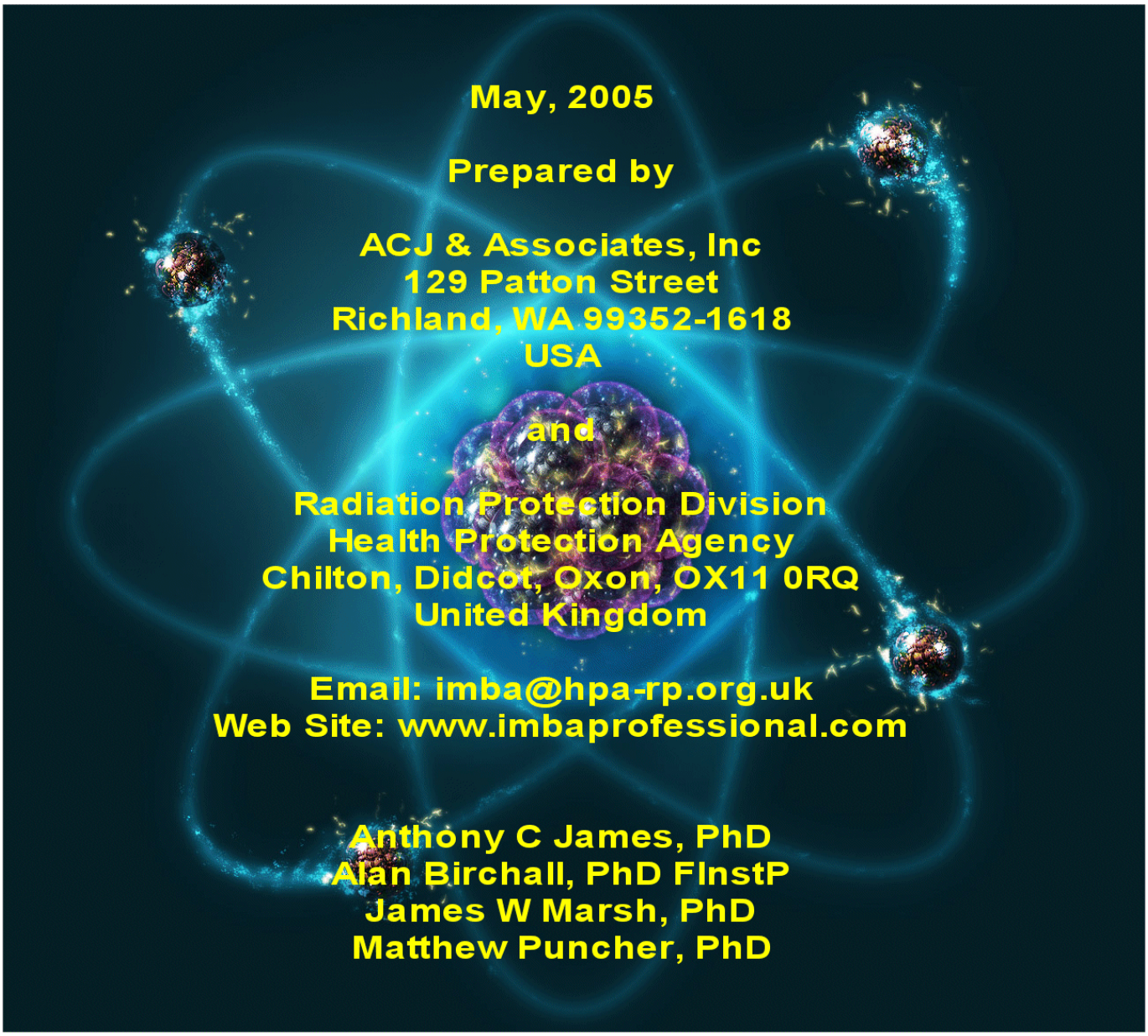
User Manual for

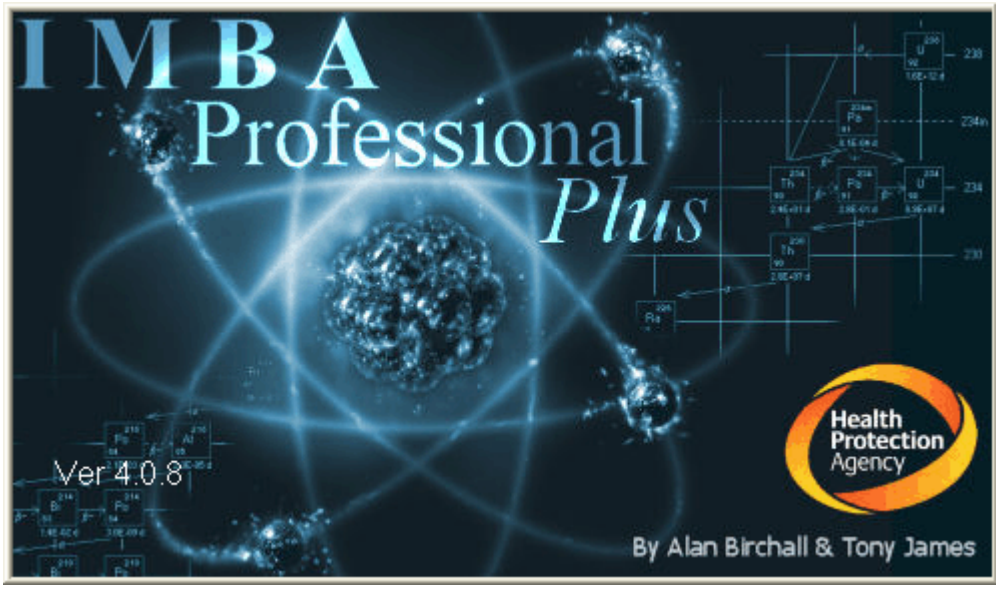
IMBA Professional Plus

(Version 4.0)



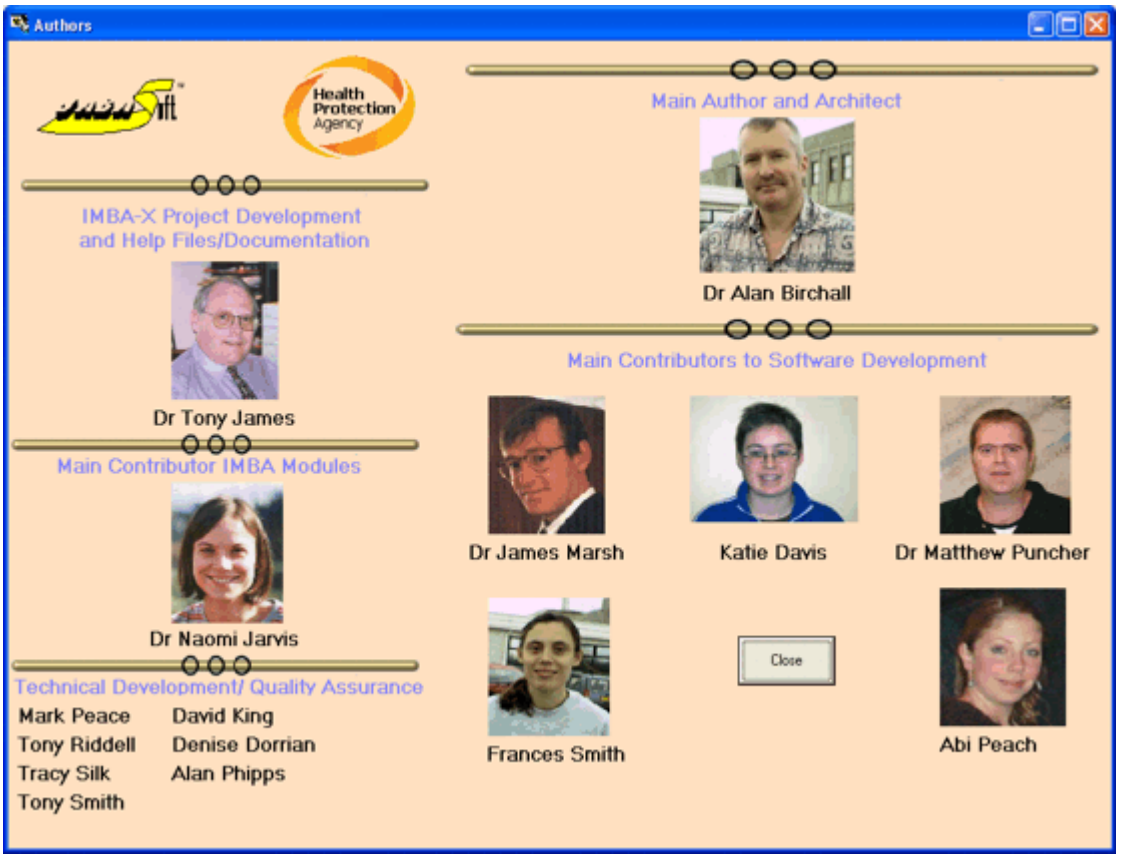
Origins of IMBA Professional Plus

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 **I**ntegrated **M**odules for **B**ioassay **A**nalysis (**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™ and IMBA Professional Series of software products (*i.e.*, all IMBA-based software applications distributed previously).

Authors and Acknowledgements



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

Dr. Tony James (ACJ & Associates, Inc.) 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.

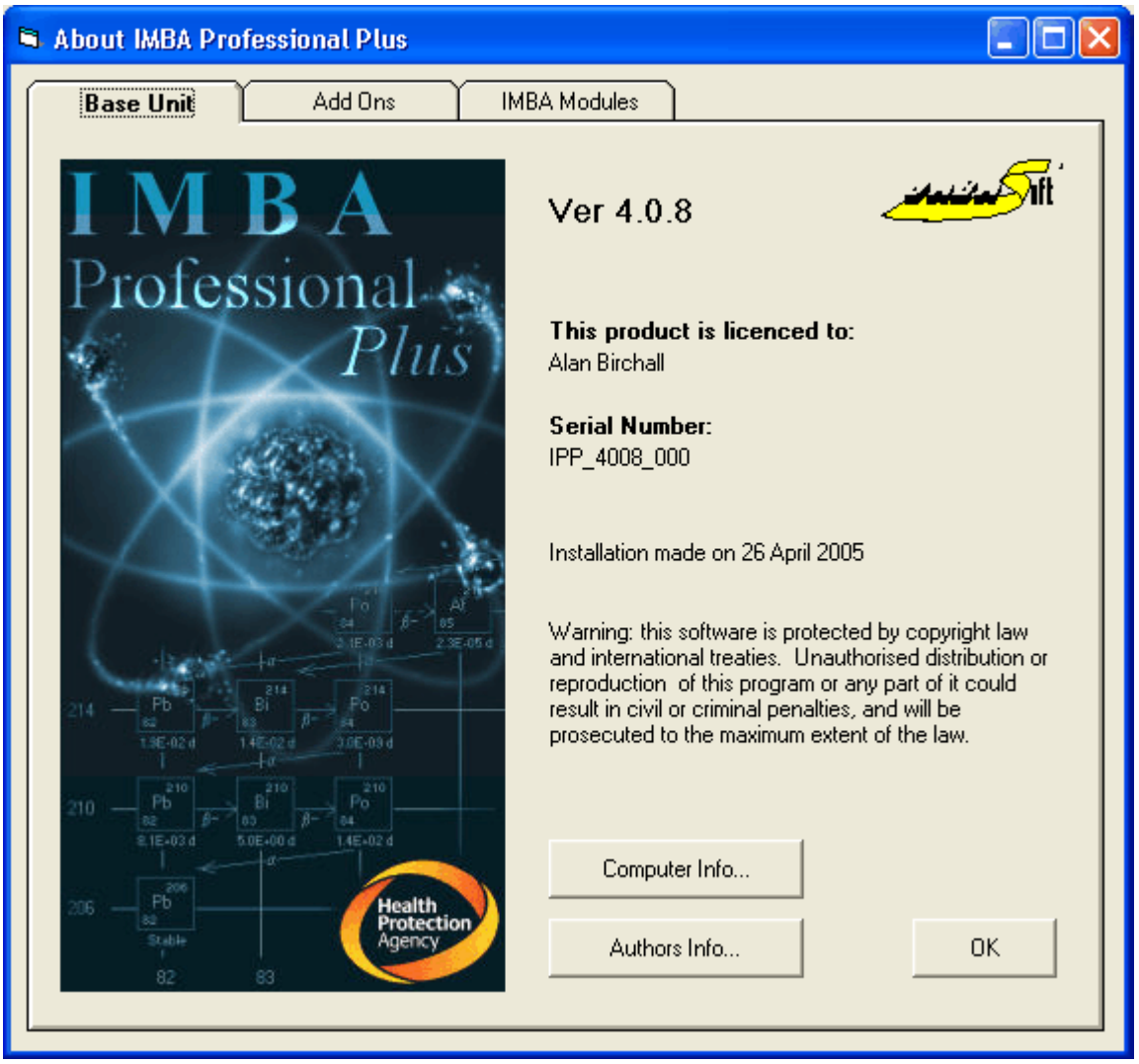
Dr. Naomi Jarvis (US Consultant) developed the extensions of NRPB's **IMBA Suite** needed for IMBA Expert™/Professional Plus to perform their specialized calculations.

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.

IMBA Professional Plus - Base Unit



IMBA Professional Plus (Version 4.0) is a compilation of features and capabilities developed for IMBA Expert™ USDOE-Edition, IMBA Expert™ CANDU-Edition, and IMBA Expert™ OCAS-Edition, with new features developed by HPA-RPD. 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** (^{140}Ba);
- **caesium** (^{134,137}Cs);
- **californium** (^{252}Cf);
- **carbon** (^{14}C) - as particulate or as gaseous or vapor forms of carbon;
- **cerium** (^{141,144}Ce);
- **chromium** (^{51}Cr);
- **cobalt** (^{57,58,60}Co);
- **curium** (^{242,243,244}Cm);
- **europium** (^{152,154,155,156}Eu);
- **hafnium** (^{181}Hf);
- **hydrogen [tritium]** (^{3}H) - 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** (^{140}La);
- **manganese** (^{54}Mn);
- **neptunium** (^{237,239}Np);
- **nickel** (^{63}Ni);
- **niobium** (^{94,95}Nb);
- **phosphorus** (^{32,33}P);
- **plutonium** (^{238,239,240,241,242}Pu);
- **promethium** (^{147}Pm);
- **protactinium** (^{231}Pa);
- **polonium** (^{210}Po);
- **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** (^{35}S) - as particulate, for both inorganic and organically incorporated sulfur -

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

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

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).

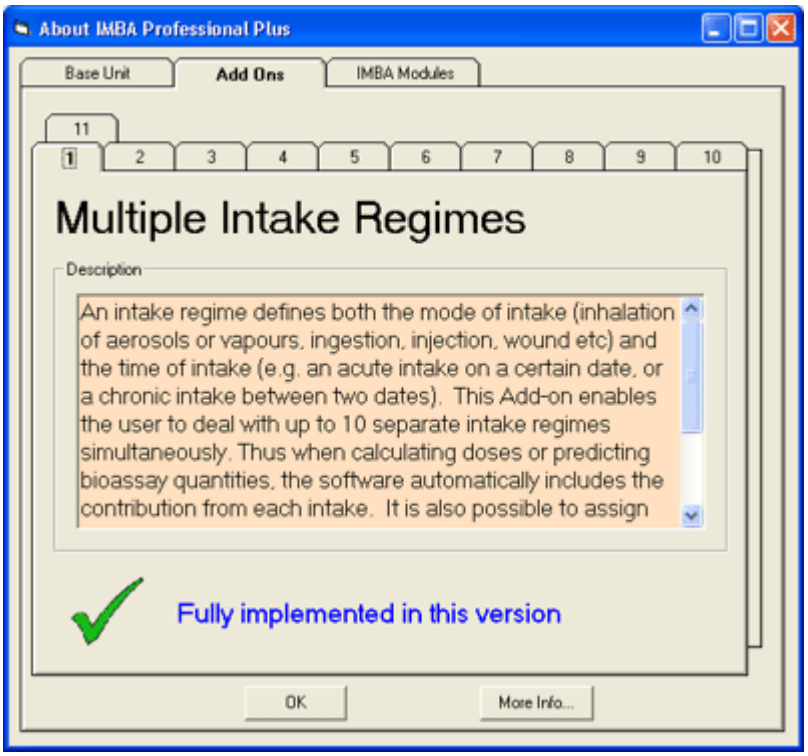
- Obtain the **best estimate** of the amount of intake - repeating the calculation with the same assumptions and data yields an identical result.
- Calculate the **committed equivalent dose to each organ or tissue -** and the **effective dose -** from an **indicator radionuclide**.
- Toggle between **ICRP60/68**, 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 Add Ons provide additional, highly specialised, fully-integrated features, which greatly enhance the software's functionality.

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 - Multiple Intake Regimes.
- Add-On 2 - Multiple Bioassay Types.
- Add-On 3 - Associated Radionuclides.
- Add-On 4 - Uranium Mixtures.
- Add-On 5 - Uptake from a Wound.
- Add-On 6 - Errors on Intake.
- Add-On 7 - Bayes Implementation.
- Add-On 8 - Tritium Tool.
- Add-On 9 - Dose Calculations for Causation.
- 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 IMBA Professional Plus web site.

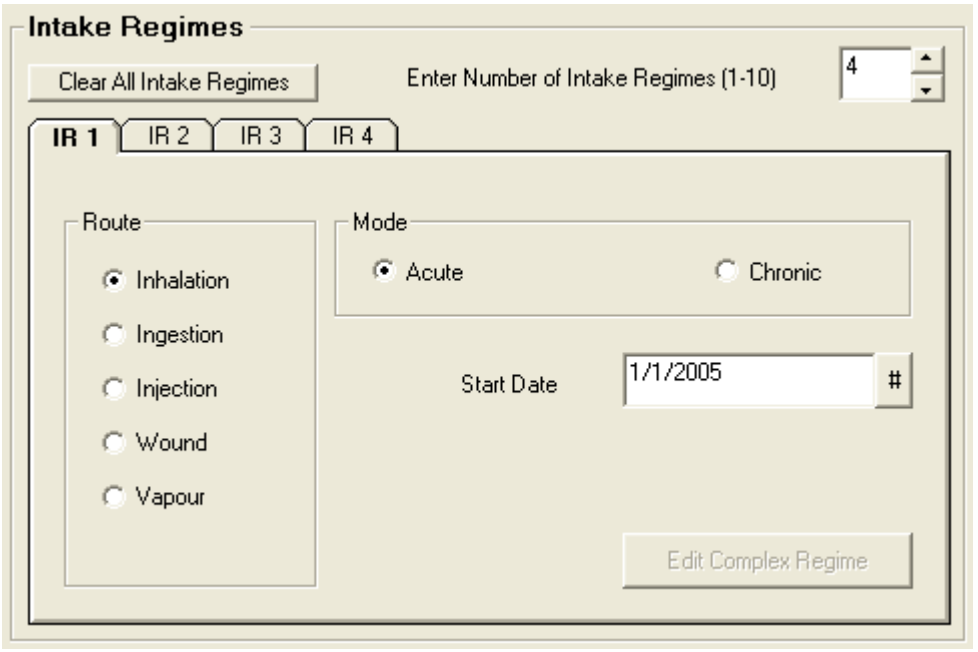
Add-On 1: Multiple Intake Regimes

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 Main screen. You select the number of intake regimes, and each intake regime (IR) can be set up independently by selecting the appropriate tab.



In the Bioassay screen, the single intake on the left hand side of the screen is replaced by the chosen number of intakes. For dose calculations, 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 Case of Multiple Intakes.
- Return to List of Add-Ons.

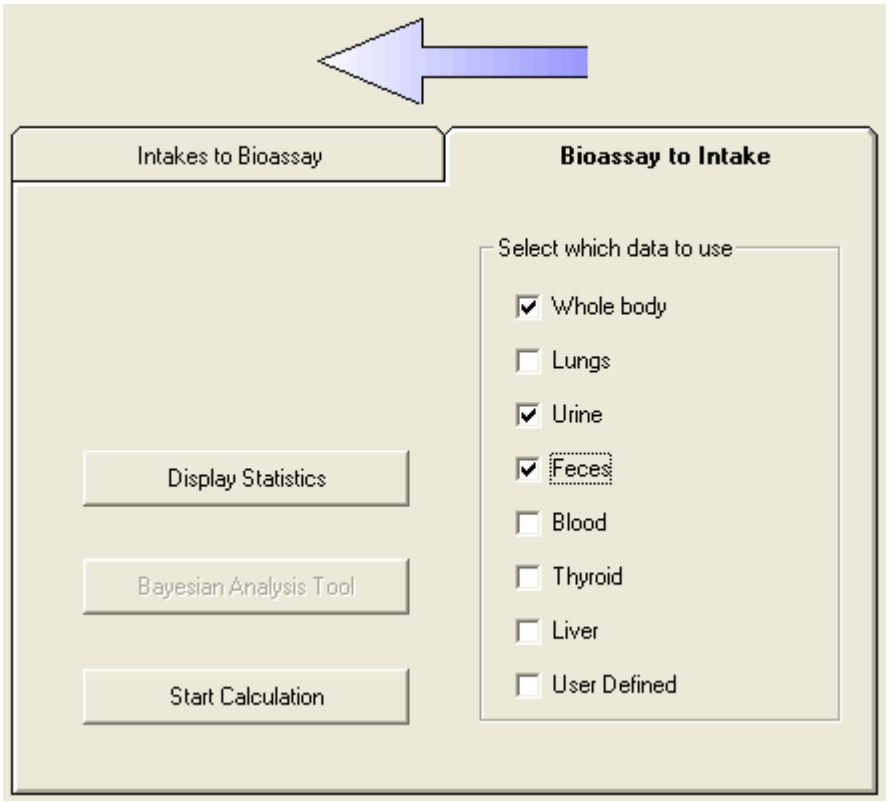
Add-On 2: Multiple Bioassay Types

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 Bioassay screen 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.



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

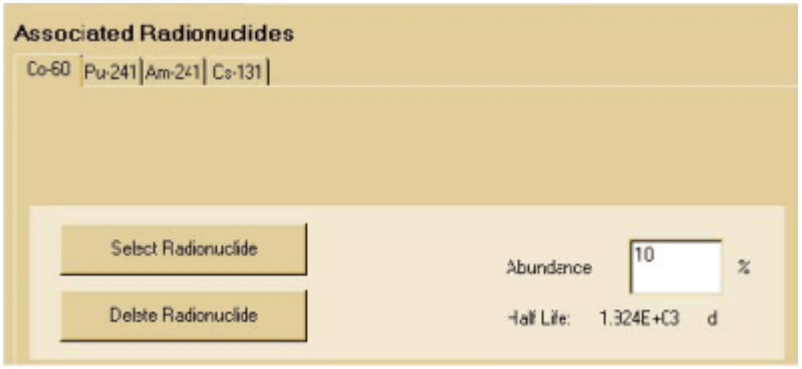
Add-On 3: Associated Radionuclides

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 associated radionuclide 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.**



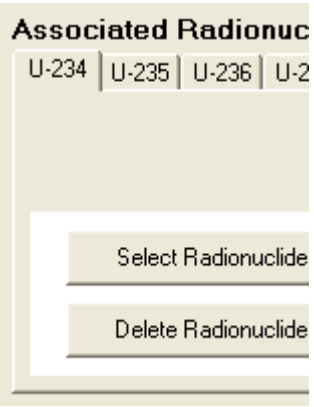
- For an example of a dose calculation involving associated radionuclides see Doses from Associated Radionuclides.

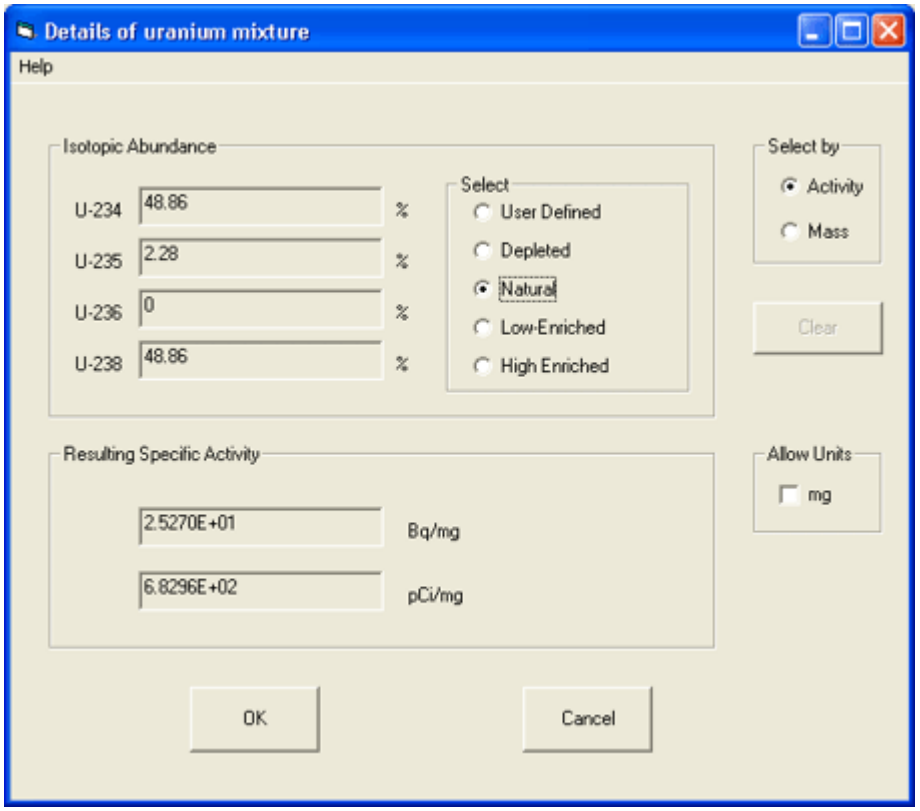
- Return to List of Add-Ons.

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.**





After exiting this screen, the uranium isotopes are automatically included as associated radionuclides with the selected abundances**. 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 Case of Uranium Isotopic Mixture.

- Return to List of Add-Ons.

Add-On 5: Uptake from a Wound

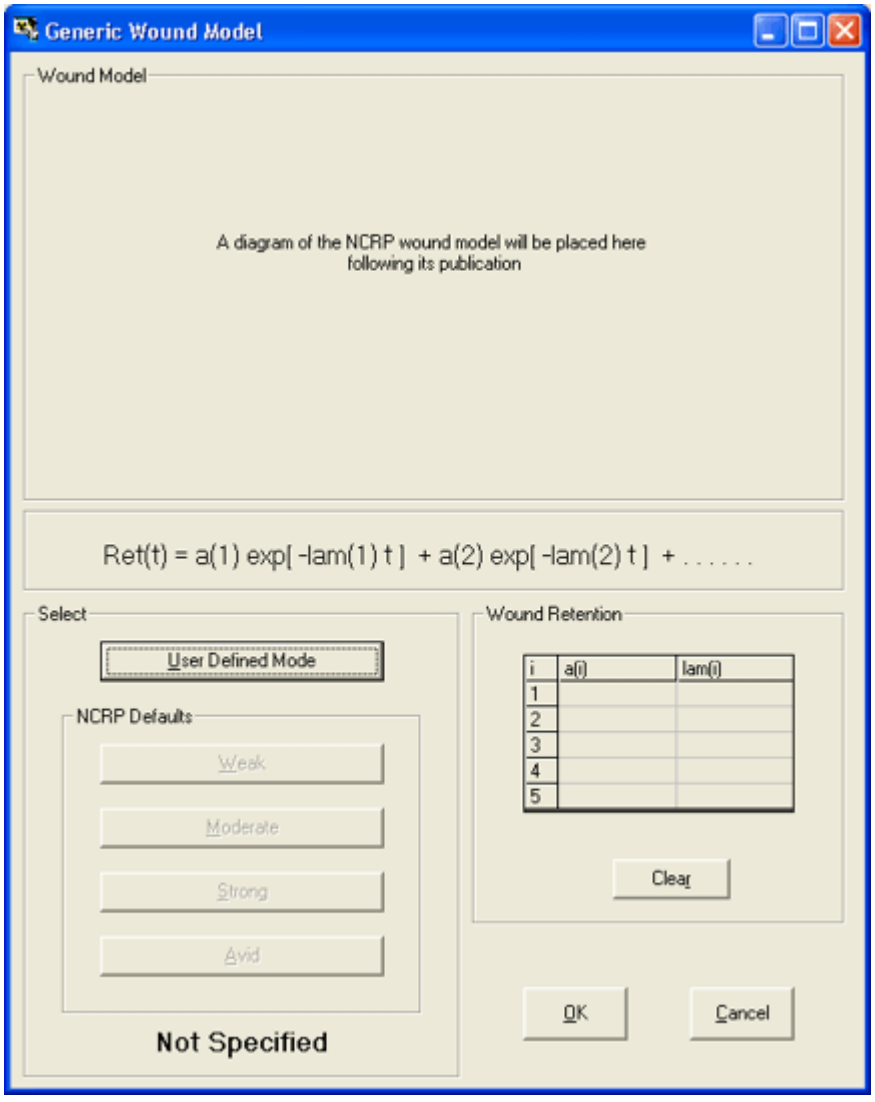
Description

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.



- For an example of a bioassay analysis and dose calculation involving a intake via a wound see Case of Wound Uptake.

- Return to List of Add-Ons.

Add-On 6: Errors on Intake

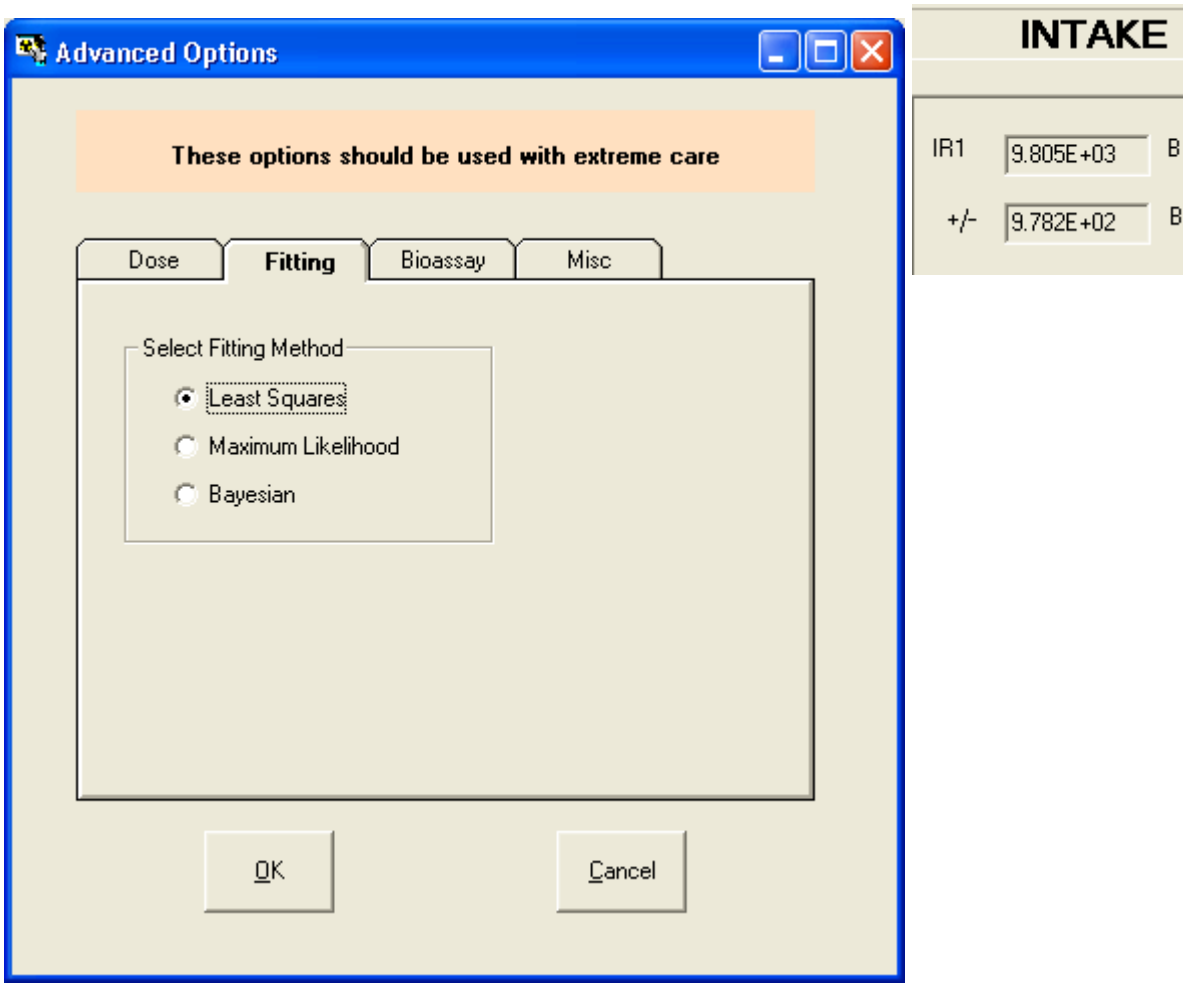
Description

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.



- For an example involving the estimation of errors on calculated values of intake see Case Evaluating Errors on Intake.
- 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 Bayesian approach 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 Multiple Intake Regimes 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 Case Implementing Bayesian Analysis.
- 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 Case Implementing Tritium Tool.
- 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 Dose Calculations for Causation.
- Return to List of Add-Ons.

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

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

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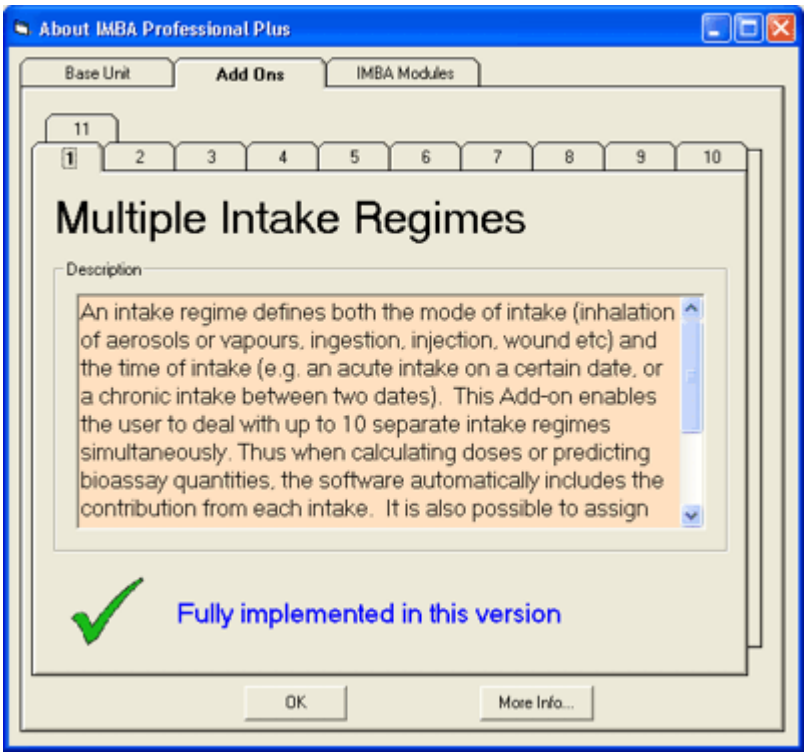
- For an example using the statistics package to evaluate an intake see Case Using Statistics Package.
- Return to List of Add-Ons.

Additional Functionality in IPP "Add-Ons"



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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 IMBA Professional Plus web site.

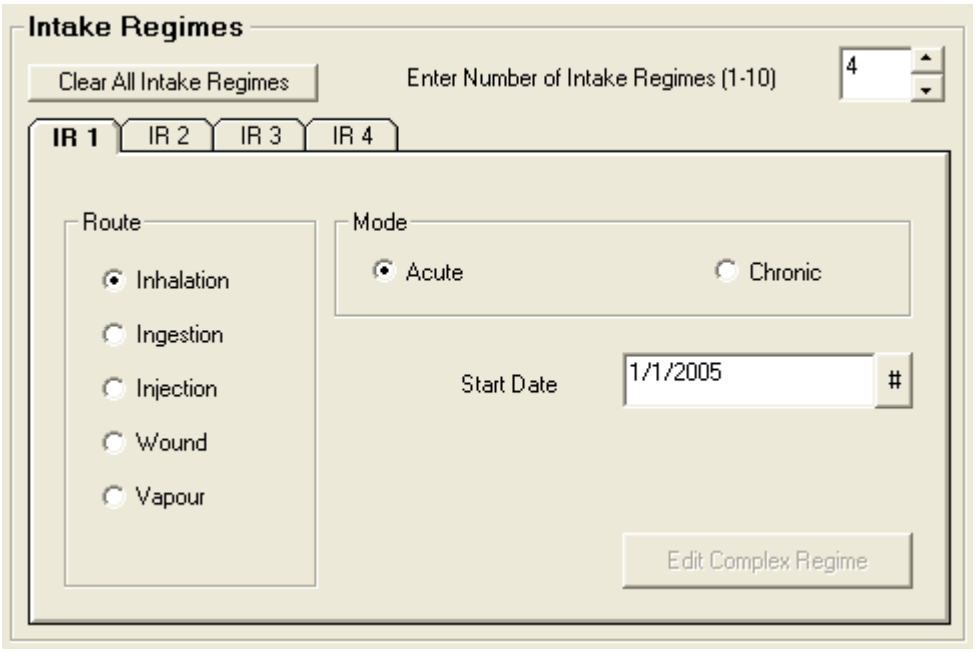
Add-On 1: Multiple Intake Regimes

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 Main screen. You select the number of intake regimes, and each intake regime (IR) can be set up independently by selecting the appropriate tab.



In the Bioassay screen, the single intake on the left hand side of the screen is replaced by the chosen number of intakes. For dose calculations, 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 Case of Multiple Intakes.
- Return to List of Add-Ons.

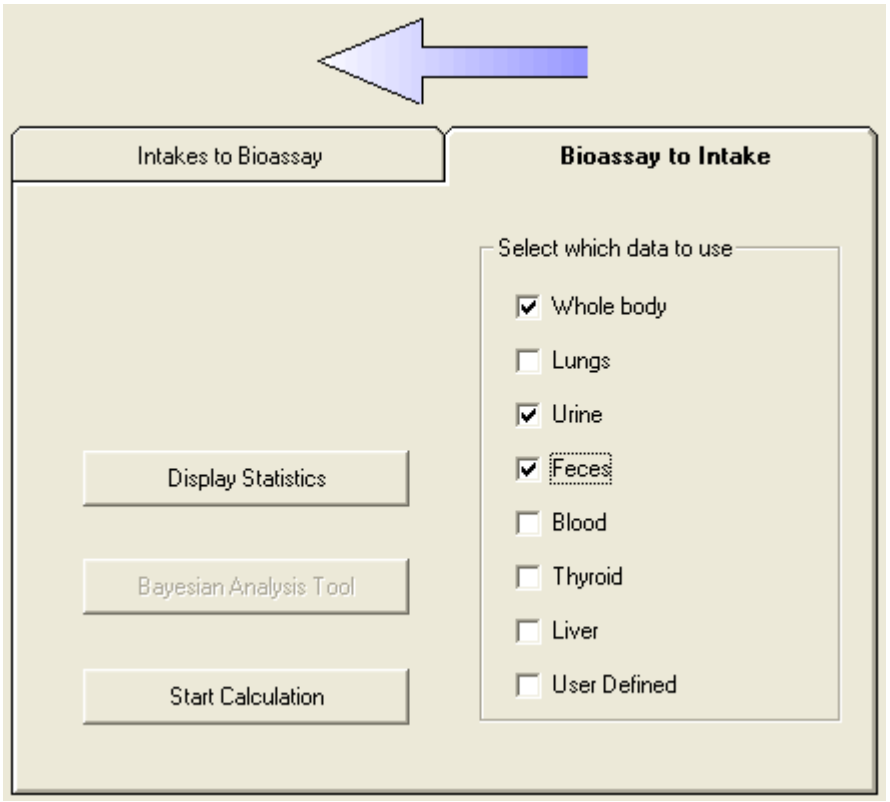
Add-On 2: Multiple Bioassay Types

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 Bioassay screen 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.



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

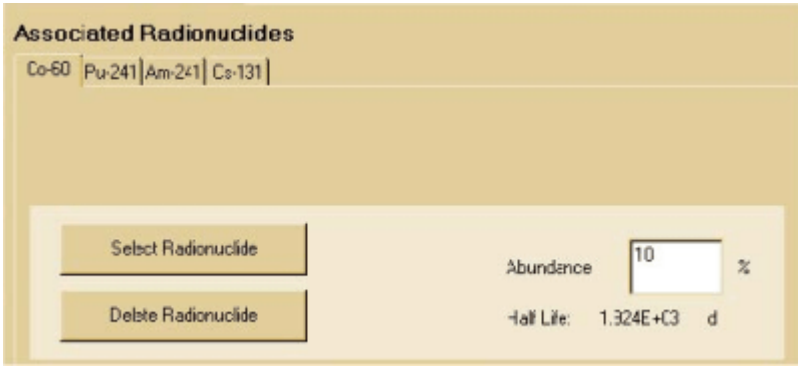
Add-On 3: Associated Radionuclides

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 associated radionuclide 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.**



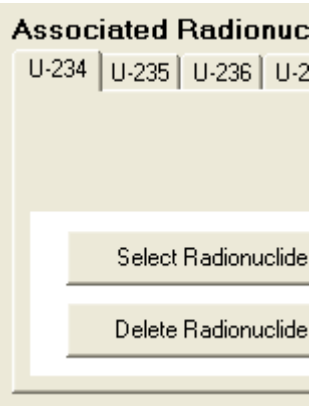
- For an example of a dose calculation involving associated radionuclides see Doses from Associated Radionuclides.

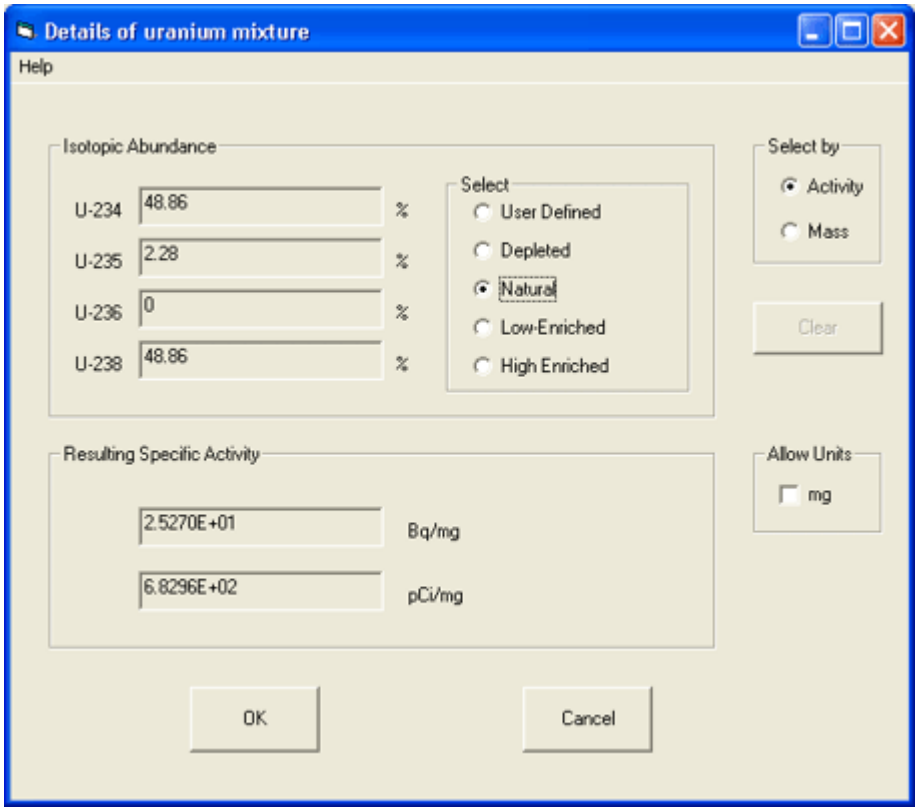
- Return to List of Add-Ons.

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.**





After exiting this screen, the uranium isotopes are automatically included as associated radionuclides with the selected abundances**. 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 Case of Uranium Isotopic Mixture.

- Return to List of Add-Ons.

Add-On 5: Uptake from a Wound

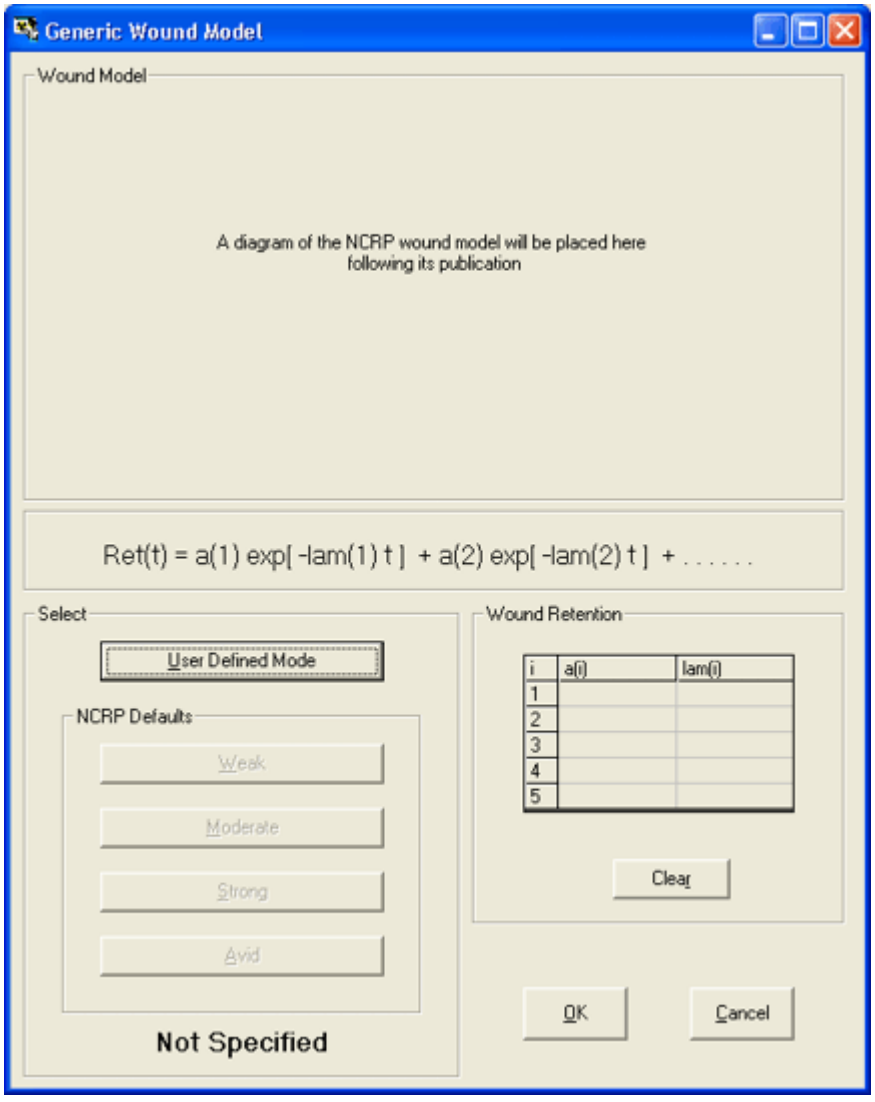
Description

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.



- For an example of a bioassay analysis and dose calculation involving a intake via a wound see Case of Wound Uptake.

- Return to List of Add-Ons.

Add-On 6: Errors on Intake

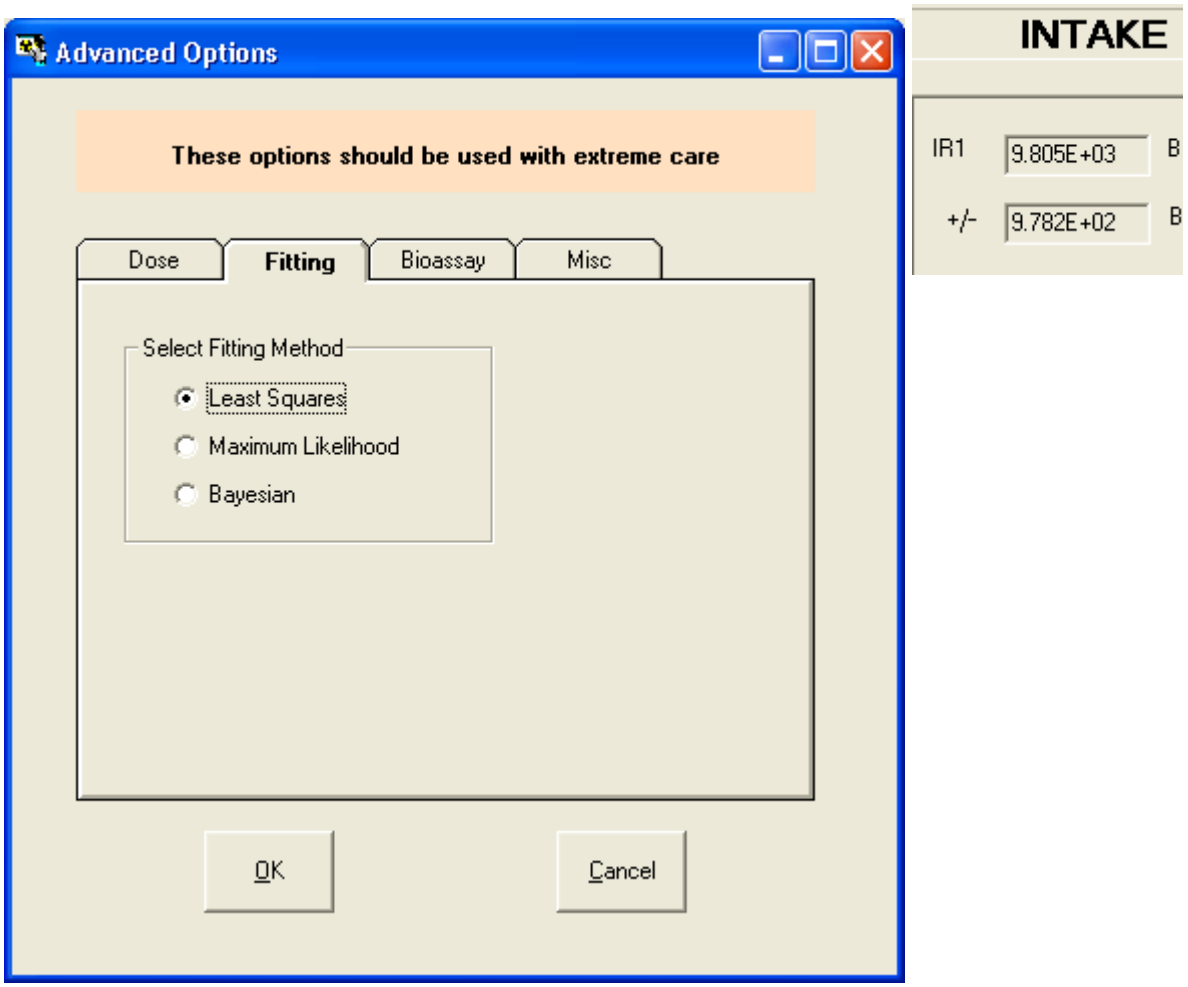
Description

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.



- For an example involving the estimation of errors on calculated values of intake see Case Evaluating Errors on Intake.
- 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 Bayesian approach 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 Multiple Intake Regimes 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 Case Implementing Bayesian Analysis.
- 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 Case Implementing Tritium Tool.
- 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 Dose Calculations for Causation.
- Return to List of Add-Ons.

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

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

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 Case Using Statistics Package.
- Return to List of Add-Ons.

"What's This?" - Visual Tour

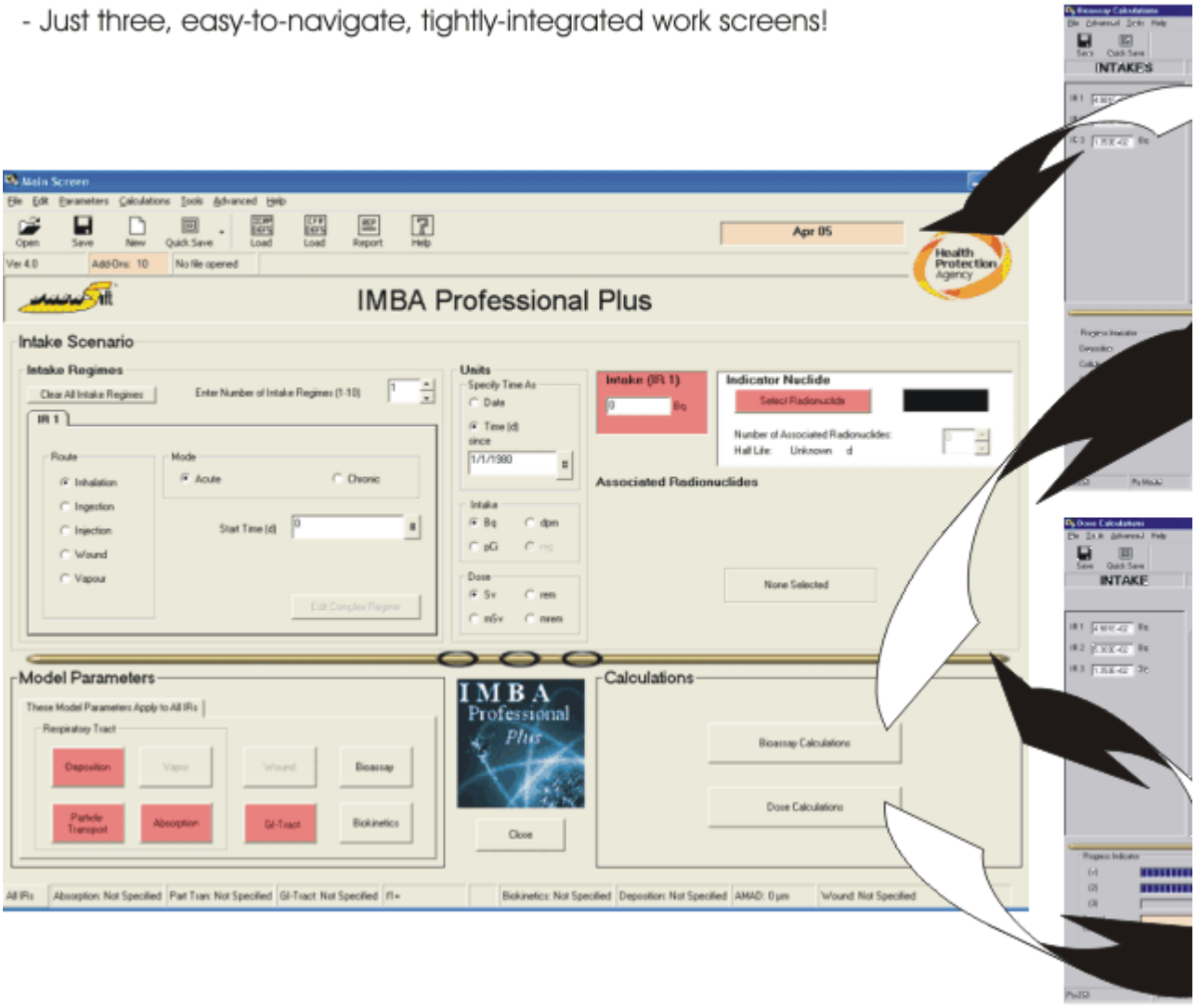
This **tour** will **guide** you through the layout and operation of IMBA Professional Plus' three working screens, and the tools provided for data entry, export, and visualization:

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

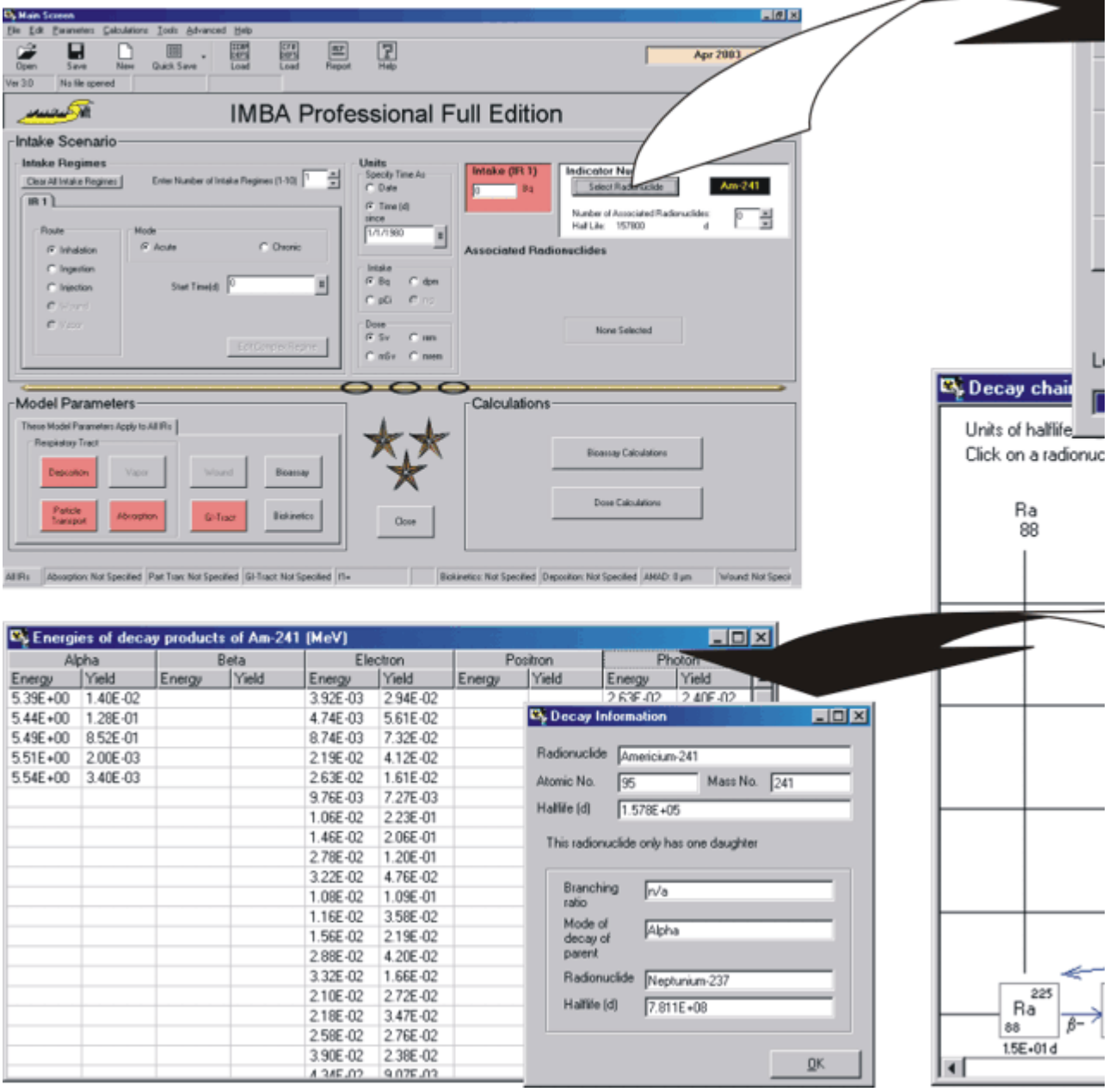
Visual Tour of Main Screen

IMBA Professional Plus

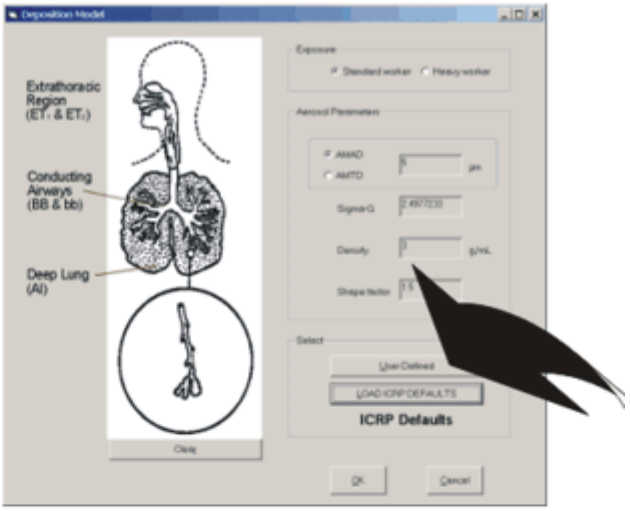
- Just three, easy-to-navigate, tightly-integrated work screens!

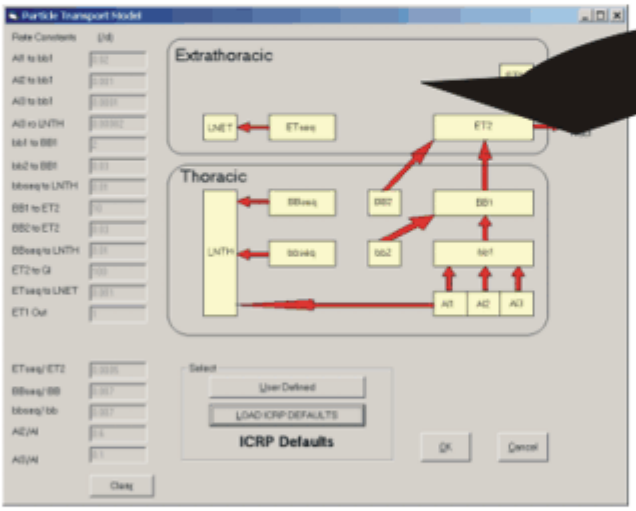


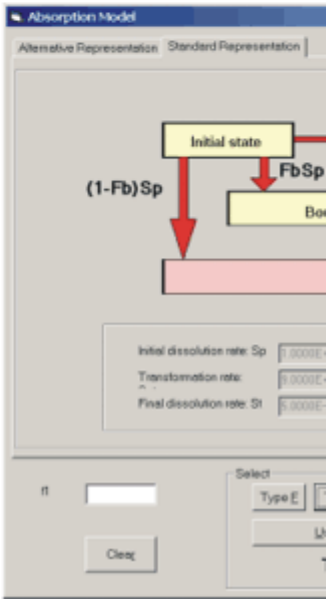
Radionuclide Database (ICRP Publication 38)



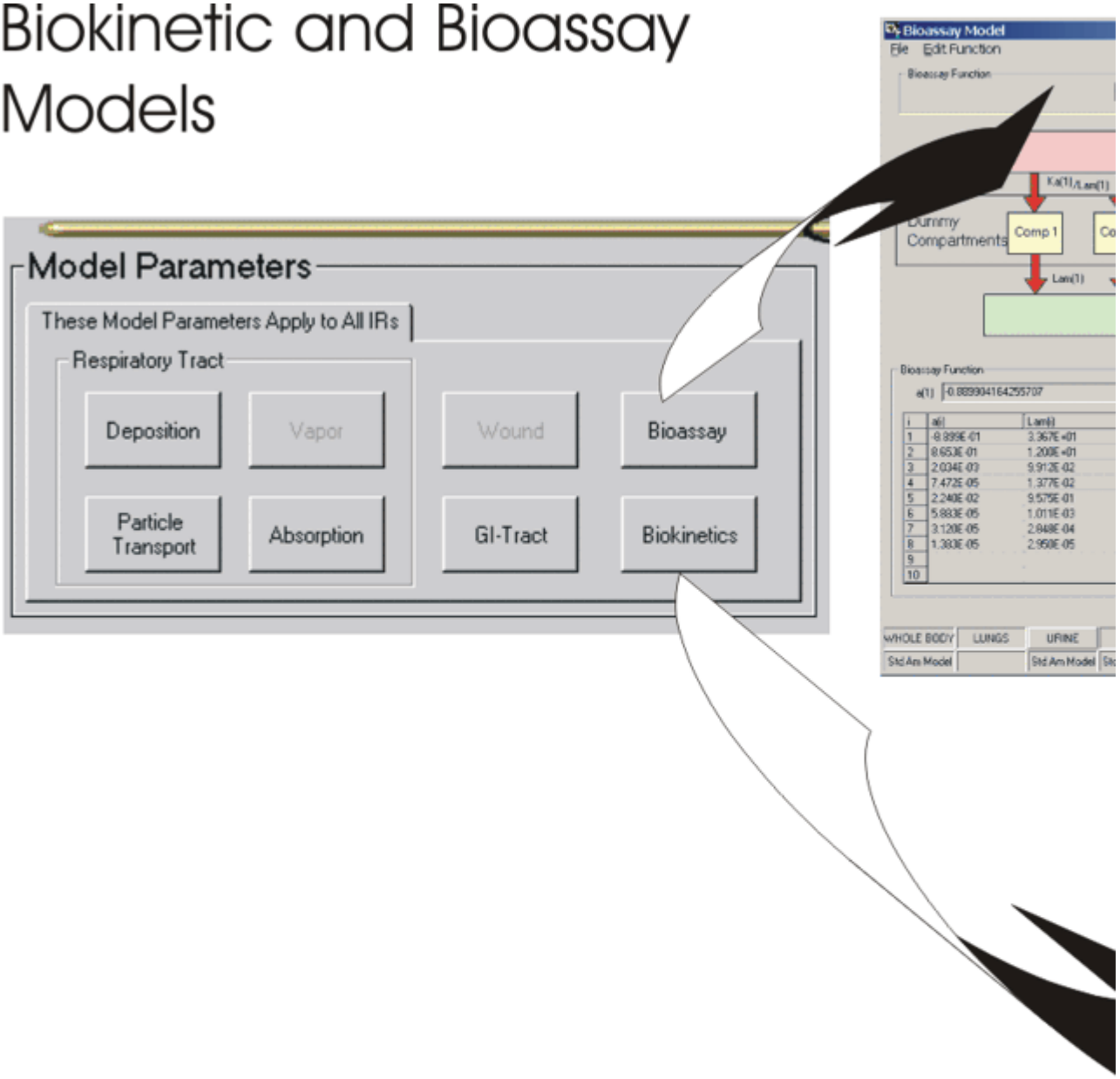
Respiratory Tract and Gut Models







Biokinetic and Bioassay Models



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).

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 Additional Functionality in "Star" and "Professional" Editions.

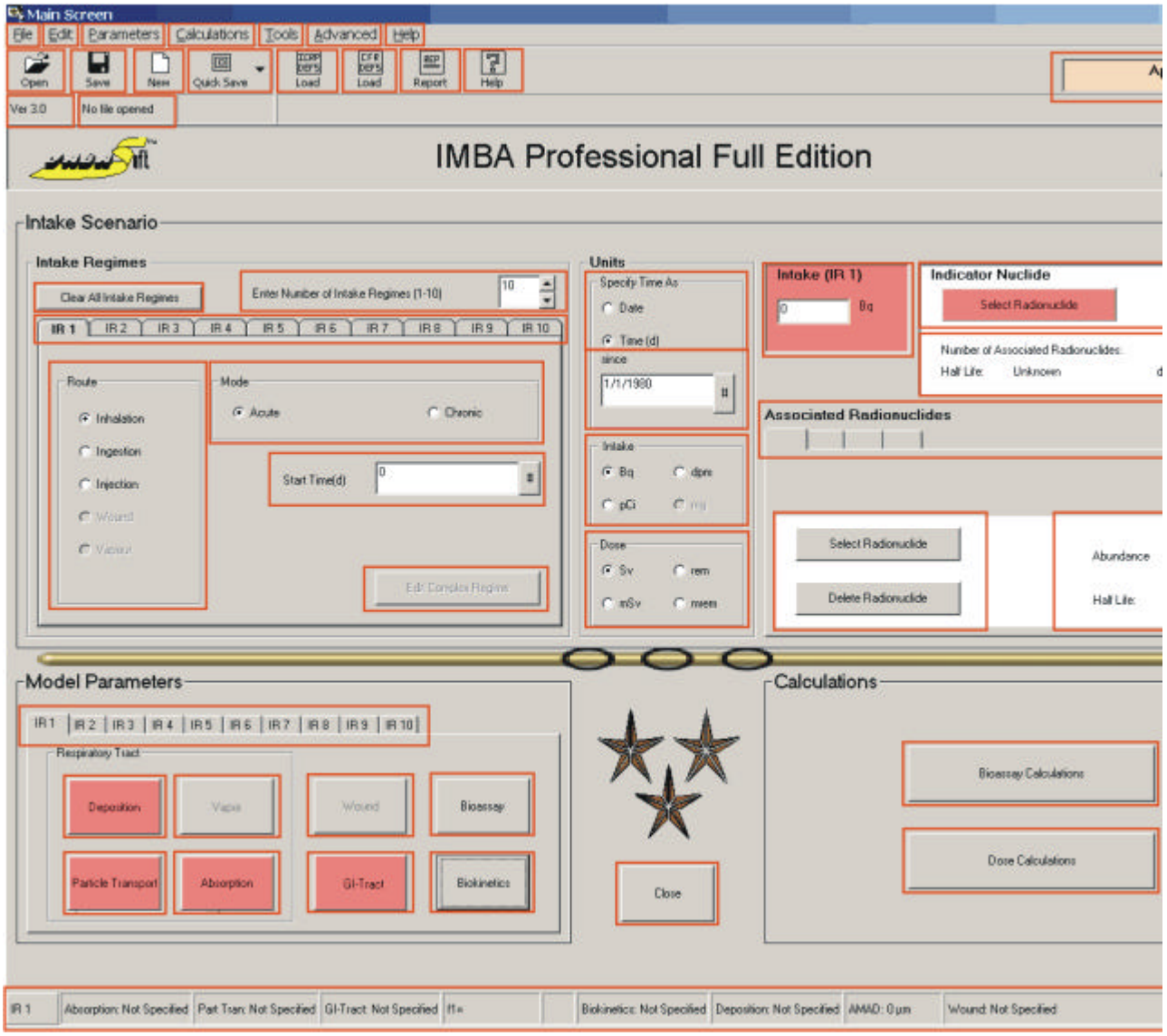
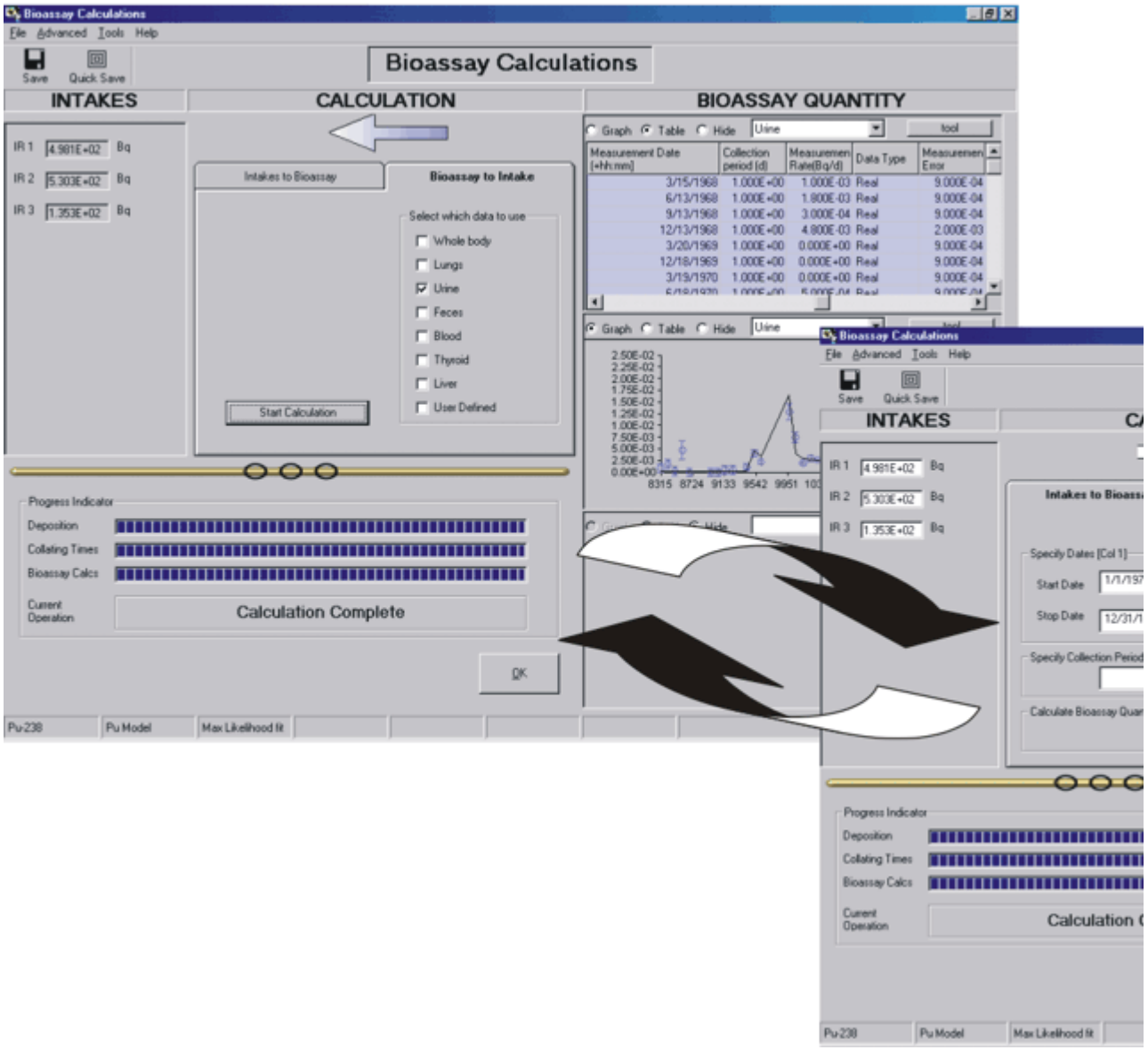


Figure 2.5. What's in the **Main Screen**?

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 Additional Functionality in "Star" and "Professional" Editions.

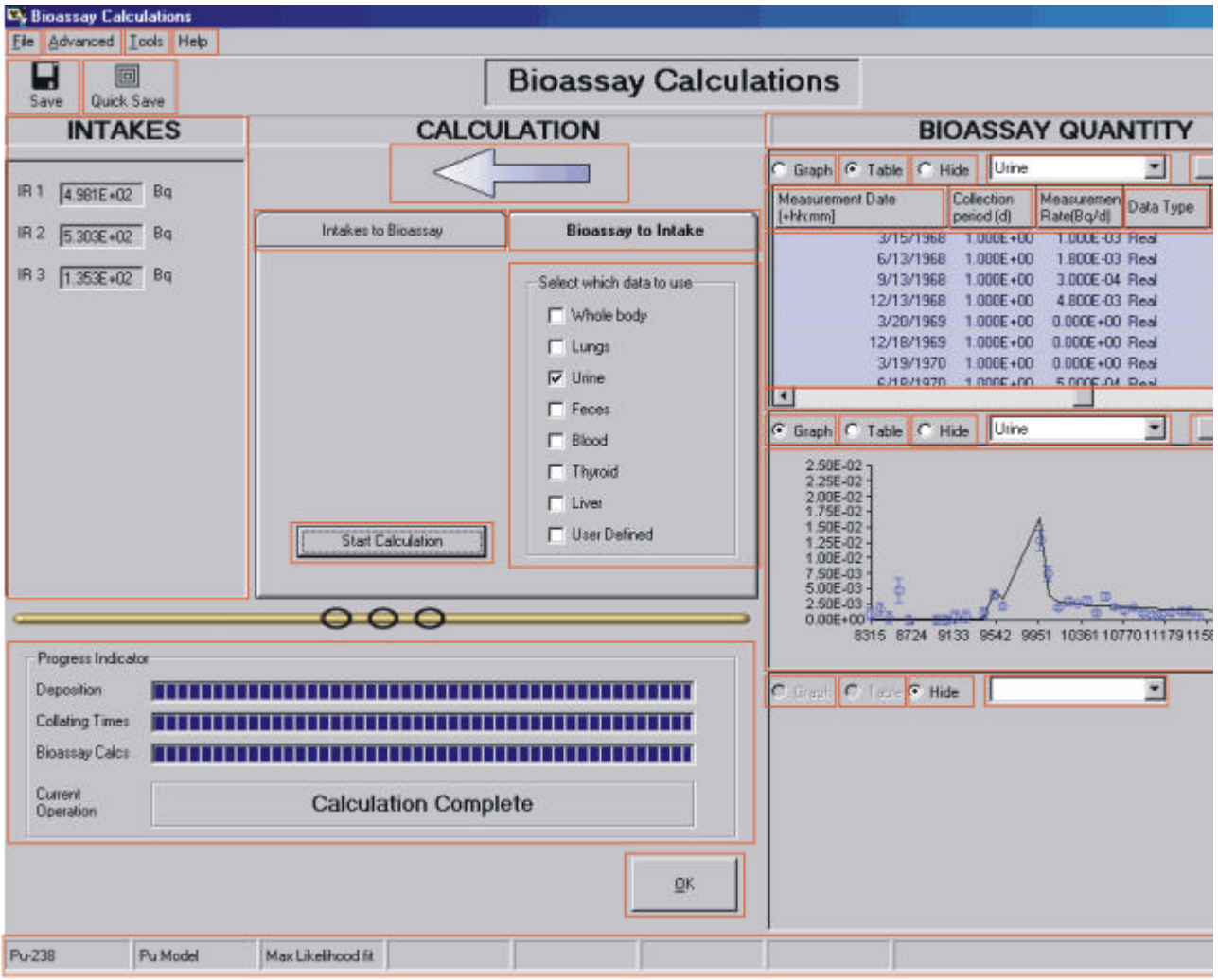


Figure 2.7. Bioassay Calculations screen in default "**Bioassay to Intakes**" mode.

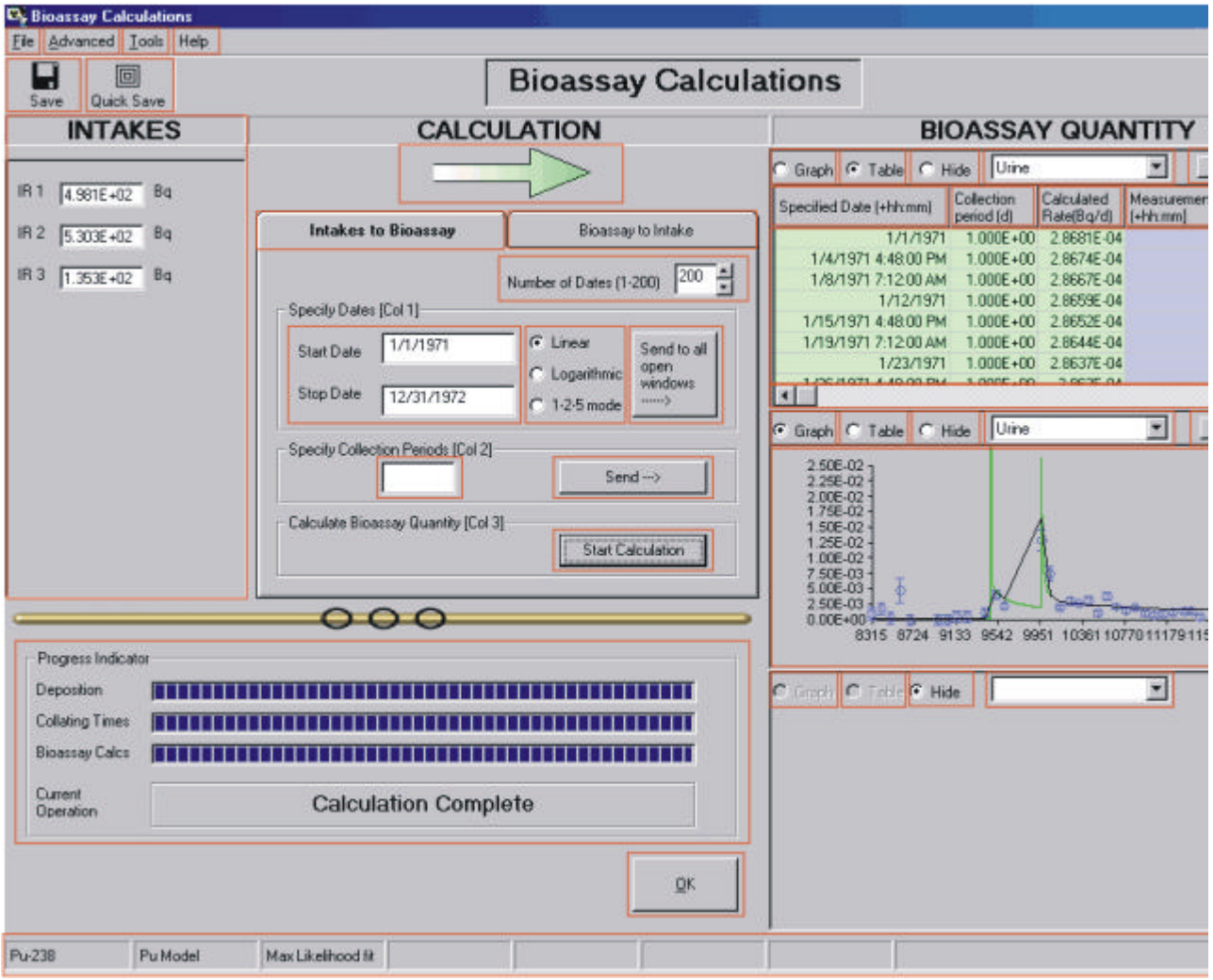
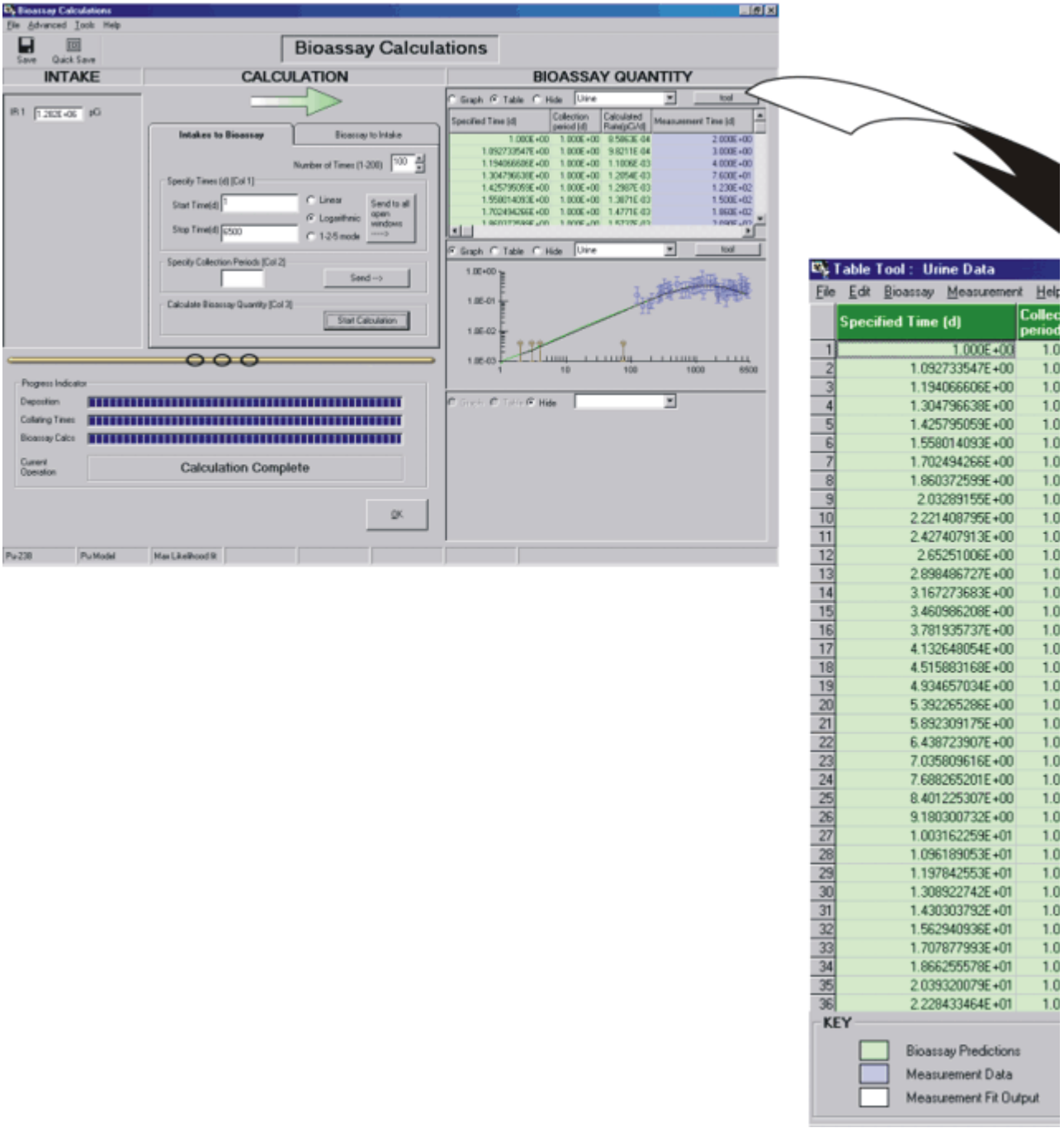


Figure 2.8. Bioassay Calculations screen with "**Intakes to Bioassay**" mode selected.

Visual Tour of the Table Tool



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

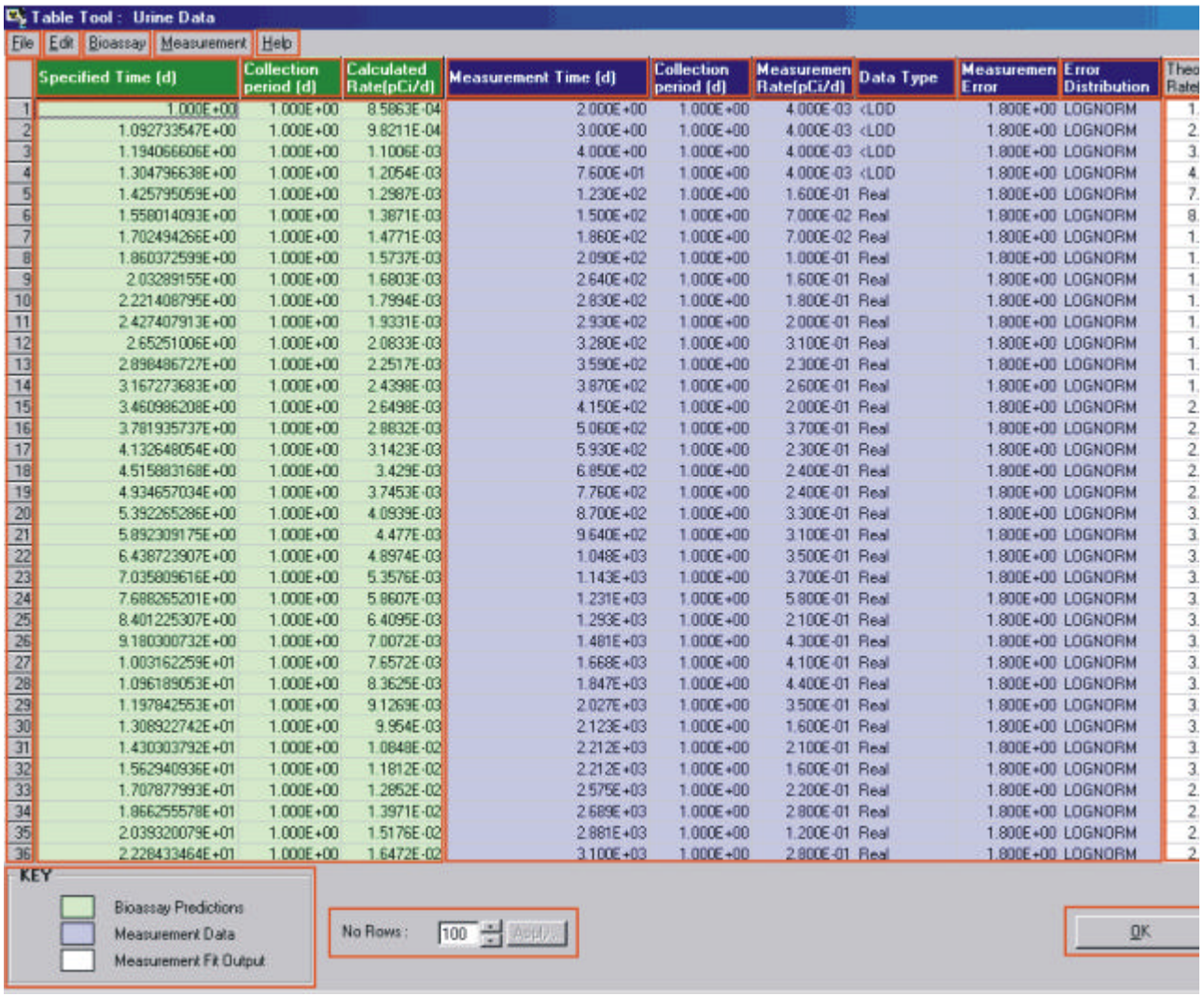
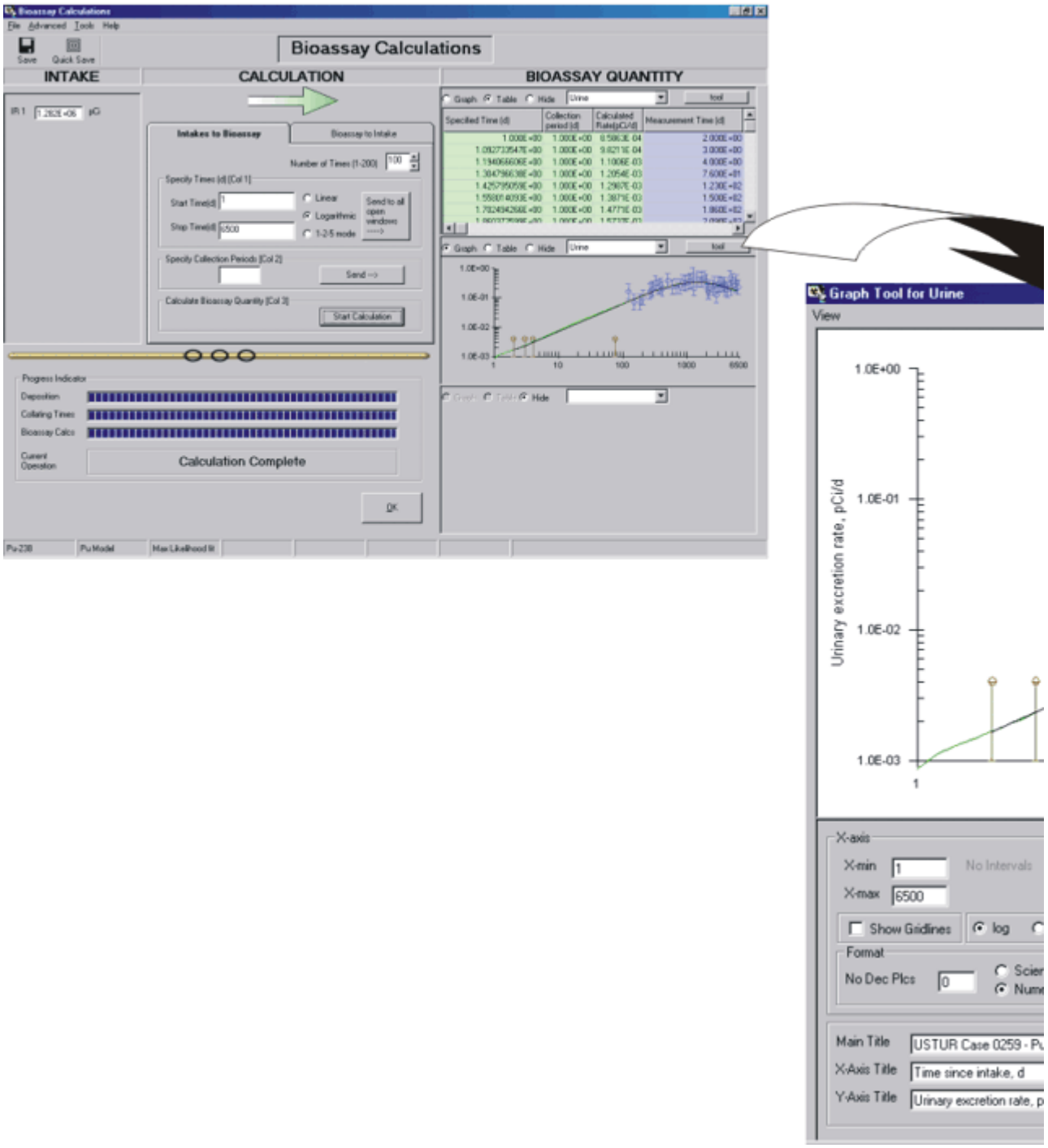


Figure 2.10. What's in the Table Tool?

Visual Tour of the Graph Tool



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

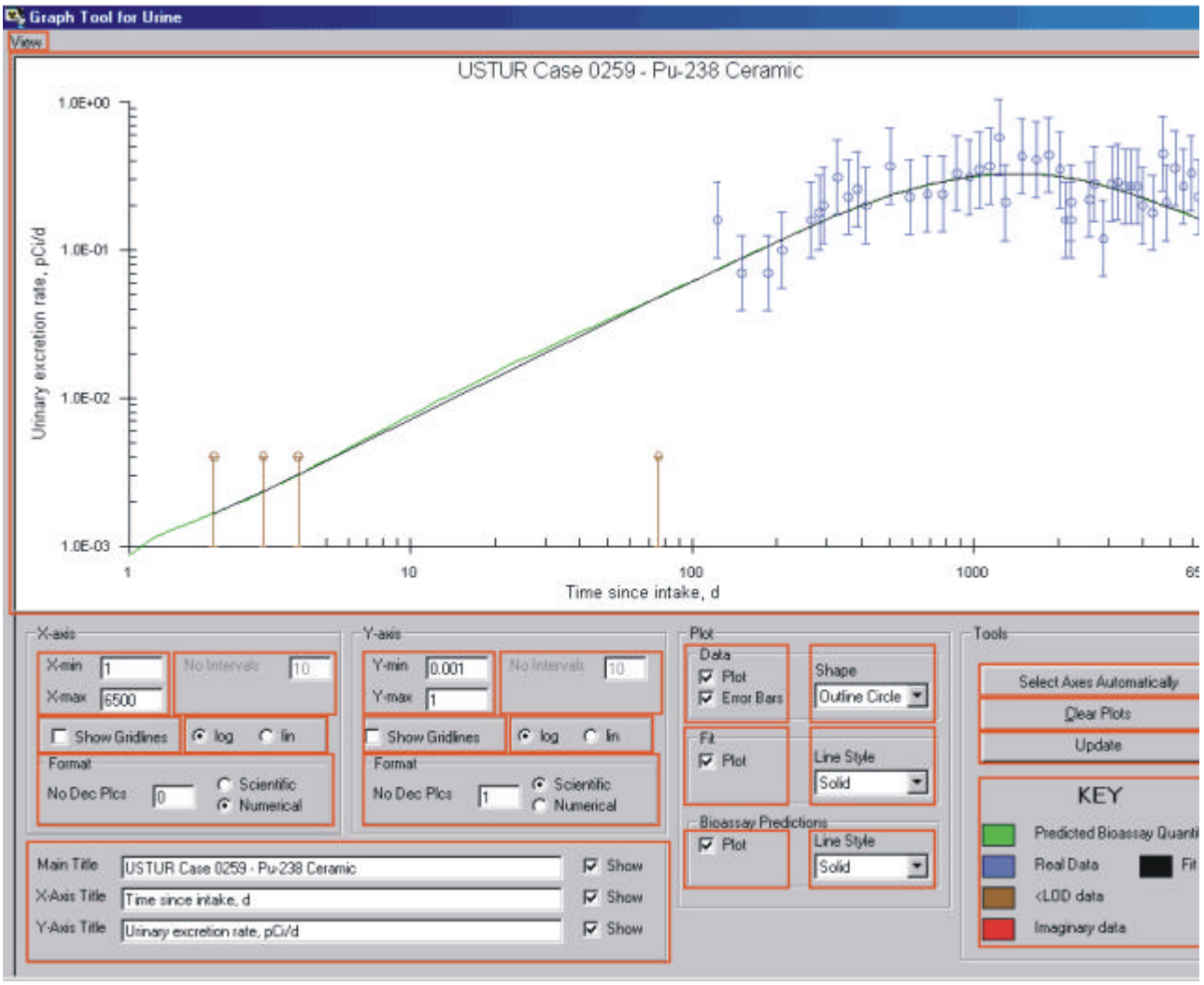
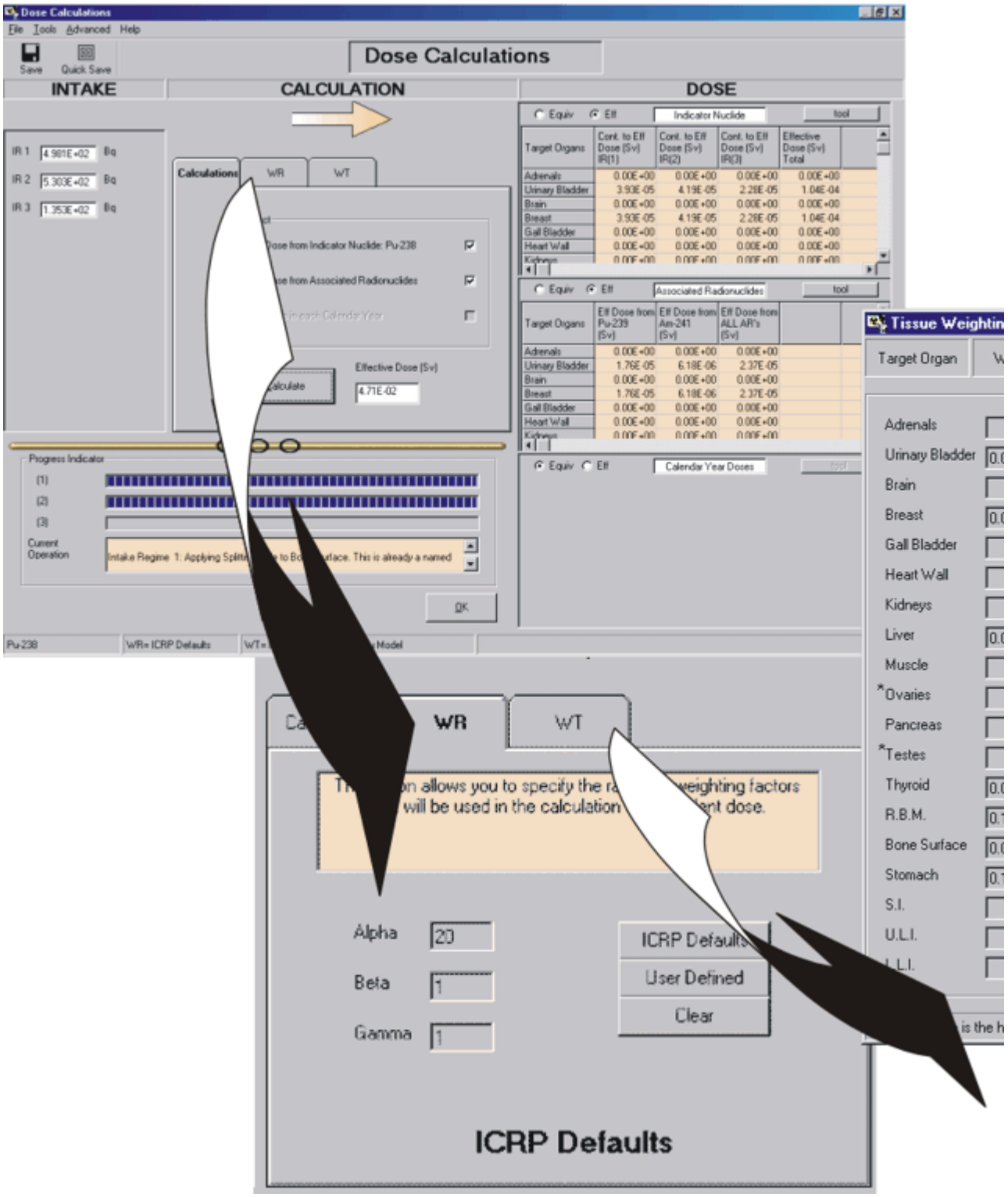


Figure 2.12. What's in the Graph Tool?

Visual Tour of Dose 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 in the figure below - for a "pop-up" description of the function of that part of the screen (and/or control).

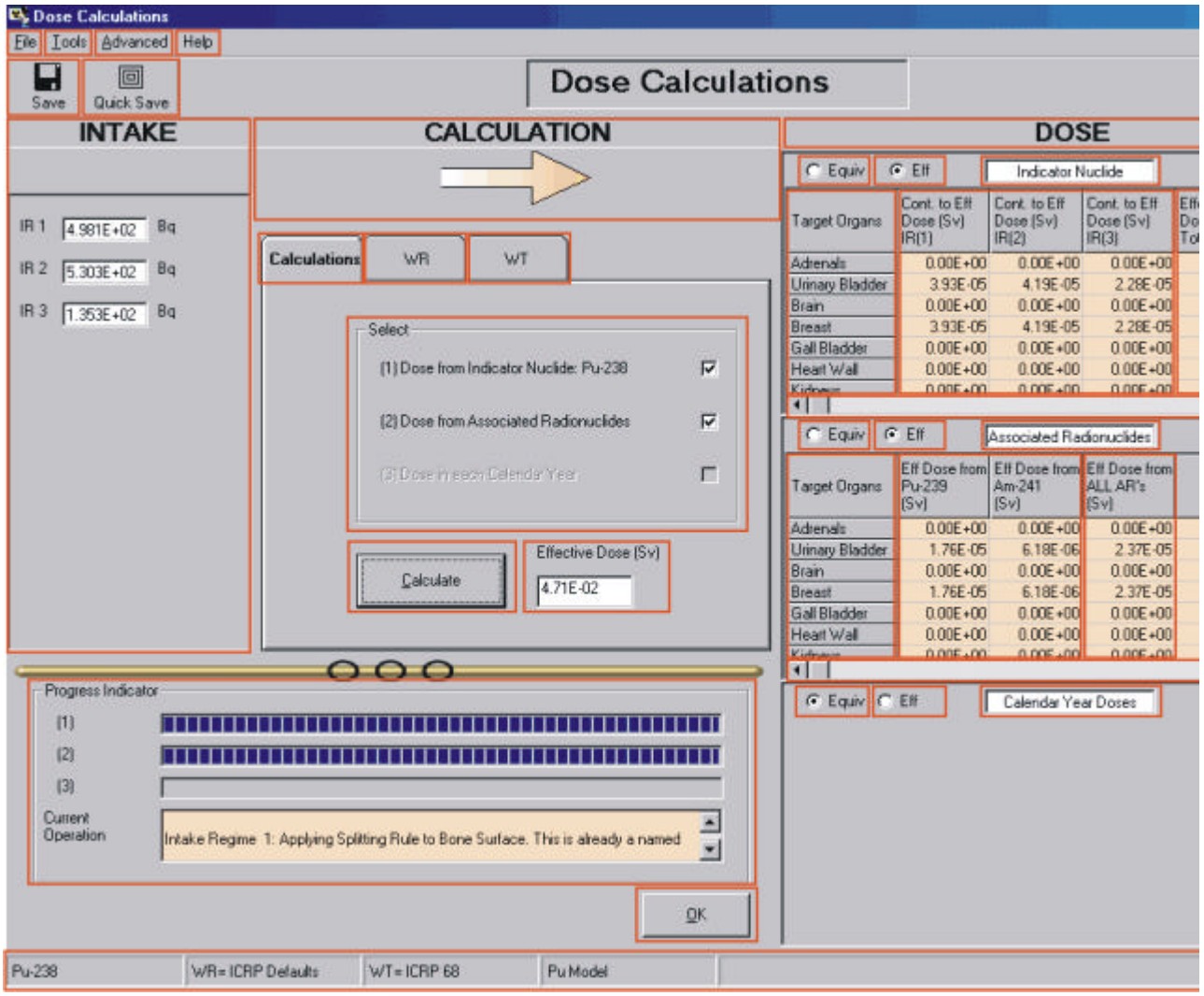


Figure 2.14. What's in the Dose Calculations screen?

Main Screen (Opening Screen)

The ***Main Screen*** (opening screen) appears when you *click* the **IMBA Professional Plus** icon - which runs **IMBA.exe**. This screen is shown in Figure 2.1.

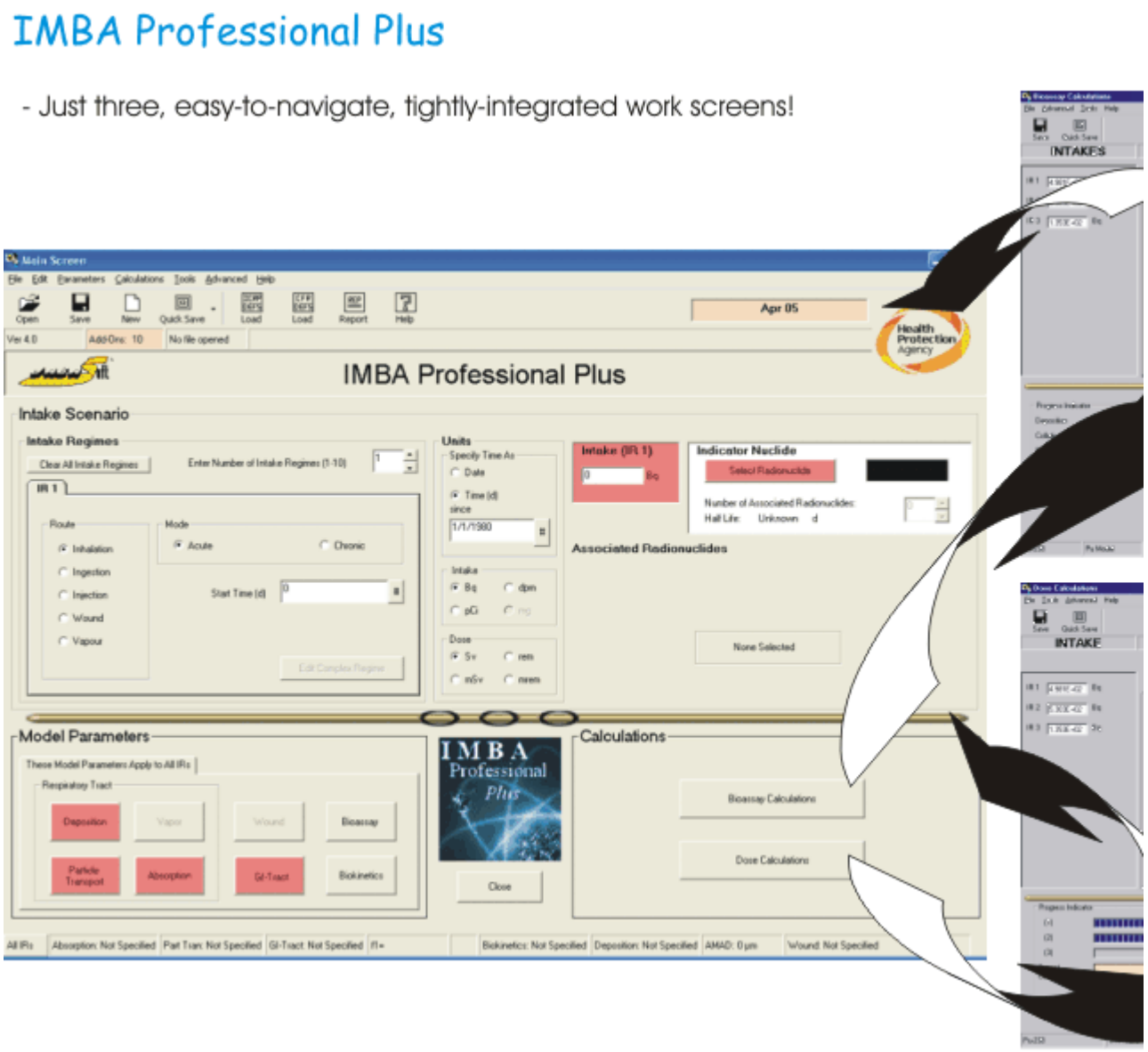


Figure 2.1. The **Main Screen** (opening screen).

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.
- Parameters menu.
- Calculations menu.
- Tools menu.
- Advanced menu.
- Help menu.

File Menu

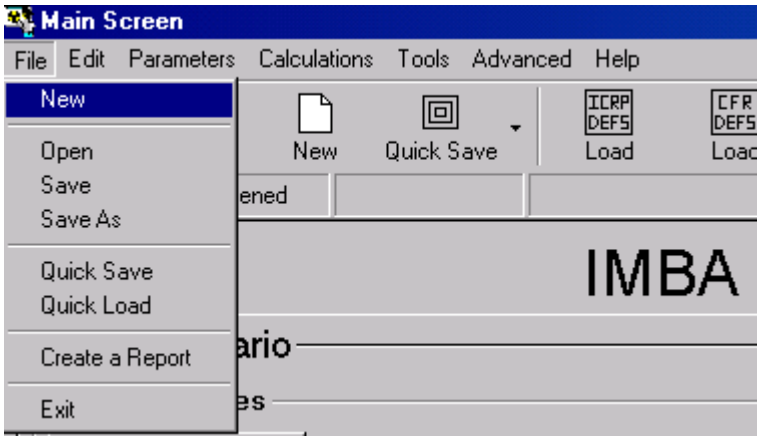


Figure 3.2. Drop-down **File** list box.

