the particle matrix remains with the plutonium "bulk" material. For the Associated Radionuclides in body organs, including 241 Pu, progeny "ingrowth" is calculated ONLY as part of the Dose Calculation.
 Note: Skeletal Retention is NOT one of the 7 "explicit" ^{Bioassay Quantities} in IMBA Professional Plus. However, the "User Defined" quantity can be set up (with the appropriate bioassay function) to represent skeletal retention. Appendix A: Technical Basis includes a suitable bioassay function for americium retention in the skeleton. This is already implemented in the parameter file "HAN-1_Am-241.ix".

Figure 4.142 shows the resulting "fit" to the 239Pu excretion rate in urine. this is a substantially more "credible" representation of the measured values than the initial "prediction" - based on ICRP default parametr values (Figure 4.134).

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Pu-239	Max Likelihood fit		

Figure 4.142. Predicted 239Pu urinary excretion rate and lung retention.

^{Note:} As with the other example cases "solved" in this ^{User Manual}, the "solutions" offered are NOT intended to be scientifically definitive. They are

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• <u>Proceed</u> to Compare Doses Calculated using ICRP Default and Optimized Parameter Values.

Dose Calculation for HAN-1 Case

We can use EITHER the "*HAN-1_Pu-239.ix*" OR the "*HAN-1_Am-241.ix*" parameter file to calculate the resulting committed effective doses - so we will use BOTH - with the <u>10CFR835</u> tissue weighting factors.

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	Calculations	WR	WT			bb	0.00E+00	0.00E+00	
		· · · ·				AI	0.005+00	0.000 +00	
						Esophagus	0.00E+00	0.00E+00	
		Select				Gonads	1.68E-01	1.68E-01	
						Spare	0.00E+00	0.00E+00	
		(1) Dose from India	cator Nuclide: Pu-239		V	Remainder	0.00E+00	0.00E+00	
						TOTAL	1.51E+01	1.51E+01	
		(2) Dose from Ass	ociated Radionuclides						
						C Equiv	🖲 Eff	Associate	ed Rac
		(3) Annual Commit	ted Doses		Ξ	Target Organs	Eff Dose from Pu-238 (rem)	Eff Dose from Pu-240 (rem)	Eff Di Pu-24 (rem)
						bb	0.00E+00	0.00E+00	0.
			Effective Dr	una (unam)		Al	0.00E+00	0.00E+00	0.
			Ellective Dit	ve (rem)		LN(TH)	0.00E+00	0.00E+00	0.
		Calculate	3.49E+01	_		Esophagus	0.00E+00 2.94E-02	0.00E+00	1
						Space	0.00E+00	0.23E-02	0
						Remainder	0.00E+00	0.00E+00	0.
						TOTAL	2.95E+00	7.47E+00	6.
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					<u>o</u> k				
Pu-239 WR= ICRP I	Defaults WT	10 CFR 835	ICRP Pu Model						

Figure 4.143. Effective doses calculated using ²³⁹Pu as the Indicator Nuclide.

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					C Equiv	€ Eff	Indic	ator N
IR1 9.875E+03 P	α 				Target Organs	Dose (rem) IR(1)	Effective Dose (rem) Total	
	Calcula	tions WR	WT		<u>bb</u>	0.00E+00	0.00E+00	
					LN(TH)	0.00E+00	0.00E+00	
					Esophagus	0.00E+00	0.00E+00	
		Select			Gonads	4.42E-02	4.42E-02	
				_	Spare	0.00E+00	0.00E+00	
		(1) Dose from Inde	cator Nuclide: Am-241	M	TOTAL	2.52E+00	2.52E+00	
					< 101%L] 2.020400	2.022400	
		(2) Dose from Ass	ociated Radionuclides	N	C Equiv	€ Eff	Associate	d Rac
		(3) Annual Commit	ted Doses	E	Target Organs	Eff Dose from Pu-238 (rem)	Eff Dose from Pu-239 (rem)	Eff Di Pu-24 (rem)
					bb	0.00E+00	0.00E+00	0.
			Effective Dose (re	ml	Al	0.00E+00	0.00E+00	0.
			Eliocare Dose he	,	LN(TH) Econhagun	0.00E+00	0.00E+00	0.
		Calculate	3.49E+01		E sopragus Gonada	2 955-02	1.695-01	0.
					Spare	0.00E+00	0.00E+00	0.
					Remainder	0.00E+00	0.00E+00	0.
					TOTAL	2.96E+00	1.51E+01	7.
		000			< (2)			
(1)							Annual C	(ommit)
(2)								
(3)								
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				<u>O</u> K				
Am-241	WR= ICRP Defaults	WT= 10 CFR 835	ICRP Am Model					

Figure 4.144. Effective doses calculated using ²⁴¹Am as the Indicator Nuclide.

As expected, the calculated total effective dose is the same - irrespective of whether specific radionuclides are defined as the Indicator Nuclide or as an Associated Radionuclide. Table 4.16 summarizes the contributions to total effective dose made by each of the 6 radionuclides involved in this example - for both of the above calculations - and the fraction of effective dose contributed by radionuclide retention in the lungs. For comparison, the Table also shows the calculated effective dose that would result from the initial assumption of Type 'S' plutonium - and all ICRP default parameter values.

Contribution from:	Optimized Parameter Values - with 239Pu as the Indicator Nuclide	Optimized Parameter Values - with 241Am as the Indicator Nuclide	<u>ICRP Default</u> <u>Parameter Values –</u> <u>Type 'S' Plutonium</u>
<u>238Pu</u>	<u>2.95</u>	<u>2.96</u>	<u>3.05</u>
<u>239Pu</u>	<u>15.1</u>	<u>15.1</u>	<u>14.9</u>
<u>240Pu</u>	7.47	<u>7.48</u>	<u>7.30</u>
<u>241Pu</u>	<u>6.82</u>	<u>6.82</u>	<u>3.93</u>

Table 4.16. Contributions to effective dose (in rem and %).

<u>242Pu</u>	<u>0.00256</u>	<u>0.00252</u>	<u>0.00247</u>
<u>241Am</u>	<u>2.52</u>	<u>2.52</u>	<u>2.44</u>
Total from All Nuclides	<u>34.9 (100%)</u>	<u>34.9 (100%)</u>	<u>31.5 (100%)</u>
Total from Lungs	<u>27.7 (79%)</u>	<u>27.7 (79%)</u>	<u>10.9 (39%)</u>

Note #1: You will have noticed that the quantity "effective dose" is remarkably "robust" (at least, for highly insoluble plutonium). In this case, the changes that we had to make to the HRTM "input" parameter values - in order to "fit" the bioassay data - changed the total effective dose only marginally from that calculated using standard ICRP default parameter values. Using "case specific" parameter values increased the calculated effective dose by just 11%!
 Note #2: However, use of "case specific" HRTM parameter values DOES have a substantial effect on the distribution of effective dose between the Lungs and other body organs. The lung dose is calculated to increase by a factor of about 2.5 (154%).