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*.

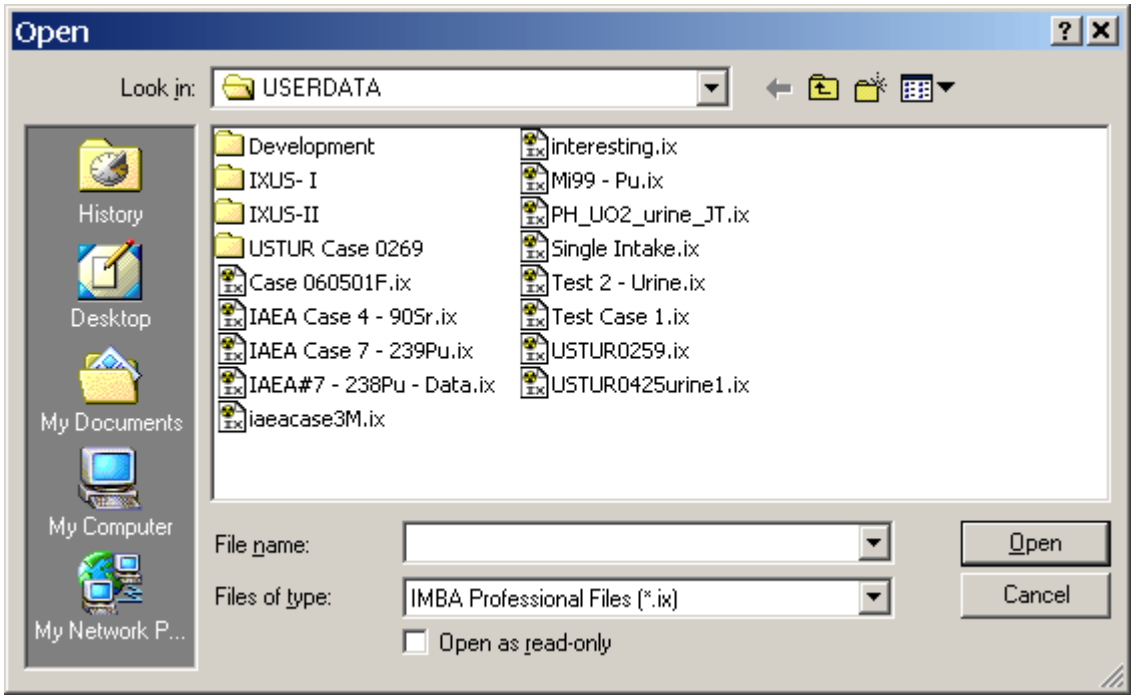


Figure 3.3. The **Open** parameter file dialog box.

Edit Menu

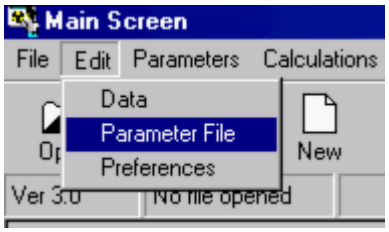


Figure 3.4. Drop-down **Edit** list box.

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).

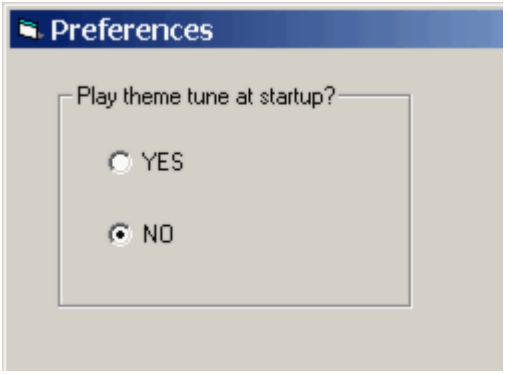


Figure 3.5. Start-up preference.

Parameters Menu

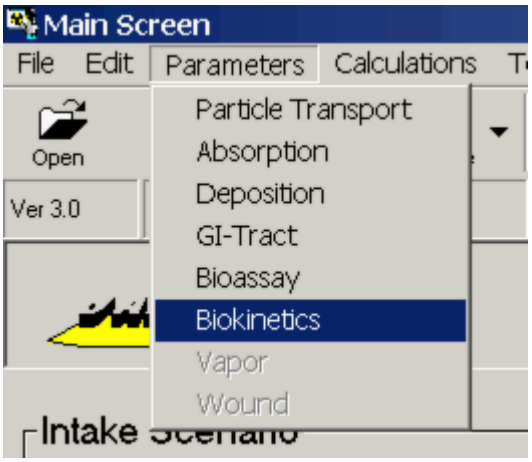


Figure 3.6. Drop-down **Parameters** list box.

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 respiratory tract model - 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** GI tract 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 bioassay quantity - 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

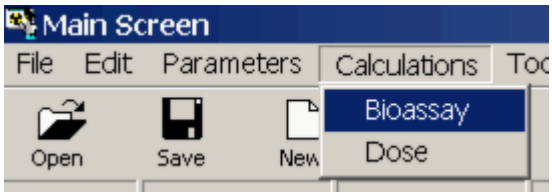


Figure 3.7. Drop-down **Calculations** list box.

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 Intake 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

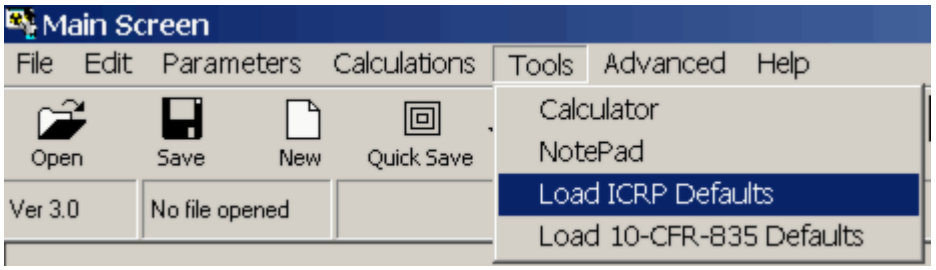


Figure 3.8. Drop-down **Tools** list box.

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):

1. the F1 Values for *** window - where "***" is the pre-selected radionuclide - so you can *select* the appropriate value of the gut uptake fraction (**f**1) for the pre-selected 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):

1. the F1 Values for *** window - where "***" is the pre-selected radionuclide - so you can *select* the appropriate value of the **gut uptake fraction** (**f**1) for the pre-selected radionuclide;

2. 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.).

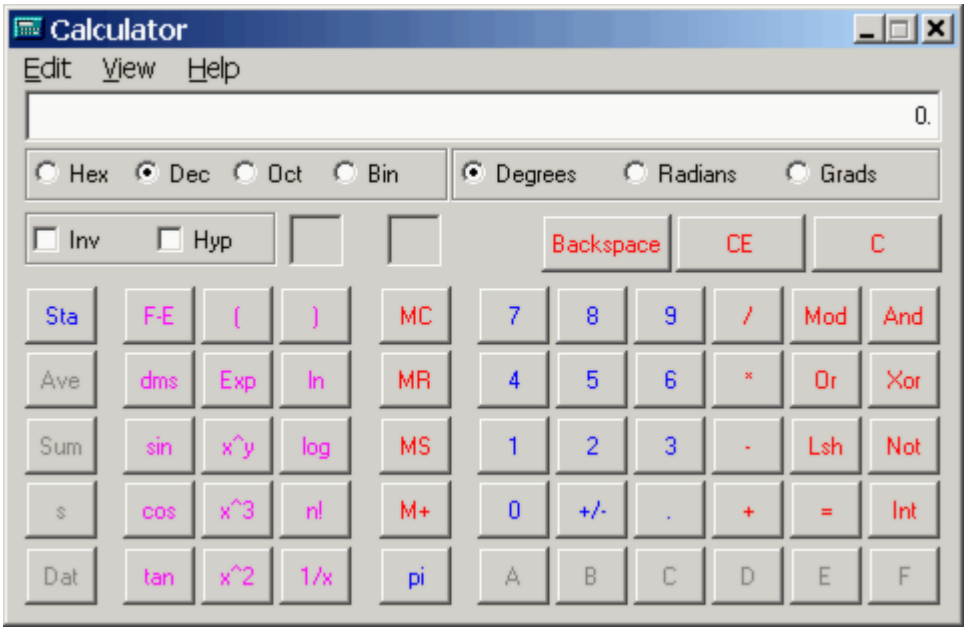


Figure 3.9. Standard Microsoft® Calculator.

Advanced Menu

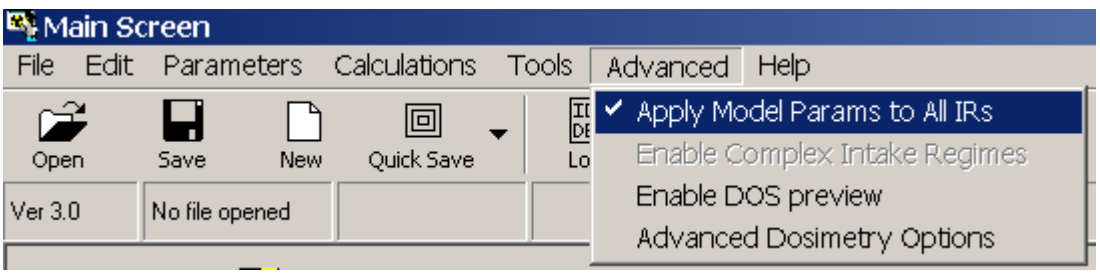


Figure 3.10. Drop-down **Advanced** list box.

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** (un-tick) 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** nuclear recoil energy from the SEEs for alpha emissions. For all Professional Series versions, the "default" is to **Include** nuclear recoil energy.

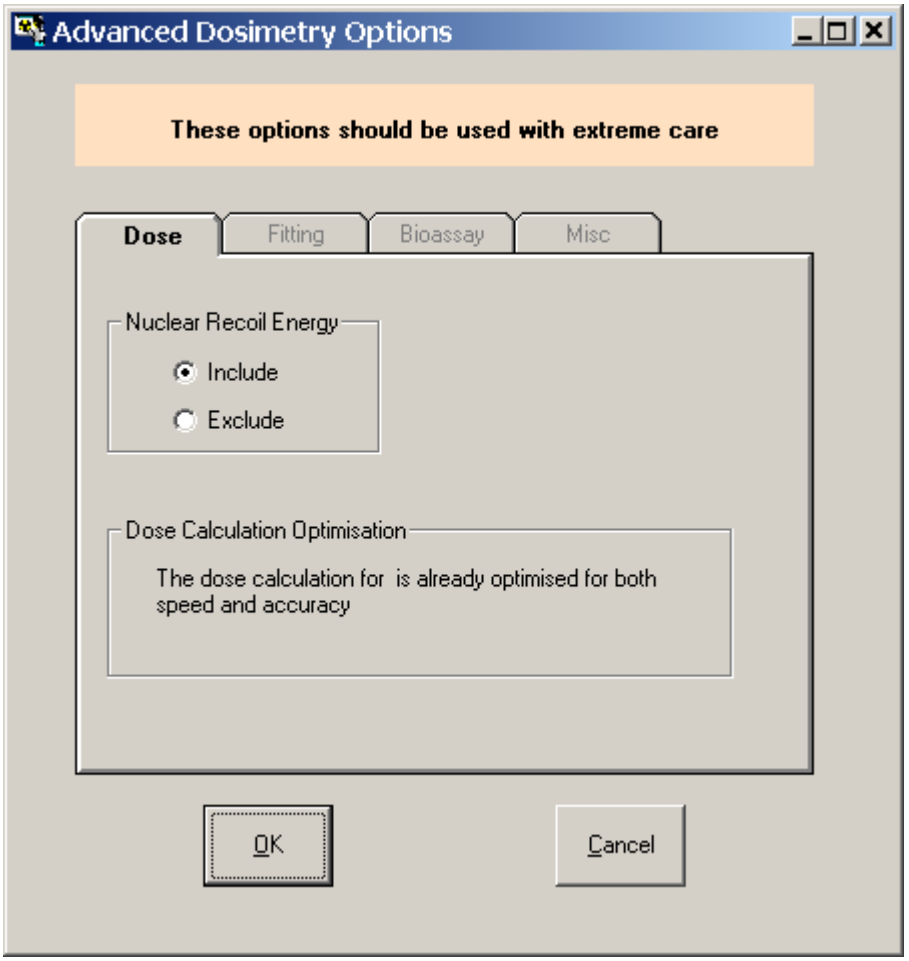


Figure 3.11. Tabs to select **Advanced Dosimetry Options**.

Help Menu

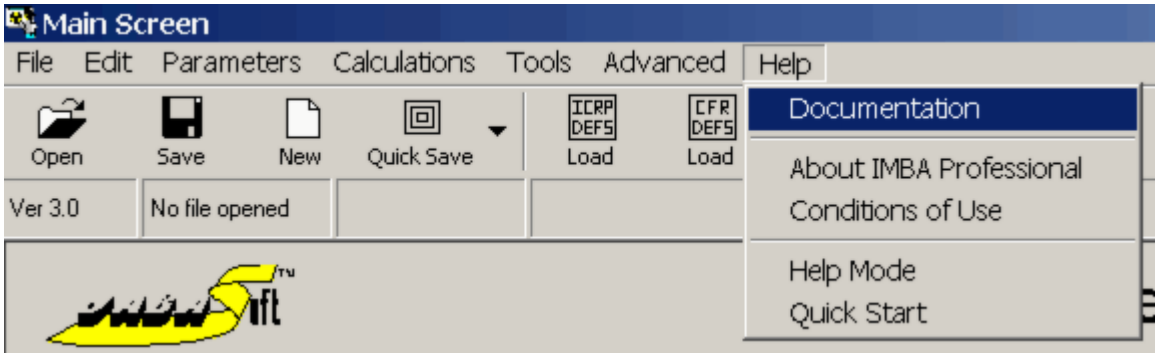


Figure 3.12. Drop-down **Help** list box.

The **Help** options are:

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

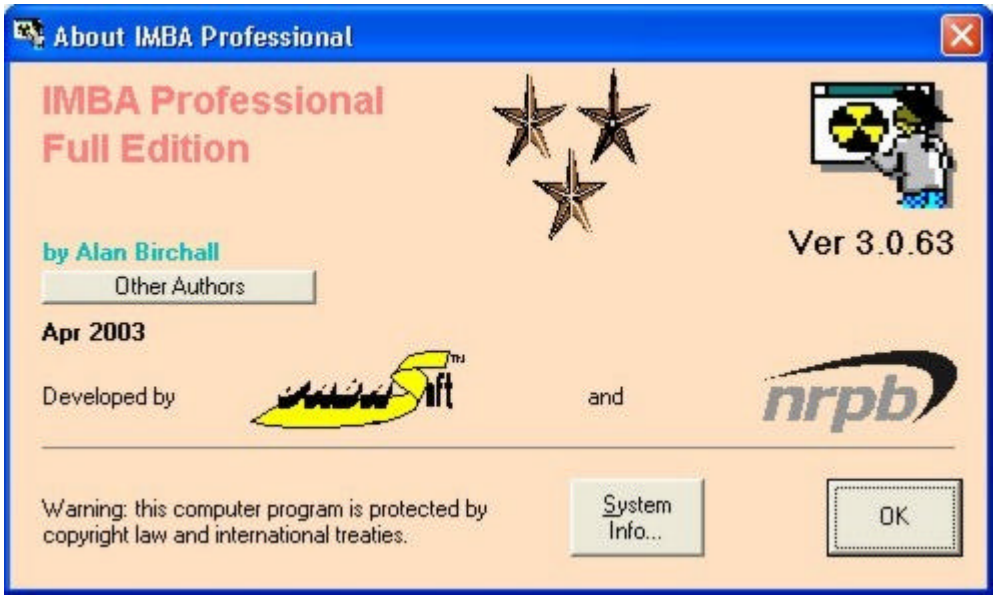


Figure 3.13. Authorship and Copyright Notice.

- **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 "**Mouse-over 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).

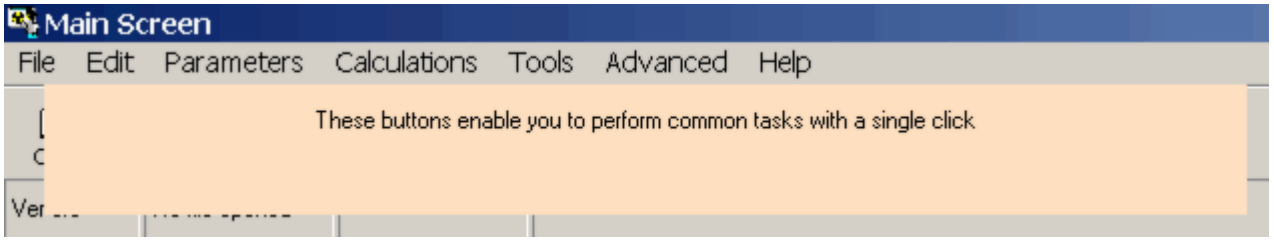


Figure 3.14. *Help Mode* message describing the function of the **Tool Bar**.

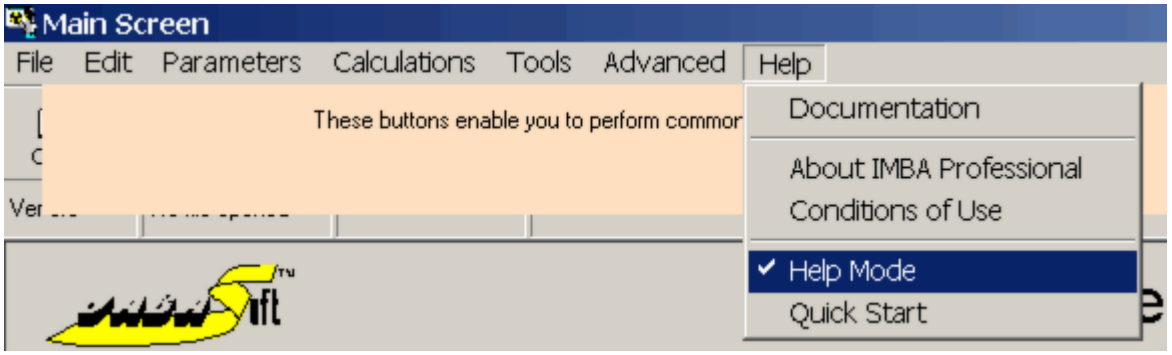


Figure 3.15. Re-click the *Help Mode* option to remove the **tick** (disable *Help Mode*).

- **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.

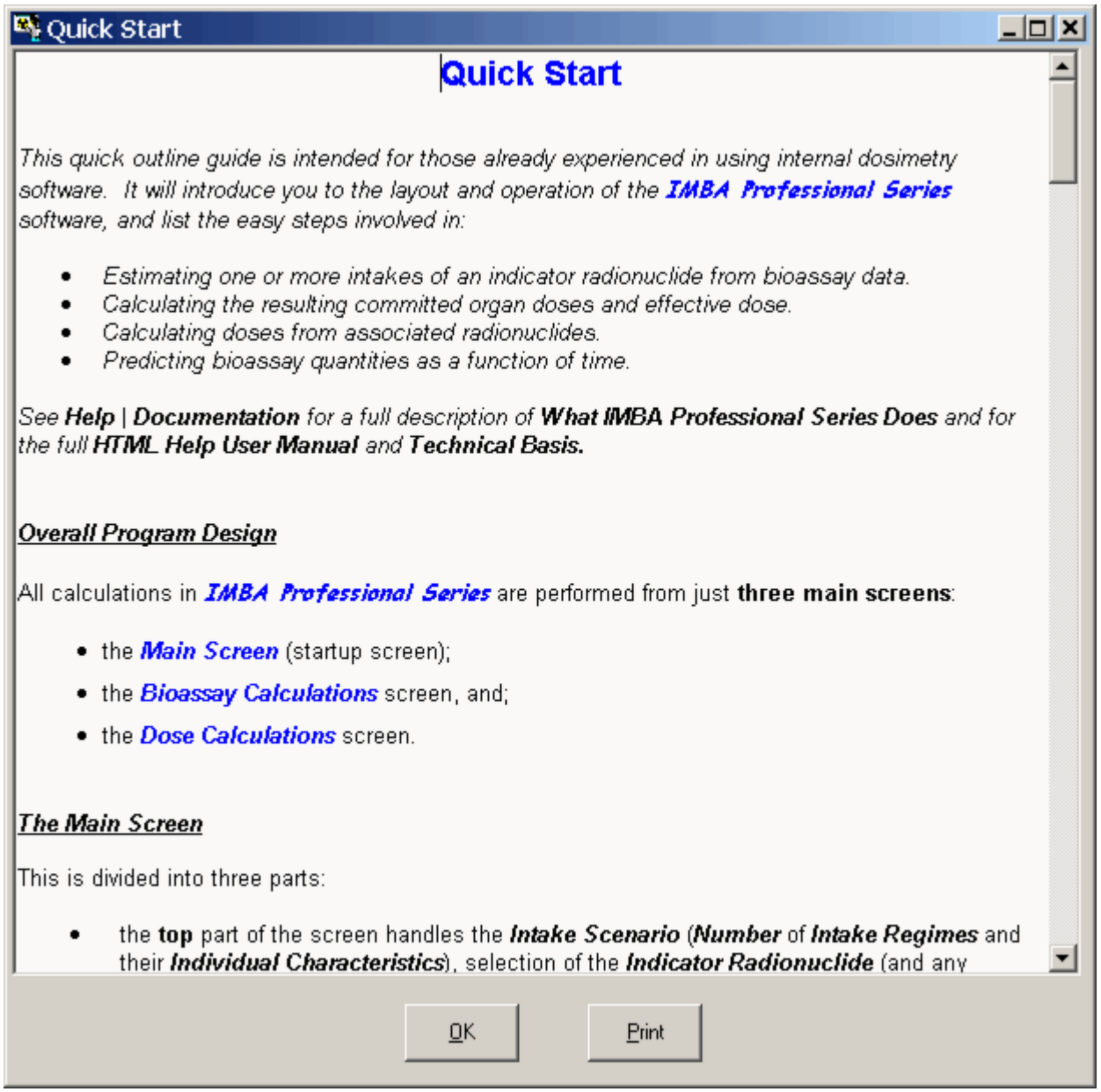
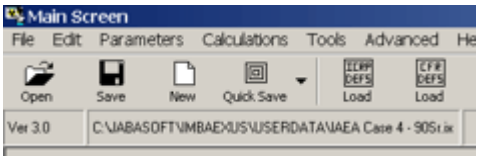


Figure 3.16. Scrollable Quick Start Help window.

Tool Buttons

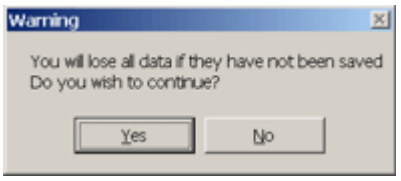
The **Tool Bar**, shown at the top-left of the *Main Screen*, just below the **Menu Bar**, contains **Tool Buttons** to let you perform common tasks with a **single click**. The tool buttons change appearance as the mouse pointer is passed over them.

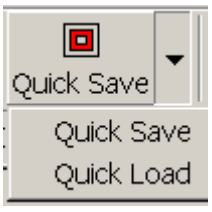
Open a **Parameter File "*.ix"** from the directory C:\JABASOFT\IMBAEXUS\USERDATA - or browse to another folder.



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 **Save** 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**."





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. **Clicking** the **button** will **Open** automatically (in sequence):
(1) the *F1 Values for* *** window - where "***" is the pre-selected radionuclide - so you can **select** the appropriate value of the gut uptake fraction (**f_1**) for the pre-selected radionuclide;
(2) the *Bioassay Model* window - to **confirm** 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**. **Clicking** the **button** will **Open** automatically (in sequence):
(1) the *F1 Values for* *** window - where "***" is the pre-selected

radionuclide - so you can **select** the appropriate value of the **gut uptake fraction** (**f**1) for the pre-selected radionuclide;
(2) the *Bioassay Model* window - to **confirm** 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 - **View** a scrollable summary of available **Help Options** (Figure 3.18).

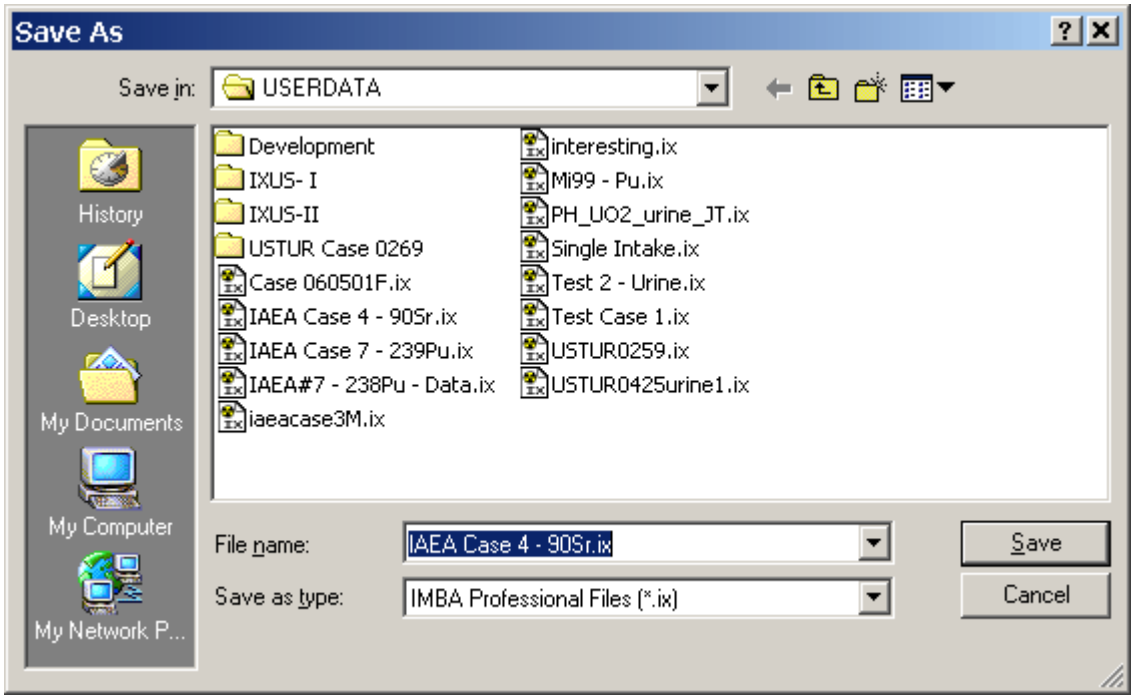


Figure 3.17. Save As dialog box.

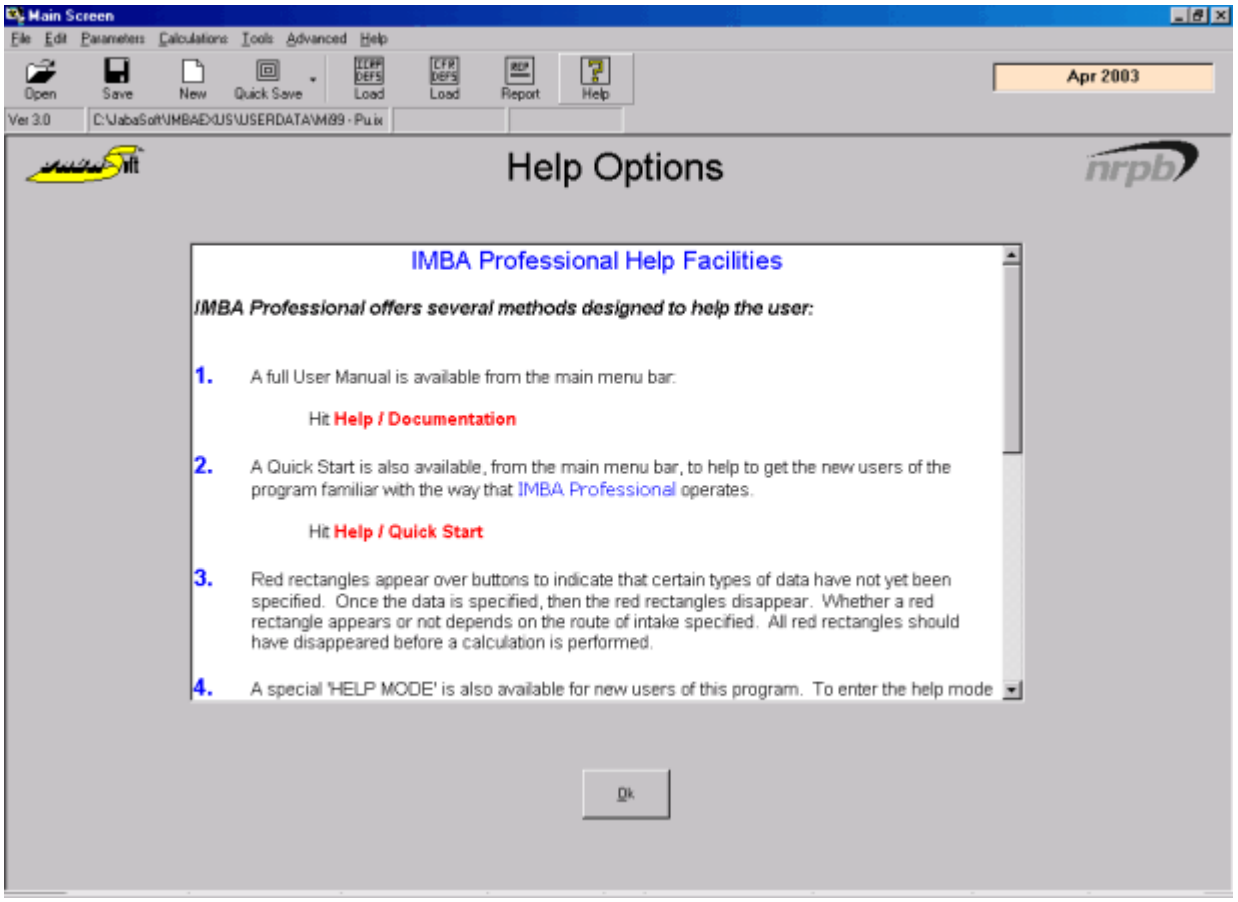


Figure 3.18. Summary of available **Help Options**.

Parameter File Bar

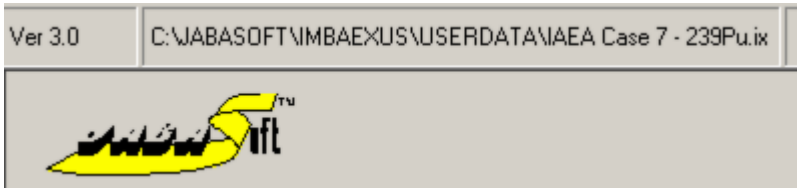


Figure 3.19. Parameter File bar.

- 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).

Key Tip: You can load **IMBA Professional** and open a selected **Parameter File** automatically - simply by double-clicking on the **file icon**! See the **Quick Start** guide for instructions.

For example, double-clicking this "**IX**" icon (in the USERDATA folder) will **Run IMBA Professional** - with the **Parameter File** "IAEA#3 - 60Co.ix" already opened.

Note: If **IMBA Professional** is already running, double-clicking on an "**IX**" icon will load and run a second copy.

Main Status Bar

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 absorption 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** - activity median aerodynamic diameter (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**.

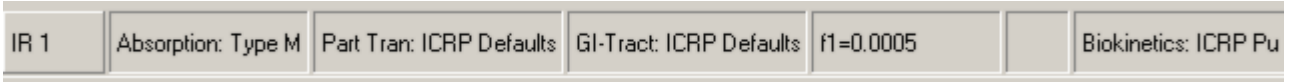


Figure 3.21. Working Status Bar - appearance for **Working** (in-use) **Parameter File**.

Intake Scenario Panel

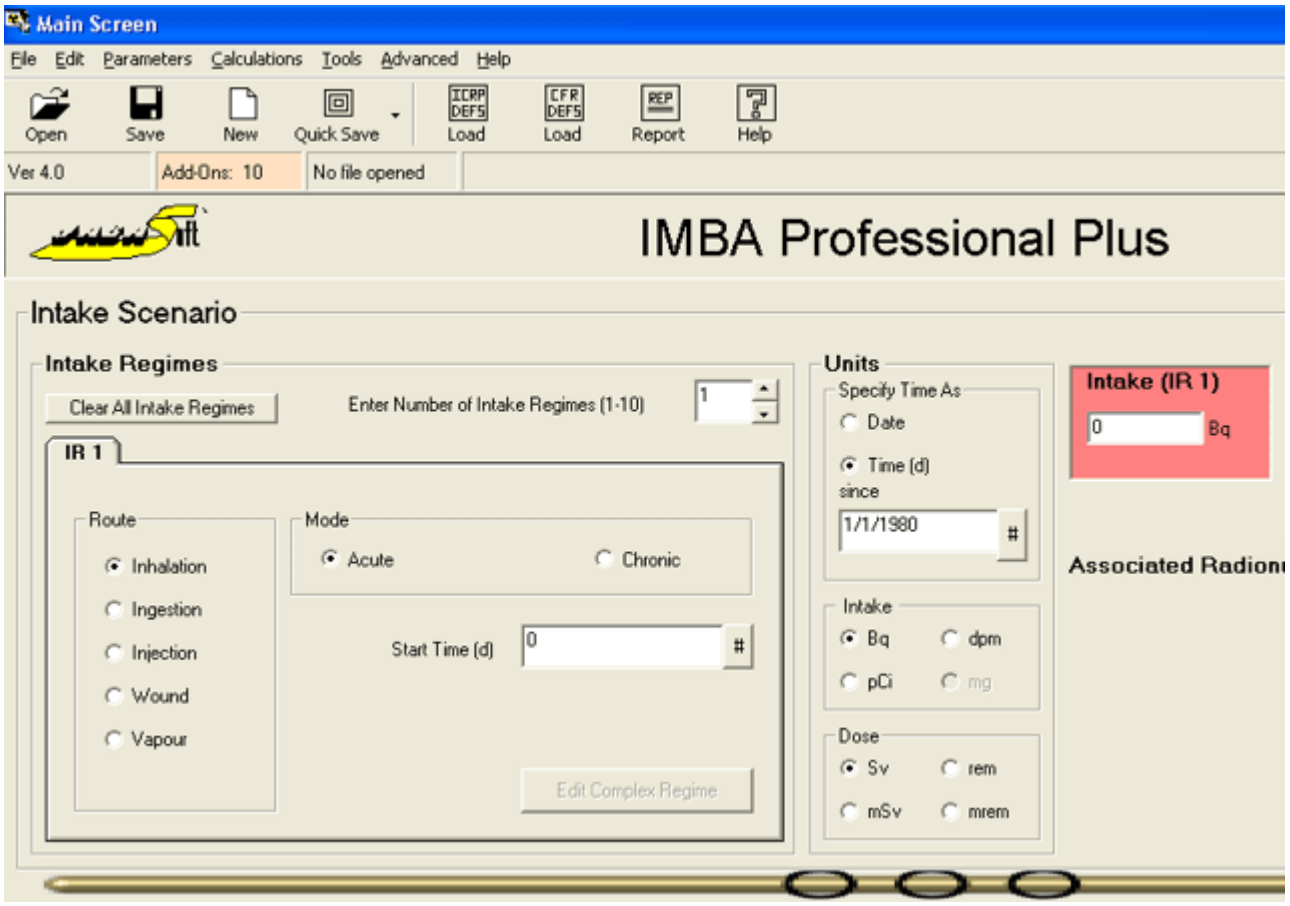


Figure 3.22. Intake Scenario panel.

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

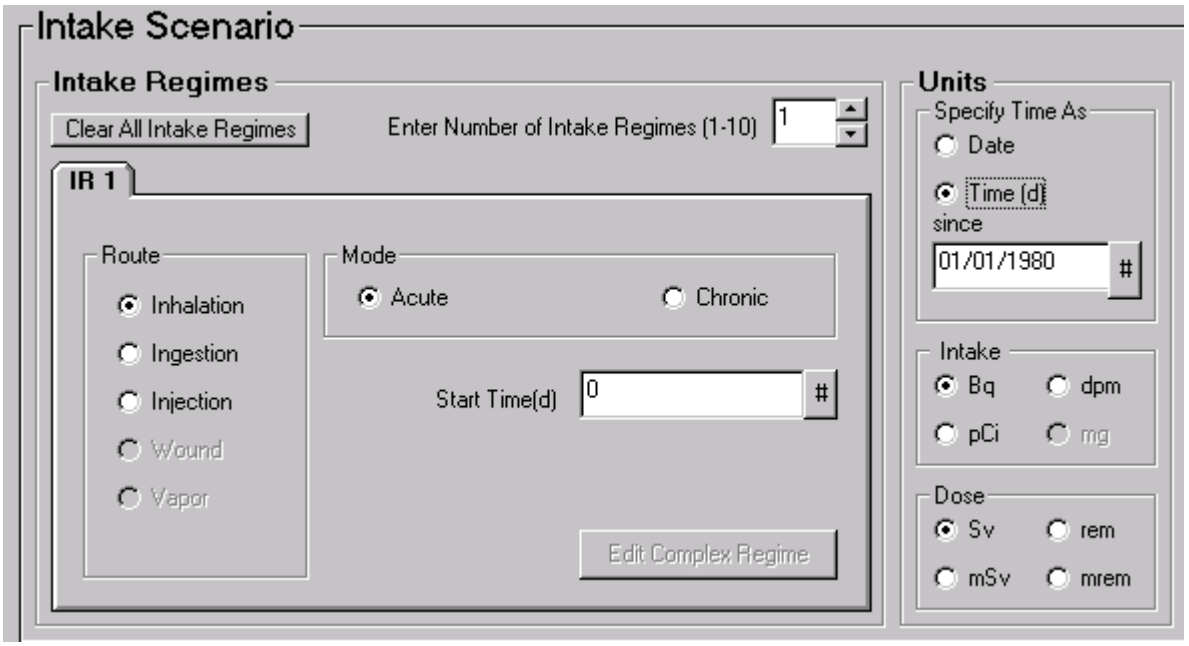


Figure 3.23. Intake Regimes sub-panel with adjacent **Units** sub-panel.

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 select 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 highlight 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 Acute or Chronic);
- the **Start Time (d)** of intake.

With the **Units** of **Time** at the default setting of "**Time (d) since**," Selecting 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 reference "**Time (d) since**" value**.** For example, with the "**Time (d) since**" time-of-day set at 07:00:

- 0, 5 - start time is the zero$_{th}$ day (at 7:00 AM), end time is the fifth day (at 7:00 AM);
- 0.4375, 6.75 - start time is the zero$_{th}$ day (at 5:30 PM), end time is the sixth day (at 1:00 AM).

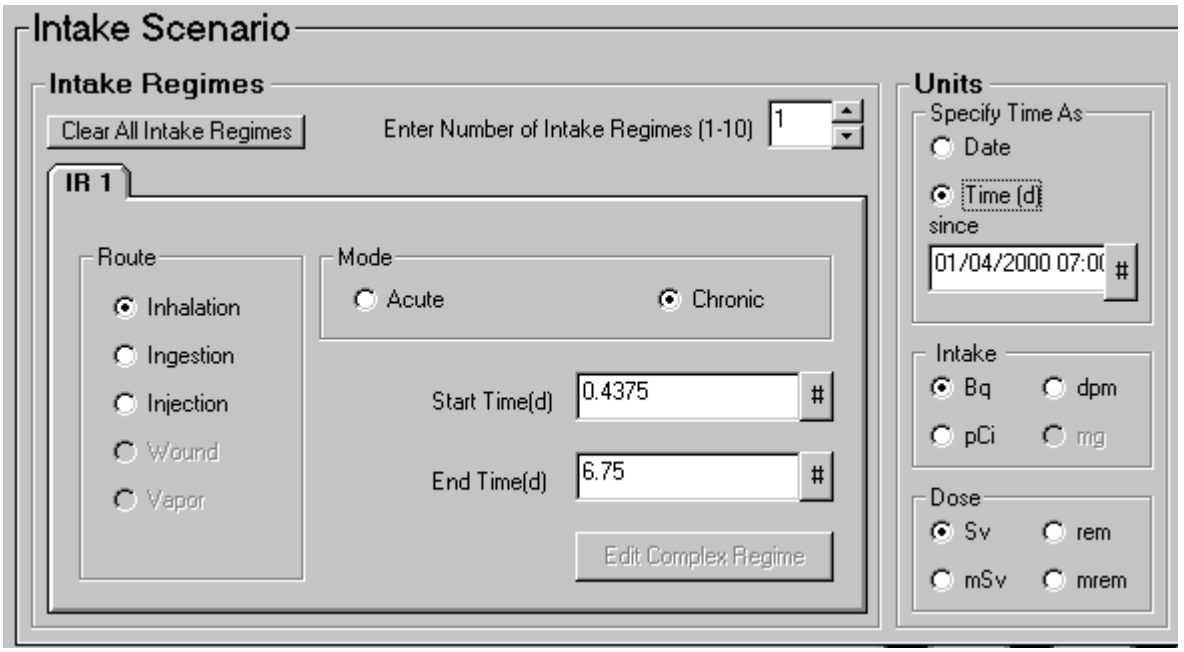


Figure 3.24. The **End Time (d)** dialog box appears when you select the **Chronic** intake **Mode** - for the displayed **IR** only.

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, i.e., 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

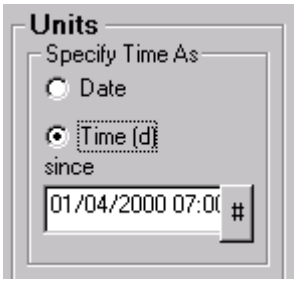


Figure 3.25. The reference "**Time (d) since**" value.

For all calculations of bioassay quantities (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 1st, 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, change 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 select:

- **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 **decimal-fraction days**.

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

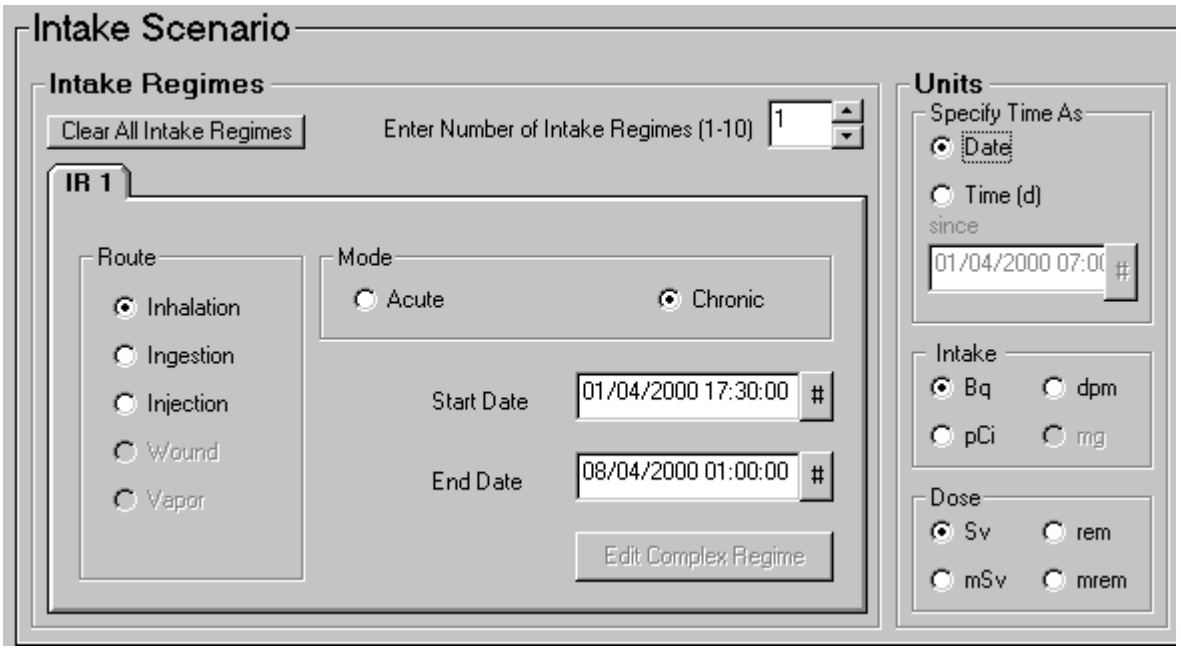


Figure 3.26. The **Start Date (and time-of-day)** and **End Date (and time-of-day)** appear automatically (in the **Chronic** intake **Mode**) when you select **Date** under "**Specify Time As**."

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 1st, 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

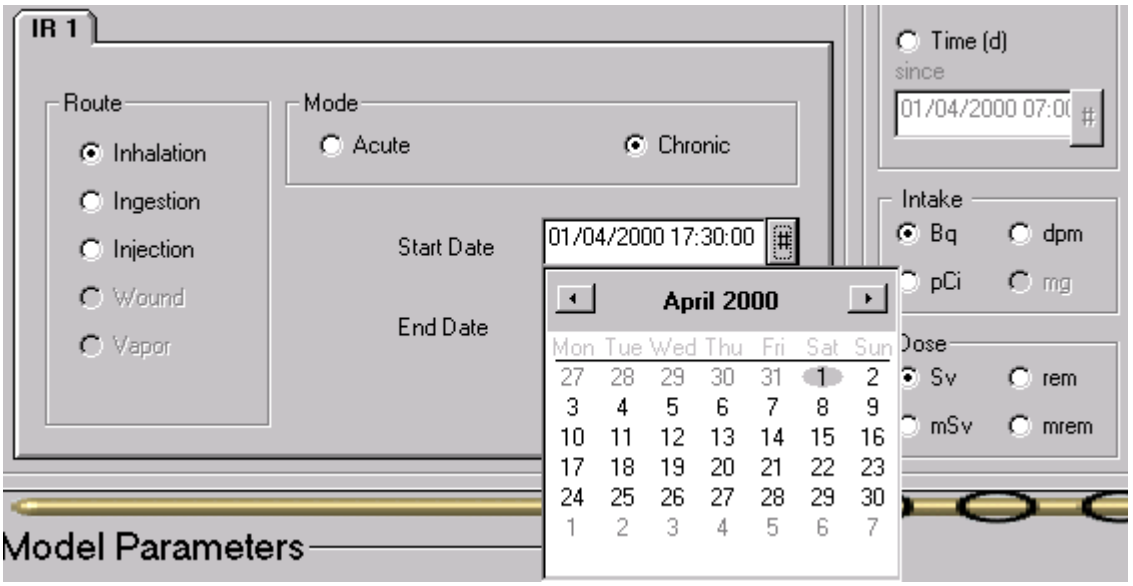


Figure 3.27. Drop-down Windows**â Calendar** for date selection.

As an alternative to typing in the full **Date** directly in the dialog box, clicking 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 arrow buttons to **scroll** backwards or forwards through the months (and years). Click 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**, click, type a "**space**," and then type 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, re-click the "**#**" sign next to the dialog box.

–

Specifying Several Intake Regimes (Star Feature)

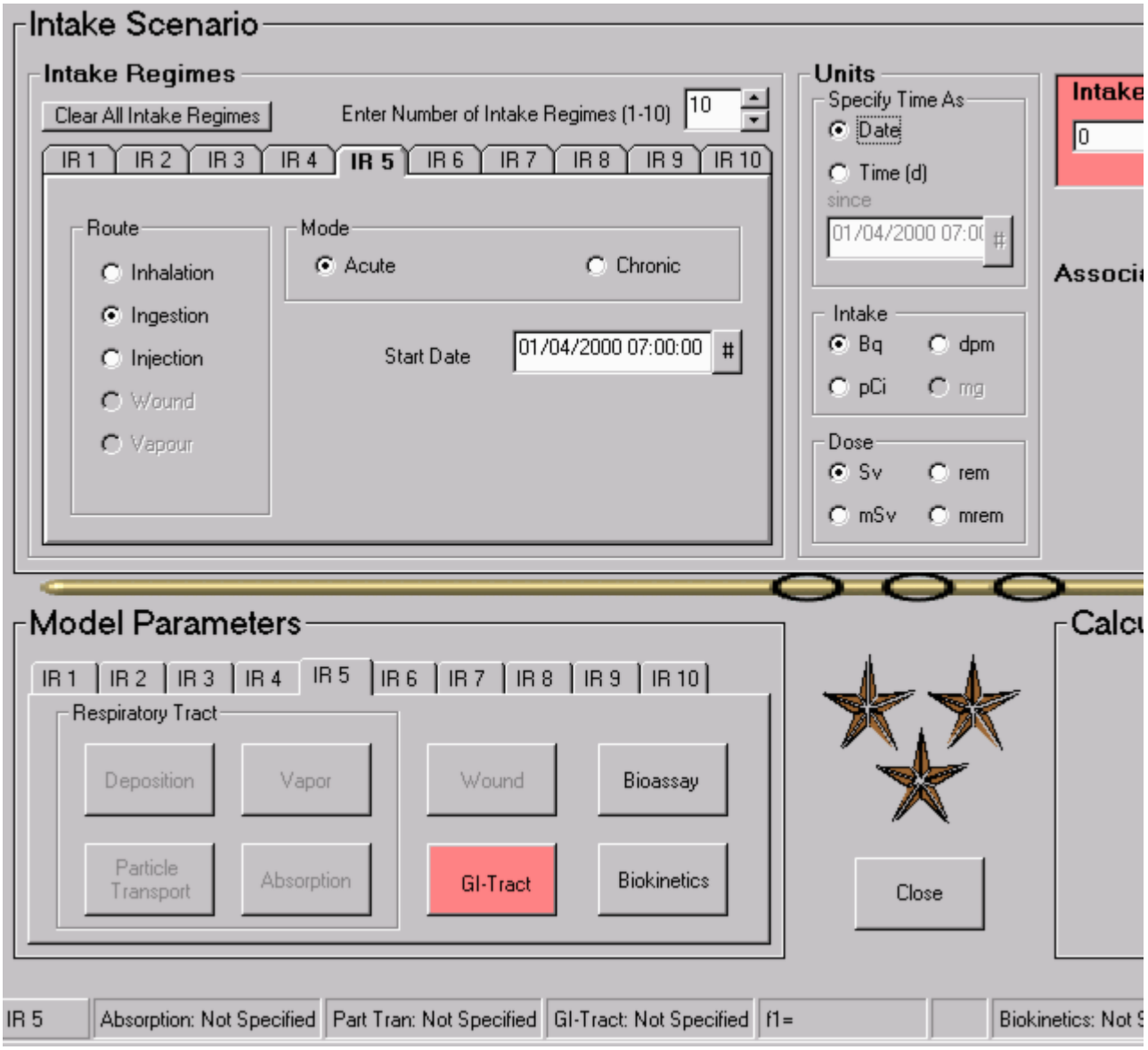


Figure 3.28. Specifying the **5th** (**IR 5**) of **10 Intake Regimes** - as an **Ingestion**.

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 Model Parameters Sub-panel). 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

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.

Warning: The selected working **Unit** of activity is used throughout IMBA_Professional. You will need to **ensure** that this activity **Unit** is **consistent** with the activity unit in which your **bioassay data** are expressed. Although the working activity **Unit** will NOT affect the calculated **value(s)** of **intake(s)**, it WILL affect crucially the **calculated doses**.

Units of Dose

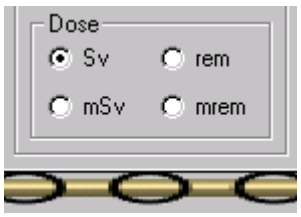


Figure 3.30. Specifying the **Units** of **Dose**.

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**.

Warning: You can change the **Unit** in which doses are displayed at will - but you MUST re-run your dose calculation to change the displayed **values** of dose accordingly.

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

Intake Amounts / Radionuclides Sub-panel

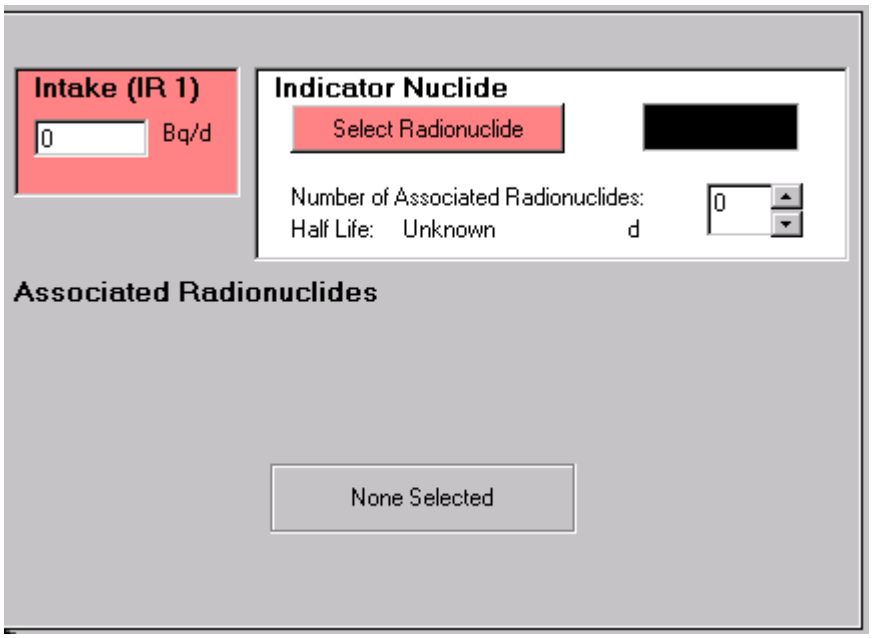


Figure 3.31. Specifying the **Indicator Nuclide** and **Intake** amount.

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 **highlighted** in red - as is the "**Select Radionuclide**" **button**. This warns that neither an **intake amount** nor an Indicator Nuclide has been defined.

Note: IMBA Professional works with a SINGLE **Indicator Nuclide** for each case study, **i.e.**, the **parameter file** holds only ONE **indicator nuclide**. If you need to assess bioassay measurements of more than one **indicator nuclide** for an individual person, you will need to set up a separate case study (**parameter file**) for each **indicator nuclide**.

Note: The **Intake (IR #)** amount applies only to the **Indicator Nuclide**. The activity of Associated Radionuclides is defined separately - as an activity **Abundance (%)** relative to the activity of the indicator nuclide.

Selecting the Indicator Nuclide

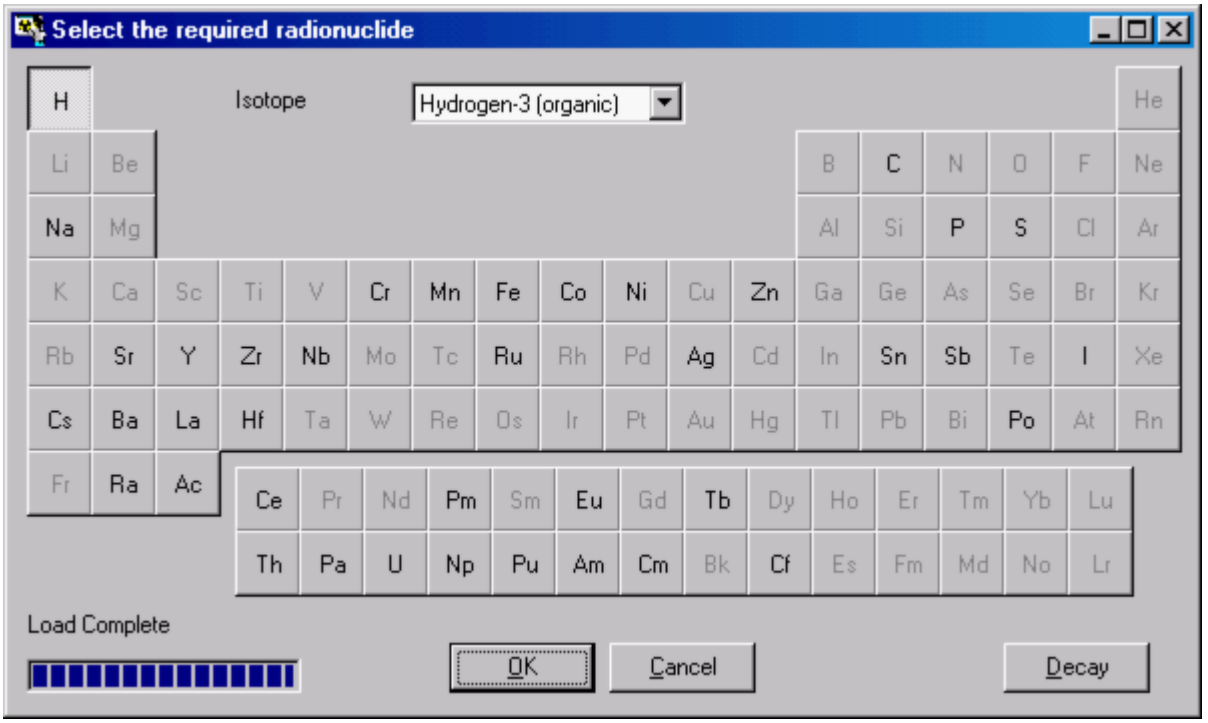


Figure 3.32. Selecting the **Indicator Nuclide** from the periodic table of the elements.

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

1. **Click** the required **element** - this puts the first **isotope** available for that element in the **Isotope** dialog box.
2. **Click** the "**down**" arrow on the **Isotope** dialog box - this displays all the available isotopes for that element.
3. **Highlight** and **click** your required **isotope** from the drop-down list - this puts your isotope in the dialog box (Figure 3.33).
4. **Click** the "**OK**" **button** 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**", **i.e.**, that your IMBA Professional Series software has "**loaded**" all of your available radionuclides. Only the IMBA Professional (Full Version) includes all 75 radionuclides. The more basic versions will automatically display fewer elements (for radioelement selection) than those shown in Figure 3.32.

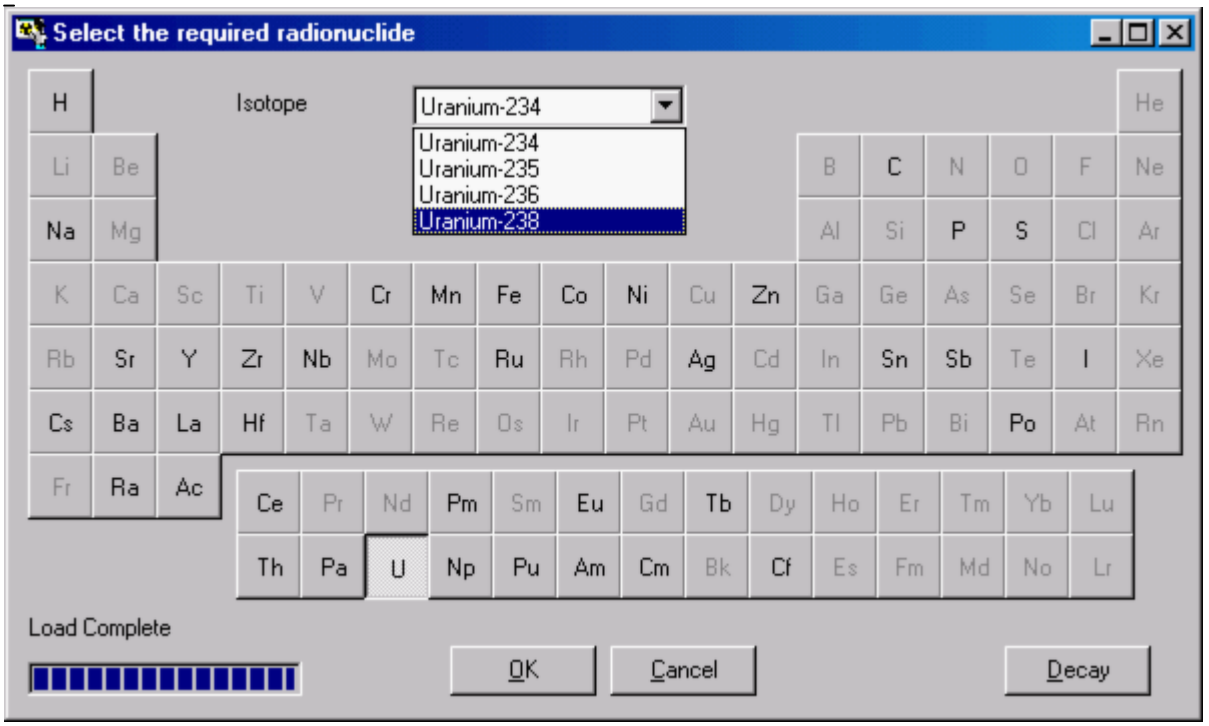


Figure 3.33. Selecting **Uranium-238** from the **Isotope** drop-down list.

Clicking "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 **highlight** on the "**Select Radionuclide**" **button** disappears.

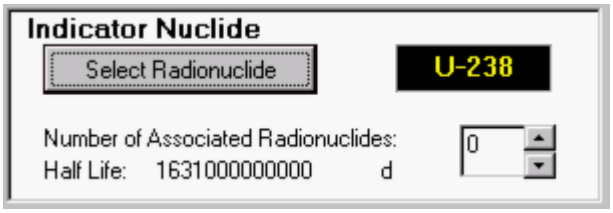


Figure 3.34. The **selected radionuclide** displayed in the **Indicator Nuclide** window.

List of Available Radionuclides (Full Version)

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

- **actinium** (^{227,228}Ac);
- **americium** (^{241,243}Am);
- **antimony** (^{124,125}Sb);
- **barium** (^{140}Ba);
- **caesium** (^{134,137}Cs);
- **californium** (^{252}Cf);
- **carbon** (^{14}C) - as particulate - a version update will include gaseous and vapour forms of carbon;
- **cerium** (^{141,144}Ce);
- **chromium** (^{51}Cr);
- **cobalt** (^{57,58,60}Co);
- **curium** (^{242,243,244}Cm);
- **europium** (^{152,154,155,156}Eu);
- **hafnium** (^{181}Hf);
- **hydrogen [tritium]** (^{3}H) - as particulate, with biokinetic models for tritiated water (HTO) and organically bound tritium (OBT) - a version update will include gaseous and vapour forms of tritium;
- **iodine** (^{125,129,131,133,134,135}I);
- **iron** (^{55,59}Fe);
- **lanthanum** (^{140}La);
- **manganese** (^{54}Mn);
- **neptunium** (^{237,239}Np);
- **nickel** (^{63}Ni);
- **niobium** (^{94,95}Nb);
- **phosphorus** (^{32,33}P);
- **plutonium** (^{238,239,240,241,242}Pu);
- **polonium** (^{210}Po);
- **promethium** (^{147}Pm);
- **protactinium** (^{231}Pa);
- **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** (^{35}S) - as particulate, for both inorganic and organically incorporated sulfur - a version update will include gaseous and vapour forms of sulphur;
- **terbium** (^{160}Tb);
- **thorium** (^{228,230,232}Th) - assuming same biokinetic model for parent and radioactive progeny - note that ICRP68 assumes independent kinetics for the progeny;
- **tin** (^{113}Sn);
- **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** (^{90}Y);
- **zinc** (^{65}Zn);
- **zirconium** (^{95}Zr).

Displaying the Decay Series

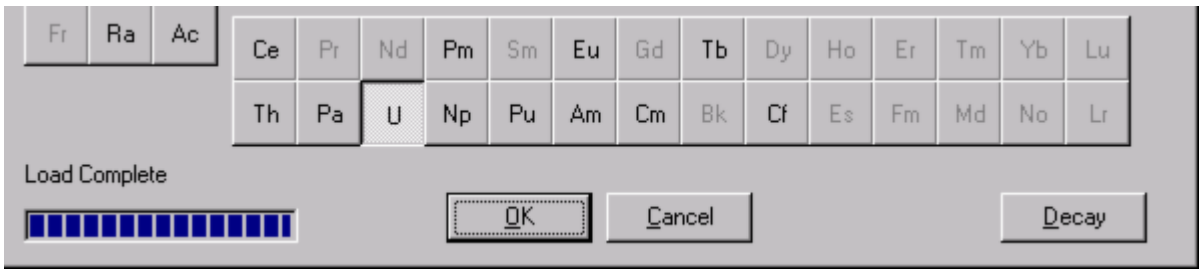


Figure 3.35. "**Decay**" button (bottom-right-corner of "**Select the required radionuclide**" window).

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).

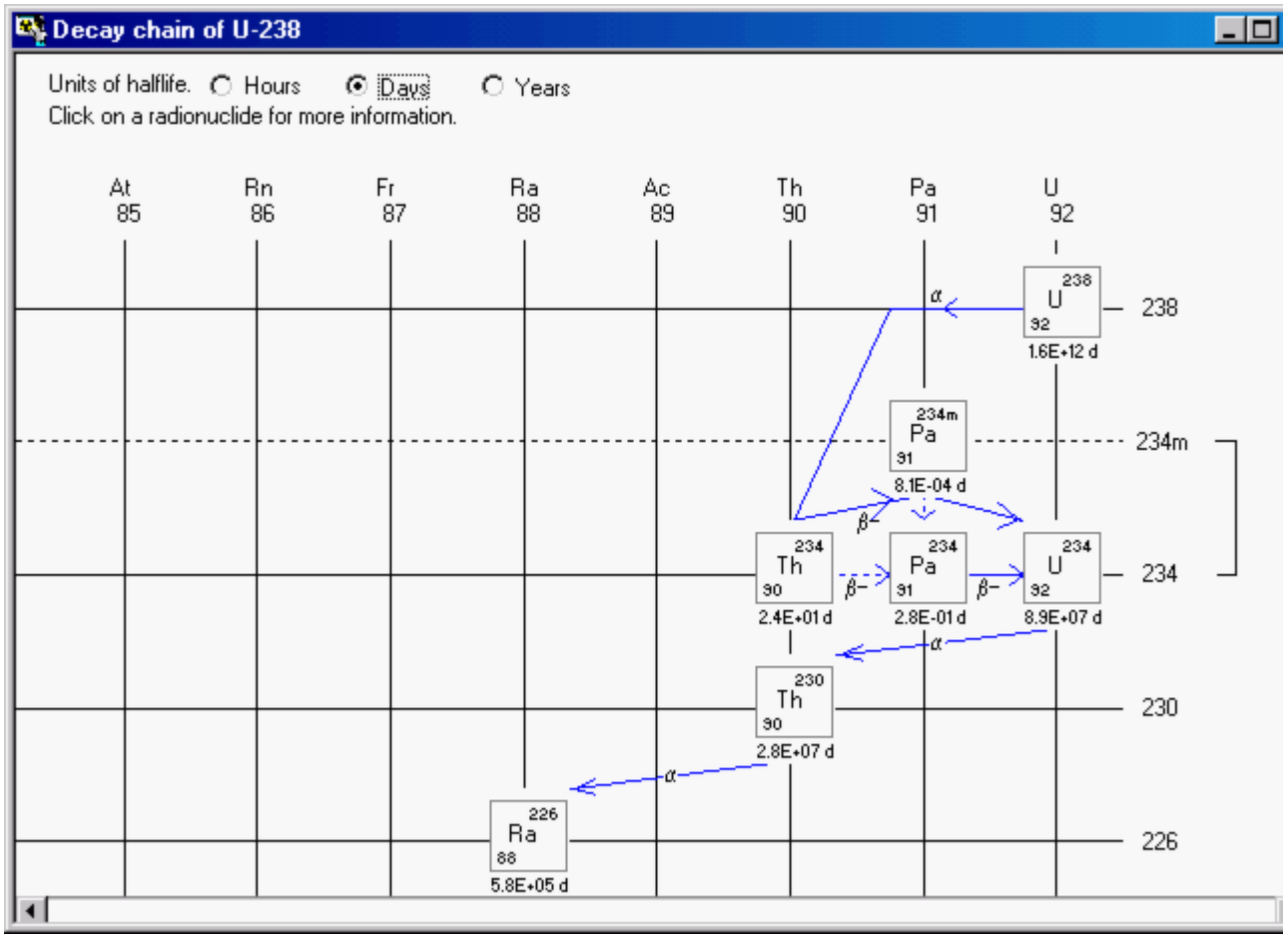


Figure 3.36. "**Decay chain of Pu-239**" window - partial view.

For a long decay chain (such as that of *238*U), 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).

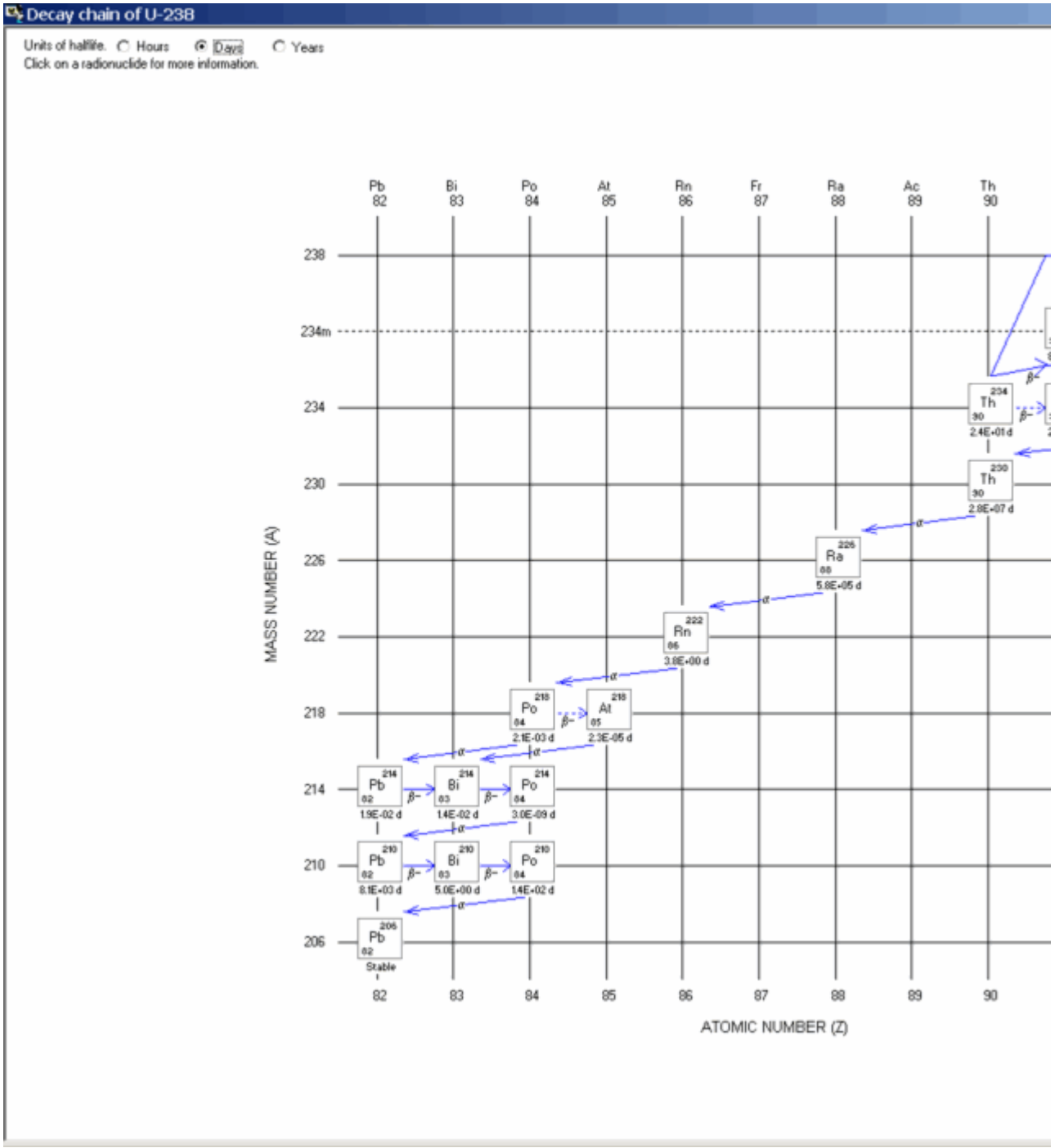


Figure 3.37. Maximized view of the whole "**Decay chain of U-238**" window.

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

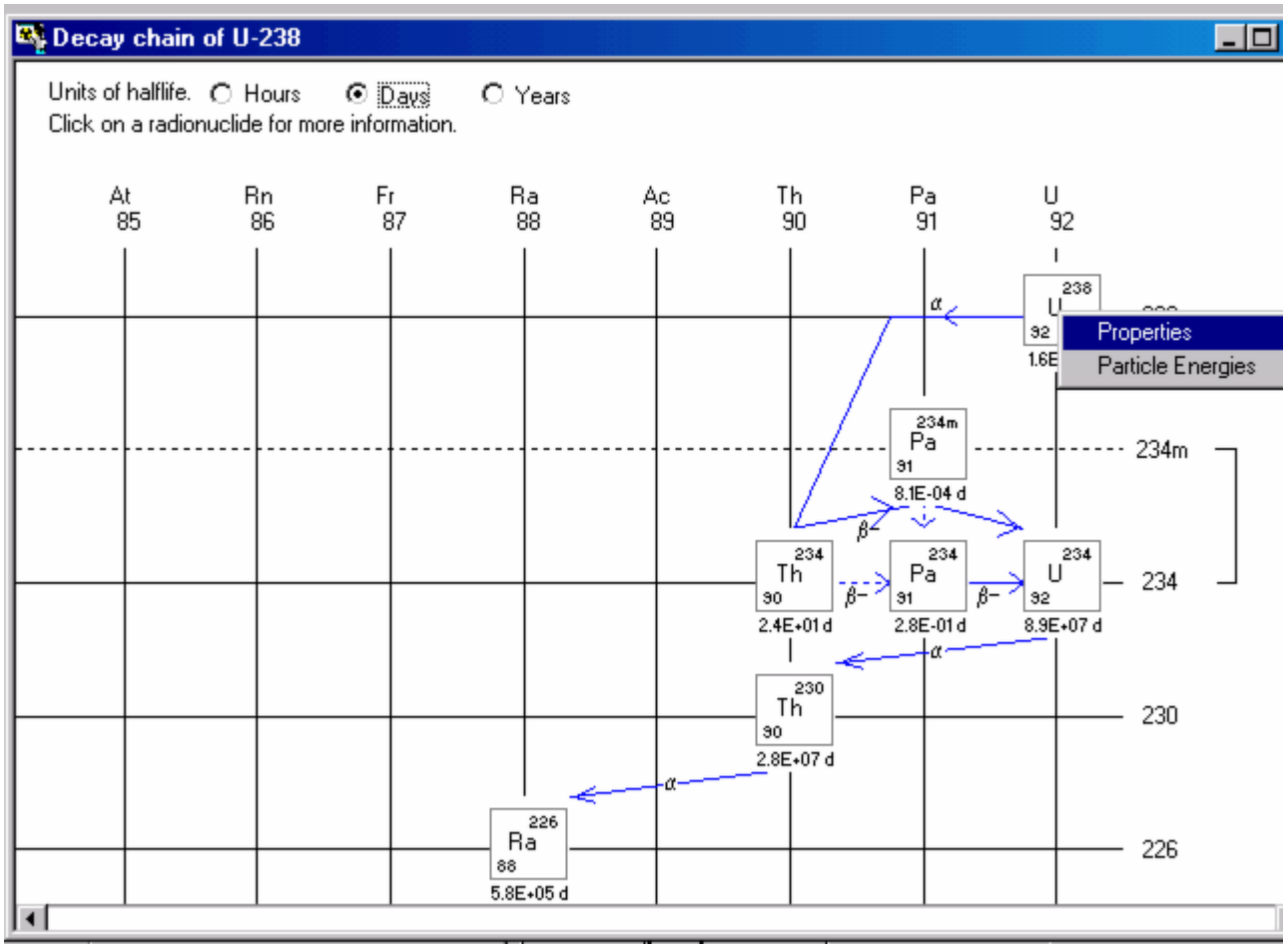


Figure 3.38. Clicking on a radionuclide for more information.

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.

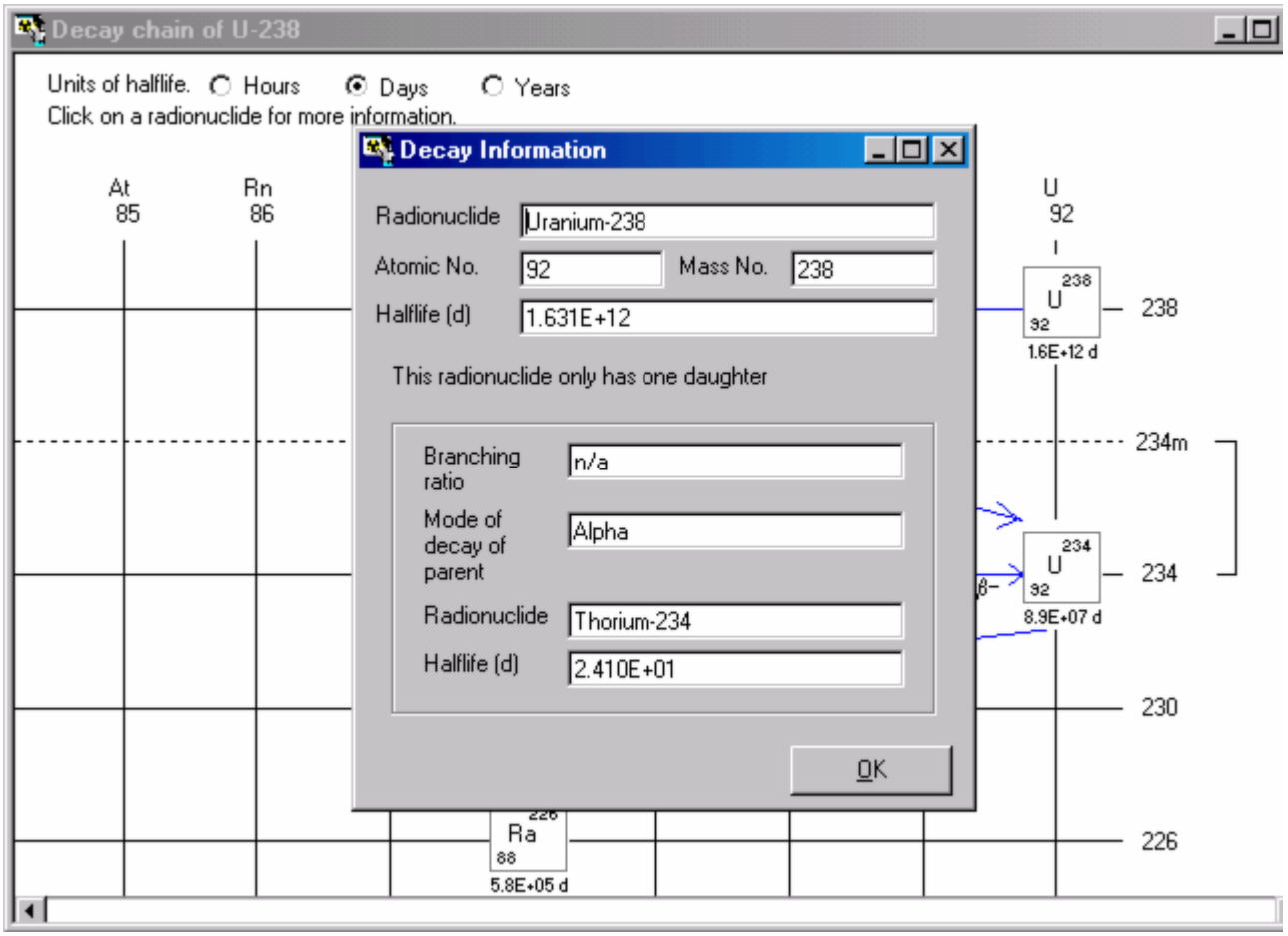


Figure 3.39. Displaying the **Decay Information** for Uranium-238.

Figure 3.39 shows the "**Decay Information**" window that appears when you *click* the "**Properties**" *option* for 238**U**. 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).

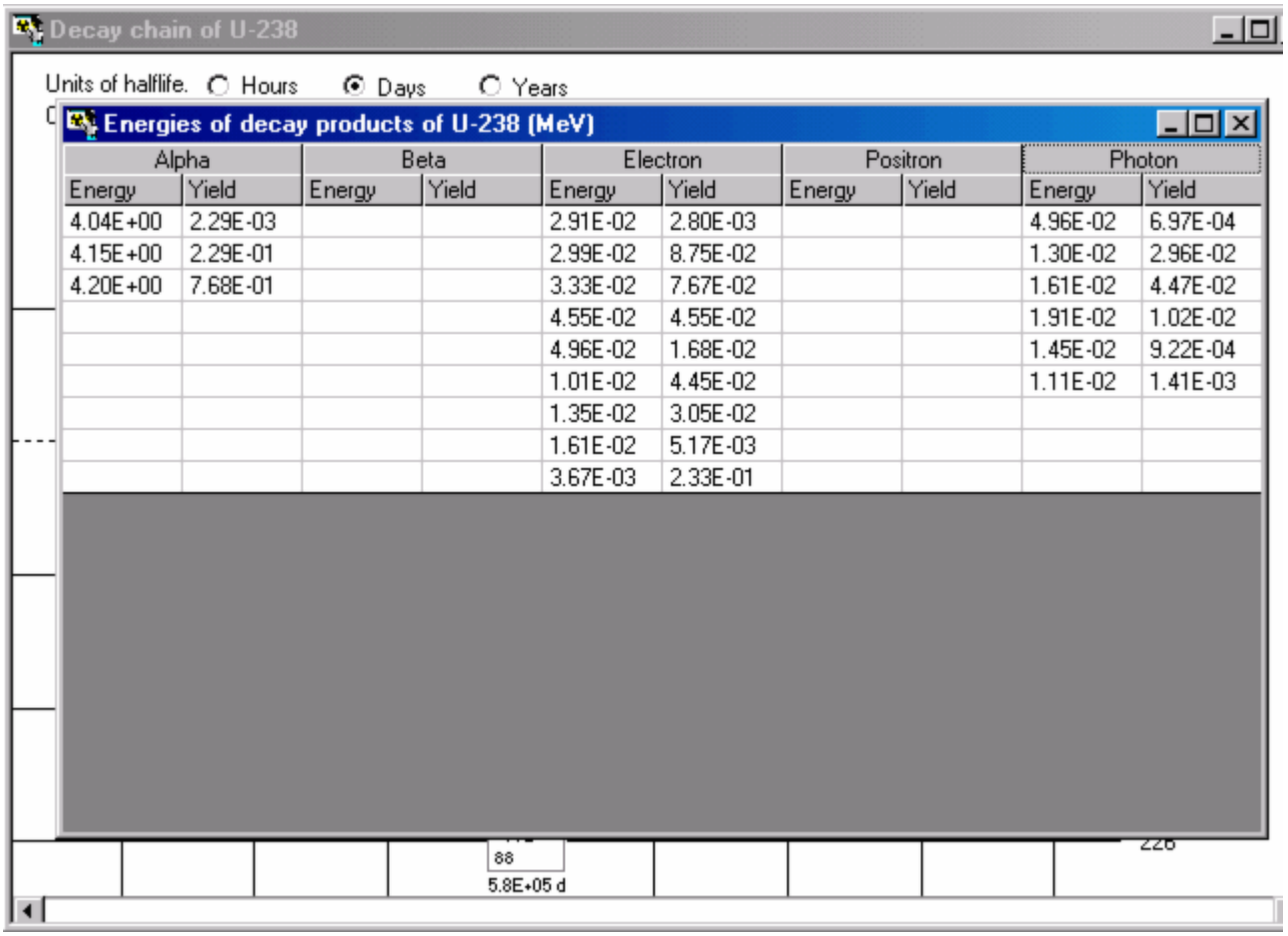


Figure 3.40. Displaying the **Energies of decay products** for Uranium -238.

Selecting Associated Radionuclides (Star Function)

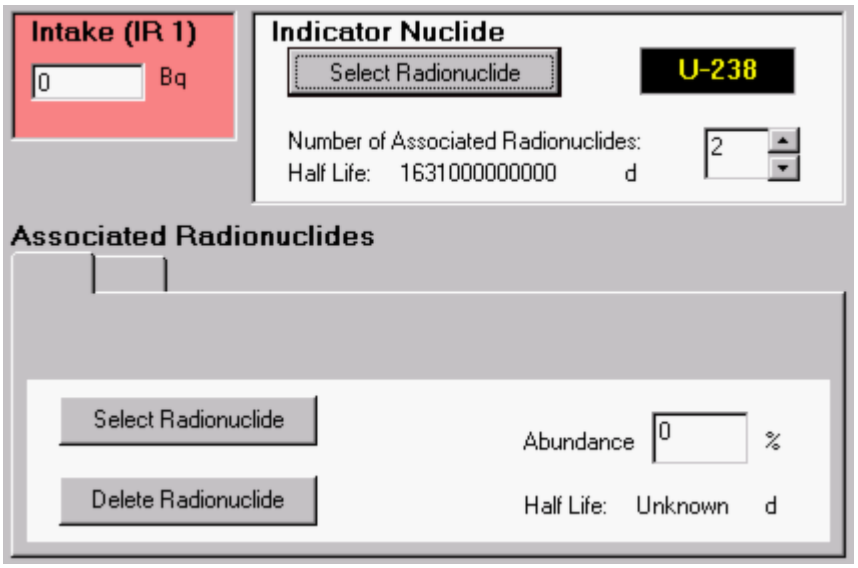


Figure 3.41. Adding **Associated Radionuclides** to the **Indicator Nuclide**.

To add one or several **Associated Radionuclides**, you first *select* the number of radionuclides required. This automatically displays the required number of blank "record

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 (^{239}**Pu** and ^{241}**Am**) set up to be associated with a hypothetical (**1 Bq**) **Intake** of the indicator nuclide (^{238}**U**). The "**Delete Radionuclide**" *button* removes the indexed associated radionuclide.

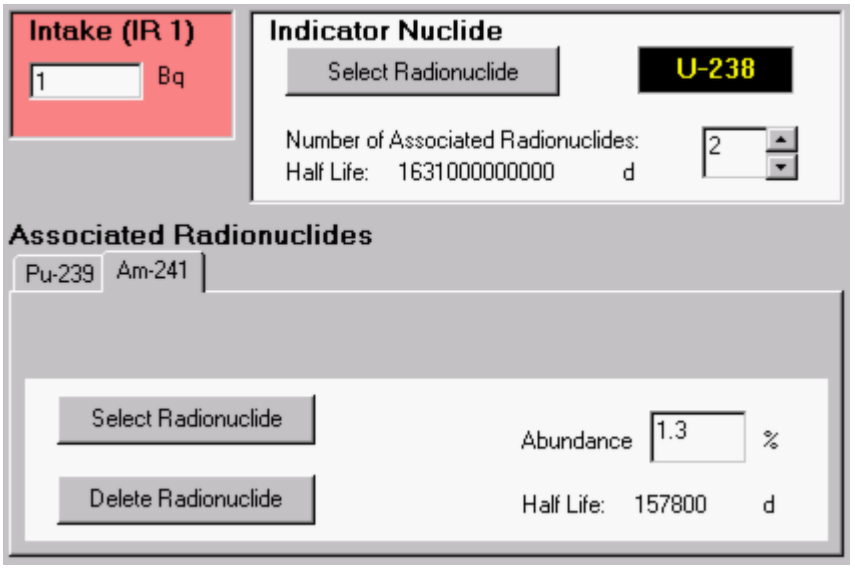


Figure 3.42. Adding ***239*Pu** and ***241*Am** as **Associated Radionuclides**.

Note: The **Associated Radionuclides** are not part of any **bioassay calculation**. All bioassay calculations are performed for the **Indicator Nuclide**. The associated radionuclides represent additional **Intakes** - that ARE included in any **dose calculation**.

Warning: If there is more than one **Intake Regime** (**IR**), then **IMBA Professional** automatically assigns the same **Associated Radionuclides** (and their specified **Abundances**) to **All IRs**. If this is **not appropriate**, you should *calculate* doses separately for each **IR** - using its own set of **Associated Radionuclides** and/or **Abundances**.

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Setting Hypothetical Intake Amounts

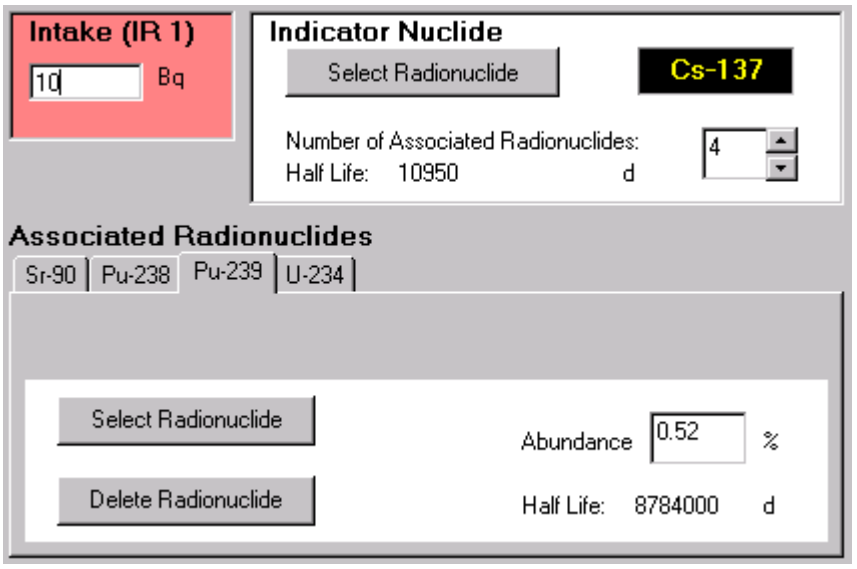

Figure 3.43. Setting a hypothetical amount for **Intake (IR 1)**.

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.

Note: The program "focus" leaves the **Intake (IR #)** dialog box immediately you carry out the next mouse *action*, *e.g.*, when you *click* on another program control.

Tip: Once you have defined the **IR(s)**, and selected the **Indicator Nuclide**, the **next step** is to proceed with setting up the Model Parameters. You can't perform any calculation in IMBA Professional without first defining the required model parameters. The program will **guide** you through the necessary procedures.

Note: Multiple Intakes are a **Star Feature**.

Model Parameters Sub-panel

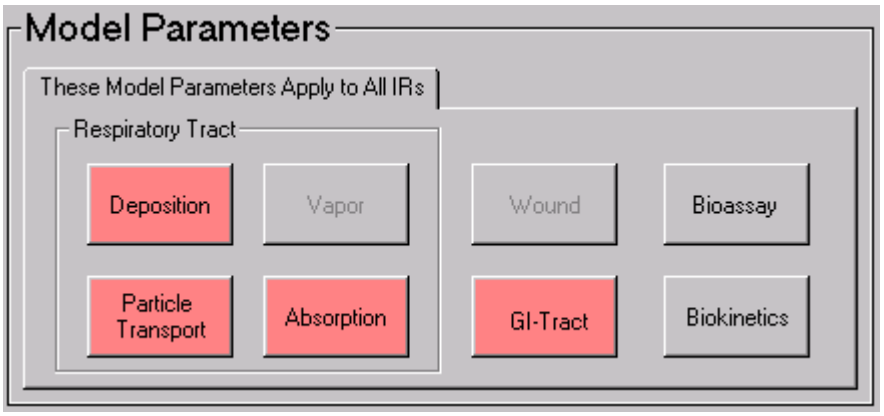

Figure 3.44. Model Parameters sub-panel at start-up - for a **New** (blank) parameter file.

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
- Absorption
- GI-Tract.

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 GI-Tract model. However, you will also need to specify the gut uptake fraction (**f1**), which is part of the "**Absorption**" model. In this case, the **absorption parameters** for the respiratory tract model are NOT required.

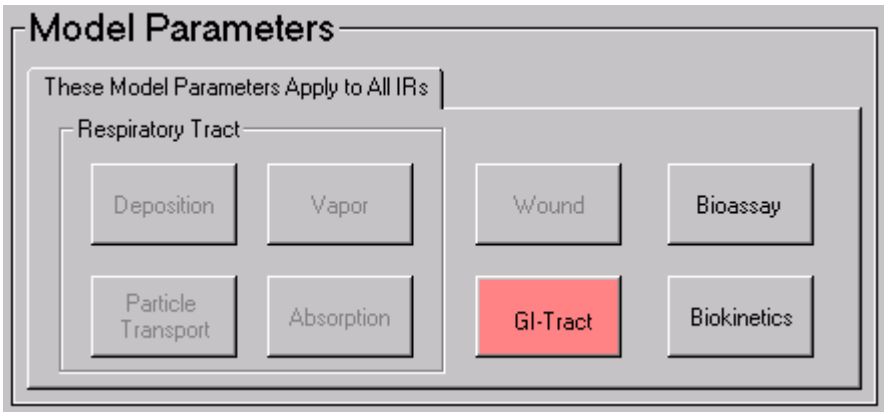

Figure 3.45. Model Parameters sub-panel for "**Ingestion**" as the **Route** of intake.

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).

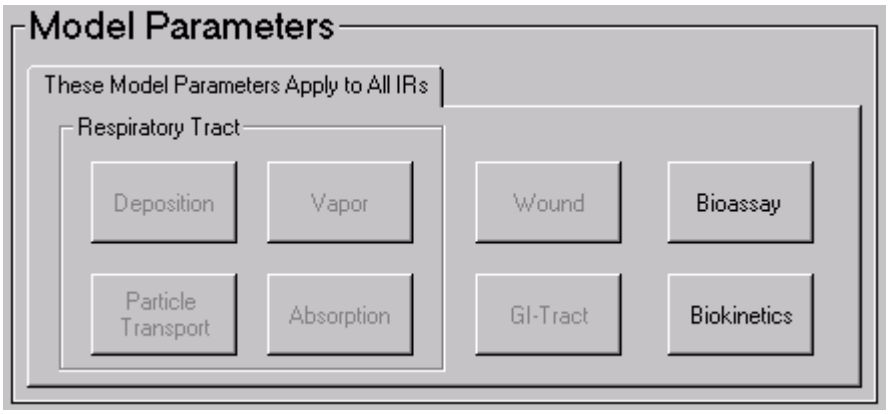

Figure 3.46. Model Parameters sub-panel for "**Injection**" as the **Route** of intake.

Deposition Parameters

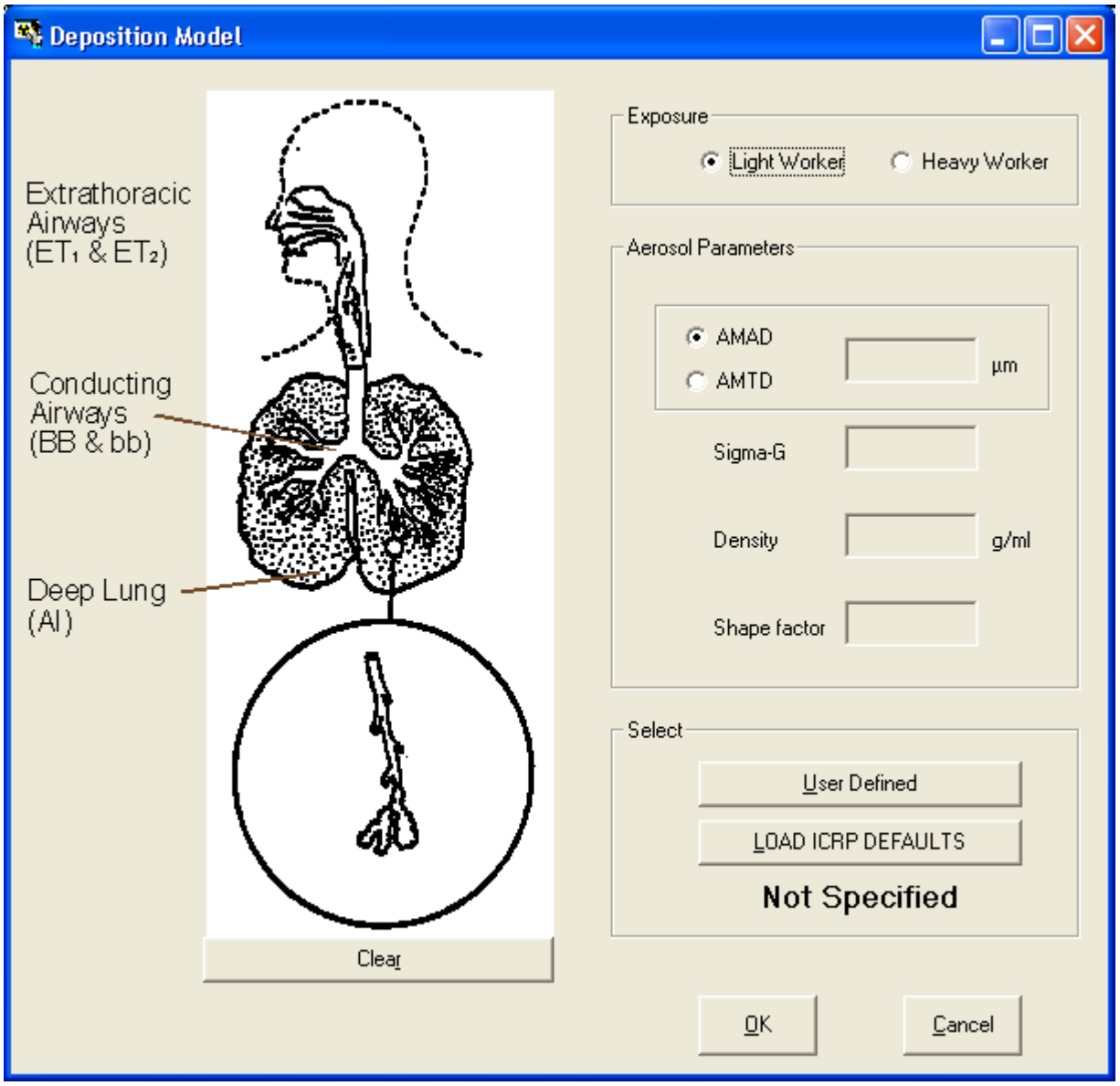

Figure 3.47. Deposition Parameters window.

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

- ***U*ser Defined**;
- ***L*OAD 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*.

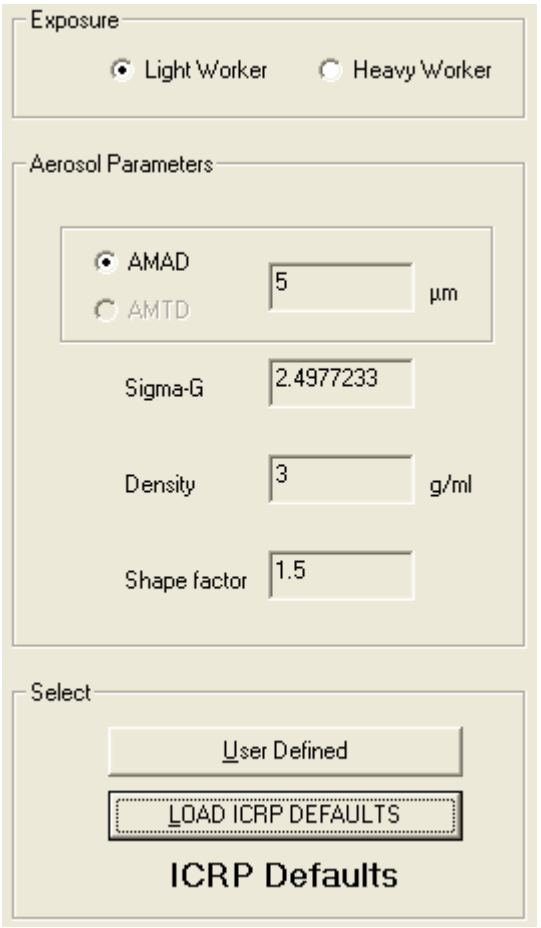

Figure 3.48. Selection of **ICRP Defaults** for **Deposition Parameters**.

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

- Standard worker - average ventilation rate 1.2 $m^3 h^{-1}$.
- AMAD - 5 µm.
- Sigma-G (s_g) - 2.4977233.
- [Particle] **Density** (ρ) - 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).

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 ICRP68 Reference 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).

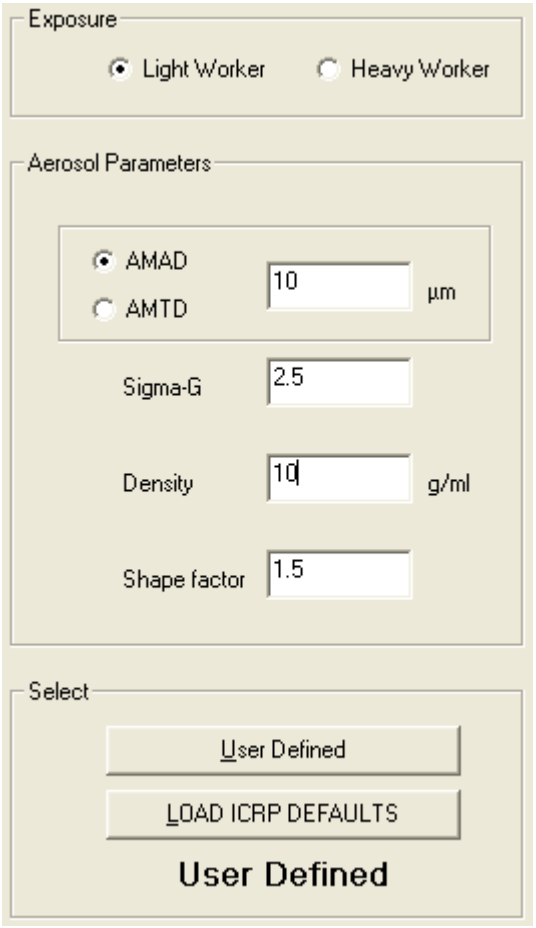

Figure 3.50. Selection of **User Defined** values for **Deposition Parameters**.

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

- AMAD - 10 µm.
- Sigma-G (s**g**) - 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).

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**.

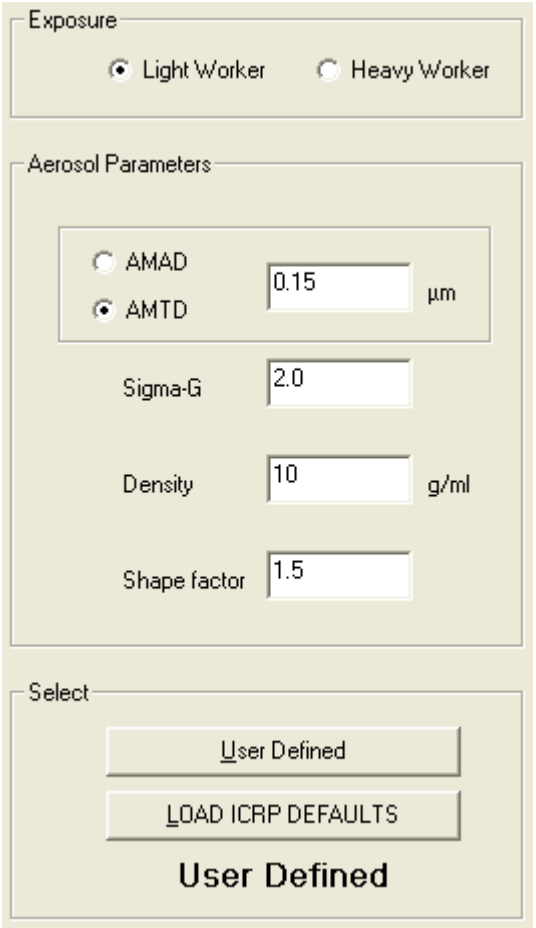

Figure 3.52. Characterizing a sub-micron aerosol by its **AMTD**.

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

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

Particle Transport Parameters

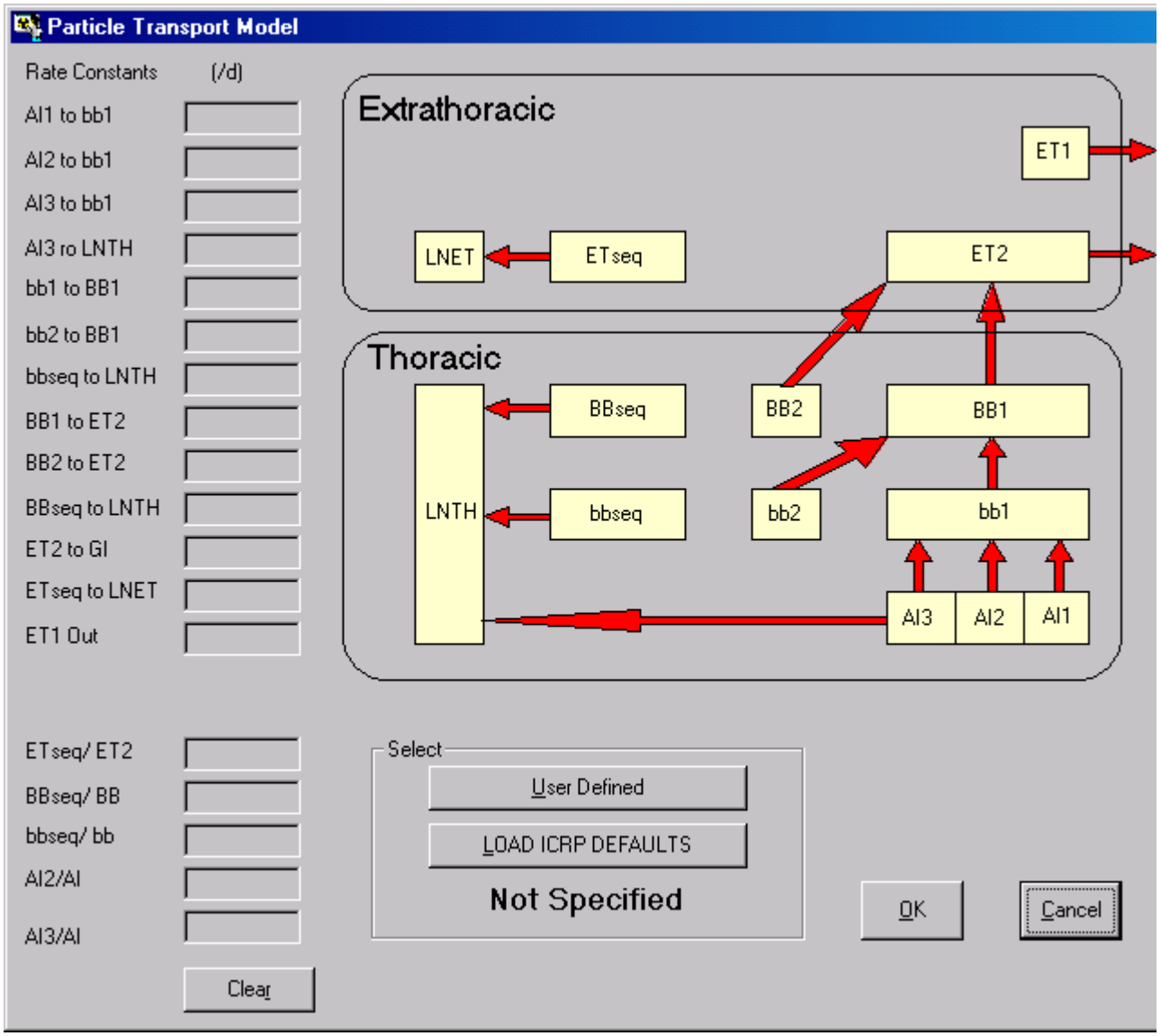

Figure 3.53. Particle Transport Model window.

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).

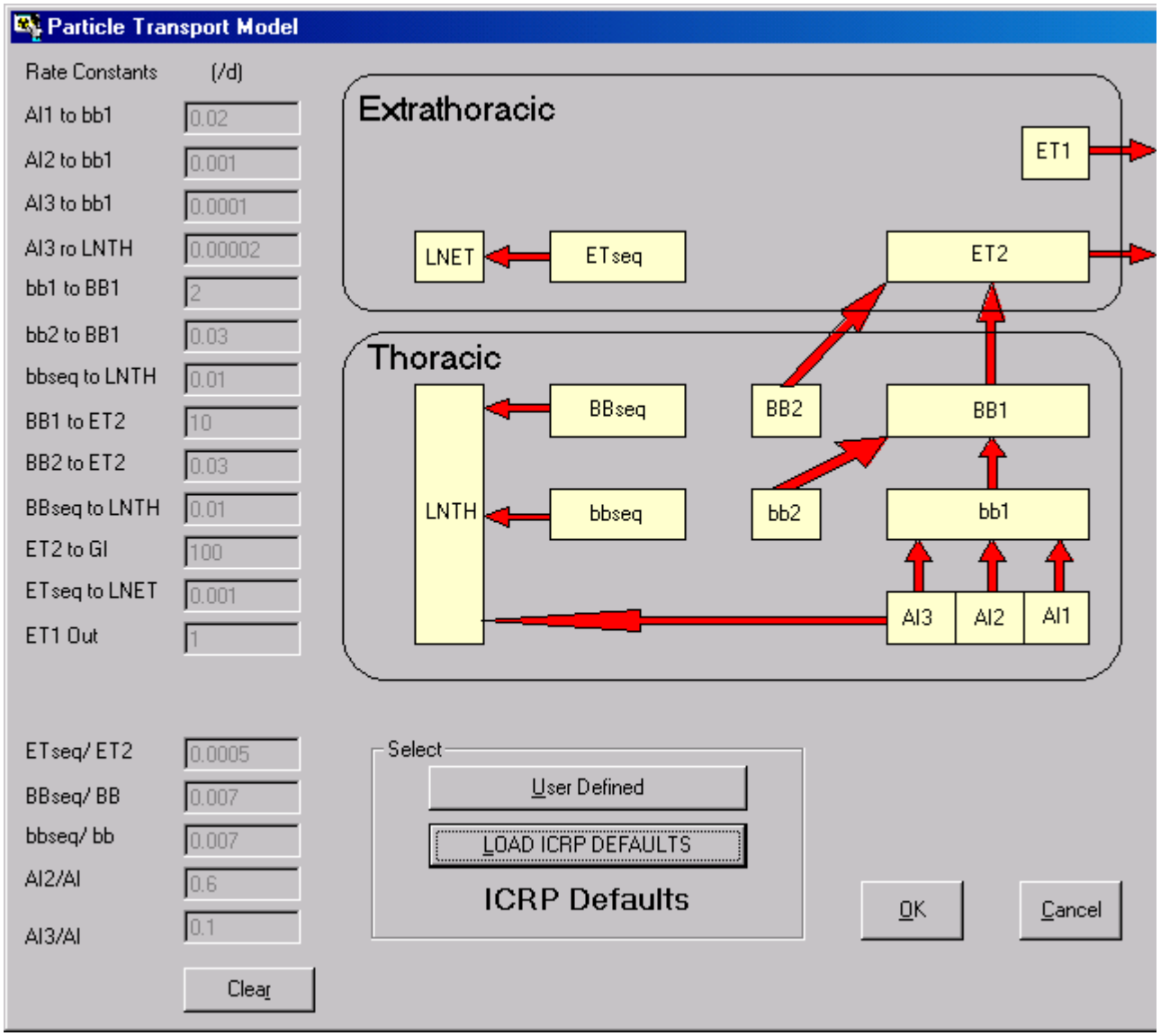

Figure 3.54. Particle Transport Model window loaded with parameter values recommended in *ICRP Publication 66* (**ICRP DEFAULTS**).

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**.

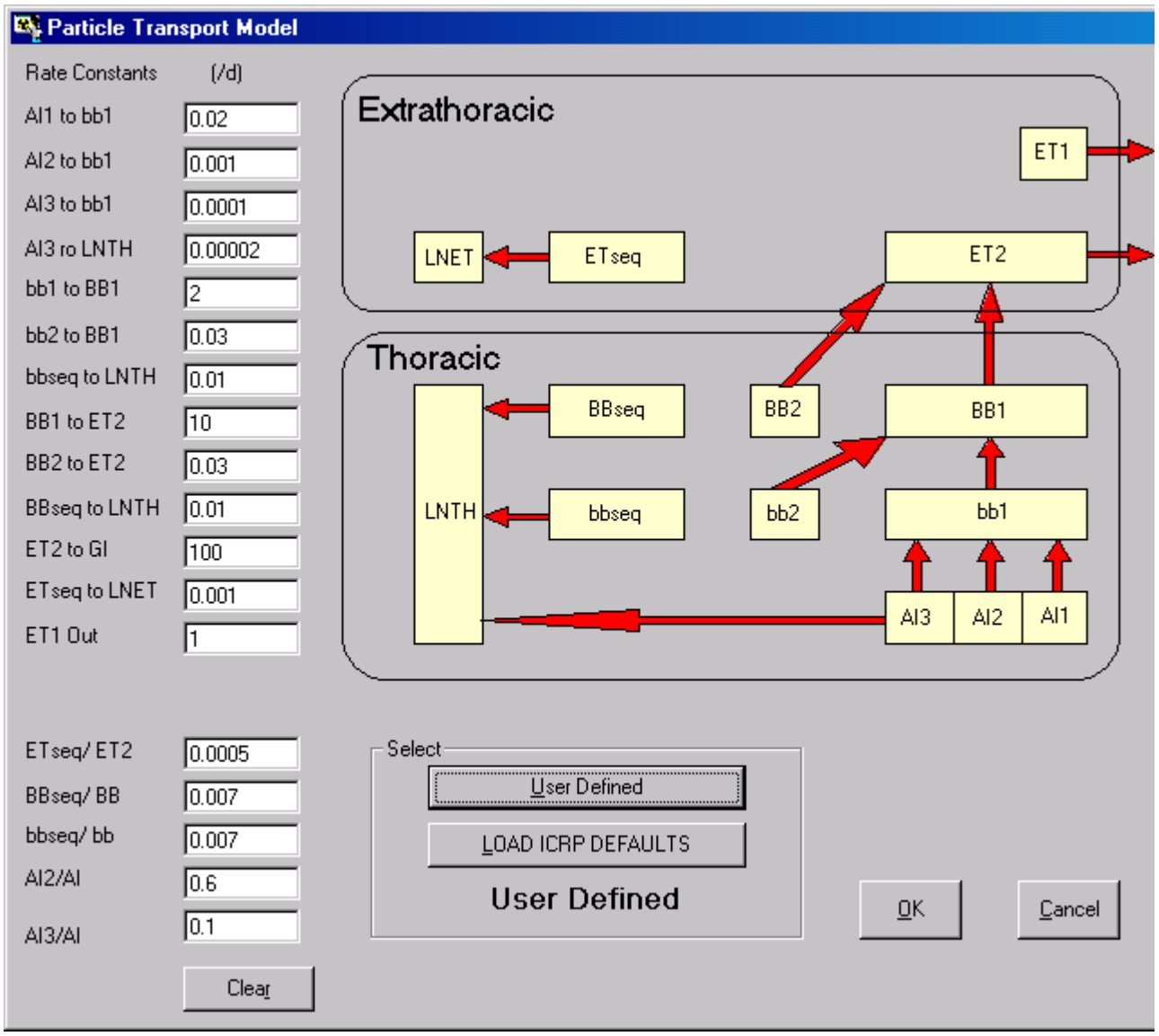

Figure 3.55. Particle Transport Model window in its "**User Defined**" mode.

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).

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

Note: If you need to, you can set the values of the particle transport parameters independently for EACH **Intake** by **Inhalation** (*i.e.*, each **IR #**).

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 absorption parameters for substitution in the *ICRP Publication 66* respiratory tract absorption model - and the associated value of the gut uptake fraction (f**1**).

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

Selecting ICRP Default Absorption Parameters

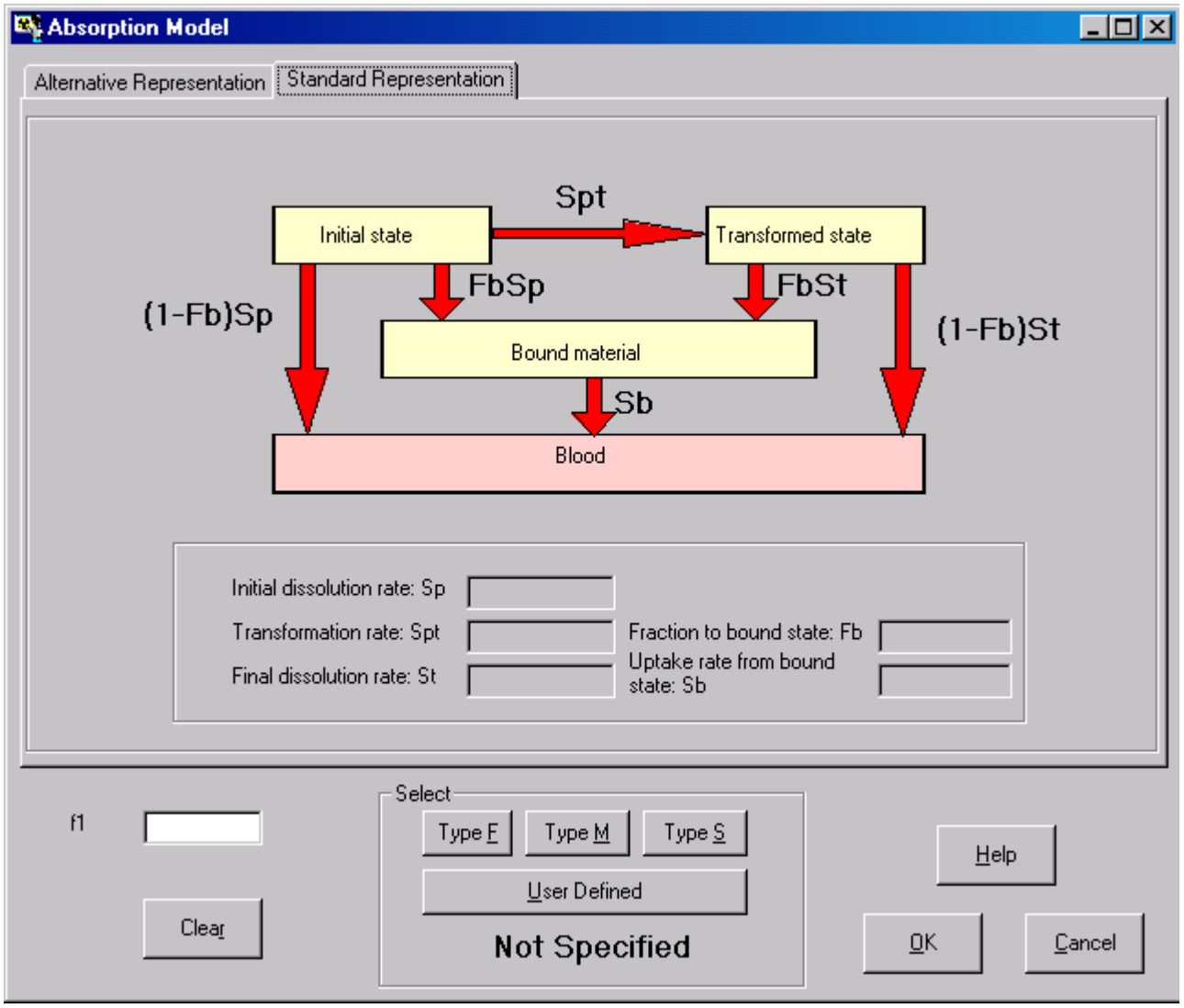

Figure 3.57. Absorption Model window.

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 (f**1**), 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**1** values for different chemical forms of the **Indicator Nuclide**. Figure 3.58 shows the **F1 values for Am** window.

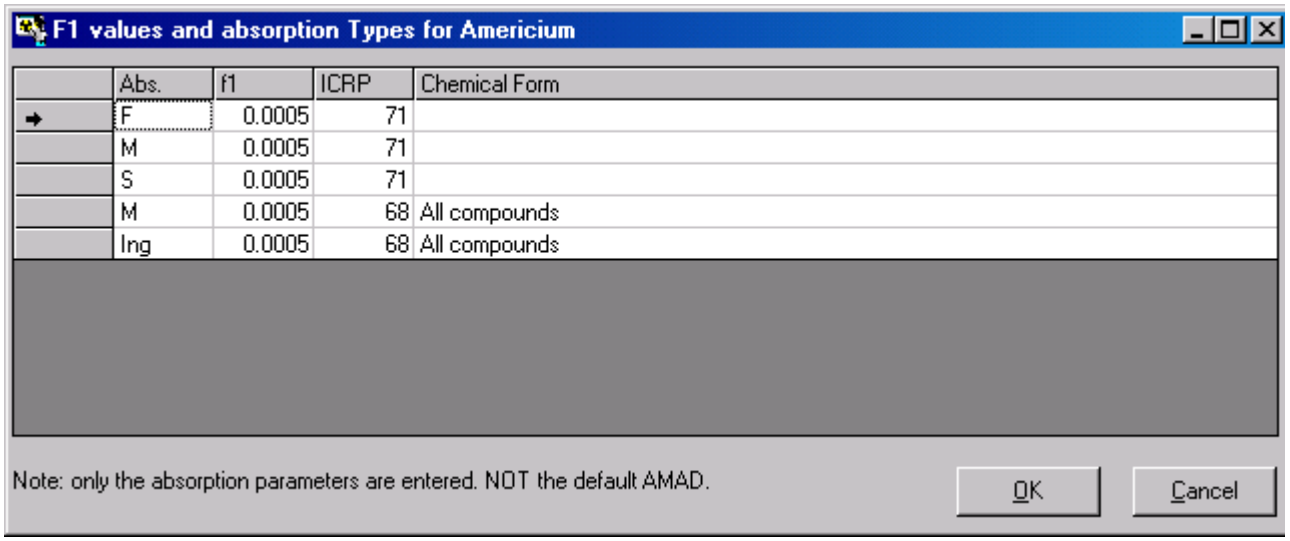

Figure 3.58. F1 values window - for **Help** in selecting the value of f**1**.

Note: If you have not previously selected the **Indicator Nuclide**, you CANNOT use the "**Help**" button in the **Absorption Model** window. In this case, IMBA Professional will display a WARNING message - prompting you to *Select* an **Indicator Nuclide**.

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.

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

Tip: ***You can also define the value of f1 in the* GI Tract Model *window. BOTH the* Absorption Model *window and the* GI Tract Model *window display the currently loaded value of f1 - 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).

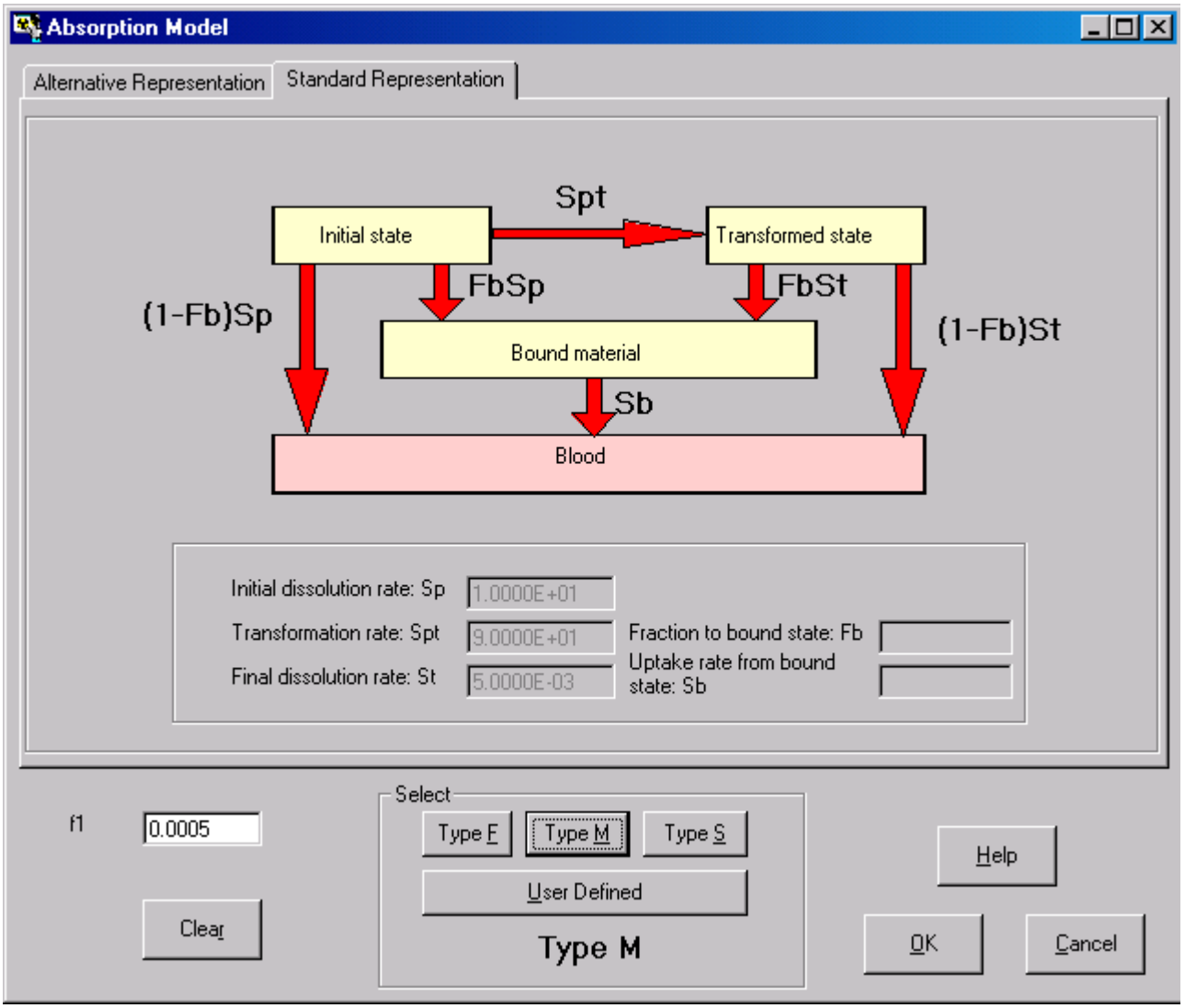

Figure 3.59. Absorption Model window with the *ICRP Publication 71* recommended f**1** value for **Type M** (Americium) loaded.

Figure 3.60. The selected **Type M** absorption behavior and the f**1** 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.

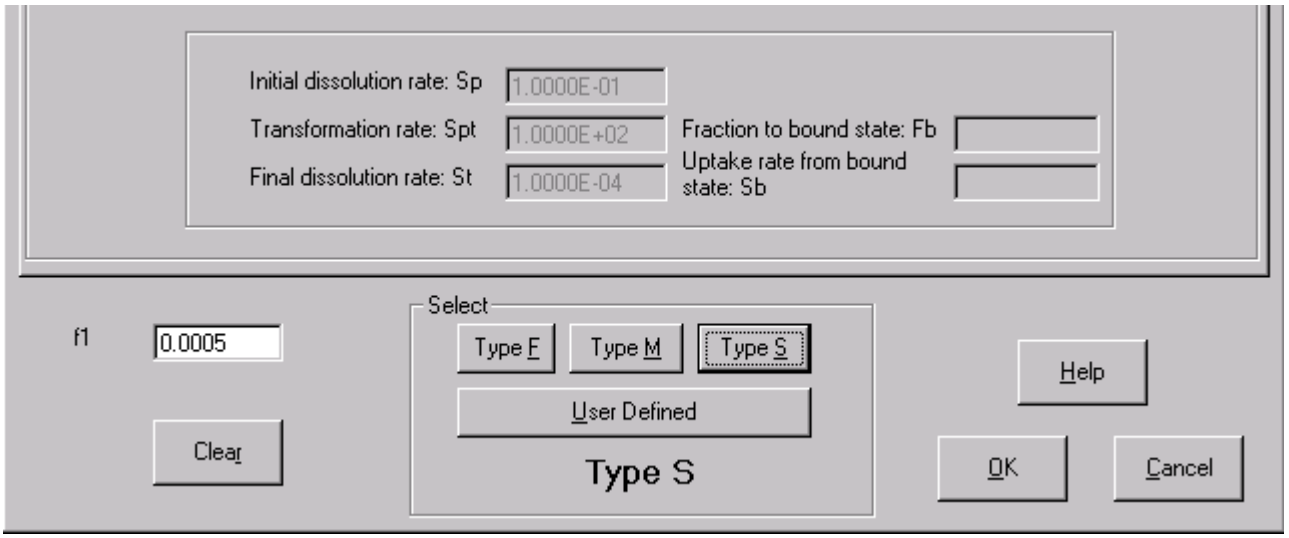

Figure 3.61. Absorption Model window after selecting "**Type** S" absorption behavior.

Warning: Selecting a different respiratory tract **Absorption Type** does NOT automatically select an appropriate value of the gut absorption fraction (f**1**). This is YOUR responsibility! The previously-loaded value of f**1** will remain in the "**f1**" dialog box until you C**lear** and/or **replace** this with a new value.

Tip: It is a good idea to go back and *click* the "H**elp**" button again - to check out the ICRP-recommended value of f**1** that is appropriate for your newly selected respiratory tract **Absorption Type**.

Note: Remember that selecting an ICRP default from the "**Help**" button loads BOTH the **Absorption Type** and f**1** value, whereas selecting the **Absorption Type** by *clicking* a "**Type**" *button* will load ONLY the **Absorption Type**.

Defining Your Own Absorption Parameters

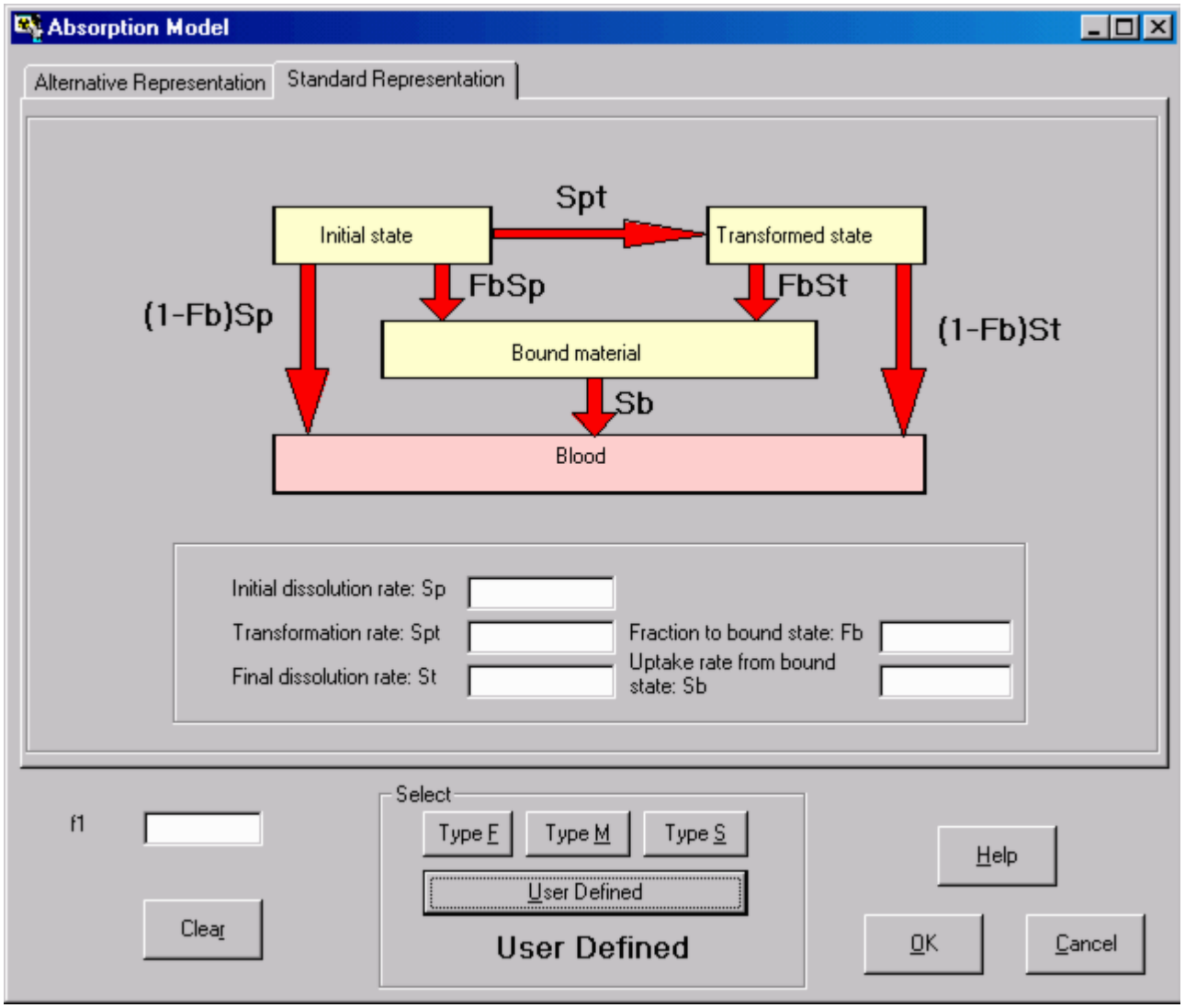

Figure 3.62. Absorption Model window for **User Defined** parameter *option*.

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** (Model of Material Absorption 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 -2 d -1;
- **s**pt = 100 d -1;
- **s**t = 10 -5 d -1;
- **f**b = 0.05;
- **s**b = 10 -3 d -1.

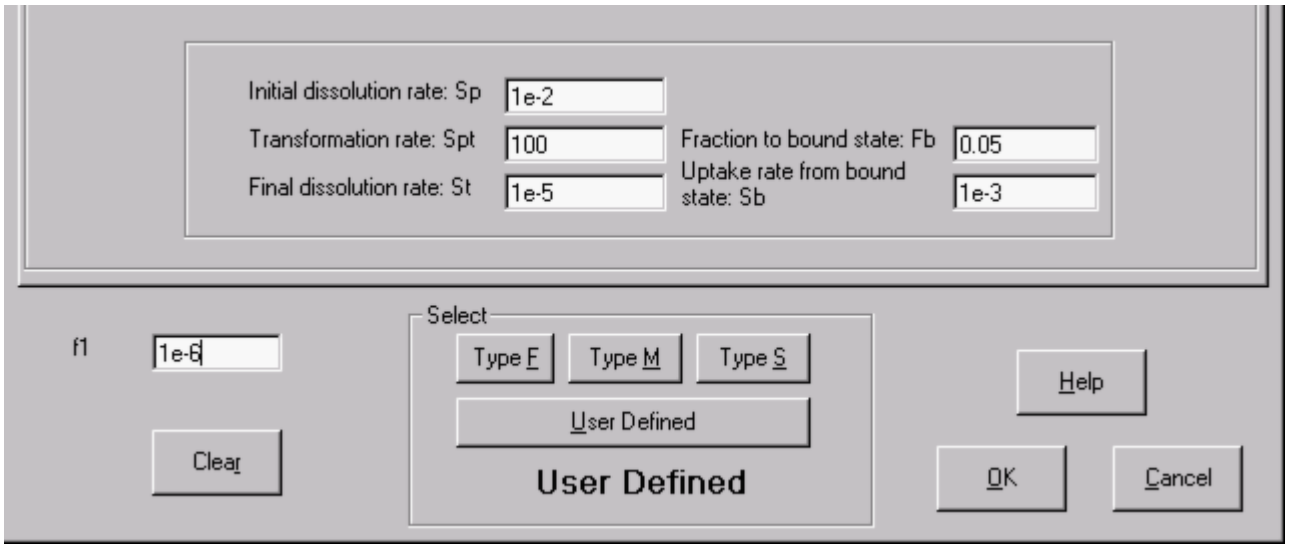

Figure 3.63. Entering your own (non-default) values of **Absorption Rates.**

Warning: The **Unit** in which **Absorption Rates** are expressed in IMBA Professional is ALWAYS "**d**$_{-1}$," *i.e.*, "**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 ICRP Publication 66:

- 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.

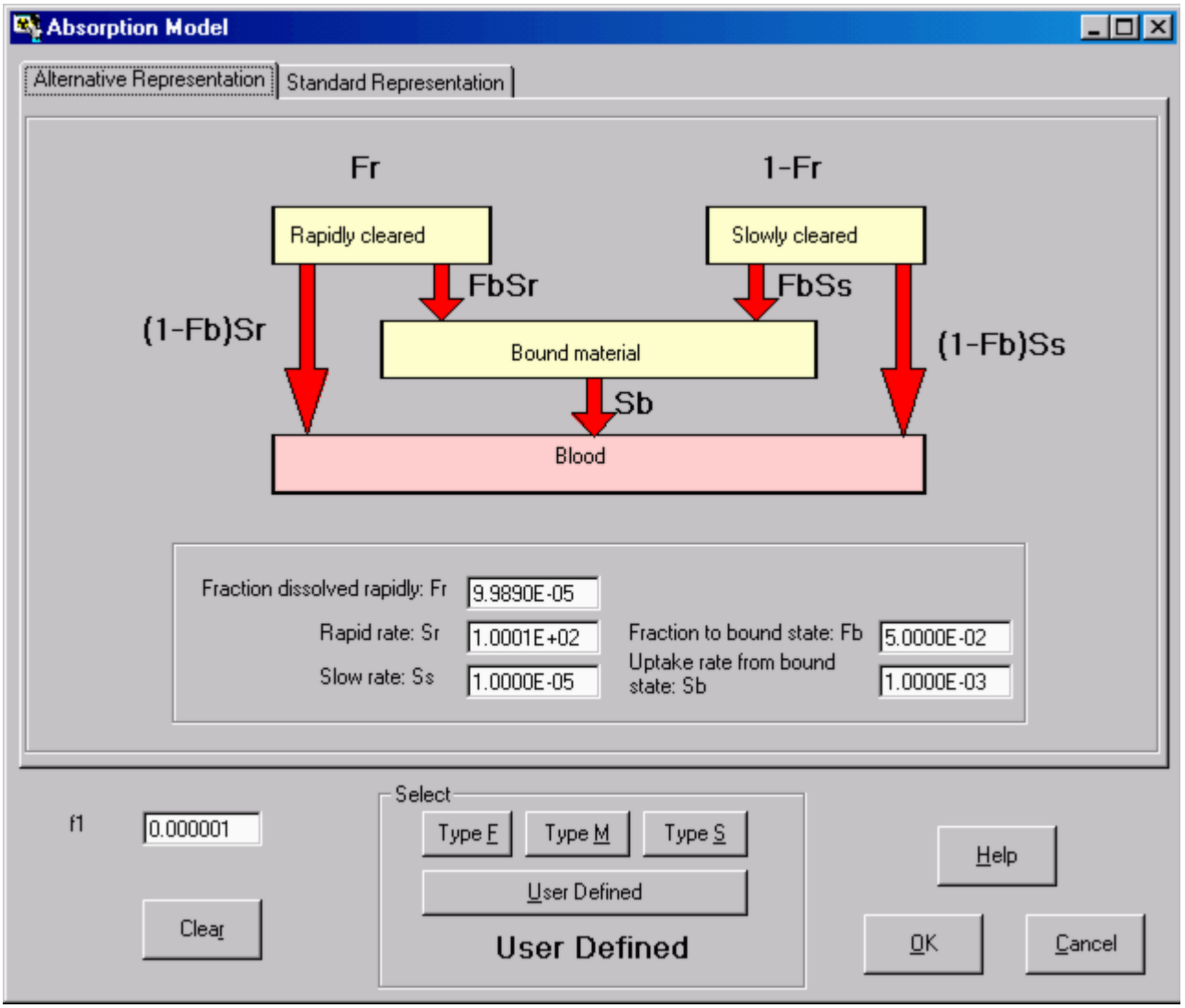

Figure 3.64. Automatically calculated **Alternative Representation** of the particle dissolution, material binding and absorption characteristics shown in Figure 3.63.

The alternative dissolution and absorption parameters are:

- **Fraction dissolved rapidly, f_r** = 9.9890 ´ 10-5;
- **Rapid rate, s_r** = 100.01 d-1;
- **Slow rate, s_s** = 10-5 d-1;
- **Fraction to bound state, f_b** = 5 ´ 10-2;
- **Uptake rate from bound state, s_b** = 10-3 d-1.

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

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

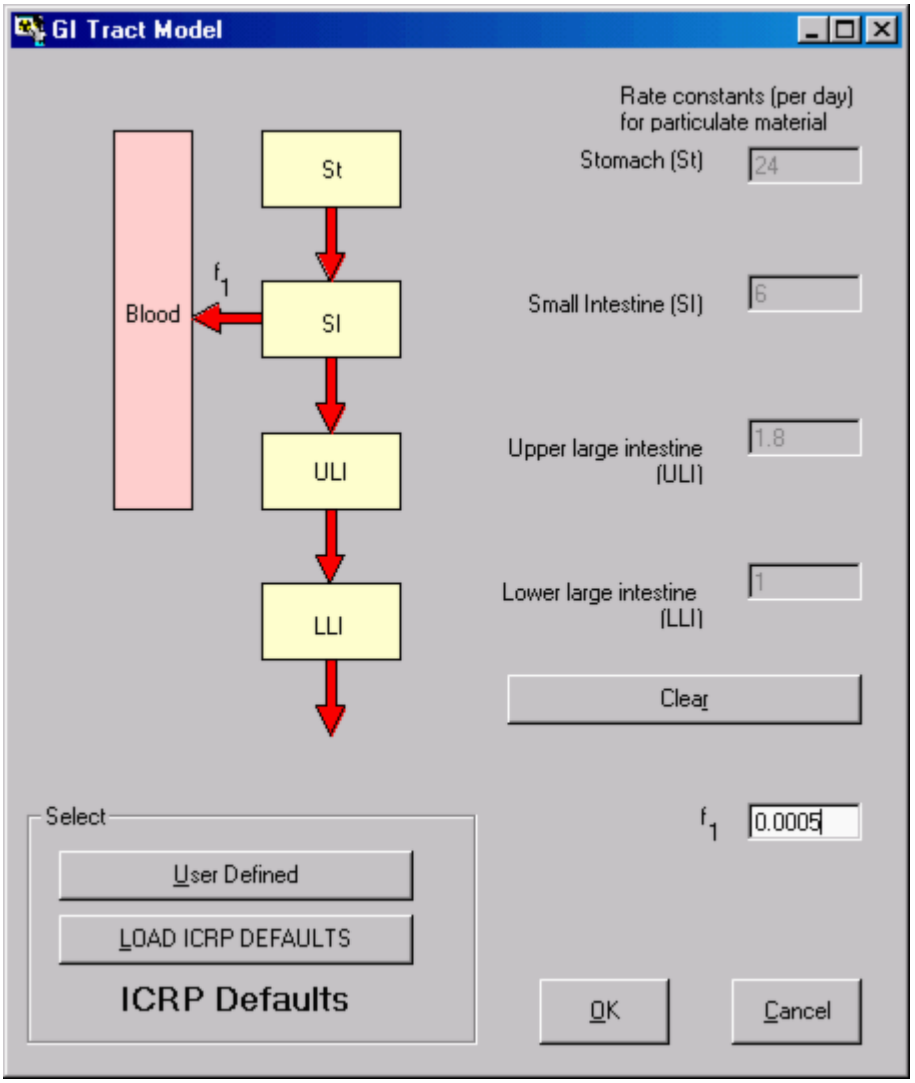

Figure 3.65. The **ICRP Publication 30 GI Tract Model** with **ICRP Default** parameter values loaded.

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

In Figure 3.65, the "**f1**" dialog box is displaying the value of "**0.0005**" for the gut absorption fraction (f***1***). If you had selected the f***1*** value earlier, **e.g.**, in the **F1 Values** window and/or the **Absorption Model** window (see Selecting ICRP Default Parameters), then the same f***1*** value would have been loaded automatically in the "**f1**" 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 "**f1**" dialog box would have appeared empty. In either case, you can type a new value of f***1*** directly into the "**f1**" dialog box (Figure 3.65).

To "look up" an appropriate ICRP-default value of f***1***, **click** the "**Help**" button in the **GI Tract**

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

Note: The f***1*** "**Help**" **button** only appears in the **GI Tract Model** window IF you have selected "**Ingestion**" as the **Route** of intake.

Note: In the f***1*** "**Help**" window, **indicate** a **row** displaying your desired f***1*** value, and then **click** "**OK**." ONLY the displayed f***1*** 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

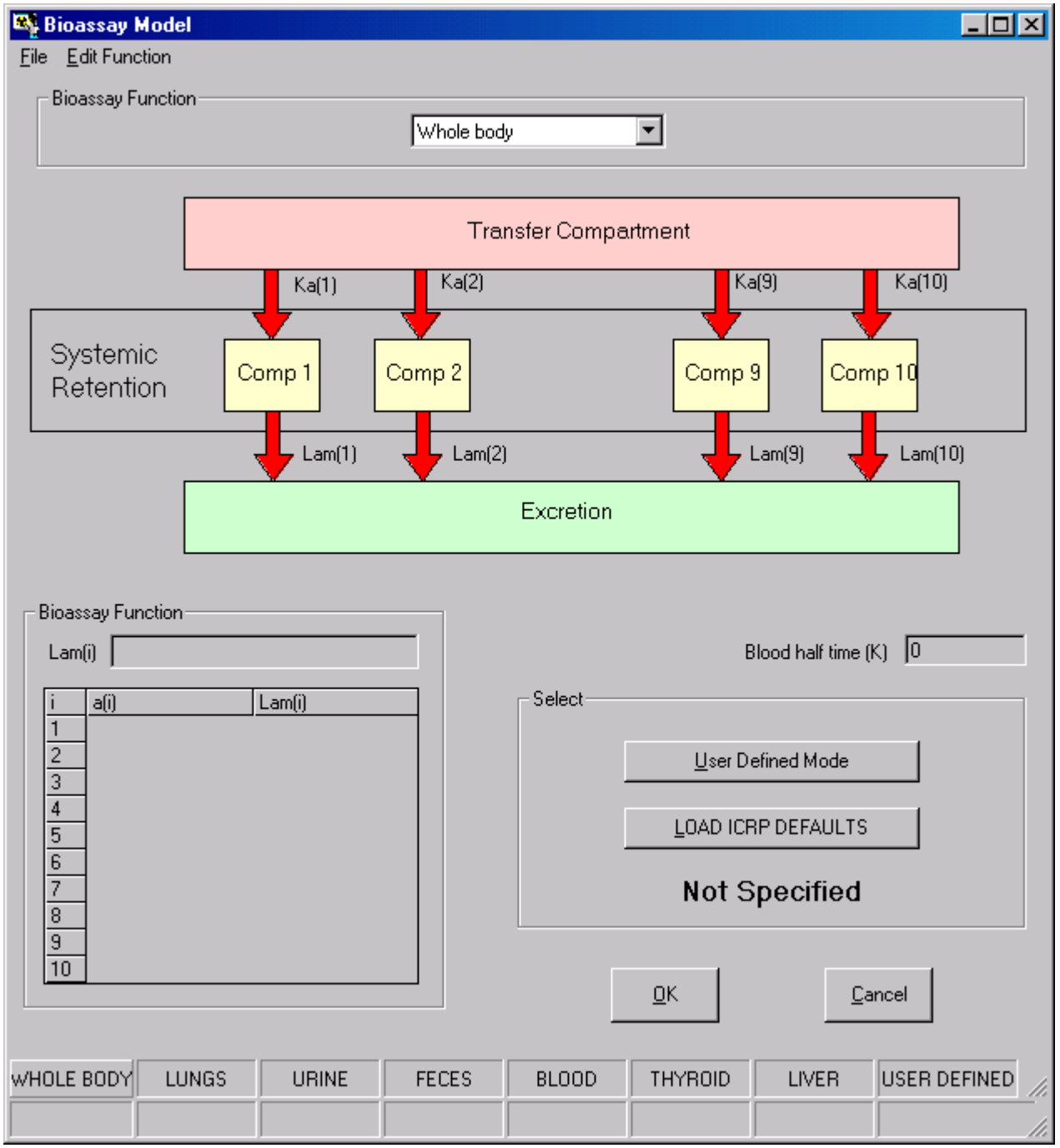

Figure 3.68. The **Bioassay Model** window.

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).

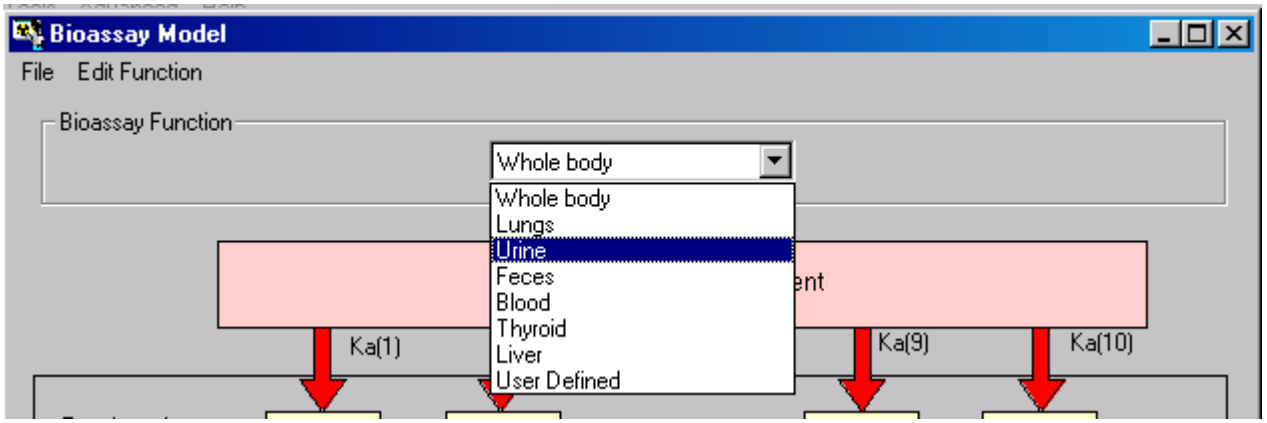

Figure 3.69. List **Bioassay** options.

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.

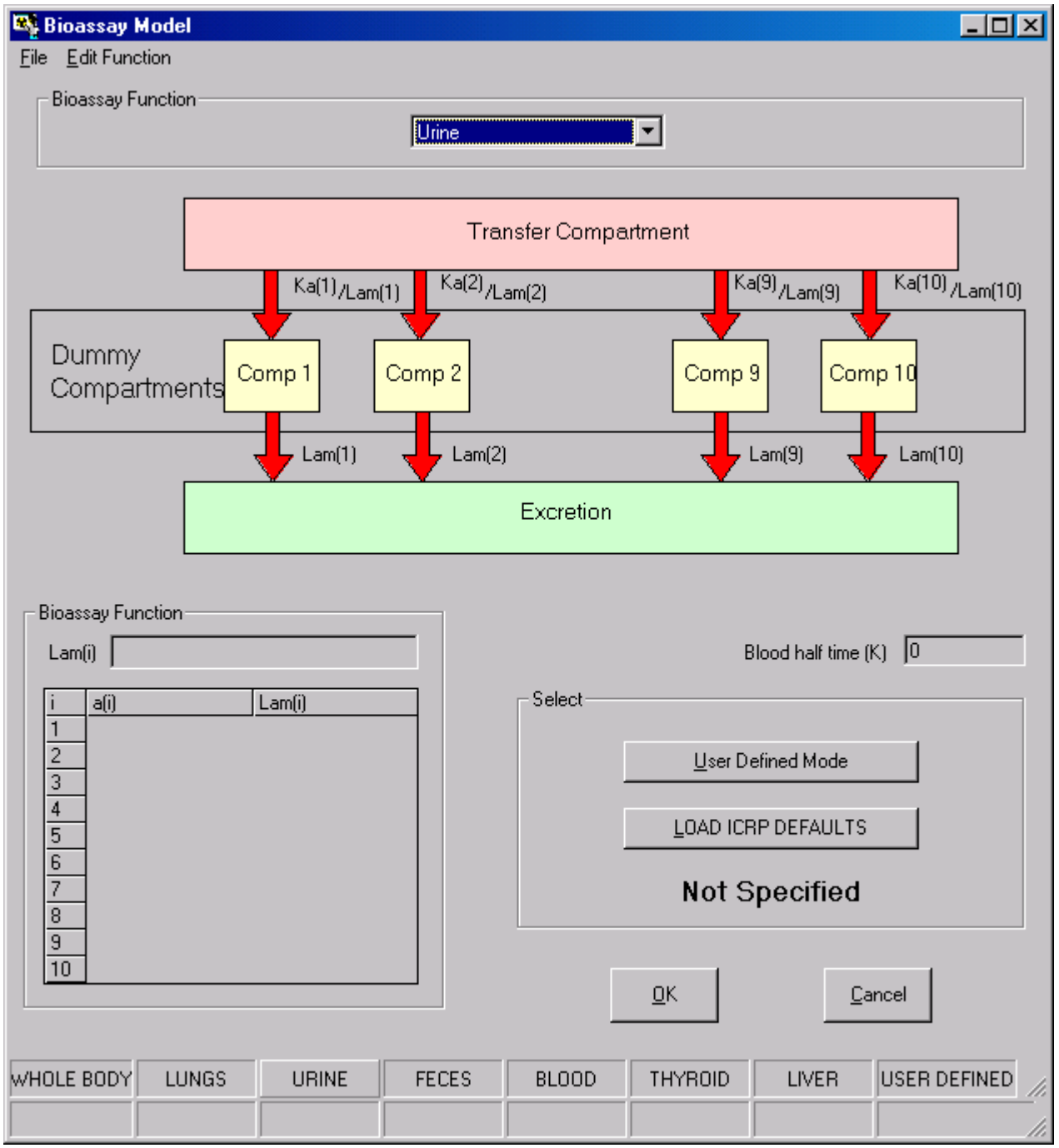

Figure 3.70. Selecting **Urine** in the **Bioassay Model** window.

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:

- ***U*ser Defined Mode**;
- ***L*OAD ICRP DEFAULTS**.

1. *"LOAD ICRP DEFAULTS" Option*

If you click the ***L*OAD 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, Fitted Excretion Functions).

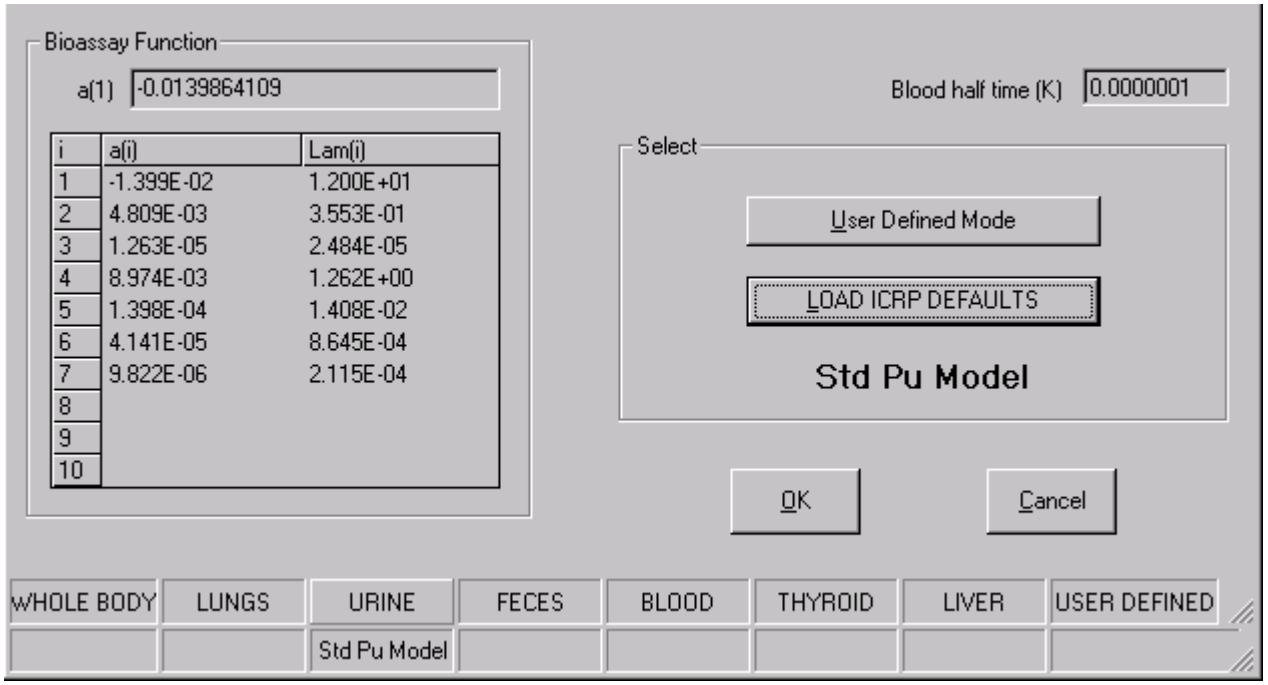

Figure 3.71. Loading the **parameters** of the **Bioassay Function** for **Pu-in-urine**.

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.

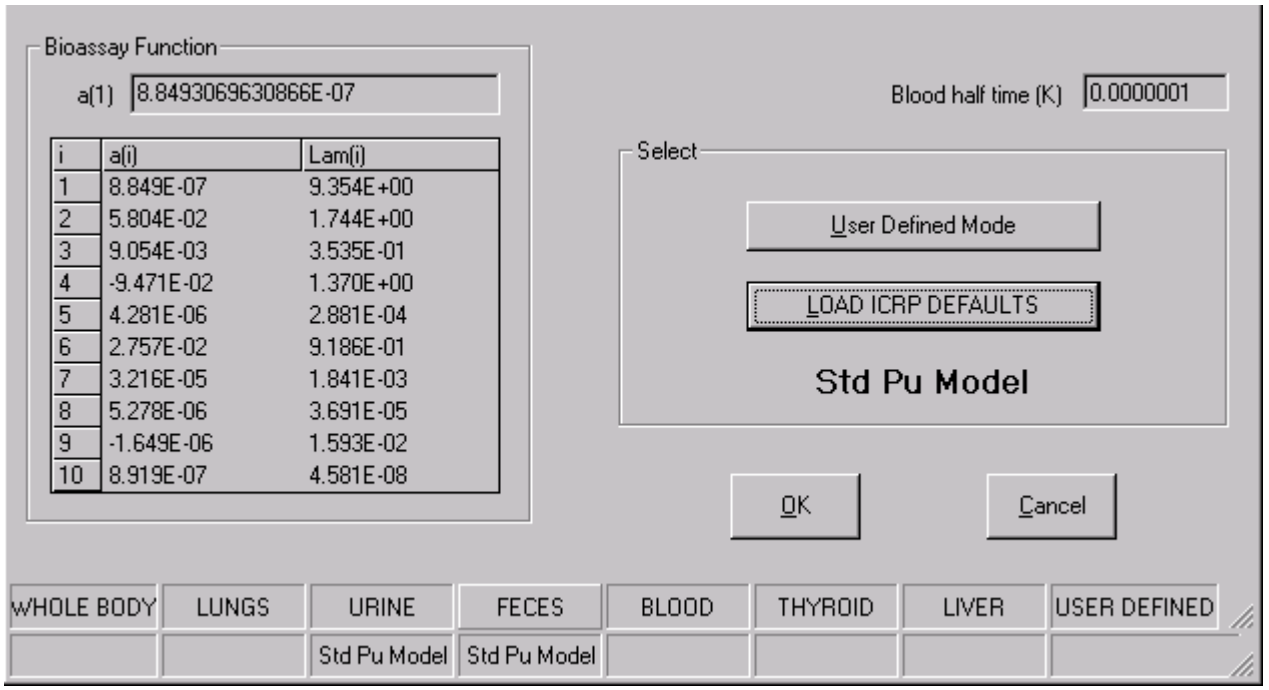

Figure 3.72. Adding the **parameters** of the **Bioassay Function** for **Pu-in-faeces**.

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. **IMBA Professional** "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**.

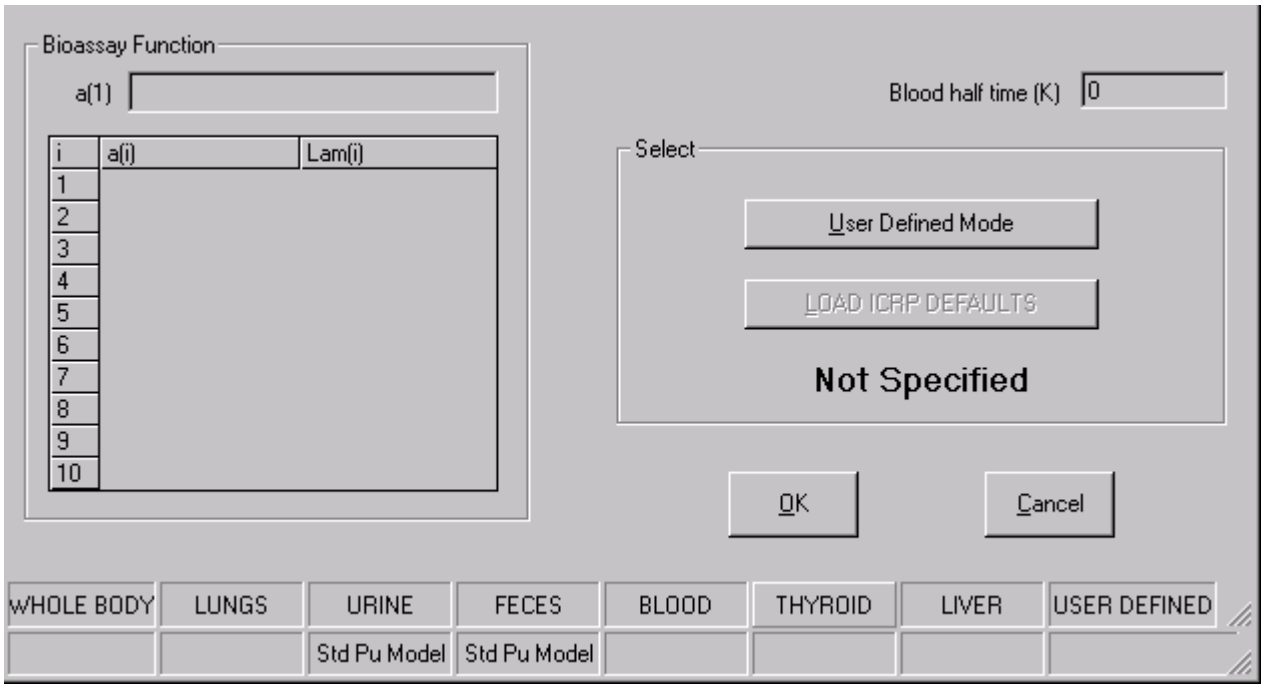

Figure 3.73. Label displayed if you try to load an "ICRP" **Bioassay Function** for **Pu-in-thyroid**.

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).

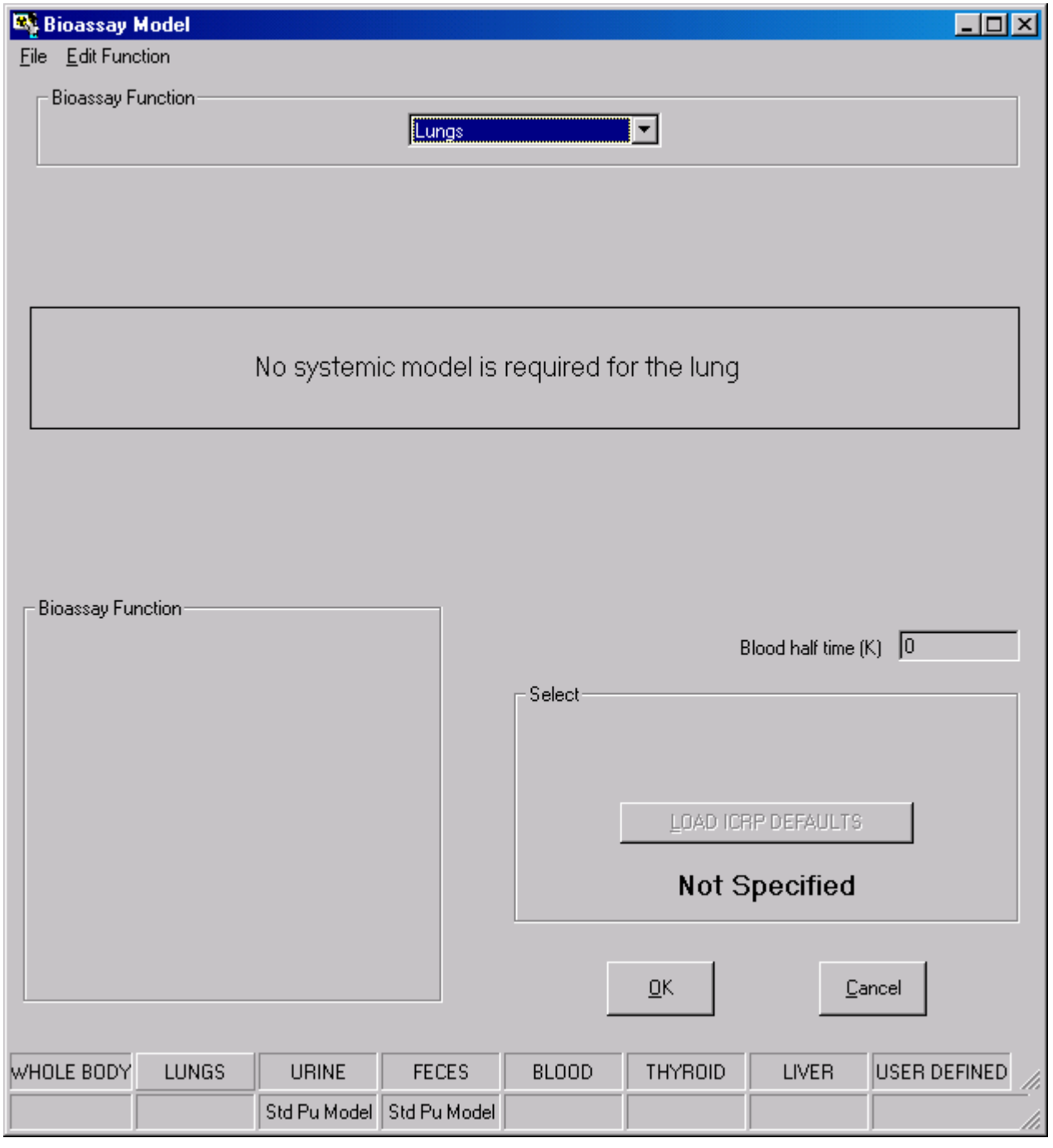

Figure 3.74. Message displayed if you try to load a **Bioassay Function** for the **Lungs**.

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.

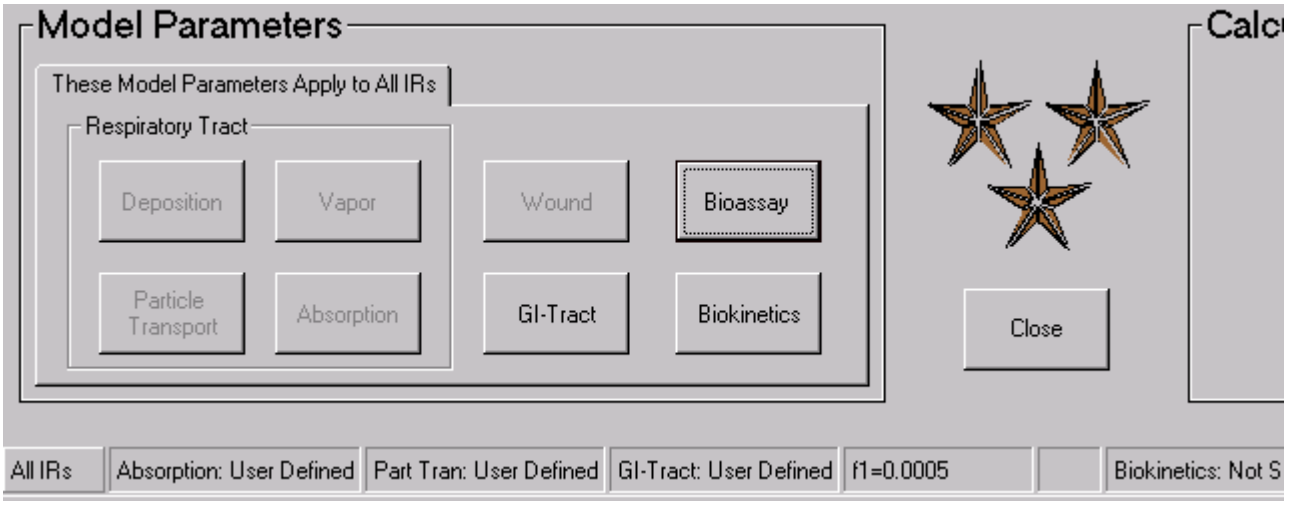

Figure 3.75. The Status Bar does NOT indicate the selected **Bioassay Functions**.

2. **"***User Defined Mode***"**

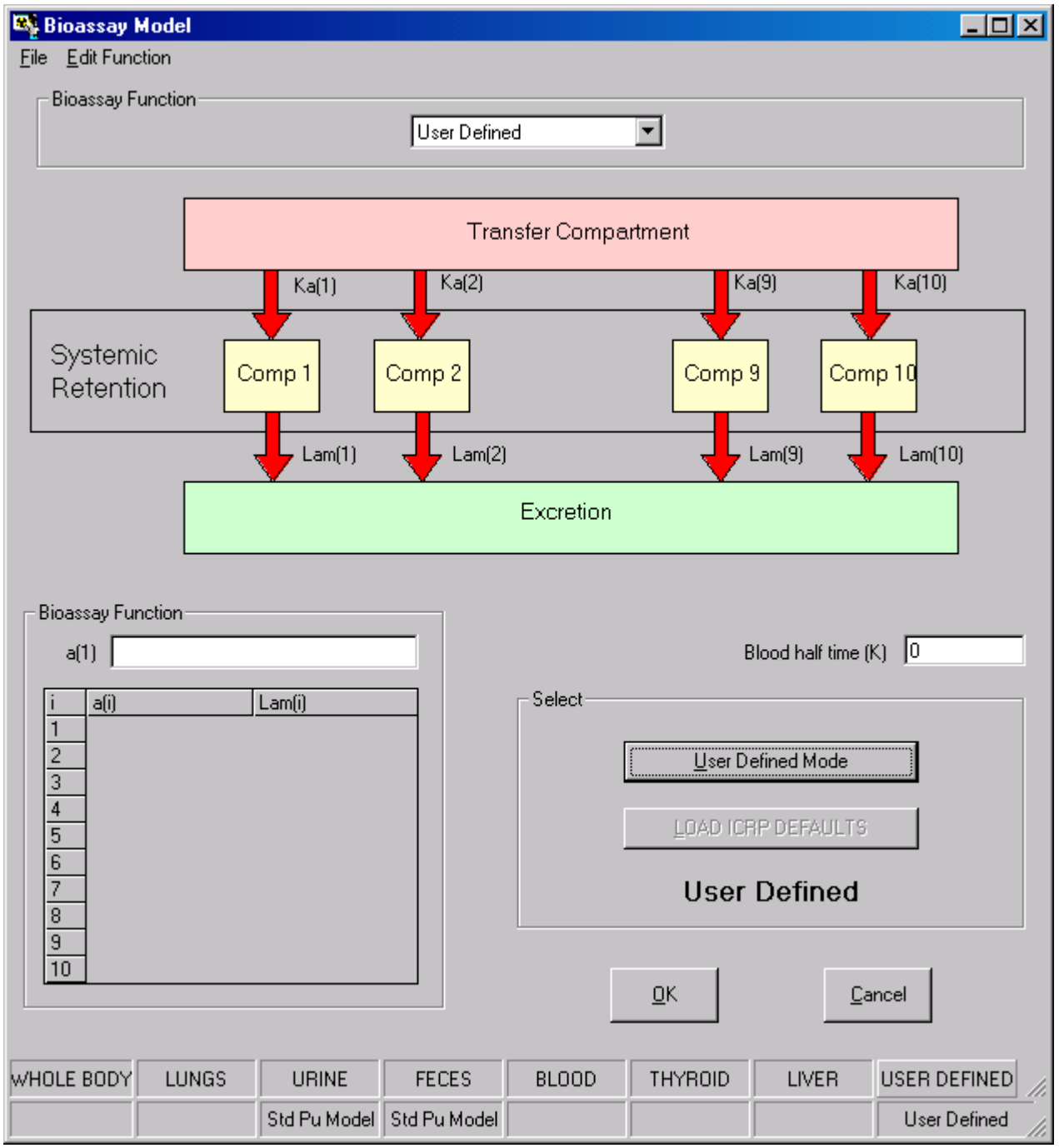

Figure 3.76. The **Bioassay Model** window in the "**User Defined Mode**."

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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**.

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

Quantity in **IMBA Professional**, then any **Dose Calculations** that you perform with ICRP-recommended "**Default**" **Biokinetic Models** may be INCONSISTENT with your **bioassay analyses**. For **Dose Calculations**, **IMBA Professional** 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 ICRP-recommended **Bioassay Models** in one operation - see "One-step Loading of All Model Parameters."

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Biokinetic Parameters

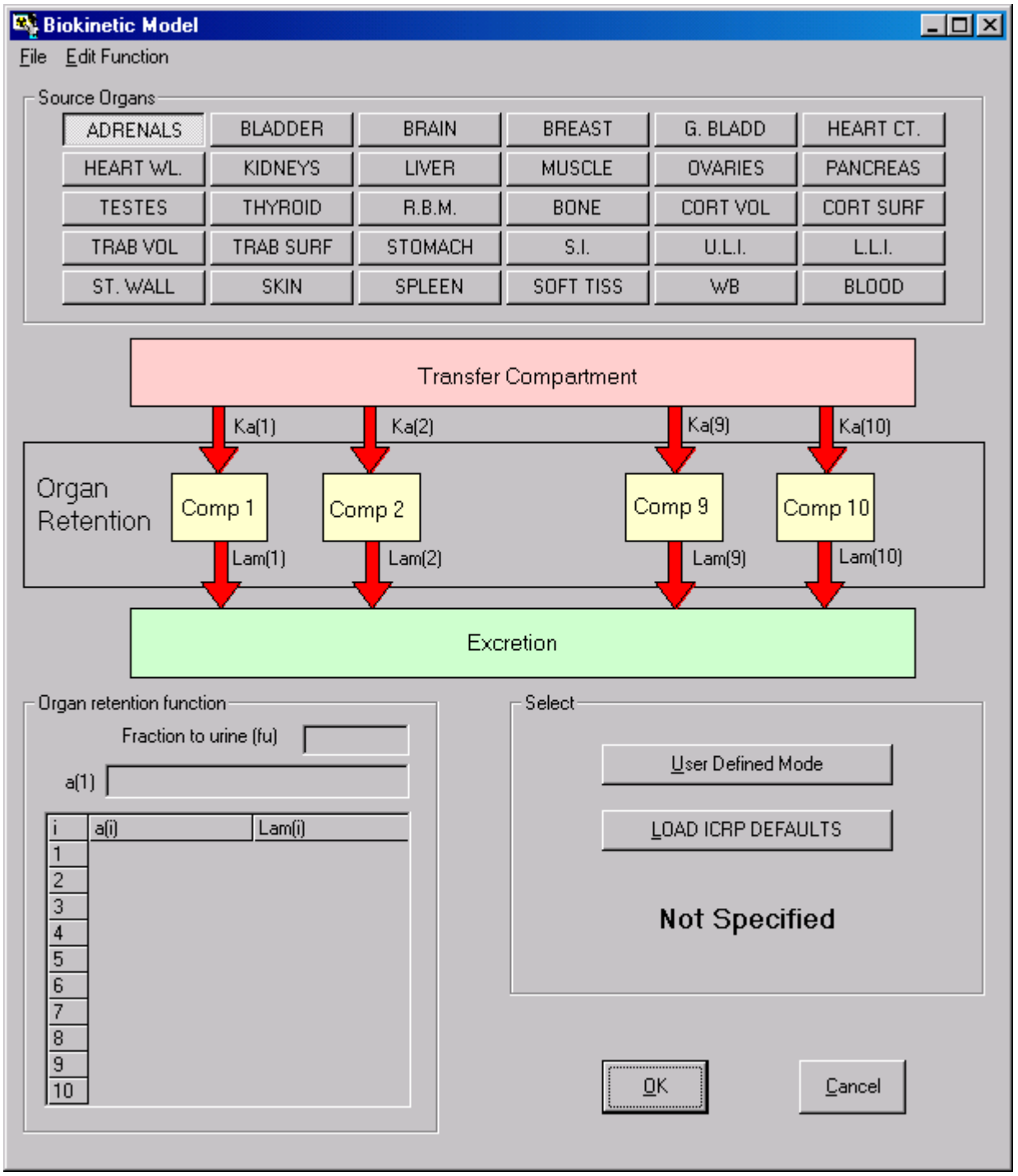

Figure 3.77. The **Biokinetic Model** window.

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 ***L*OAD 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*

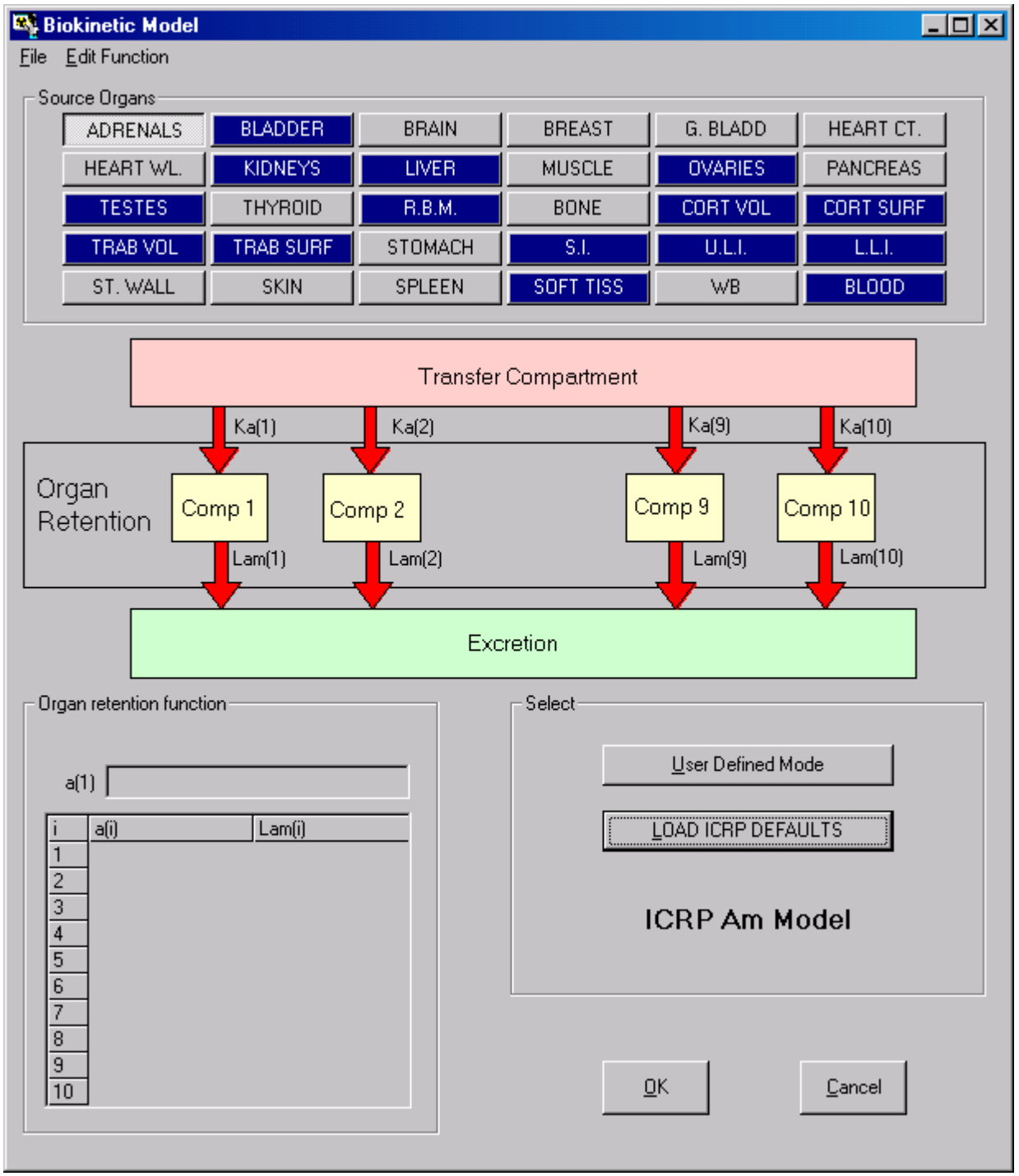

Figure 3.78. Loading the **ICRP Default** Biokinetic Models for americium.

Clicking the *L***OAD ICRP DEFAULTS** button automatically loads the fitted retention functions 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**.

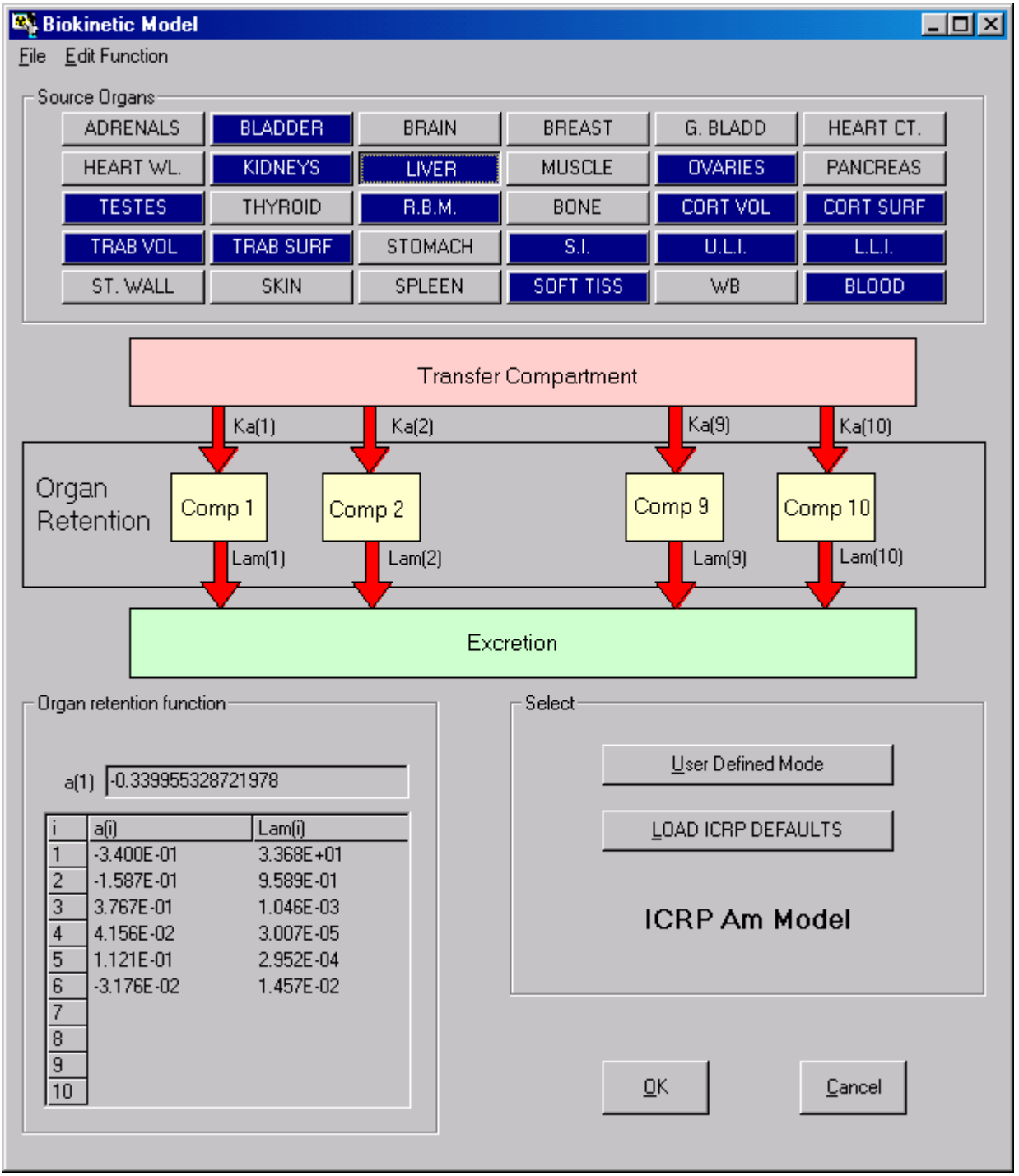

Figure 3.79. The **retention function** for americium in liver.

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**.

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 "*U***ser 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 "*U***ser Defined Mode**" button.

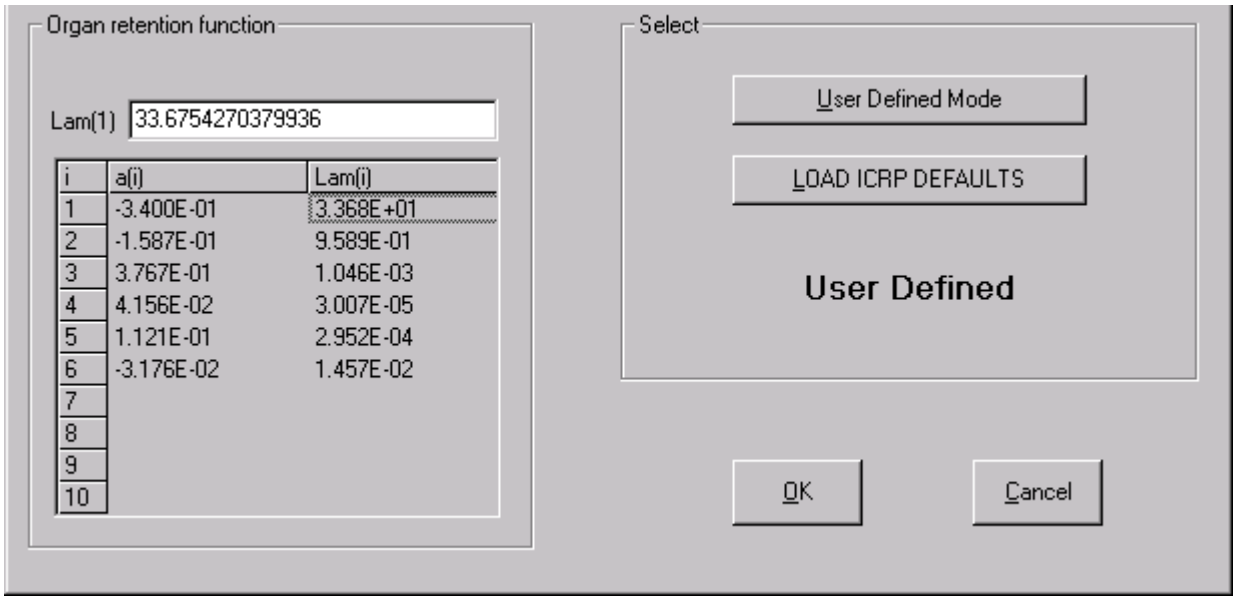

Figure 3.81. The "**User Defined Mode**" for re-defining the **retention function** for americium in liver.

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 *U***ser Defined Mode**, the **Status Bar** will indicate this (Figure 3.82) - even if you make no change to an "ICRP-default" parameter value.

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

Tip: You can re-load ALL of the "ICRP-default" parameter values by re-clicking the "*L***OAD 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.

Warning: If you substitute a different Source Organ **retention function** for any "ICRP-default" **Bioassay Model** in **IMBA Professional**, then the **Dose Calculations** that you perform may NOT be valid for ALL Source/Target Organ combinations. **IMBA Professional** 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*

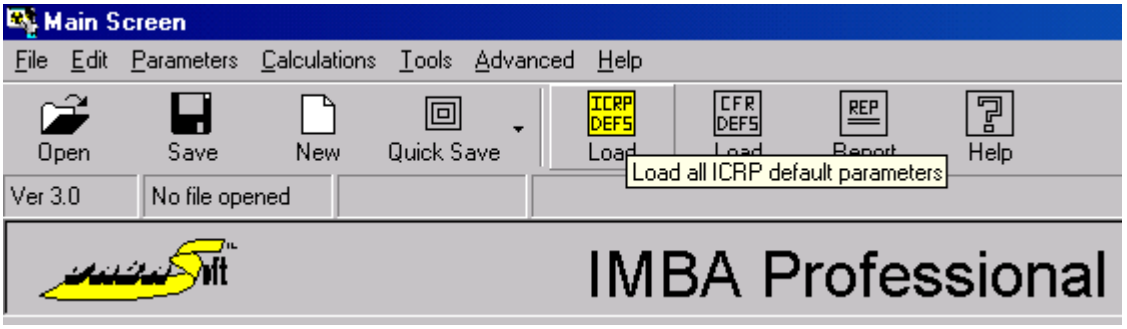

Figure 3.83. The "**ICRP DEFS Load**" tool button.

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).

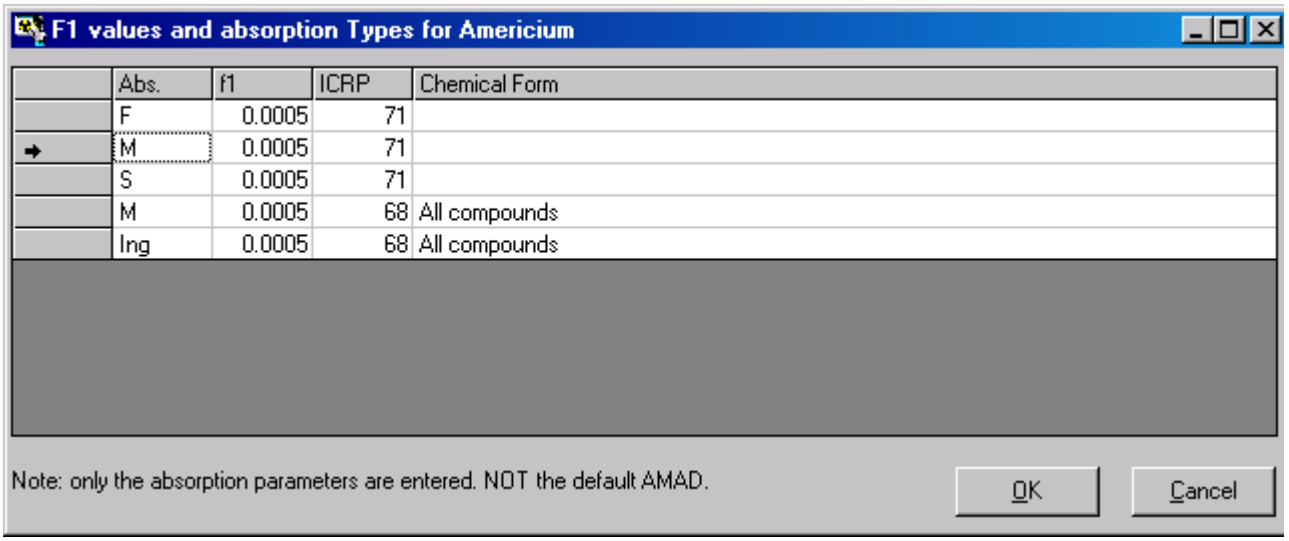

Figure 3.84. The "**F1 values for Am**" window for selecting both the **Absorption Type** and ***f1*** value for americium.

Select the **row** with your required combination of ICRP-default **Absorption Type** and ***f1*** 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.

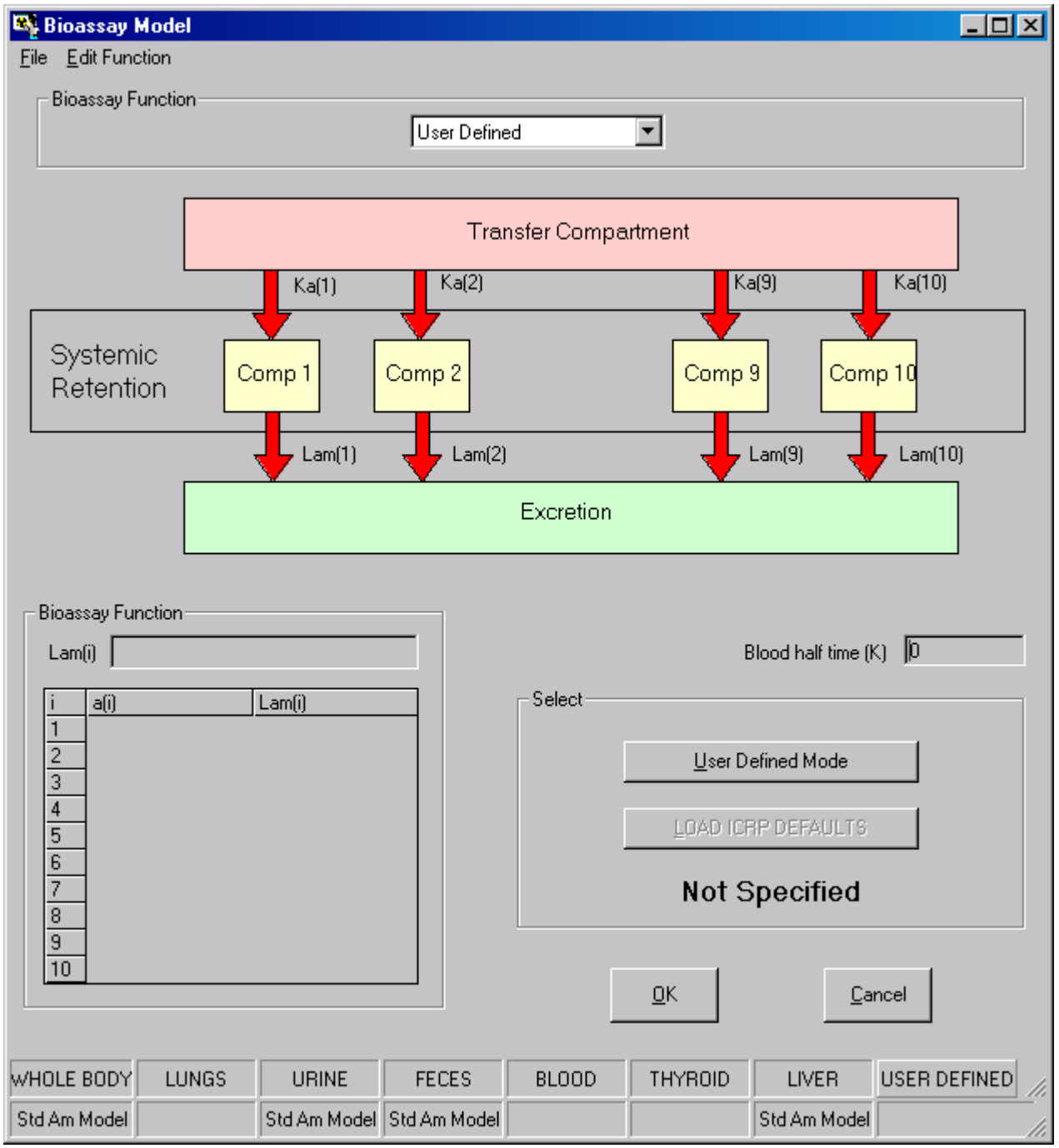

Figure 3.85. The **Bioassay Model** window confirming that ALL **ICRP-default** parameters have been loaded.

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**;
- ***f1*** - "**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**."

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**, ICRP's Dosimetric Quantities).

2. *10-CFR-835 Prescribed Parameters*

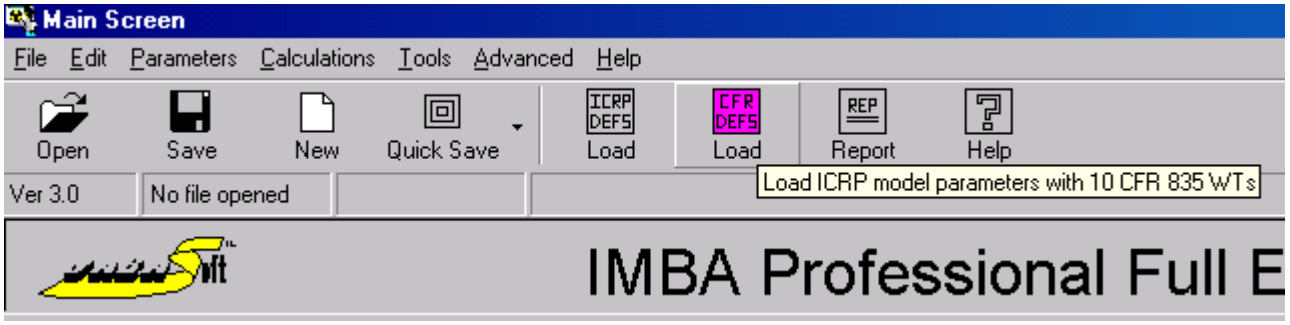

Figure 3.87. The "**CFR DEFS Load**" tool button.

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 **ICRP-DEFAULT Absorption Type** and ***f1*** value. When you then click "**OK**", **IMBA Professional** will load ALL of the **ICRP-DEFAULT Biokinetic Model** AND **Bioassay Model** parameters. **However**, 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).

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.

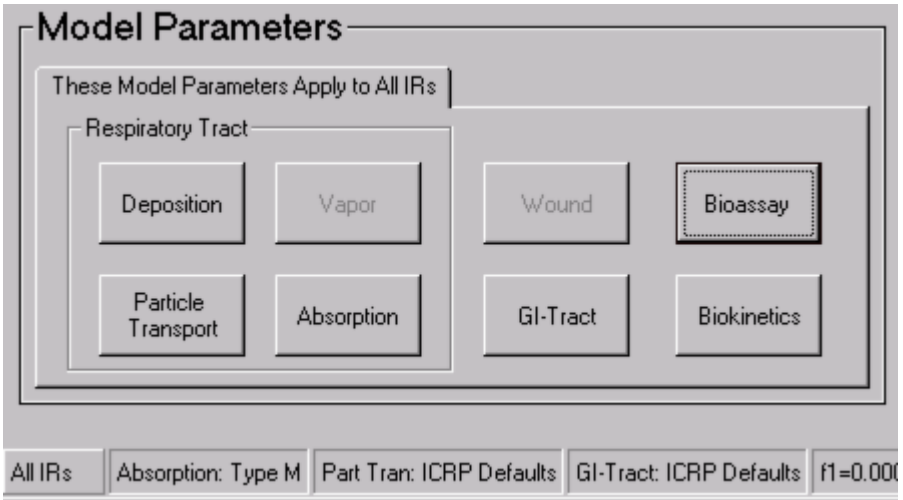

Figure 3.88. The **Model Parameters** sub-panel and **Status Bar** in the "**These Model Parameters Apply to All IRs**" mode.

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**, **Sg**, **r** and **SF** - in **model #1**), or **Absorption Parameters** (**Absorption Type** and **f1** 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).

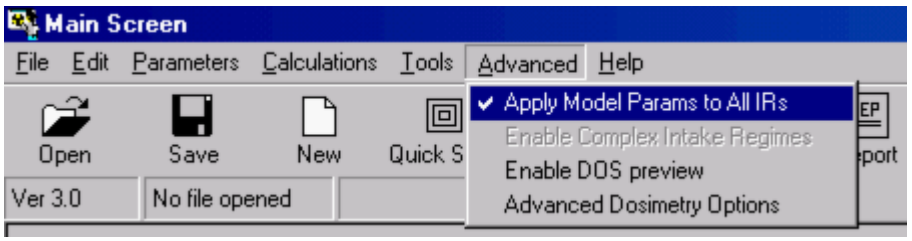

Figure 3.89. De-selecting "**Apply Model Params to ALL IRs**" in **Advanced** menu.

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).

Note: In this "*independent models*" mode, the **Index Tabs** in the **Intake Regimes** and **Model Parameters** sub-panels are linked. You can change the displayed **IR #**, and its associated set of **Models**, by *clicking* a new **IR # Tab** in *either* sub-panel.

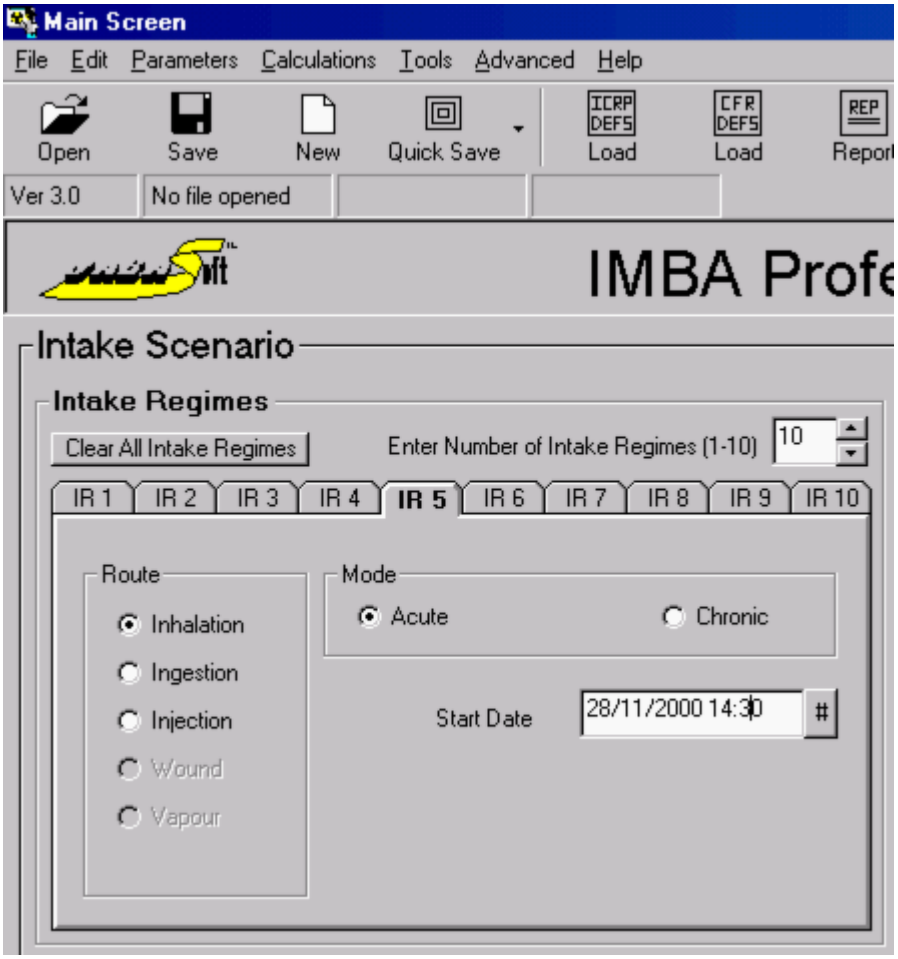

Figure 3.90. Display mode for setting up model parameters *independently* for each **IR**.

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

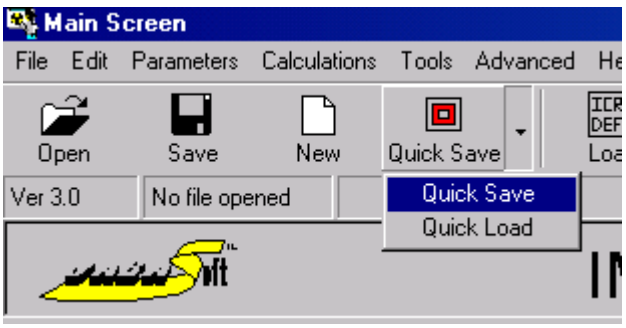

Figure 3.91. The "Quick Save" *tool button* for **Saving All Model Parameters** (and calculated results).

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**, *e.g.*, to save your work periodically as you proceed through setting up a complex case study.

Note: The "**Quick Save**" *tool button* 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 name** 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 *clicking* **S**ave.

Note: *Selecting* **"File | Save"** from the **Menu Bar** performs exactly the same function as the "**Save**" *tool button*.

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 name**" *dialog box* (Figure 3.92) always appear when you select "**File | Save As**" from the **Menu Bar** (in the **Main Screen**).

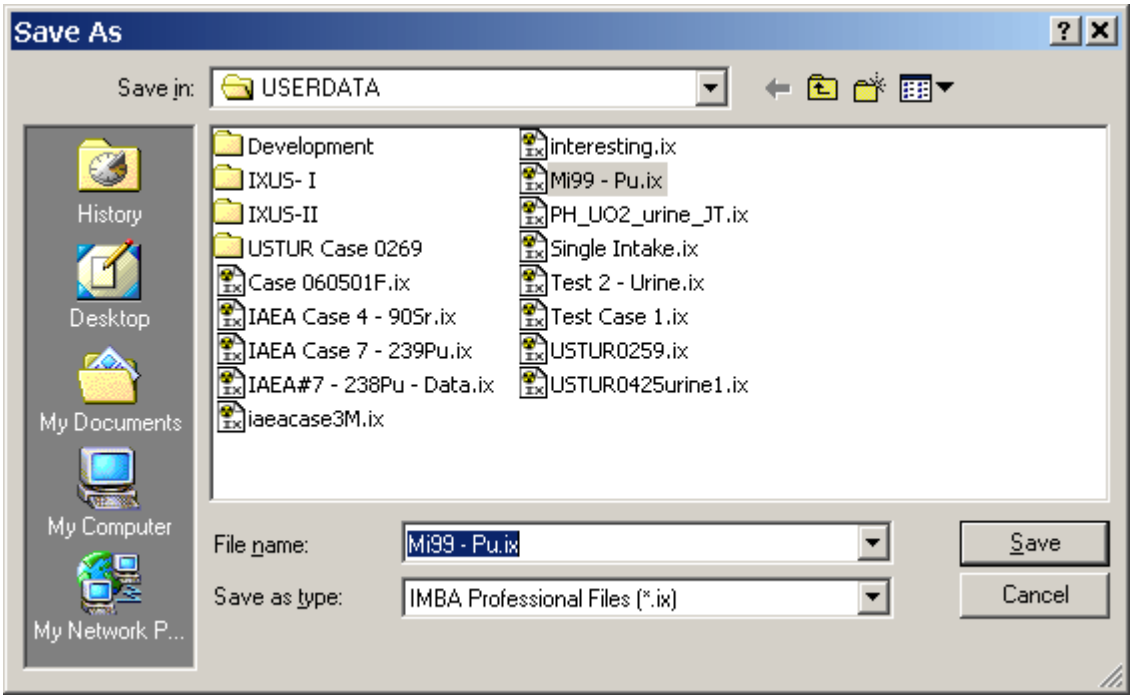

Figure 3.92. The "**Save As**" dialog box opened automatically by the "**Save**" *tool button* when no **Parameter File** name has been specified.

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

Click "Mi99 - Associated Radionuclides.ix" 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

case.

Mi99_Associated_Radionuclides.ix

```
UNITS
Date
Bq
6/9/1945
UNITS2
Sv
INTAKE REGIMES
 1
 3
 1 ,        1 ,        0,         0
 1 ,        1 ,        9464,      0
 1 ,        1 ,        9956,      0
 1 ,        1 ,        0,         0
 1 ,        1 ,        0,         0
 1 ,        1 ,        0,         0
 1 ,        1 ,        0,         0
 1 ,        1 ,        0,         0
 1 ,        1 ,        0,         0
 1 ,        1 ,        0,         0
RADIONUCLIDE
Pu-238
Pu
ASSOCIATED RADIONUCLIDES
 2
 2
Pu-239
 3.5
Am-241
 0.8
*
 0
*
 0
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 0
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0
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

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 , *

9417.7 , 1.0000E+00 , 2.8520E-04 , 10873 , 1.0000E+00 , 2.0000E-03 , Real , 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 , * , * , * , * , * , * , * , *

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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 ,  * , * , * , * , * , * , * , *
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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 ,  * , * , * , * , * , * , * , *
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9839.6 , 1.0000E+00 , 2.2832E-03 ,  * ,* ,* ,* ,* ,* ,* ,*
9843.2 , 1.0000E+00 , 2.2741E-03 ,  * ,* ,* ,* ,* ,* ,* ,*
9846.9 , 1.0000E+00 , 2.2649E-03 ,  * ,* ,* ,* ,* ,* ,* ,*
9850.6 , 1.0000E+00 , 2.2558E-03 ,  * ,* ,* ,* ,* ,* ,* ,*
9854.2 , 1.0000E+00 , 2.2471E-03 ,  * ,* ,* ,* ,* ,* ,* ,*
9857.9 , 1.0000E+00 , 2.2383E-03 ,  * ,* ,* ,* ,* ,* ,* ,*
9861.6 , 1.0000E+00 , 2.2296E-03 ,  * ,* ,* ,* ,* ,* ,* ,*
9865.2 , 1.0000E+00 , 2.2213E-03 ,  * ,* ,* ,* ,* ,* ,* ,*
9868.9 , 1.0000E+00 , 2.2128E-03 ,  * ,* ,* ,* ,* ,* ,* ,*
9872.6 , 1.0000E+00 , 2.2045E-03 ,  * ,* ,* ,* ,* ,* ,* ,*
9876.2 , 1.0000E+00 , 2.1964E-03 ,  * ,* ,* ,* ,* ,* ,* ,*
9879.9 , 1.0000E+00 , 2.1884E-03 ,  * ,* ,* ,* ,* ,* ,* ,*
9883.6 , 1.0000E+00 , 2.1803E-03 ,  * ,* ,* ,* ,* ,* ,* ,*
9887.3 , 1.0000E+00 , 2.1725E-03 ,  * ,* ,* ,* ,* ,* ,* ,*
9890.9 , 1.0000E+00 , 2.1649E-03 ,  * ,* ,* ,* ,* ,* ,* ,*
9894.6 , 1.0000E+00 , 2.1572E-03 ,  * ,* ,* ,* ,* ,* ,* ,*
9898.3 , 1.0000E+00 , 2.1496E-03 ,  * ,* ,* ,* ,* ,* ,* ,*
9901.9 , 1.0000E+00 , 2.1423E-03 ,  * ,* ,* ,* ,* ,* ,* ,*
9905.6 , 1.0000E+00 , 2.1349E-03 ,  * ,* ,* ,* ,* ,* ,* ,*
9909.3 , 1.0000E+00 , 2.1277E-03 ,  * ,* ,* ,* ,* ,* ,* ,*
9912.9 , 1.0000E+00 , 2.1207E-03 ,  * ,* ,* ,* ,* ,* ,* ,*
9916.6 , 1.0000E+00 , 2.1135E-03 ,  * ,* ,* ,* ,* ,* ,* ,*
9920.3 , 1.0000E+00 , 2.1065E-03 ,  * ,* ,* ,* ,* ,* ,* ,*
9923.9 , 1.0000E+00 , 2.0998E-03 ,  * ,* ,* ,* ,* ,* ,* ,*
9927.6 , 1.0000E+00 , 2.0929E-03 ,  * ,* ,* ,* ,* ,* ,* ,*
9931.3 , 1.0000E+00 , 2.0862E-03 ,  * ,* ,* ,* ,* ,* ,* ,*
9934.9 , 1.0000E+00 , 2.0797E-03 ,  * ,* ,* ,* ,* ,* ,* ,*
9938.6 , 1.0000E+00 , 2.0730E-03 ,  * ,* ,* ,* ,* ,* ,* ,*
9942.3 , 1.0000E+00 , 2.0665E-03 ,  * ,* ,* ,* ,* ,* ,* ,*
9945.9 , 1.0000E+00 , 2.0603E-03 ,  * ,* ,* ,* ,* ,* ,* ,*
9949.6 , 1.0000E+00 , 2.0539E-03 ,  * ,* ,* ,* ,* ,* ,* ,*
9953.3 , 1.0000E+00 , 2.0476E-03 ,  * ,* ,* ,* ,* ,* ,* ,*
9956.9 , 1.0000E+00 , 2.6302E-02 ,  * ,* ,* ,* ,* ,* ,* ,*
9960.6 , 1.0000E+00 , 1.8373E-02 ,  * ,* ,* ,* ,* ,* ,* ,*
9964.3 , 1.0000E+00 , 1.5694E-02 ,  * ,* ,* ,* ,* ,* ,* ,*
9968 , 1.0000E+00 , 1.3637E-02 ,  * ,* ,* ,* ,* ,* ,* ,*
9971.6 , 1.0000E+00 , 1.2015E-02 ,  * ,* ,* ,* ,* ,* ,* ,*
9975.3 , 1.0000E+00 , 1.0656E-02 ,  * ,* ,* ,* ,* ,* ,* ,*
9979 , 1.0000E+00 , 9.5457E-03 ,  * ,* ,* ,* ,* ,* ,* ,*
9982.6 , 1.0000E+00 , 8.6574E-03 ,  * ,* ,* ,* ,* ,* ,* ,*
9986.3 , 1.0000E+00 , 7.9026E-03 ,  * ,* ,* ,* ,* ,* ,* ,*
9990 , 1.0000E+00 , 7.2771E-03 ,  * ,* ,* ,* ,* ,* ,* ,*
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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 , * ,* ,* ,* ,* ,* ,* ,*
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
0.000000987605 , 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
0.000000871155 , 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
0.0000001
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
0.000000987605 , 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
0.000000871155 , 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
0.000000987605 , 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
0.000000871155 , 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
0.000000987605 , 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
0.000000871155 , 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
0.0000001
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
0.000000987605 , 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
0.000000871155 , 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
0.000000987605 , 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
0.000000871155 , 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
0.000000987605 , 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
0.000000871155 , 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
0.0000001
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
0.000000987605 , 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
0.000000871155 , 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
0.000000987605 , 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
0.000000871155 , 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
0.000000987605 , 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
0.000000871155 , 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
0.6
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
PARAMETERS ABSORPTION
Type M
Normal
0.099955
100
0.005
0
0
Type M
Normal

0.099955
100
0.005
0
0
User Defined
Normal
0.09955
100
0.05
0
0
Type M
Normal
0.099955
100
0.005
0
0
Type M
Normal
0.099955
100
0.005
0
0
Type M
Normal
0.099955
100
0.005
0
0
Type M
Normal
0.099955
100
0.005
0
0
Type M
Normal
0.099955
100
0.005
0
0
Type M
Normal

0.099955
100
0.005
0
0
Type M
Normal
0.099955
100
0.005
0
0
Type M
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
1.8

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
1.8
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
1.8
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
0.000000835345 , 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
-0.0000002501 , 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
 0.000000378586 , 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
0.000000835345 , 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
-0.0000002501 , 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
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 0.0101238 , 6.13083E-03
 0.0579437 , 2.48708E-04
STOMACH
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S.I.
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-0.00000145591 , 5.94293E+00
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 0.00000374311 , 2.30152E-03
 0.000000378586 , 2.30125E-04
-0.00000161905 , 3.72082E-01
-0.00000331261 , 3.63339E-01
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-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
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 0.583868 , 1.13111E+00
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 0.00000439178 , 2.42701E-04
 0.00000567754 , 2.56698E-05
 0.00947443 , 3.57888E-01
 0.0000139771 , 1.77924E-03
ST. WALL
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SKIN
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SPLEEN
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SOFT TISS
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 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
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BLOOD
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 0.372409 , 3.55291E-01
 0.000166134 , 2.78392E-04
 0.000219279 , 2.67517E-05
-0.000289855 , 7.10001E-03
TAB 3
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ICRP Pu Model
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-0.001165681225 , 1.19987E+01
 0.000011659 , 1.41314E-02
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 0.000401149 , 3.55543E-01
 0.000747544 , 1.26294E+00
 0.000000835345 , 2.18047E-04
 0.00000106043 , 2.50778E-05
BRAIN
 0
BREAST
 0
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G. BLADD
0
HEART CT.
0
HEART WL.
0
KIDNEYS
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-0.0104525 , 3.55064E-01
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0.000290264 , 1.24857E-04
0.000458568 , 4.25213E-04
0.0103148 , 1.39221E-02
0.00052571 , 2.16919E-05
LIVER
5
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-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
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0.000080518 , 2.14761E-05
-0.000824848 , 1.98367E-04
-0.0000799751 , 3.89897E-01
PANCREAS
0
TESTES
5
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0.000258506 , 2.12454E-05
-0.000918511 , 2.11593E-04
-0.000259102 , 3.89940E-01
THYROID
0

R.B.M.
6
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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
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-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
-0.0000002501 , 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
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-0.00000258125 , 1.30481E+00
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 0.00000374311 , 2.30152E-03
 0.000000378586 , 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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-0.00000119168 , 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
```

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 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
 0.000000835345 , 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
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CORT VOL
6
-0.24714990438 , 8.53426E-05
0.00000209448 , 1.26224E+00
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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
-0.0000002501 , 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
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0.00000374311 , 2.30152E-03

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U.L.I.
 9
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 0.00330195 , 3.55146E-01
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-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
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 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
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WB
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BLOOD
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0.000219279 , 2.67517E-05
-0.000289855 , 7.10001E-03
TAB 5
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ICRP Pu Model
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0.000401149 , 3.55543E-01
0.000747544 , 1.26294E+00
0.000000835345 , 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

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 0.239998 , 2.68343E-05
 0.295656 , 1.85293E-04
-0.237545 , 3.35067E-04
MUSCLE
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OVARIES
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 0.000080518 , 2.14761E-05
-0.000824848 , 1.98367E-04
-0.0000799751 , 3.89897E-01
PANCREAS
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TESTES
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 0.000258506 , 2.12454E-05
-0.000918511 , 2.11593E-04
-0.000259102 , 3.89940E-01
THYROID
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R.B.M.
 6
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 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
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-0.000033387 , 6.87895E-03
 0.0237225 , 2.94142E-04
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 0.318626 , 2.89246E-05
TRAB VOL
 7
 0.0000190871 , 1.25850E+00
-0.133532 , 7.76870E-04
-0.0000002501 , 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
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-0.00000145591 , 5.94293E+00
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 0.00000374311 , 2.30152E-03
 0.000000378586 , 2.30125E-04
-0.00000161905 , 3.72082E-01
-0.00000331261 , 3.63339E-01
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U.L.I.
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 0.000002311 , 3.69827E-04
 0.00000151967 , 1.02814E-05
 0.00000229533 , 6.21726E-05
L.L.I.
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-0.6345 , 1.16251E+00
 0.583868 , 1.13111E+00
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 0.00000439178 , 2.42701E-04
 0.00000567754 , 2.56698E-05
 0.00947443 , 3.57888E-01
 0.0000139771 , 1.77924E-03
ST. WALL
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SKIN
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SPLEEN
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SOFT TISS
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 0.00845648 , 3.66703E-03
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-2.80238 , 1.33343E+00
 0.0848507 , 8.41887E-04
 0.20465 , 3.51307E-01
-1.96433 , 1.94455E-05
WB
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BLOOD
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 0.000219279 , 2.67517E-05
-0.000289855 , 7.10001E-03
TAB 6
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1
ICRP Pu Model
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0.000401149 , 3.55543E-01
0.000747544 , 1.26294E+00
0.000000835345 , 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
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-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
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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
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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
-0.0000002501 , 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
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-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
0.000000378586 , 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 7
 1
ICRP Pu Model
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ADRENALS
 0
BLADDER
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-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
0.000000835345 , 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
-0.0000002501 , 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
 0.000000378586 , 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 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
 0.000000835345 , 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
-0.0000002501 , 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
 0.000000378586 , 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 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
 0.000000835345 , 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
-0.0000002501 , 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
0.000000378586 , 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 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
0.000000835345 , 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
-0.0000002501 , 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
0.000000378586 , 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
PARAMETERS DEPOSITION
ICRP Defaults
light
AMAD
5
2.4977233
3
1.5
ICRP Defaults
light
AMAD
5
2.4977233
3
1.5
ICRP Defaults
light
AMAD
0.5
2.4977233
3
1.5
ICRP Defaults
light
AMAD
5
2.4977233
3
1.5
ICRP Defaults
light
AMAD
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ICRP Defaults
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AMAD
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2.4977233

3
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ICRP Defaults
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ICRP Defaults
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AMAD
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3
1.5
ICRP Defaults
light
AMAD
5
2.4977233
3
1.5
ICRP Defaults
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AMAD
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2.4977233
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1.5
PARAMETERS WOUND
Not Specified
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Not Specified
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FITTING BIOASSAY QUANTITY
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GRAPHS
False
Whole body GRAPH
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False
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False
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False
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False
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Lungs GRAPH
0
100

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False
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False
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False
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False
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Urine GRAPH
8315
12406
10
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False
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False
0
0.025
10
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False
2
True
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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.;

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REPORT DETAILS

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Calculations Sub-panel

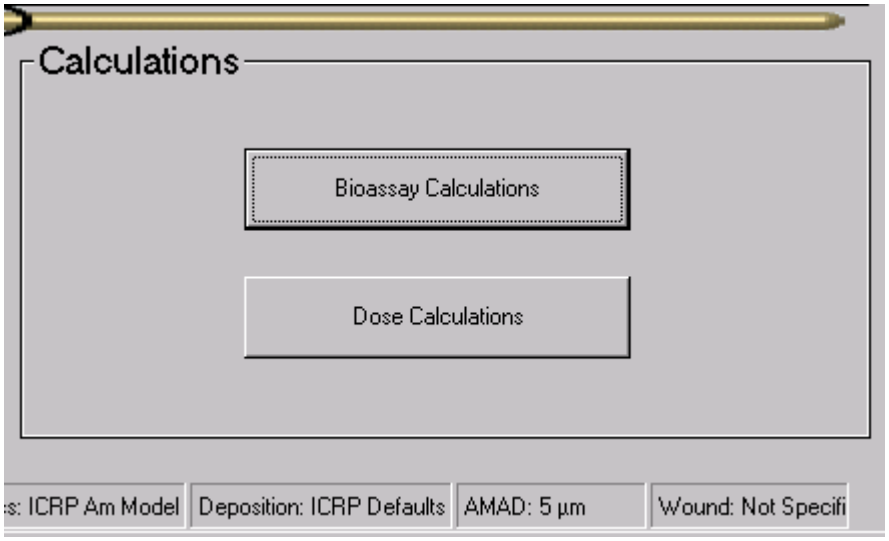


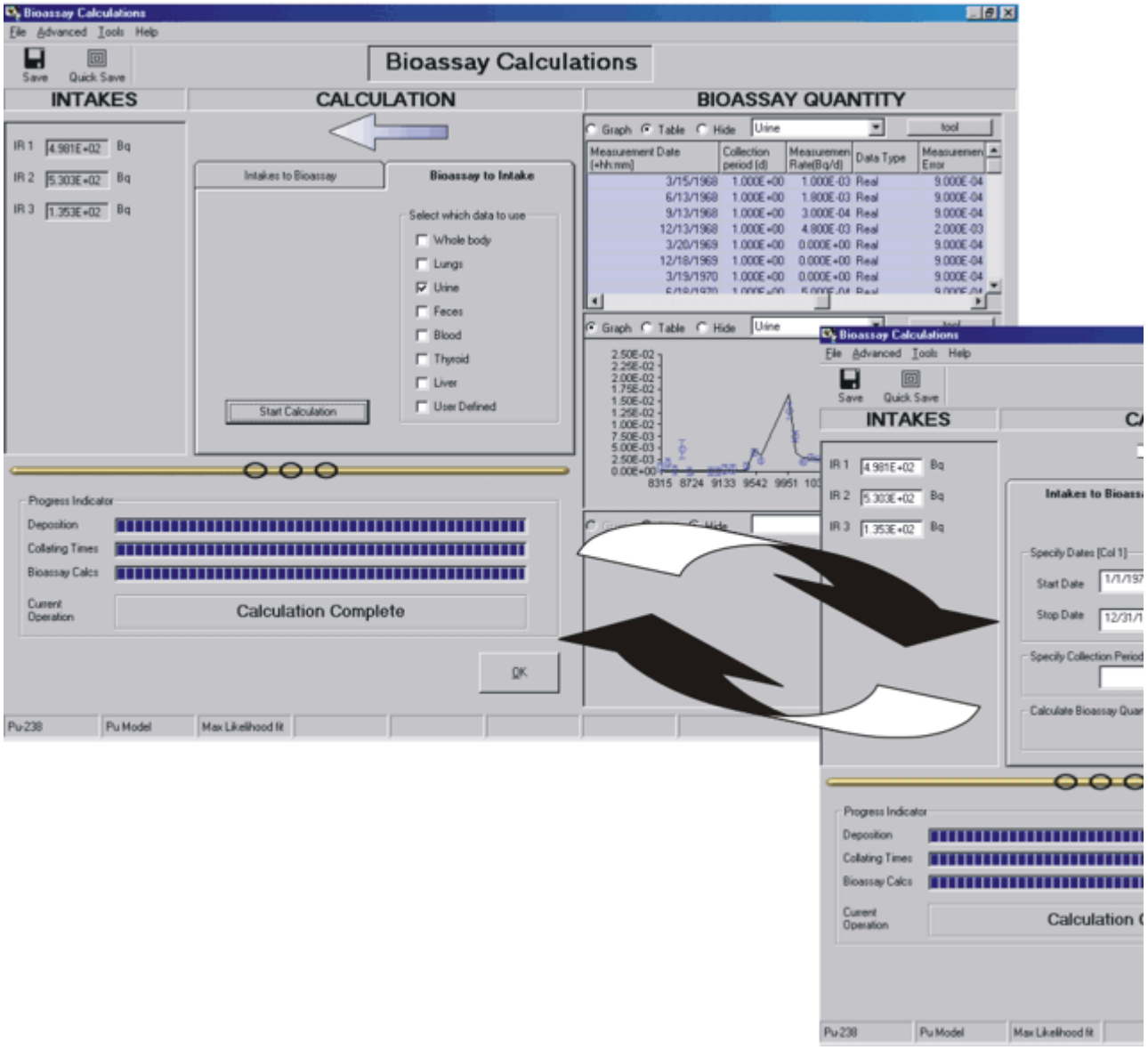
Figure 3.93. The **Calculations** Sub-panel.

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**);

- Dose Calculations - **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:

1. 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**.

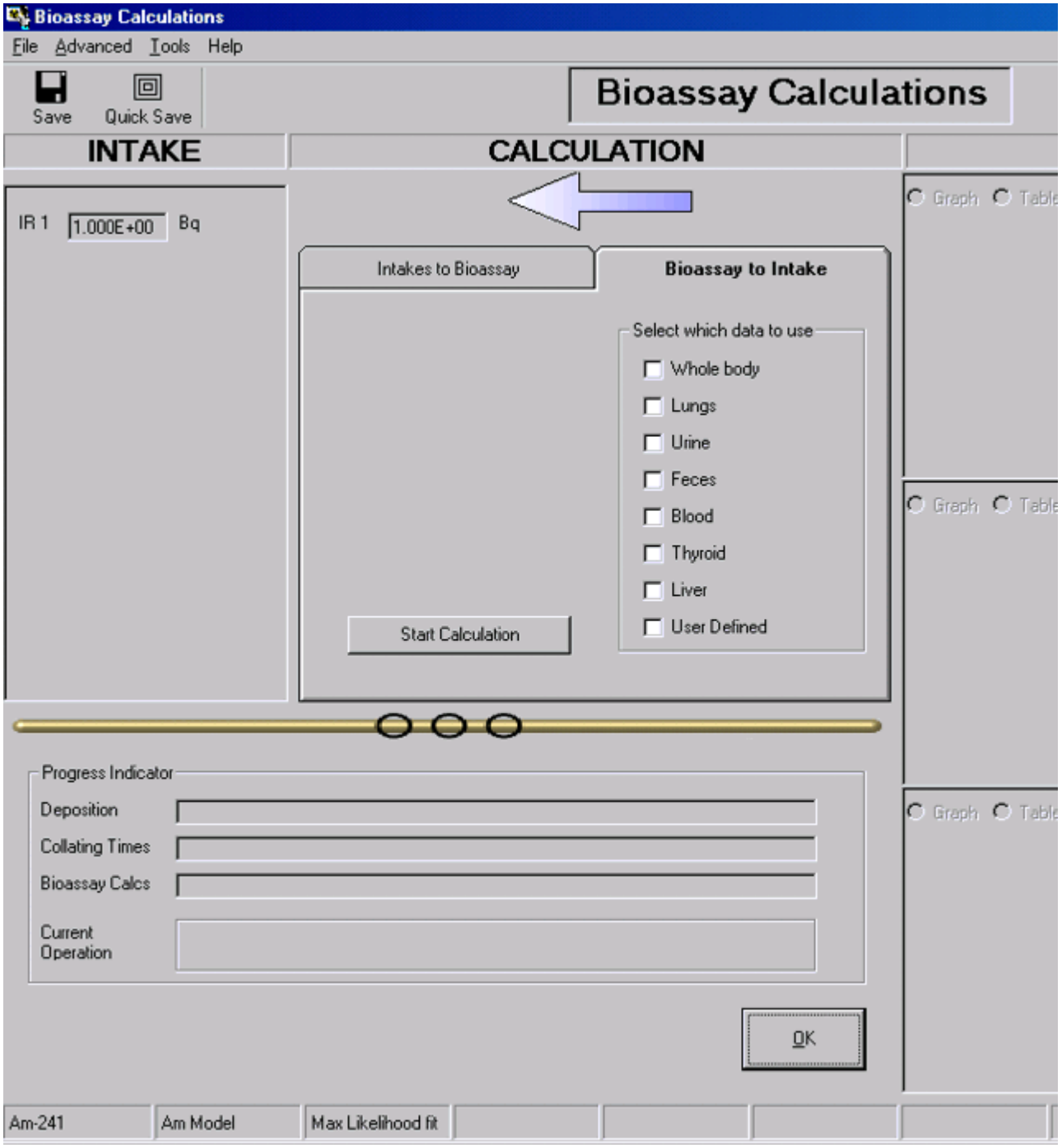


Figure 4.1. The **Bioassay Calculations** screen.

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.
- Tools menu.
- Help menu.

Bioassay File Menu

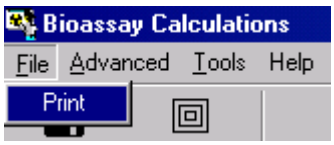


Figure 4.2. Drop-down bioassay **File** list box.

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

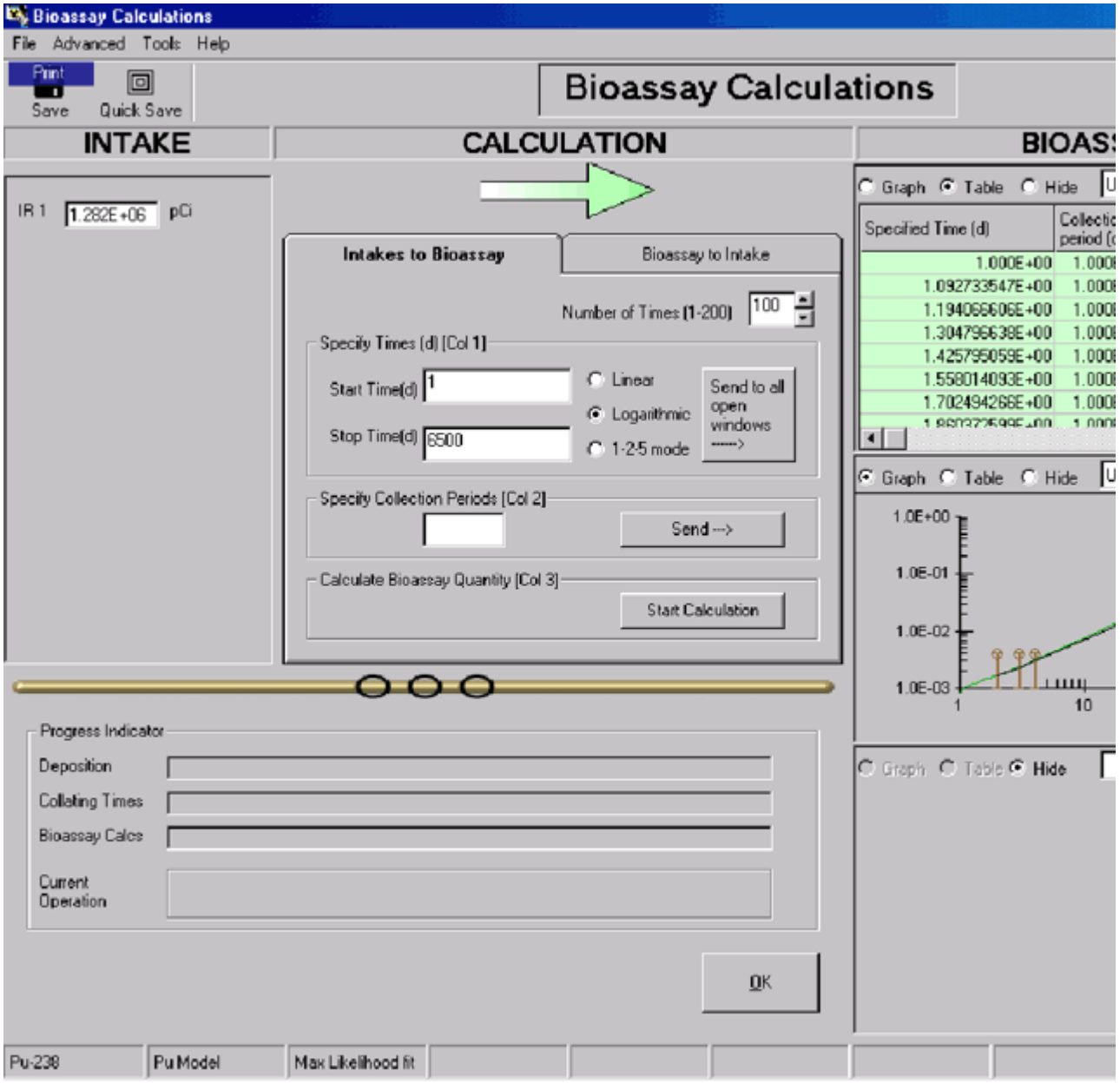


Figure 4.3. Printed screen dump of **Bioassay Calculations** screen.

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

Bioassay Advanced Menu

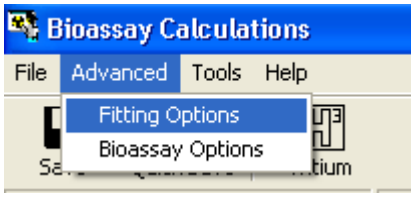


Figure 4.4. Advanced menu ***options for*** Bioassay Calculations***.***

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).***

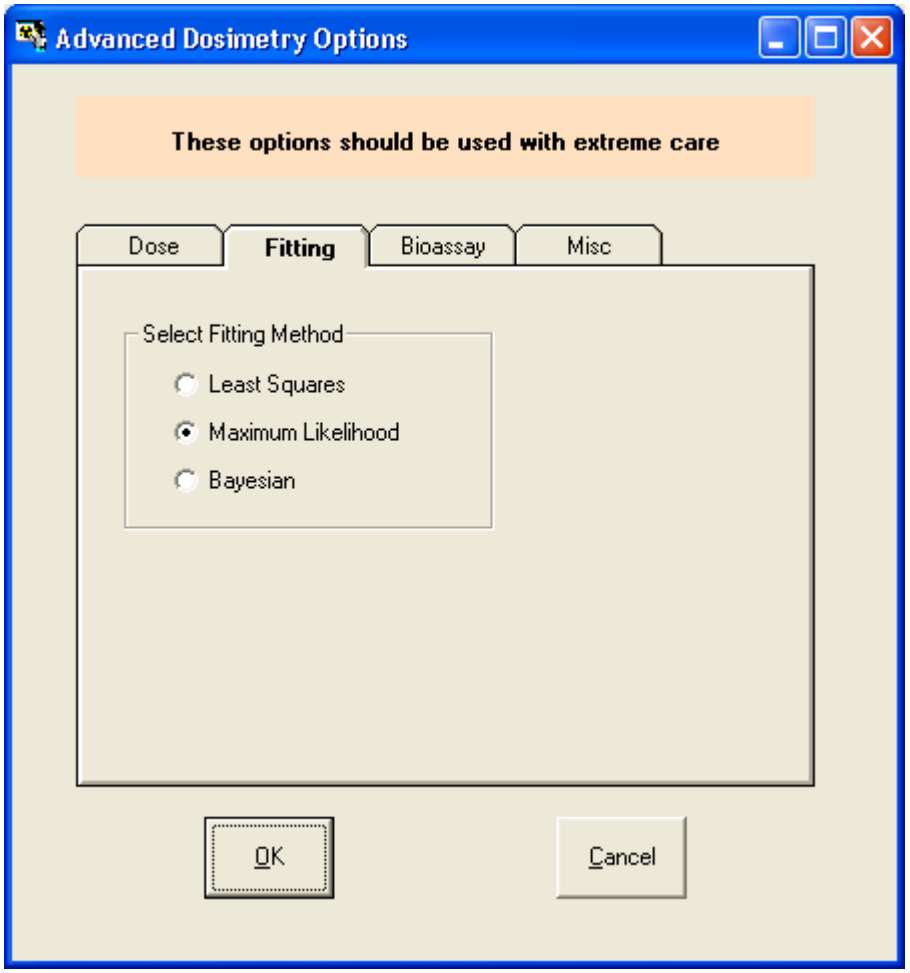


Figure 4.5. ***Selecting*** Fitting ***options in the*** Advanced Dosimetry Options window***.***

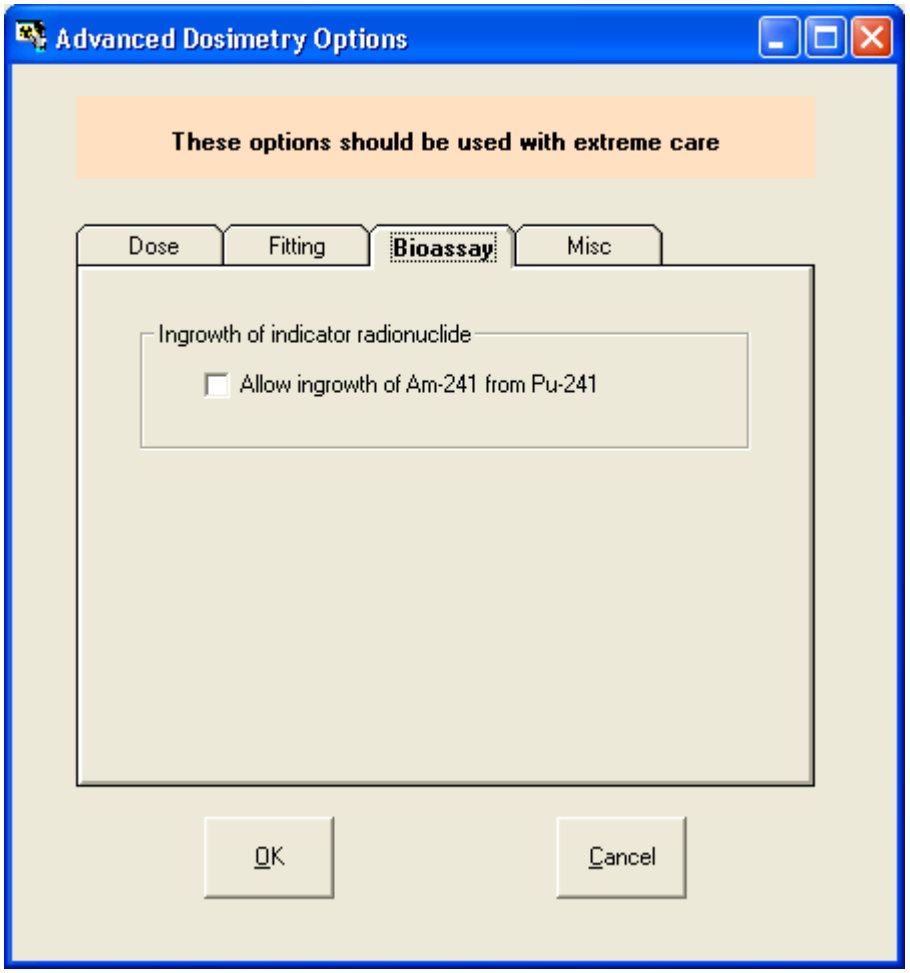


Figure 4.6. ***Enabling the*** Bioassay option ***to measure ingrowth of*** ^{241}Am ***activity (from*** ^{241}Pu***).***

Bioassay Tools Menu

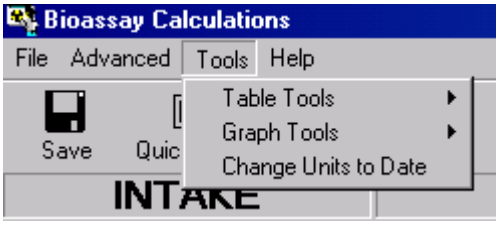


Figure 4.7. Drop-down ***Bioassay Tools*** list box.

The Bioassay Tools options are:

- ***Table Tools*** - Enable you to open the Table Tool (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 Graph Tool (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.

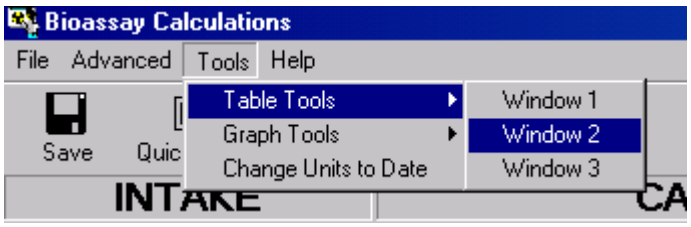


Figure 4.8. Drop-down list of ***Bioassay Quantity*** windows for using ***Table Tools***.

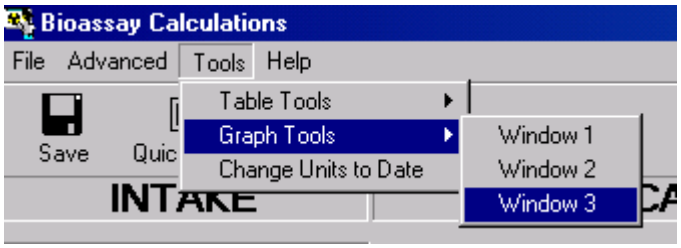


Figure 4.9. Drop-down list of ***Bioassay Quantity*** windows for using ***Graph Tools***.

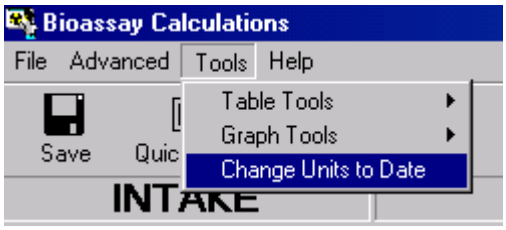


Figure 4.10. Toggle control to change the ***Time Units***.

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

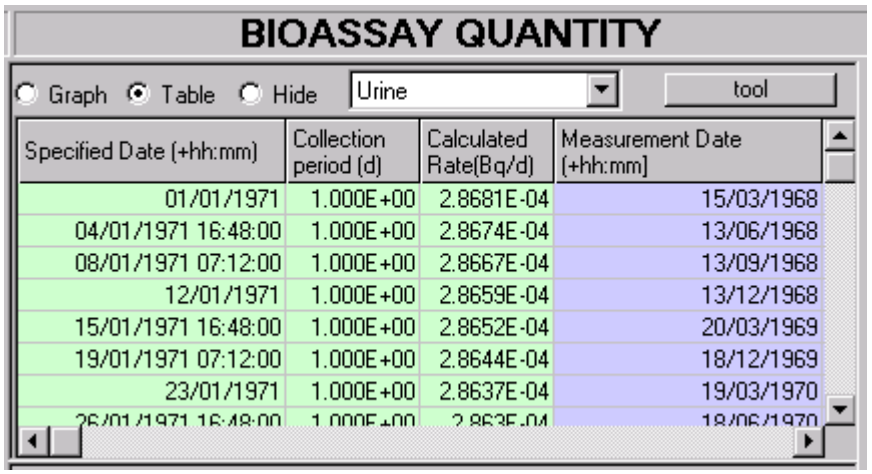


Figure 4.11. Displaying when samples were taken as a ***Date (+hh:mm)*** as the alternative to the default display of ***Time (d)***.

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.

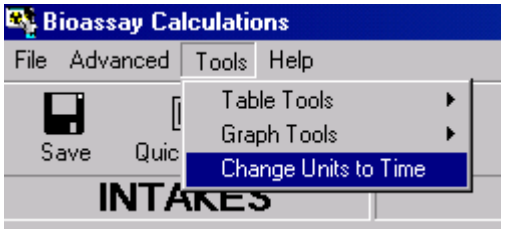


Figure 4.12. "***Change Units***" label switches automatically to enable toggling between ***Time*** and ***Date***.

Bioassay Help Menu

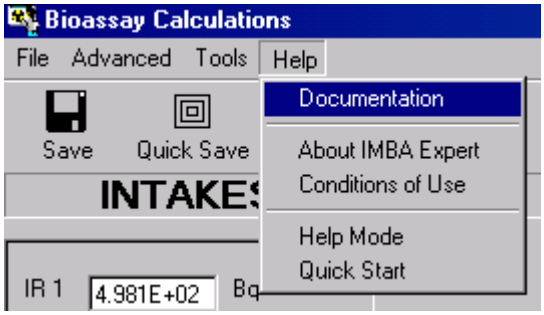


Figure 4.13. Drop-down **Bioassay Help** list box.

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

Bioassay Save Icons

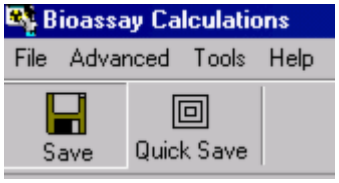


Figure 4.11. **Bioassay Save** icon.

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**").

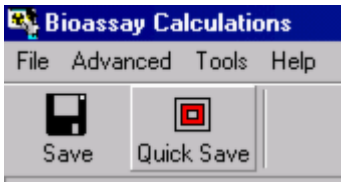


Figure 4.12. Bioassay Quick Save icon.

Closing the Bioassay Calculations Screen

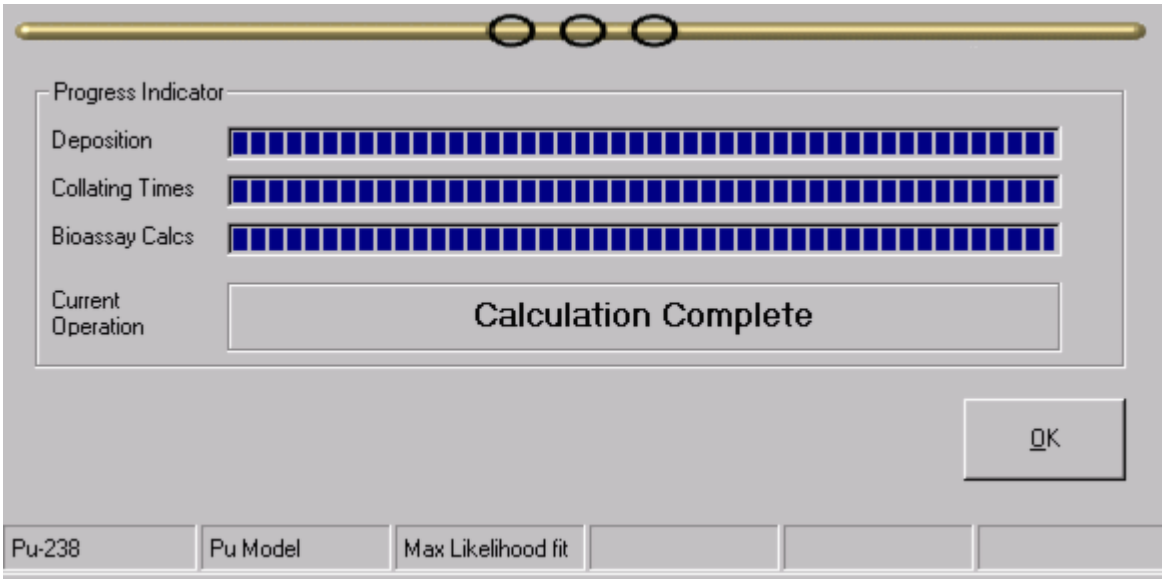


Figure 4.13. The "O**K**" button for closing and exiting the **Bioassay Calculations** screen.

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

Warning: ***Using the "**OK**" button to** close **the** Bioassay Calculations **screen leaves all of the values that were displayed (and the current values of non-displayed bioassay data) in** memory**. It does NOT automatically** save **these values to the** Parameter File**. You must choose to do this yourself - by** clicking **the "**Save**" icon. If you** exit *IMBA Professional* **without first** saving **the** Parameter File**, any updated parameter values will be** lost**.***

Tip: ***You can also** exit **the** Bioassay Calculations **screen by** clicking **the Windows® "**X**" in the top-right corner of the screen. Again, this leaves the bioassay data in** memory**, but NOT** saved **to the** Parameter File**.***

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** - Bioassay Quantity (Measurements) to estimated Intake(s) - as indicated by a **blue** arrow (Figure 4.14).

2. From **left** to **right** - value(s) of Intake(s) to predicted Bioassay Quantity - 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**").

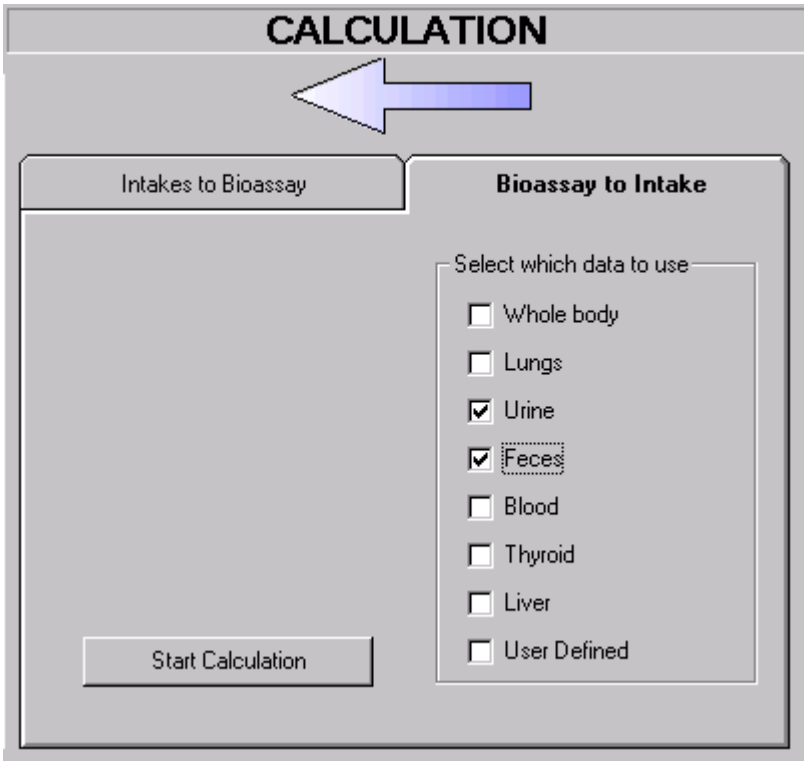


Figure 4.14. Bioassay calculation set as "**Bioassay to Intake**" and indicated by a **blue** arrow.

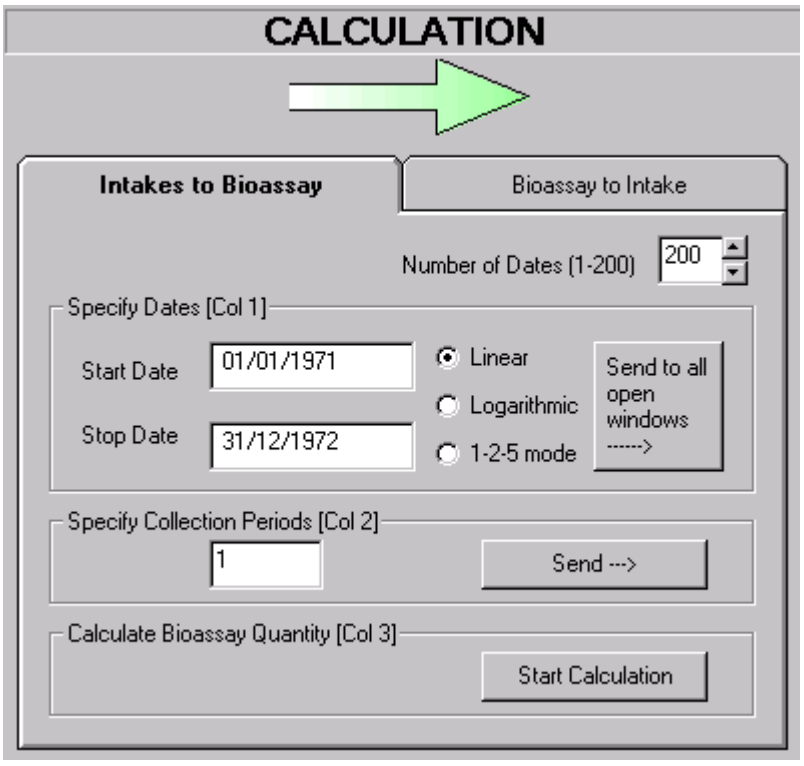


Figure 4.15. Bioassay calculation set as "**Intakes to Bioassay**" and indicated by a **green** arrow.

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**).

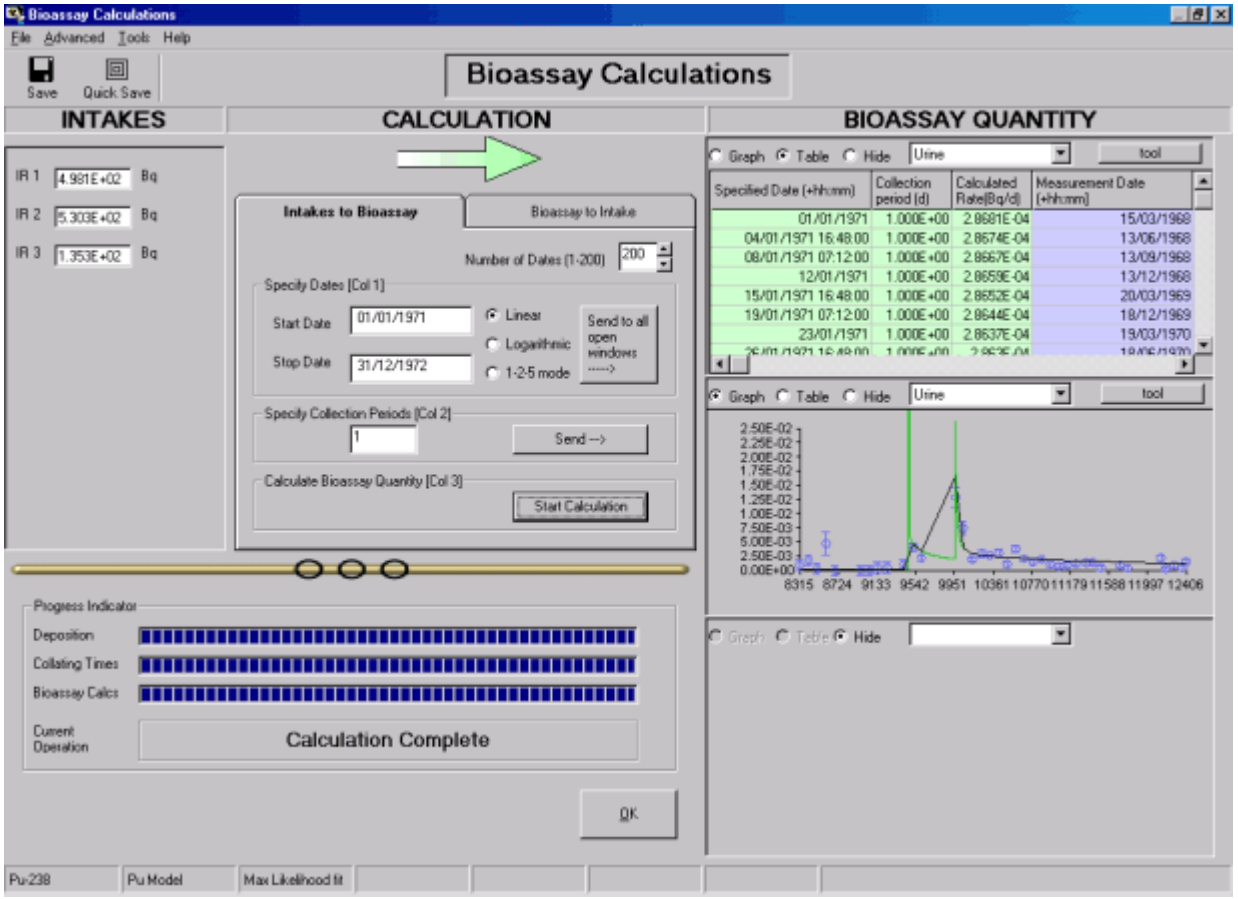


Figure 4.16. "**INTAKES**" sub-panel displays **Intake** amounts for up to 10 **Intake Regimes** (**IRs**).

Am-241 As Indicator Of Plu-241

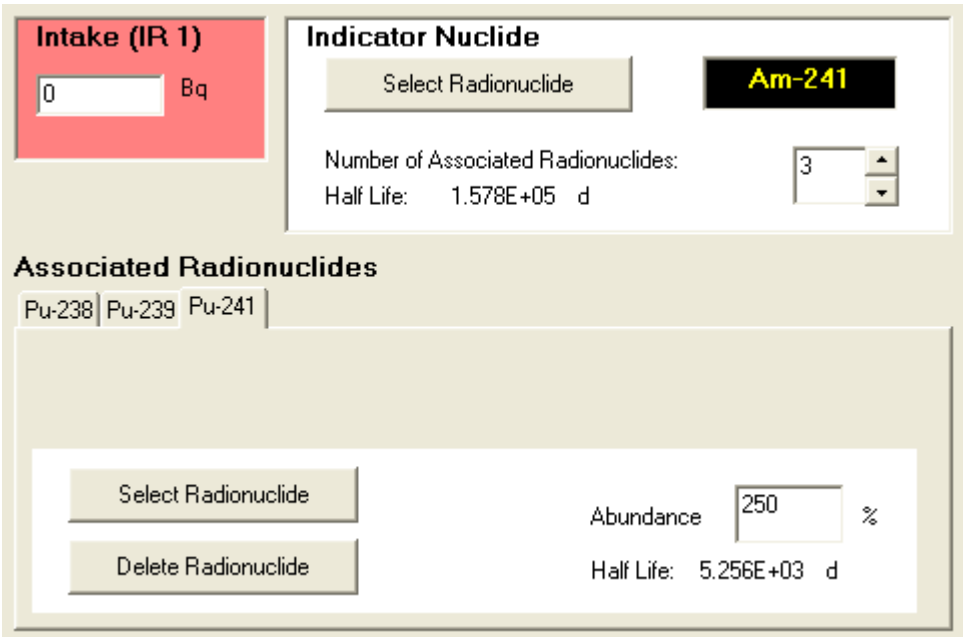


Figure 4.17. Combination of 241**Am** as the Indicator Nuclide and 241**Pu** as an Associated Radionuclide.

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 ^{241}**Pu**, higher sensitivity for lung counting can often be achieved by measuring the activity of the ^{241}**Am** progeny (59.5 keV and 35.7% abundance **g-ray**) rather than the low-energy and low-abundance **L X-rays** emitted by ^{239}**Pu** (and ^{238}**Pu**). For particulate material retained in the respiratory tract, it is reasonable to assume that the absorption of ^{241}**Am** (from the particle matrix) will occur at the same rate(s) as that of the plutonium isotopes. Thus, the ^{241}**Am** activity measured in the lungs should be a good indicator of the parent ^{241}**Pu** activity, and thus the total retained plutonium activity. However, account must be taken of the 14-y decay half-life of ^{241}**Pu**, and the subsequent in-growth of the ^{241}**Am** activity. IMBA Professional Plus includes a special tool to enable this decay and in-growth to be accounted for automatically. Thus, measurements of ^{241}**Am** 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 ^{241}**Am** as the Indicator Nuclide and ^{241}**Pu** 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).

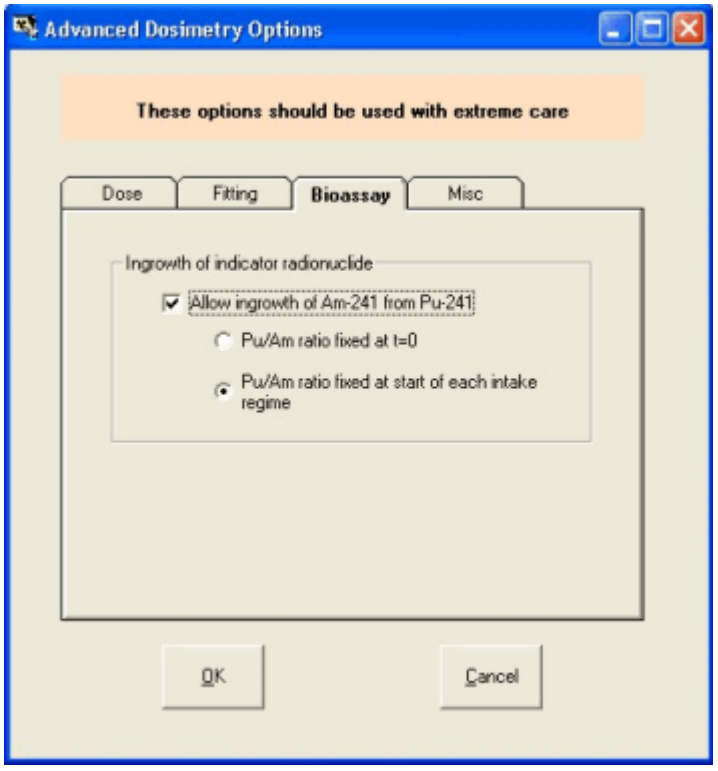


Figure 4.18. Bioassay option to track "in-growth" of ^{241}**Am** as the Indicator Nuclide for ^{241}**Pu** in the lungs.

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

Important Note: IMBA Professional Plus also calculates the in-growth of 241Am from 241Pu in all systemic organs. However, this calculation assumes that the 241Am produced from decay of 241Pu in systemic organs has the same biokinetic behavior as the parent 241Pu (i.e., the 241Pu **Associated Radionuclide**).

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.

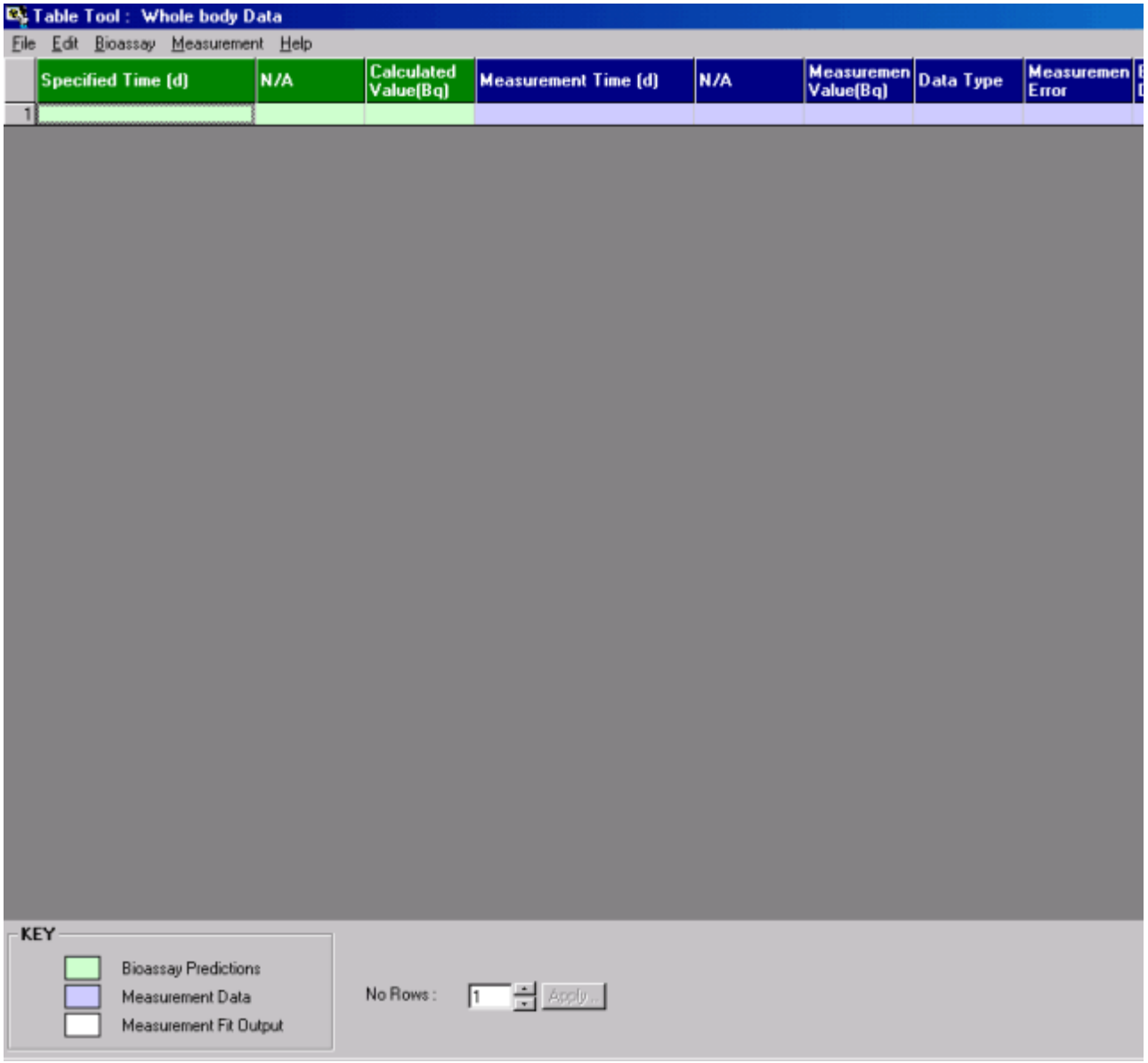


Figure 7.1. Table Tool before data entry - with "Whole body" as the Bioassay Quantity.

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 ^{60}Co (Single Intake example), there are **8** values of whole-body activity. So, in that case:

- Ensure 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.
- Click the "**Apply**" button to the right of the dialog box.

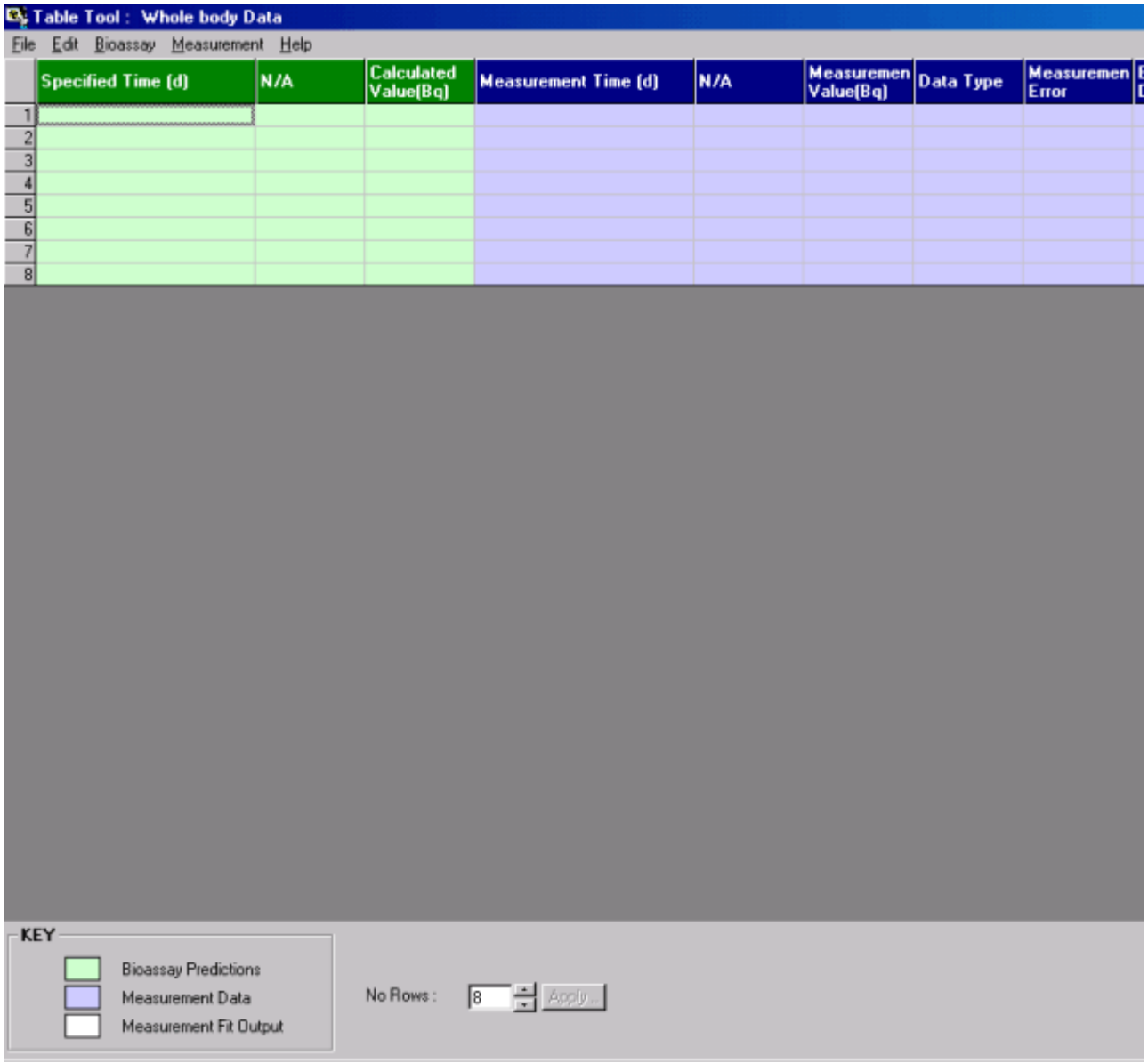


Table 7.2. Table Tool with **8** rows opened.

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** - leave 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**).

Important: ***Since*** IMBA Professional ***uses the*** Maximum Likelihood Method ***to "fit" the measured data, you MUST complete*** all six measurement data columns ***(shown with the blue background in Figure 7.2), including appropriate values for the*** Data Type***,*** Measurement Error***, and*** Error Distribution ***- for*** every data point ***(every row displayed in the data table).***

Note: ***You can specify the*** Data Type ***- and all other error parameters -*** individually for each data point***.***

You have three **options** for entering the **measured bioassay data**:

1. Type this in manually (cell by cell - or block of cells).
2. Copy a block of data into the **Table Tool** from a Windows® application using the Windows® clipboard.
3. Read 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 clicked. 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 highlighted.

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.

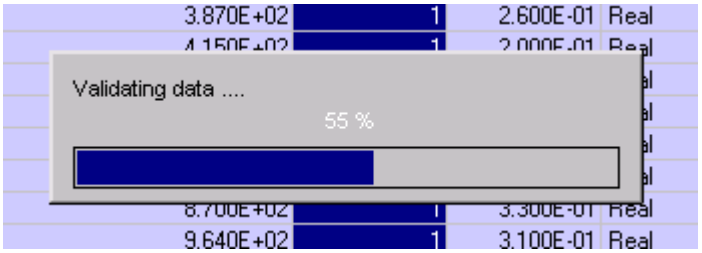


Figure 7.3. Data Validation.

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**");
- Proceed to **Step #10** in the **multiple intake** example ("**Graphing the Data - Multiple Intakes**").

Or:

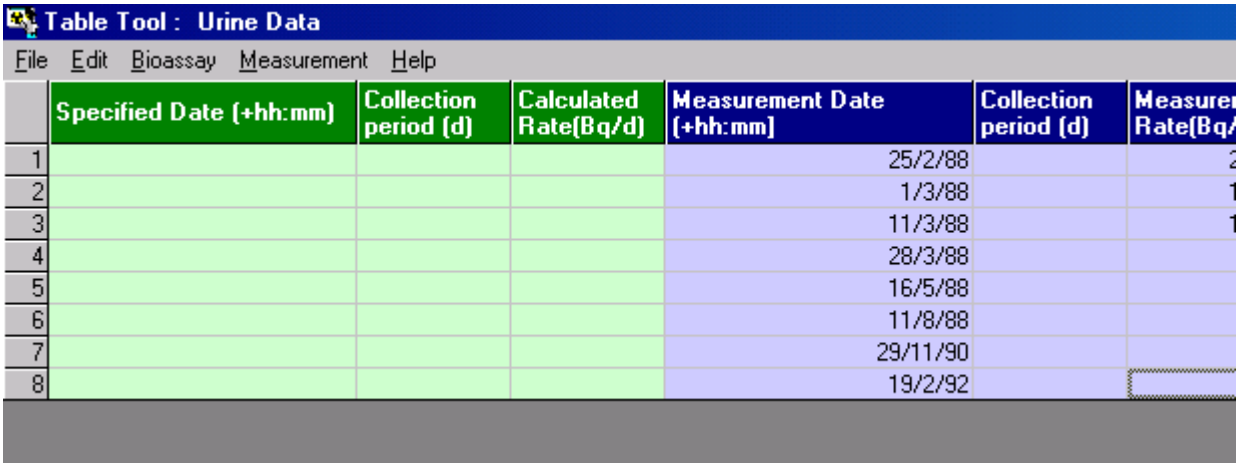
- Return to the **case description** and list of steps for the **single intake** example.
- Return to the **case description** and list of steps for the **multiple intakes** example.

For a comprehensive **catalog** of the features and functions of the **Table Tool**, see Visual Tour 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).

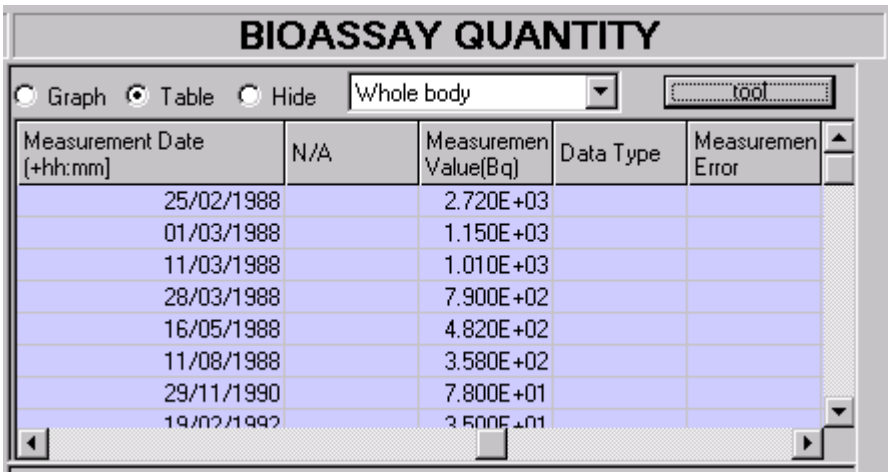


	Specified Date (+hh:mm)	Collection period (d)	Calculated Rate(Bq/d)	Measurement Date (+hh:mm)	Collection period (d)	Measure Rate(Bq/
1				25/2/88		2
2				1/3/88		1
3				11/3/88		1
4				28/3/88		
5				16/5/88		
6				11/8/88		
7				29/11/90		
8				19/2/92		

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).



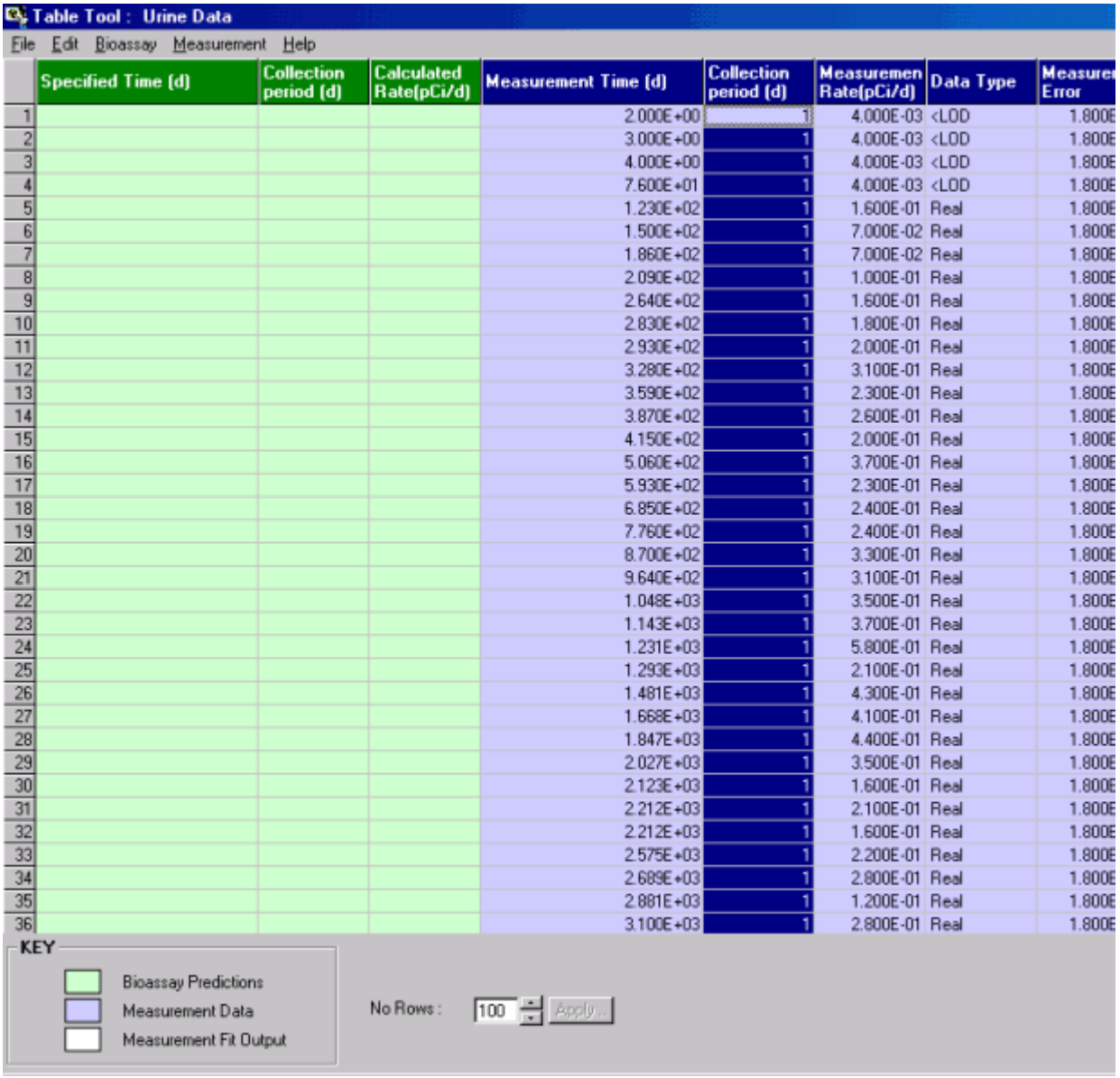
Measurement Date (+hh:mm)	N/A	Measuremen Value(Bq)	Data Type	Measuremen Error
25/02/1988		2.720E+03		
01/03/1988		1.150E+03		
11/03/1988		1.010E+03		
28/03/1988		7.900E+02		
16/05/1988		4.820E+02		
11/08/1988		3.580E+02		
29/11/1990		7.800E+01		
19/02/1992		3.500E+01		

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	1.800E
2				3.000E+00	1	4.000E-03	<LOD	1.800E
3				4.000E+00	1	4.000E-03	<LOD	1.800E
4				7.600E+01	1	4.000E-03	<LOD	1.800E
5				1.230E+02	1	1.600E-01	Real	1.800E
6				1.500E+02	1	7.000E-02	Real	1.800E
7				1.860E+02	1	7.000E-02	Real	1.800E
8				2.090E+02	1	1.000E-01	Real	1.800E
9				2.640E+02	1	1.600E-01	Real	1.800E
10				2.830E+02	1	1.800E-01	Real	1.800E
11				2.930E+02	1	2.000E-01	Real	1.800E
12				3.280E+02	1	3.100E-01	Real	1.800E
13				3.590E+02	1	2.300E-01	Real	1.800E
14				3.870E+02	1	2.600E-01	Real	1.800E
15				4.150E+02	1	2.000E-01	Real	1.800E
16				5.060E+02	1	3.700E-01	Real	1.800E
17				5.930E+02	1	2.300E-01	Real	1.800E
18				6.850E+02	1	2.400E-01	Real	1.800E
19				7.760E+02	1	2.400E-01	Real	1.800E
20				8.700E+02	1	3.300E-01	Real	1.800E
21				9.640E+02	1	3.100E-01	Real	1.800E
22				1.048E+03	1	3.500E-01	Real	1.800E
23				1.143E+03	1	3.700E-01	Real	1.800E
24				1.231E+03	1	5.800E-01	Real	1.800E
25				1.293E+03	1	2.100E-01	Real	1.800E
26				1.481E+03	1	4.300E-01	Real	1.800E
27				1.668E+03	1	4.100E-01	Real	1.800E
28				1.847E+03	1	4.400E-01	Real	1.800E
29				2.027E+03	1	3.500E-01	Real	1.800E
30				2.123E+03	1	1.600E-01	Real	1.800E
31				2.212E+03	1	2.100E-01	Real	1.800E
32				2.212E+03	1	1.600E-01	Real	1.800E
33				2.575E+03	1	2.200E-01	Real	1.800E
34				2.689E+03	1	2.800E-01	Real	1.800E
35				2.881E+03	1	1.200E-01	Real	1.800E
36				3.100E+03	1	2.800E-01	Real	1.800E

Figure 7.6. Entering the same value in a highlighted block of cells.

Tip: Highlight ***the*** whole ***data column with a single click - by*** right-clicking ***the column*** heading ***- "***Collection Period (d)***" 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.

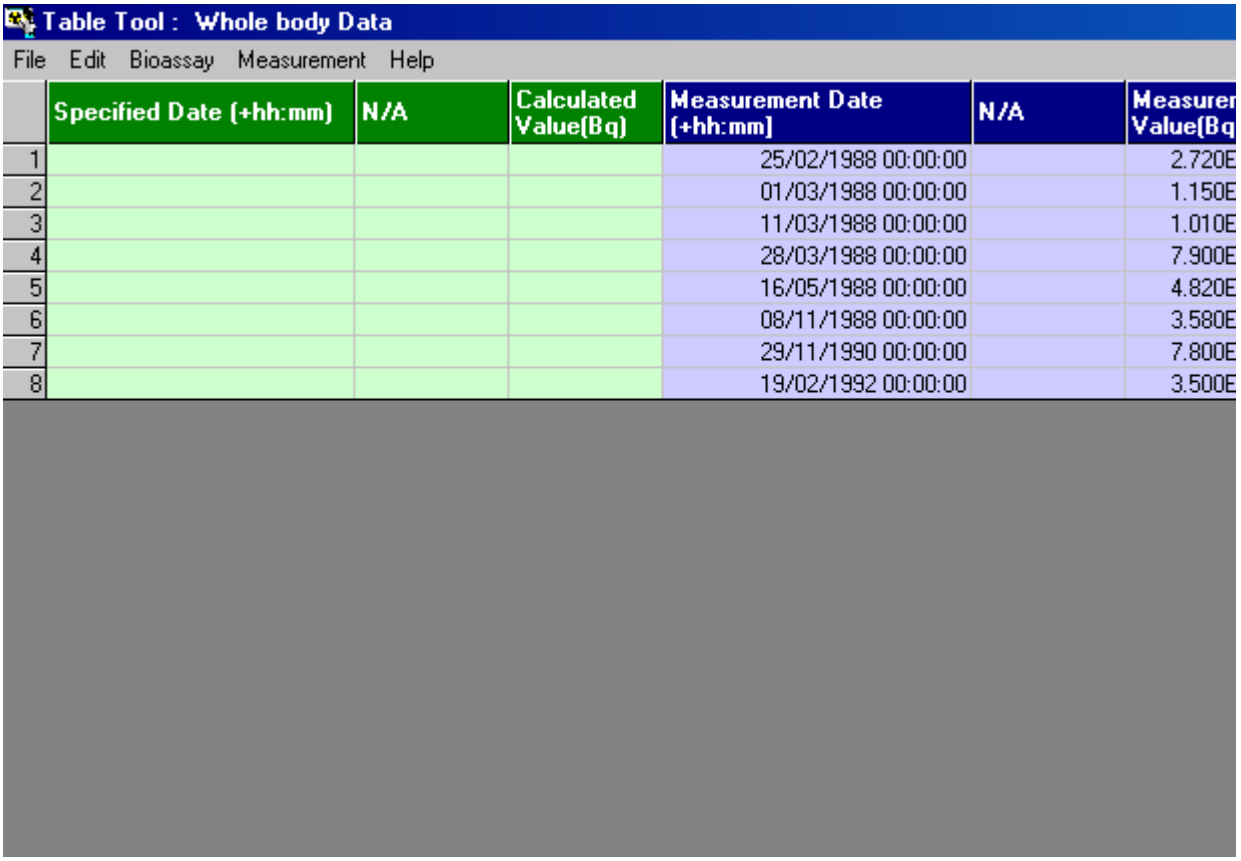


Figure 7.7. Drop-down menu for entering the "**Data Type**."

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.

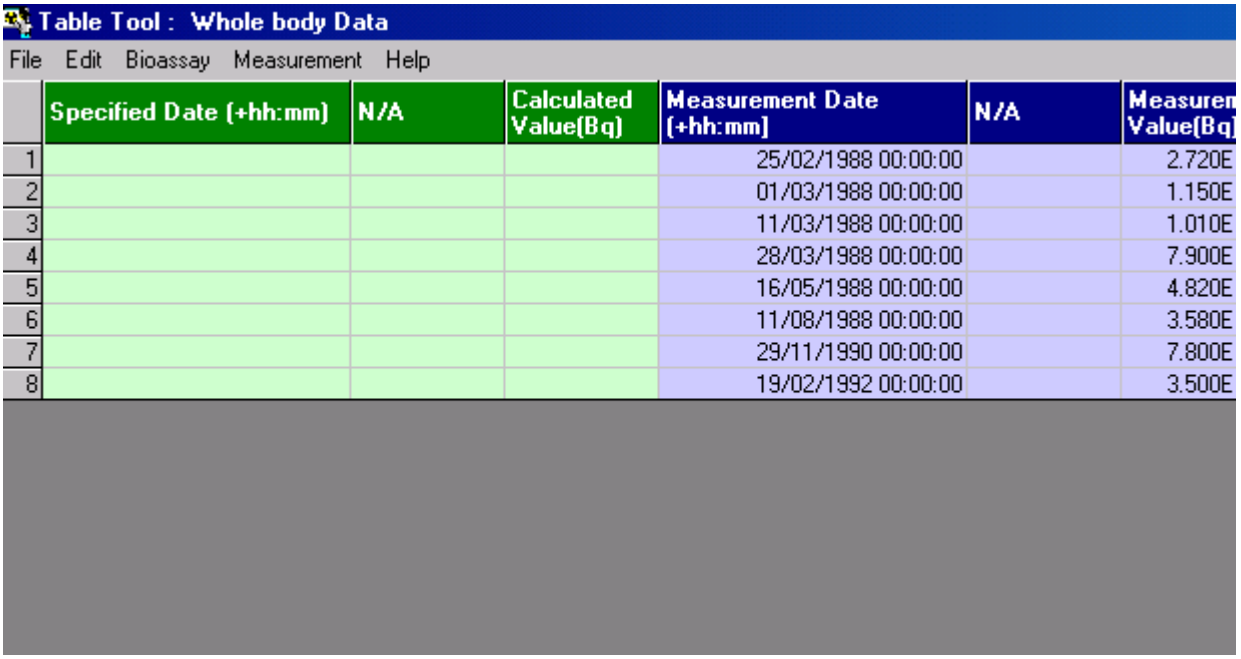


Figure 7.9. Drop-down menu to "**Generate Errors**."

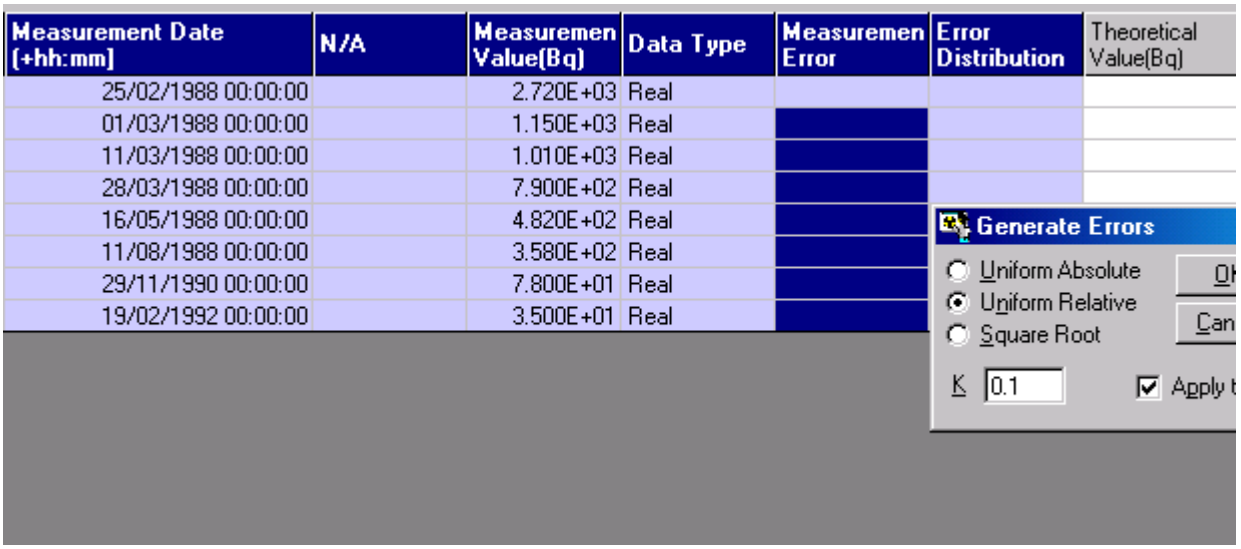


Figure 7.10. The "Generate Errors" window.

In the "generate Errors" window:

- "**Uniform Relative**" error is set by default - or select alternative;
- "A**pply 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).

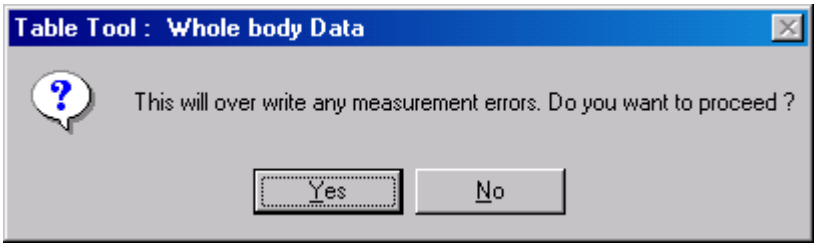


Figure 7.11. **Warning** message before overwriting measurement errors.

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.

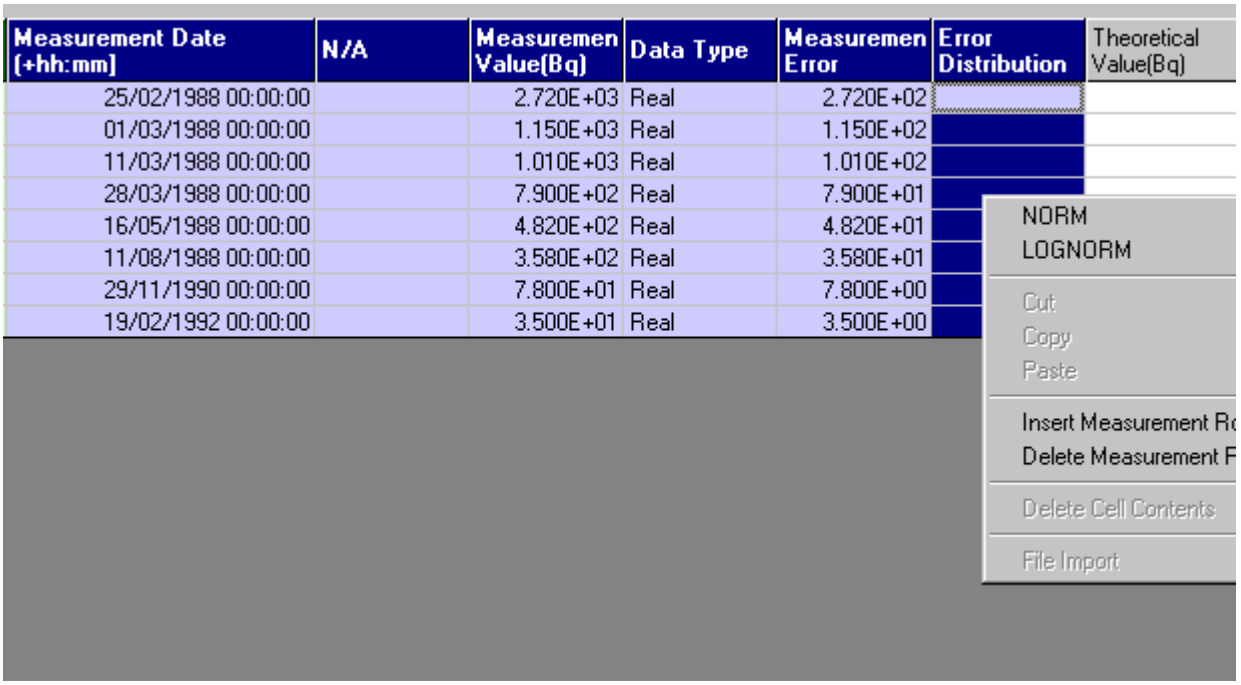


Figure 7.12. Selecting a **Normal** distribution for each error value.

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

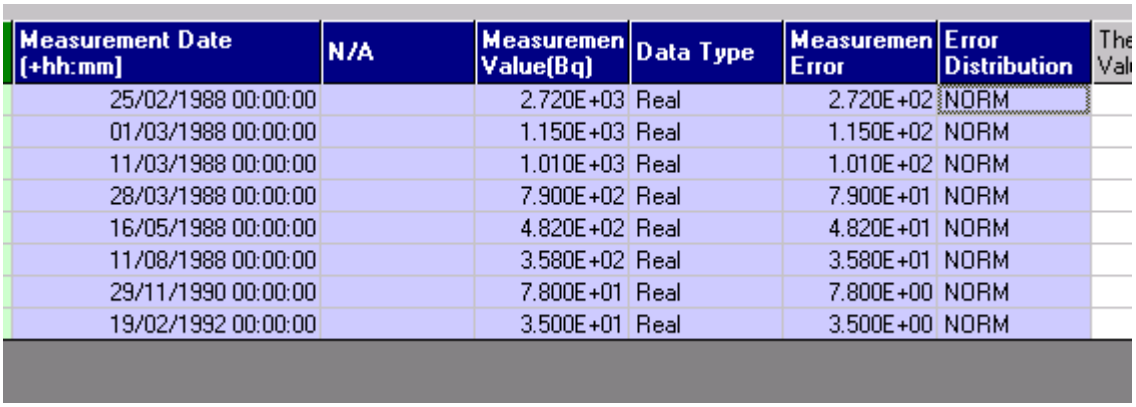
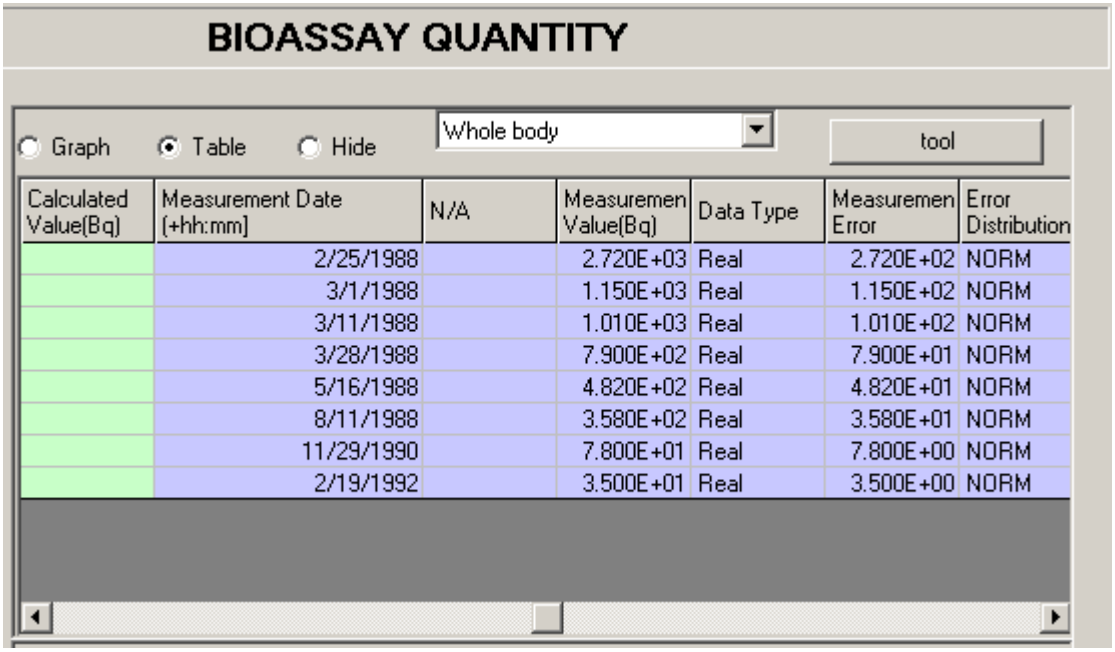


Figure 7.13. Completed measurement data in **Table Tool**.

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.



Calculated Value(Bq)	Measurement Date (+hh:mm)	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

Figure 7.14. Completed **Bioassay Quantity** table of data.

Tip: Right-clicking on any cell in the data table enables you to "**Insert**" or "**Delete**" a **whole row** of measurement data. This automatically **opens** a new "blank" row (below the row that you clicked on), or **deletes** the row that you clicked on, respectively. This does NOT interfere with any rows of values in the first three columns of the **Table Tool** (with green background), which relate to the "**predicted**" bioassay values. The "green" and "blue" columns of the **Table Tool** operate independently.

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.
- Return 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:

1. *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;
4. *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.

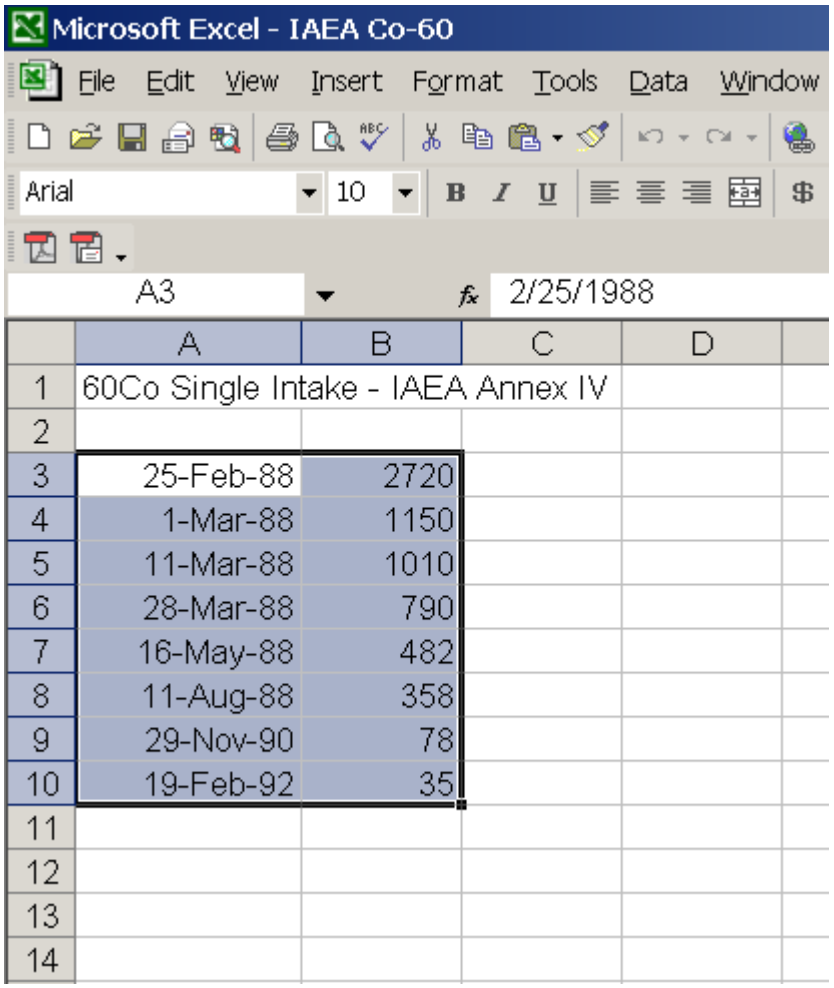
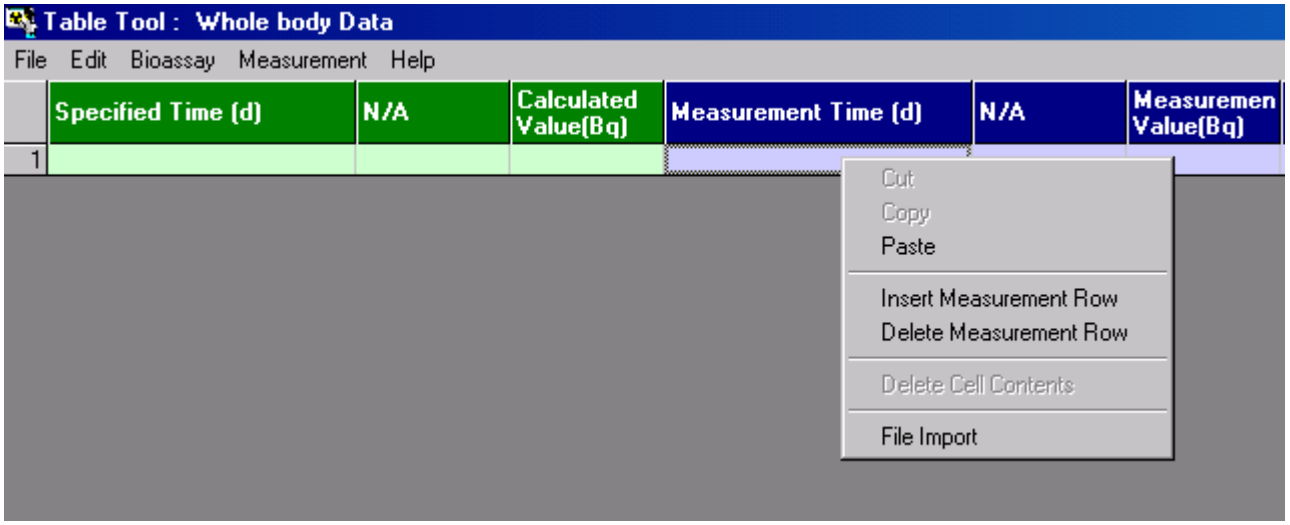


Figure 7.15. Highlighting a block of data in Microsoft Excel spreadsheet for copying to the Windows® clipboard.



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);
- "P**aste**" 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).

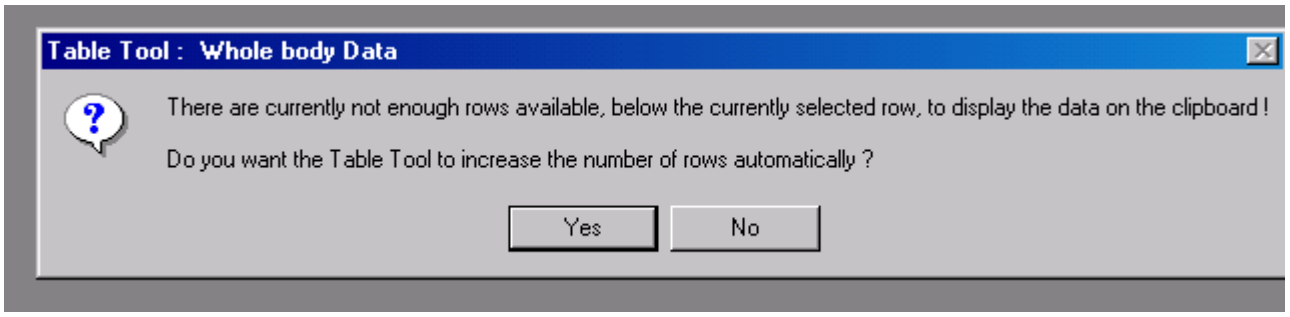
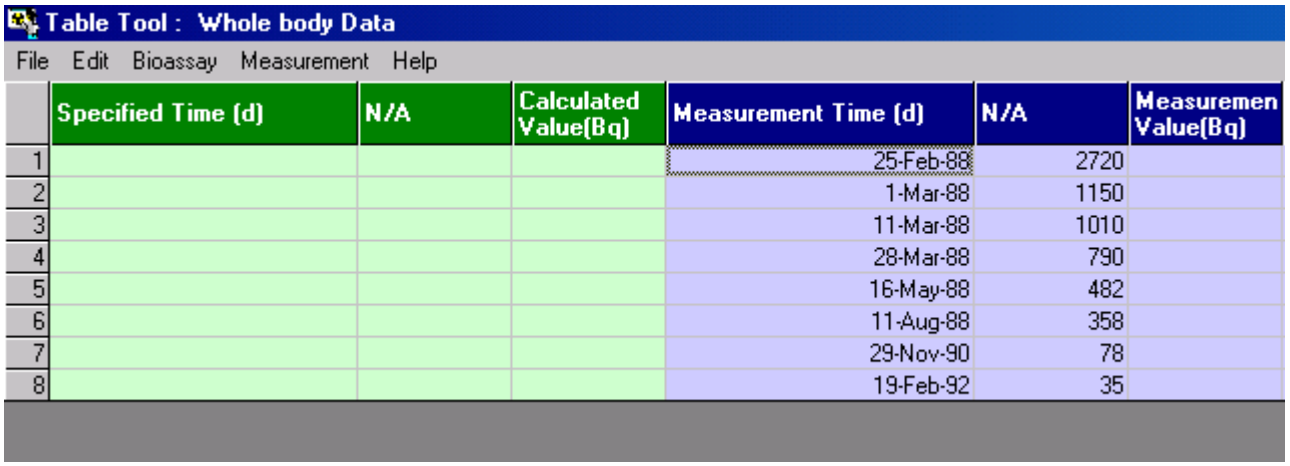


Figure 7.17. Warning notice.



	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**".

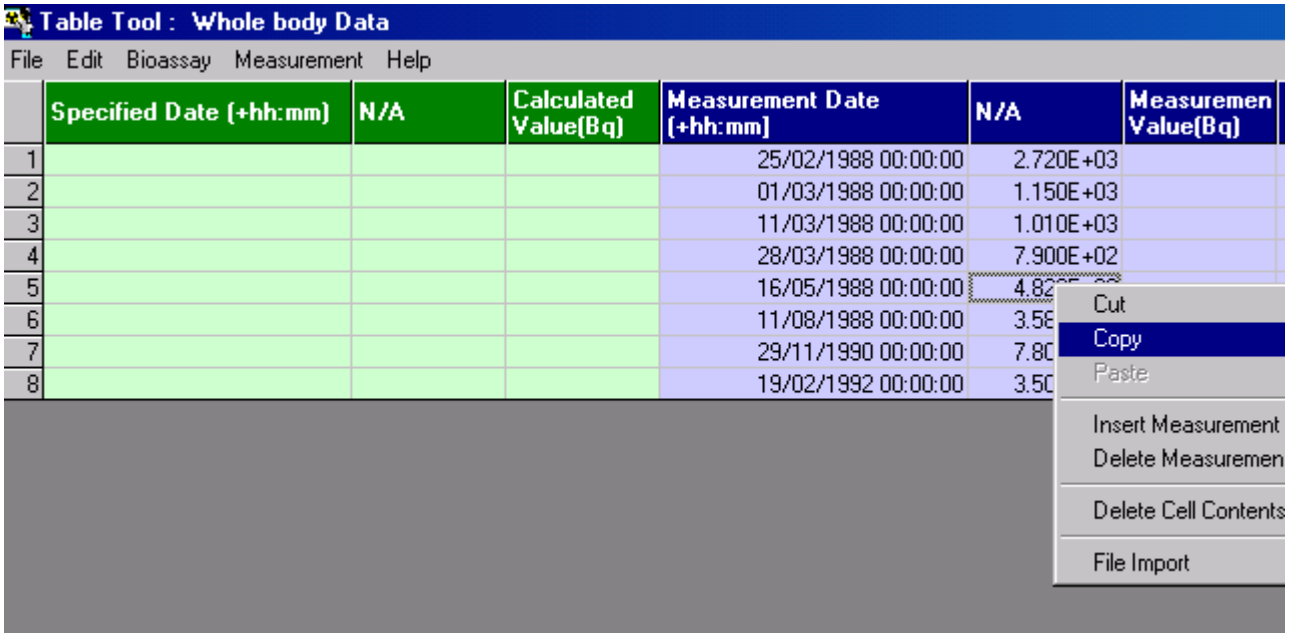


Figure 7.19. Moving a column of data in the **Table Tool**.

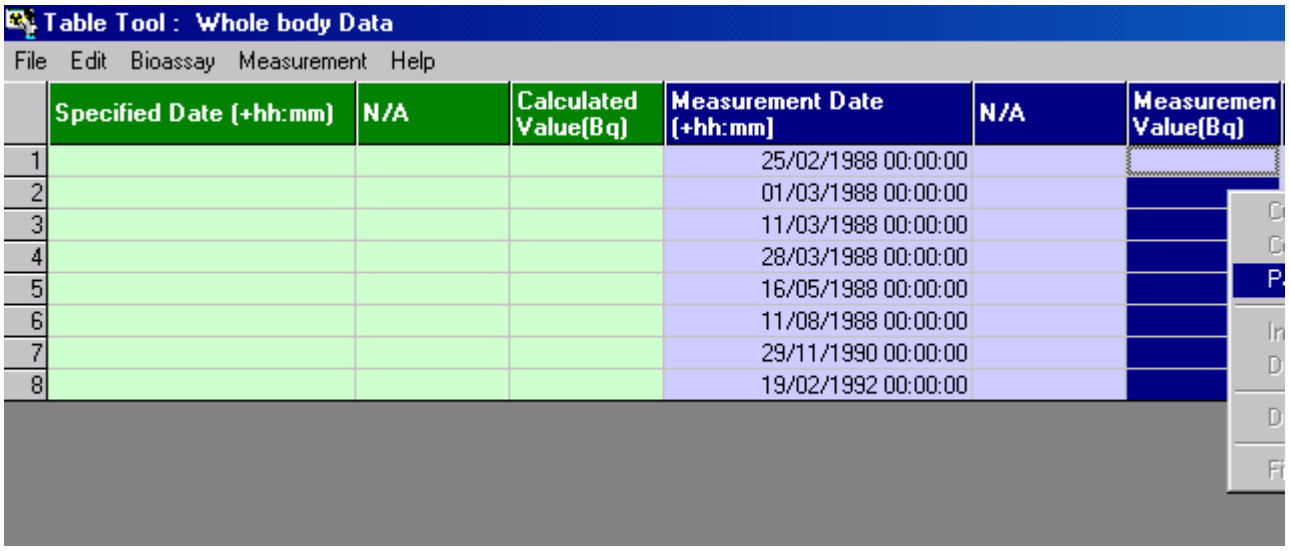


Figure 7.20. Pasting data to the target cells.

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 manual data entry. 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.

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

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

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

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

Importing a Data File

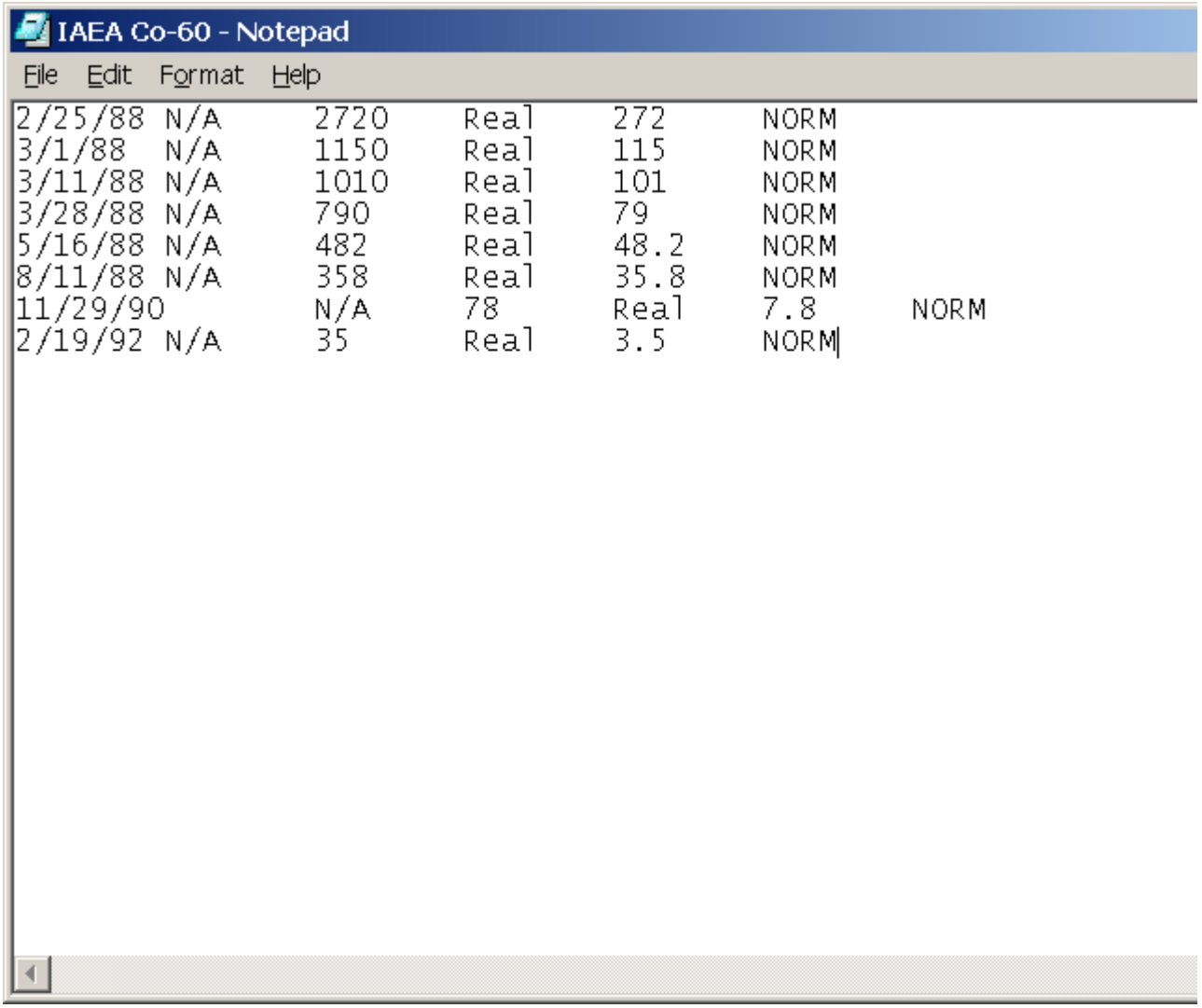


Figure 7.21. Tab delimited text file ("**IAEA Co-60.txt**") holding measurement data.

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**".

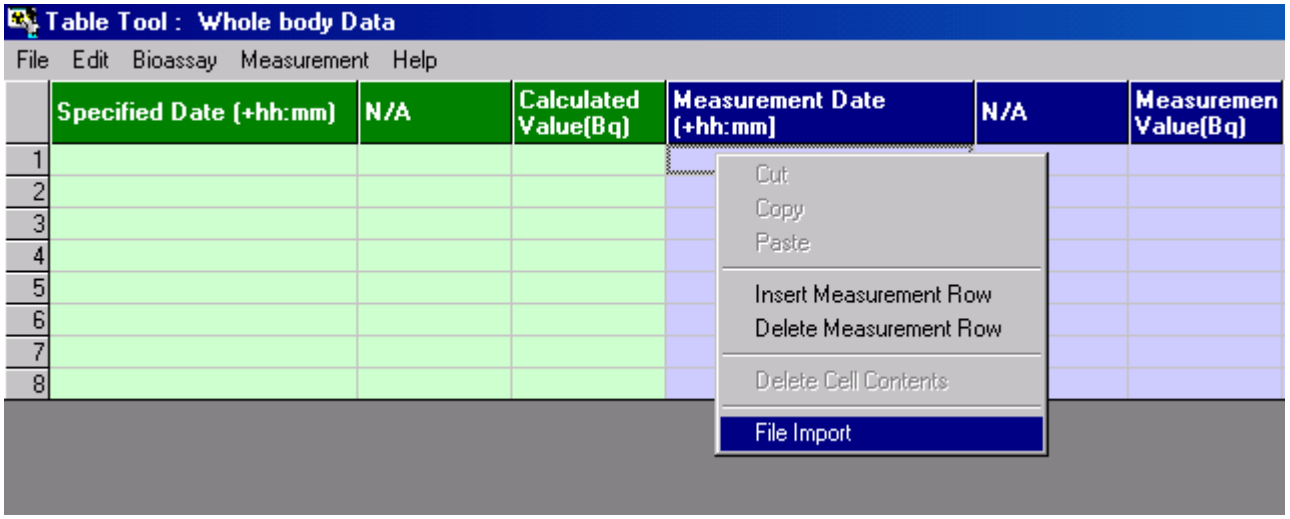


Figure 7.22. "**File Import**" menu.

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.

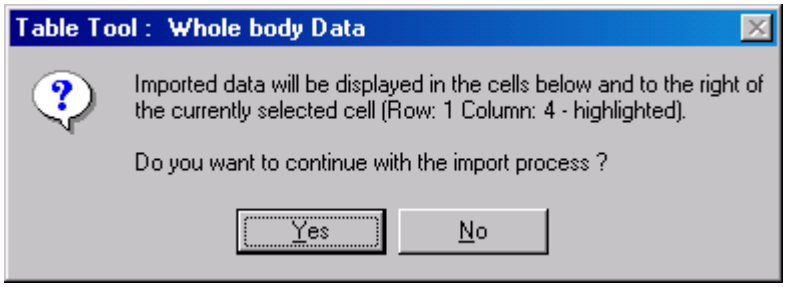


Figure 7.23. Notice to confirm the target location in the data table.

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.

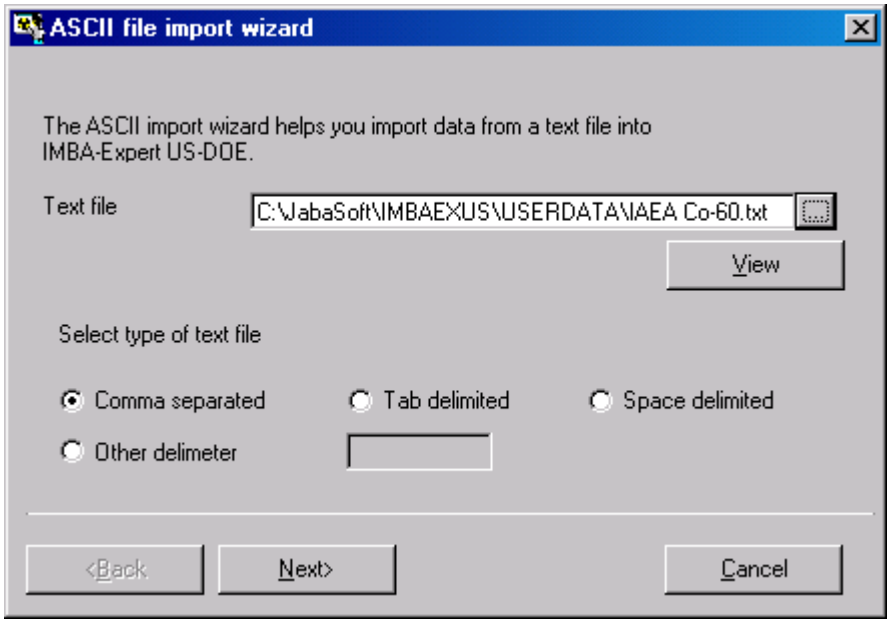


Figure 7.24. ASCII file import wizard for browsing to the **data text file** containing measurement data.

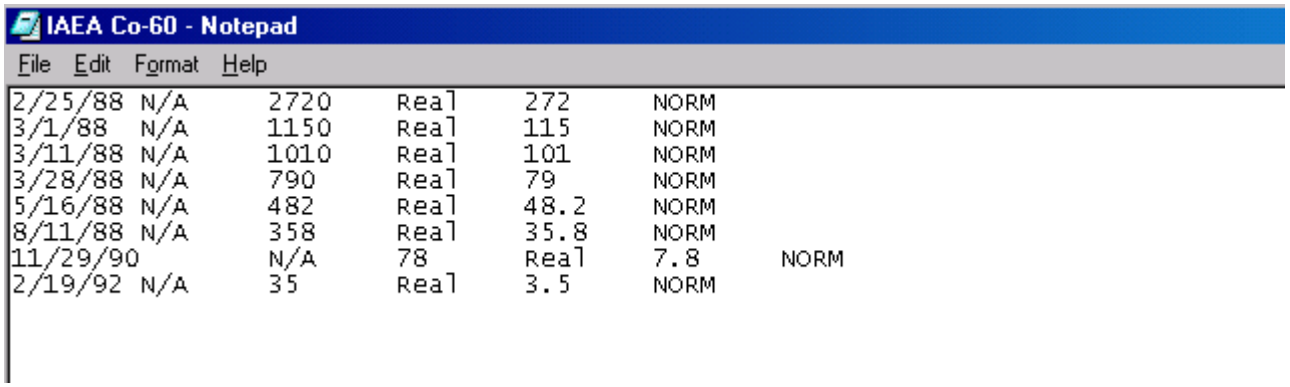


Figure 7.25. Text data file viewed in the **ASCII file import wizard**.

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).

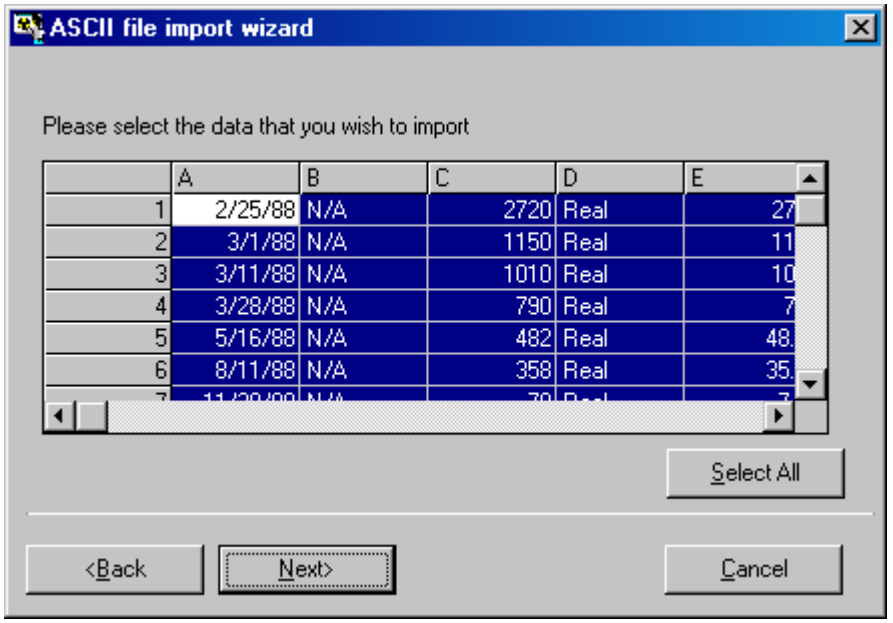


Figure 7.26. Selecting the data in the ASCII text file to **import** into the **Table Tool**.

Click "N**ext**". 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).

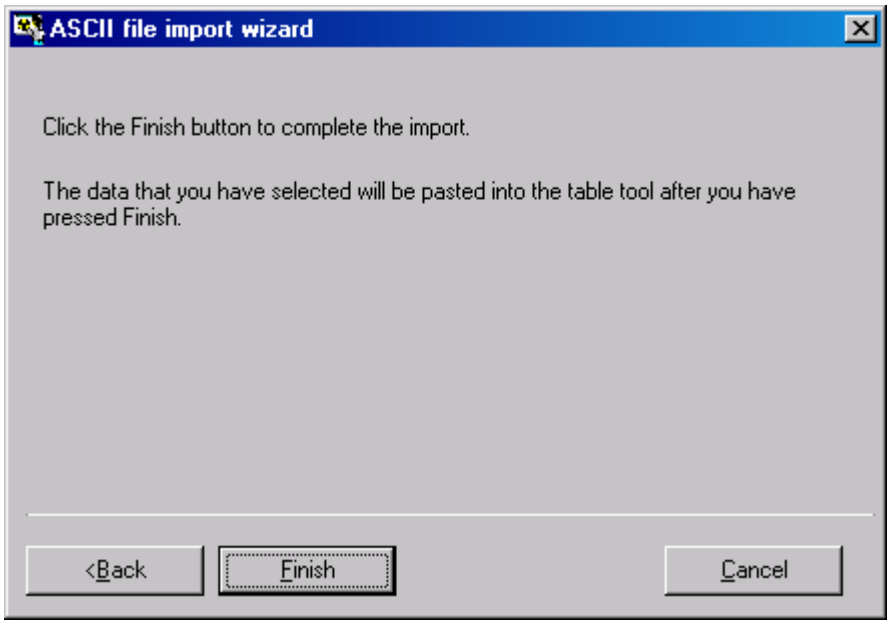
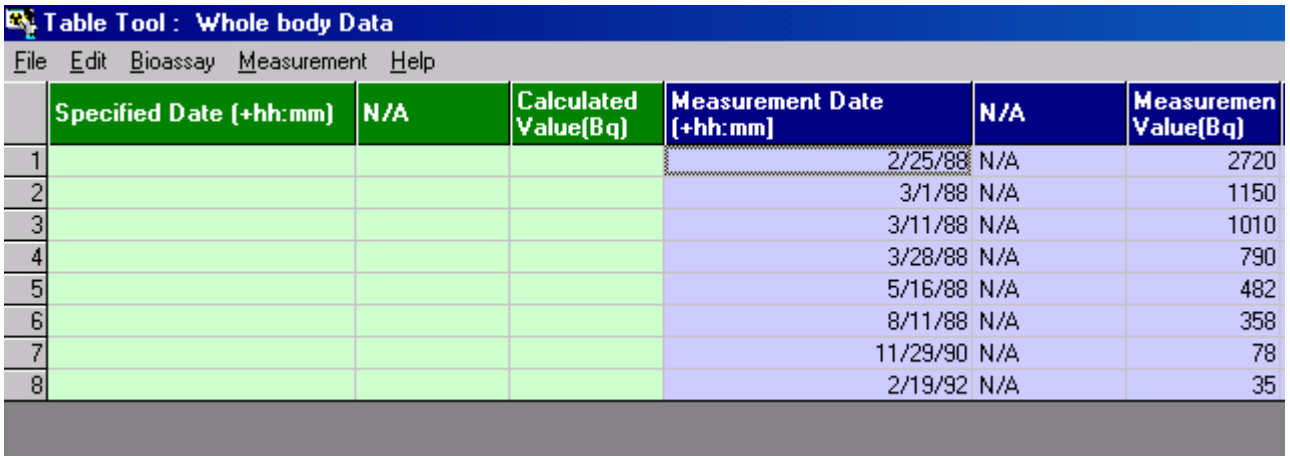


Figure 7.27. Reminder that you are about to paste data into the Table Tool.

Click "F**inish**" to proceed with your data import (Figure 7.28) - or "C**ancel**" this.

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.



	Specified Date (+hh:mm)	N/A	Calculated Value(Bq)	Measurement Date (+hh:mm)	N/A	Measuremen Value(Bq)
1				2/25/88	N/A	2720
2				3/1/88	N/A	1150
3				3/11/88	N/A	1010
4				3/28/88	N/A	790
5				5/16/88	N/A	482
6				8/11/88	N/A	358
7				11/29/90	N/A	78
8				2/19/92	N/A	35

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).

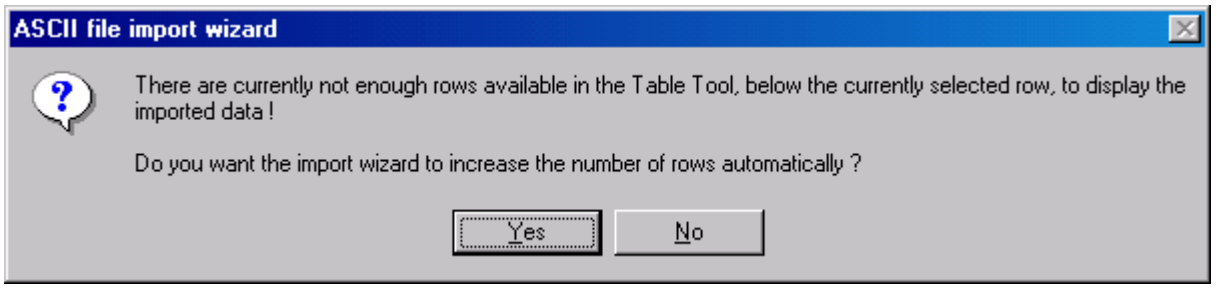


Figure 7.30. Warning message if there are **too few rows** opened in the **Table Tool** to receive imported data.

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**.

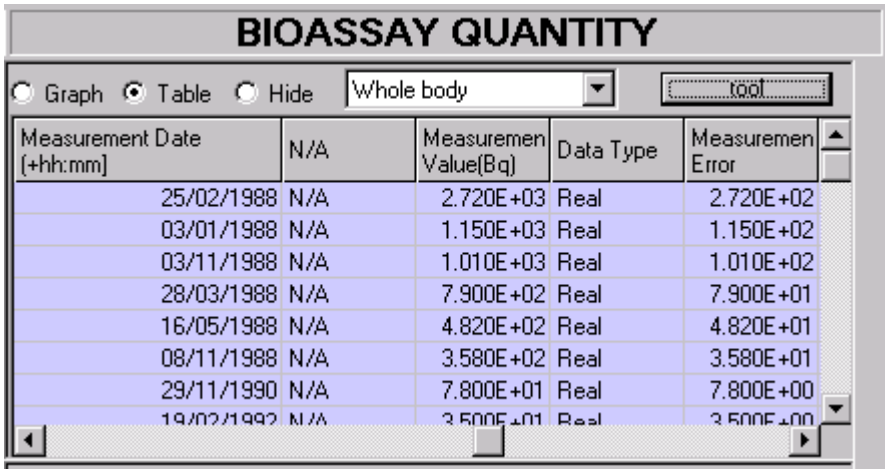


Figure 7.31. Imported data as it appears in the **Bioassay Quantity** window.

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**:

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

Graph Tool for Viewing the Data and Fit

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

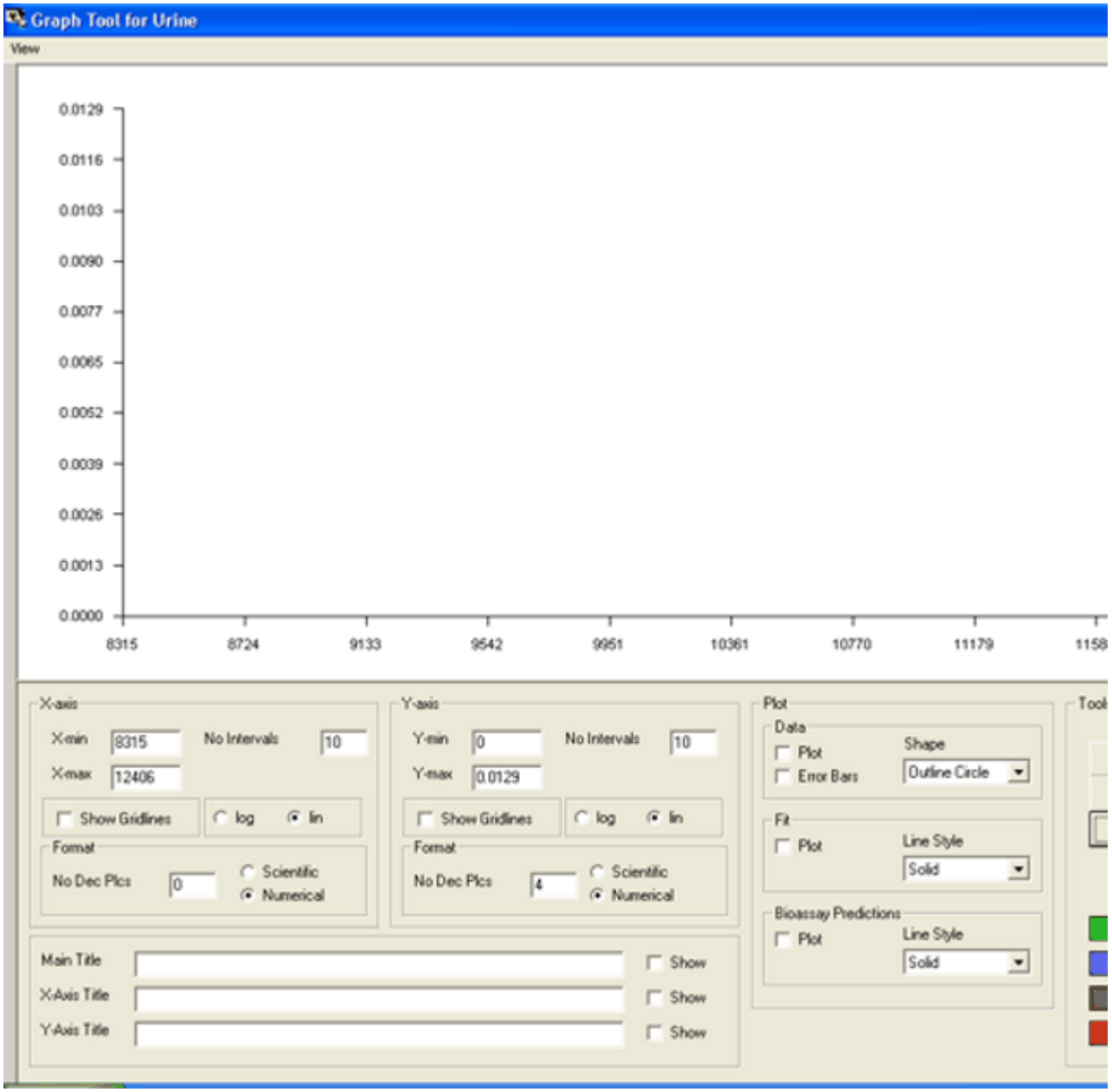


Figure 8.1. Selecting Axes Automatically in the **Graph Tool**.

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**."

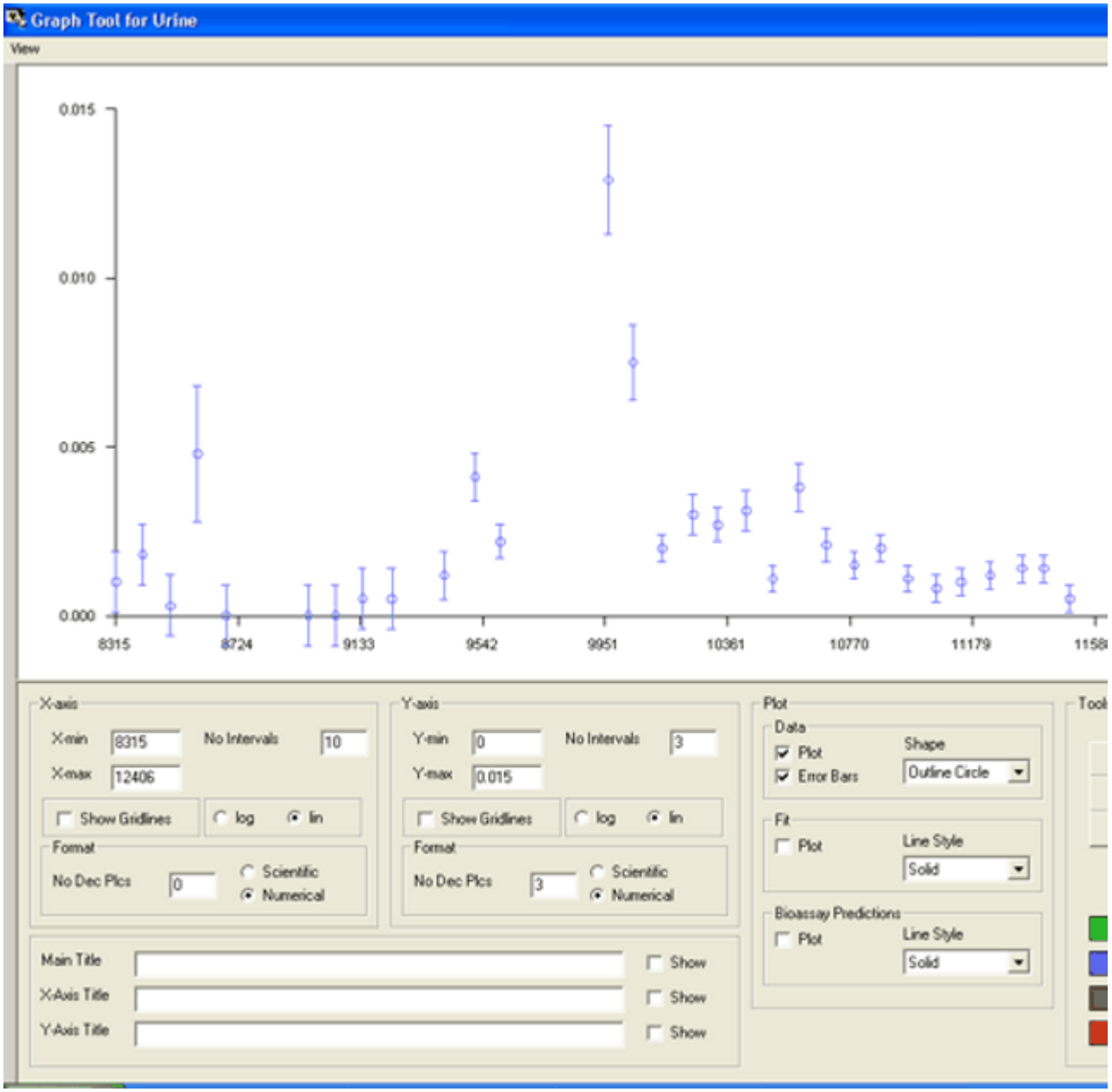


Figure 8.2. Plotting the **data points** and **error bars**.

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).

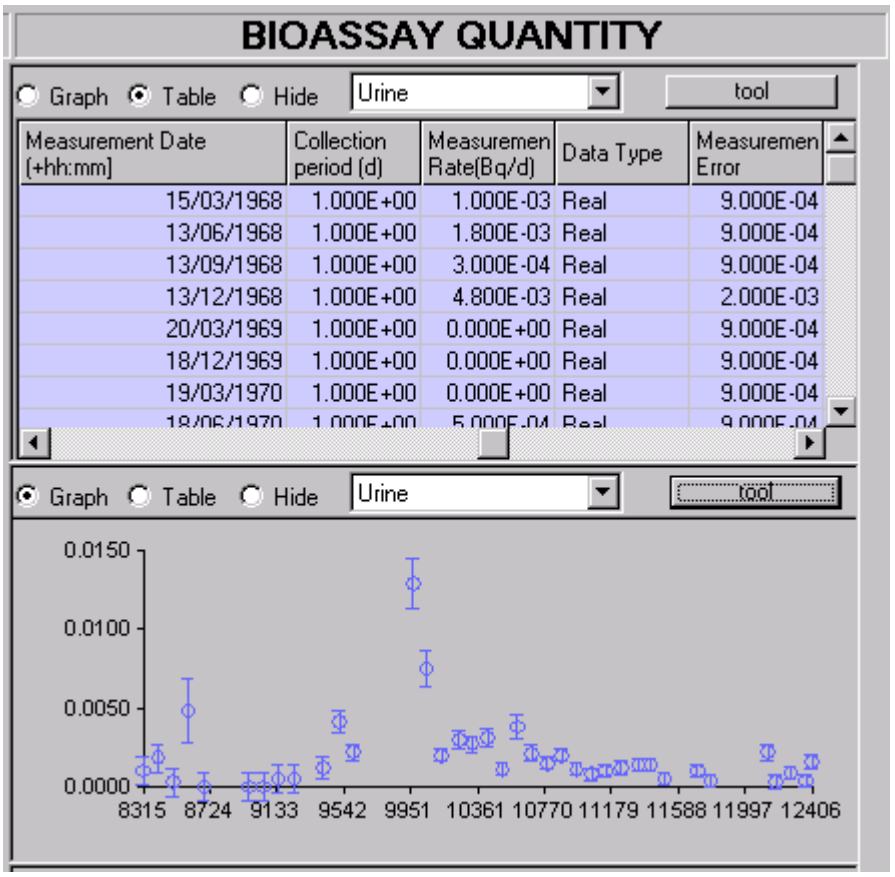


Figure 8.3. Graph of Whole body **data and error bars** displayed in **Bioassay Quantity** window.

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:

- Proceed to the **Multiple Intakes Calculation** (**Step #11**);
- Return 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

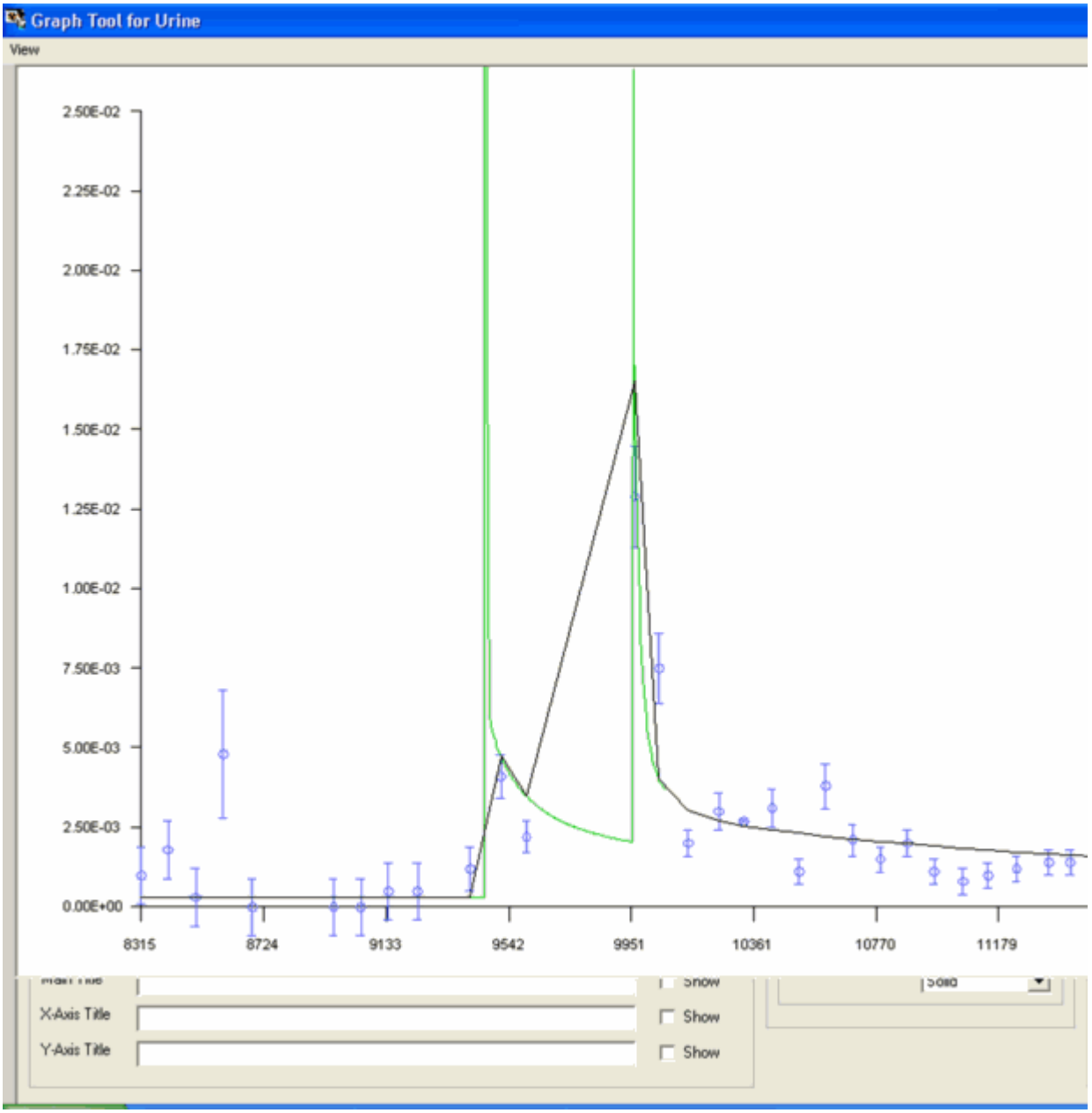


Figure 8.4. Maximised view of the Graph.

Clicking View | Maximise (from the View 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**).

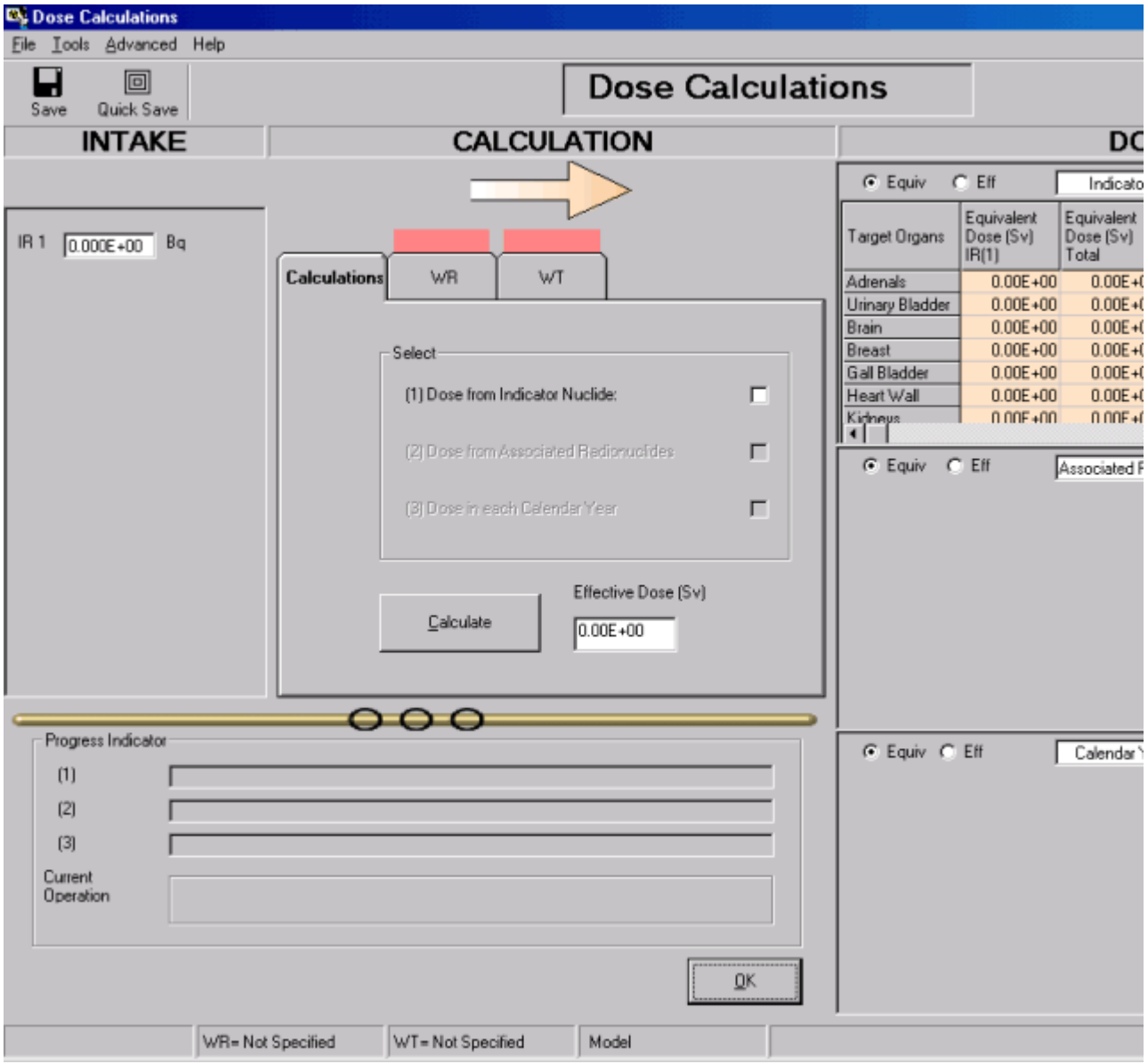


Figure 5.1. The **Dose Calculations** screen.

The screen is divided into these functional parts:

- Menu Bar.
- **Intake** sub-panel.
- **Calculation** sub-panel.
- **Calculation Progress Indicator**.
- **Dose Results** windows.

Dose Calculations Menus

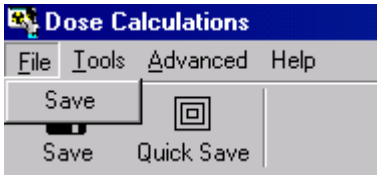


Figure 5.2. Dose Calculations Menus.

These are:

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

Dose Calculation Tools

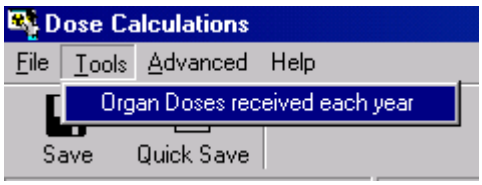


Figure 5.3. Tool to open "**Equivalent Doses to Selected Organ Calculated in Each Calendar Year**" window.

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 IMBA Expert™ OCAS-Edition) is provided in IMBA Professional Plus, Add-On 9, Dose Calculation For Causation. 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 (http://www.cdc.gov/niosh/ocas/ocasirep.html#irep).

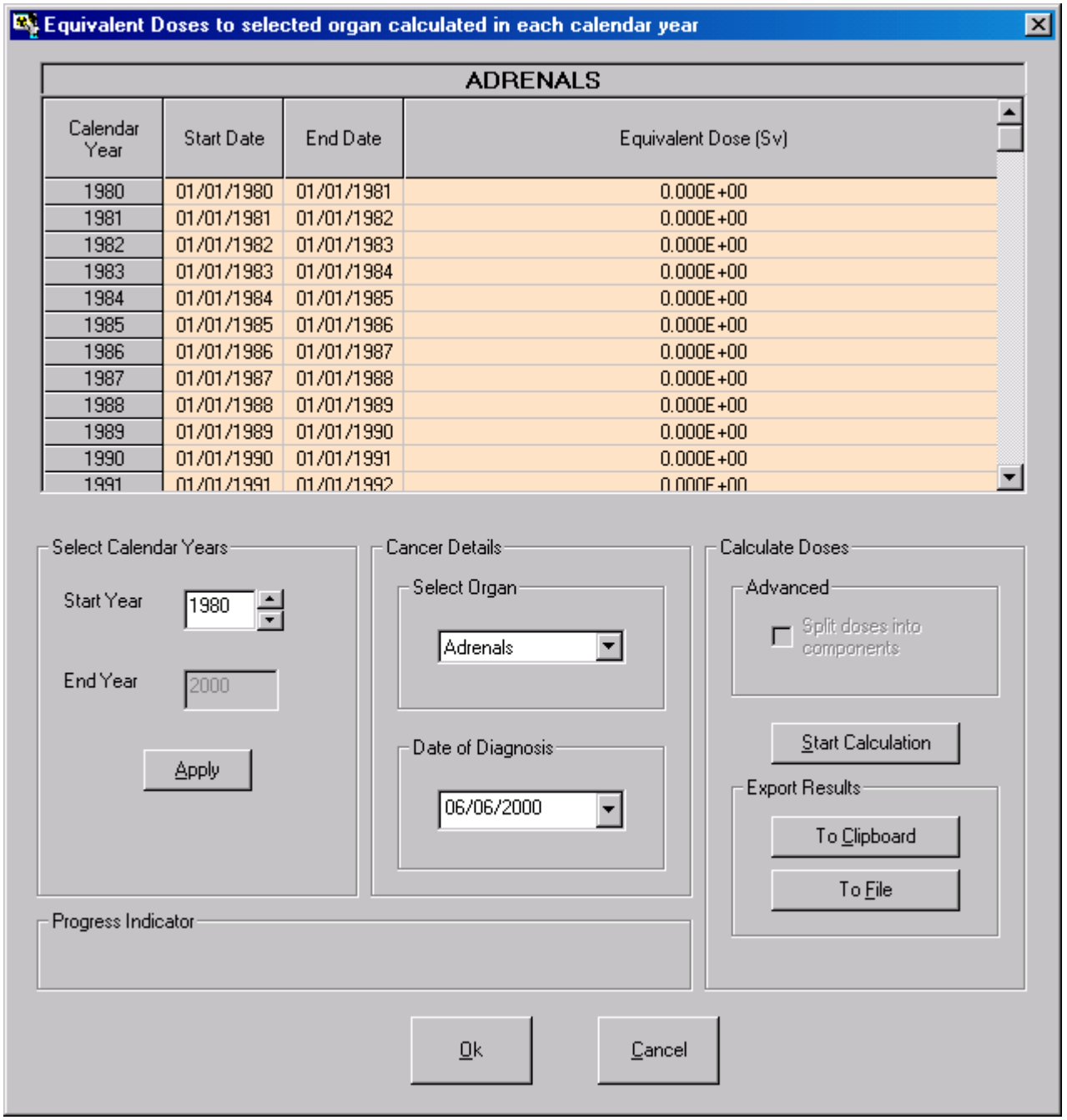


Figure 5.4. Window used to calculated equivalent doses received by a specified organ in each year.

Advanced Dose Calculations Menu

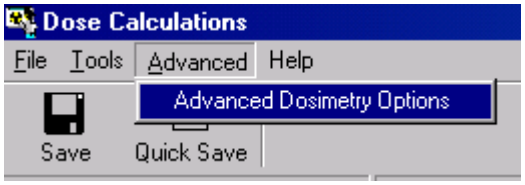


Figure 5.5. Tool to open the "**Advanced Dosimetry Options**" window.

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

- Exclude nuclear recoil energy from the SEEs for alpha emissions.
- Use **Bayesian Analysis** in the bioassay fitting procedure.
- Use measurements of Am-241 activity to evaluate Pu-241 content.
- Miscellaneous special functions - reserved for the future.

Nuclear Recoil Energy in SEE

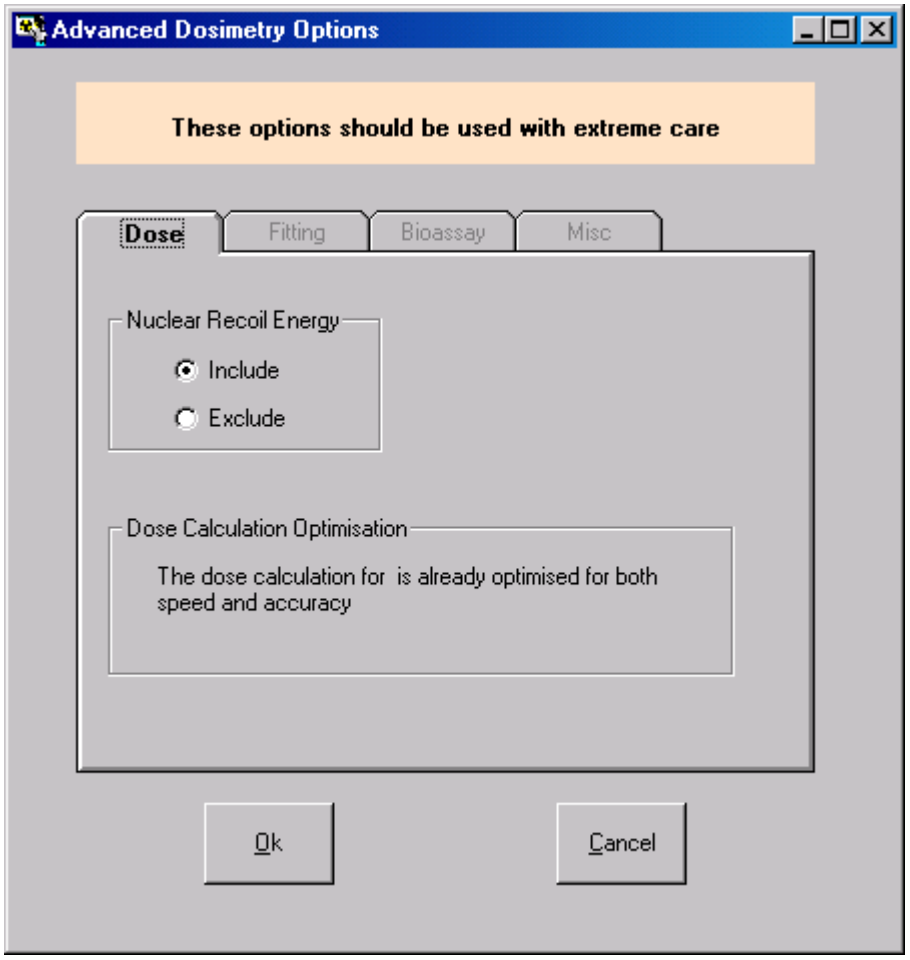


Figure 5.6. Advanced Dosimetry Options window showing option to **Exclude nuclear recoil energy** from the **SEEs** for alpha emissions.

In the basic software version (*IMBA Professional* Lite-Edition), 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 Bioassay Calculations screen (Advanced Menu).

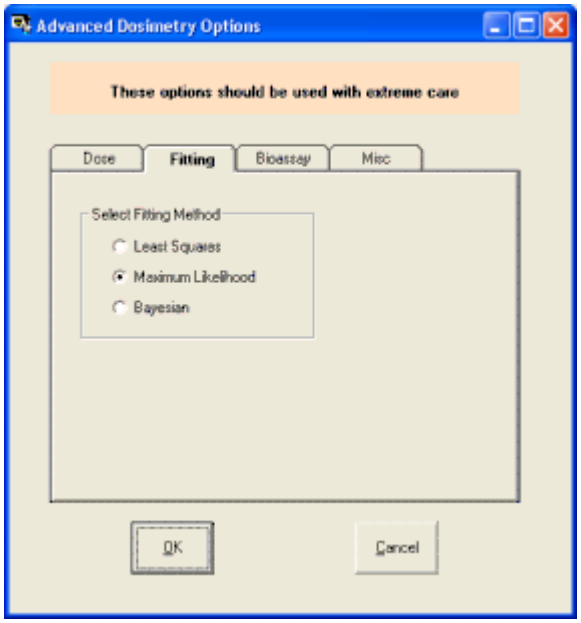


Figure 5.7. "Fitting" Options window.

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 automatically when the **Indicator Nuclide** is defined as ^{241}**Am**, AND ^{241}**Pu** is included in the list of **Associated Radionuclides**. See Case Of Am-241 In-growth as an example.

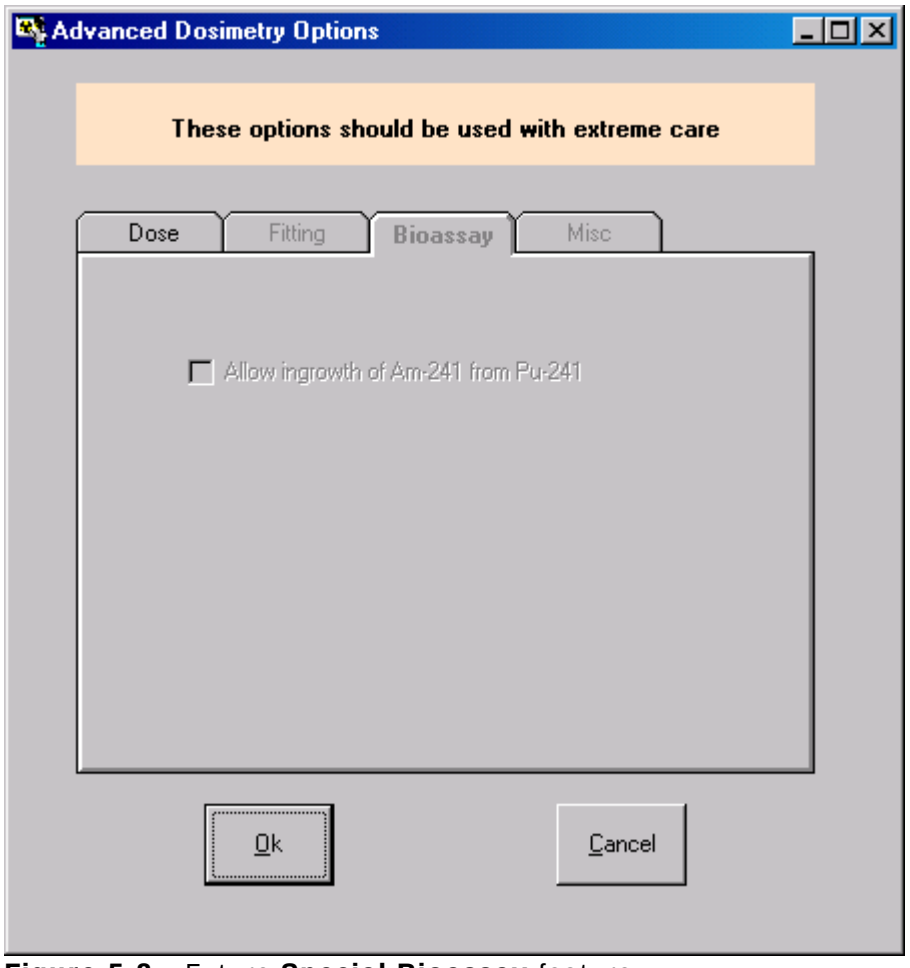


Figure 5.8. Future **Special Bioassay** feature.

Specify Intakes In Mass Units (mg)

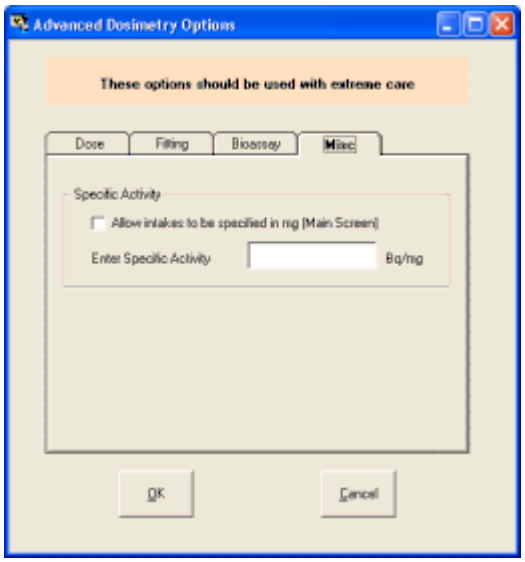


Figure 5.9. "Miscellaneous" Option - Use of **"Mass"** as the **Unit of Intake**.

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).

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).

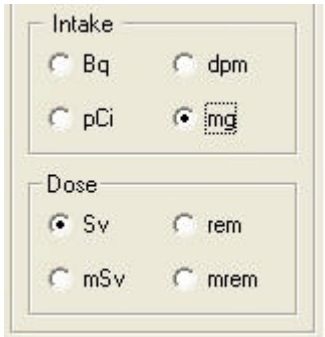


Figure 5.11. "**mg**" **Unit of Intake** enabled.

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

Intake Sub-Panel - Dose Calculations

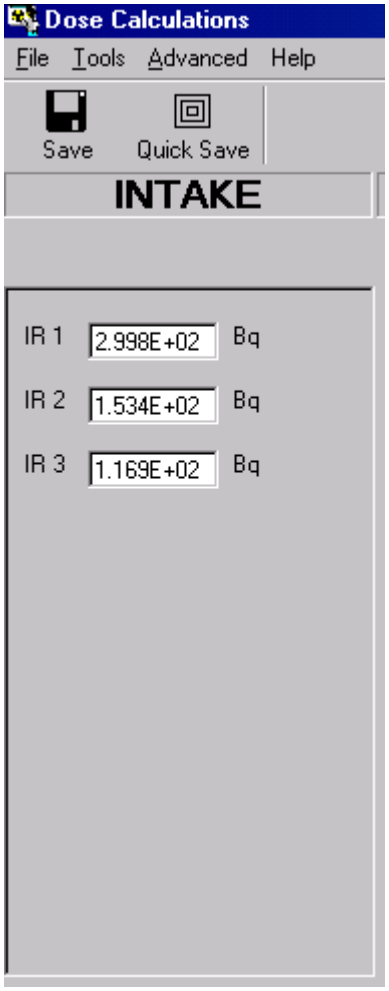


Figure 5.12. Intake sub-panel.

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 Example of Estimating Multiple Intakes using the Miller et al. (1999) data. You can also enter hypothetical values of intake, or values from other sources, directly in the **Intake** dialog boxes.

Dose Calculations Sub-Panel

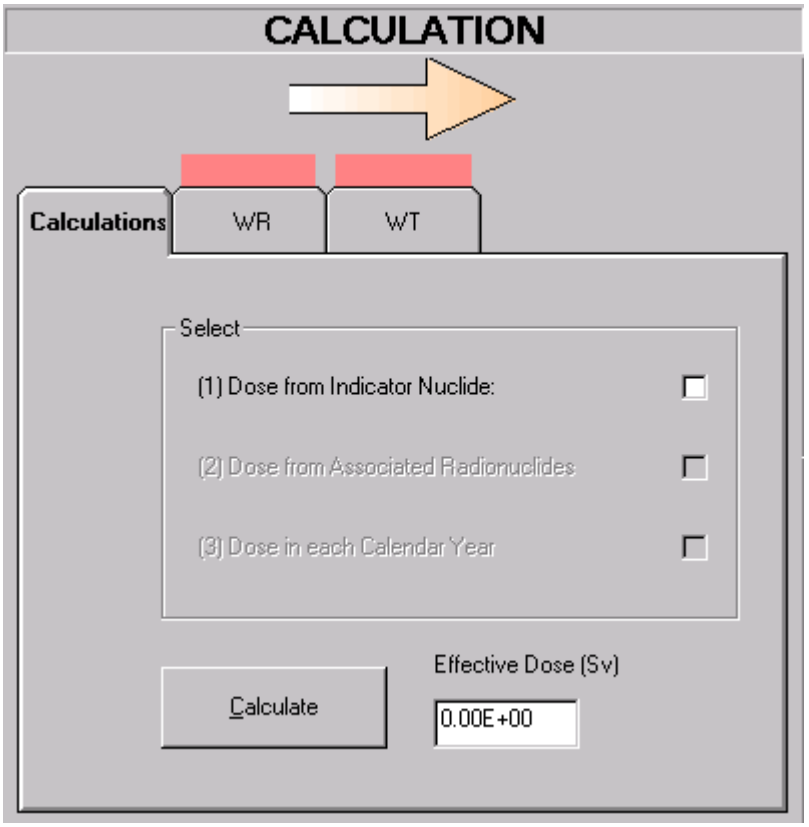


Figure 5.13. Dose Calculation sub-panel at start-up.

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 Miller et al. (1999) example case, let's assume that each intake of ^{238}Pu was associated with two additional radionuclides, ^{239}Pu and ^{241}Am. Let's hypothesize that the ^{239}Pu activity concentration in the inhaled material was 15% of the indicator ^{238}Pu value, and the ^{241}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.

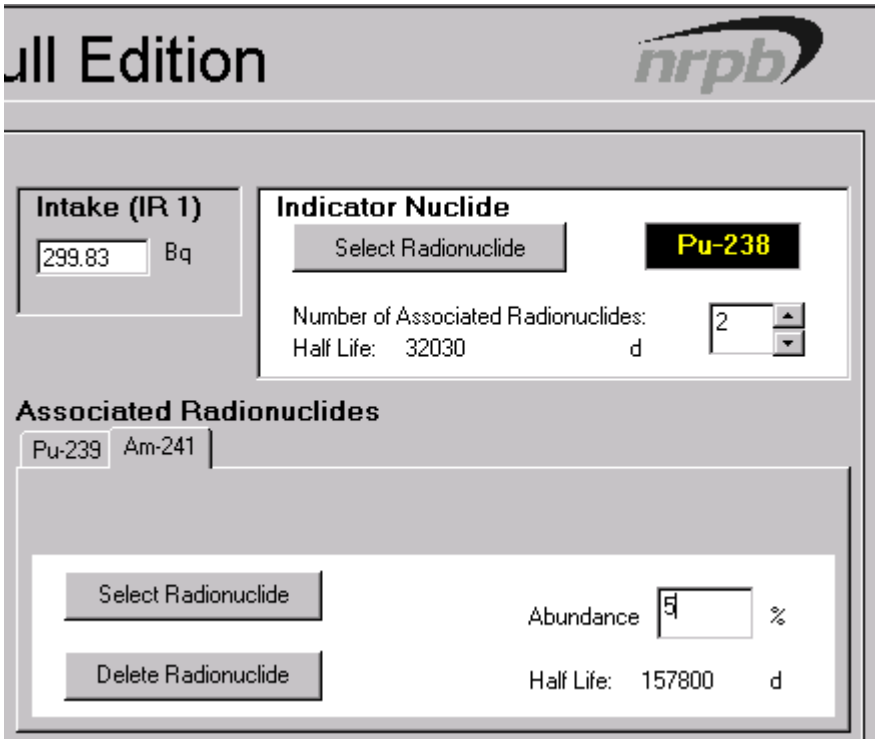


Figure 5.14. Example of two **Associated Radionuclides**, with ^{238}**Pu** as the **Indicator Nuclide**.

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**".

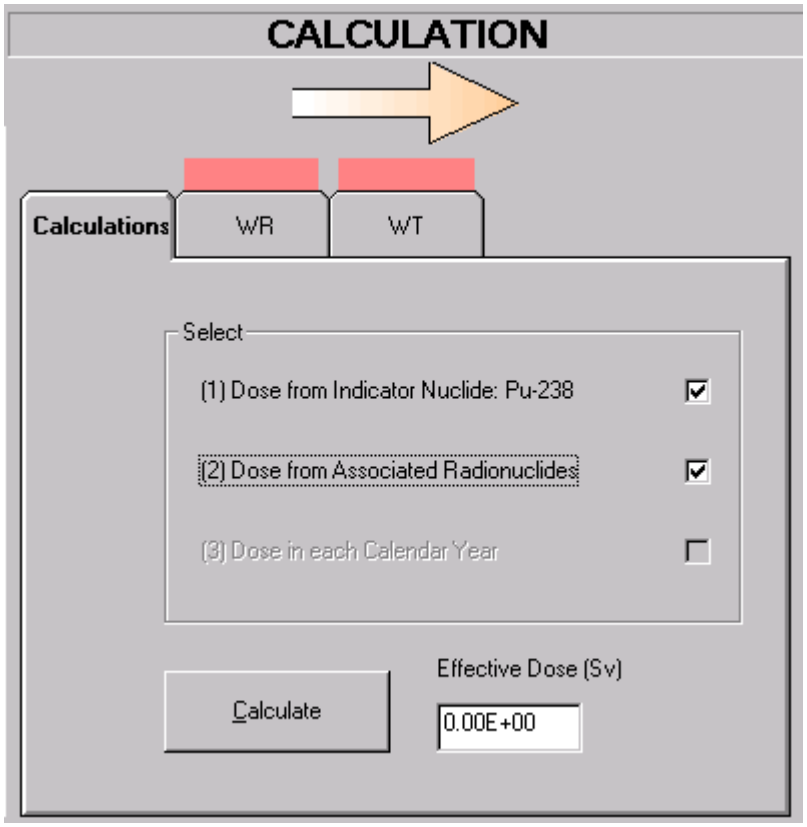


Figure 5.15. Dose Calculation sub-panel for case with **Associated Radionuclides**.

Defining the Radiation Weighting

Factor

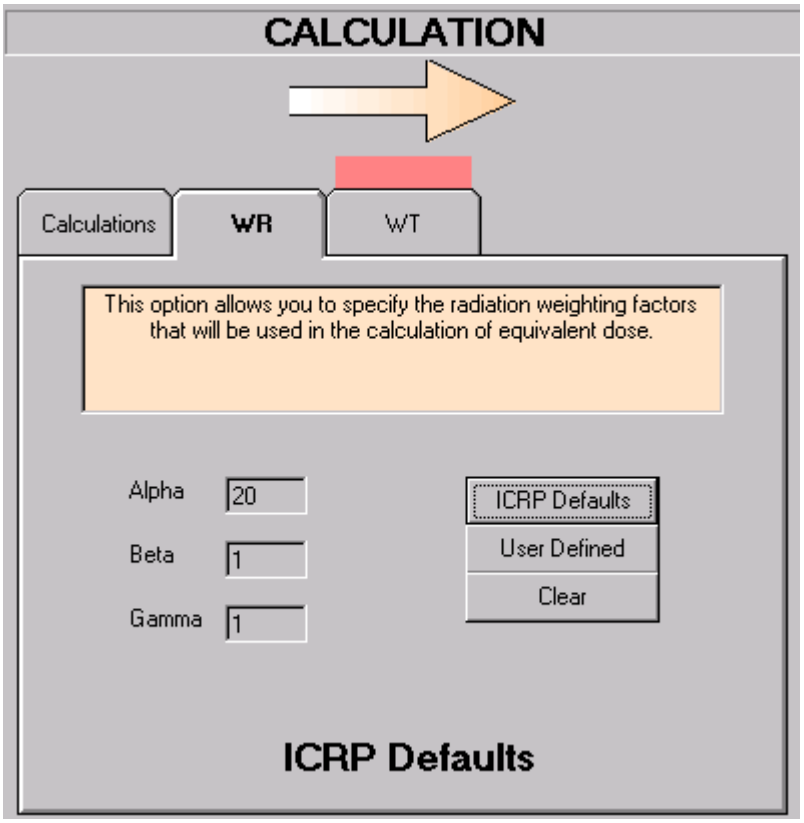


Figure 5.16. Selection of **ICRP-recommended Radiation Weighting Factors**.

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

Selecting the Tissue Weighting Factors

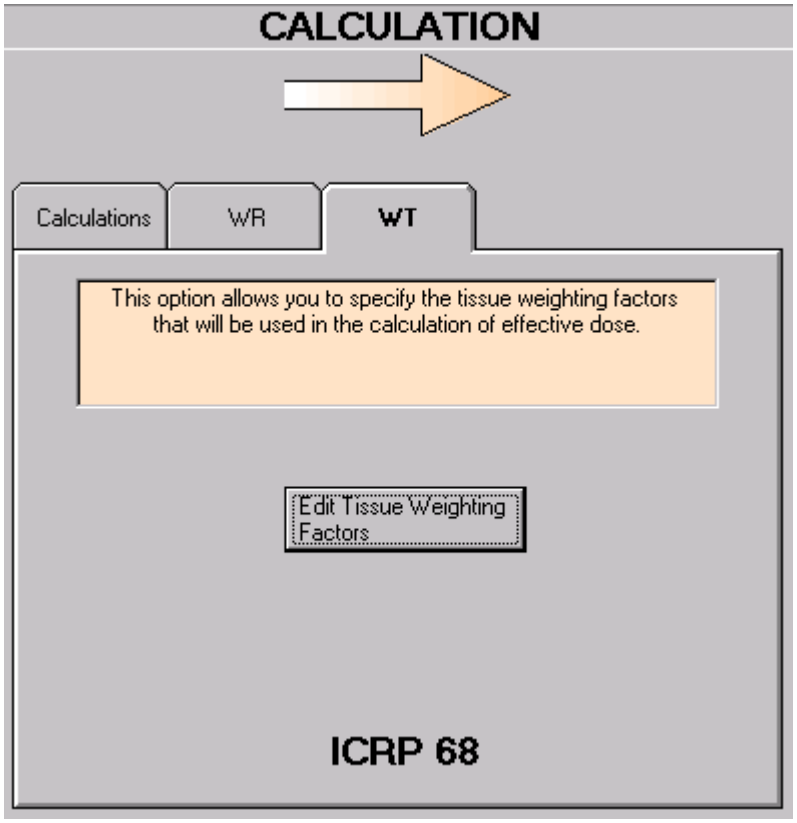


Figure 5.17. Selection of **ICRP60/68 Tissue Weighting Factors** and **Remainder Tissue Rules**.

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).

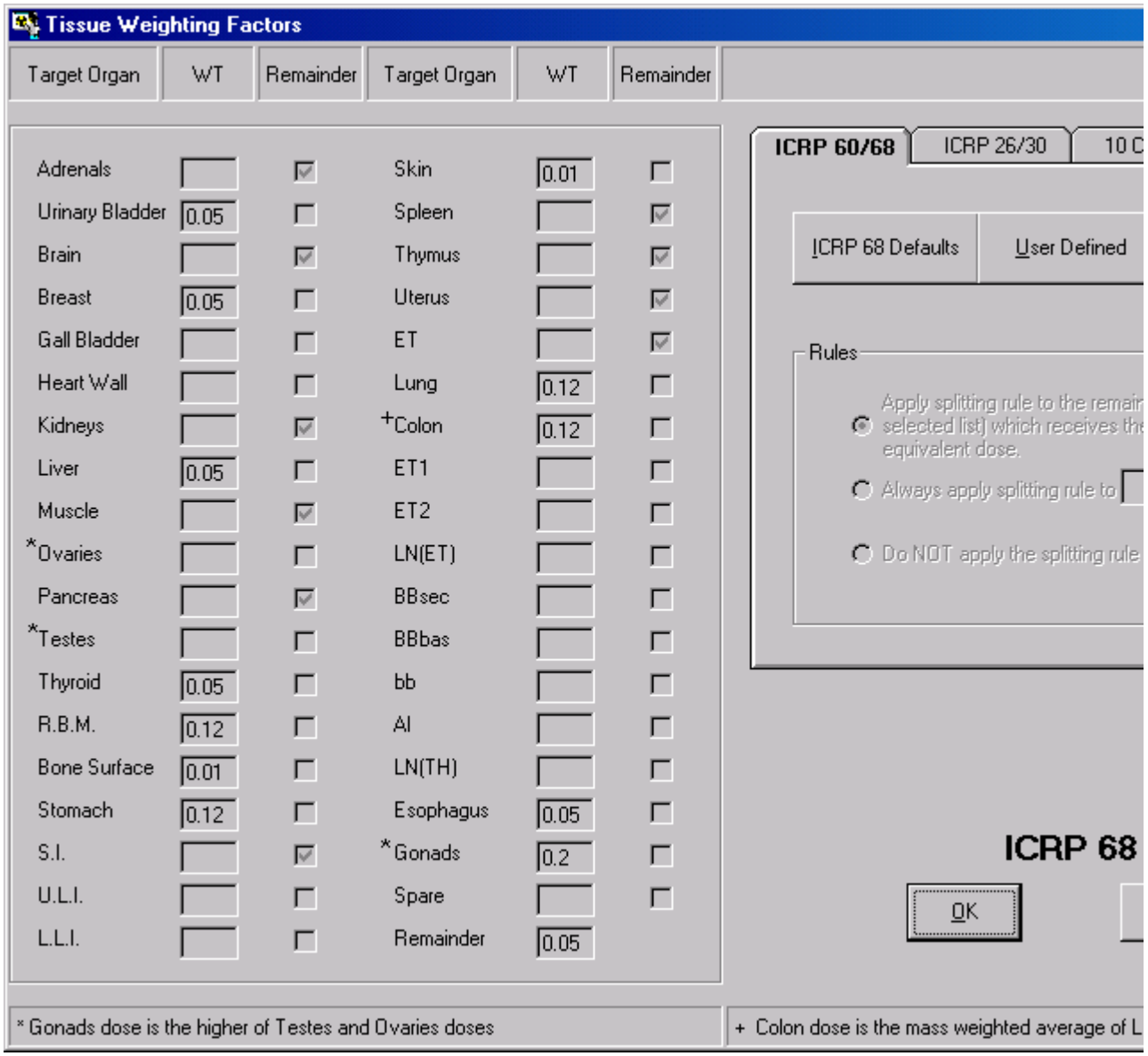


Figure 5.18. The **Tissue Weighting Factors** window.

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

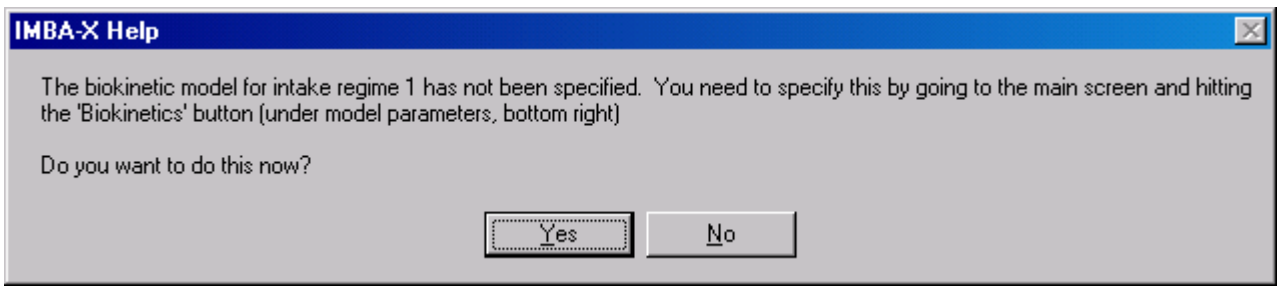


Figure 5.19. Warning Notice to select a **Biokinetic Model** for the **Indicator Nuclide**.

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.

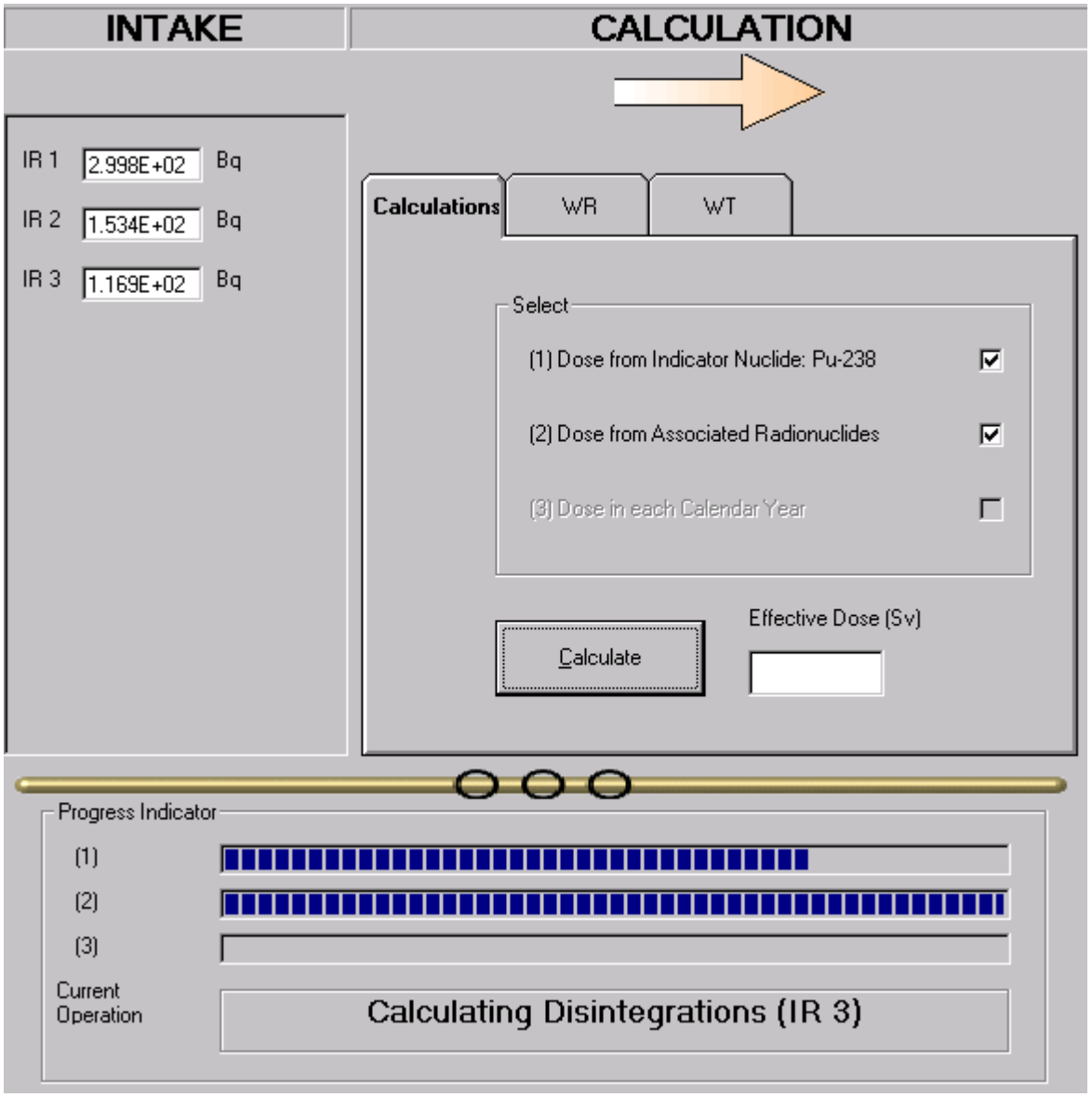


Figure 5.20. Progress Indicator shows what calculation is currently being performed.

Dose Results Windows

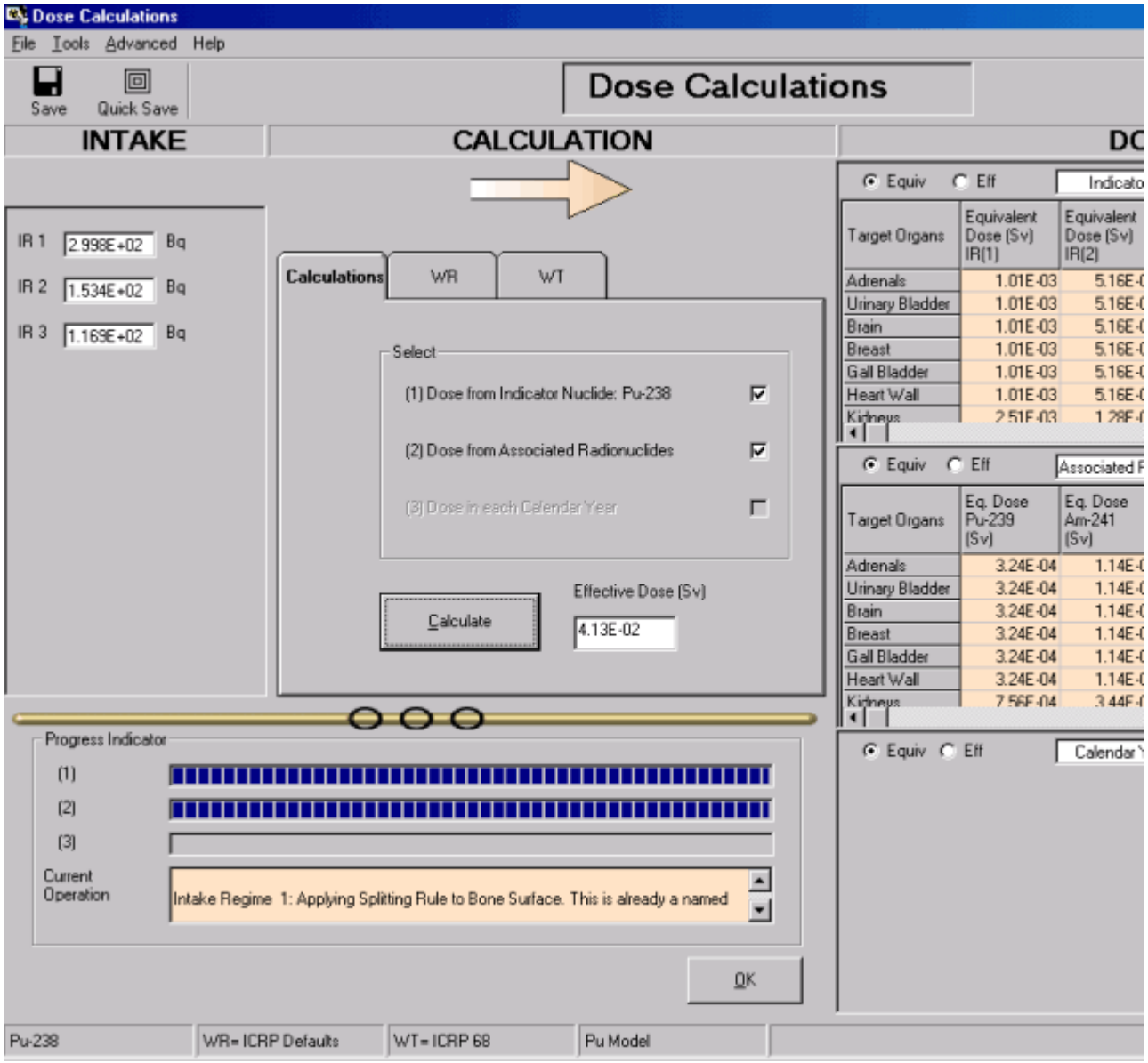


Figure 5.21. Displayed results of a completed **Dose Calculation** set to show **Equivalent Doses** in the "**Dose**" windows.

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**.

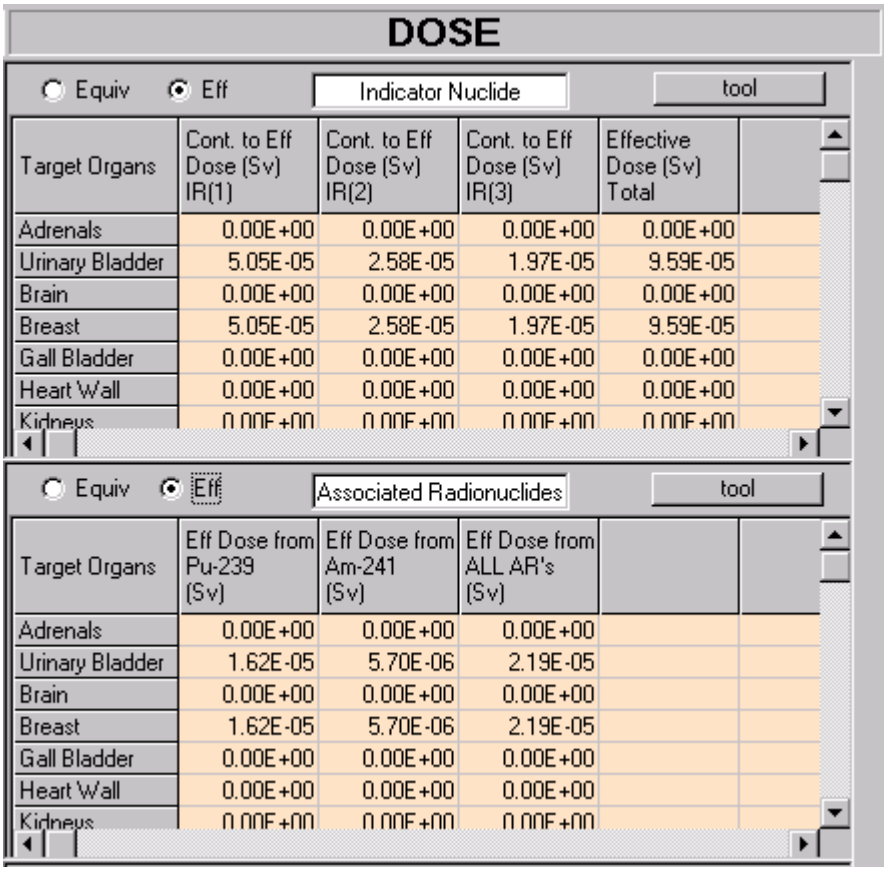


Figure 5.22. Displayed results of a completed **Dose Calculation** set to show **Effective Doses** in the "**Dose**" windows.

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**."

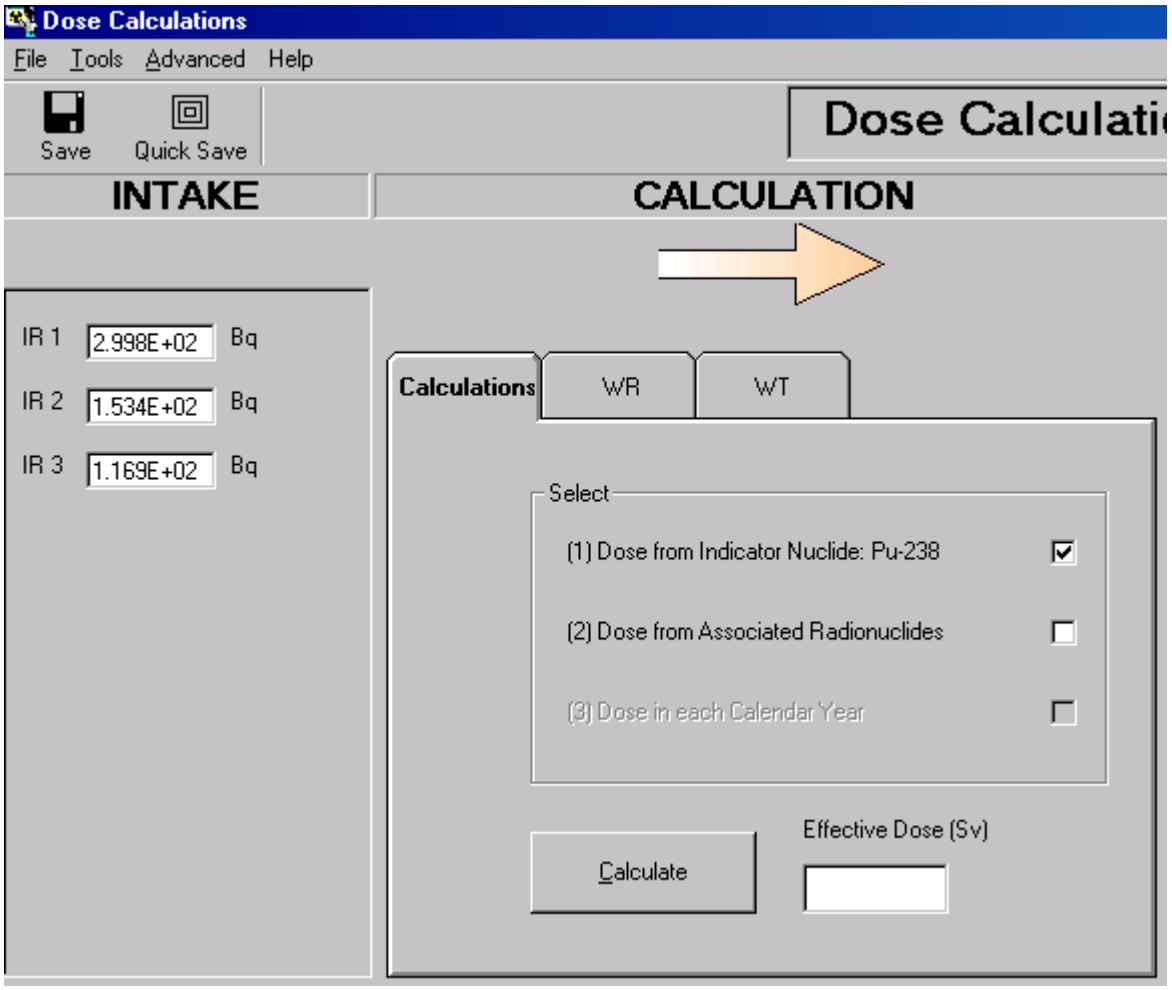


Figure 5.23. Checking the "**Dose from indicator radionuclide (Pu-238)**" dialog *box* in the **Dose Calculations** screen.

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**" sub-panel. If the values of w_R have NOT already been specified, the "**WR**" *tab* will appear as in Figure 5.24.

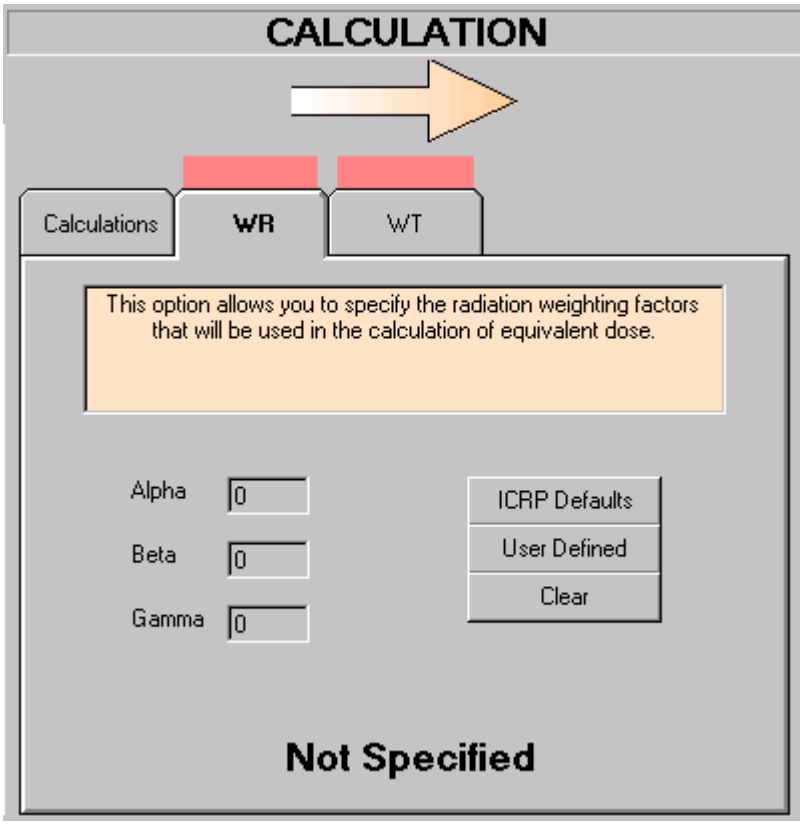


Figure 5.24. "**WR**" *tab* before values of the radiation weighting factor have been defined.

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

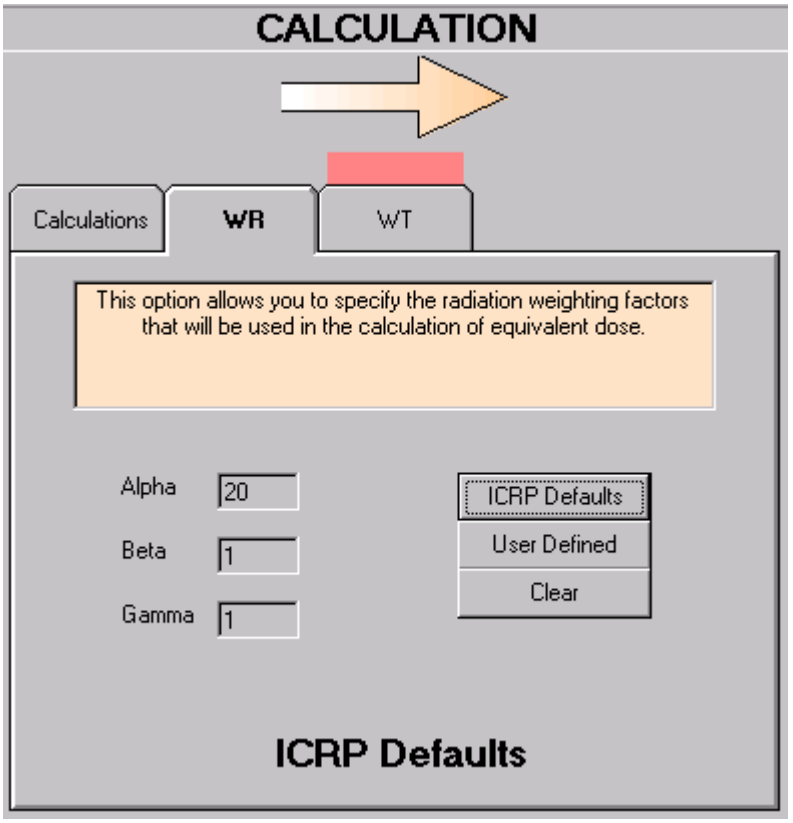


Figure 5.25. Loading the **ICRP Default** values of radiation weighting factor.

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

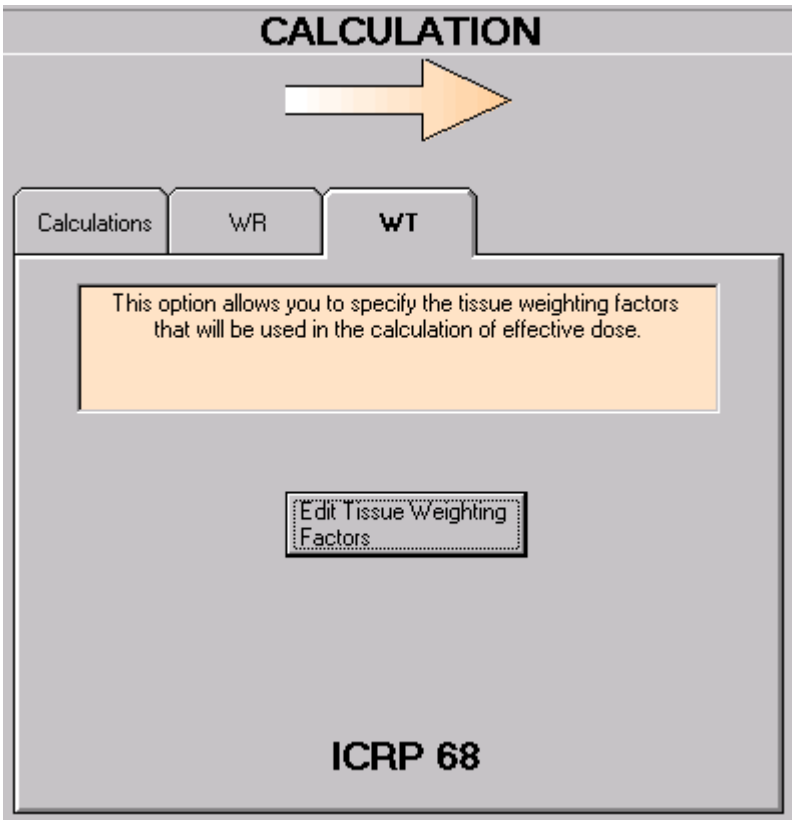


Figure 5.26. Selection of **ICRP60/68** tissue weighting factors.

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.

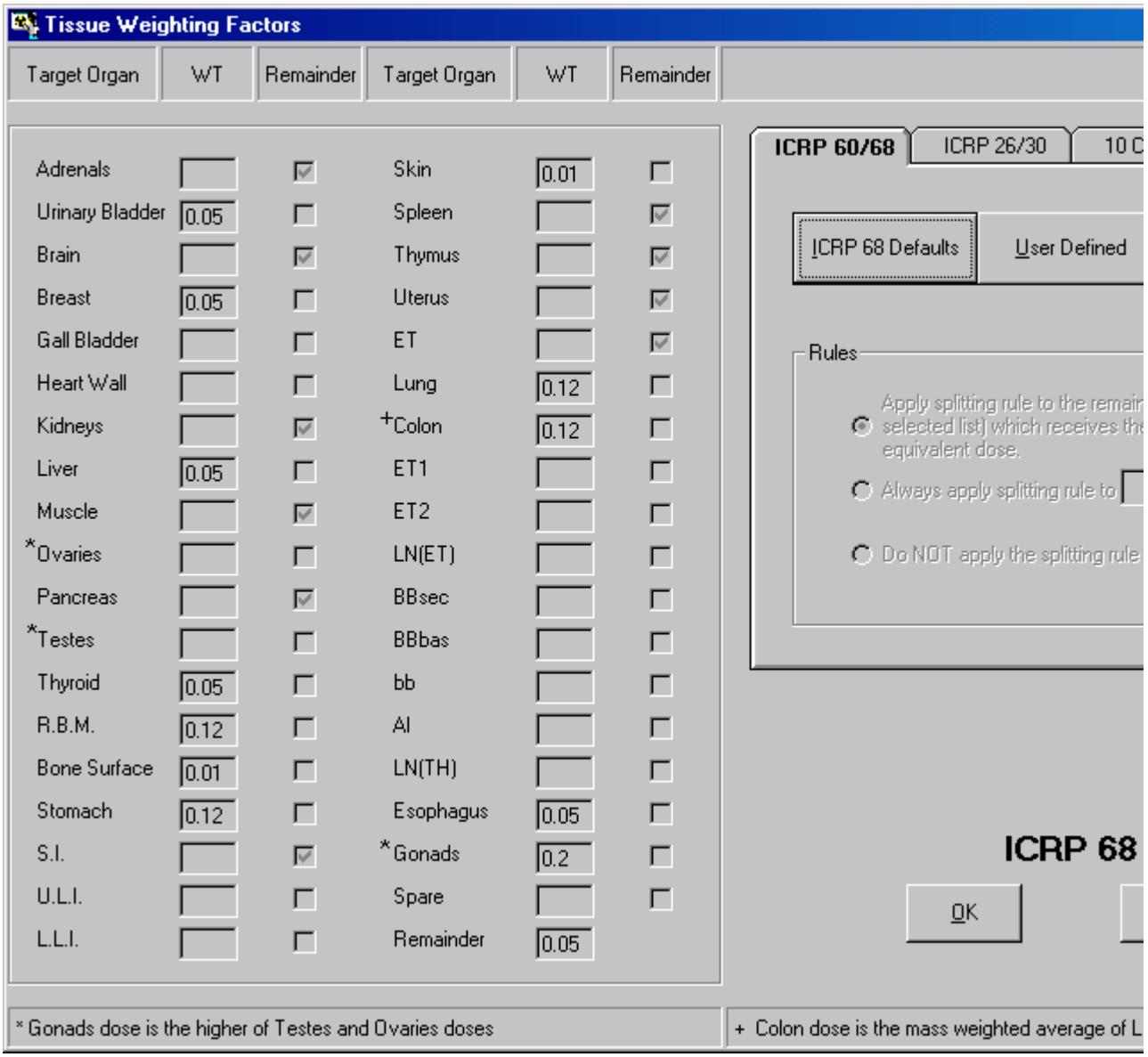


Figure 5.27. Selection of **ICRP60/68** values for the tissue weighting factors and **ICRP60/68** remainder tissue rules.

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**.

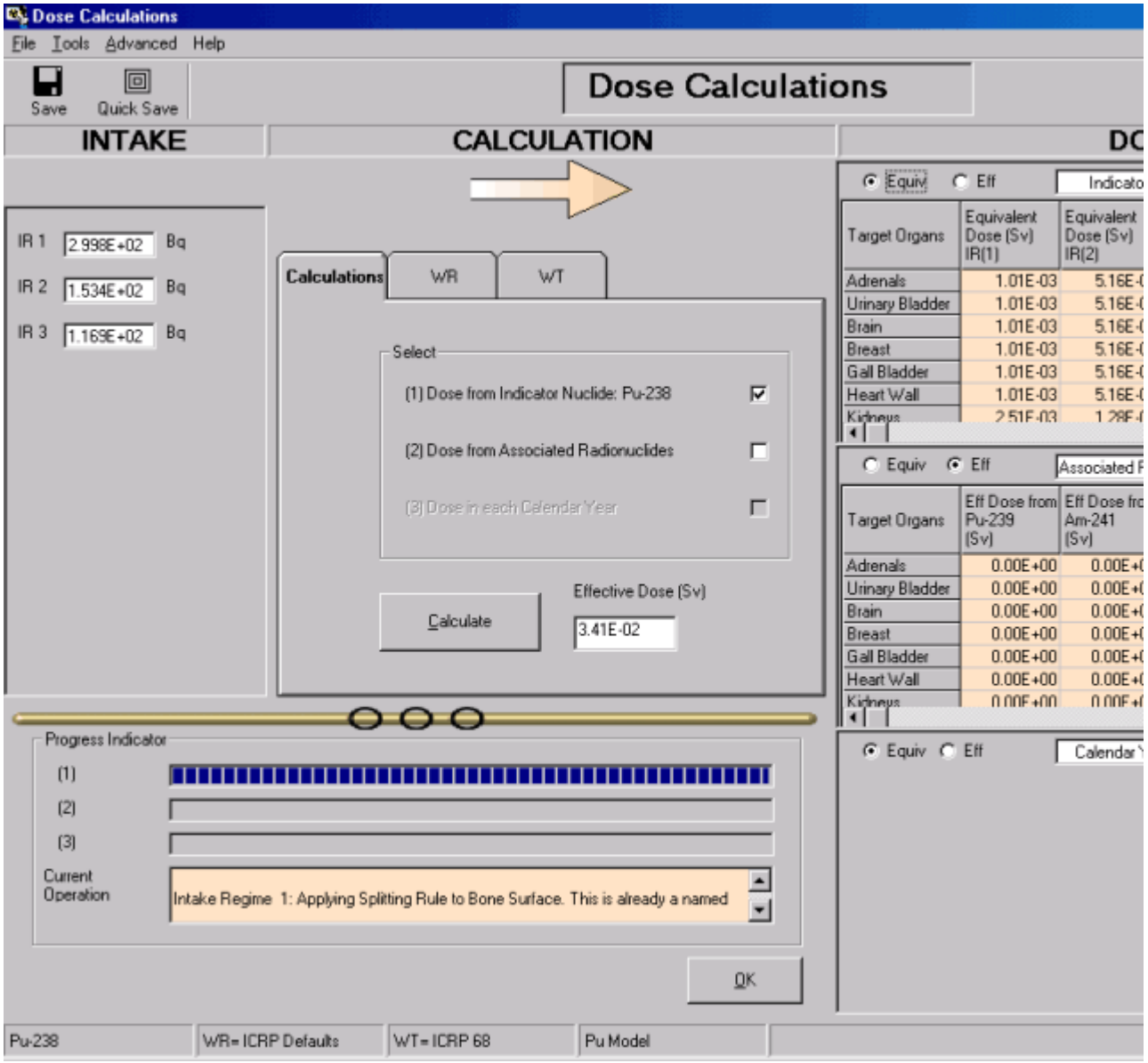


Figure 5.28. Calculated values of **Equivalent Dose** (for the **Indicator Radionuclide**).

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).

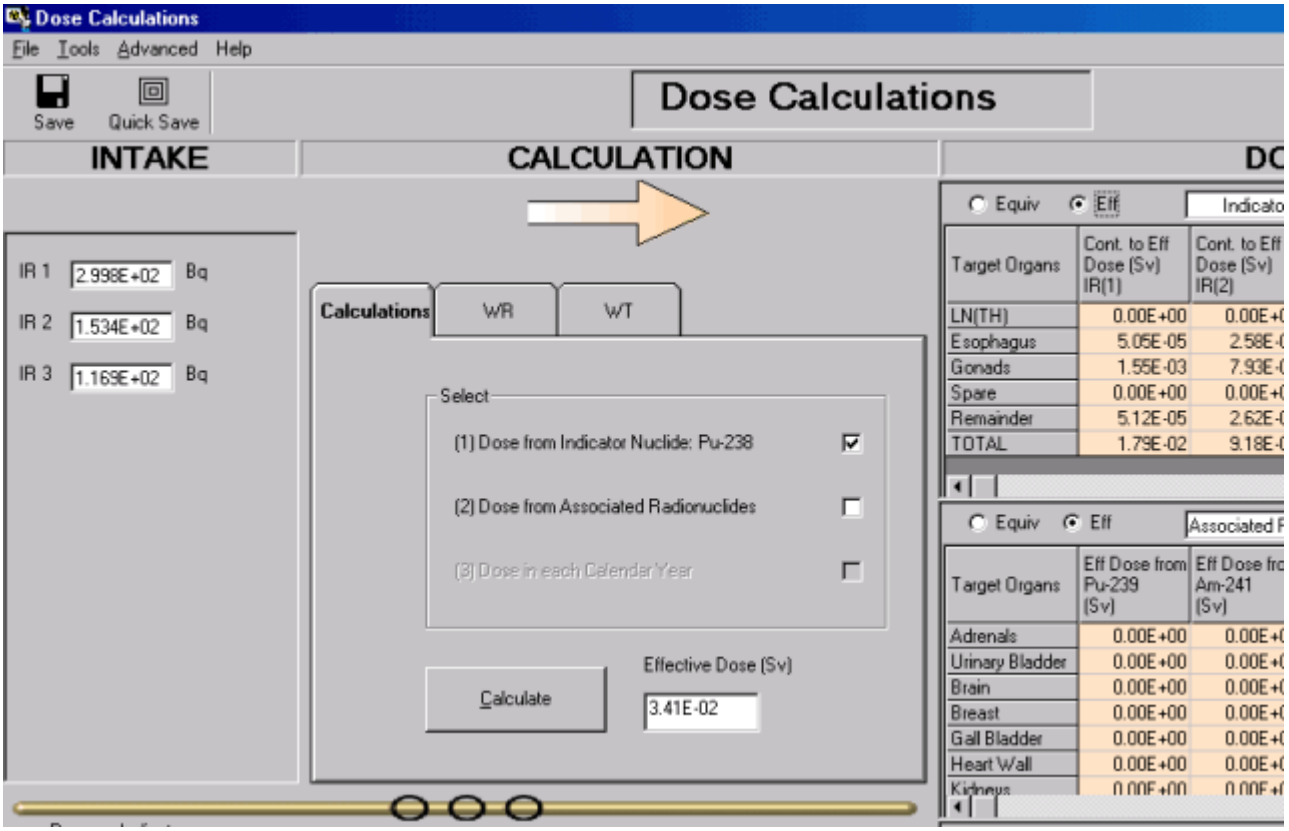


Figure 5.29. Displaying the **TOTAL Effective Dose** resulting from each intake (and the contributions from each target organ).

The values of **Effective Dose** that are calculated to result from **each separate intake** (in the **multiple intakes** example case) are:

- E***IR1*** **= 17.9 mSv** (1.8 rem);
- E***IR2*** **= 9.2 mSv** (0.9 rem);
- E***IR3*** **= 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 Optimizing the Intake Estimation), 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 Associated Radionuclides are calculated at the same time as those from the **Indicator Nuclide** - see Dose Results Windows. 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**).
2. *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 "C**alculate**" *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 multiple 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 Case of Wound Uptake - requires Add-On 5.
- Calculations involving the estimation of errors on calculated values of intake see Case Evaluating Errors on Intake - requires Add-On 6.
- Calculation involving Bayesian analysis of intake see Case Using Bayesian Analysis - requires Add-On 7.
- Calculation involving Case Implementing Tritium Tool - 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 Dose Calculations for Causation - requires Add-On 9.
- Calculation using external measurements of ^{241}**Am** activity as an indicator of plutonium activity in the lungs see Case of Am-241 In-growth - requires Add-On 10.
- Calculation using the statistics package to evaluate an intake see Case Using Statistics Package - 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 IAEA (1999) - see their Annex IV Case 3. The data are whole-body activity measurements of 60Co 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 24th, 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, 1988	**790**
May 16, 1988	**482**
August 11, 1988	**358**
November 29, 1990	**78**
February 19, 1992	**35**

- View **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. Select the Indicator Nuclide - in the Main Screen.
2. Define the Reference Date - in the Main Screen.
3. Select the Reference Activity Units - in the Main Screen.
4. Select the Bioassay Model and other required Model Parameters - in the Main Screen.
5. Define the Intake Regime (IR1) - in the Main Screen.
6. Select - in the Bioassay Calculations screen - the Bioassay Quantity as "Whole body" (for display in the top Bioassay Quantity window).
7. Enter the bioassay data - using the data entry "tool" in the Bioassay Quantity window.
8. Graph the bioassay data - using the graph set up "tool" in Bioassay Quantity 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 multiple intakes with unknown intake parameters (Star Function). This example demonstrates an iterative optimization of the Model Parameters.

Indicator Nuclide for Single Intake

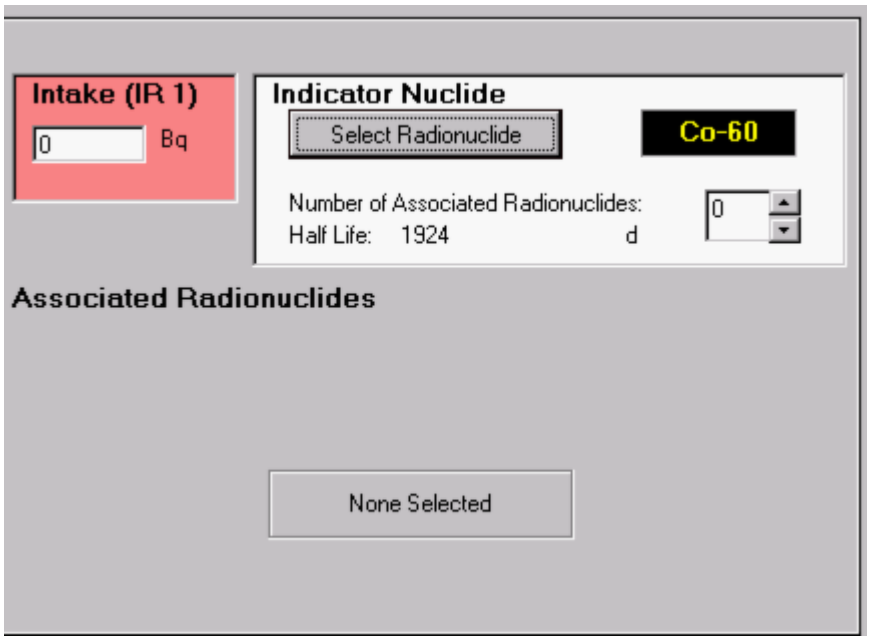


Figure 4.17. **Selecting the Indicator Nuclide (60Co).**

Select **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**.**

Tip: **In this example case, we are using bioassay data to** calculate the intake**. 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 **value of** Intake **in the dialog boxes in both the** Main Screen **and** Bioassay Calculations **screen.**

This completes Step #1 **of the** single intake **example:**

- Proceed **to the next step.**
- Return **to the case description and list of steps.**

Reference Date for Single Intake

IMBA Professional **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.**

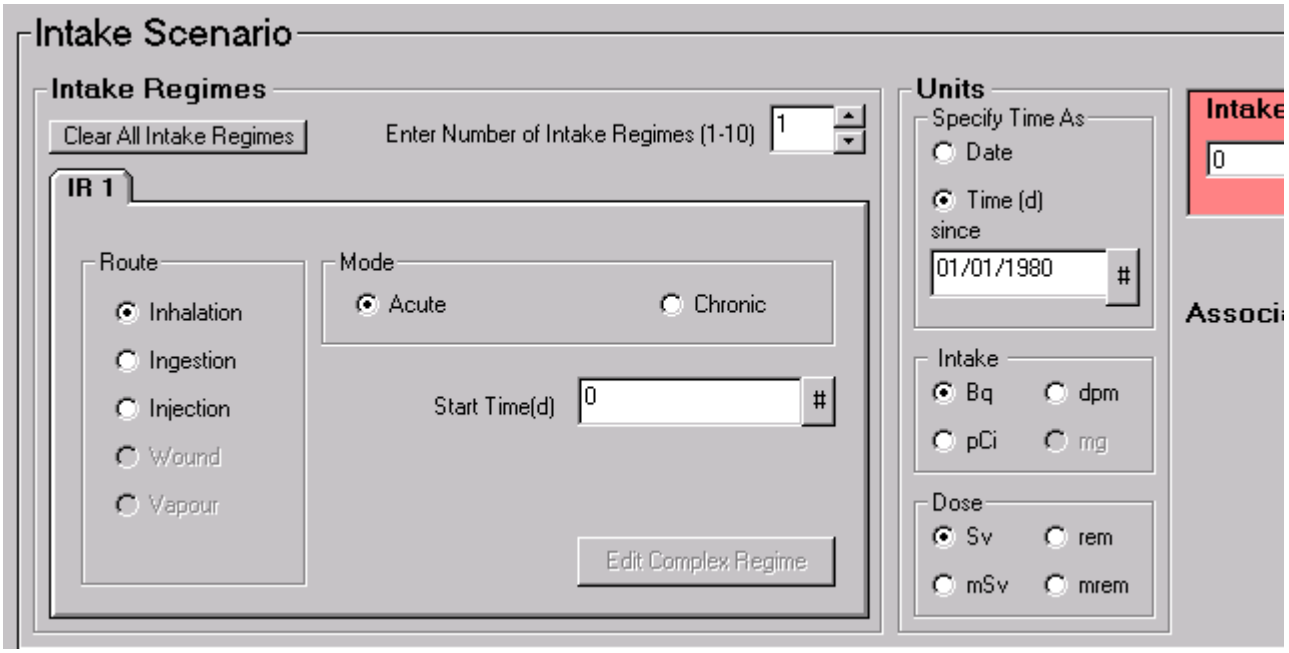


Figure 4.18. **Default "since" date loaded at start-up.**

In this example case, the intake occurred on February 24th, 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).

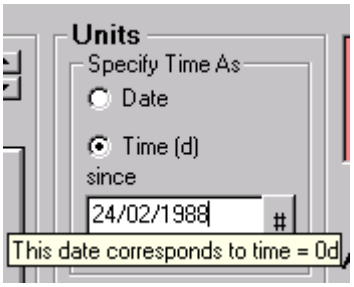


Figure 4.19. **Entering the Reference Date.**

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.

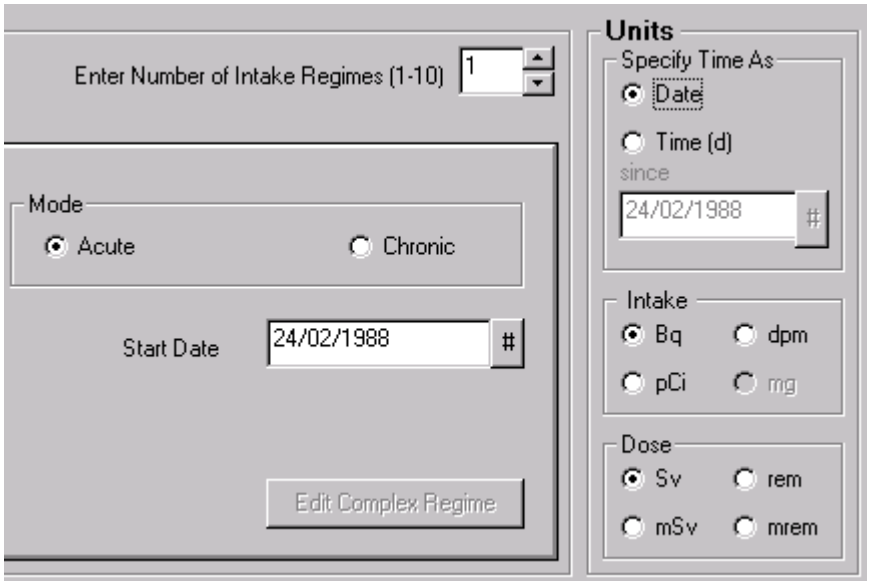


Figure 4.20. **Switching the Units of Time to Date.**

Notice that the "Start Time (d)" value of "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.**
- Return **to the case description and list of steps.**

Reference Activity Units for Single Intake

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 4.21).
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.**
- Return **to the case description and list of steps.**

Select Required Model Parameters for Single Intake

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**).**

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** IMBA Professional **will** prompt **you for each missing model definition** before **proceeding with a calculation.**

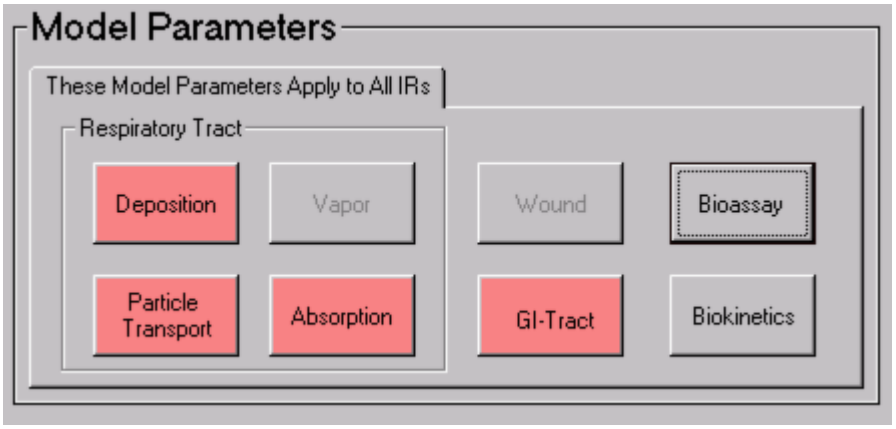


Figure 4.22. Bioassay **button for selecting the** Bioassay Model**.**

Bioassay model (for example of single 60Co intake)

For the Bioassay **model, select the "**Standard Co Model**" for** whole-body retention **(Figure 4.23):**

- select **"**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);**
- click **the "**LOAD ICRP DEFAULTS**" button;**
- click **"**OK**".**

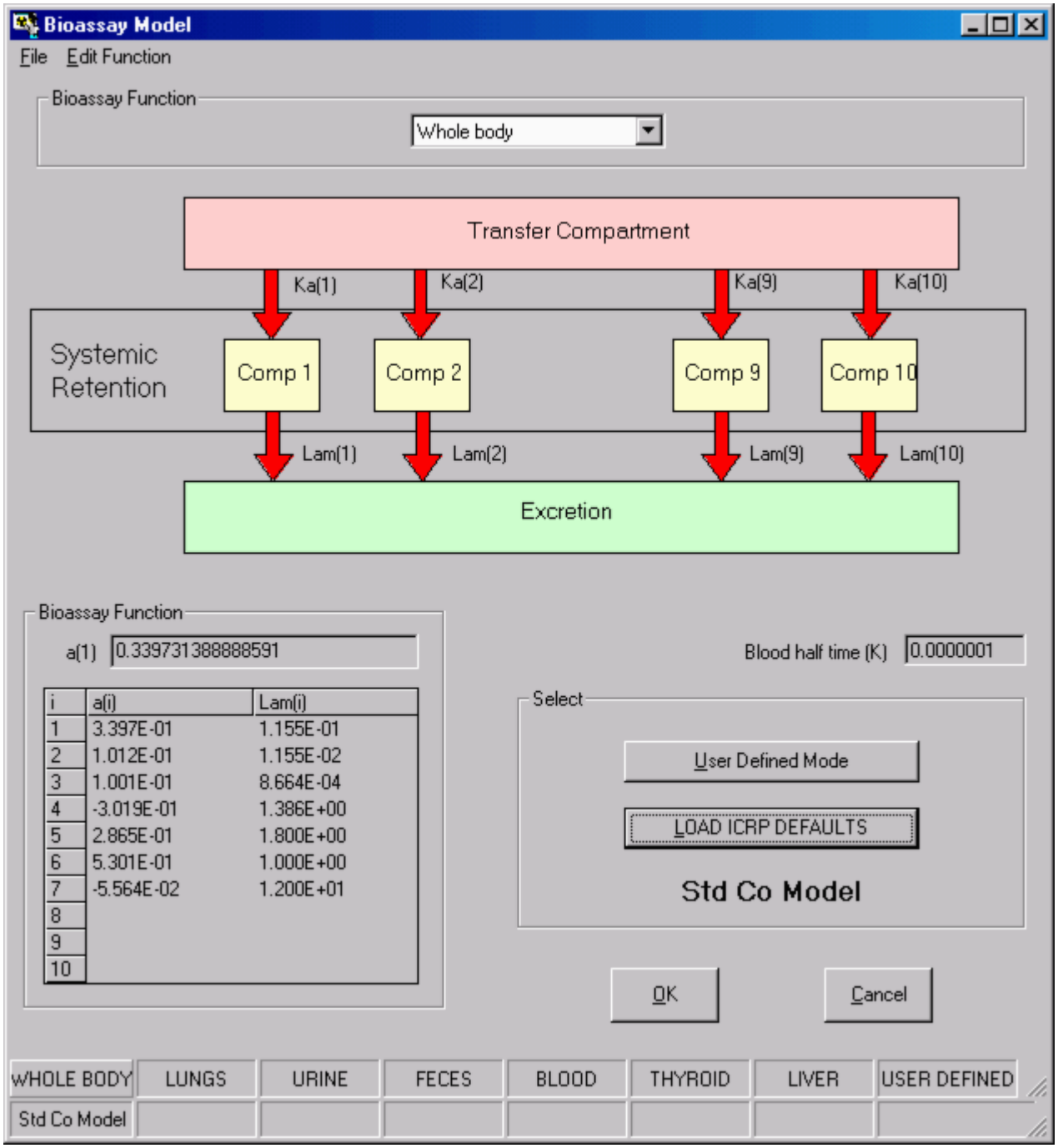


Figure 4.23. Standard Co Model **for** Whole body **selected as the** Bioassay Model**.**

Deposition model (for example of single 60Co intake)

For the Deposition model**, select the "**Light worker**" (Figure 4.24):**

- click **the "**LOAD ICRP DEFAULTS**" button;**
- **click "**OK**".**

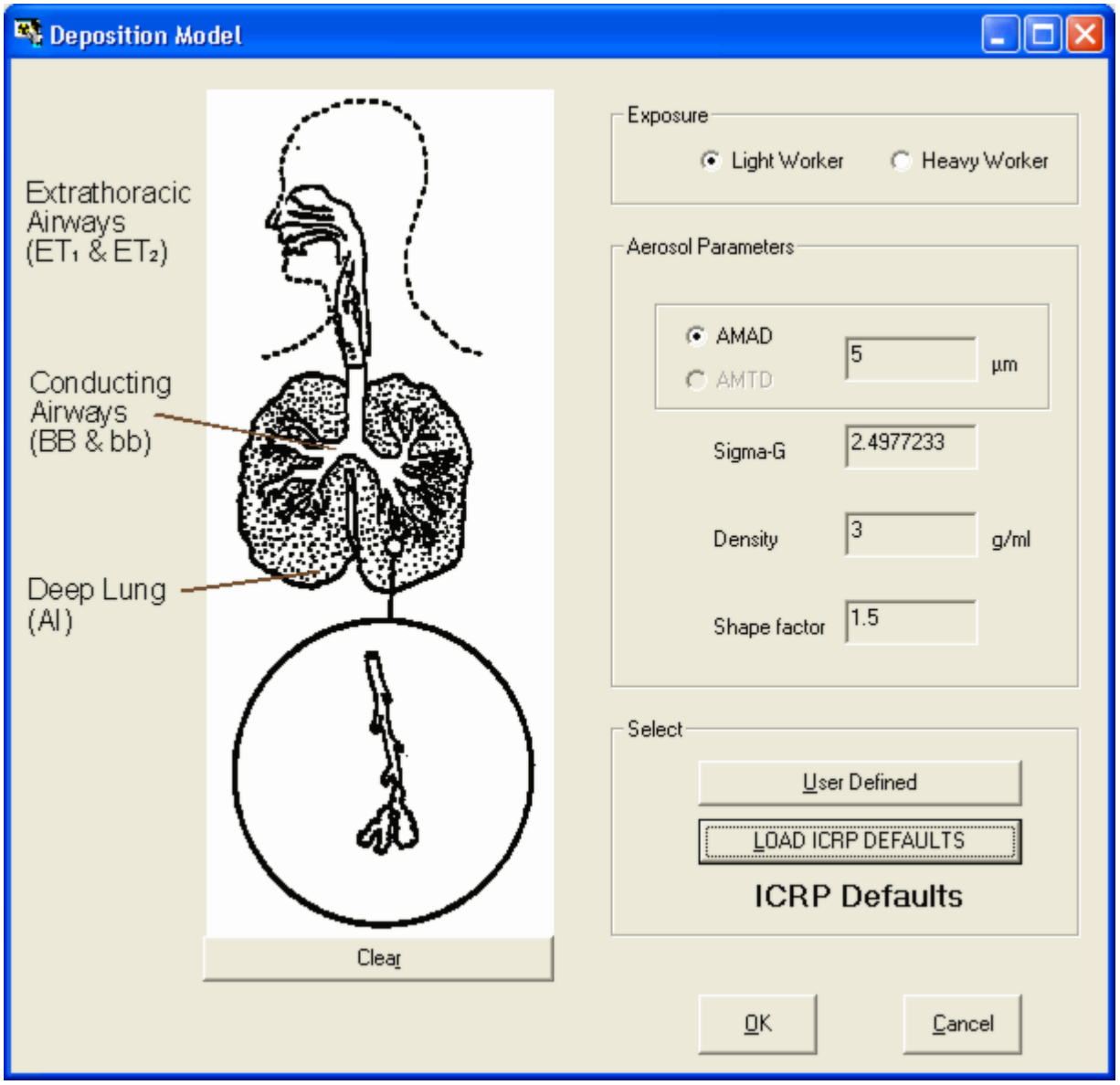


Figure 4.24. **Selecting the** Deposition Model **for a** Light worker**.**

Particle transport model (for example of single 60Co intake)

For the Particle Transport **model (Figure 4.25):**

- click **the "**LOAD ICRP DEFAULTS**" button;**
- click **"**OK**".**

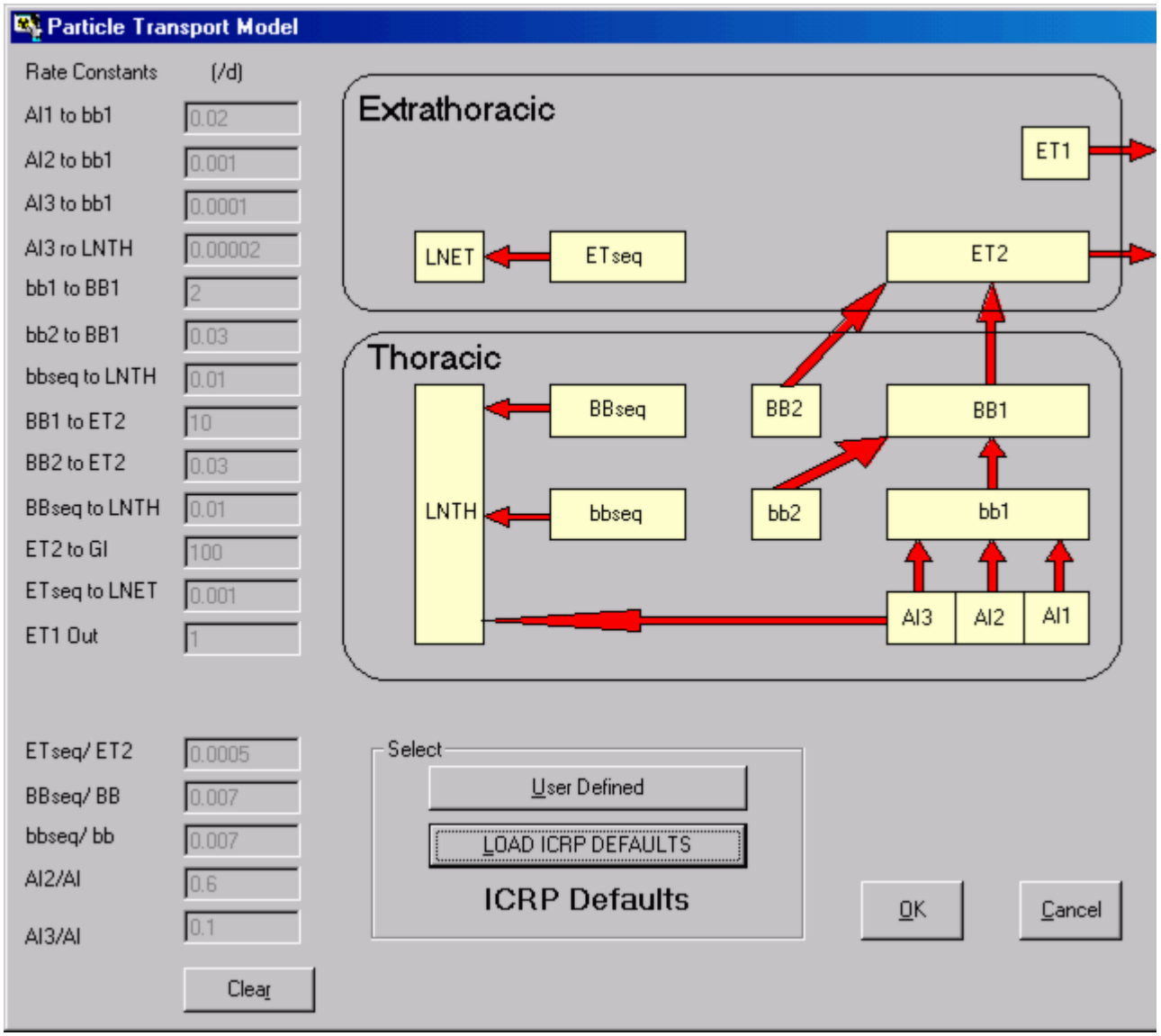


Figure 4.25. **Selecting the** ICRP Default Particle Transport Model**.**

Absorption model (for example of single 60Co intake)

For the Absorption **model, select the** Type M ICRP Default **model (Figure 4.26) - see** Cobalt Biokinetic Model **(**Technical Basis Section**):**

- click **the "**Type M**" button;**
- click **"**OK**".**

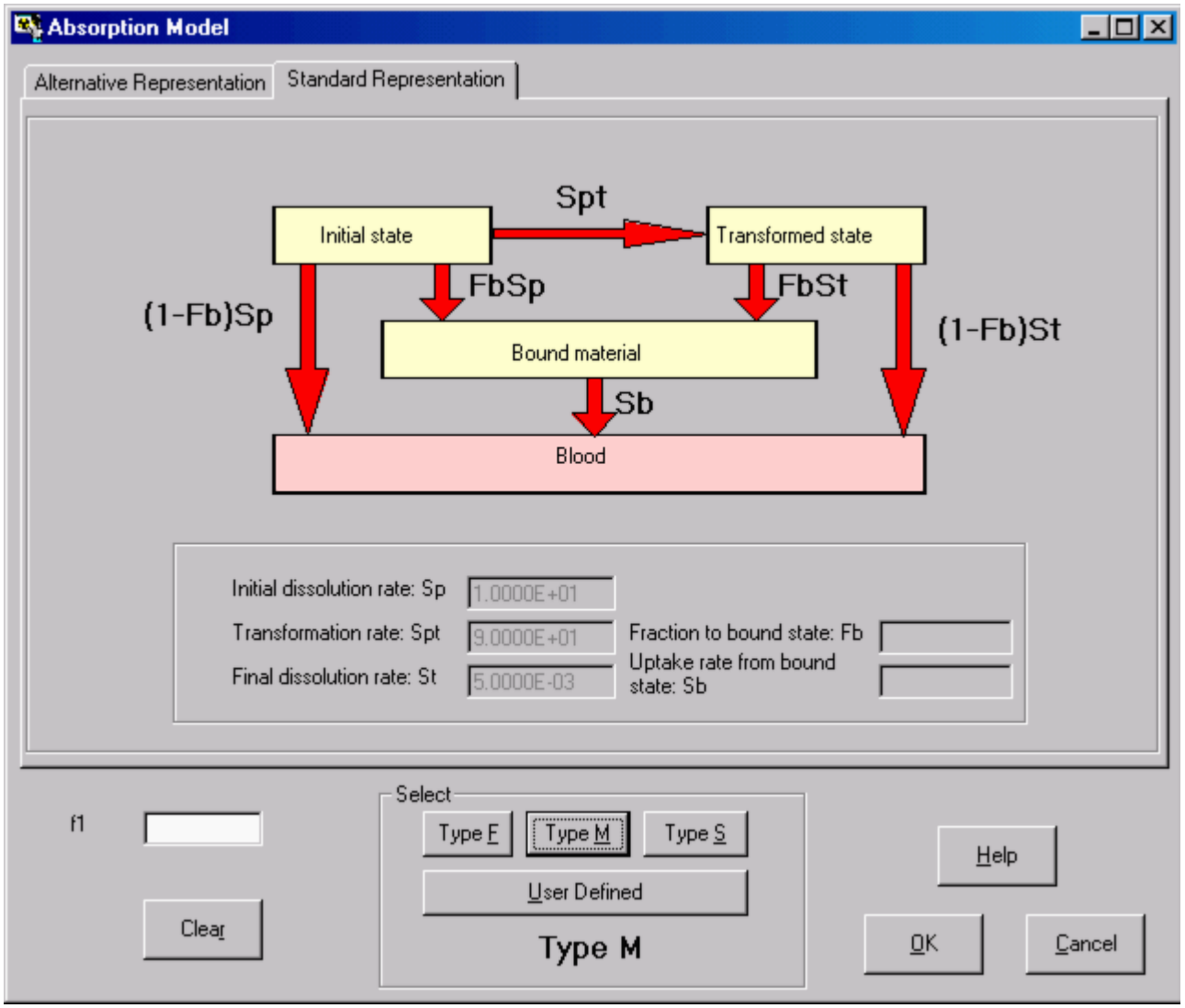


Figure 4.26. Selecting the Type M Absorption Model.

To **select** an appropriate (ICRP-recommended) value of f_1:

- **click** the "Help" button (Figure 4.26);
- **select** the "Abs.: M" row (Figure 4.27);
- **click** "OK".

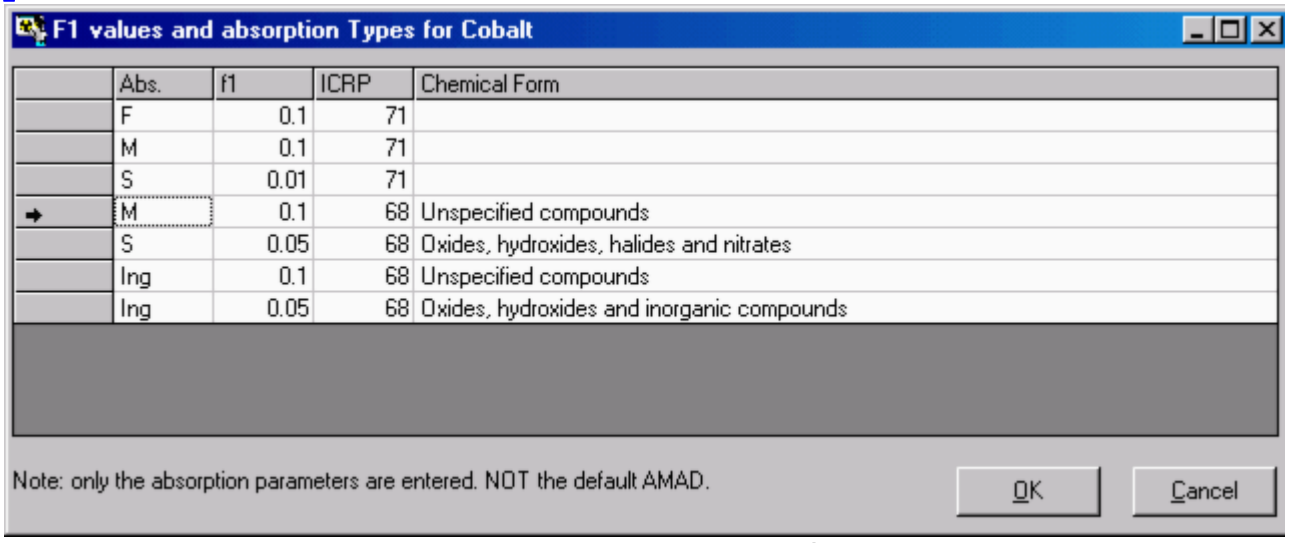


Figure 4.27. **Selecting the ICRP-recommended value of f_1.**

GI-Tract model (for example of single 60Co intake)

For the GI-Tract model, select LOAD ICRP DEFAULTS (Figure 4.28):

- **click the "LOAD ICRP DEFAULTS" button;**
- **click "OK".**

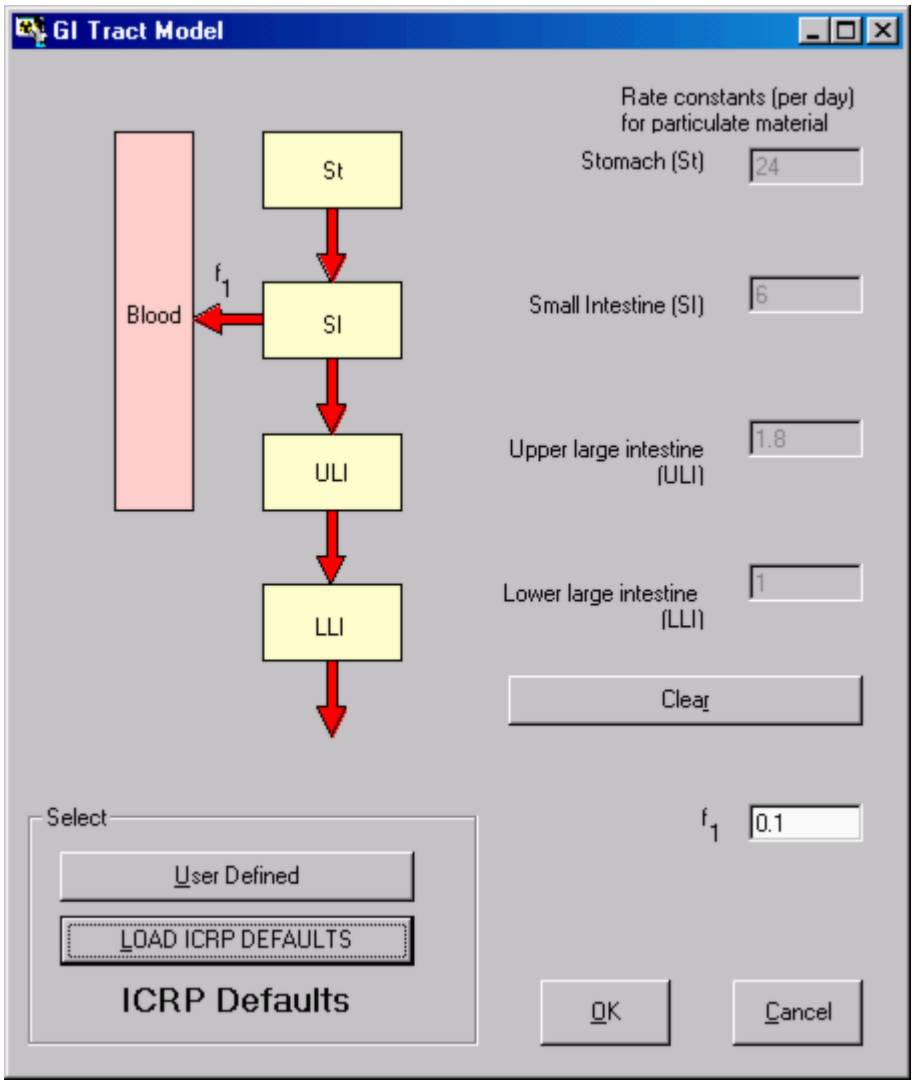


Figure 4.28. Selecting the ICRP Default GI-Tract Model.

This completes the definition of ALL Model Parameters required to calculate the Intake of 60Co in the IAEA (1999) 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 f_1.**

This completes Step #4 of the single intake example:

- **Proceed to the next step.**
- **Return 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).

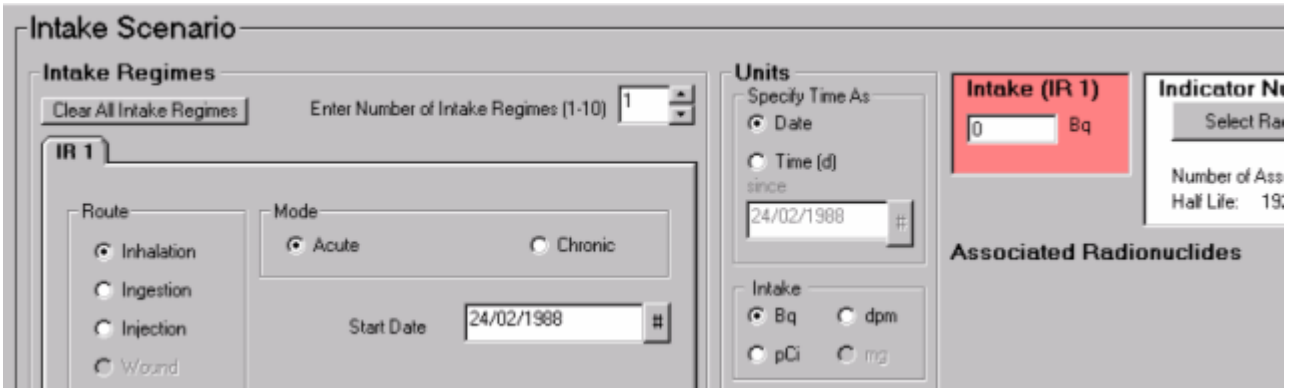


Figure 4.29. **IR1** defined (by default) as **Acute Inhalation**.

This completes **Step #5** in the **single intake** example:

- Proceed to the next step.
- Return to the case description and list of steps.

Select Whole Body Activity as Bioassay Quantity

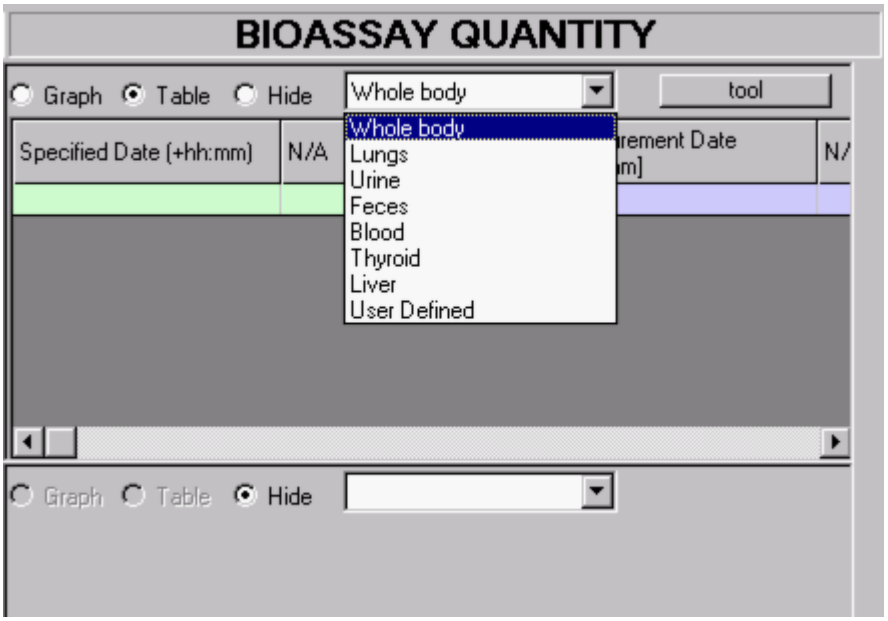


Figure 4.30. Drop-down **Bioassay Quantity** list box.

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:

- Click 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), select "**Whole body**" from the drop-down list box (Figure 4.30).

This "opens" 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**).

Note: When it is first opened, the data **Table** in the **Bioassay Quantity** window has only one row. This window is designed to display data values, and NOT for data entry. Since no data have yet been entered, there are no data to display at this stage. The "**tool**" button opens the **Table Tool** for your selected **Bioassay Quantity**. This provides the **tools** that you will use to enter (and/or edit) the **bioassay data** - in the next step.

Tip: Use the **scroll bar** below the open **Bioassay Quantity** window to view additional columns (to the right) that are related to **measured bioassay data**.

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

IMBA Professional 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 Table Tool. This will enable you to enter (and/or edit) the **whole-body activity** data.

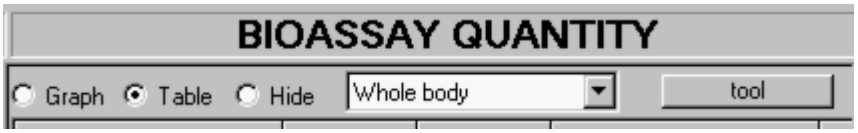


Figure 4.31. Bioassay Quantity window set to hold "**Whole body**" data - with active "**tool**" button.

- See Using the Table Tool (**Step #7** in the **single intake** example):
- Return to the case description and list of steps.

Graphing the Data

IMBA Professional 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 Graph Tool.

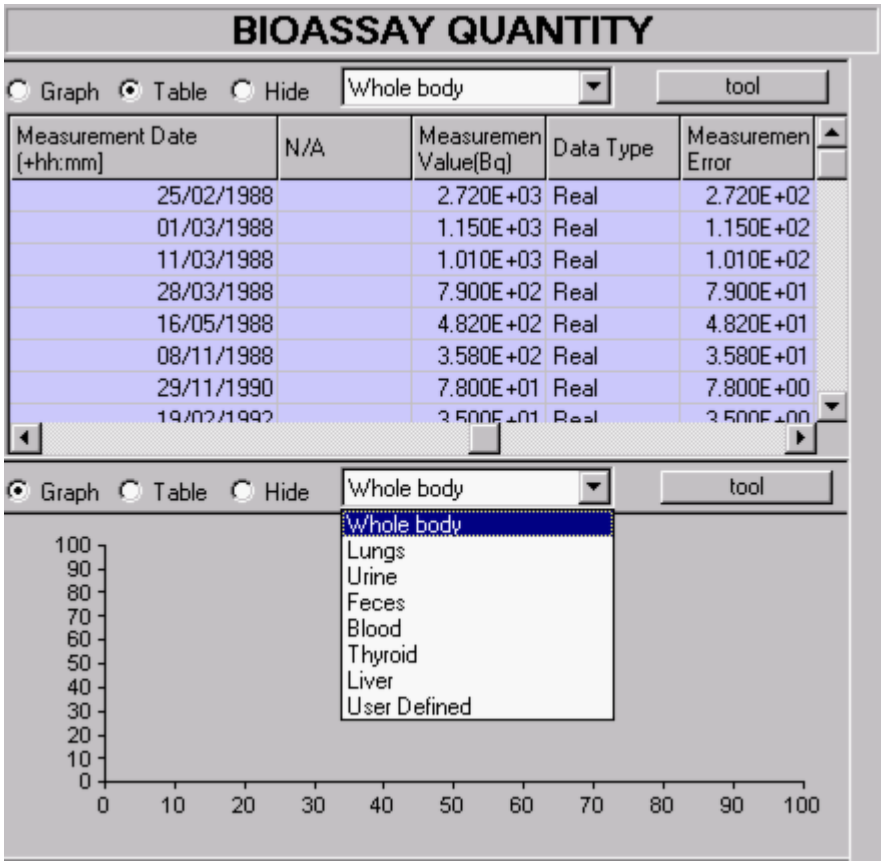


Figure 4.32. Opening a **Graph** window for the **Whole body bioassay quantity**.

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):
- Return 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**.

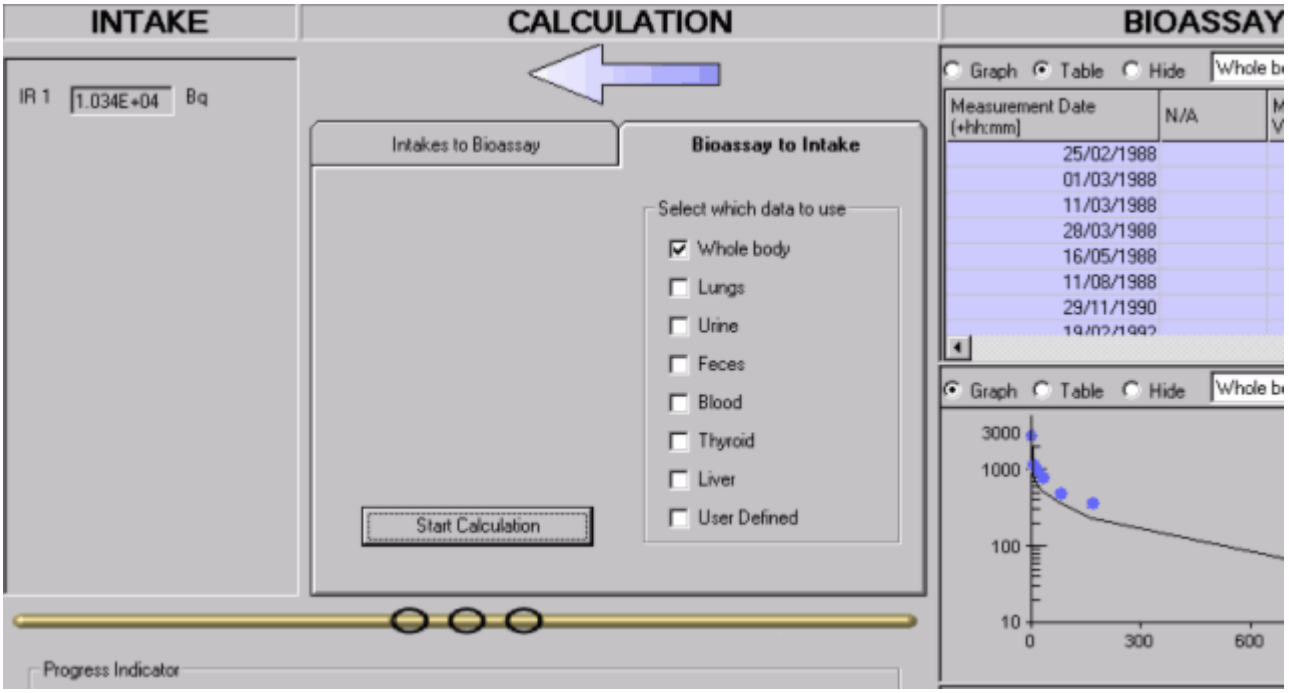


Figure 4.33. Calculated **Intake** amount with corresponding **best fit** to the data.

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 reviewing, and if necessary making reasonable changes to, one or more of the assumed **Model Parameters** (see Improving the Data Fit).

Improving the Data Fit

In this example case (single intake of 60Co by inhalation), the **fit** to the data is clearly improved by varying the assumed aerosol Activity Median Aerodynamic Diameter (AMAD) from the 5-µm default value recommended by **ICRP** - to an **AMAD of 1 µm** (with sg = **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**.

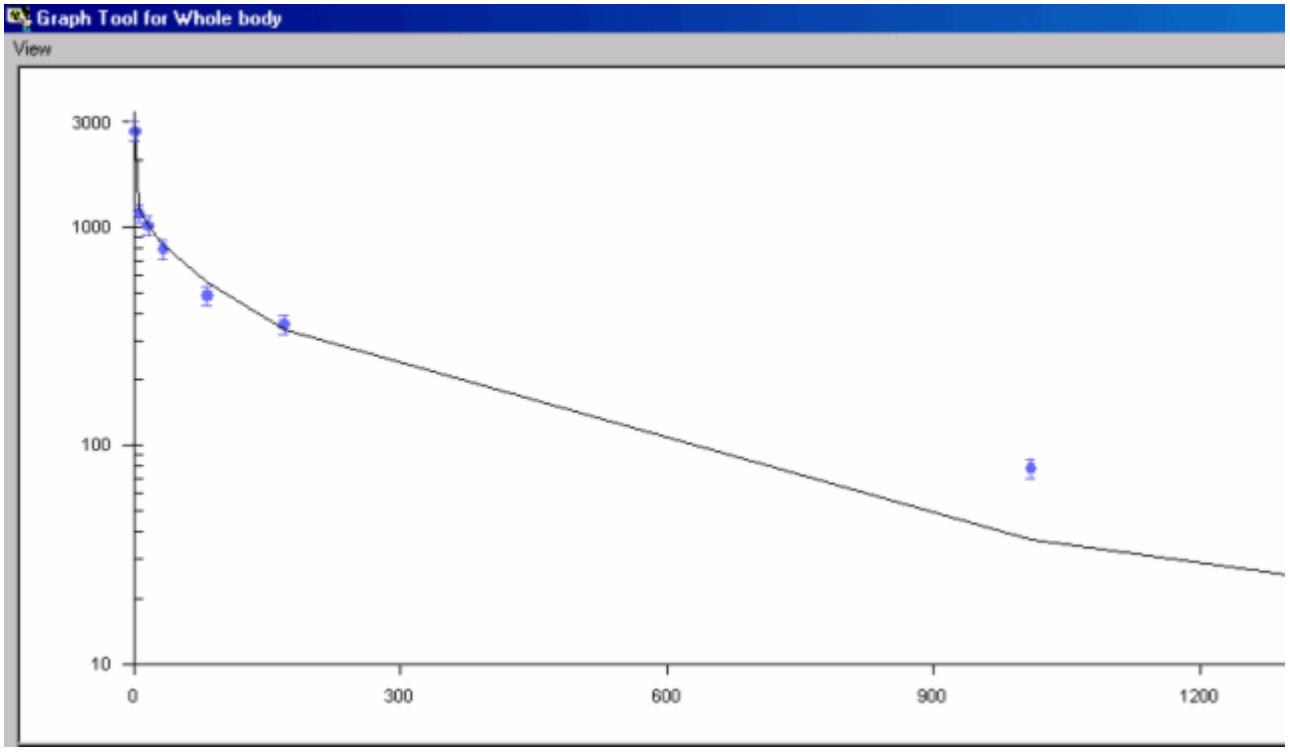


Figure 4.34. Improved data fit obtained by **changing** the value of aerosol **AMAD**.

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:

- Return to the case description and list of steps.
- Follow a more complex example involving the calculation of multiple intakes 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 Miller et al. (1999) - see their Appendix 2. The data are urinary excretion measurements of 238Pu in 37 samples taken from March 15th, 1968 through May 28th, 1979. The worker concerned had several intakes (by inhalation) of mixed 239Pu/238Pu:

1. In the mid-1950s - and assumed for analysis purposes to have occurred on June 9th, 1945.
2. On May 8th, 1971.
3. 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 21st, 1972 (mid-way between the prior- and post-intake sample dates). No information about the physical properties of the 239Pu/238Pu 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-1) ± 1 SD
March 15, 1968	1 ± 0.9
June 13, 1968	1.8 ± 0.9
September 13, 1968	0.3 ± 0.9
December 13, 1968	4.8 ± 2
March 20, 1969	0 ± 0.9
December 18, 1969	0 ± 0.9
March 19, 1970	0 ± 0.9
June 18, 1970	0.5 ± 0.9
September 24, 1970	0.5 ± 0.9
March 18, 1971	1.2 ± 0.7
June 29, 1971	4.1 ± 0.7
September 22, 1971	2.2 ± 0.5
September 18, 1972	12.9 ± 1.6
December 8, 1972	7.5 ± 1.1
March 15, 1973	2 ± 0.4
June 27, 1973	3 ± 0.6
September 17, 1973	2.7 ± 0.5
December 21, 1973	3.1 ± 0.6
March 21, 1974	1.1 ± 0.4
June 17, 1974	3.8 ± 0.7
September 16, 1974	2.1 ± 0.5
December 18, 1974	1.5 ± 0.4
March 17, 1975	2 ± 0.4
June 16, 1975	1.1 ± 0.4
September 19, 1975	0.8 ± 0.4
December 12, 1975	1 ± 0.4
March 17, 1976	1.2 ± 0.4
July 2, 1976	1.4 ± 0.4
September 12, 1976	1.4 ± 0.4
December 8, 1976	0.5 ± 0.4
June 24, 1977	1 ± 0.4
September 15, 1977	0.4 ± 0.4
September 1, 1978	2.2 ± 0.5
October 20, 1978	0.3 ± 0.4
January 18, 1979	0.9 ± 0.4
April 20, 1979	0.4 ± 0.4
May 28, 1979	1.6 ± 0.4

- View list of steps for estimating multiple intakes.

Steps in Multiple Intake Calculation - Making 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 Reference Date - in the **Main Screen**.
3. Select the Reference Activity Units - 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 Date of Each Intake - in the **Main Screen**.
8. Select - in the **Bioassay Calculations Screen** - the Bioassay Quantity as "**Urine**" (for display in the top **Bioassay Quantity** window).
9. Enter the bioassay data - using the data entry "**tool**" in the **Bioassay Quantity** window.

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.

Tip: When you are familiar with the operation of IMBA Professional, you will find that the initial **Steps 1 through 10** can be performed in any order (to suit your own working style) - just as long as ALL of the parameter and data values have been defined BEFORE you click the "**Start Calculation**" button.

Important: If you have missed a step, IMBA Professional will prompt you to carry this out - but only if the required data values are **missing** (null).

Warning: It is your responsibility to check that ALL of the model parameters have been set to your specific requirements. IMBA Professional will use whatever values are in memory when you click the "**Start Calculation**" button.

Indicator Nuclide for Multiple Intakes

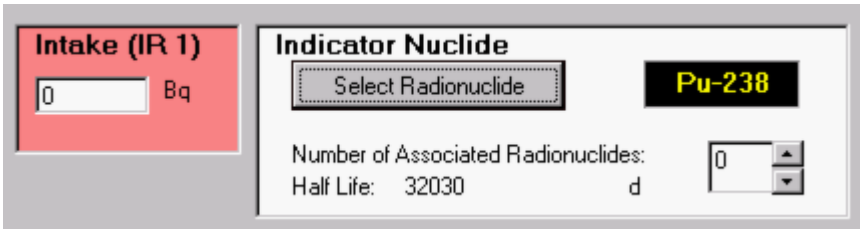


Figure 4.35. **Selecting the** Indicator Nuclide (238Pu)**.**

Select **the** Indicator Nuclide **(**238**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** 238**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

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 1**st**, 1980) is loaded at start-up.**

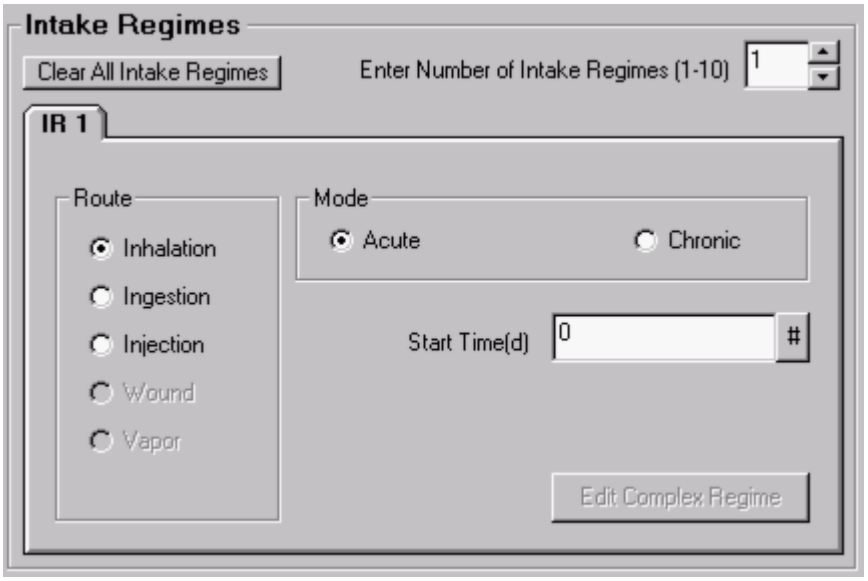


Figure 4.36. **Default "**since**" date loaded at start-up.**

In the example case, the earliest date of interest is June 9th**, 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).**

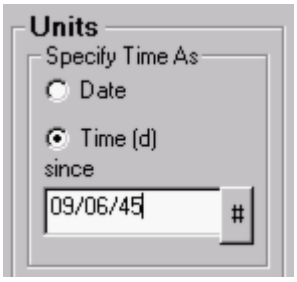


Figure 4.37. **Entering the** Reference Date**.**

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**.**

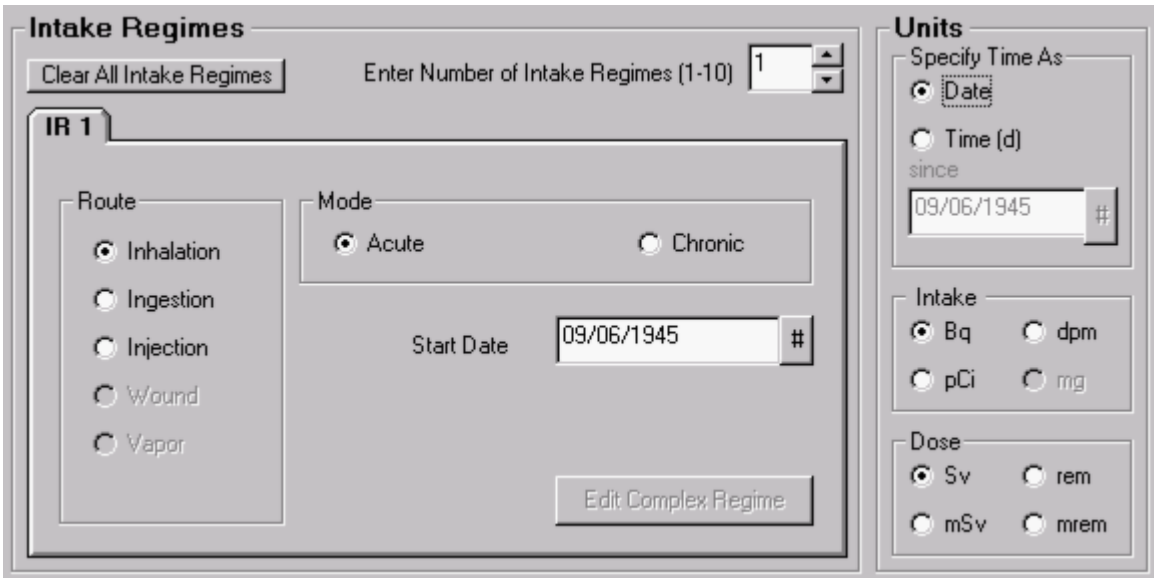


Figure 4.38. **Switching the** Units of Time **to** Date**.**

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.**

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** multiple intakes **example:**

- Proceed **to the next step.**
- Return **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-1**. Therefore, the required** Unit of Activity **is "**Bq**."**

Figure 4.39. **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 **in the** multiple intakes **example:**

- Proceed **to the next step.**
- Return **to the** case description **and list of steps.**

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**.**

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.**
- 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.**

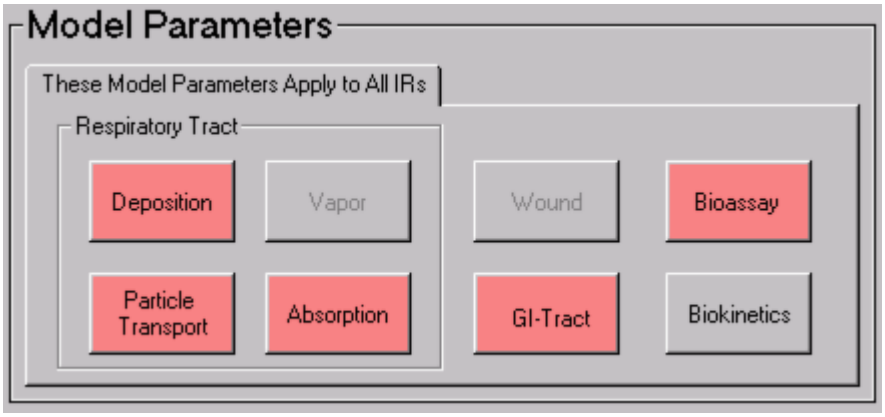


Figure 4.40. Bioassay **button for selecting the** Bioassay Model**.**

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 **"**OK**."**

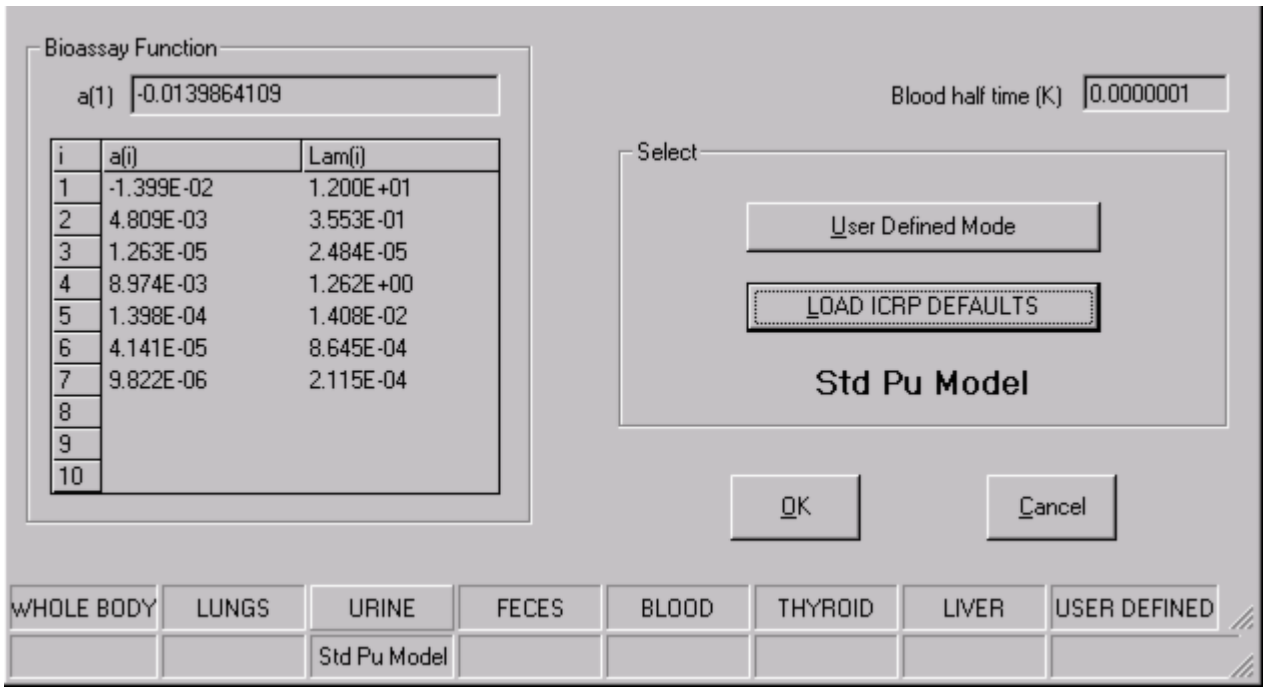


Figure 4.41. Standard Pu Model **for** Urine **selected as the** Bioassay Model**.**

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**."**

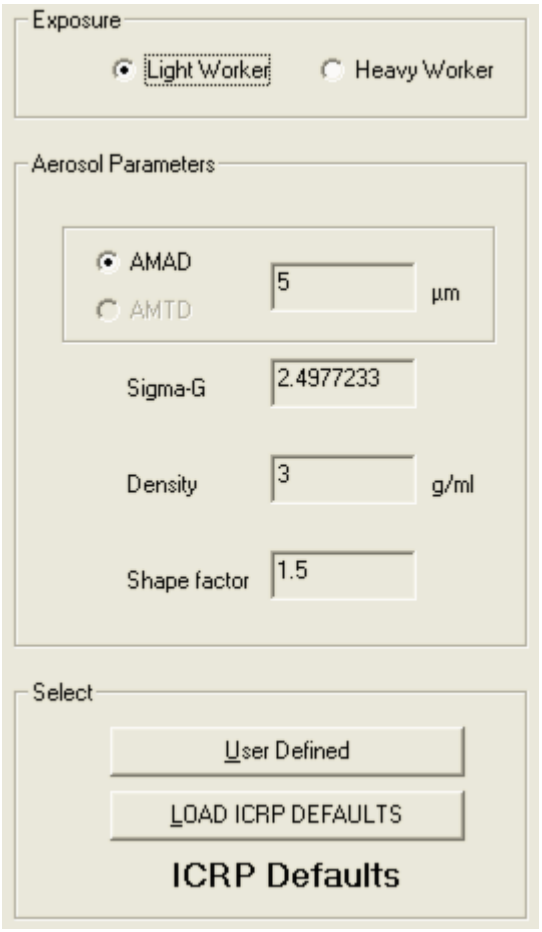


Figure 4.42. **Selecting the** Deposition Model **for a** Light worker**.**

Particle transport model

For the Particle Transport **model (Figure 4.43):**

- click **the "**LOAD ICRP DEFAULTS**"** button**;**
- click **"**OK**."**

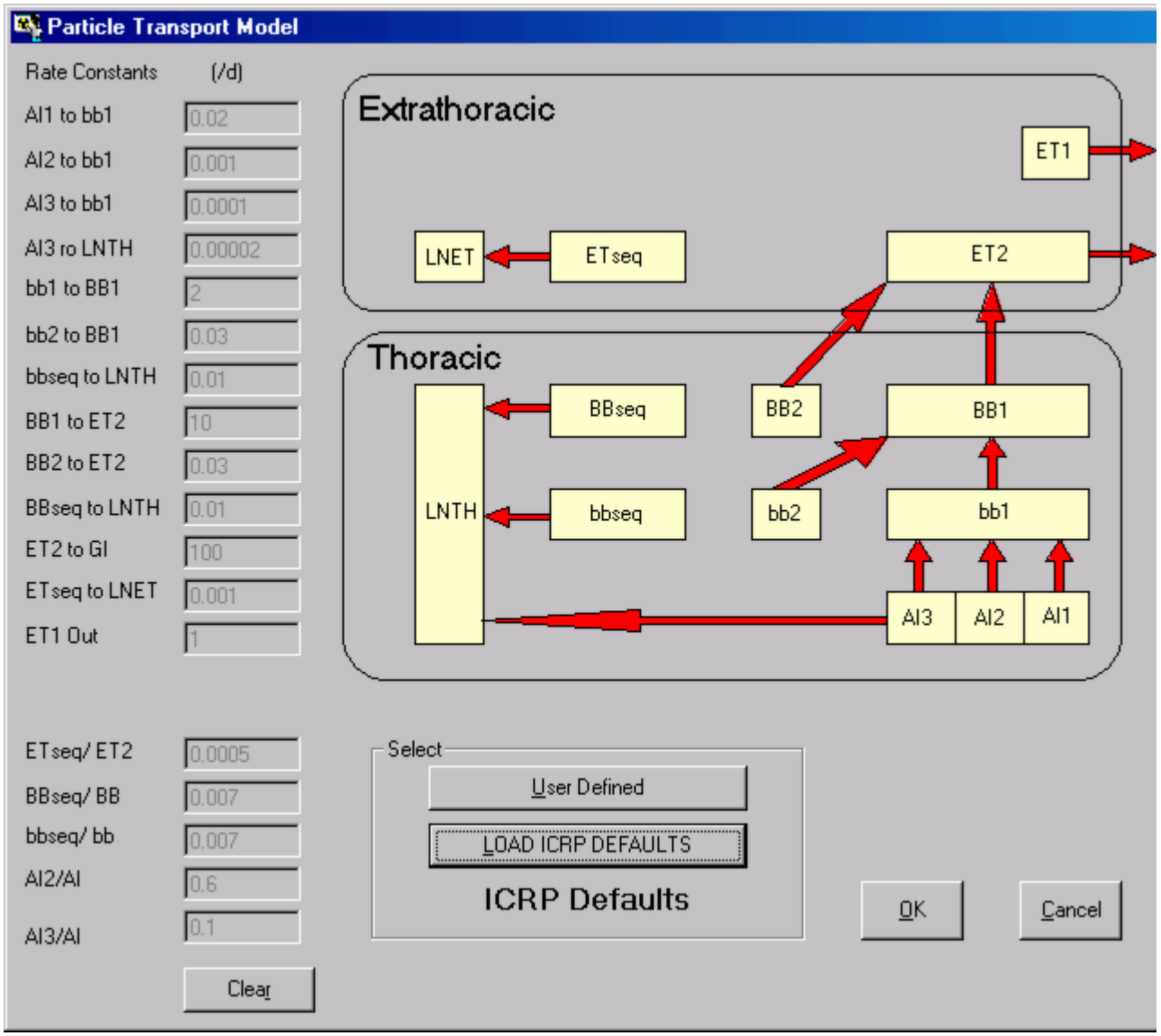


Figure 4.43. **Selecting the** ICRP Default Particle Transport Model**.**

Absorption model (for example of multiple 238Pu 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 M**"** button**;**
- click **"**OK**."**

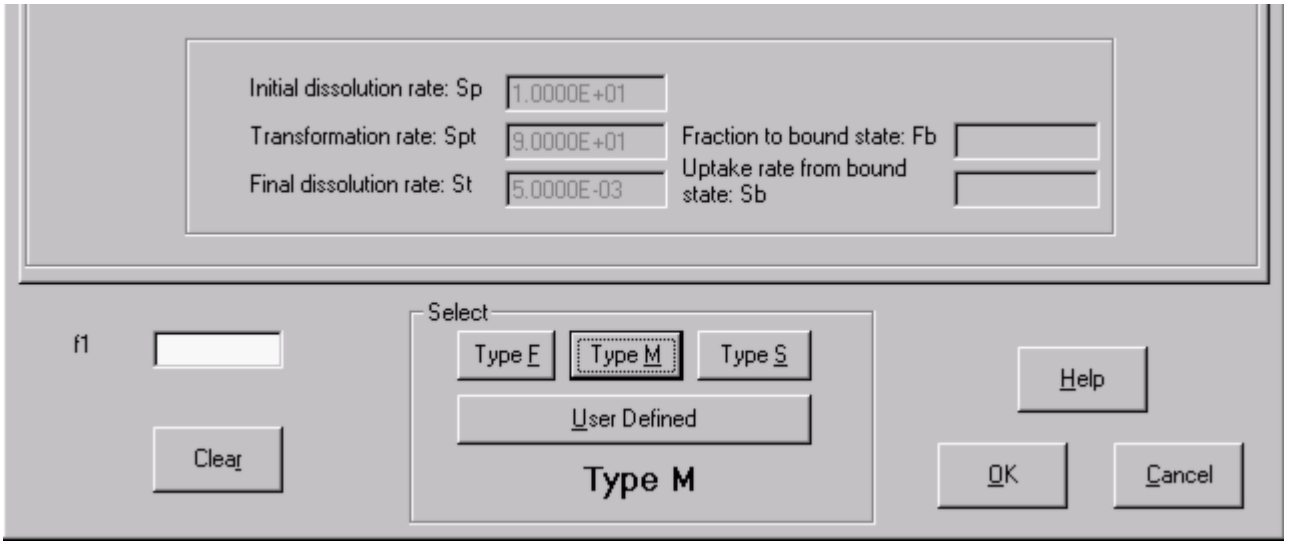


Figure 4.44. **Selecting the** Type M Absorption Model**.**

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**."**

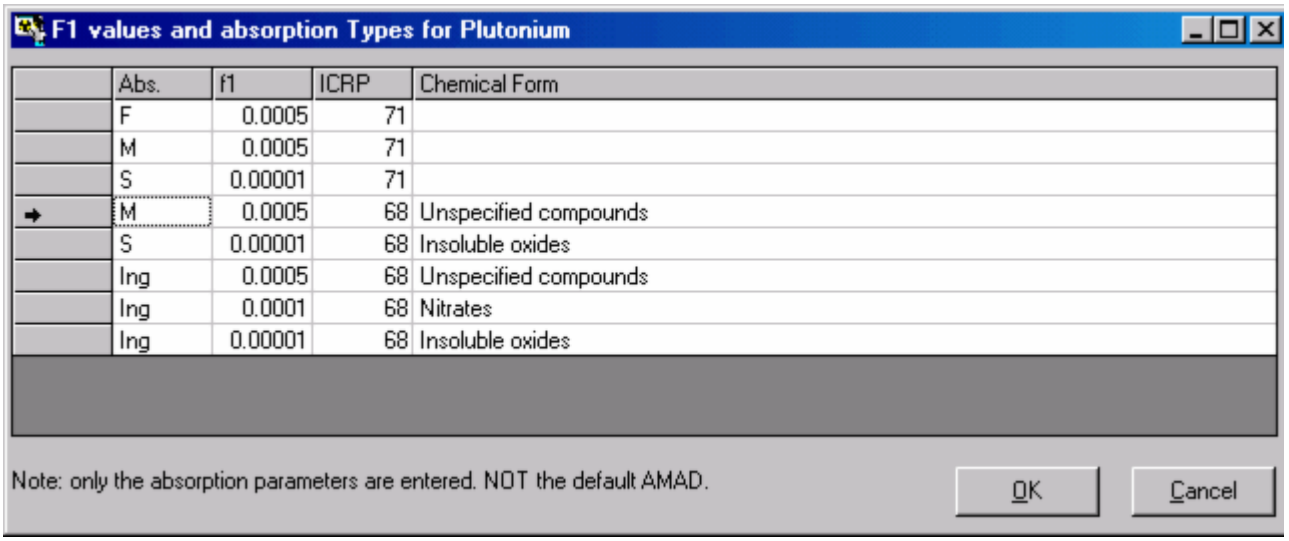


Figure 4.45. **Selecting the** ICRP-recommended **value of** f1**.**

GI-Tract model

For the GI-Tract **model,** select LOAD ICRP DEFAULTS **(Figure 4.46):**

- click **the "**LOAD ICRP DEFAULTS**"** button**;**
- click **"**OK**."**

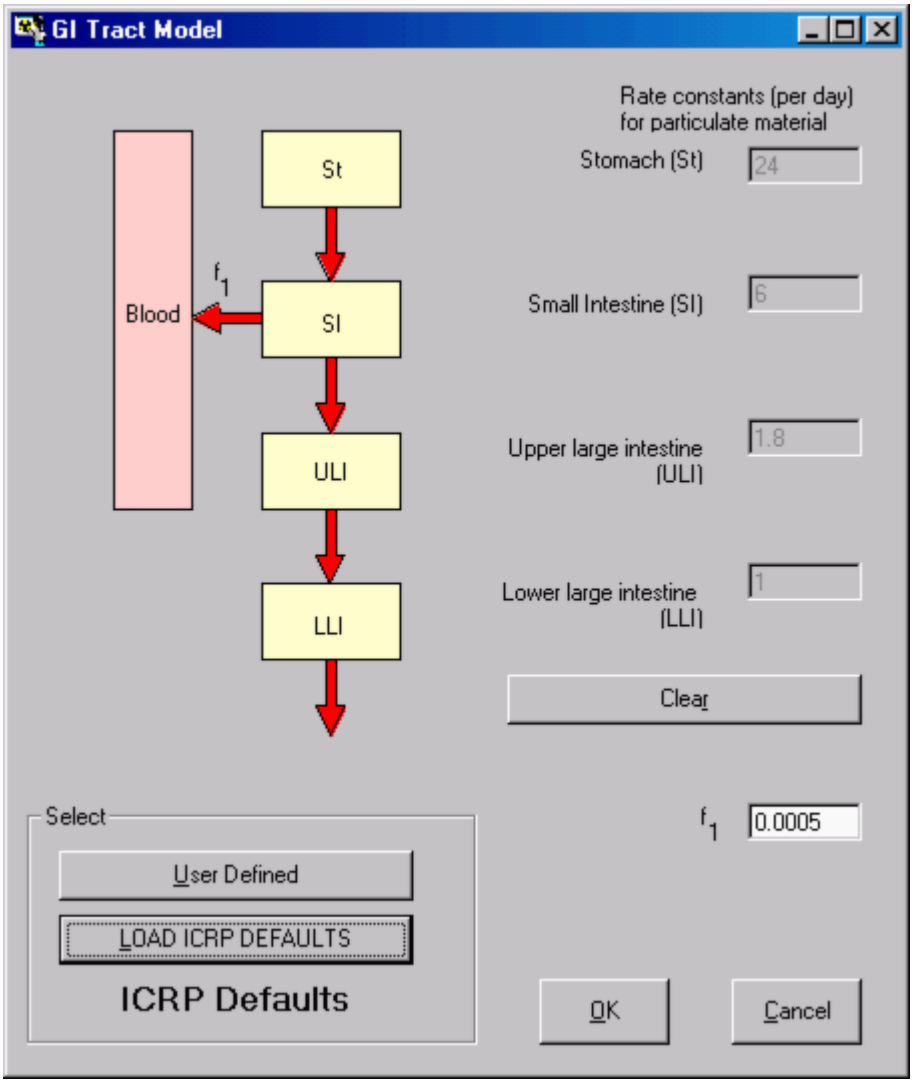


Figure 4.46. **Selecting the** ICRP Default GI-Tract Model**.**

This completes the definition of ALL Model Parameters **required to calculate the (3)** Intakes **of** 238**Pu in the** Miller at al. (1999) example case.

Key Tip: **Don't forget that 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 just the** Absorption Model **(**i.e.**, type of absorption behaviour) and the value of** f1**.**

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)

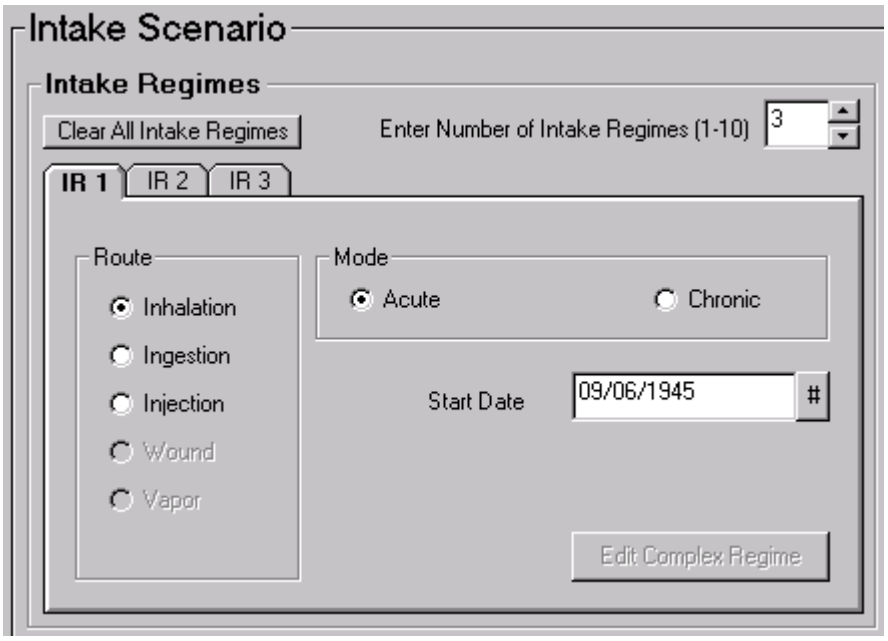


Figure 4.47. **Selecting 3 separate Intake Regimes (IRs).**

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.**
- Return **to the case description and list of steps.**

Select Independent Model Parameters

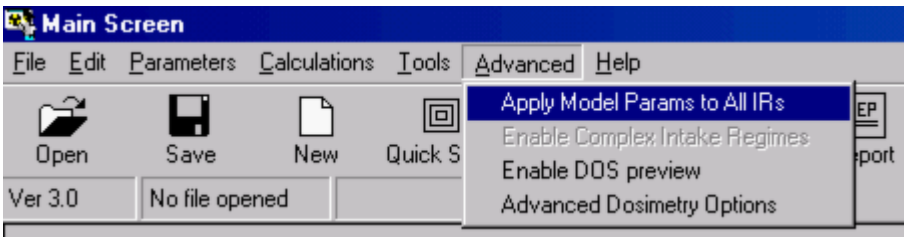


Figure 4.48. Un-checking "Apply Model Params to All IRs" in the "Advanced" menu.

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 1 Intake Regime - AND you have un-checked 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#.

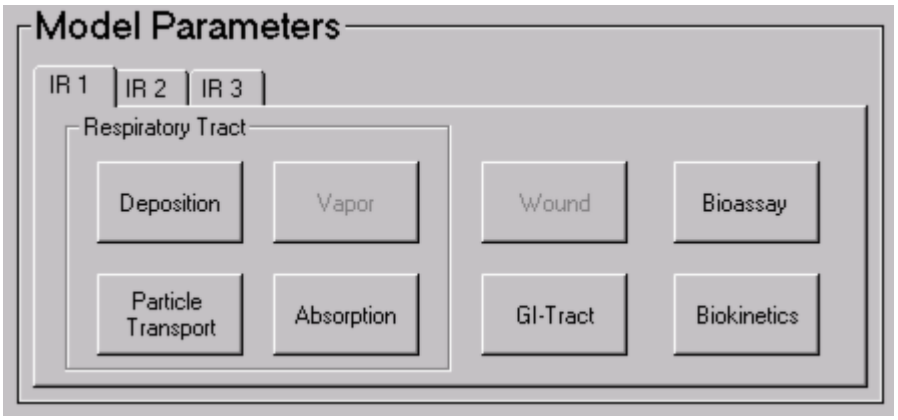


Figure 4.49. Individual IR# tabs for setting up Model Parameters specific to each IR.

This completes Step #6 in the multiple intakes example:

- Proceed to the next step.
- Return to the case description and list of steps.

Defining the Date of Each Intake

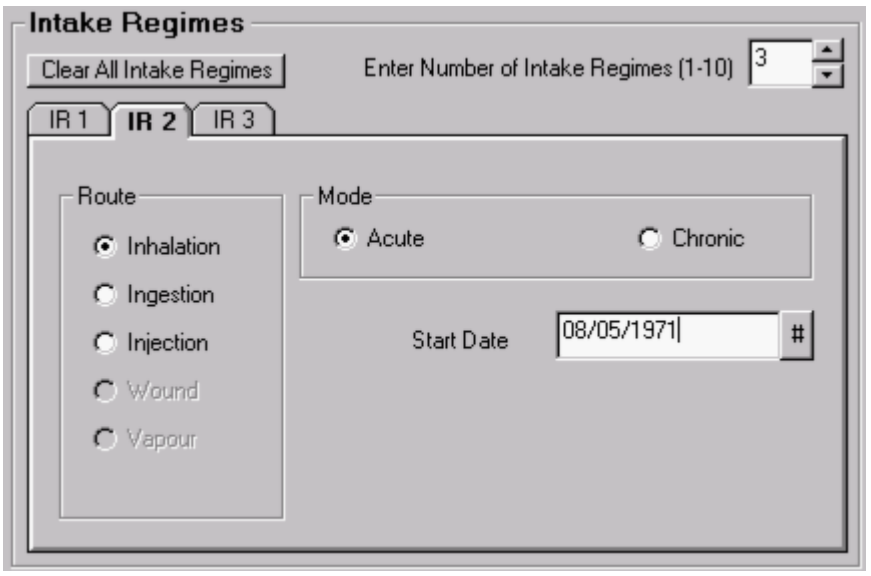


Figure 4.50. **Setting the** Date **of** IR 2 **as May 8**th**, 1971.**

Once you have specified independent model parameters **for** all IRs**, you simply** click **on each** IR # tab **displayed in the "**Intake Regimes**" sub-panel to** specify **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 8**th**, 1971;**
- enter **the estimated "**Start Date**" of** IR 3 **as March 21**st**, 1972.**

Note: **In this example, all 3 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

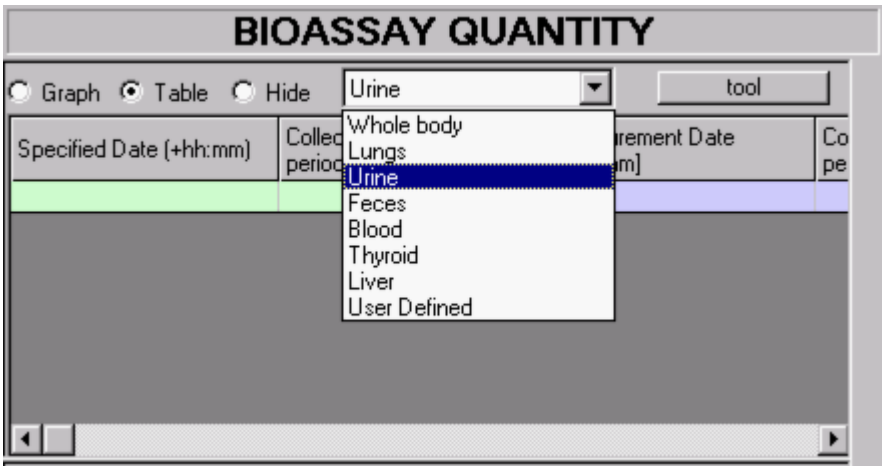


Figure 4.51. **Drop-down** Bioassay Quantity **list box.**

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**).**

Note: **When it is first opened, the data** Table **in the** Bioassay Quantity **window has only one row. This window is designed to display data values, and NOT for data entry. Since no data have yet been entered, there are no data to display at this stage. The "**tool**" button** opens **the** Table Tool **for your selected** Bioassay Quantity**. This provides the** tools **that you will use to** enter **(and/or** edit**) the** bioassay data **- in the next step.**

Tip: **Use the** scroll bar **below the open** Bioassay Quantity **window to** view **additional columns (to the right) that are related to** measured bioassay data**.**

This completes Step #8 **in the** multiple intakes **example:**

- Proceed **to the next step.**
- Return **to the** case description **and list of steps.**

Data Entry - Multiple Intake Example

IMBA Professional provides a "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:

- Enter "37" in the "Number of Rows" dialog box (bottom panel, left-of-center - see Figure 4.52).
- Click the "Apply" button to the right of the dialog box.

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.**

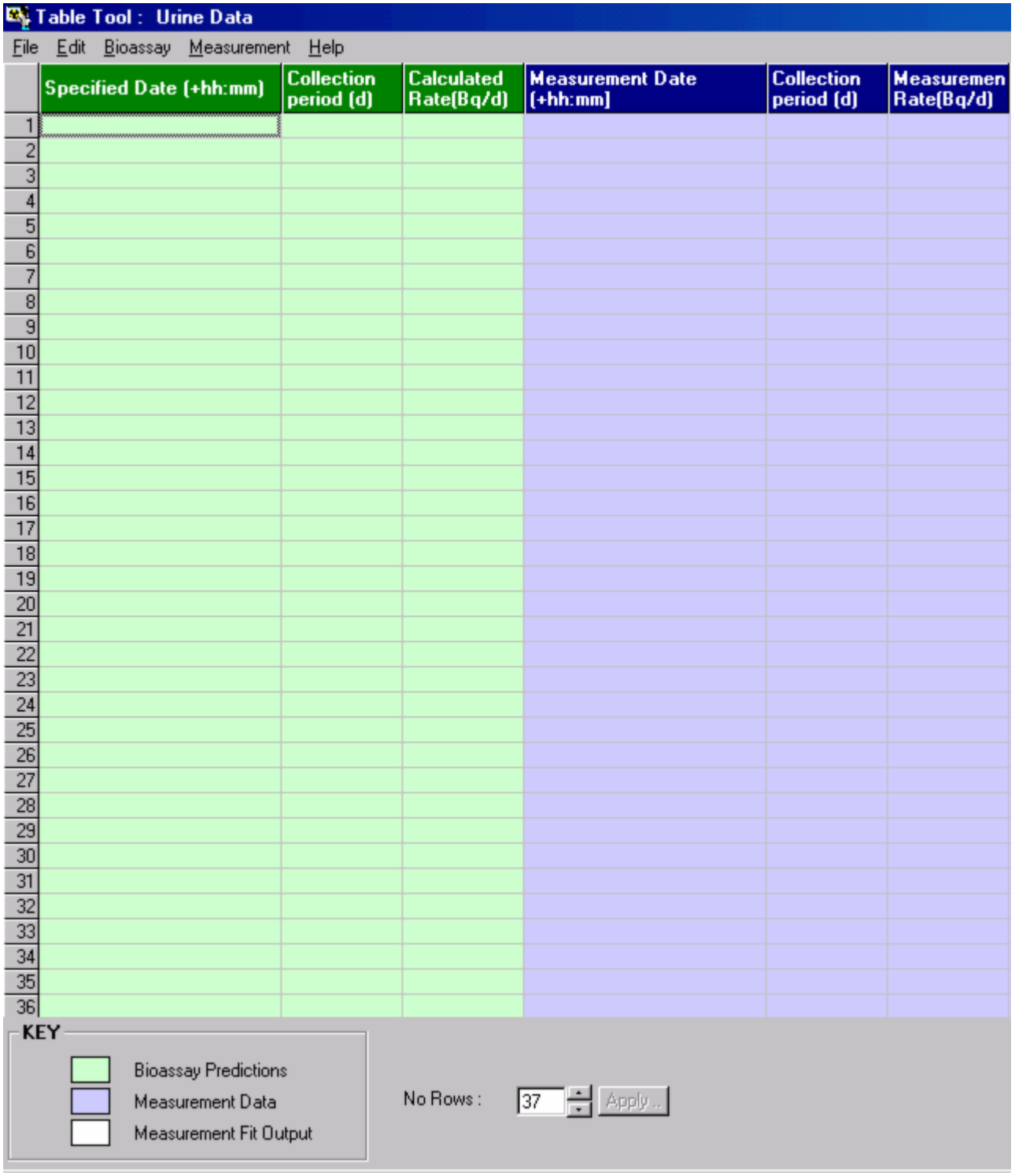


Table 4.52. Table Tool **with** 37 **rows opened.**

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.**

Graphing the Data - Multiple Intakes

IMBA Professional 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 "Urine" and "Graph" for display in the second Bioassay Quantity window (Figure 4.53). Then click the "tool" button to open the Graph Tool.

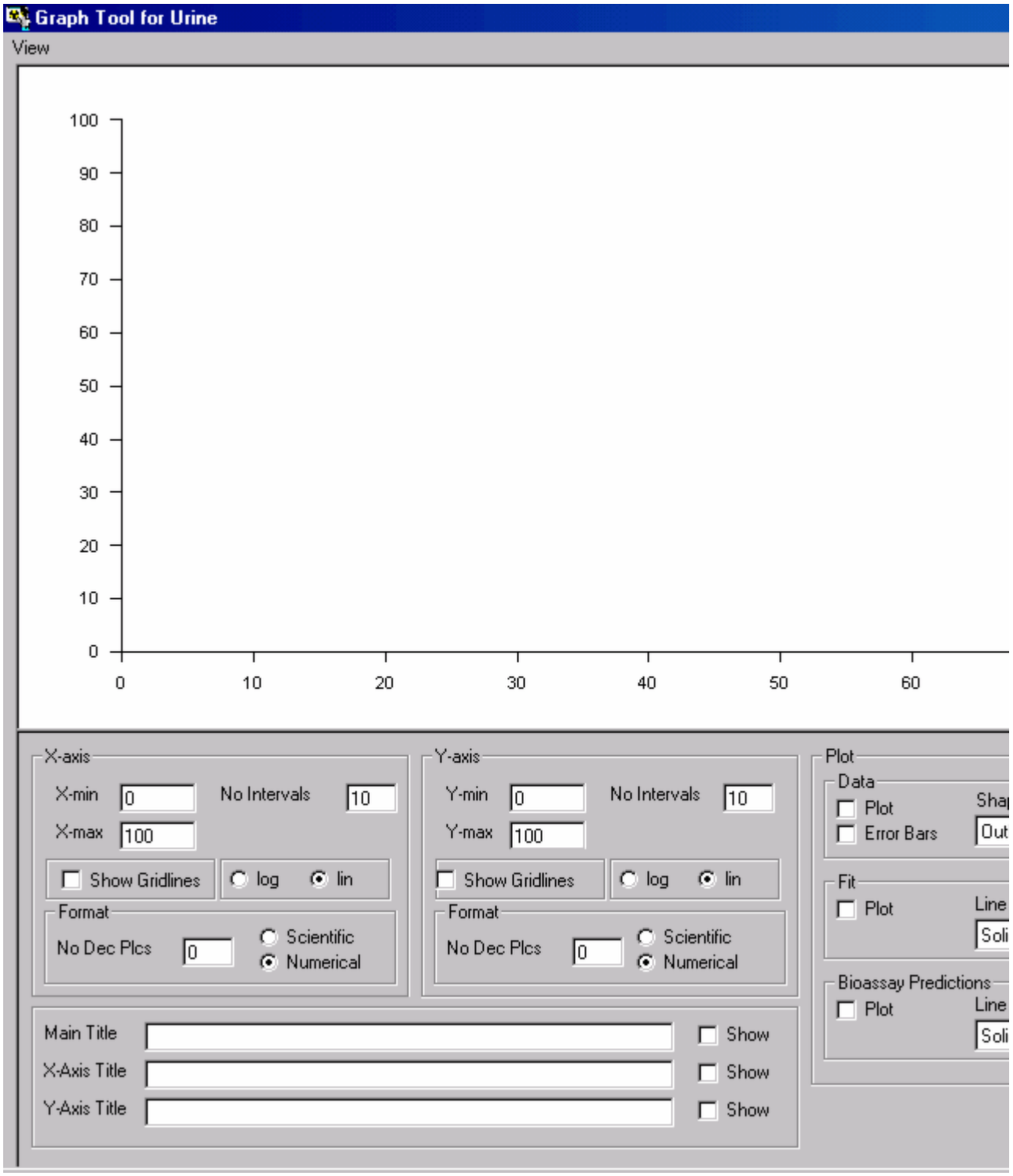


Figure 4.53. **Opening a Graph window for the Urine bioassay quantity.**

- **See** Graph Tool for Viewing Data and Fit (Step #10 **in the** multiple intakes **example):**
- Return **to the** case description **and list of steps.**

Calculating the Intake Amounts

Before you can calculate **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):**

- check **the** Urine box**.**

If you forget to do this, you will be prompted.

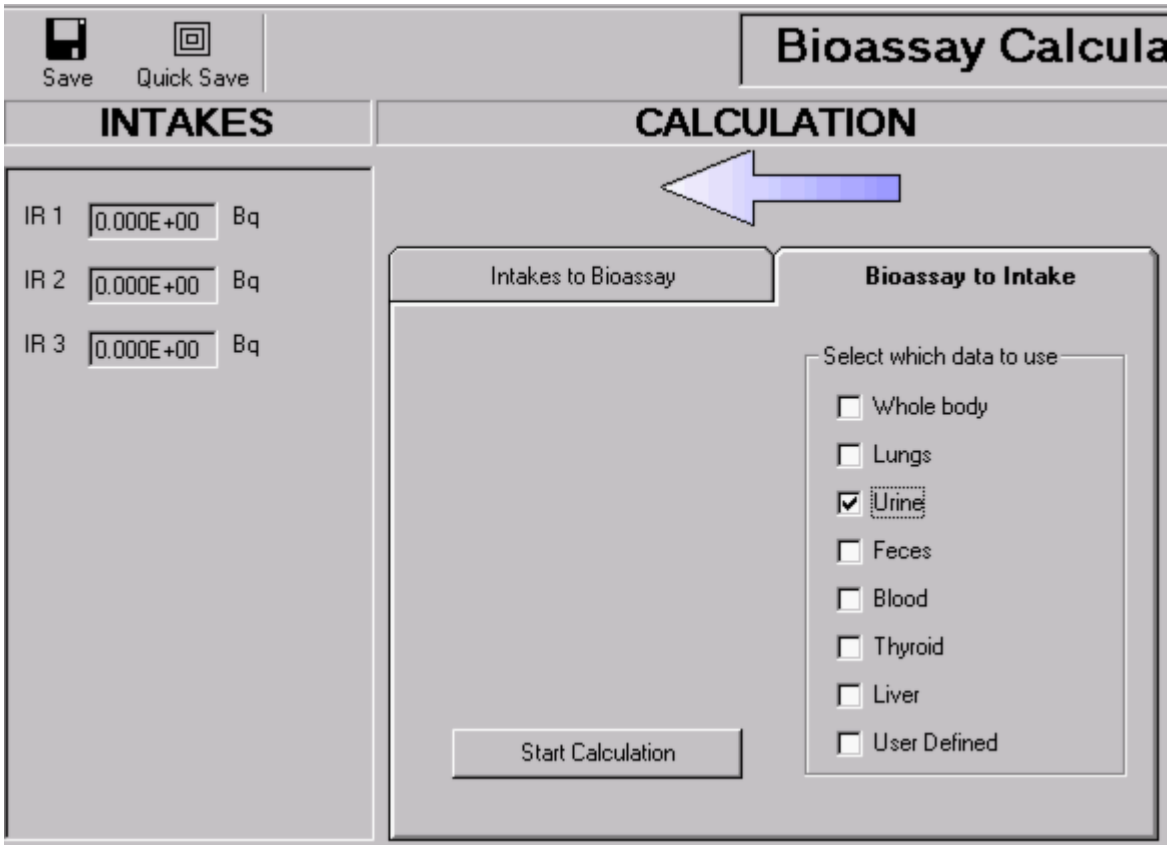


Figure 4.54. **Selecting** Urine **as the** Bioassay Quantity **to use to estimate** Intakes**.**

To calculate **the** maximum likelihood estimate **of the** Intake **amounts:**

- click **the "**Start Calculation**"** button **(Figure 4.55).**

This will:

- display **automatically the** Intake **amounts for all three** Intake Regimes (IR1, IR2 and IR3)**;**
- plot **automatically the corresponding** fit **to the** data points **(see Figure 4.55) - provided that the "**Plot Fit**"** box **was** checked **in the** Graph Tool**.**

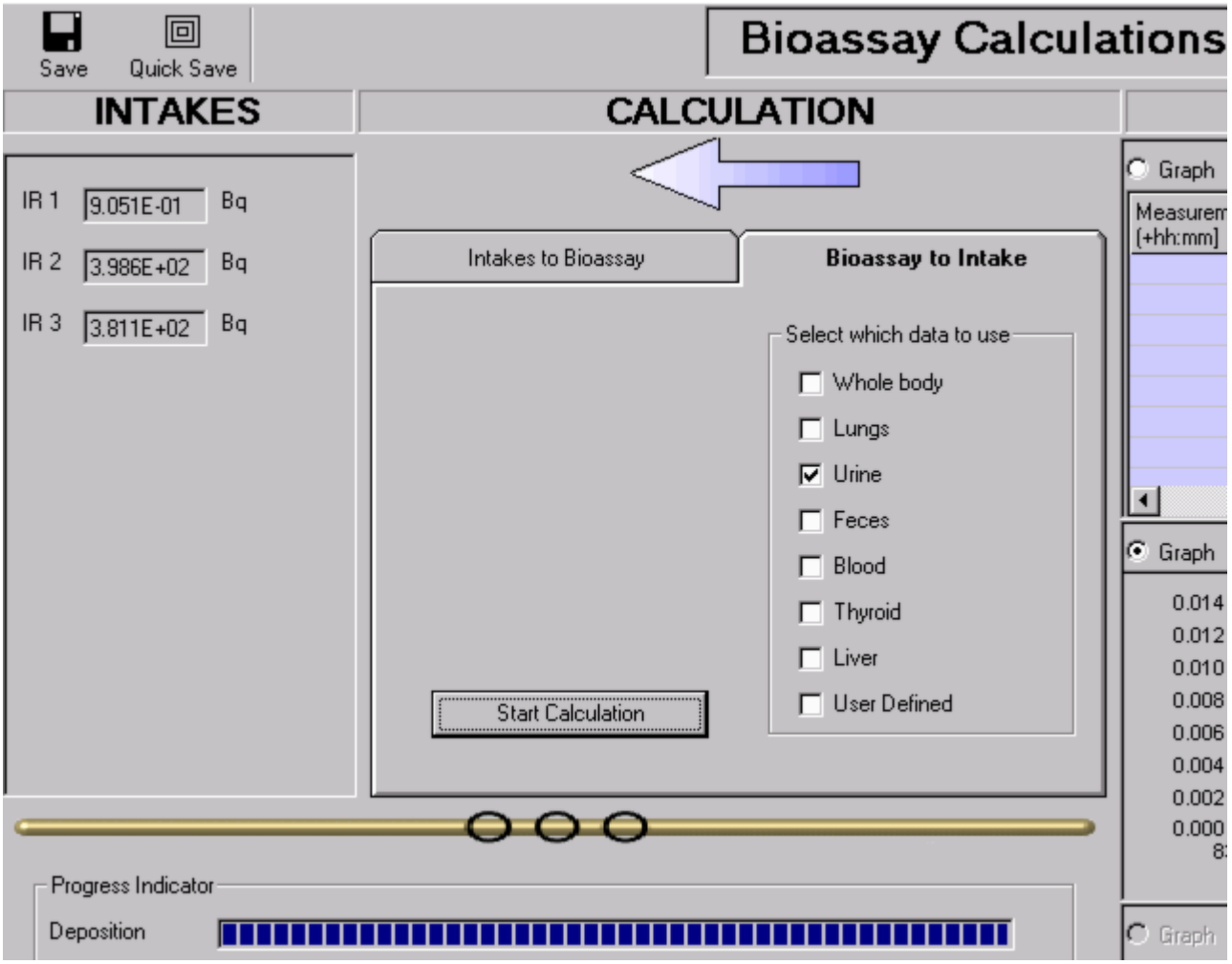


Figure 4.55. **Calculated Intakes with corresponding best fit to the data (for assumed Type M absorption behavior).**

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 review, and modify 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 f1 = 0.00001 - and recalculating the intake amounts, gives the result shown in Figure 4.56.

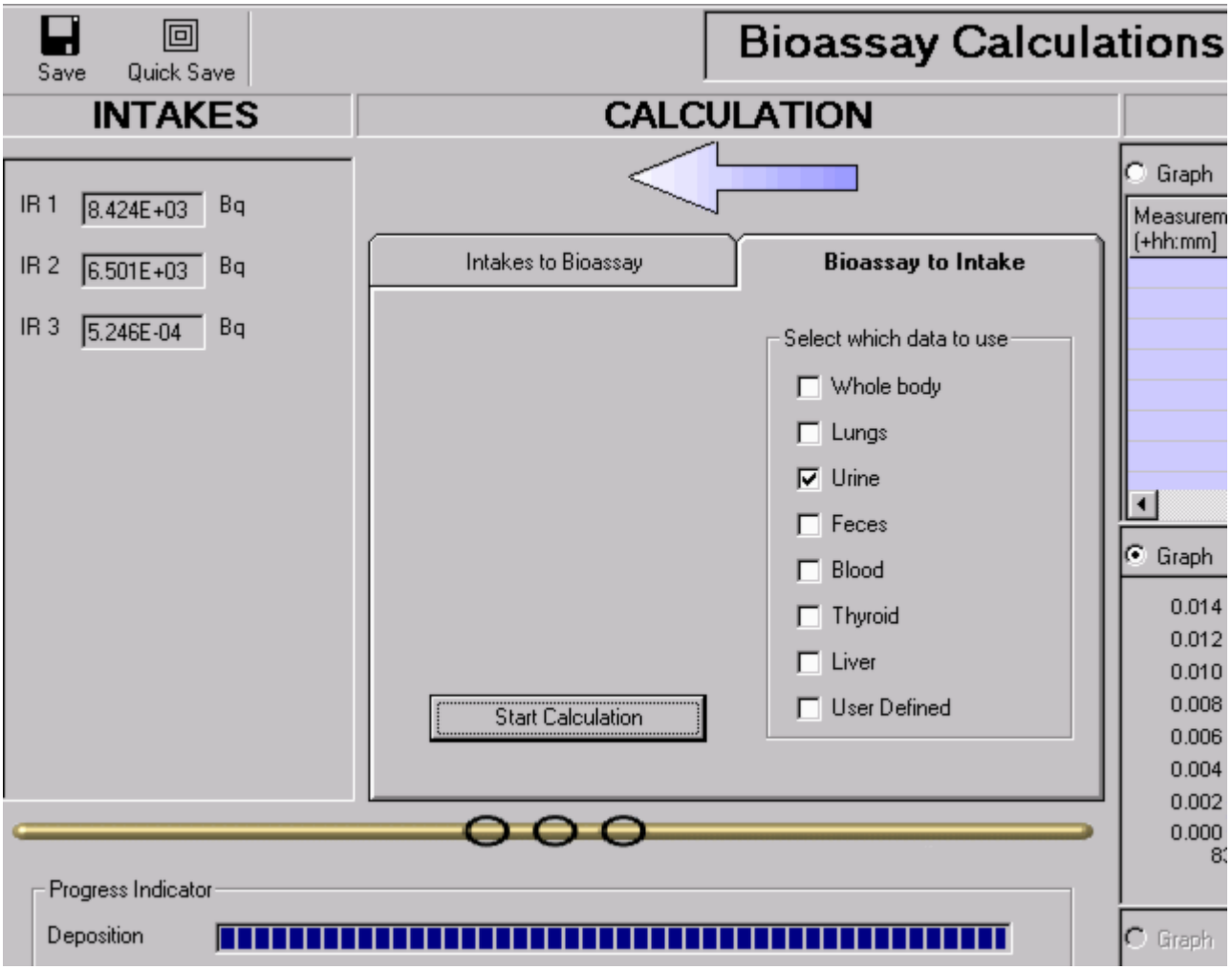


Figure 4.56. **Calculated Intakes with corresponding best fit to the data for assumed Type S absorption behaviour.**

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, IMBA Professional 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

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**.**
- Return **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.

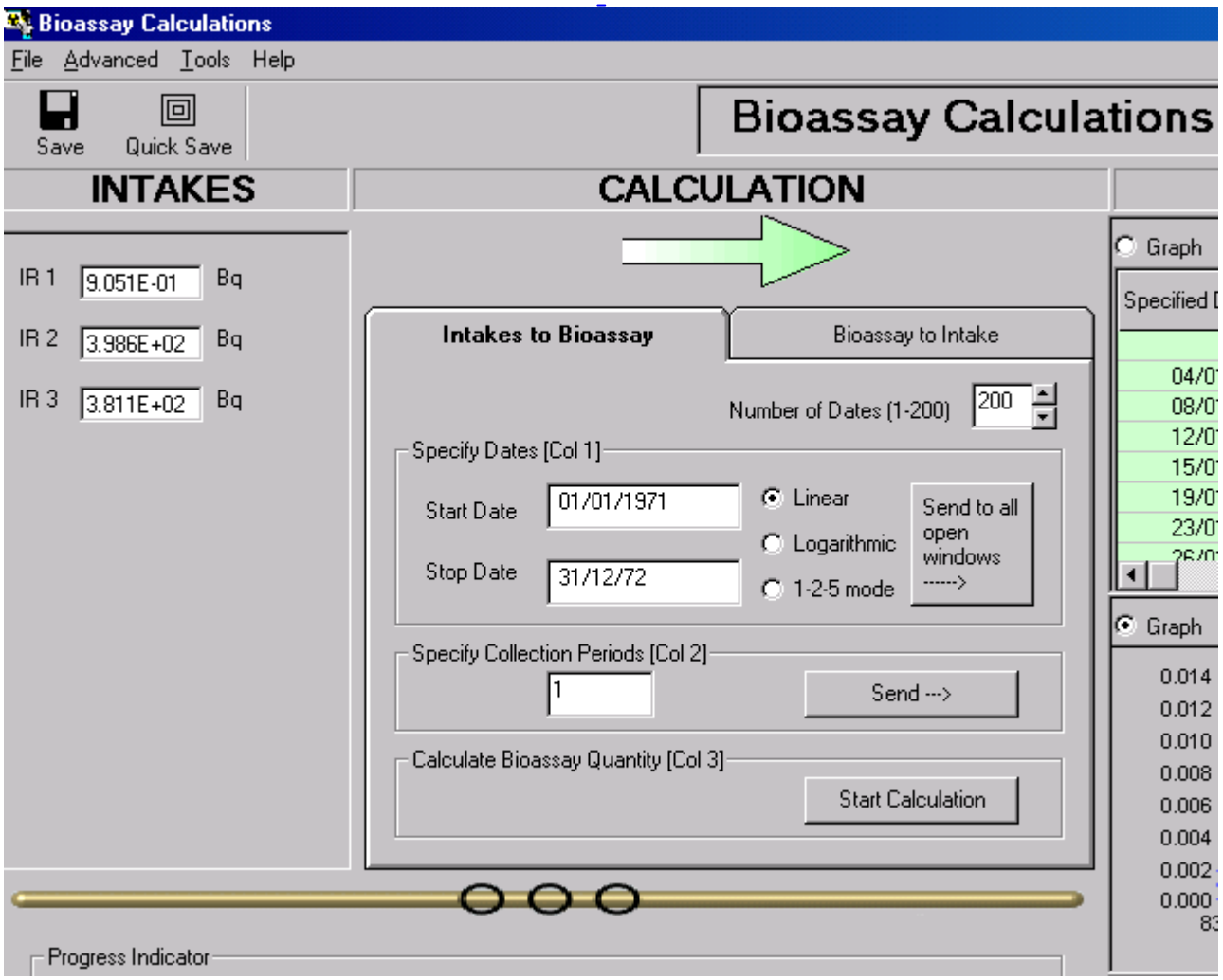


Figure 4.57. Setting up a series of times at which to predict the bioassay quantity.

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.

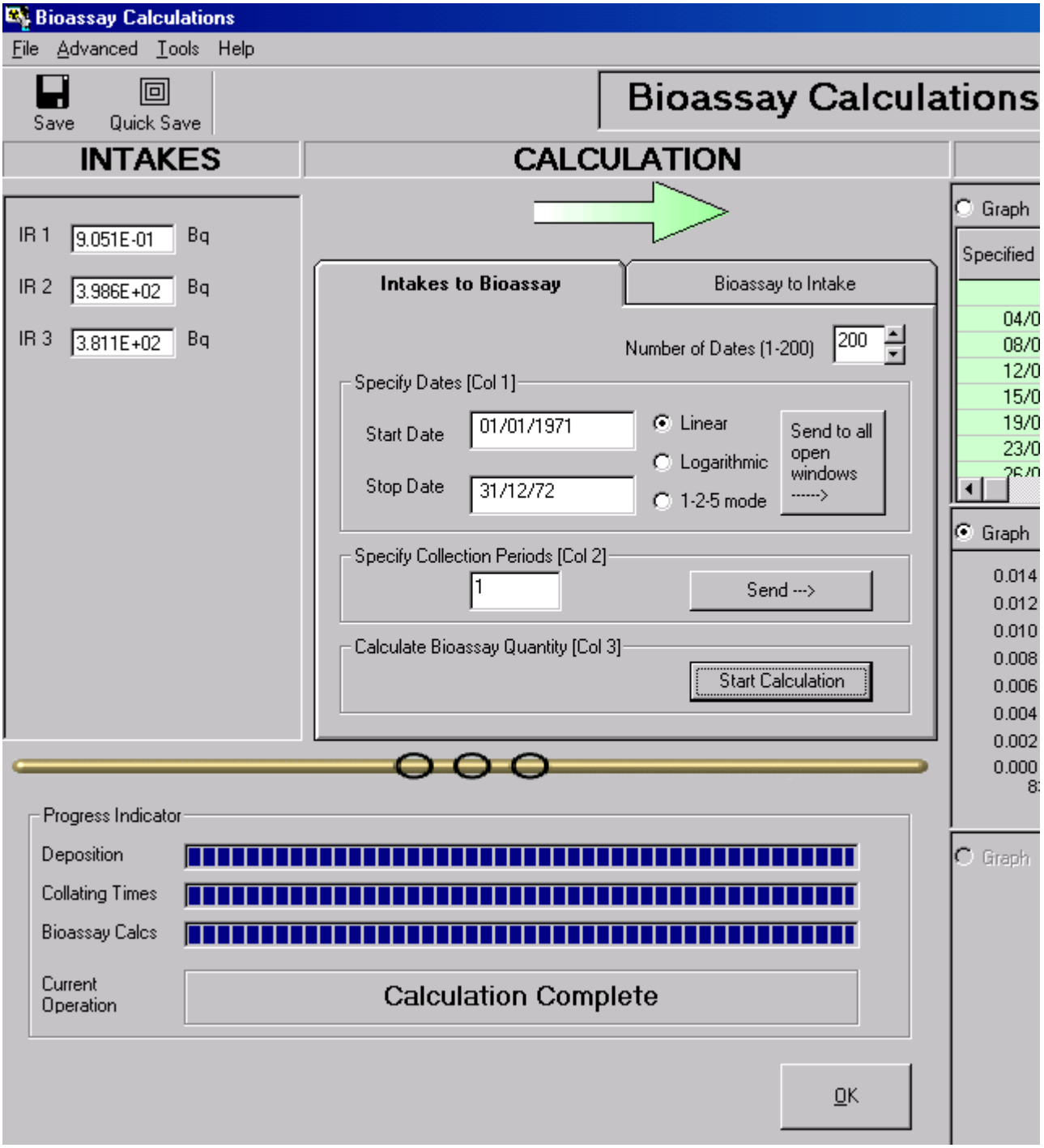


Figure 4.58. Predicted bioassay quantity displayed in the Bioassay Quantity window.

Warning: If you are using a slow processor (< 400 MHz), you will have to wait several minutes for the calculation of 200 excretion values to finish.

Tip: If your processor is too slow, decrease the number of time points.

Plotting the predicted bioassay quantity

This is done in the Graph Tool (Figure 4.59):

- click the "Select Axes Automatically" button ("Tools" sub-panel);
- check the "Plot" dialog box under "Bioassay Predictions" ("Plot" sub-panel).

The predicted values of the bioassay quantity will automatically be added to the graph of the data (as a green curve).

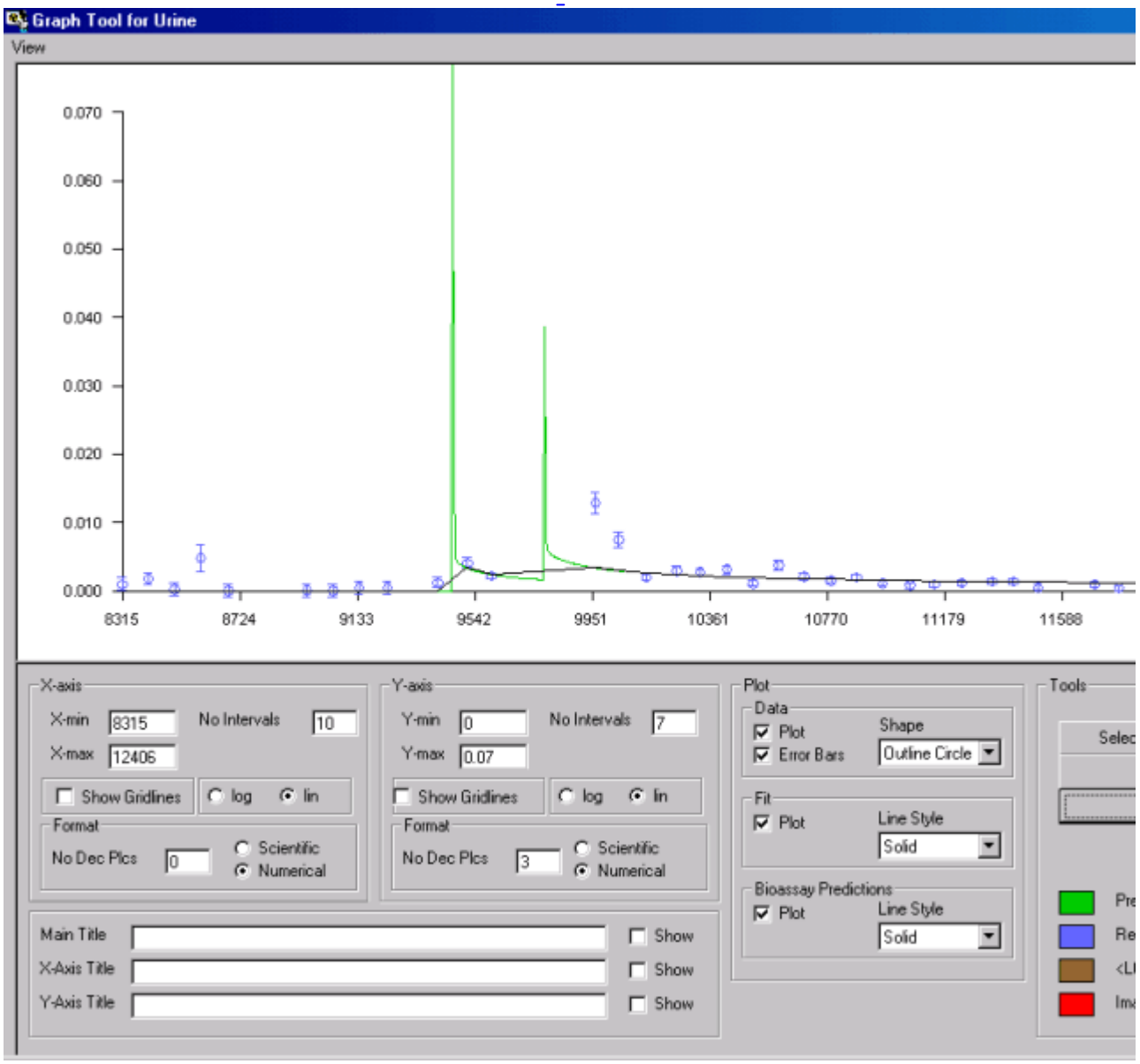


Figure 4.60. Curve of predicted bioassay quantity displayed in Bioassay Quantity window.

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. the predicted early urinary excretion for the known intake time (IR2) is substantially higher than the next measured value (at 9,516 d);
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.

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.

To test this interpretation:

- in the Main Screen, change the assumed "Start Date" for IR3 to "11/9/72";
- back in the Bioassay Calculations screen, "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:

- IR1 = 0 Bq;
- IR2 = 355.9 Bq;
- IR3 = 367.7 Bq.

Figure 4.62 shows the enlarged plot in the Graph Tool.

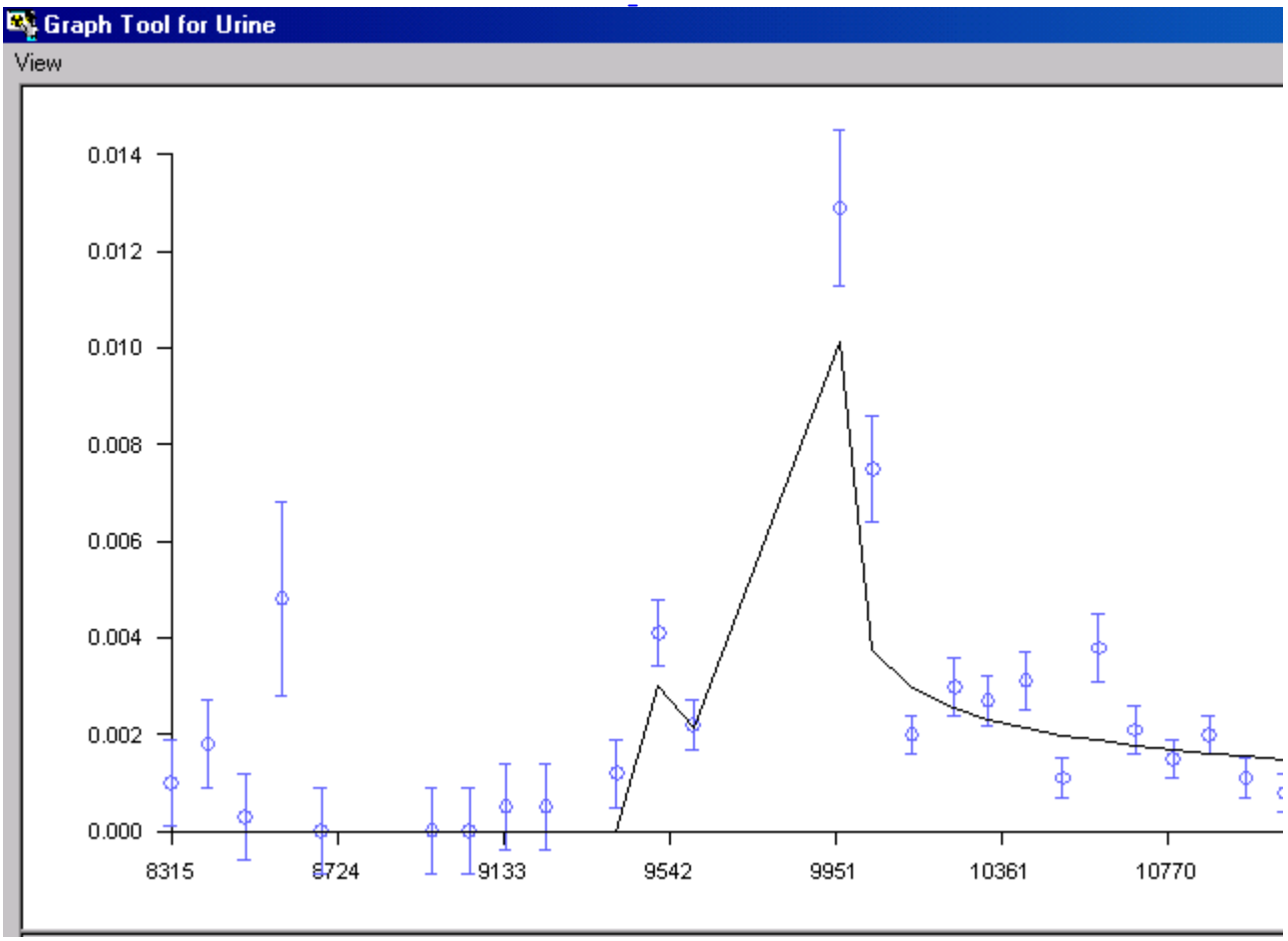


Figure 4.62. Improved data fit obtained by refining the assumed date of intake for IR3.

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.

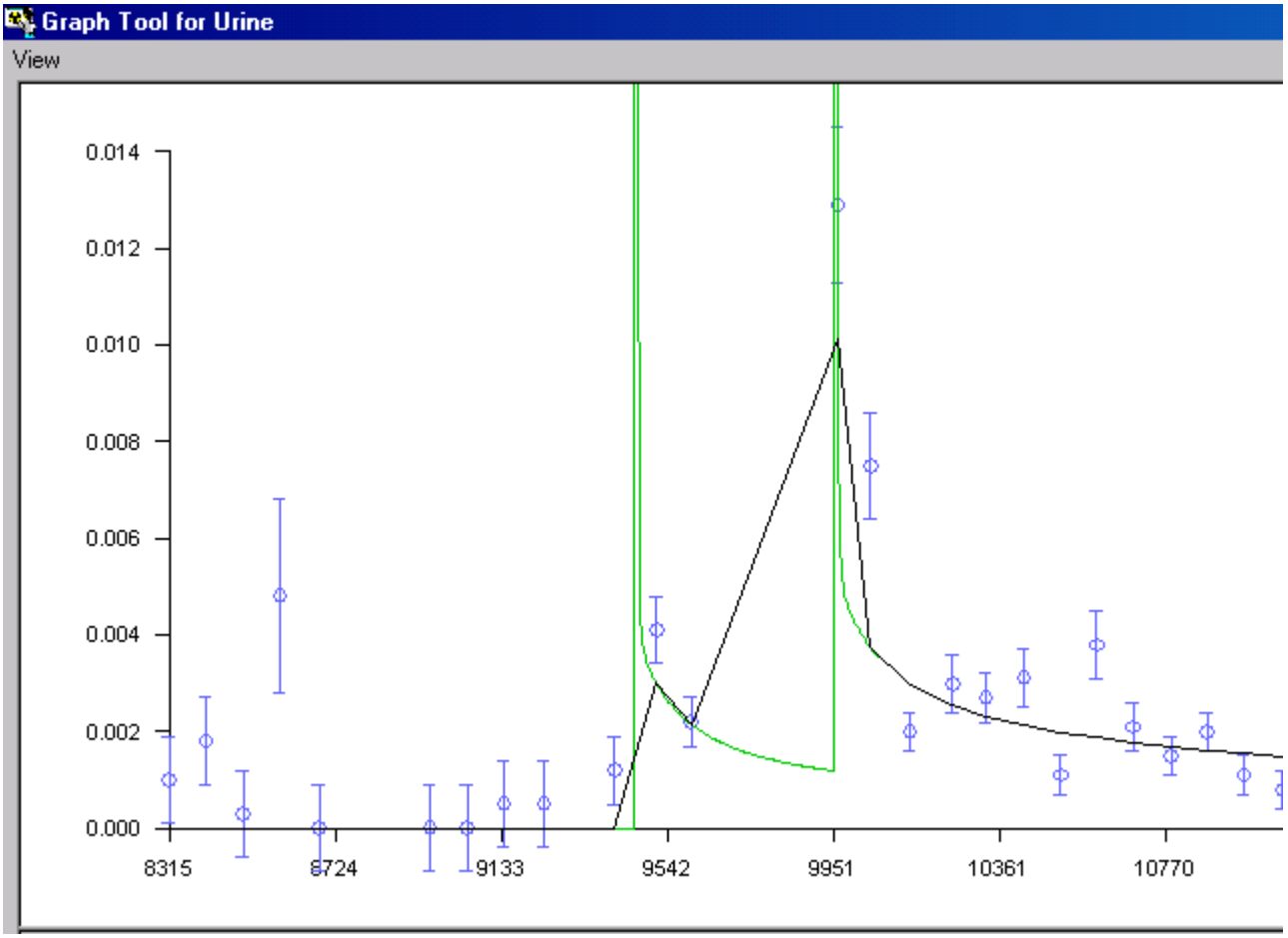


Figure 4.63. Predicted rapid changes in urinary excretion from IR2 and IR3.

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 arrow), click the "Start Calculation" button.

The result is shown in Figure 4.64.

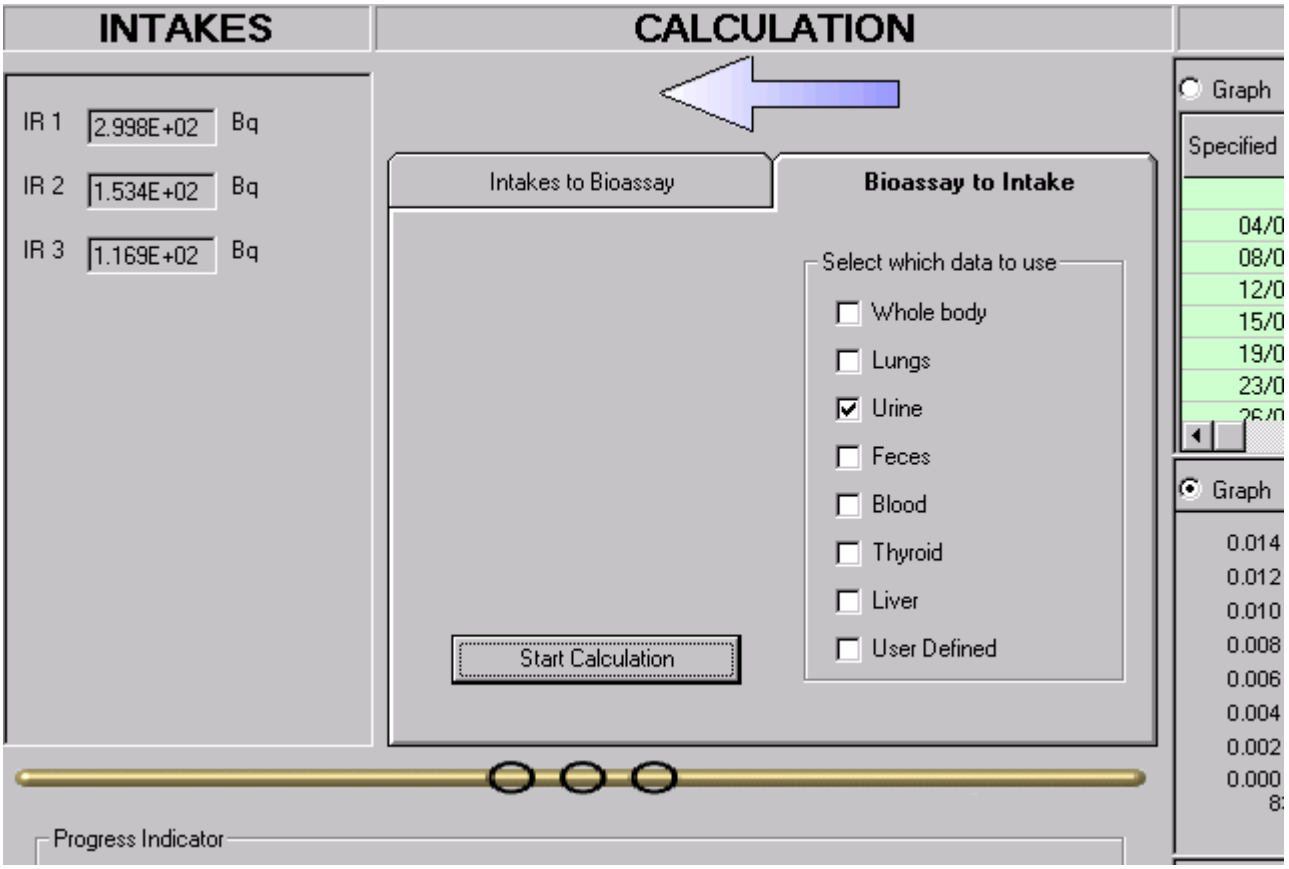


Figure 4.64. Calculating new intake amounts for an increased absorption rate for IR3.

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:

- IR1 = 299.8 Bq;
- IR2 = 153.4 Bq;
- IR3 = 116.9 Bq.

Figure 4.65 shows the enlarged plot in the Graph Tool.

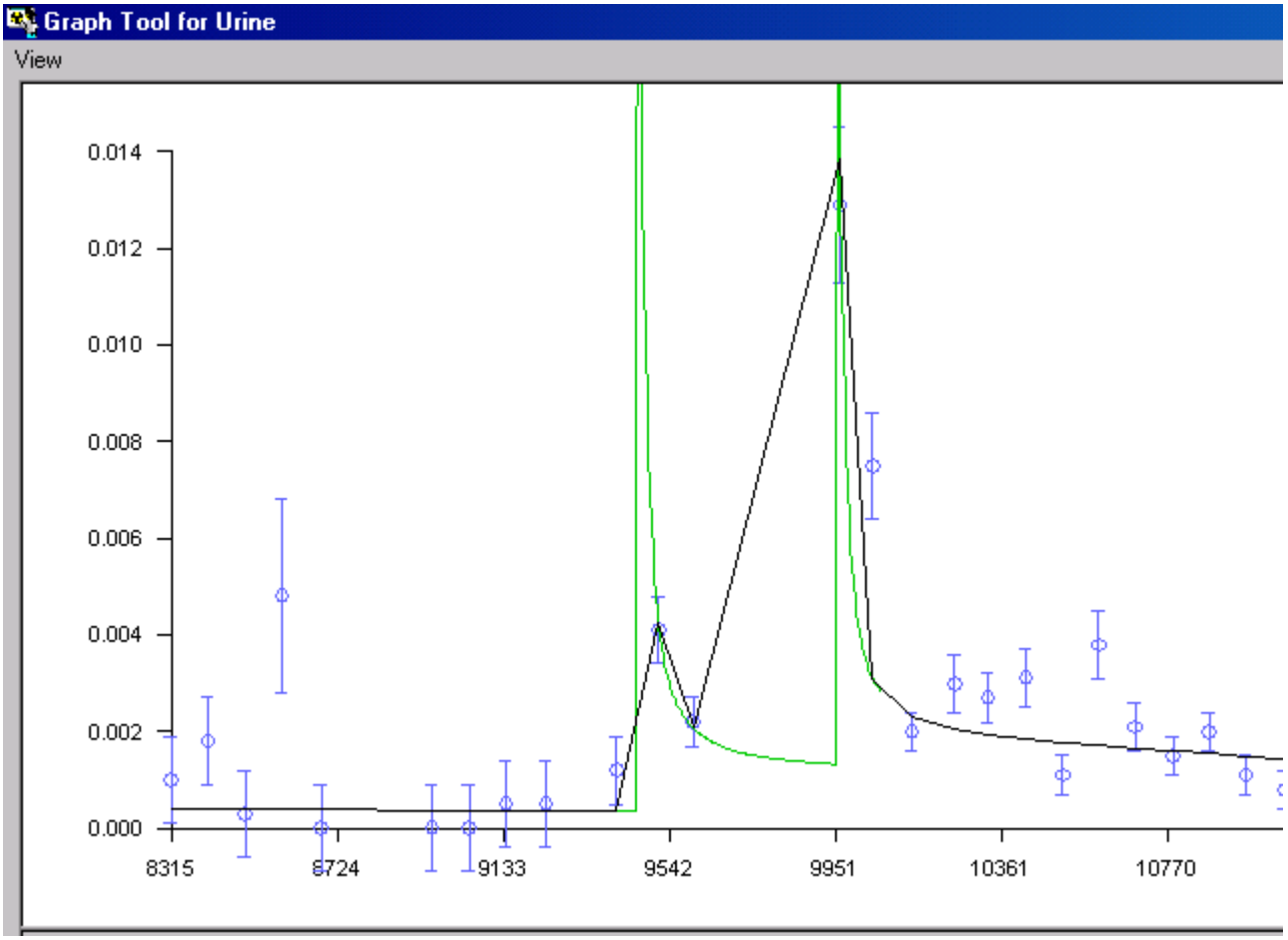


Figure 4.65. Improved data fit by refining the assumed absorption rate for IR3.

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

This example is taken from IAEA (1999) - 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 90Sr", 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.

Table 4.3. **90Sr/90Y whole body activity measurements.**

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 4.4. **90Sr urine activity measurements.**

Sample date	Collection period (h)	Daily excretion rate (kBq d-1)
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. 90**Sr faecal activity measurements.**

Sample date	Collection period (h)	Daily excretion rate (kBq d-1)
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**

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:

1. assume **appropriate** errors**;**
2. assume **ICRP-recommended** bioassay models**;**
3. test **hypothetical** intake scenarios**;**
4. evaluate **the** likely intake**;**
5. evaluate **the** likely dose**.**

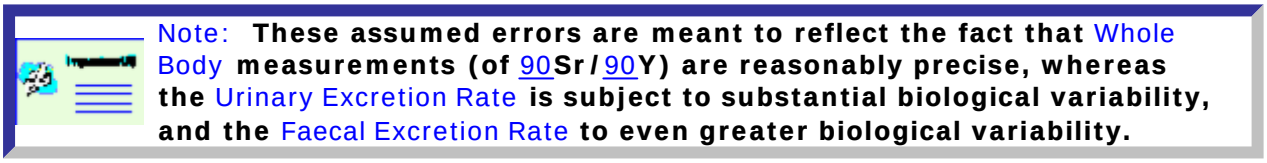
Error Assumptions - Multiple Bioassay Quantities

No information on the magnitude of measurement errors is available in this example case**. 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** $^{90}Sr/^{90}Y$**) 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.

Table Tool : Whole body Data

File Edit Bioassay Measurement 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.

Table Tool : Urine Data

File Edit Bioassay Measurement 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.**

Table Tool : Feces Data

File Edit Bioassay Measurement 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 Error Values):

- 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).**

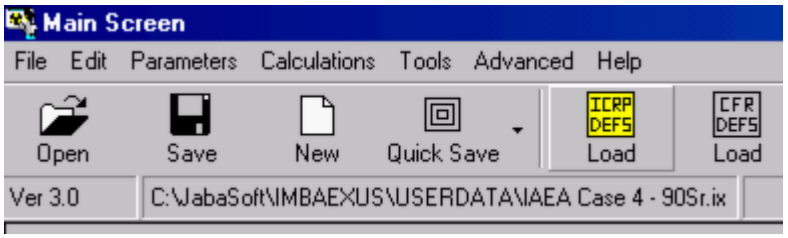


Figure 4.71. **The "**ICRP DEFS Load**" icon for specifying use of all ICRP** default **models.**

You will be prompted to select an "f1 Value**" and "**Absorption Type**" for the** 90Sr **material (Figure 4.72).** Select **type "**M**".**

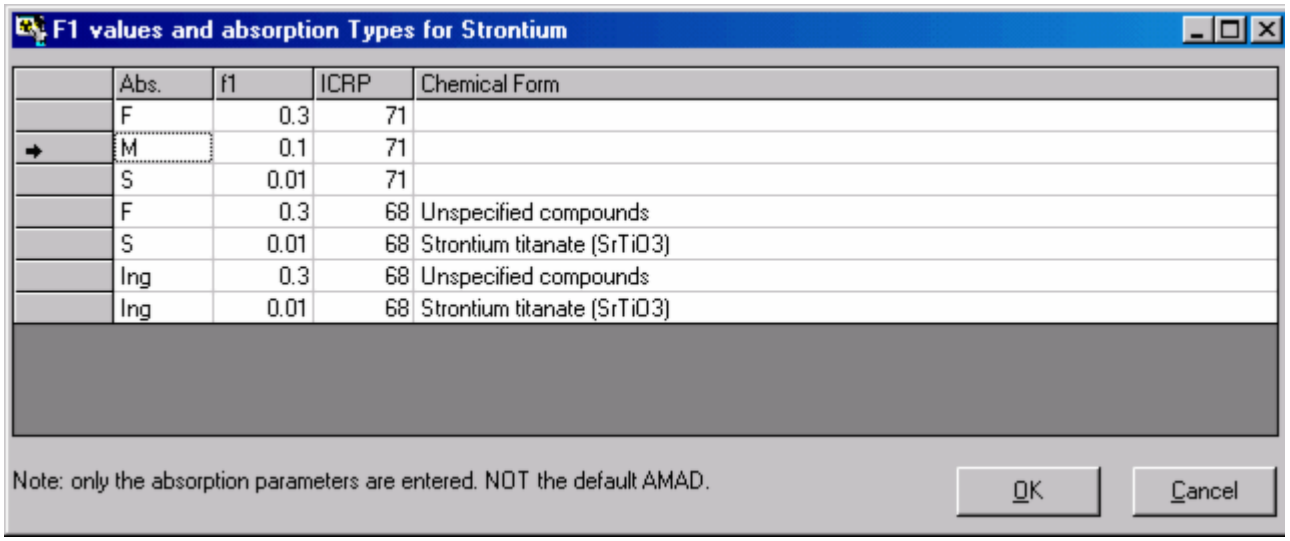


Figure 4.72. **Selecting the f1 value and absorption type for** Strontium**.**

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).**

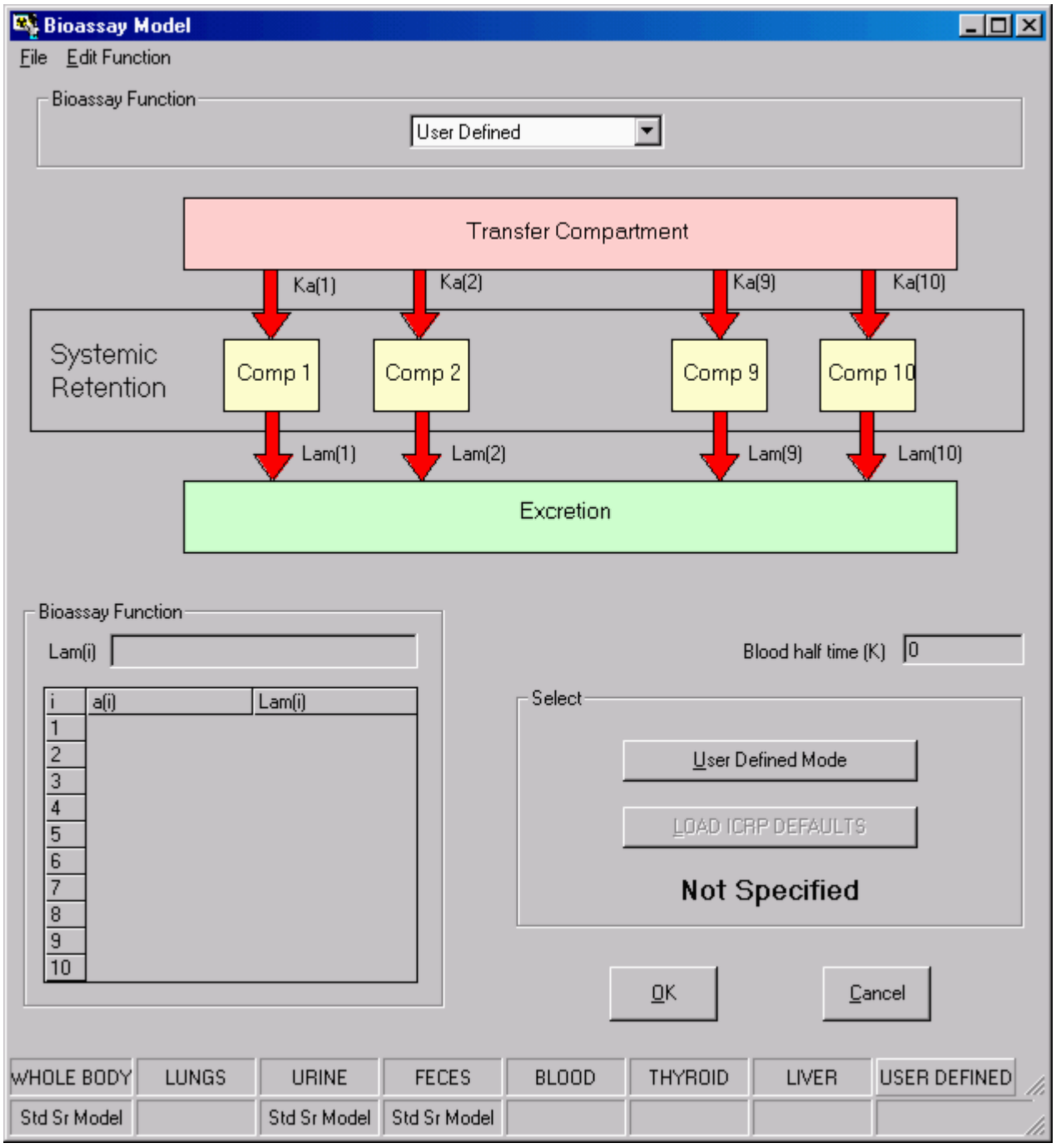


Figure 4.73. **Confirming that the "**Std Sr Model**" has been loaded for** Whole Body**,** Urine **and** Faeces**.**

This completes Step #2 **in the** multiple bioassay quantities **example (loading** Standard ICRP Bioassay Models **for** Strontium **):**

- Proceed **to** Hypothetical Intake Scenarios**.**
- Return **to the** case description **and list of steps.**

Hypothetical Intake Scenarios - Multiple Bioassay Quantities

The nature of the intake was unknown in this case (IAEA Case #4) - so let's try to get IMBA Professional 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 IMBA Professional use the bioassay data (whole body, urine and faeces) simultaneously to "choose" the most likely scenario.

Important Note: **The availability of 3 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).

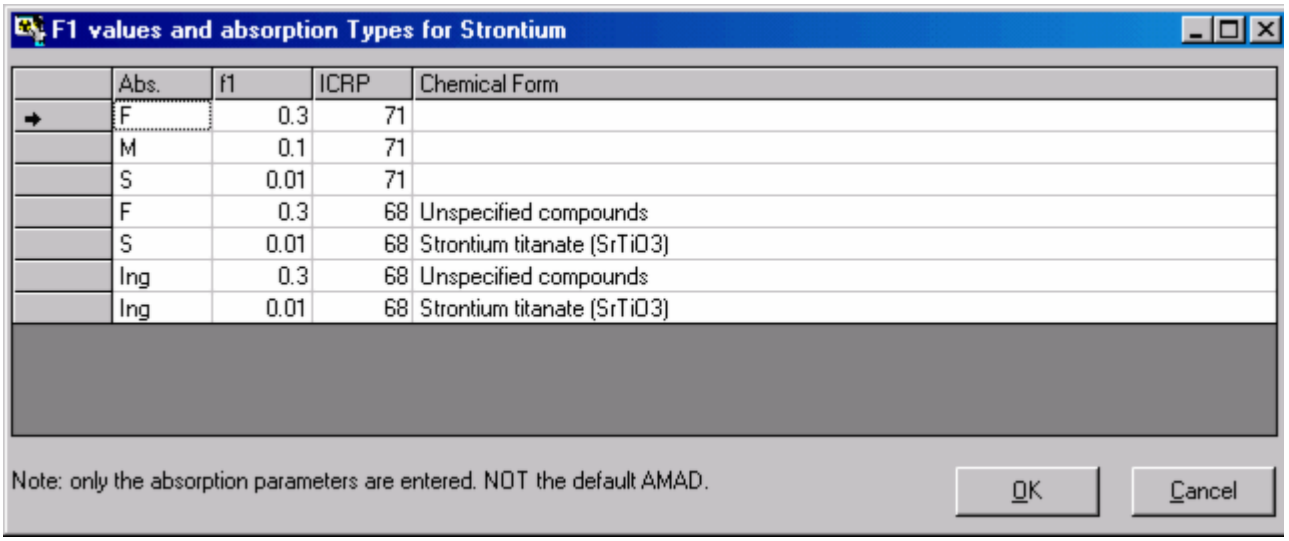


Figure 4.74. **ICRP's currently recommended "default" values for Strontium gut uptake fraction and absorption Type.**

Let's try setting up 4 hypothetical (but possible) intake scenarios, and seeing if IMBA Professional 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 4 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).

Note: **In this case, the actual intake probably occurred on November 24th, 1990 - about five days before the first whole body count and urine sample. The "Start Date" for each hypothetical (acute) intake is therefore set to "24/11/90".**

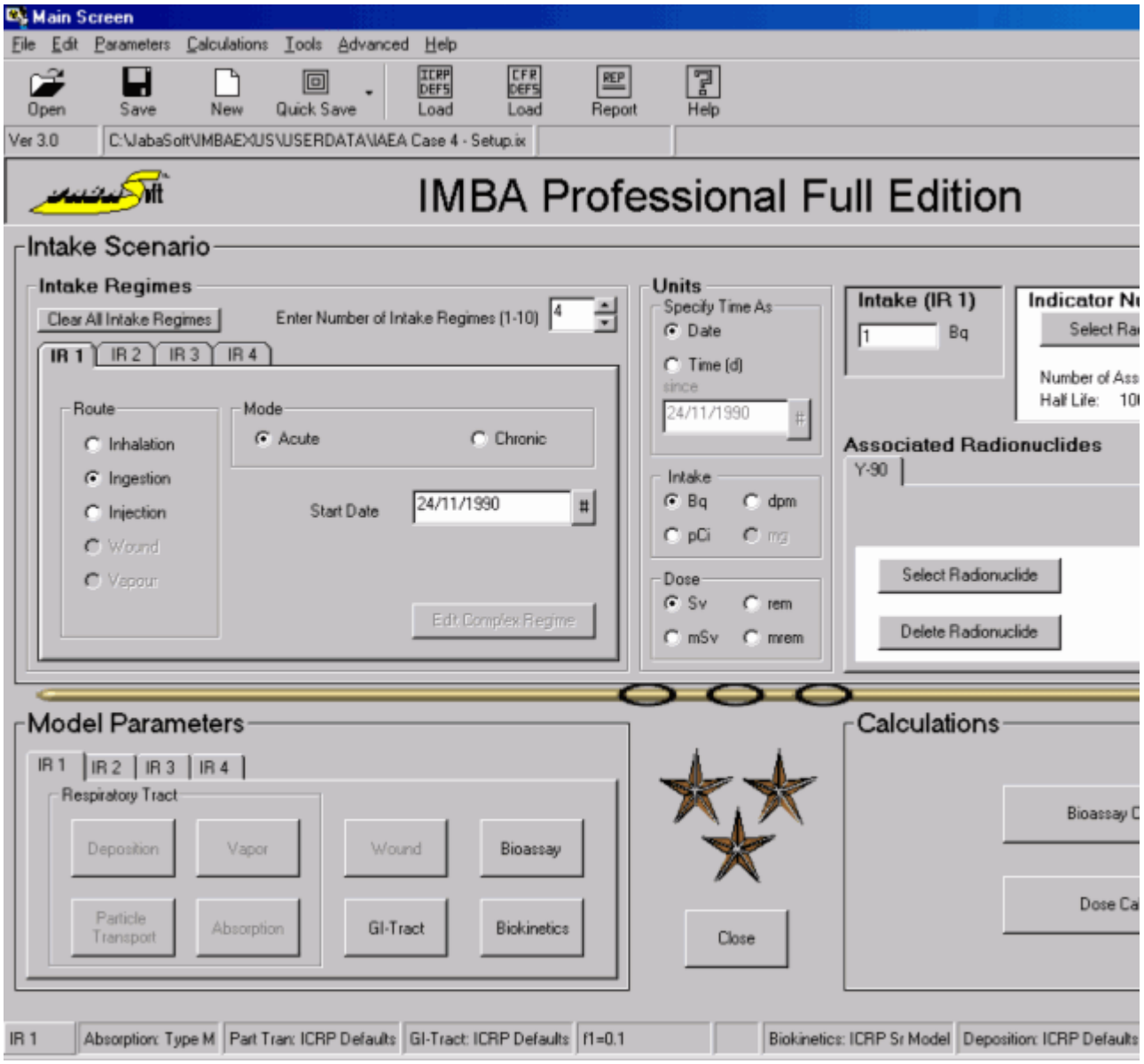


Figure 4.75. **First hypothetical intake regime (IR1) set up as "Ingestion" with f1 = 0.1.**

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.

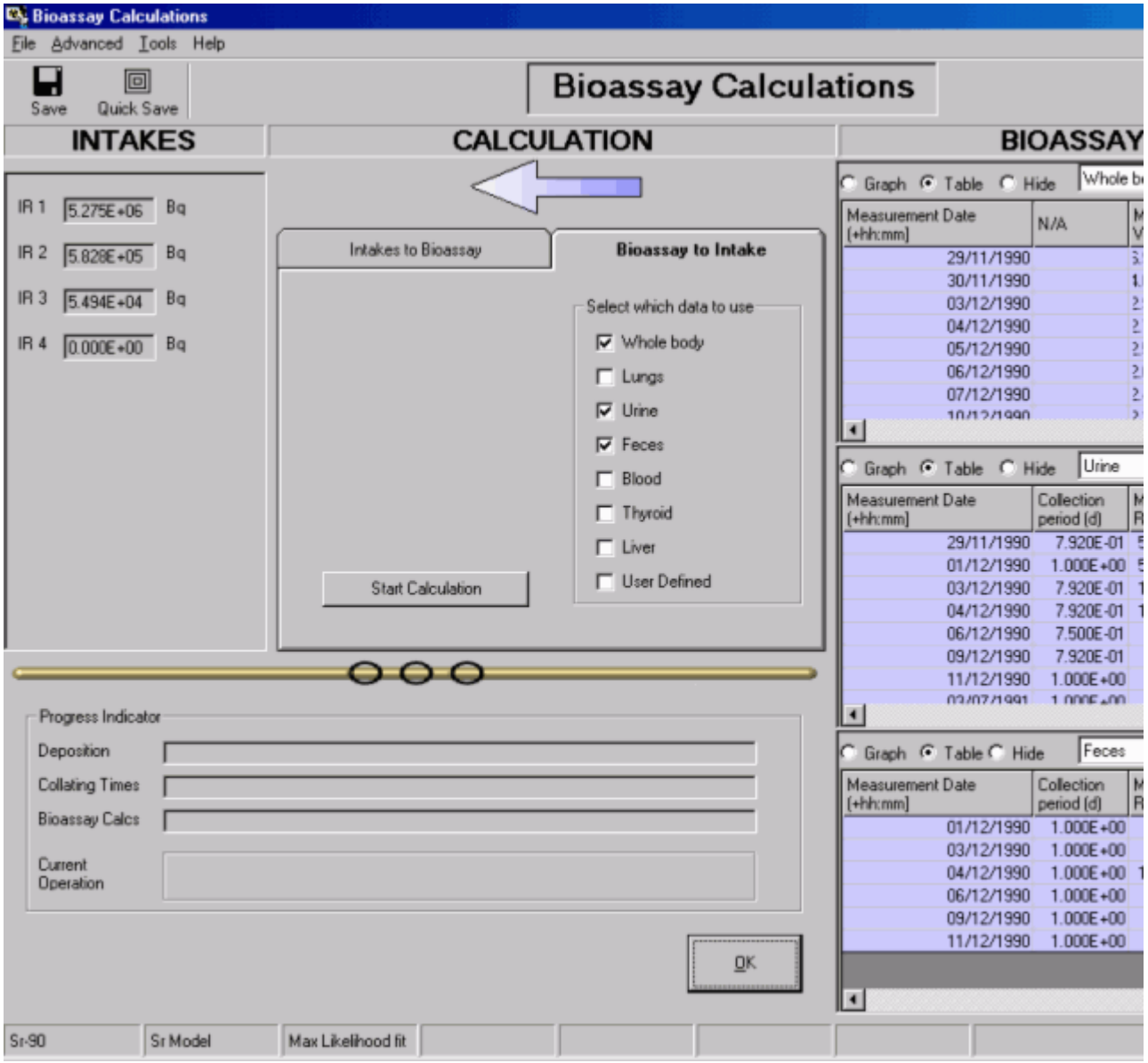


Figure 4.76. **Calculated amounts of 4 hypothetical intakes.**

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.

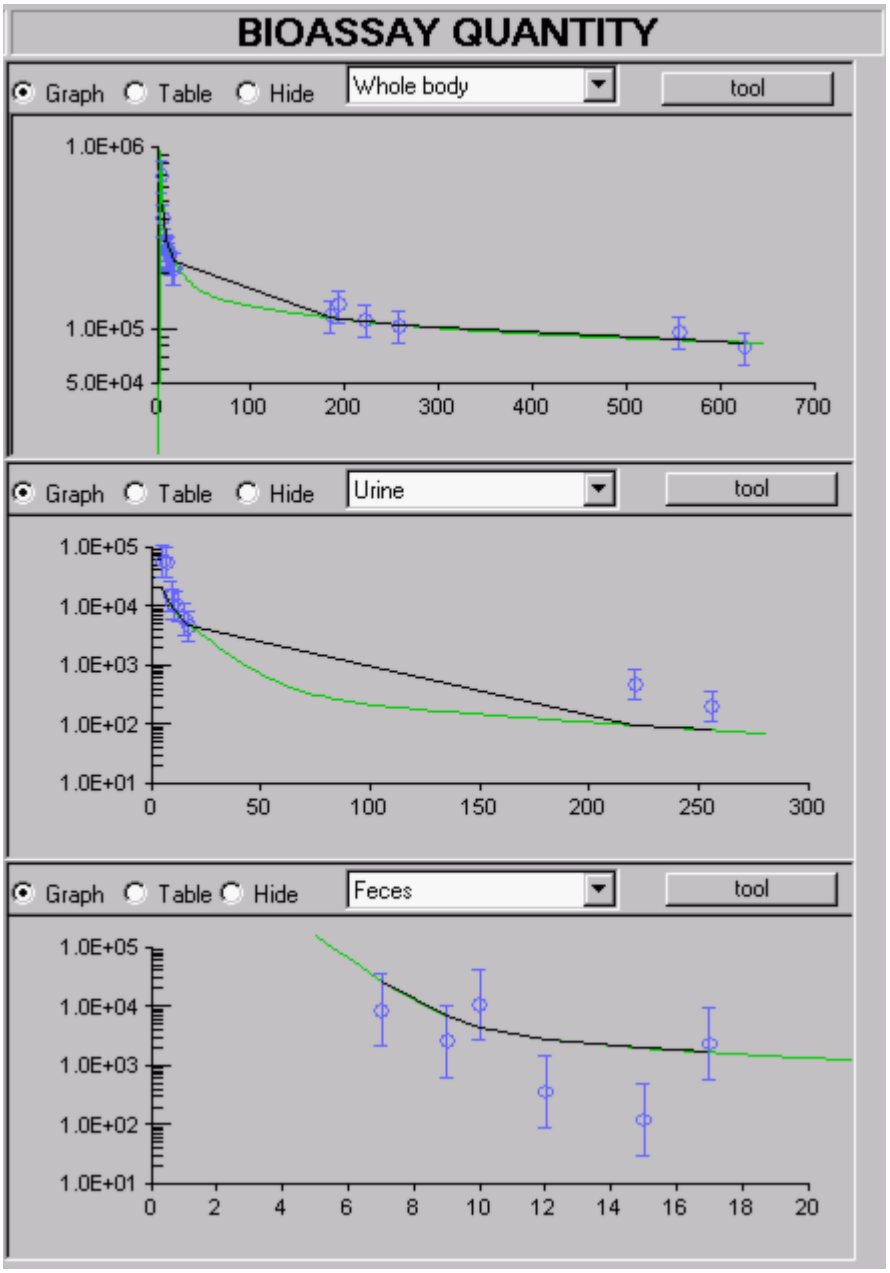


Figure 4.77. **Overall fits to the bioassay data given by a combination of 4 hypothetical acute intakes.**

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 f1 = 0.3) and inhalation (Type "F" with various assumed values of the AMAD), as follows:

- IR1 **- Ingestion - with f1 = 0.3.**
- IR2 **- Inhalation - Type "F" absorption - with AMAD = 5 µm (ICRP default aerosol);**
- IR3 **- Inhalation - Type "F" absorption - with AMAD = 20 µm;**
- IR4 **- Inhalation - Type "F" absorption - with AMAD = 100 µm.**

Figure 4.78 shows the result.

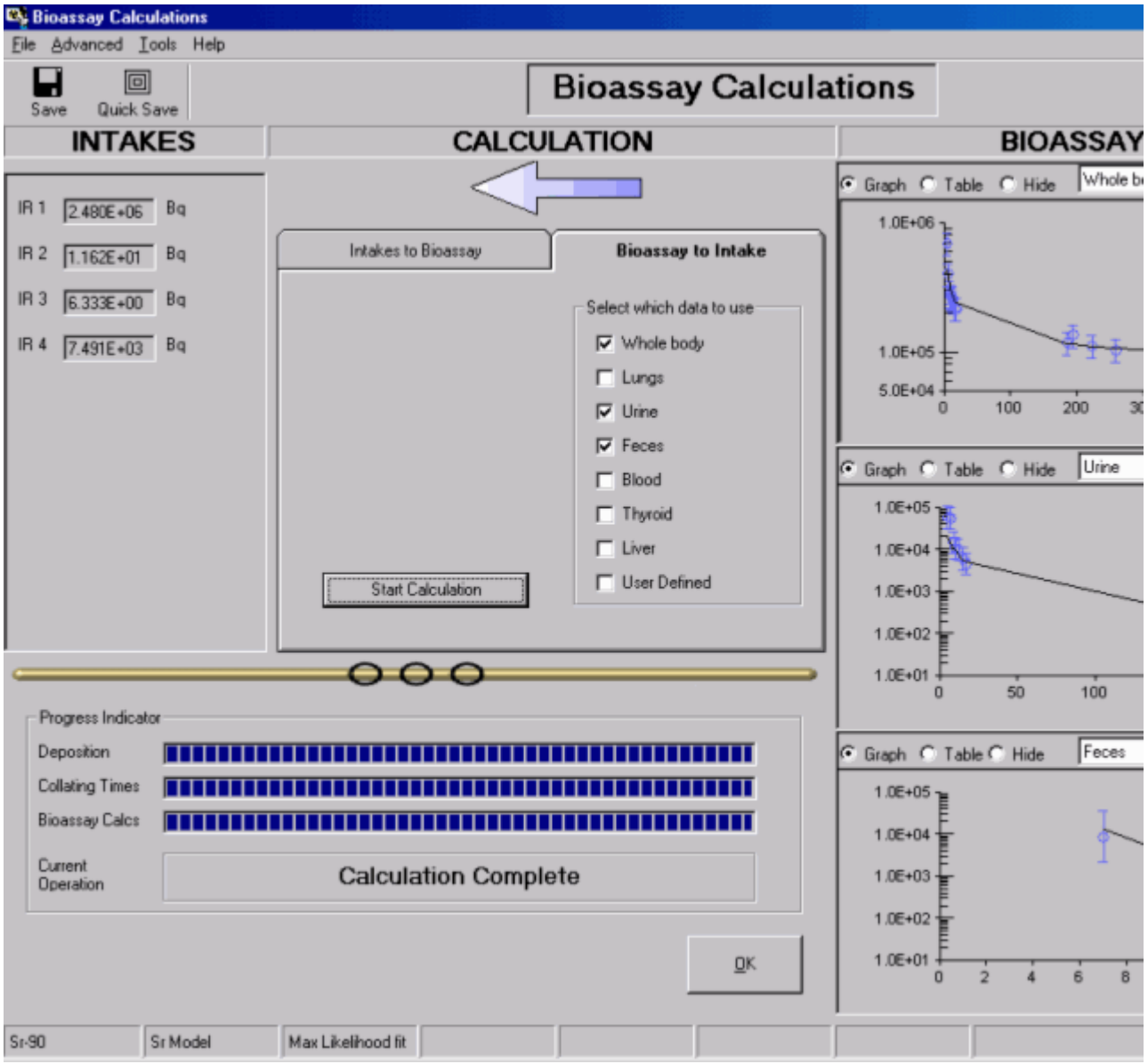


Figure 4.78. **Intake amounts calculated for 4 hypothetical (simultaneous) intake scenarios.**

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.

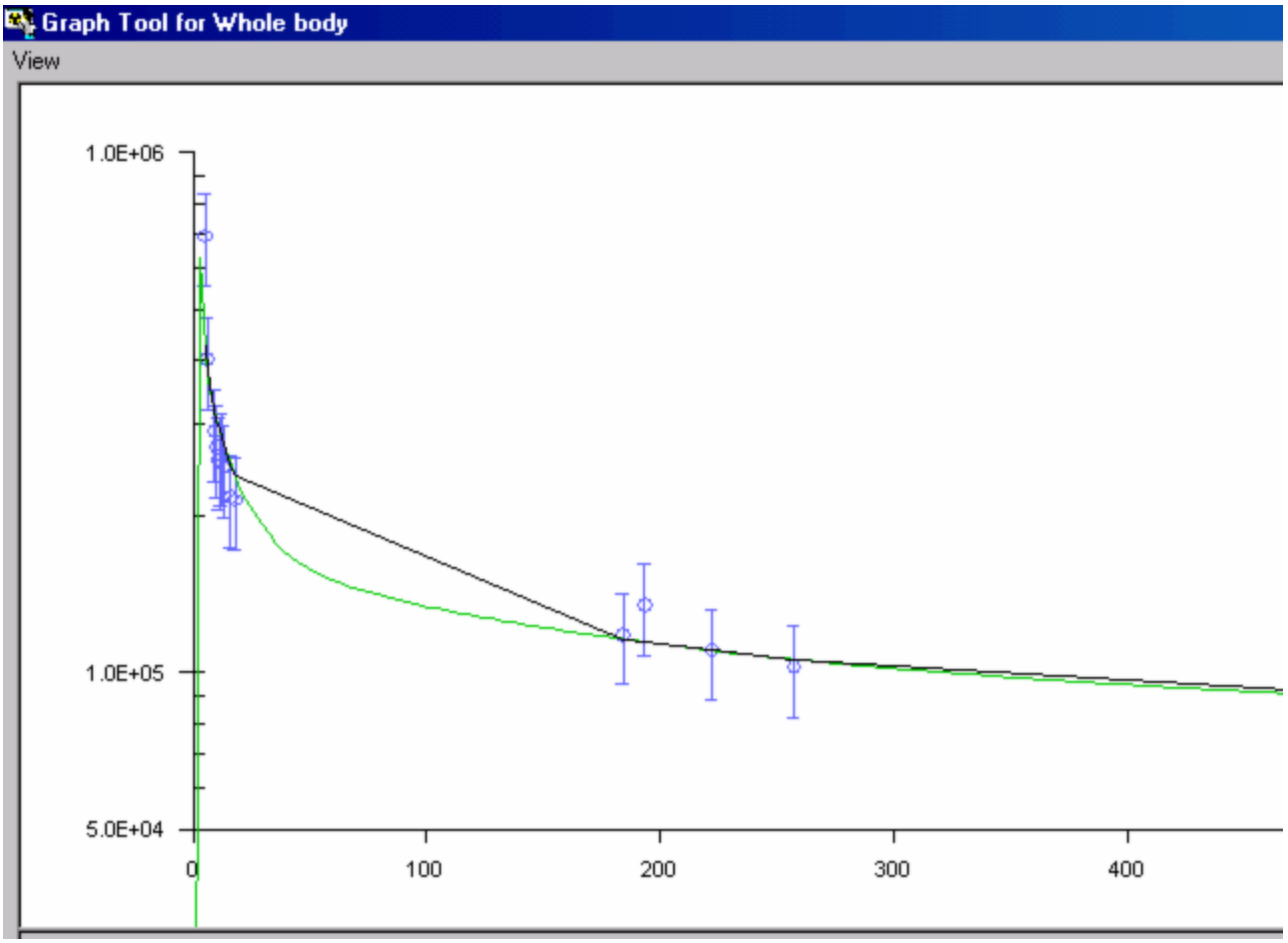


Figure 4.79. Graph Tool **plot of** whole body **data.**

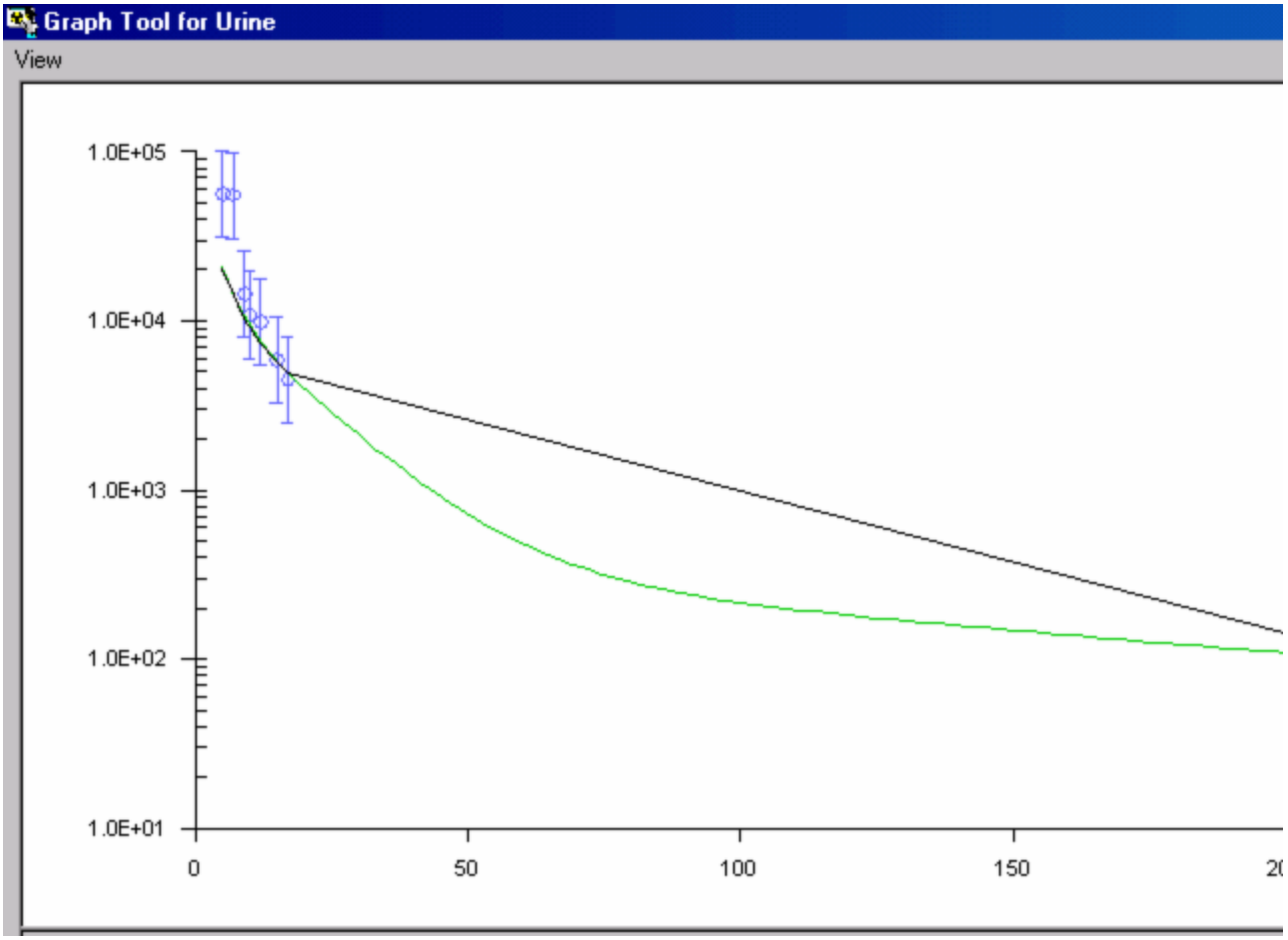


Figure 4.80. Graph Tool **plot of** urine **data.**

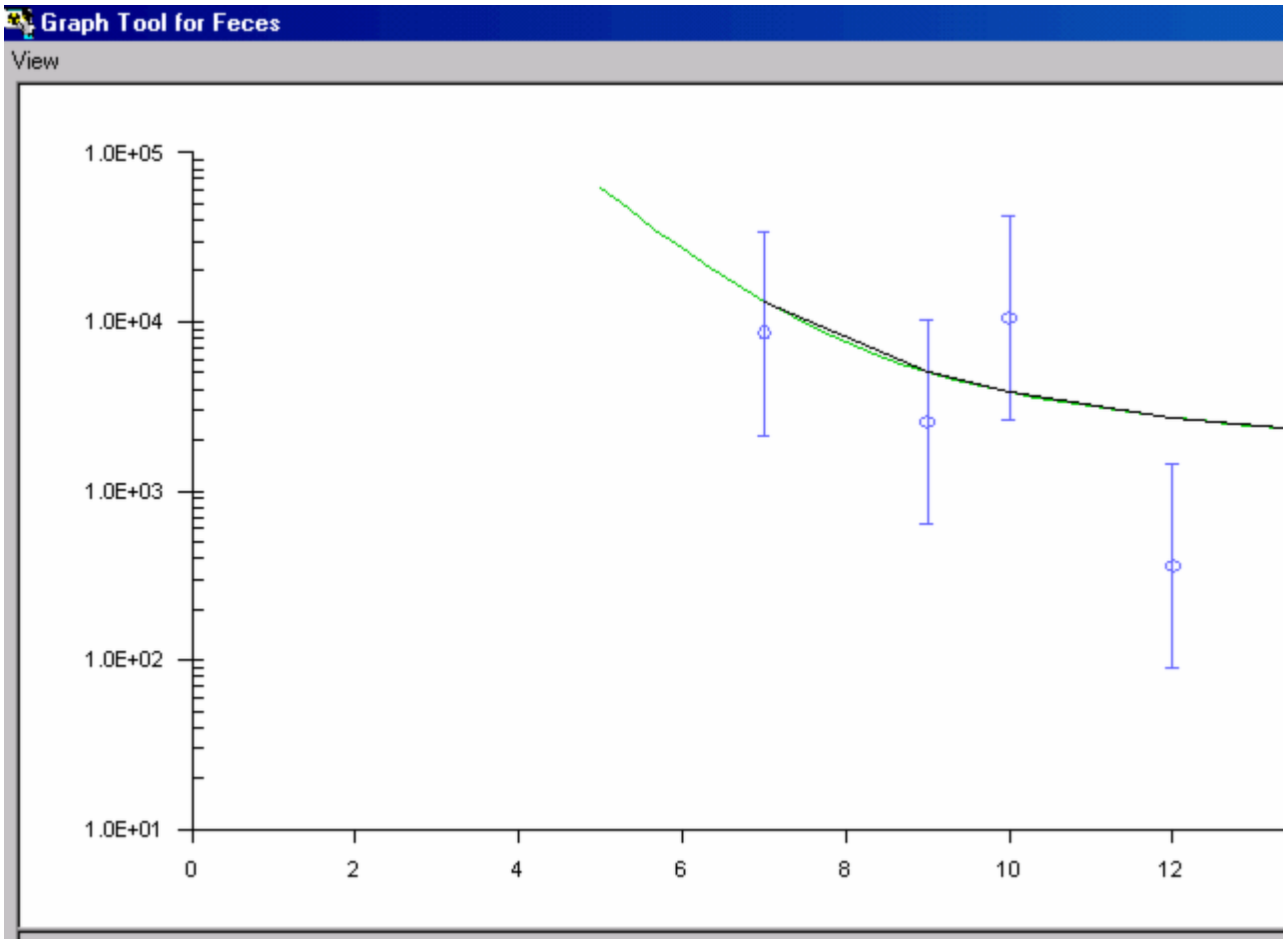


Figure 4.81. Graph Tool **plot of** faecal **data.**

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-µm-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**.**

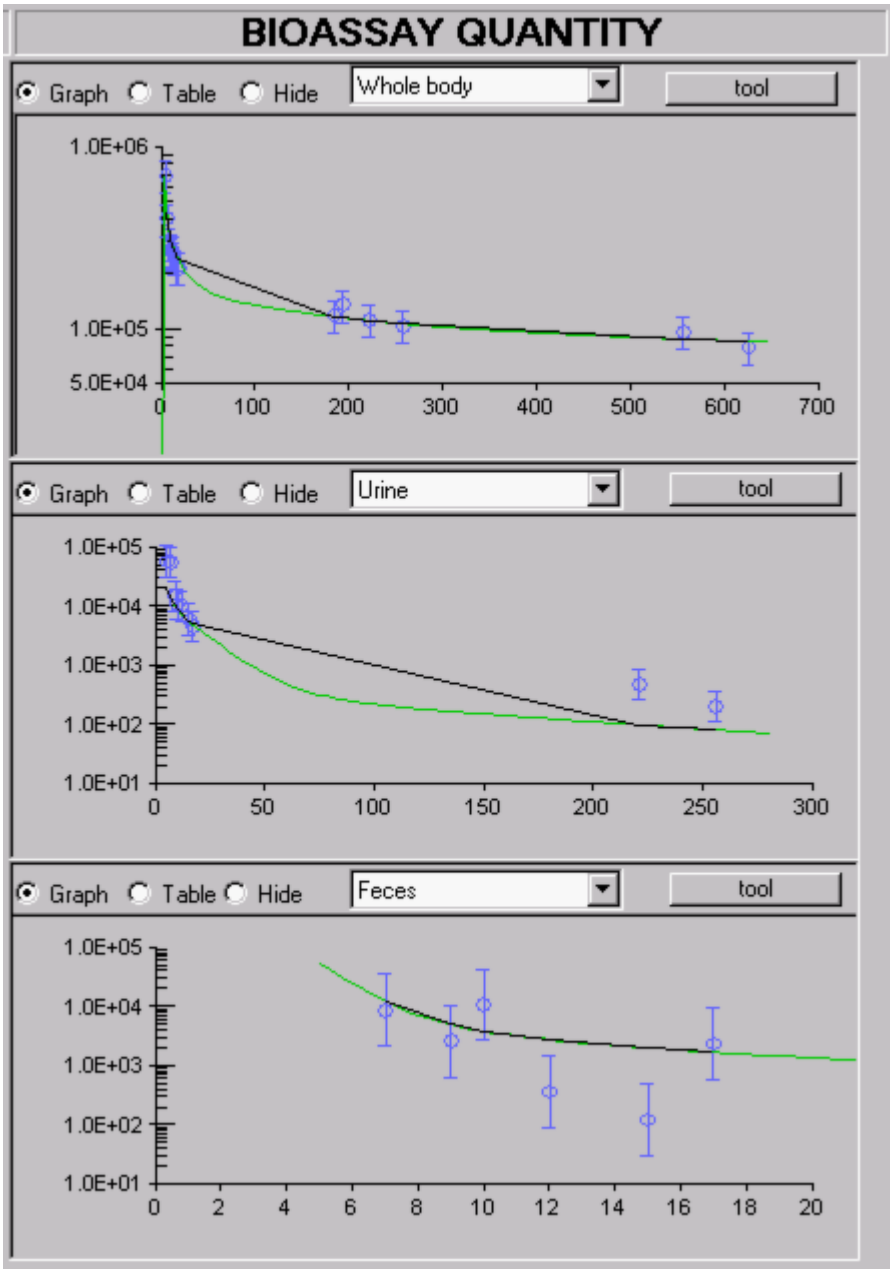


Figure 4.82. **"Best Fit" to the bioassay data obtained when the intake is assumed to be by ingestion.**

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," IMBA Professional 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.

Tip: IMBA Professional is designed to make it easy for you to test a range of hypothetical intake scenarios - when knowledge of the conditions of intake is sparse (as is often the case). It is then just as easy (and quick) to examine the implications of the most likely scenarios for dose.

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.**
2. **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.

Note: The Associated Radionuclide (90**Y**) is included in the dose calculations. The ICRP-recommended biokinetic models are assumed for both 90**Sr** and 90**Y**, and also the ICRP68 radiation and tissue weighting factors.

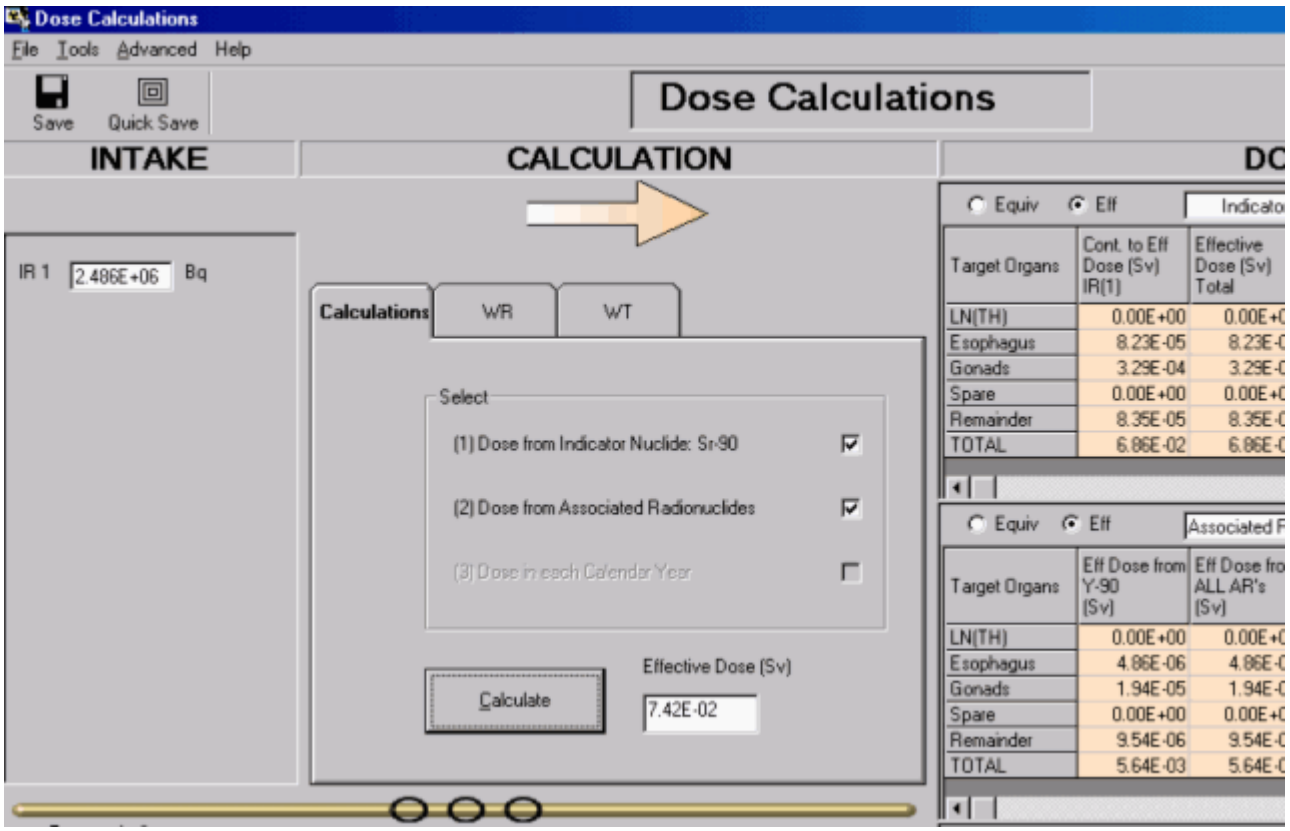


Figure 4.83. **Effective doses calculated for** ingestion **of** 90**Sr/**90**Y powder.**

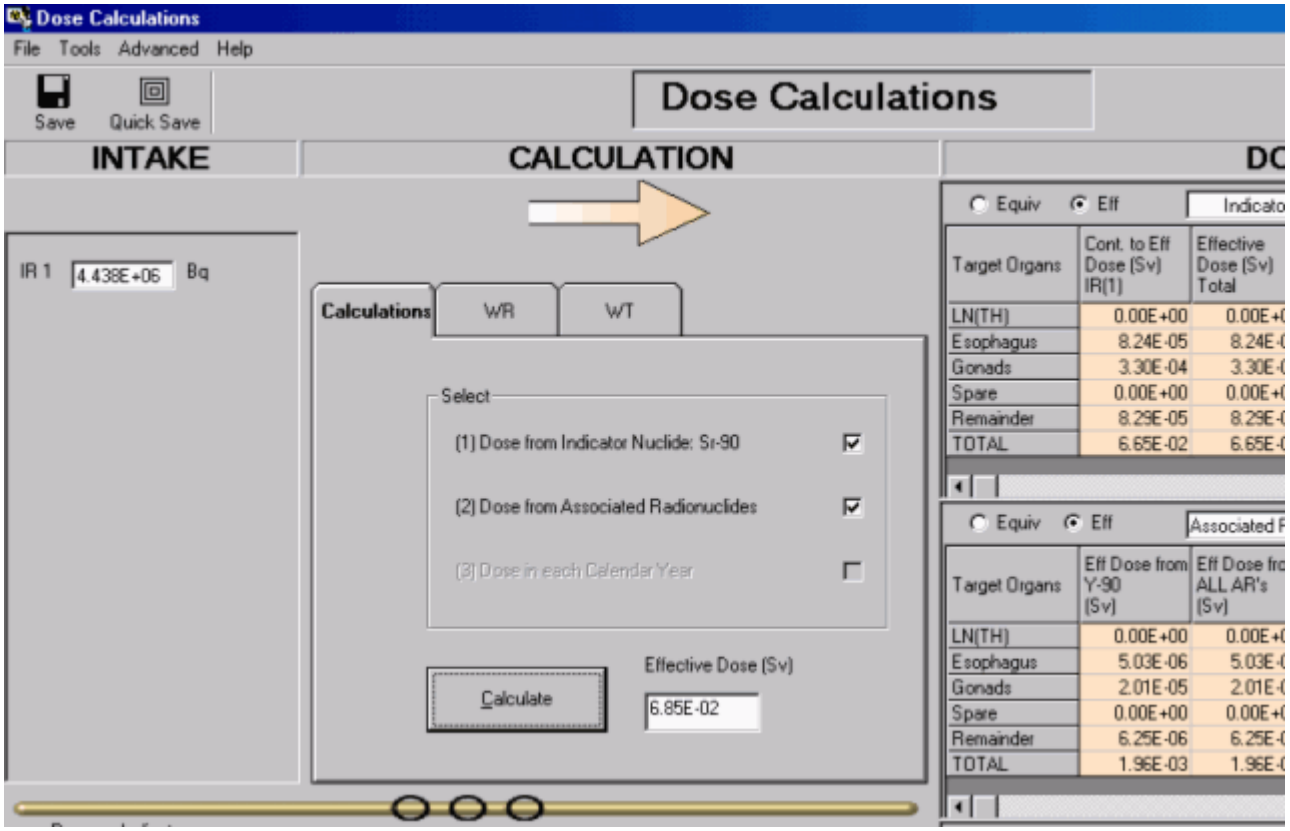


Figure 4.84. **Effective doses calculated for inhalation of $^{90}Sr/^{90}Y$ aerosol (100-µm-AMAD, Type "F").**

Table 4.6. **Comparison of effective doses calculated by assuming intake by ingestion or inhalation.**

Route of Intake	Effective Dose from ^{90}Sr (mSv)	Effective Dose from ^{90}Y (mSv)	Total Effective Dose (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**.**

Note: The Associated Radionuclide (^{90}Y) is included in the dose calculations. The ICRP-recommended biokinetic models are assumed for both ^{90}Sr and ^{90}Y, and also the ICRP68 radiation and tissue weighting factors.

This completes the final step in the multiple bioassay quantities example (Evaluating the Dose):

- Return to the case description and list of steps.

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 µm.
- 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 IMBA Professional Plus 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

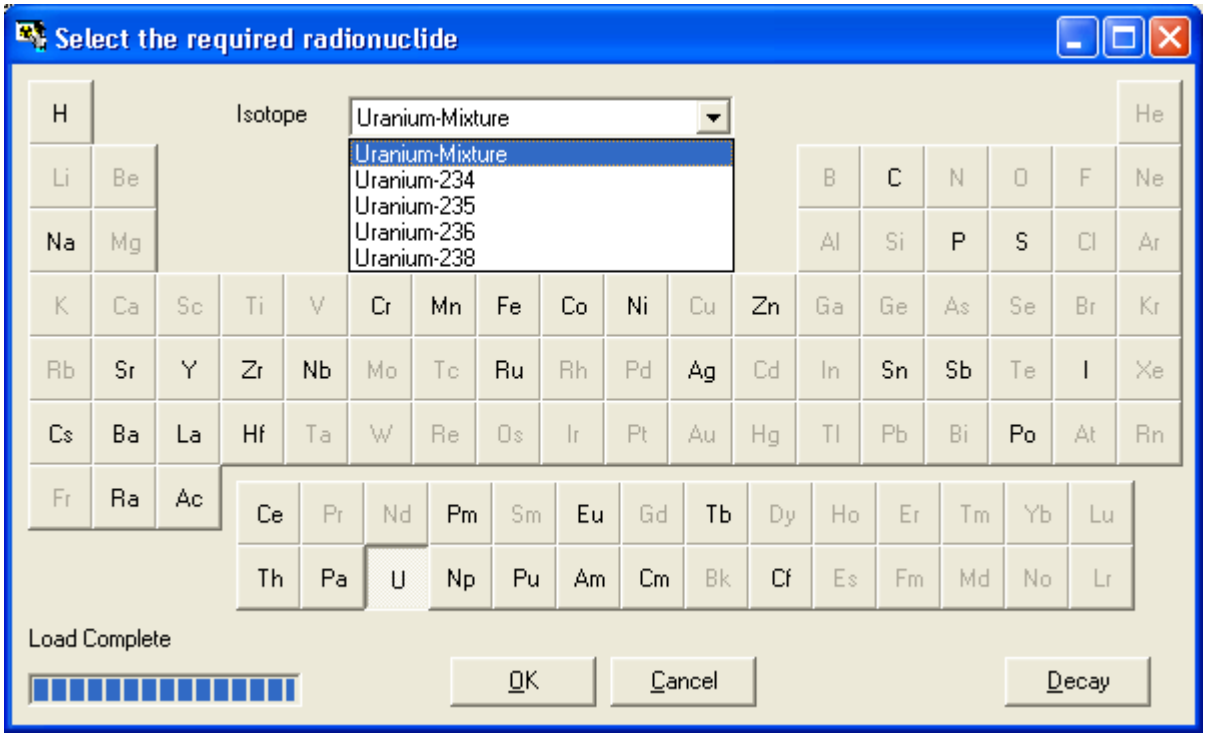


Figure 4.92. Selecting Uranium-Mixture as the Indicator Nuclide.

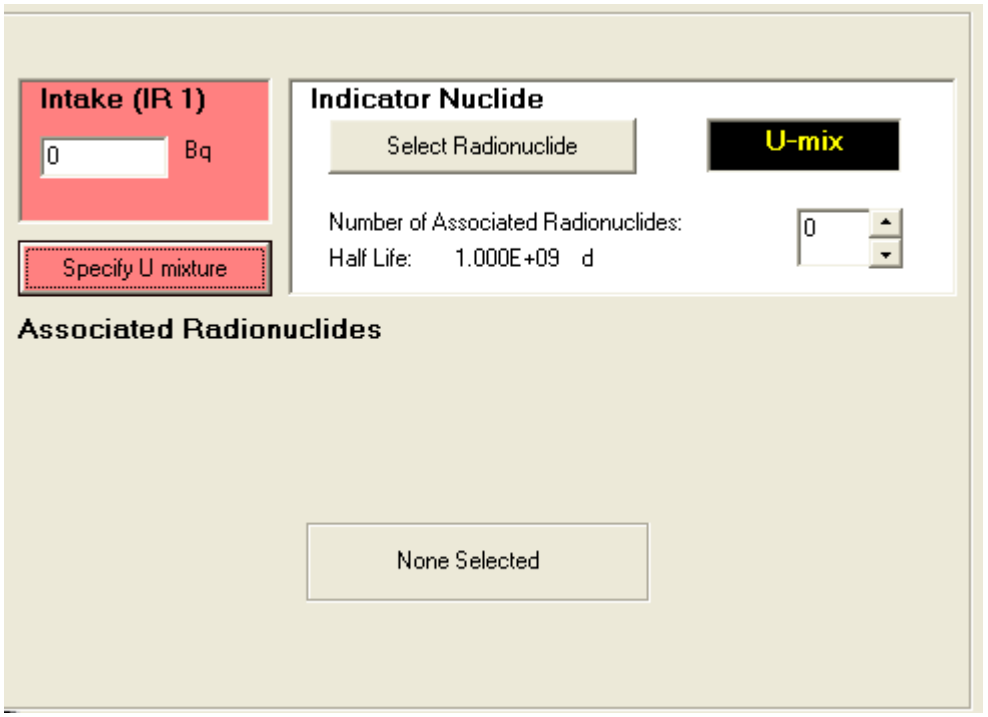


Figure 4.93. "Specify U mixture" button.

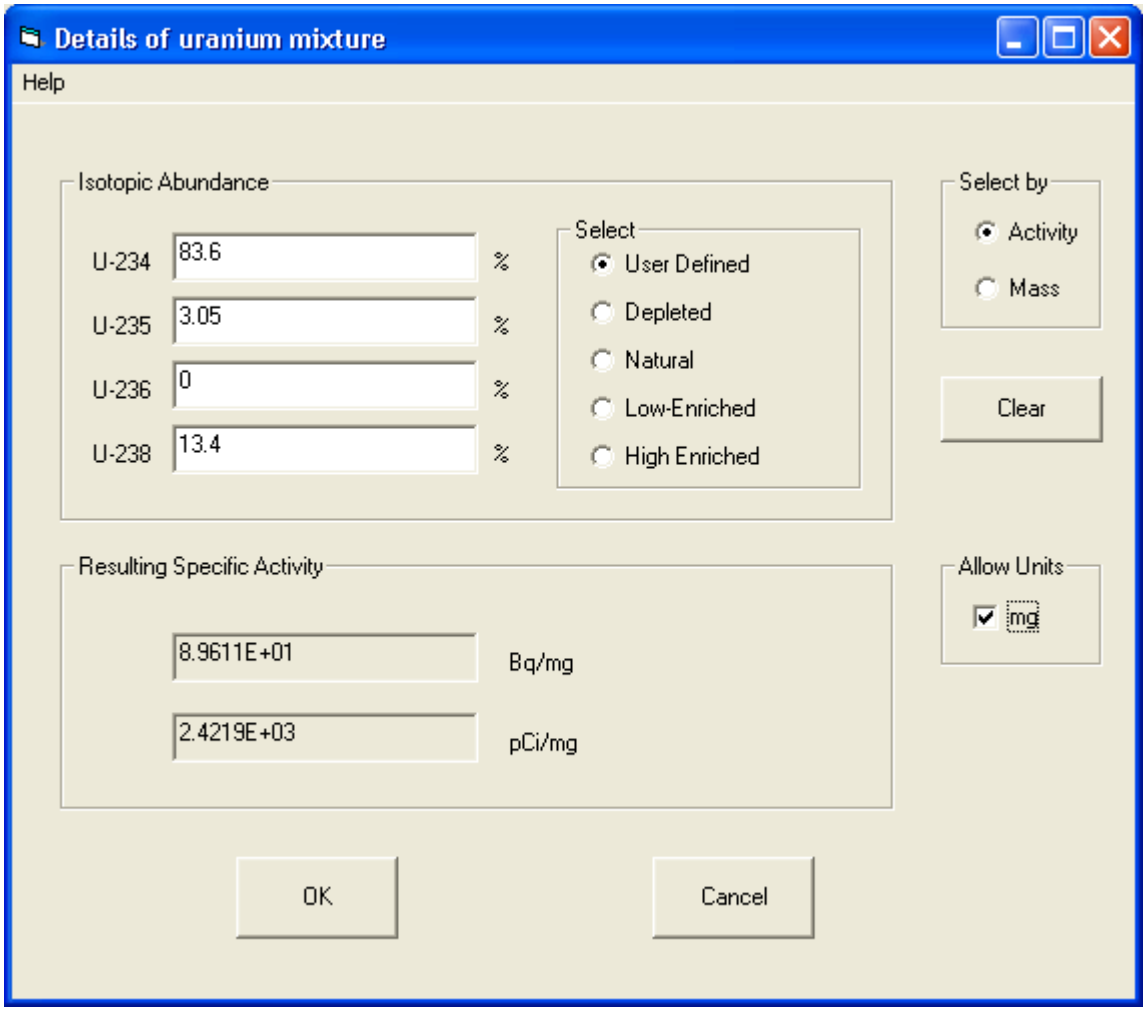


Figure 4.94. User Defined details of uranium mixture with resulting specific activity.

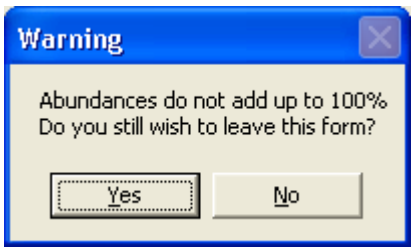


Figure 4.95. Warning notice.

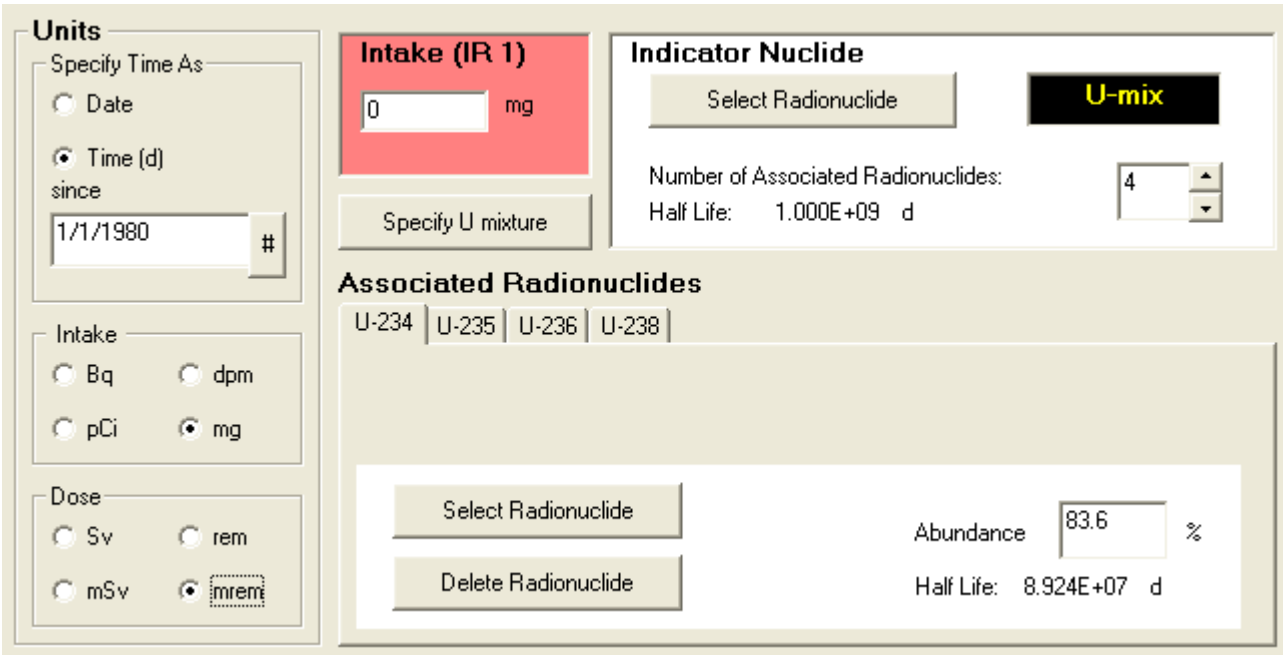


Figure 4.96. Selected U-mix showing Associated Radionuclides and "mg" Intake Unit.

To define the isotopic composition and measurement unit for the uranium mixture:

1. Select "Uranium-Mixture" as the Indicator Nuclide (Figure 4.92).
2. Click the "Specify U mixture" button (Figure 4.93).
3. Enter the Isotopic Abundance values (% by Activity in this case), check the Allow Units "mg" box (Figure 4.94), and click "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".

Note #1: The calculated specific activity of the defined uranium mixture is automatically displayed in the "details of uranium mixture" window" (Figure 4.94).

Note #2: The individual uranium isotopes (**234**U, **235**U, **236**U and **238**U) are automatically loaded as Associated Radionuclides. This is done in readiness for the Dose Calculation.

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 Table Tool of IMBA Professional Plus. Note that:

- **These are real 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 bioassay quantity) is the calculated daily uranium excretion rate - in µg d-1.**
- **We have assumed a lognormal error distribution, with a sg of 1.8. This is a more realistic representation of the data variability than the reported measurement uncertainties. The measurement uncertainties do NOT represent the sytematic (biological) variability in urinary excretion - which is substantially greater.**

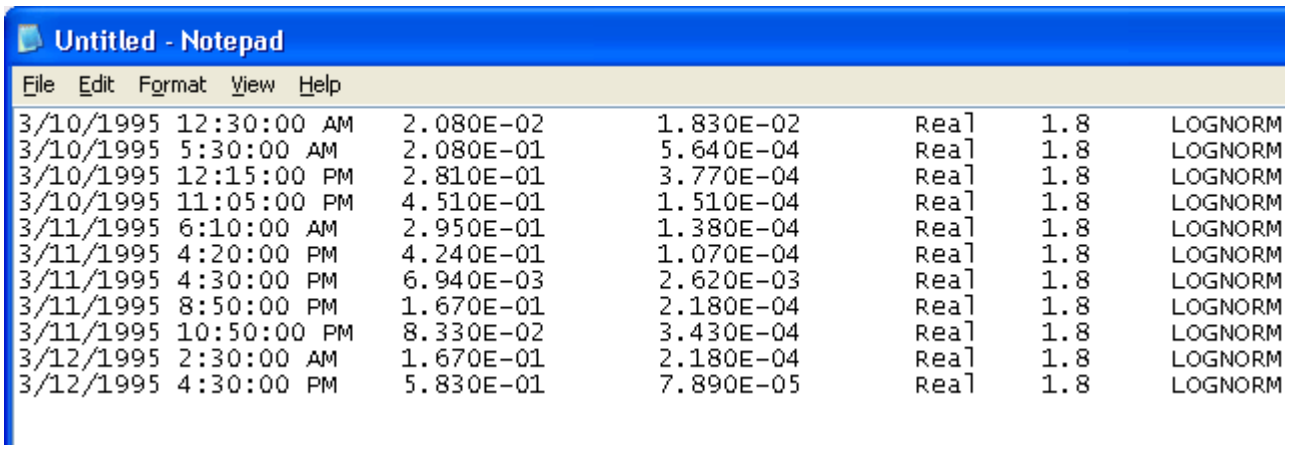


Figure 4.97. **Uranium-in-urine bioassay data set.**

Tip: **The reported (normal) measurement errors are given in the data file "IU_URINE_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 2nd Step in the uranium isotopic mixture example:

- Proceed to Enter Fecal Data.
- Return 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 real 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 lognormal error distribution, with a sg of 3.0 ,c.f., sg = 1.8 for the urine data. This is a more realistic representation of the variability in fecal excretion rate than the reported measurement uncertainties. The raw measurement uncertainties drastically underestimate the sytematic (biological) variability in fecal excretion.**

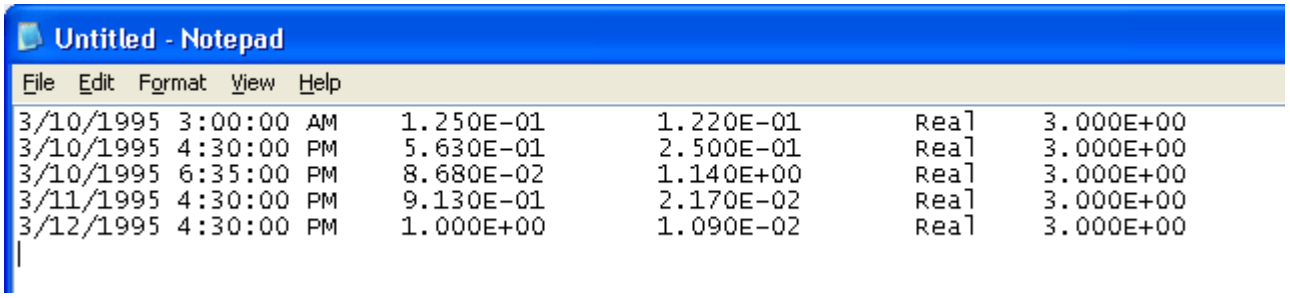


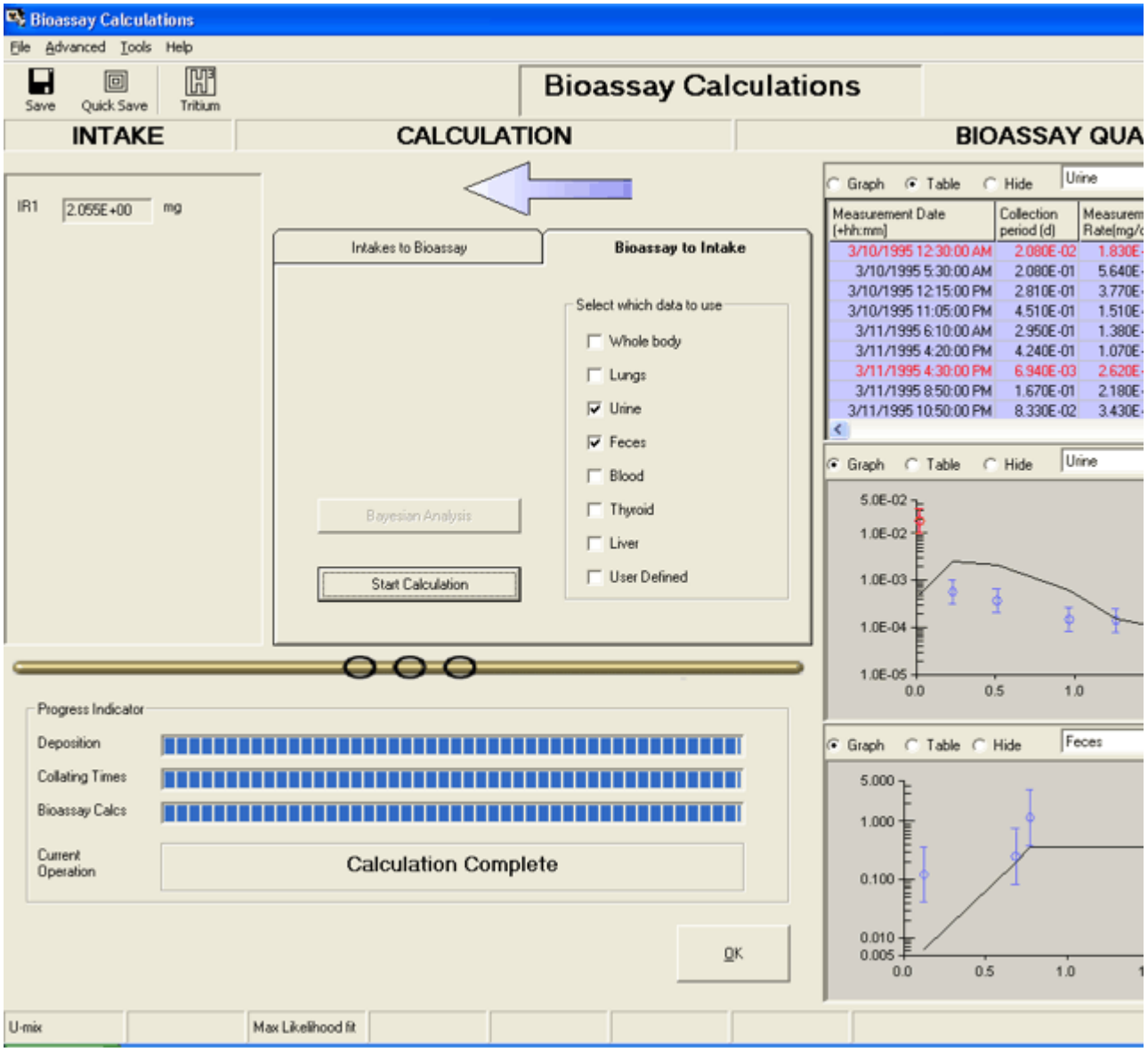
Figure 4.98. **Uranium-in-feces bioassay data set.**

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:

- Proceed to Initial Joint Analysis of Urine/Fecal Data.
- Return to the case description and list of steps.

Initial Joint Analysis of Urine/Fecal Data



4.99. **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:

- Acute inhalation**, at** t = 0.
- Aerosol characteristics **-** AMAD/MMAD **= 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.
- GI-Tract transport parameters - ICRP66 Default.
- Gut uptake fraction (f1) - 0.002 (ICRP68 - highly insoluble uranium compounds: UO2, U3O8).
- Two reported uranium-in-urine outlier values have been excluded from the "fit":
  - the first value (from the sample collected 30 minutes after the intake) is assumed to result from sample contamination. the rate of excretion of uranium in urine following an acute intake requires several hours to "build up" - it does NOT decrease over this period.
  - the seventh value (from the sample collected at about 1.8 d after the intake) is also assumed to result from sample contamination.

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 predicted urinary excretion rate falls off more rapidly than the measured values.
- After the first day, the observed urinary excretion rates are relatively constant.
- The predicted fecal excretion rate peaks at approximately the same time 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 an order of magnitude lower than the measured rate.
- After the measured "peak" in fecal excretion of uranium (during the first day), the measured excretion rate is about an order of magnitude lower than that predicted.

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 relatively constant source of intake. The obvious candidate is dietary intake.

This completes the 4th Step in the uranium isotopic mixture example:

- Proceed to Correct for Dietary Uranium Intake.
- Return to the case description and list of steps.

Correct for Dietary Uranium Intake

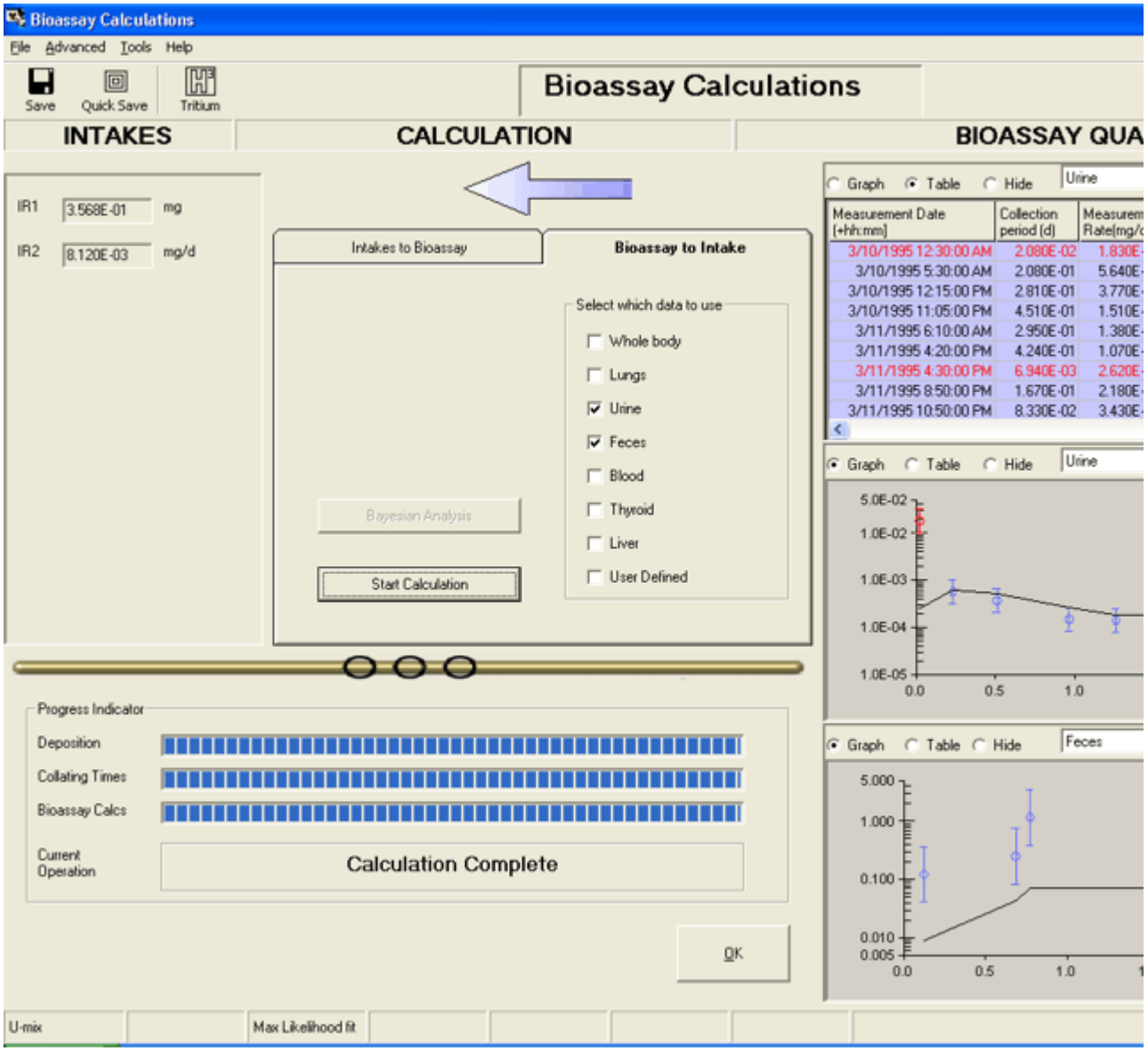


Figure 4.100. **Data "fit" for assumed combination of acute inhalation with background chronic ingestion.**

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 gut uptake fraction, f1 = 0.02, i.e., 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 µg/d) fitted on the assumption of 'moderate' absorption (corresponding to the assumed f1 value of 0.02). In fact, the data shows that the early fecal excretion rates were about an order of magnitude higher than the fitted rates - without significantly influencing urinary excretion. This can only happen if the chronically ingested material has a substantially lower value of f1 than we assumed here, i.e., the dietary uranium is significantly less readily absorbed. So, we can expect to improve the data "fit" by finding more appropriate parameter values, i.e., by optimizing the intake model.

This completes the 5th Step in the uranium isotopic mixture example:

- Proceed to Optimize Intake Model Parameters.
- Return to the case description and list of steps.

Optimize Intake Model Parameters

In reality, the "background" dietary intake would have been "natural" uranium, and not "LEU" - as assumed in the previous analysis. Therefore a different conversion factor to mass 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 3.55 - in the ratio of the specific activities of LEU:U-Nat (approximately 2,422:683). 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.**

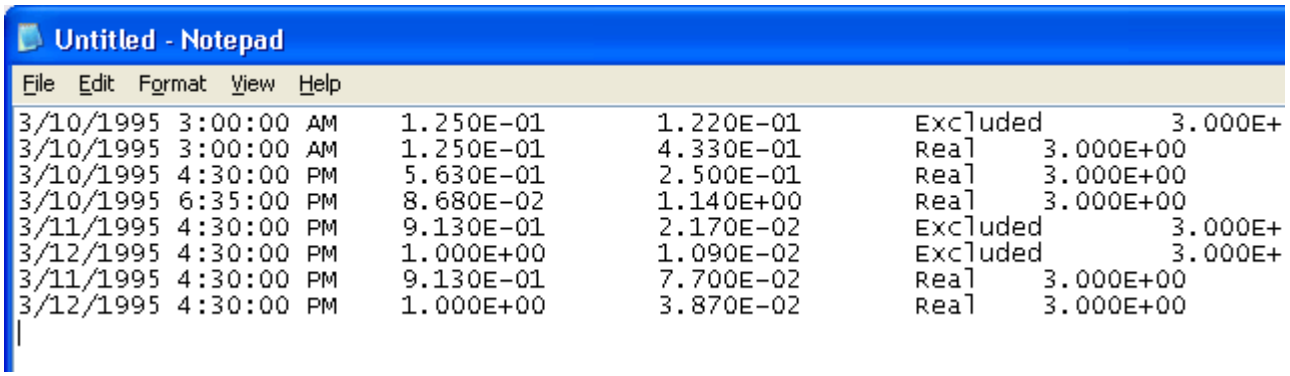


Figure 4.101. **Adjusting the 1st, 4th and 5th values of uranium mass excretion rates for the specific activity of natural uranium.**

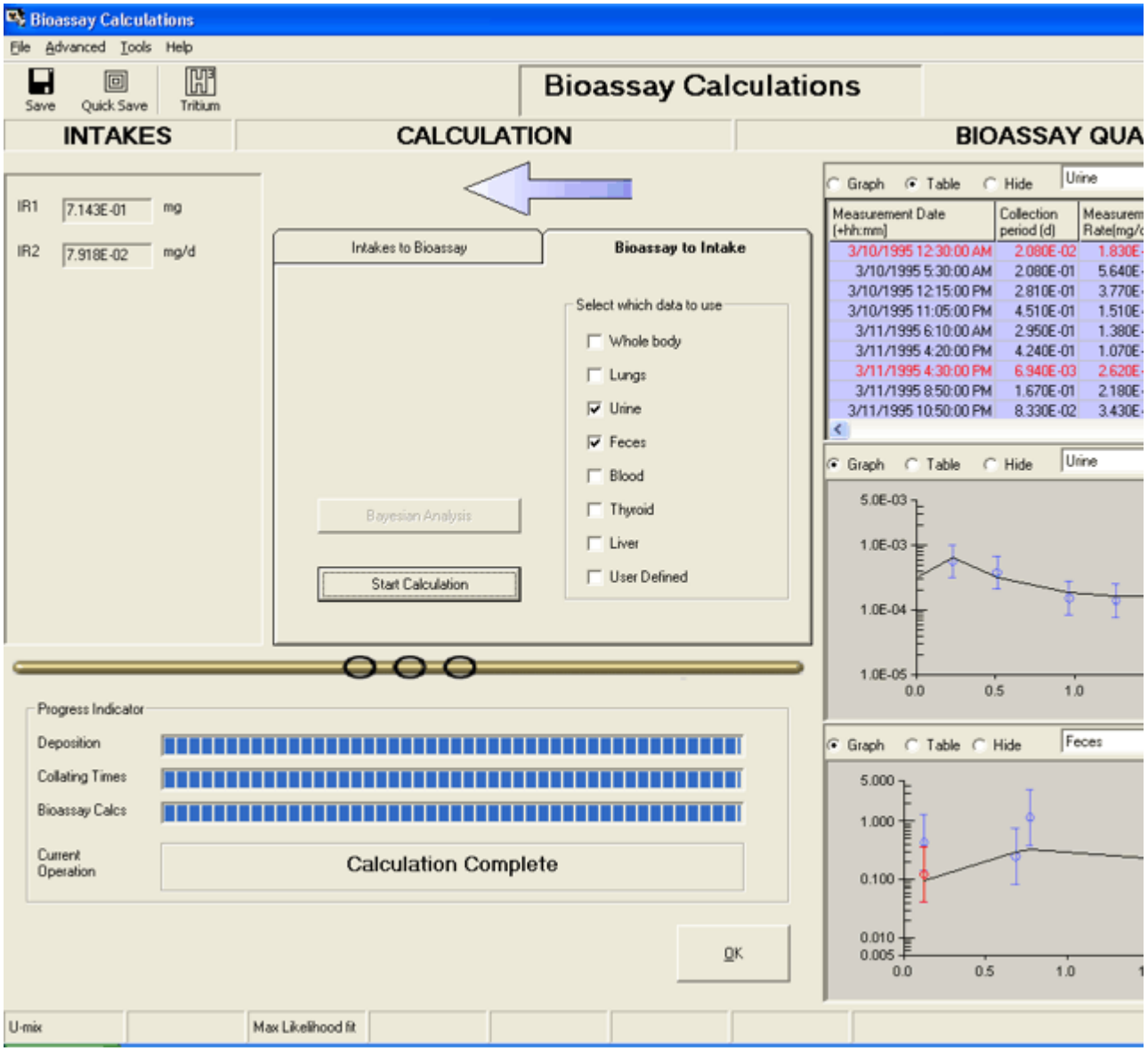


Figure 4.102. **Data "fit" obtained by "optimizing" intake and GI-tract model parameter values - with adjusted "baseline" fecal uranium mass excretion rates.**

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 f1 value for the acute inhalation (IR1) to 0.0002 (from the "default" value of** 0.002**).**
2. Reducing **the f1 value for the "background" chronic dietary intake (IR2) to 0.002 (from the "default" value of** 0.02**).**
3. Doubling **the rate of transport through the SI to 12 d-1 (from the "default" value of** 6 d-1**).**
4. Doubling **the rate of transport through the ULI to 3.6 d-1 (from the "default" value of** 1.8 d-1**).**
5. Doubling **the rate of transport through the LLI to 2 d-1 (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.**

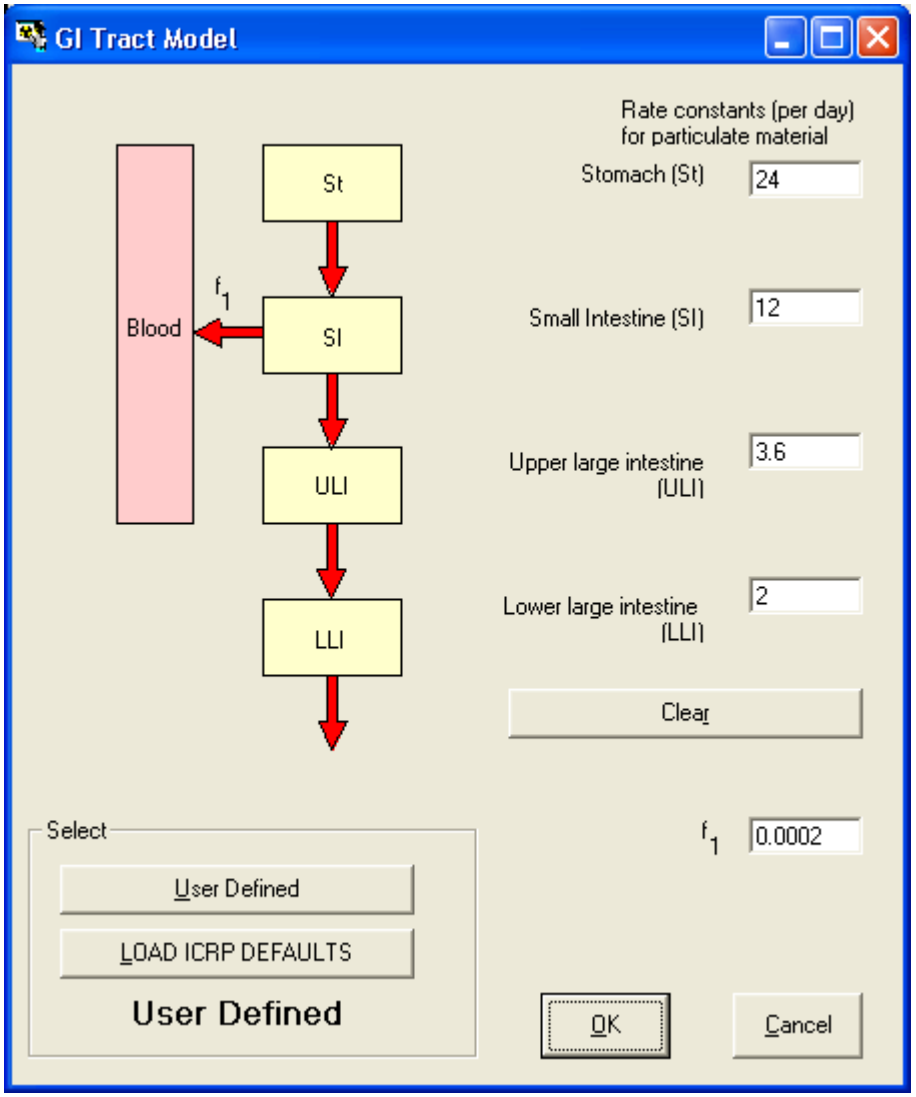


Figure 4.103. **"User Defined" values of rate constants in the GI Tract model.**

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 6th Step in the uranium isotopic mixture example:

- Proceed to Committed Doses from U-Mixture.

- Return 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 79.2 µg d-1 (assumed here to have started at 0:00 AM on March 10th, 1975).**

As for all dose calculations, for this "Uranium Mixture" case, you calculate the resulting committed doses by clicking 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 (IR1).

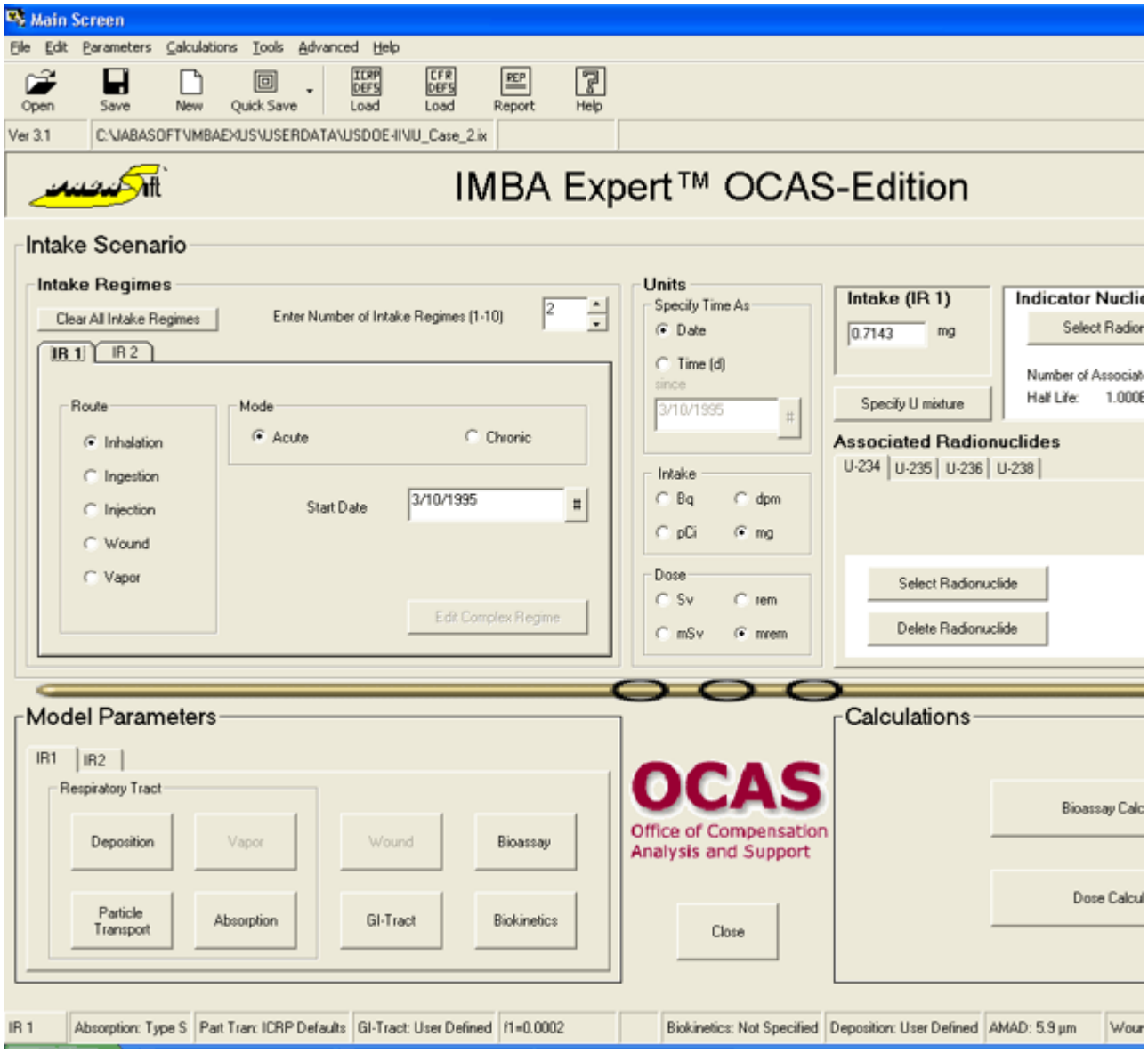


Figure 4.104. "Dose Calculations" button for calculating committed doses for a Uranium Mixture (treated as Associated Radionuclides).

For this example, we have:

- Checked "mrem" as the dose unit (Figure 4.104).
- Reduced the number of intake regimes to ONE (IR1) - also shown in Figure 4.104.
- Selected the "ICRP Default" values of radiation weighting factor (wR) - in the "Dose Calculations" screen.
- Selected the "10CFR835 Default" values of tissue weighting factor (wT).
- Checked the "Dose from Associated Radionuclides" box .
- Checked the "Dose Committed in Each Calendar Year" box.
- Selected the "Speed" calculation option from the Advanced | Advanced Dosimetry Options | Dose menu (Figure 4.105 - see also Appendix A: Effect of Merging SEEs).
- Clicked the "Calculate" button.

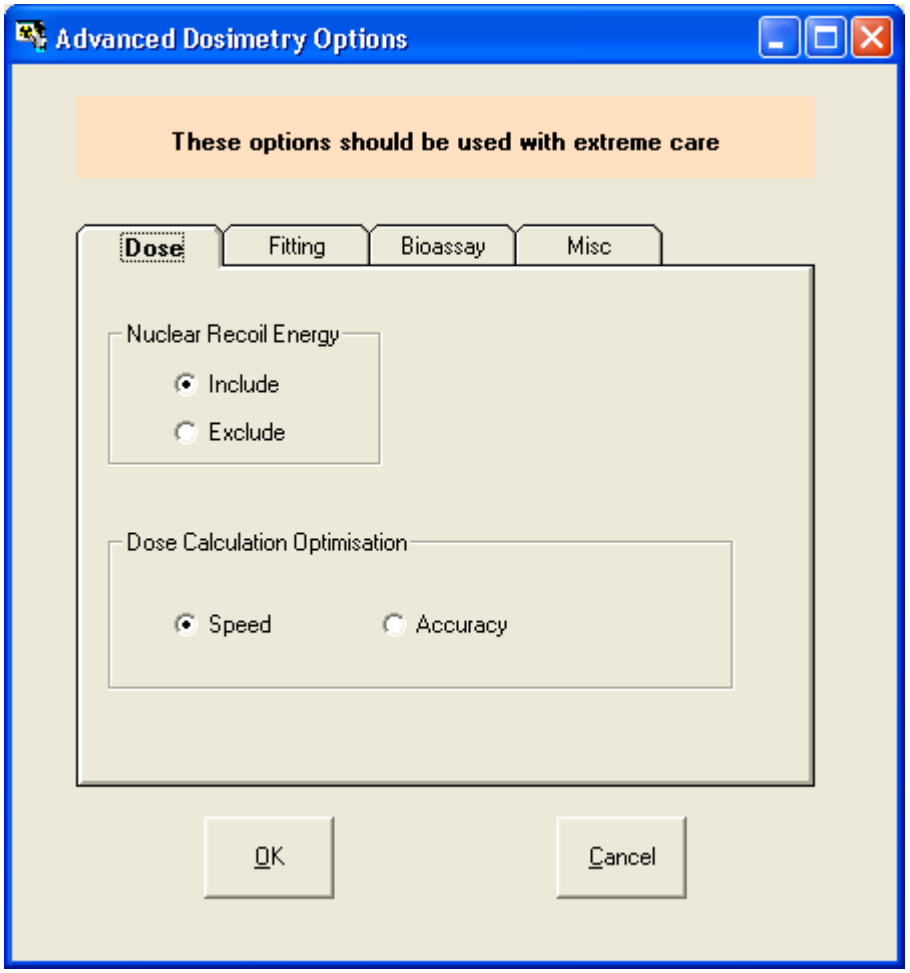


Figure 4.105. **Selecting the "Speed" option - to "merge" the initial short-lived progeny of 235U and 238U.**

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 Appendix C: Dose Quality Assurance 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.

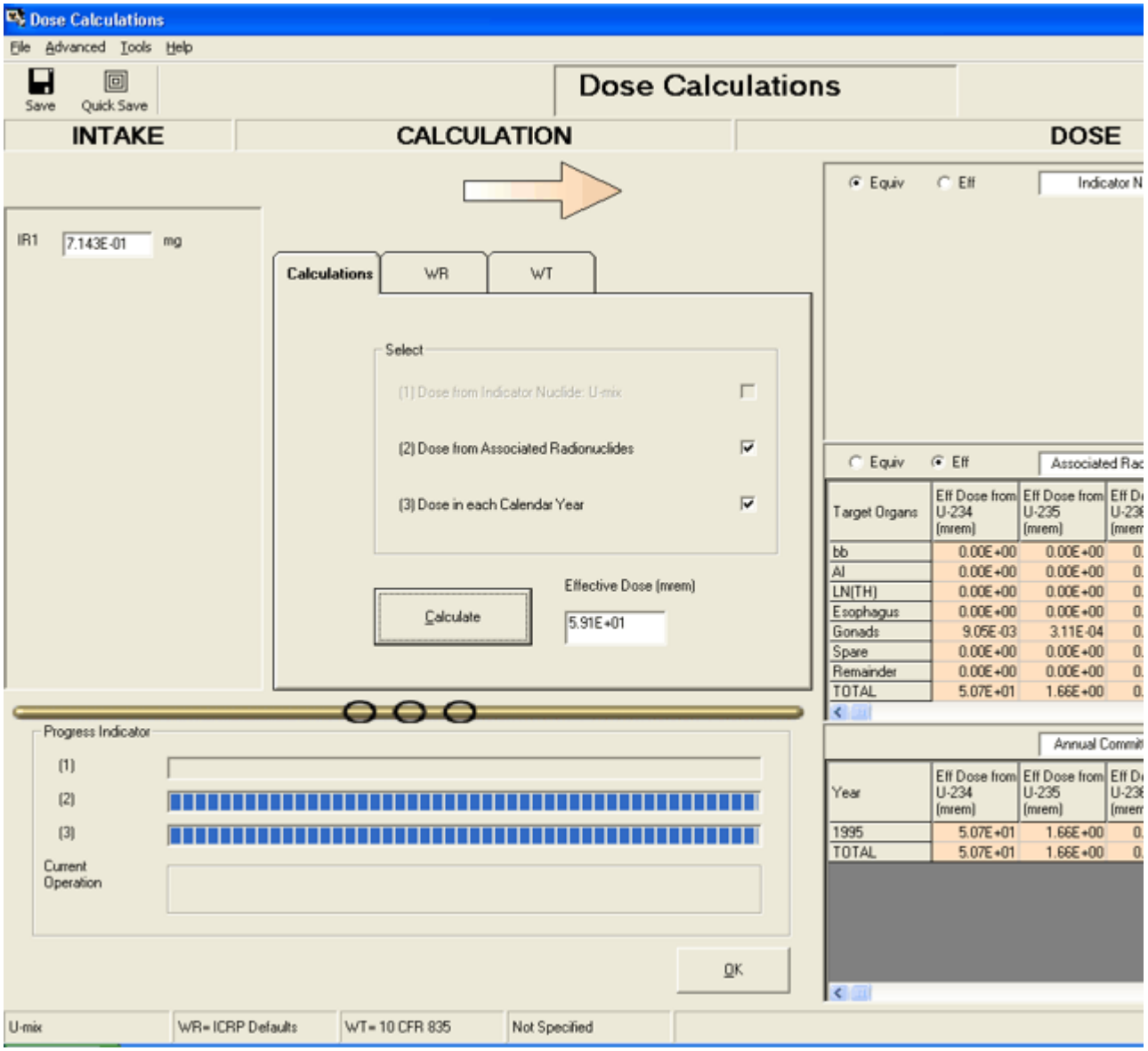


Figure 4.106. **Calculated total effective dose together with the year in which it was committed.**

Figure 4.106 shows that:

- **The committed effective dose from the estimated acute intake of LEU (IR1 = 0.714 mg) is 59.1 mrem.**

This completes the Last Analytical Step in the uranium isotopic mixture example:

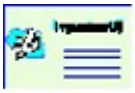
- Proceed to Published Data on "Background" U-in-Urine.
- Return to the case description and list of steps.

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 µg/d, with a standard deviation of 0.11 µg/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.**



Note: The above data were reported as volumetric concentration (µg/L). They have been converted here to the daily excretion rate, assuming the New Reference Man (ICRP 2002b) value of 1.6 L/d urinary output.

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 µg/d. The value of 0.19 µg/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.

- Proceed 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 (f1 value of 0.02)

- **Joint analysis of the measured urinary and fecal uranium mass excretion rates gave an estimated (acute) LEU intake of 0.357 mg - with a corresponding committed effective dose of 29.6 mrem.**

"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 (± 0.246 mg standard error). The corresponding estimate of committed effective dose is 47.6 mrem (± 20.4 mrem standard error). In this case, reasonable agreement with the value of 59.1 mrem derived by more exhaustive analysis is fortuitous.**

Note #2: **The value of 0.575 mg acute LEU intake obtained using 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 ^{125}I 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 ^{125}I activity at the wound site had fallen to about 3.5% of the original measurement. At 7 d, the ^{125}I activity at the wound site remained at about 3.5% of the original measurement. At 13 d, the ^{125}I activity at the wound site had dropped to about 1.8%.

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	5,000 ± 2,000
-151	2,000 ± 3,000
0.1	6,000 ± 2,000
4	14,000 ± 3,000

7	10,000 ± 3,000
13	15,000 ± 3,000
34	16,000 ± 3,000
75	3,000 ± 3,000
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.

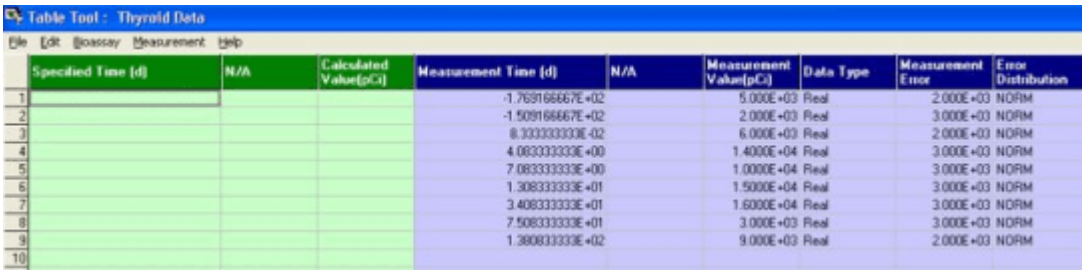


Figure D.147. Input data on thyroid uptake of 125I with assumed error distribution.

In this example, we will:

- **Set up a** "Wound" intake scenario**.**
- Test "default" assumed value(s) for the uptake rate(s) from the wound to blood.
- Derive the most likely absorption rate(s) from the wound to blood.
- Calculate the Bayesian "Posterior Probability Distribution" of the intake amount.

Setting Up Wound Intake

The necessary steps (carried out in the Main Screen) are:

1. Set the Reference Date, i.e., the Date and Time of the incident.
2. Select the Indicator Nuclide, i.e., Iodine-125.
3. Select the "Wound" radio button to define the Intake Scenario – in the "Model Parameters" panel (Figure D.148).

Selecting "Wound" as the Intake Scenario will automatically activate the "Wound" model button (displayed in pink in Figure D.148).

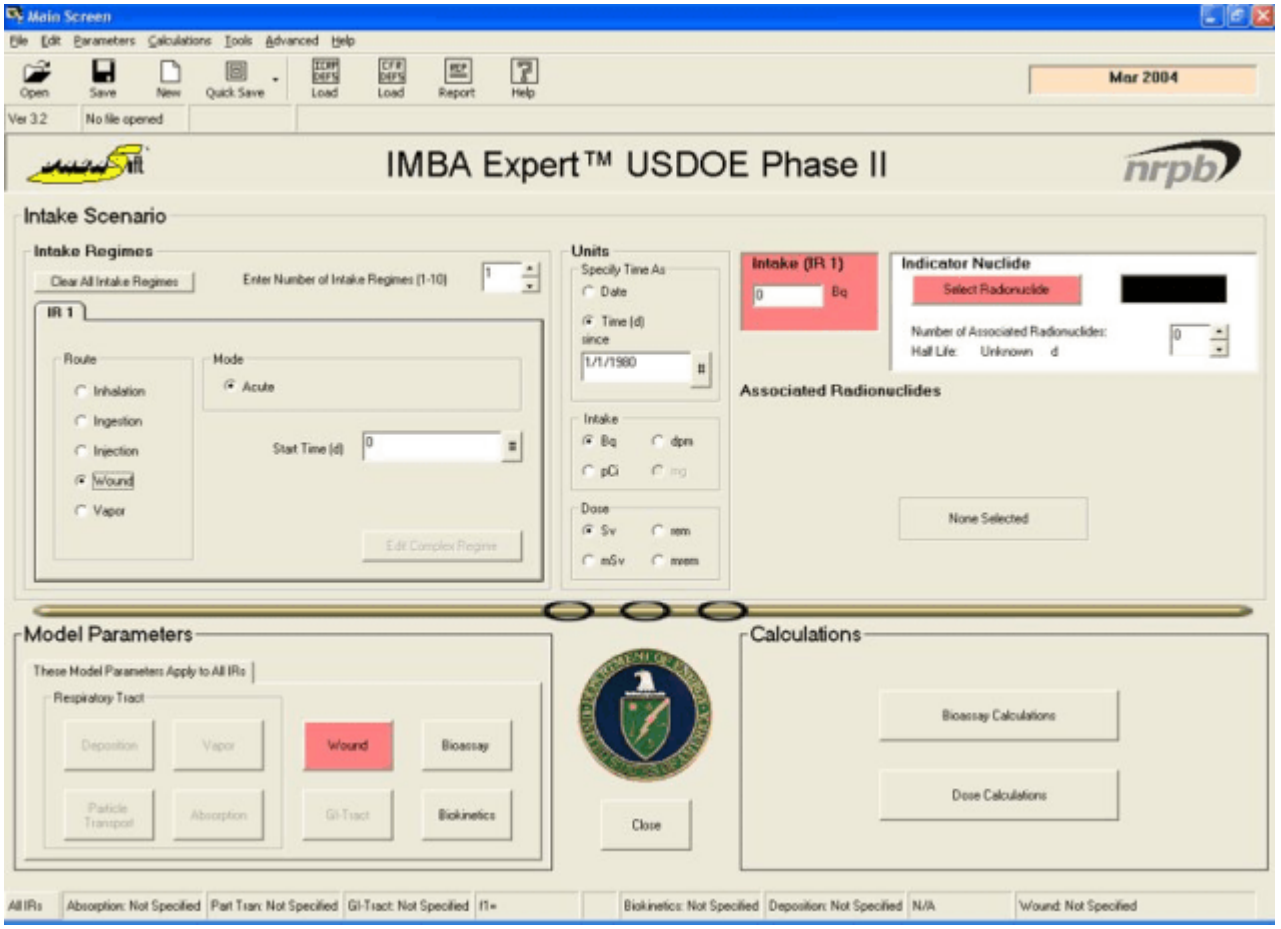


Figure D.148. Main Screen with activated button to define the "Wound" model.

Click the "Wound" model button to open the 'Generic Wound Model' window (Figure D.149).

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 "generic" form of "wound model", 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 "User Defined Mode" by clicking the so-named button (Figure D.150).

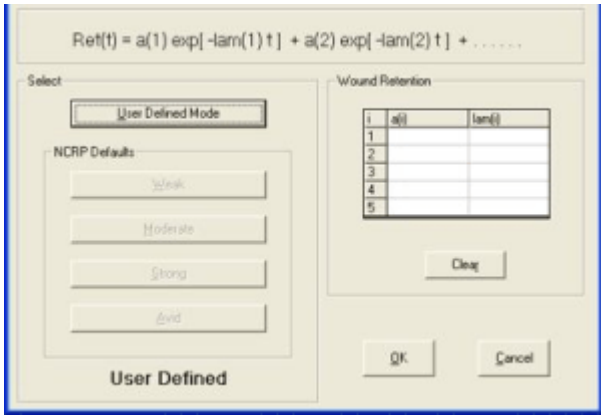


Figure D.150. User Defined Mode for entering a "Wound Retention" function.

For all compounds of iodine, ICRP Publication 68 (ICRP 1994b) recommended Type 'F' to represent absorption from the respiratory tract (at a characteristic rate of 100 d-1), with a GI-tract absorption fraction of 1. Therefore, as a first "guess", it is reasonable to assume very rapid uptake of the 125I "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):

- a(1) = 1;
- lam(1) = 100 d-1.

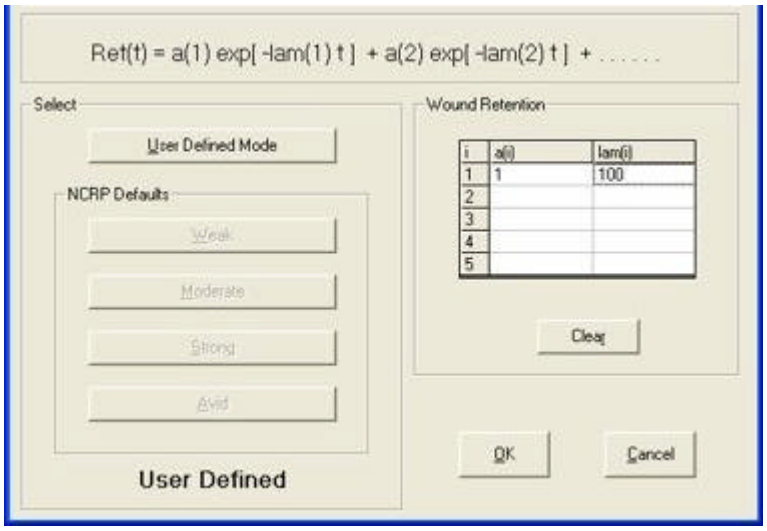


Figure D.151. Setting the rate constant for retention in a wound as 100 d-1.

In the next section, we will test how well this assumed rapid eleimination rate from the wound site "fits" the measured time-course of 125I uptake and retention in the thyroid.

- Proceed to the next step in this example case.
- Return to the case description.

Test Default Absorption Rates

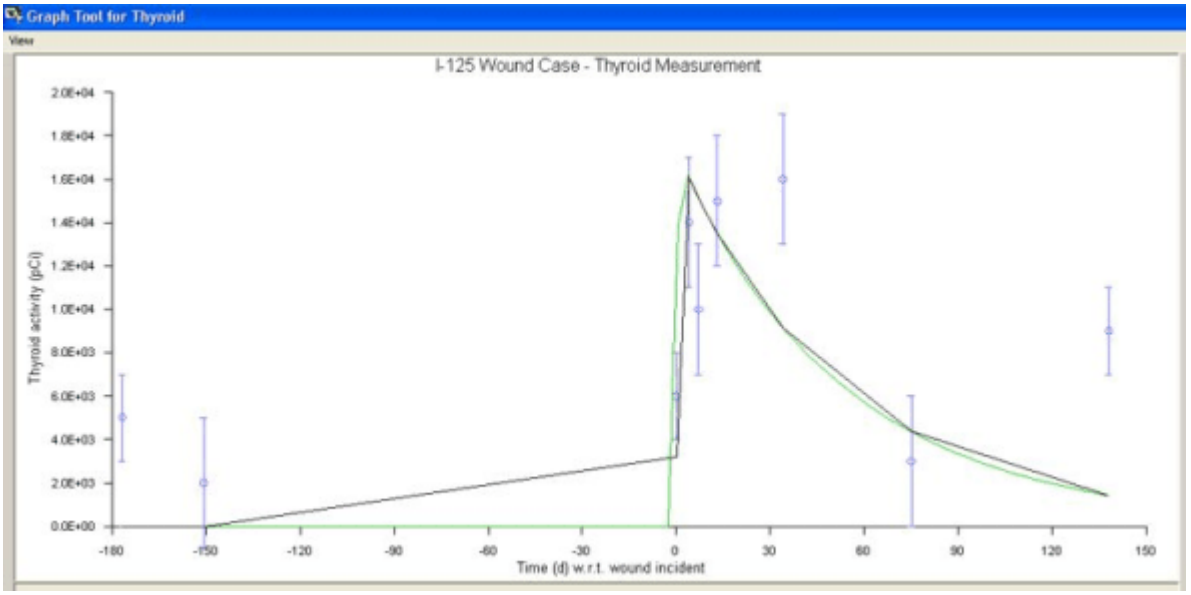


Figure D.152. Thyroid uptake and retention predicted for 'rapid' release of 125I from the wound site to the blood.

The assumed uptake rate of 100 d-1 accounts well for the observed rapid initial uptake of 125I by the thyroid, but not for the apparent "retention" of 125I in the thyroid up to 34 d after the incident. The calculated total value of the c2 statistic (as shown in the Table Tool – Figure D.153) is 32.2. This is substantially higher than the "expected" value (= 9), which is equal to the number of data points.

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	Real	2.000E+03	NORM	0.000E+00	6.250E+0(
-1.509166667E+02		2.000E+03	Real	3.000E+03	NORM	0.000E+00	4.444E-01
8.333333333E-02		6.000E+03	Real	2.000E+03	NORM	3.2291E+03	1.920E+0(
4.083333333E+00		1.4000E+04	Real	3.000E+03	NORM	1.6273E+04	5.741E-01
7.083333333E+00		1.0000E+04	Real	3.000E+03	NORM	1.5341E+04	3.169E+0(
1.308333333E+01		1.5000E+04	Real	3.000E+03	NORM	1.3664E+04	1.984E-01
3.408333333E+01		1.6000E+04	Real	3.000E+03	NORM	9.2471E+03	5.067E+0(
7.508333333E+01		3.000E+03	Real	3.000E+03	NORM	4.4193E+03	2.235E-01
1.380833333E+02		9.000E+03	Real	2.000E+03	NORM	1.434E+03	1.431E+01

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 c2, and these points are clearly NOT related to the incident (at time t = 0). Thus, the appropriate value of c2 to consider is that related to the 7 data points obtained "post-incident". This value is 25.5.

We can conclude that the assumption of an uptake rate of 100 d-1 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.

- Proceed to the next step in this example case.
- Return to the case description.

Most Likely Wound Uptake Rate(s)

IMBA Professional Plus allows up to 10 intakes to be analyzed simultaneously. In this case, and many others for which critical intake scenario 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 range of hypothetical values, and letting IMBA Professional Plus "rank" these values according to the amount of intake that it calculates for each. In this example, both the observed thyroid "retention" and the measured retention of contamination on the worker's hand 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 'wound' intakes at time t = 0. The 'hypothetical' rates tested are:

- IR1 = 100 d-1;
- IR2 = 0.2 d-1;
- IR3 = 0.1 d-1;
- IR4 = 0.05 d-1;
- IR5 = 0.02 d-1;
- IR6 = 0.01 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 c2 are shown in Figure D.155 (as displayed in the Table Tool).

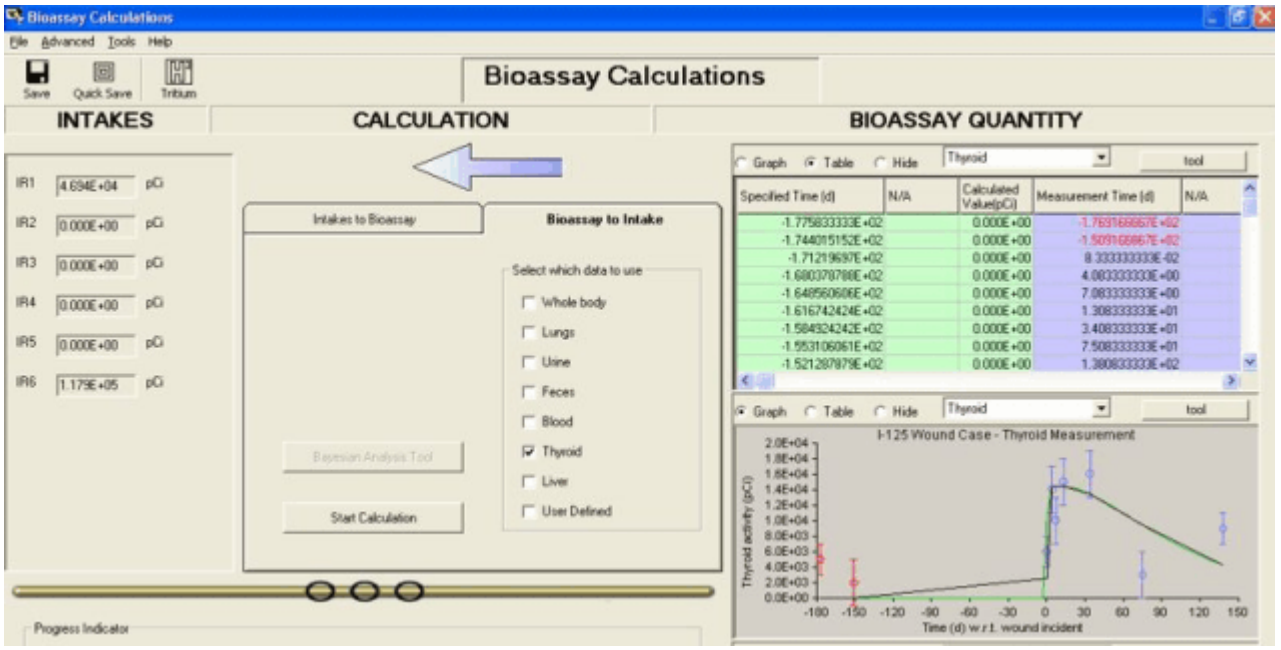


Figure D.154. Data 'fit' obtained with 6 hypothetical absorption rates.

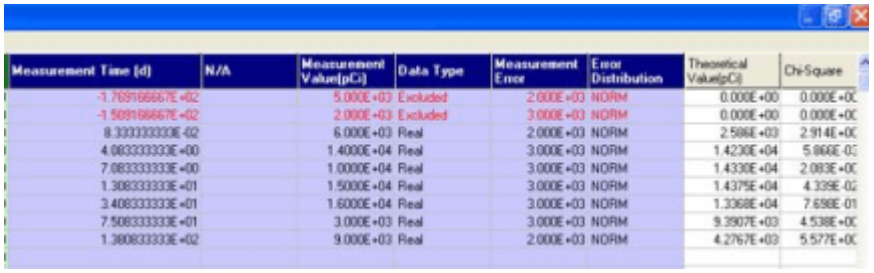


Figure D.155. Calculated values of c2 for 6 hypothetical absorption rates.

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-1 and 71.5% the slowest assumed absorption rate of 0.01 d-1. The total c2 is now reduced to 17.1. This is significantly lower than the previous value (obtained for 100% absorption at a rate of 100 d-1), but it is still significantly higher than the "expected" value (for the 7 residual data points).

However, the largest c2 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 "excluded" in the Table Tool (as we did for the first 2 data points – prior to the incident). The effect of excluding the last data point from the 'fit' is shown in Figure D.156.

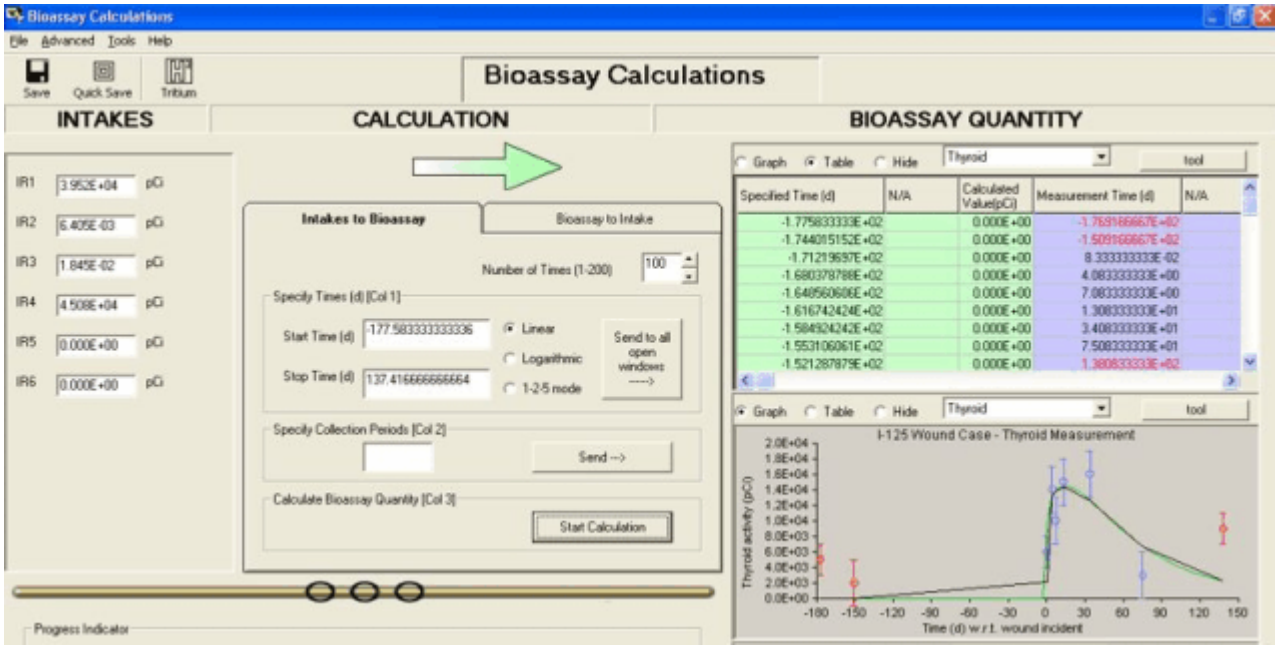
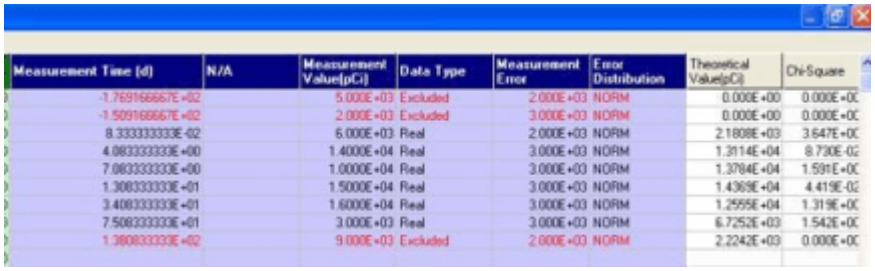


Figure D.156. Data 'fit' obtained by excluding the data point at 138 d.

Treating the data point at 138 d as an "outlier" clearly improved the 'fit' of predicted thyroid retention of 125I to the remaining 6 measured values. The resulting values of c2 are shown in Figure D.157 (from the Table Tool).



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+00
-1.509166667E+02		2.000E+03	Excluded	3.000E+03	NORM	0.000E+00	0.000E+00
8.333333333E-02		6.000E+03	Real	2.000E+03	NORM	2.180BE+03	3.647E+00
4.083333333E+00		1.4000E+04	Real	3.000E+03	NORM	1.3114E+04	8.730E-02
7.083333333E+00		1.0000E+04	Real	3.000E+03	NORM	1.3784E+04	1.591E+00
1.308333333E+01		1.5000E+04	Real	3.000E+03	NORM	1.4369E+04	4.419E-02
3.408333333E+01		1.6000E+04	Real	3.000E+03	NORM	1.2555E+04	1.319E+00
7.508333333E+01		3.000E+03	Real	3.000E+03	NORM	6.7252E+03	1.542E+00
1.380833333E+02		9.000E+03	Excluded	2.000E+03	NORM	2.2242E+03	0.000E+00

Figure D.157. Calculated values of c2 after excluding the data point at 138 d.

The The total c2 is now reduced to 8.2, 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-1 and 53.3% assigned an absorption rate of 0.05 d-1. The corresponding 'retention function' is:

$$R_{thyroid}(t) = 0.467\exp(-100t) + 0.533\exp(-0.05t) \quad \ldots\ldots\ldots(D.1).$$

This function can now be entered directly in the 'Generic Wound Model' window to define the most likely absorption behavior for the single acute intake in this case (Figure D.158).

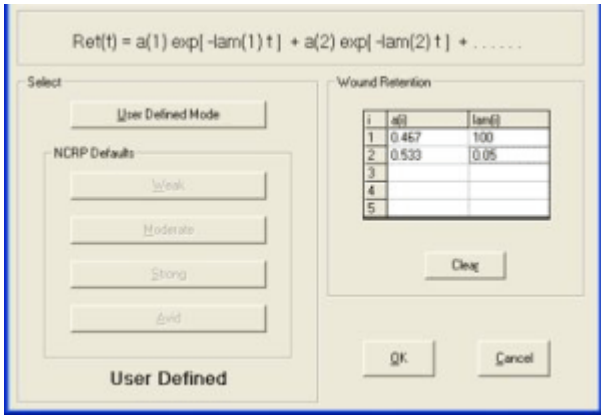


Figure D.158. Derived absorption behavior of 125I needle-puncture wound.

In the next section, we use the integrated Bayesian Analysis 'tool' to calculate the posterior probability distribution of intake for this case.

- Proceed to the next step in this example case.
- Return to the case description.

Bayesian Probability of Wound Intake

Having entered the derived retention function [in the form of Equation (D.1)], we can now use Bayesian Inference 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.

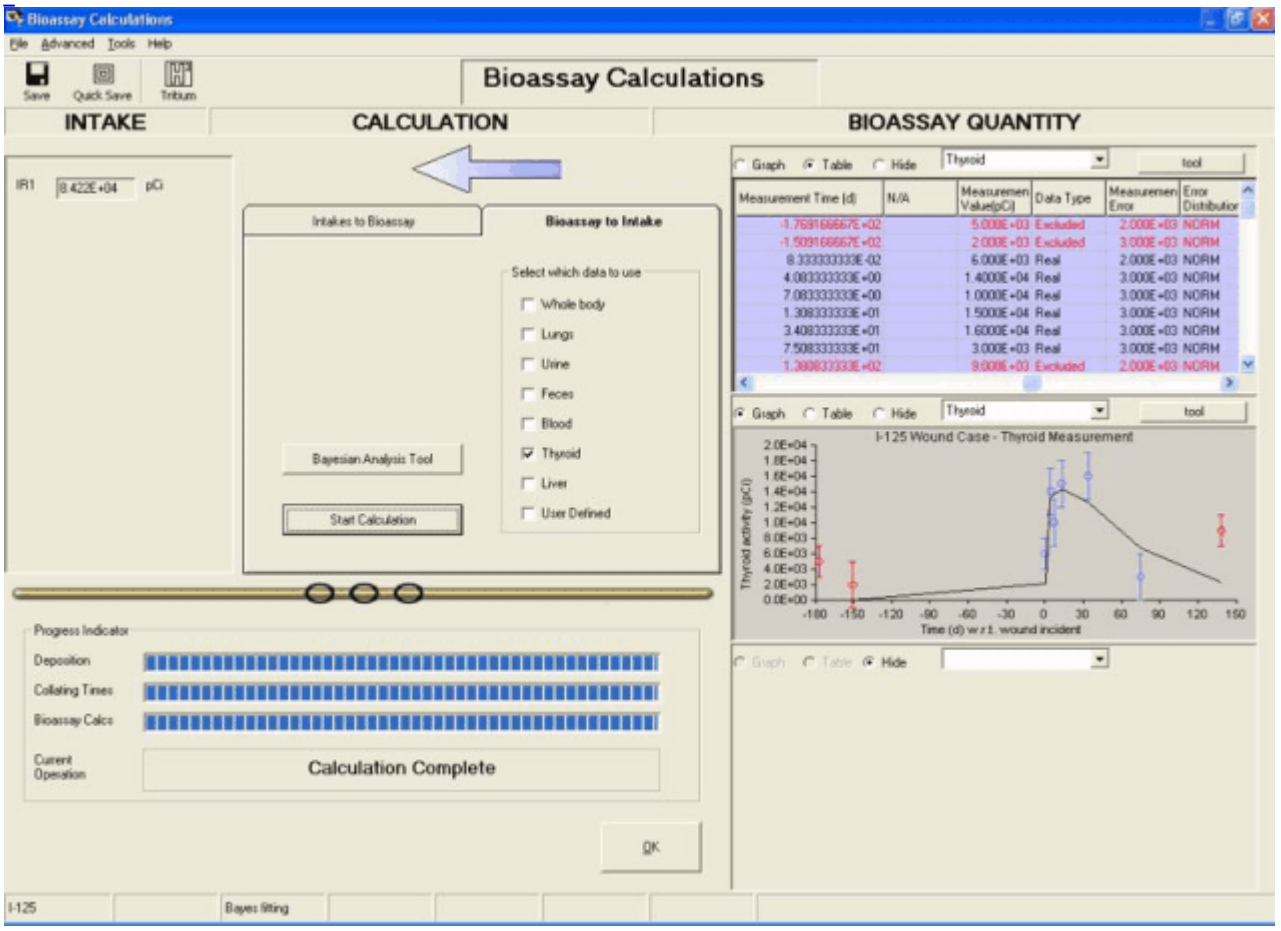


Figure D.159. Calculated mean value of the intake distribution using the 'Bayesian' fitting option.

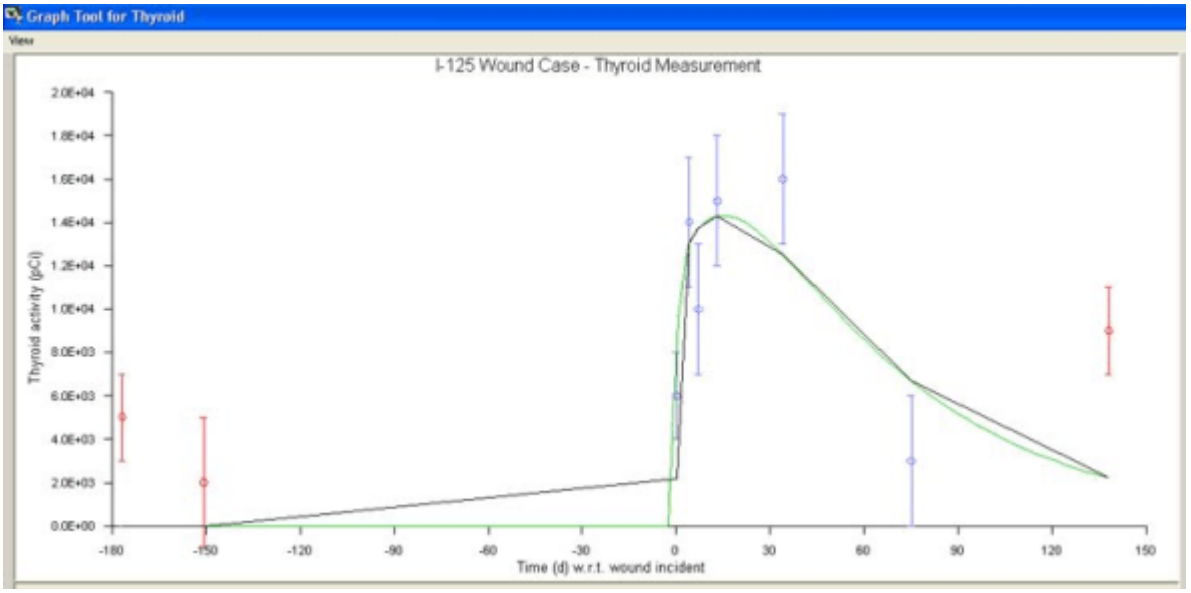


Figure D.160. Dat 'fit' obtained with derived wound retention function.

In the 'Bayesian Analysis Tool' (Figure D.161), we will select a 'Uniform' prior probability distribution of intake, over the range 1 pCi to 1,000,000 pCi (1 µCi).

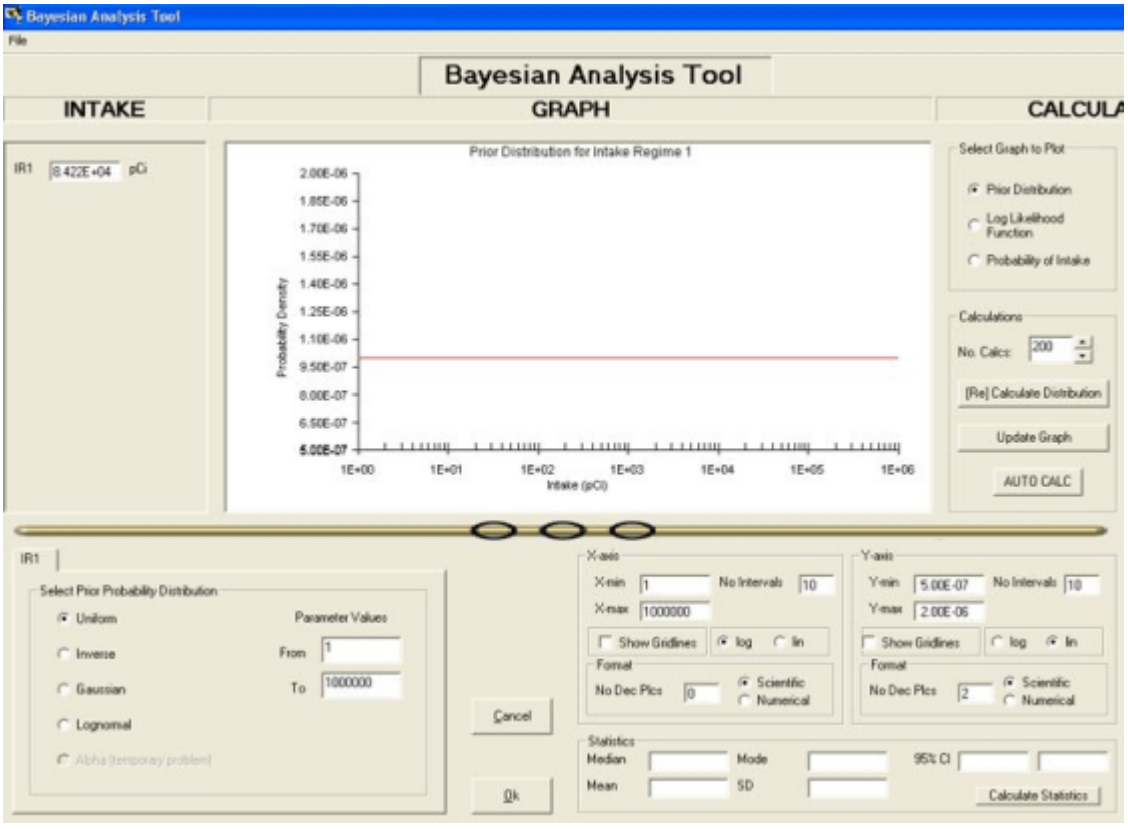


Figure D.161. Selecting a 'Uniform' prior in the 'Bayesian Analysis Tool'.

The calculated 'Log-Likelihood Function' is shown in Figure D.162.

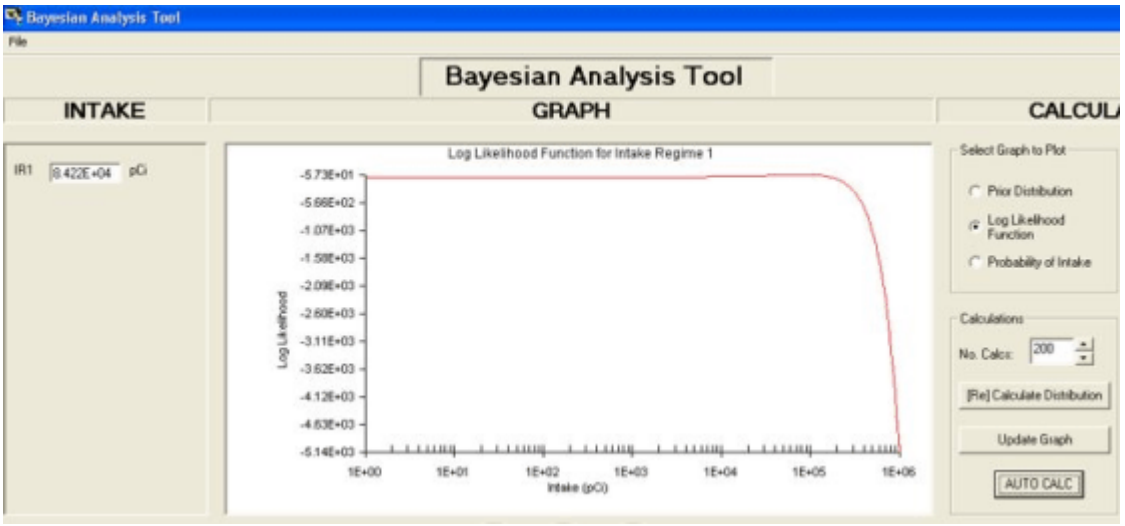


Figure D.162. Calculated Log-Likelihood intake distribution for 125I wound case (with 'Uniform' prior).

The resulting calculated 'posterior' probability distribution for the intake amount is shown in Figure D.163.

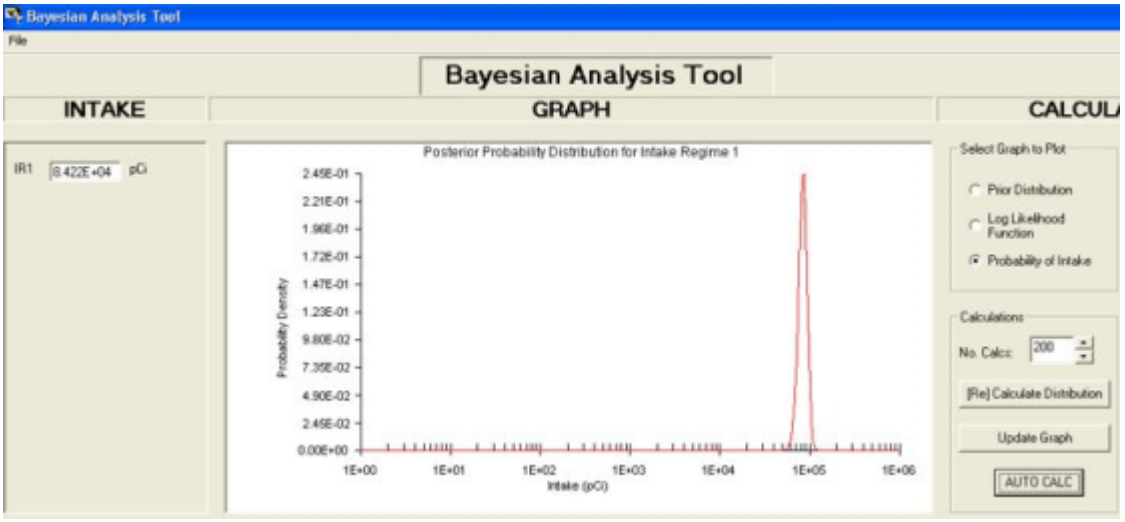


Figure D.163. Calculated posterior probability distribution for the amount of intake.

The calculated 'statistics' of the posterior probability distribution are shown in Figure D.164.

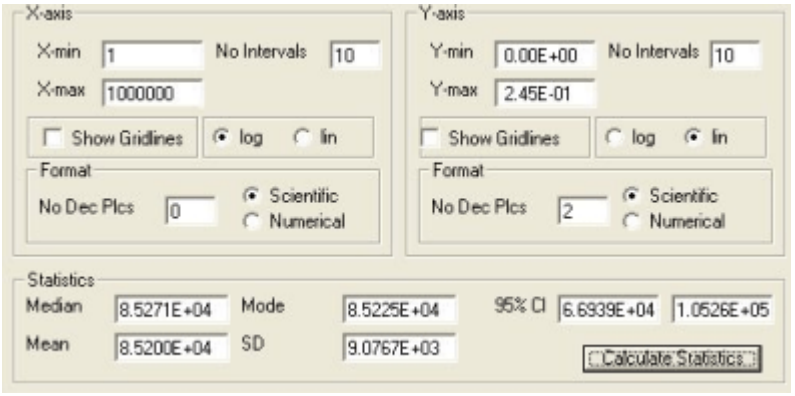


Figure D.164. Calculated 'statistics' of the posterior probability distribution.

The calculated '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 – 105,260 pCi.

Case Using the Least Squares Fitting Method - Requires Add-On 6

To illustrate the use of the least squares fitting method for evaluating the error on an estimated intake, we will re-analyze the first example case (IAEA 1999) - which is stored in the parameter file "[Install Drv]:\\JABASOFT\IMBAEXUS\USERDATA\Demo\IAEA Case 3 - 60Co.ix". 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 Table 4.1.

Note: **The least squares fitting method can be used only in cases involving a single intake - with REAL (explicit) error values on each data point, and a single bioassay quantity.**

To use the least squares fitting method, you select this option in the Bioassay Calculations screen (Figures 4.145 and 4.146) - and click "OK".

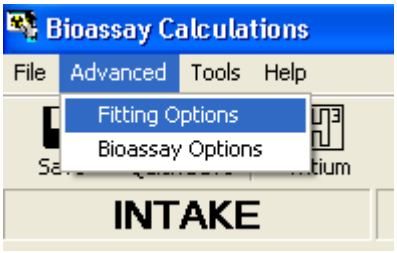


Figure 4.145. Opening the "Fitting Options" menu.

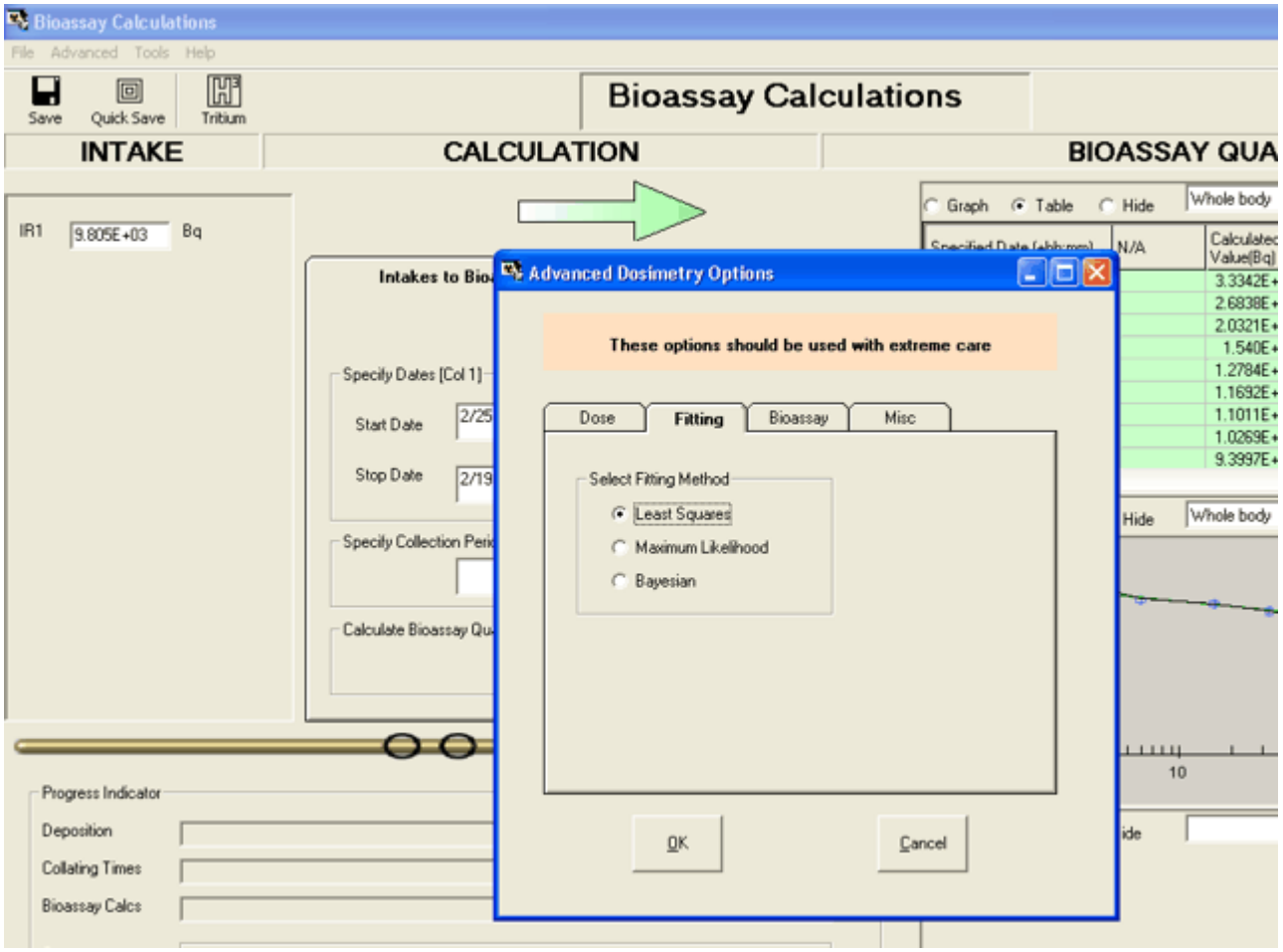


Figure 4.146. Selecting the "Least Squares" Fitting option.

Back in the Bioassay Calculations screen, you then click the Blue arrow - to re-calculate the amount of Intake (IR1) from the tabulated bioassay data. The result is shown in Figure 4.147.

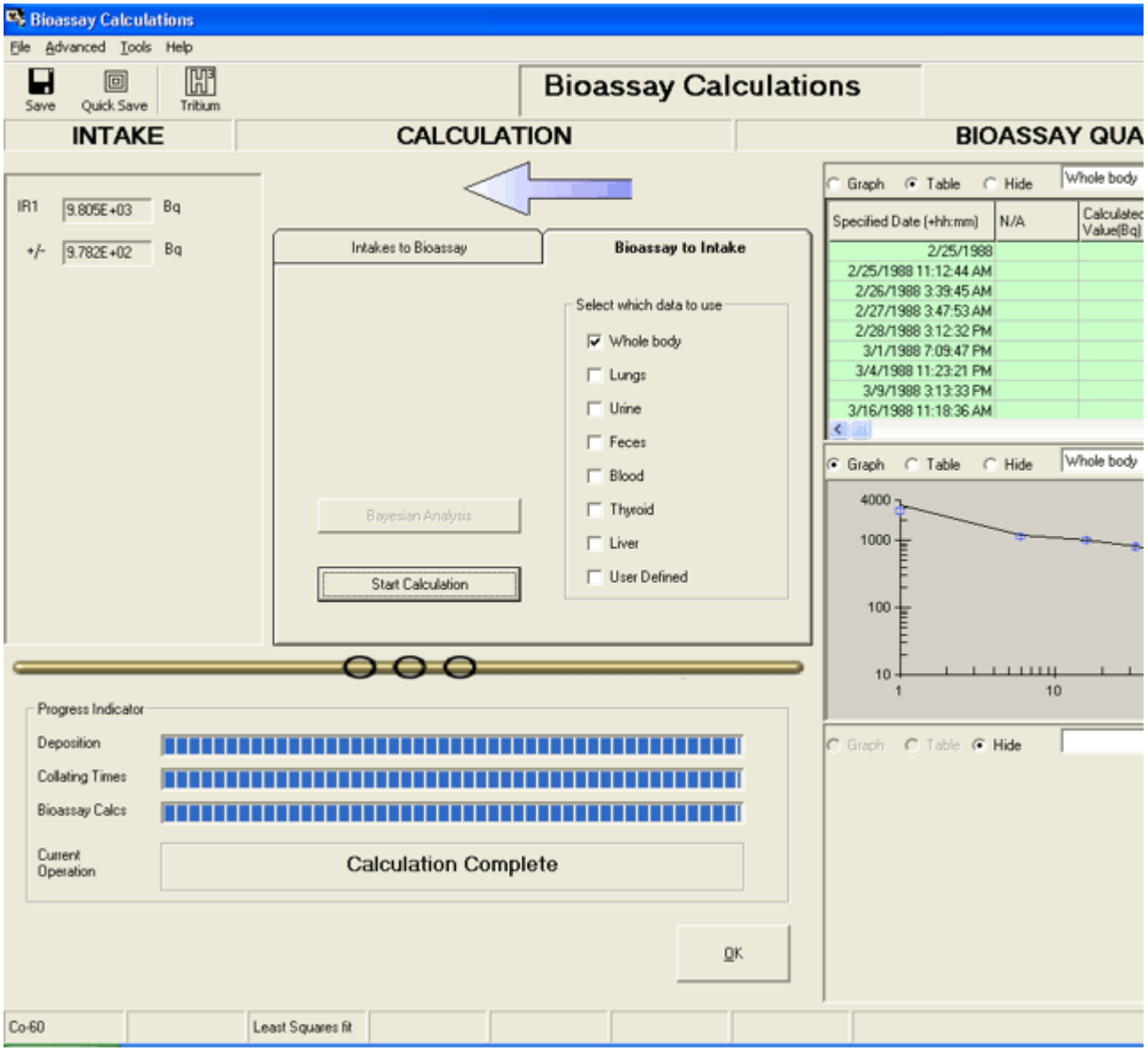


Figure 4.147. Result of least squares fitting for "IAEA Case 3 - 60Co".

As expected, the calculated value of IR1 is 9,805 Bq - the same value as calculated by the maximum likelihood method. However, the least squares method also calculates the standard error on this estimated intake - in this case ± 978.2 Bq.

Note: **More precisely, the calculated values of intake differ in the fith significant figure - 9,805.1 Bq for the least squares method c.f. 9,804.8 Bq for the maximum likelihood method. This (computational) difference is trivial.**

To further illustrate the application of the least squares fitting method, we can use this to "fit" the 241Am chest-counting data from the HAN-1 case. Figure 4.148 shows the result - for the "optimized" set of HRTM model parameters. The least squares method calculates an intake of 9,875 pCi (± 114.2 pCi standard error) - c.f., the same value (9,875 pCi) obtained with maximum likelihood fitting.

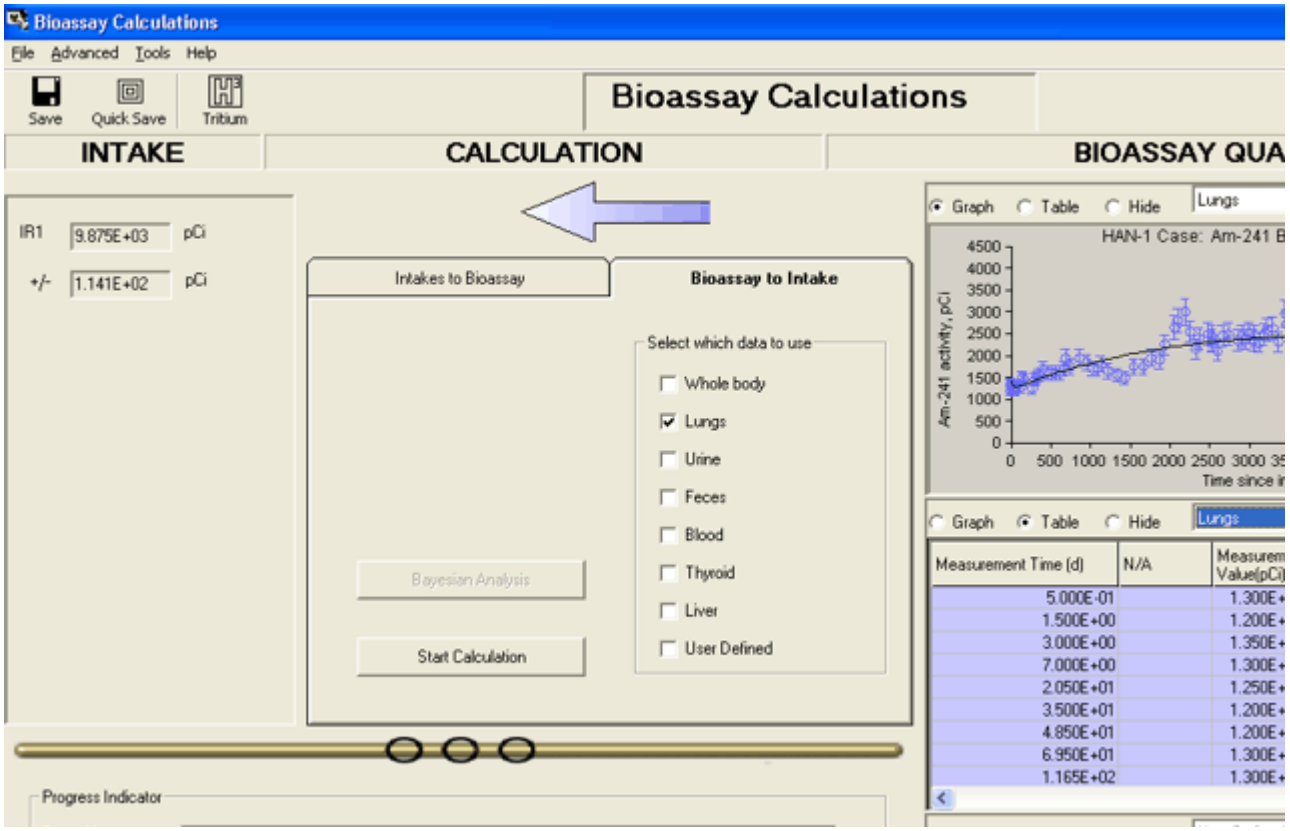


Figure 4.148. Least squares "fit" of the bioassay data in the HAN-1 case.

It is also of interest to re-analyze the HAN-1 case using the least squares method - with the (inappropriate) assumption of all ICRP Default HRTM parameter values and Type 'S' absorption behavior (Figure 4.149).

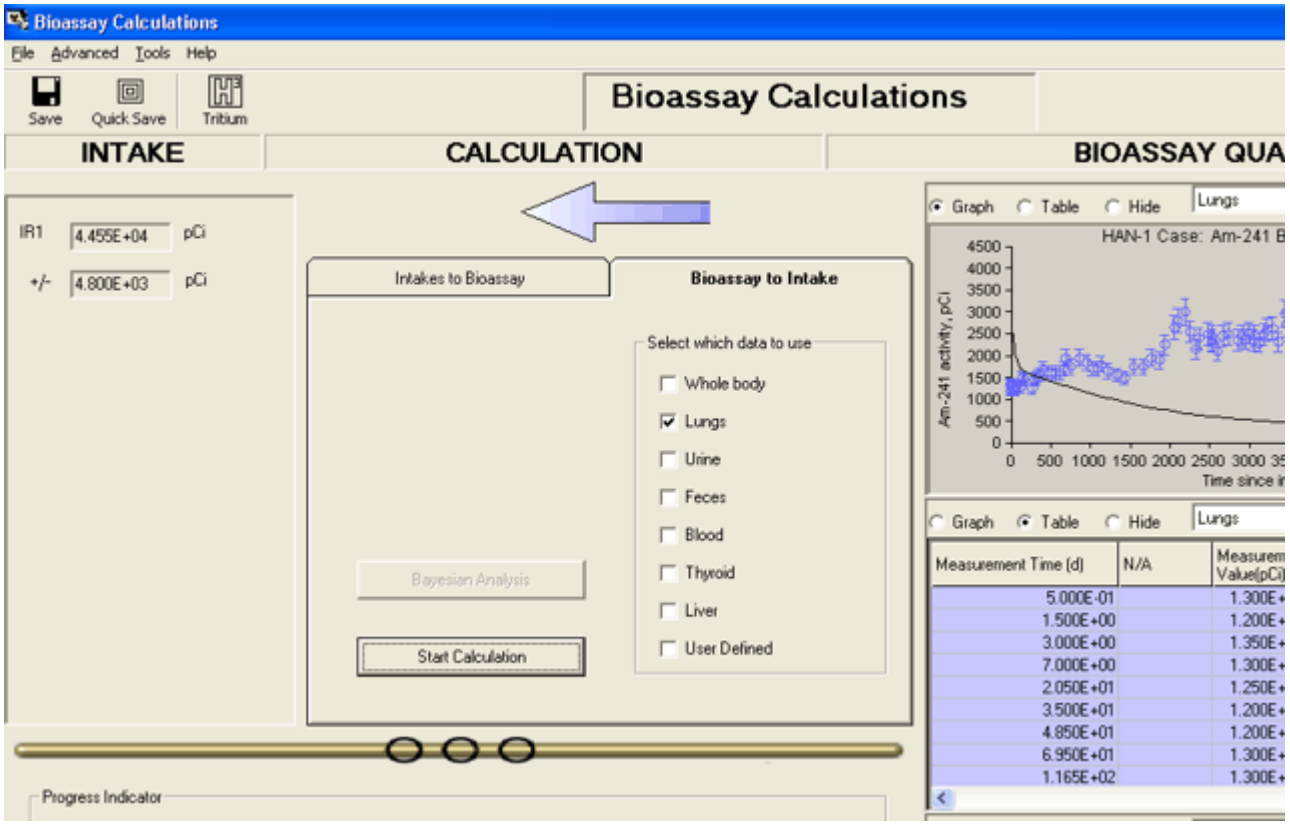
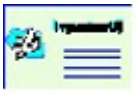


Figure 4.149. Using the least squares method to analyze the HAN-1 case with ICRP default

parameter values.

Again, the least squares method calculates the same (to the fourth significant figure) value for the intake amount (44,550 pCi) as the maximum likelihood method - with a calculated standard error of ± 4,800 pCi - c.f., 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 underlying model assumptions. Hence, the relative 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** c2-sum statistic.

Case Using Bayesian Analysis - Requires Add-On 7

To illustrate the use of the Bayesian inference in the fitting procedure, we will again re-analyze the first example case (IAEA 1999) - stored in the parameter file "[Install Drv]:\\JABASOFT\IMBAEXUS\USERDATA\Demo\IAEA Case 3 - 60Co - Bayes.ix". 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 Table 4.1.

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 in this version of the software.

To use the "Bayesian" Fitting option, you must first select this - from the Bioassay Calculation screen's Advanced | Fitting Options menu (Figure 4.150).

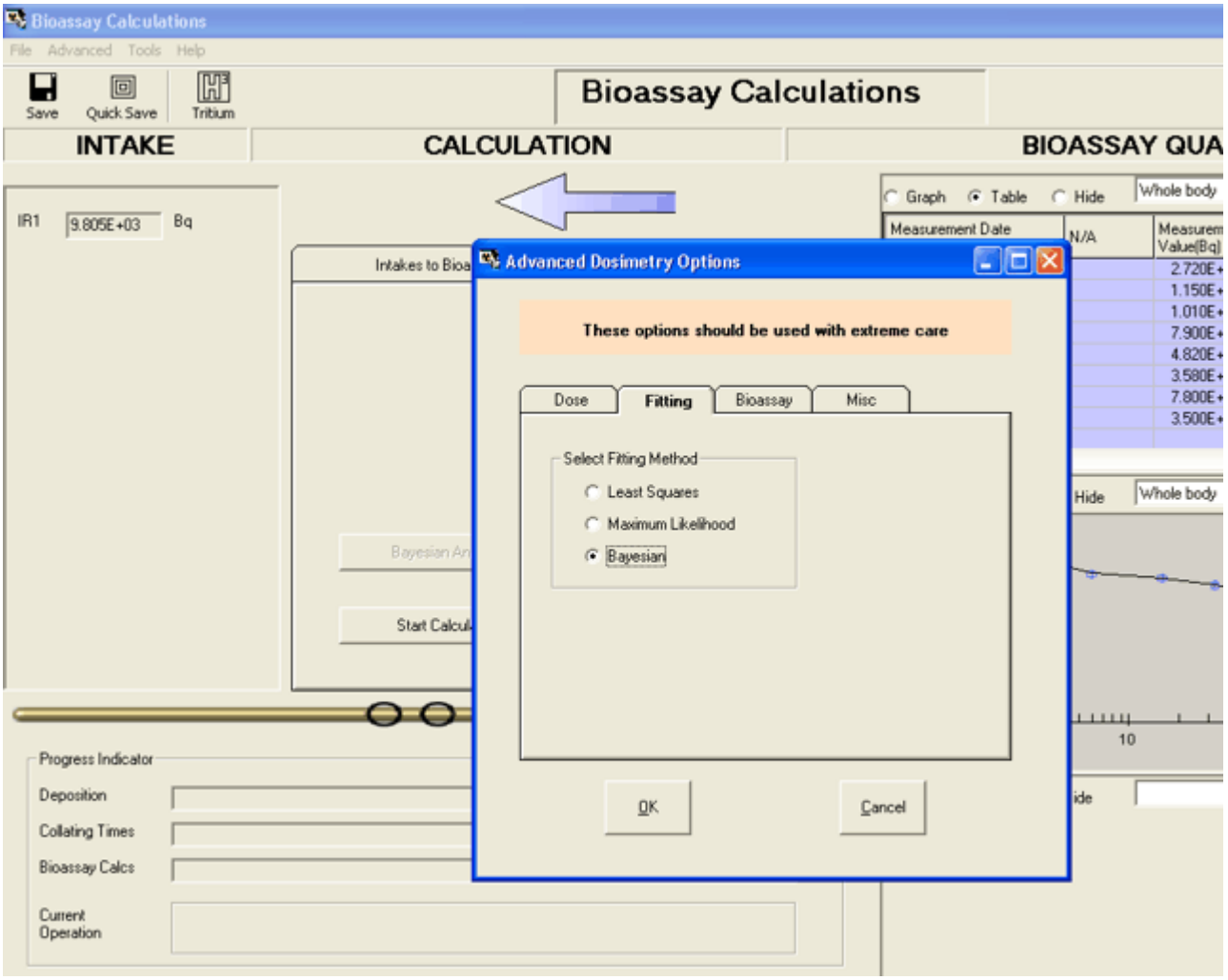


Figure 4.150. **Selecting the "Bayesian" Fitting option.**

This will activate the "Bayesian Analysis" button in the Bioassay Calculations screen (Figure 4.151).

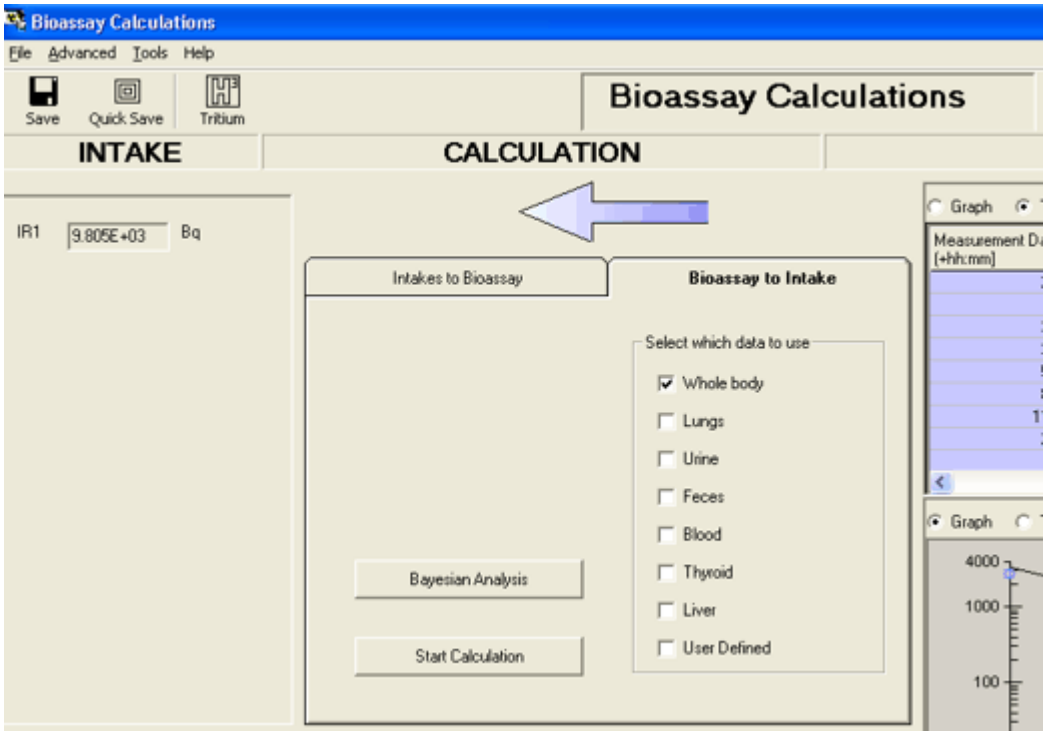


Figure 4.151. **"Bayesian Analysis" button activated.**

Clicking the "Bayesian Analysis" button opens a new screen - the Bayesian Analysis tool (Figure 4.152).

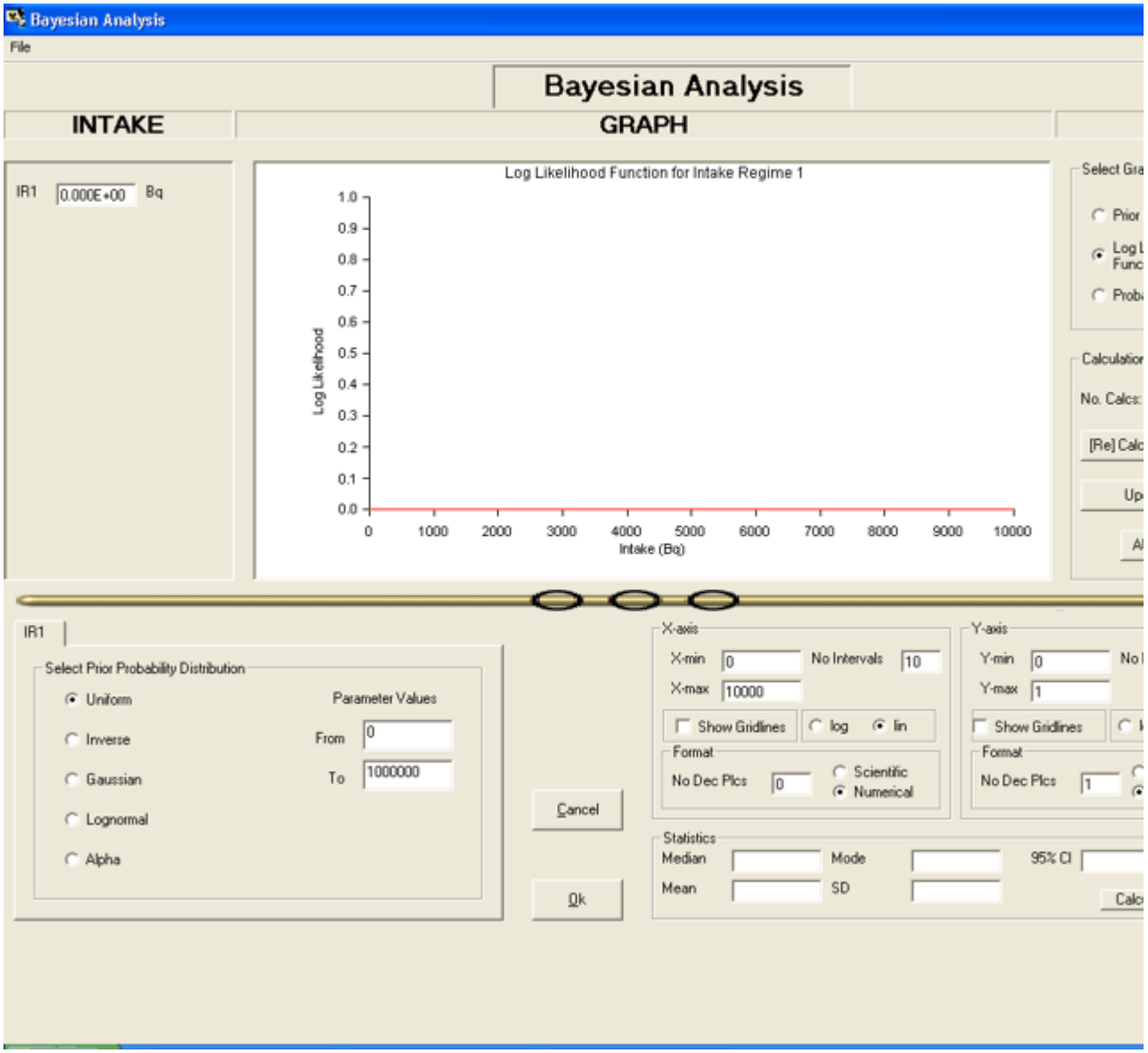


Figure 4.152. Bayesian Analysis **screen as it appears for a "New" case - with no bioassay data loaded.**

Tip: Figure 4.152 shows the "default" settings of the Bayesian Analysis tool - for the type of prior (defaulted to "Uniform"), the X- and Y-axis 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 (e.g., using the maximum likelihood or least squares method), the X-axis in the Bayesian Analysis tool will "auto-range" accordingly - when the tool is opened (Figure 4.153).

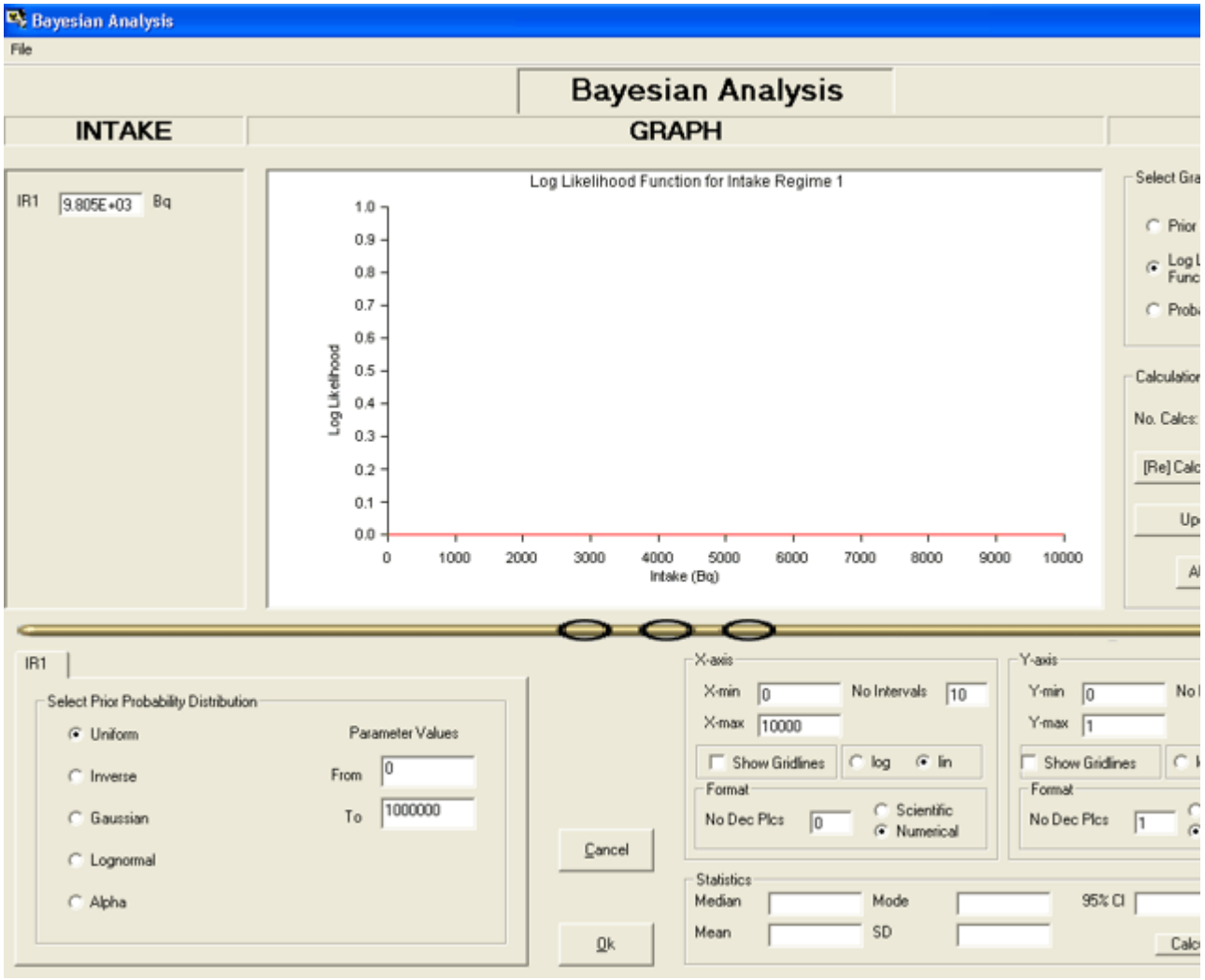


Figure 4.153. "Auto-ranging" of X-axis when the intake amount (IR1) has already been calculated.

Note: The Y-axes also "auto-ranges" when you calculate the other types of probability distribution. However, the X-axis DOES NOT. You have to choose the appropriate X-axis range - to include the whole calculated distribution.

In this section of the User Manual, we will show how each type of "Prior Distribution" affects the calculated "Log Likelihood Function" and the posterior probability distribution of intake ("Probability of Intake") in the "IAEA Case 3" ^{60}Co whole body monitoring example - as follows:

- Uniform prior.
- Inverse prior.
- Gaussian prior.
- Lognormal prior.
- 'Alpha' prior.

Probability Distribution of Intake Assuming a Uniform Prior

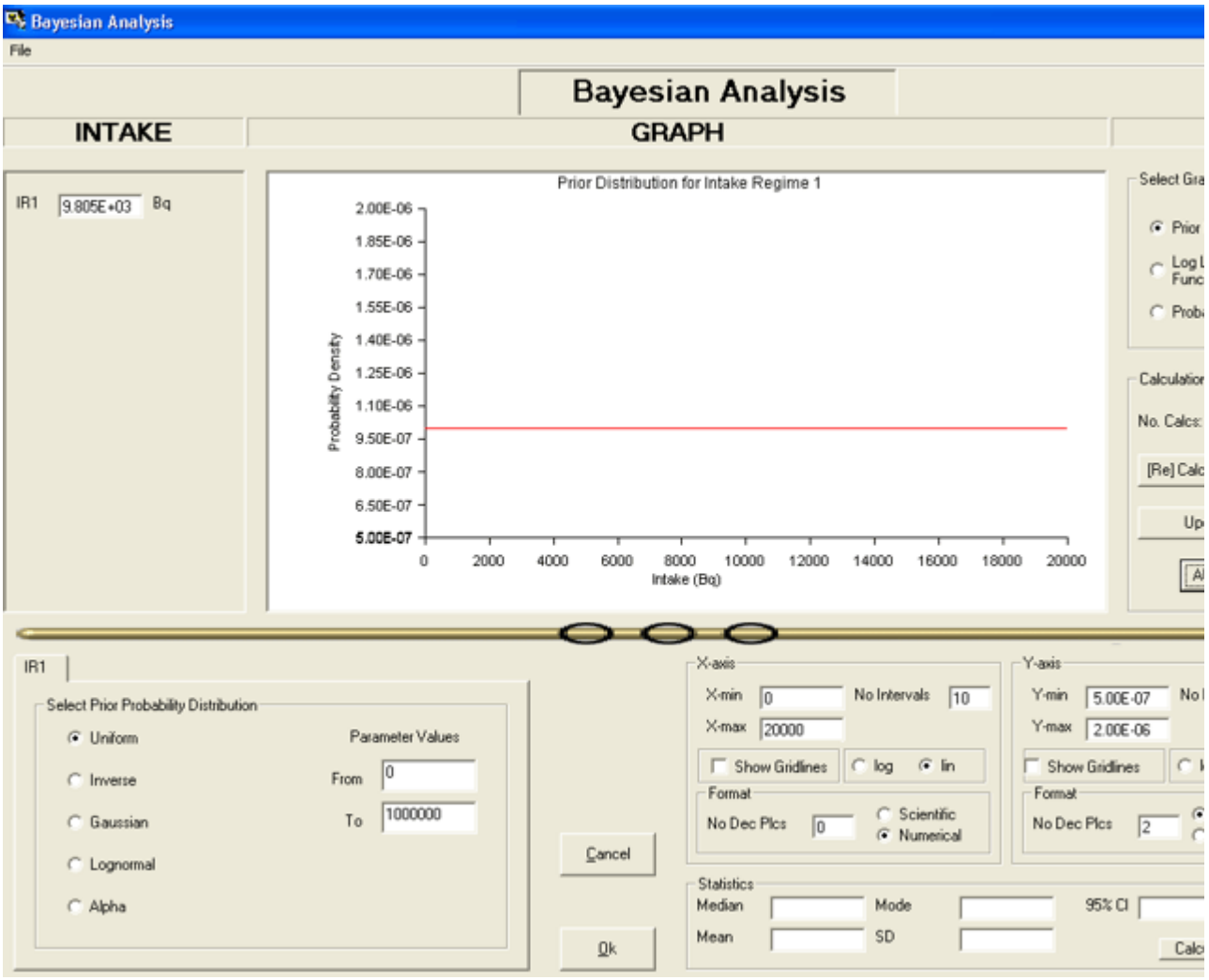
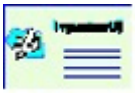


Figure 4.154. "Prior Distribution" calculated (and displayed) over a suitable X-axis range.

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 Log Likelihood Function, you simply click its radio button - and click "AUTO CALC" again. The calculated Log Likelihood Function is shown in Figure 4.155.

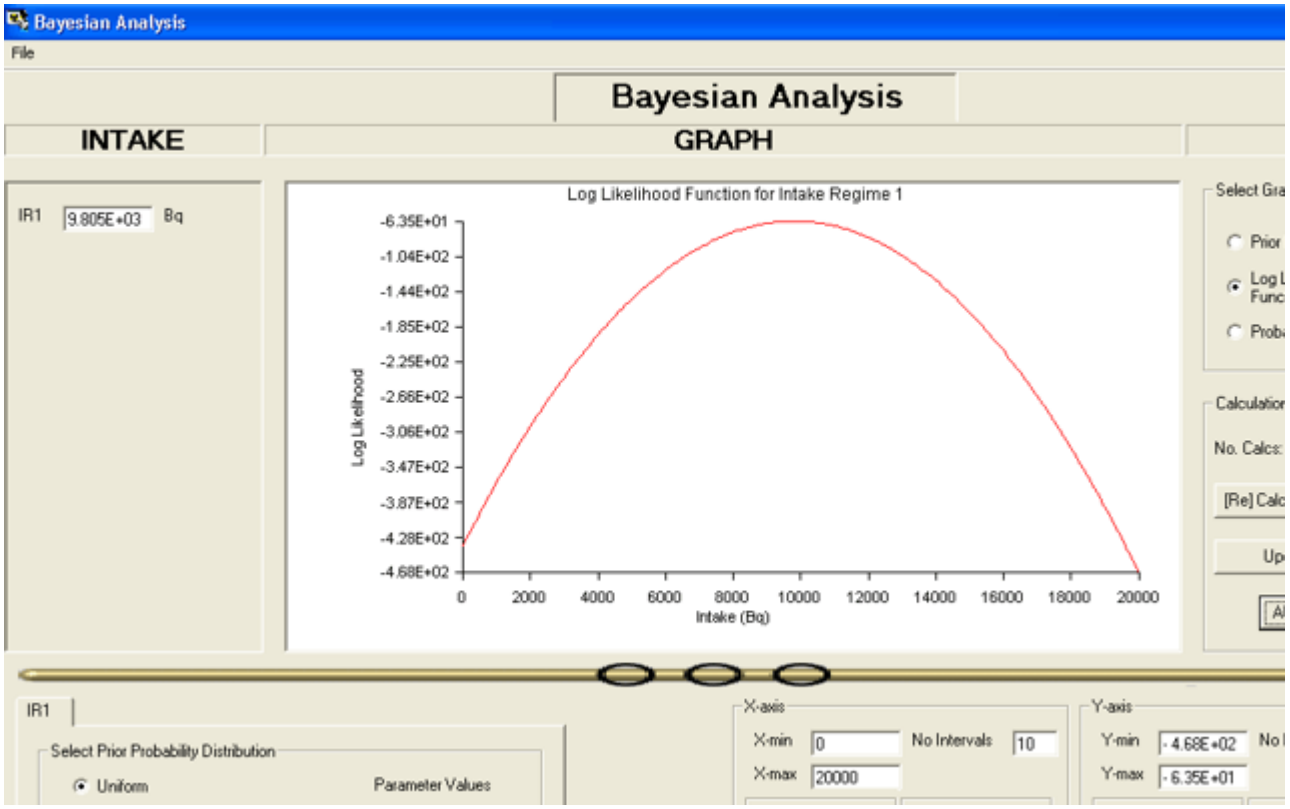
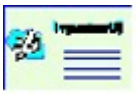


Figure 4.155. Calculated Log Likelihood Function.

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|I), 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 (I). 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.

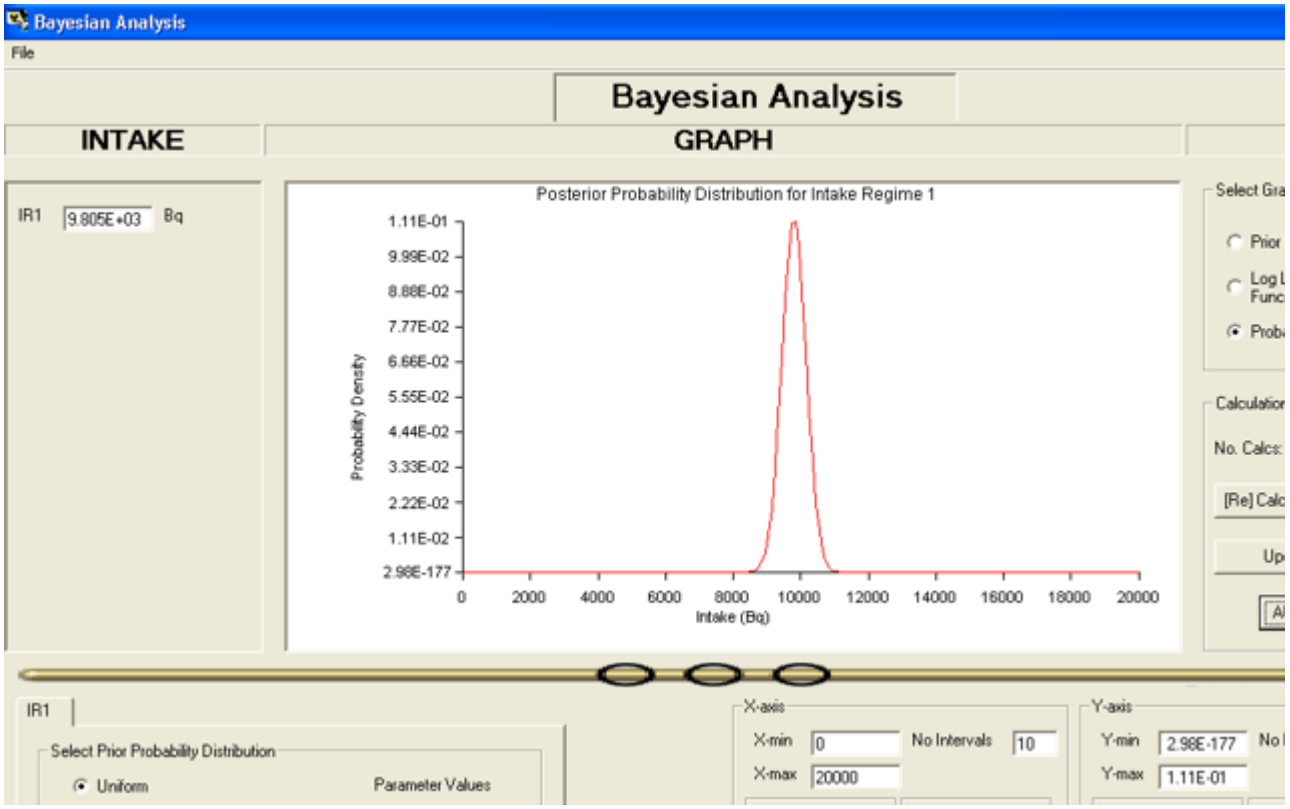


Figure 4.156. Calculated Probability of Intake - for a uniform prior.

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).

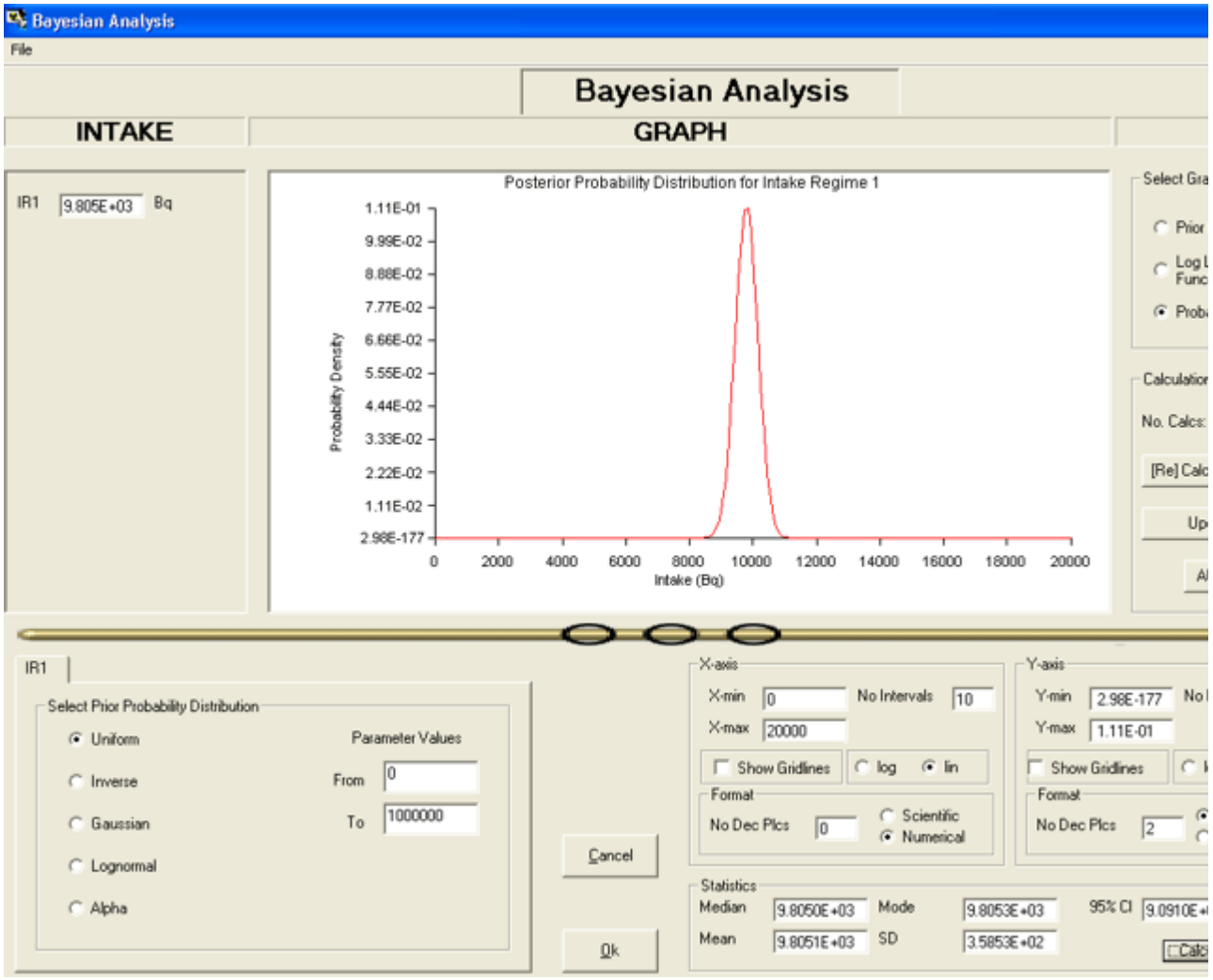


Figure 4.157. Calculating and displaying the statistical parameters of the posterior probability distribution of intake.

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.

Note #1: This distribution is very close to normal (symmetrical).

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 least squares - 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

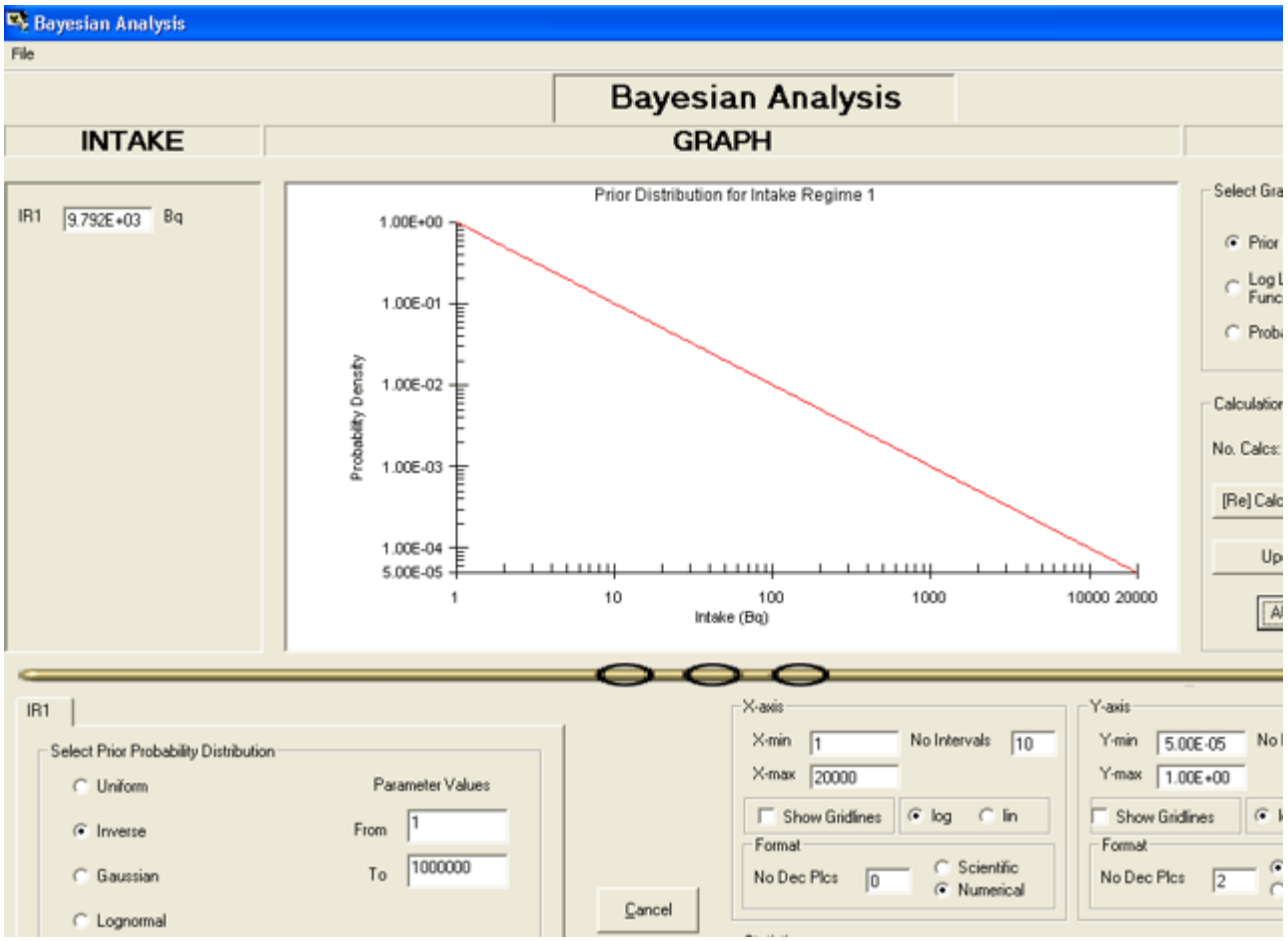


Figure 4.158. Inverse prior - plotted on Log-Log axes.

The Inverse prior probability distribution is shown in Figure 4.158. With this prior, the calculated median value of the intake distribution is 9,793 Bq (c.f., 9,805 Bq for the uniform prior). The calculated Log Likelihood Function (which is independent of the prior) was shown in Figure 4.155 (for the uniform prior).

The calculated posterior probability distribution of intake is shown in Figure 4.159, together with the calculated statistical parameters of this distribution.

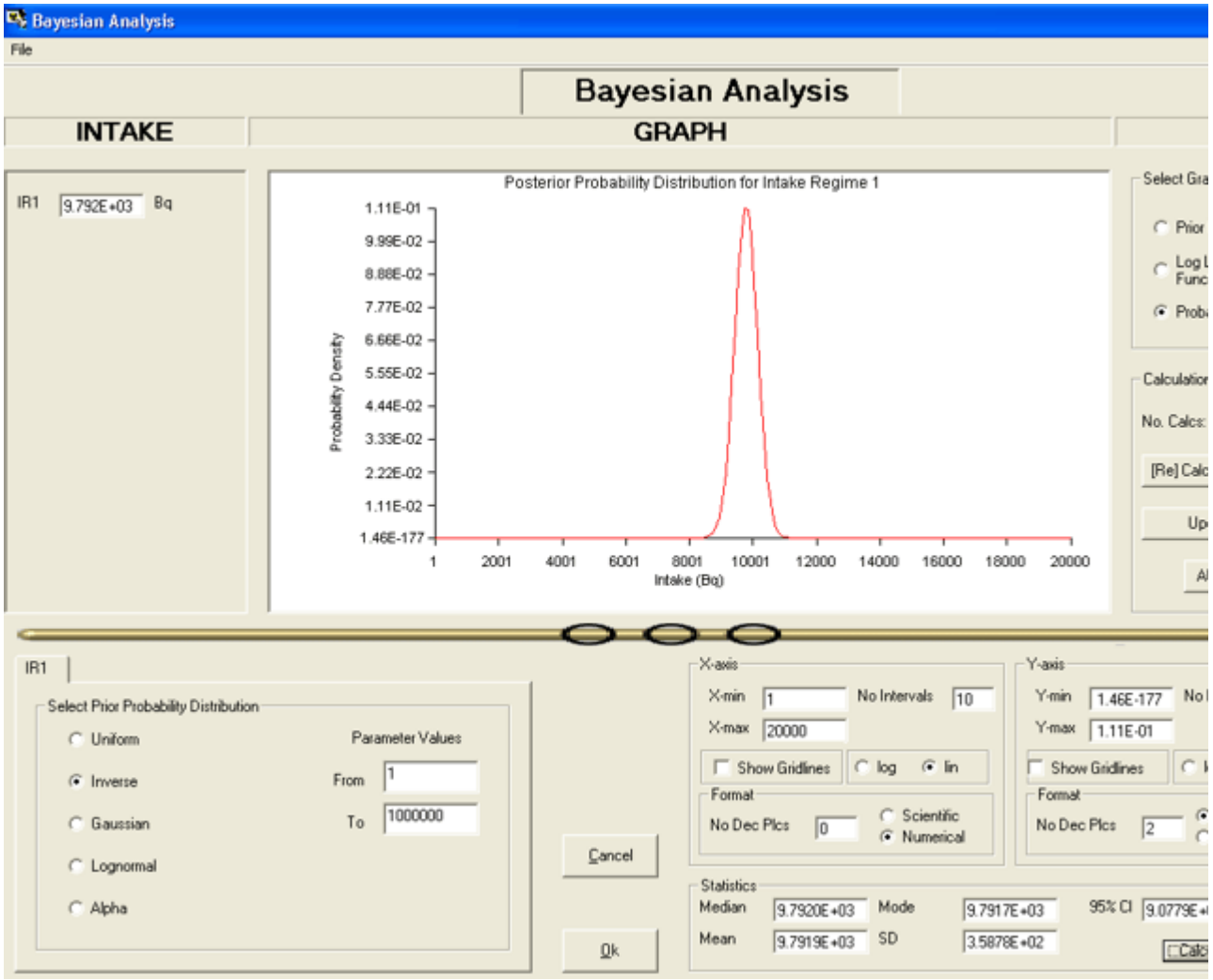


Figure 4.159. Posterior probability distribution of intake calculated for the inverse prior.

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 normal (symmetrical) - as was the case for the uniform prior. However, the distribution has been shifted (very slightly) to lower values of the median, mean and mode.

Probability Distribution of Intake

Assuming a Gaussian Prior

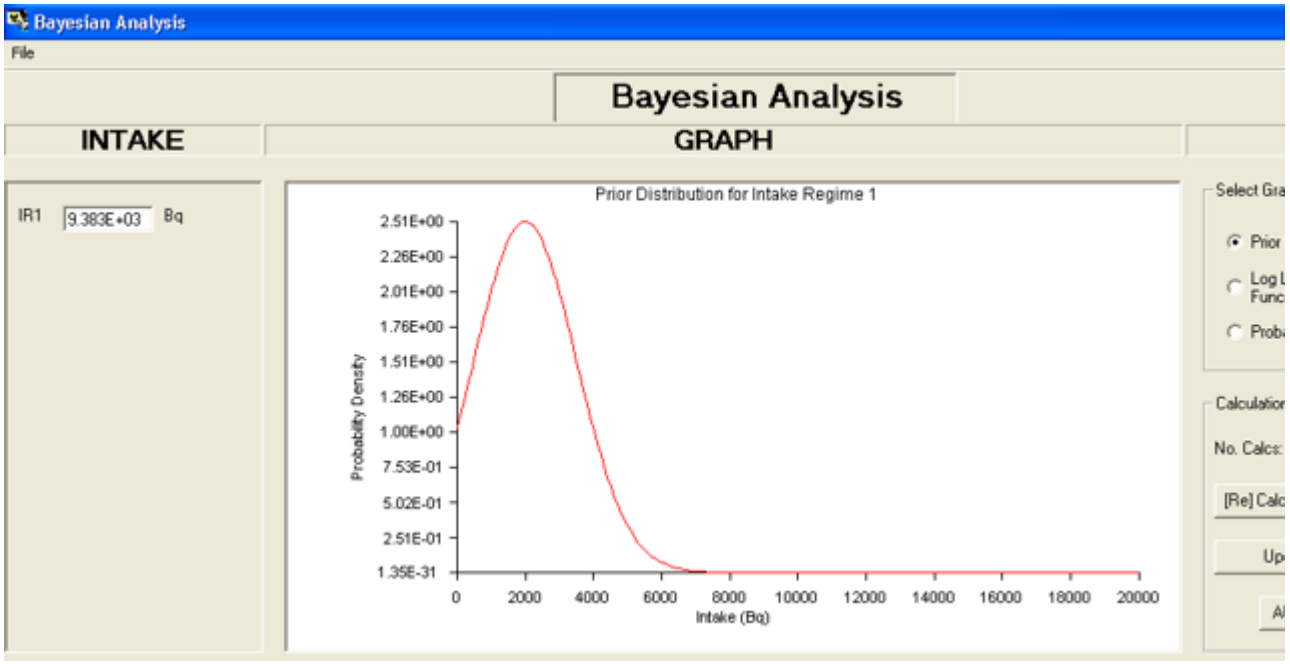


Figure 4.160. Example of a Gaussian prior.

A Gaussian prior probability distribution is shown in Figure 4.160. The median (= mean) of this distribution is 2,000 Bq, and the standard deviation 1,500 Bq. With this prior, the calculated median value of the intake distribution is 9,383 Bq (c.f., 9,805 Bq for the uniform prior). The calculated Log Likelihood Function (which is independent of the prior) was shown in Figure 4.155 (for the uniform prior).

The calculated posterior probability distribution of intake is shown in Figure 4.161, together with the calculated statistical parameters of this distribution.

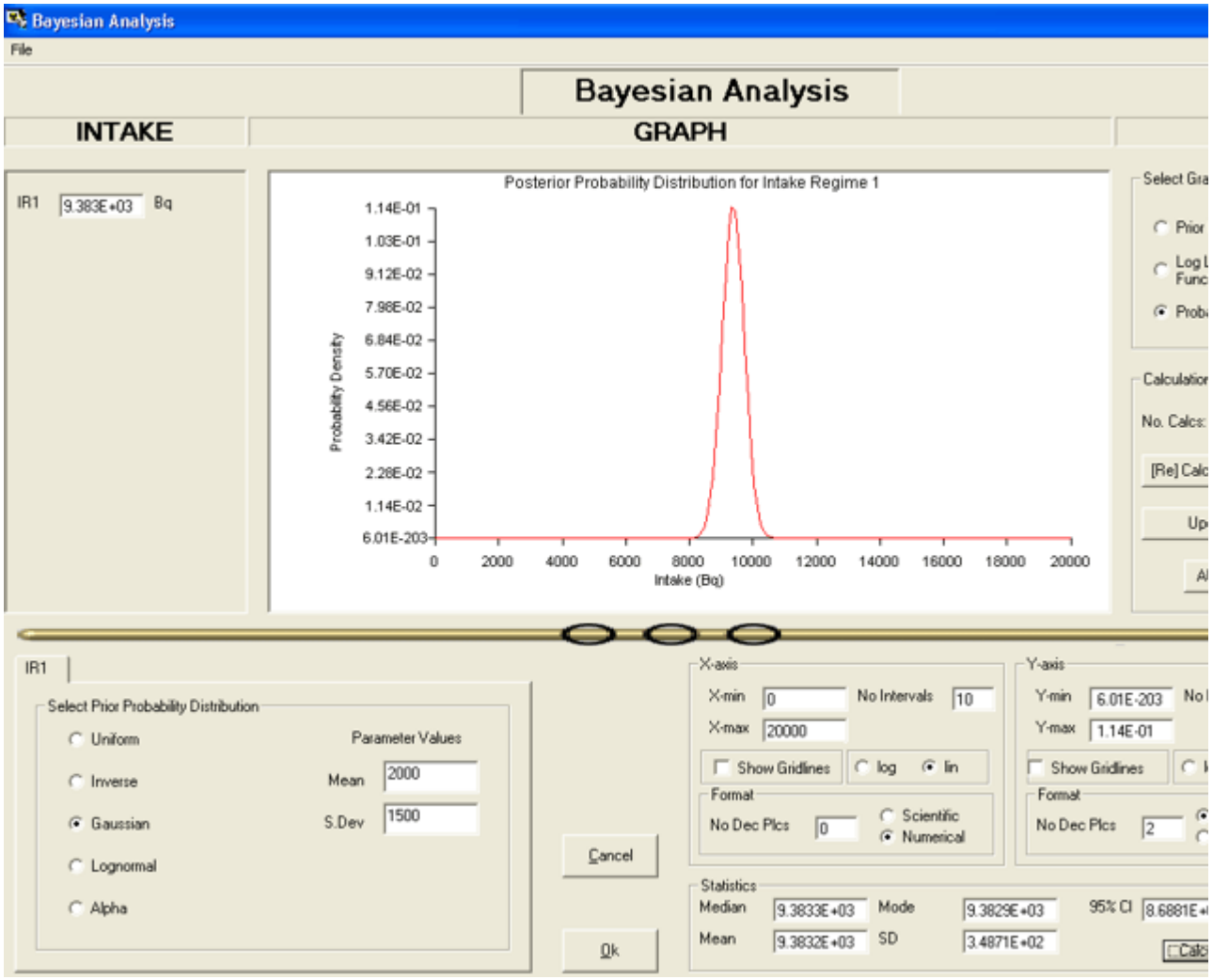


Figure 4.161. Posterior probability distribution of intake calculated for a Gaussian prior.

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 normal (symmetrical) - as was the case for the uniform prior. However, in this example, the distribution has been shifted to lower values of the median, mean and mode. The amount of "shift" depends on BOTH the assumed median (= mean) value AND the standard deviation of the Gaussian prior.

Probability Distribution of Intake Assuming a Lognormal Prior

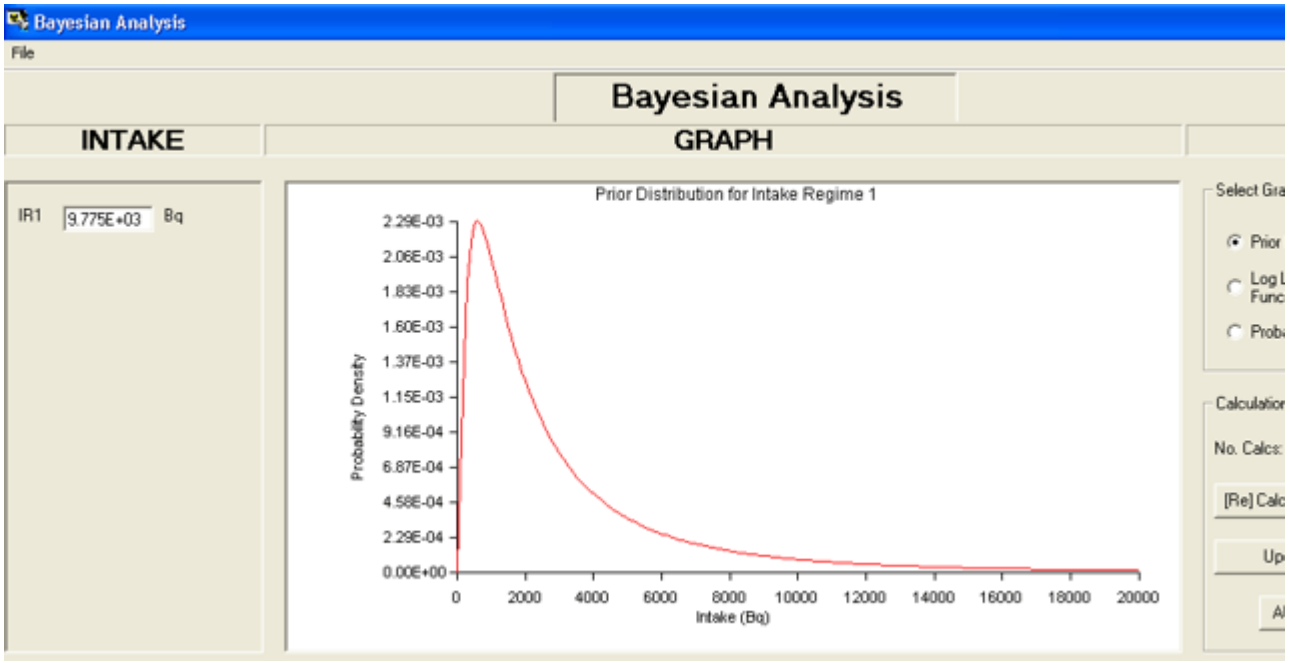


Figure 4.162. Example of a Lognormal prior.

A Lognormal prior probability distribution is shown in Figure 4.162. The median ([1] mean) of this distribution is 2,000 Bq, and the geometric standard deviation is 3. With this prior, the calculated median value of the intake distribution is 9,775 Bq (c.f., 9,805 Bq for the uniform prior). The calculated Log Likelihood Function (which is independent of the prior) was shown in Figure 4.155 (for the uniform prior).

The calculated posterior probability distribution of intake is shown in Figure 4.163, together with the calculated statistical parameters of this distribution.

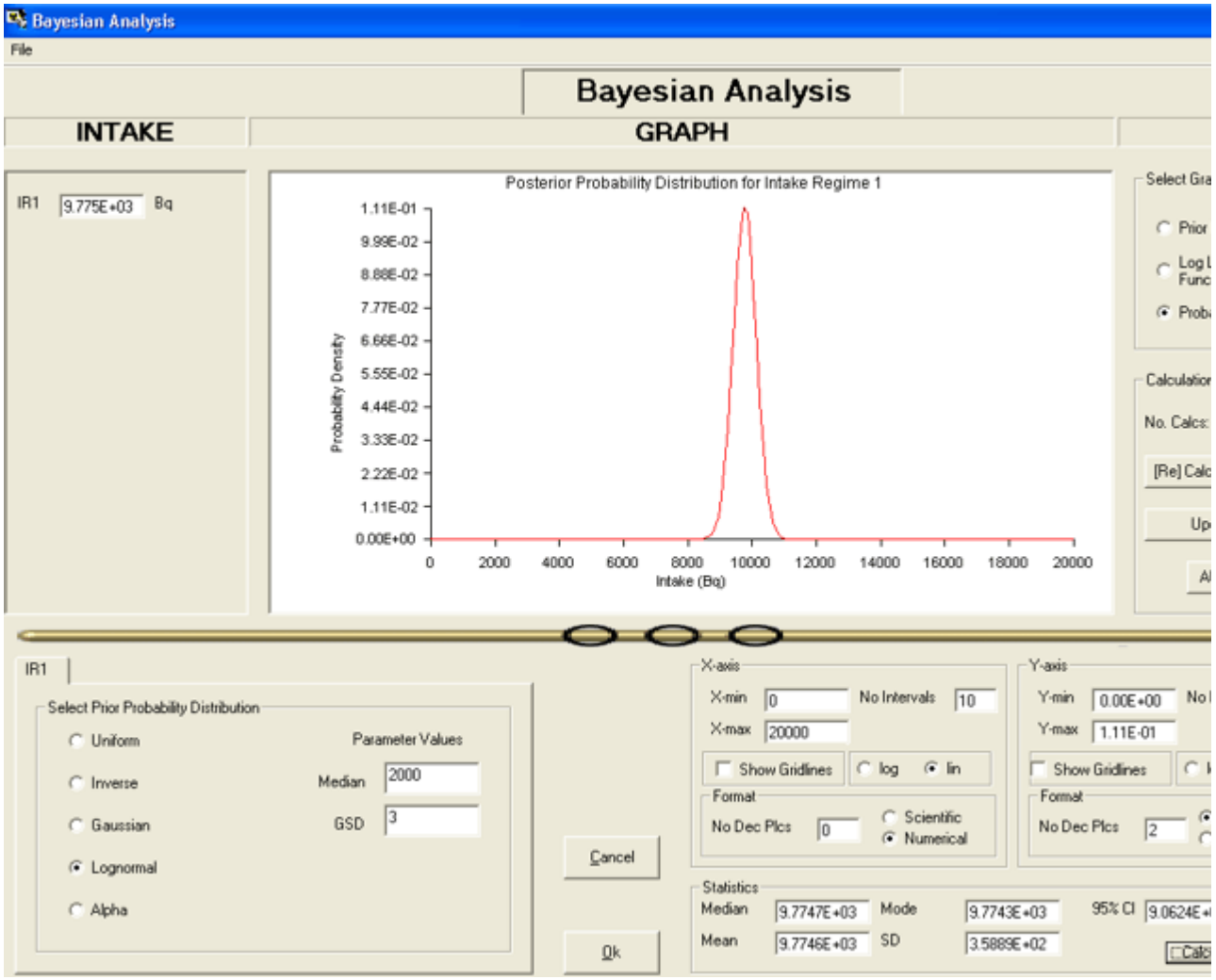


Figure 4.163. Posterior probability distribution of intake calculated for a Lognormal prior.

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 normal (symmetrical) - as was the case for the uniform prior. However, in this example, the distribution has been shifted to marginally lower values of the median, mean and mode. The amount of "shift" depends on BOTH the assumed median ([1] mean) value AND the geometric standard deviation of the Lognormal prior.

Probability Distribution of Intake Assuming an 'Alpha' Prior

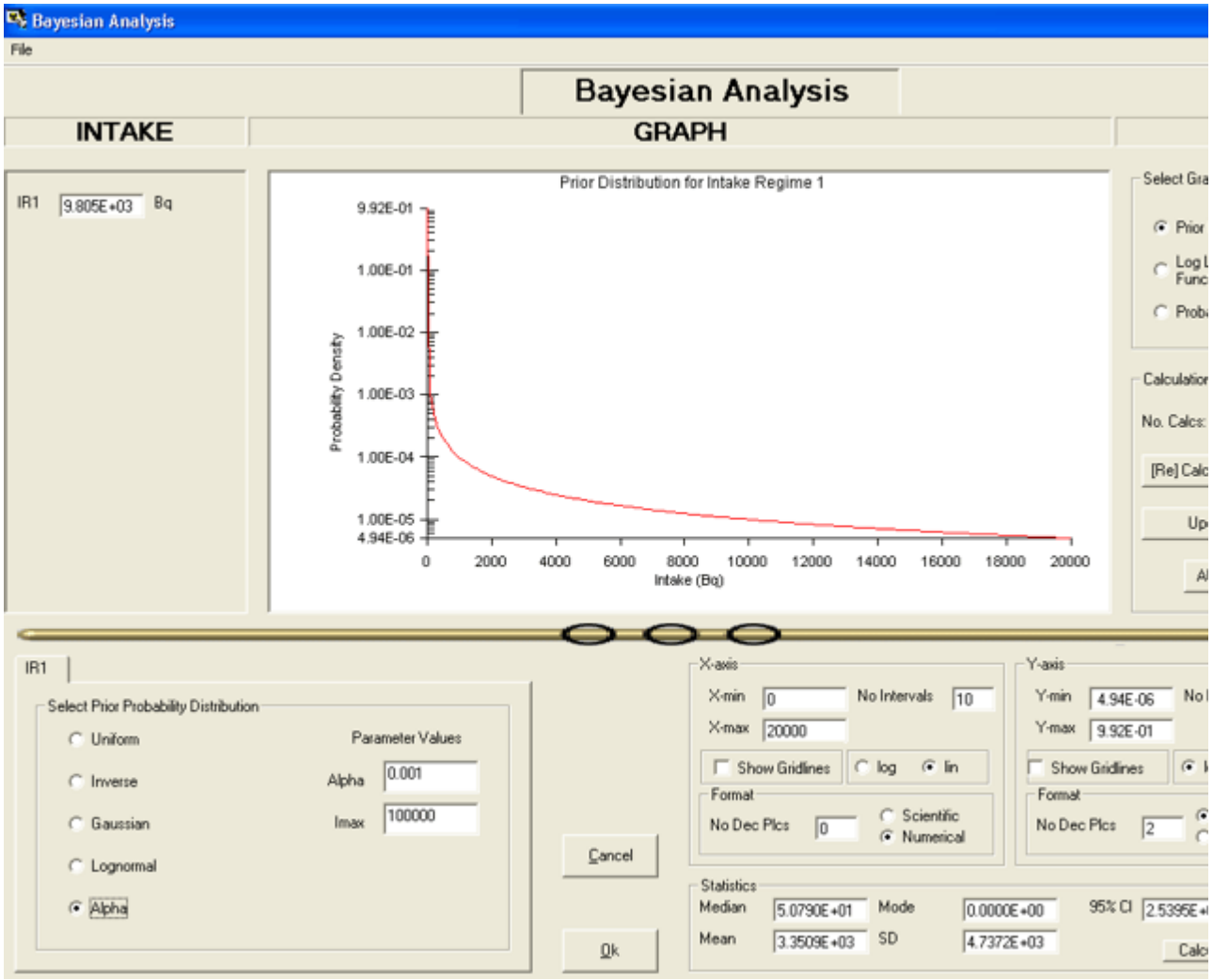


Figure 4.164. Example of an 'Alpha' prior.

An 'Alpha' 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 median of this distribution is 50.79 Bq, with a very large standard deviation of 4,737.2 Bq. With this prior, the calculated median value of the intake distribution is 9,805 Bq - which is identical to the value for the uniform prior. The calculated Log Likelihood Function (which is independent of the prior) was shown in Figure 4.155 (for the uniform prior).

The calculated posterior probability distribution of intake is shown in Figure 4.165, together with the calculated statistical parameters of this distribution.

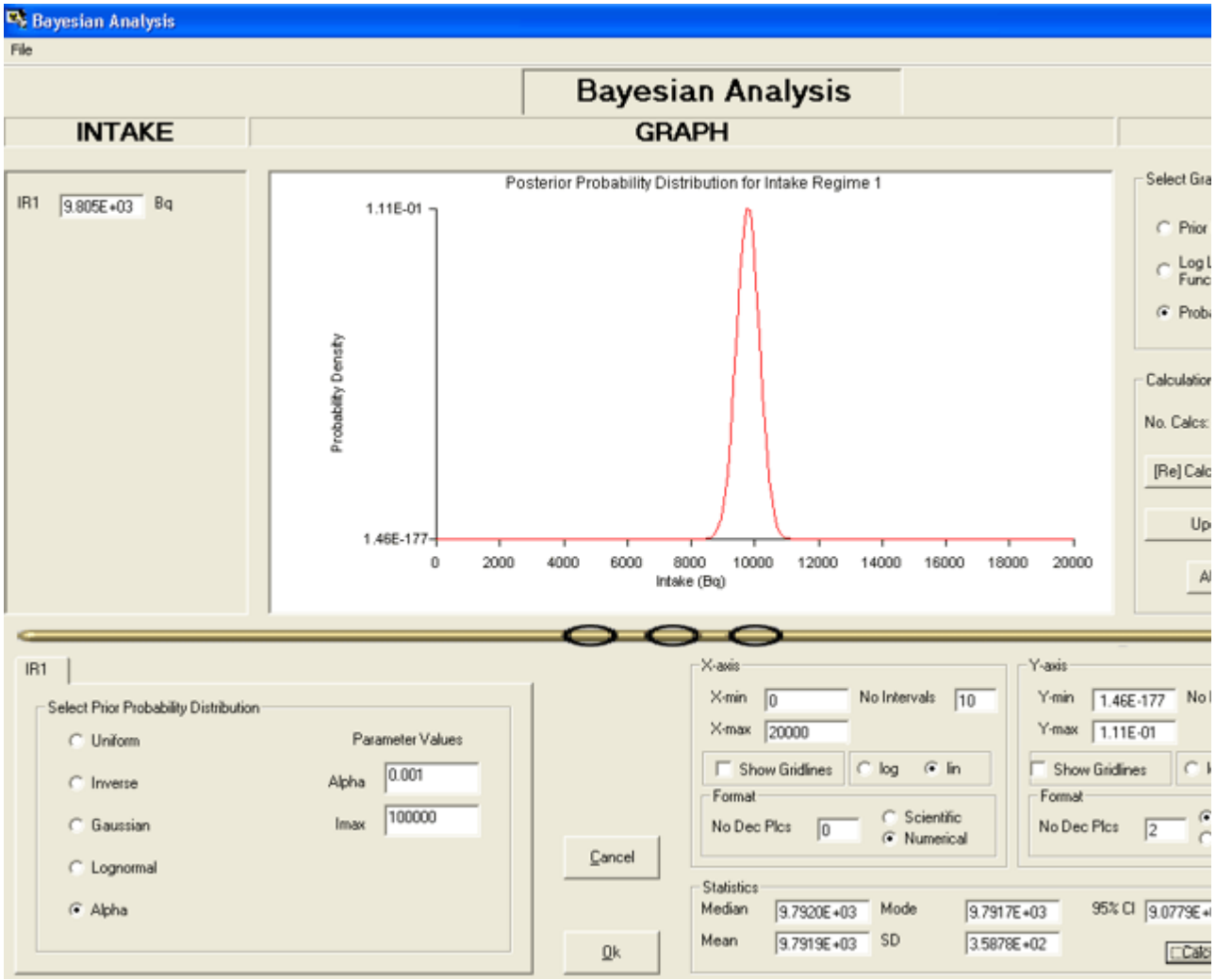


Figure 4.165. Posterior probability distribution of intake calculated for an 'Alpha' prior.

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 normal (symmetrical) - as was the case for the uniform prior. However, in this example, the distribution has been shifted to marginally lower values of the median, mean and mode.

Case ImplementingTritium Tool - Requires Add-On 8

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 IMBA Professional Plus) is provide in the ACSII 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_Tritium.txt - Notepad

File Edit Format View Help

7.000E+00	4.98750E+05	Real	1.800E+00	LOGNORM
1.400E+01	2.83500E+05	Real	1.800E+00	LOGNORM
2.100E+01	6.95625E+05	Real	1.800E+00	LOGNORM
2.800E+01	5.74875E+05	Real	1.800E+00	LOGNORM
3.500E+01	1.26000E+05	Real	1.800E+00	LOGNORM
4.200E+01	1.12875E+05	Real	1.800E+00	LOGNORM
4.900E+01	9.4500E+04	Real	1.800E+00	LOGNORM
5.600E+01	4.7250E+04	Real	1.800E+00	LOGNORM
6.300E+01	8.6625E+04	Real	1.800E+00	LOGNORM
7.000E+01	8.4000E+04	Real	1.800E+00	LOGNORM
7.700E+01	3.6750E+04	Real	1.800E+00	LOGNORM
8.400E+01	2.6250E+04	Real	1.800E+00	LOGNORM
1.050E+02	7.0875E+04	Real	1.800E+00	LOGNORM
1.120E+02	3.6750E+04	Real	1.800E+00	LOGNORM
1.190E+02	5.2500E+04	Real	1.800E+00	LOGNORM
1.260E+02	3.9375E+04	Real	1.800E+00	LOGNORM
1.330E+02	3.9375E+04	Real	1.800E+00	LOGNORM
1.400E+02	5.5125E+04	Real	1.800E+00	LOGNORM
1.540E+02	5.250E+03	Real	1.800E+00	LOGNORM
1.610E+02	3.4125E+04	Real	1.800E+00	LOGNORM
1.680E+02	7.875E+03	Real	1.800E+00	LOGNORM
1.750E+02	1.0500E+04	Real	1.800E+00	LOGNORM
1.820E+02	5.2500E+04	Real	1.800E+00	LOGNORM
1.890E+02	4.7250E+04	Real	1.800E+00	LOGNORM
1.960E+02	3.9375E+04	Real	1.800E+00	LOGNORM
2.020E+02	1.05000E+05	Real	1.800E+00	LOGNORM
2.100E+02	8.4000E+04	Real	1.800E+00	LOGNORM
2.310E+02	5.5125E+04	Real	1.800E+00	LOGNORM
2.380E+02	3.1500E+04	Real	1.800E+00	LOGNORM
2.590E+02	1.05000E+05	Real	1.800E+00	LOGNORM
2.730E+02	9.9750E+04	Real	1.800E+00	LOGNORM
2.800E+02	1.07625E+05	Real	1.800E+00	LOGNORM
2.870E+02	1.023750E+06	Real	1.800E+00	LOGNORM
2.940E+02	3.67500E+05	Real	1.800E+00	LOGNORM
3.010E+02	5.53875E+05	Real	1.800E+00	LOGNORM
3.080E+02	2.33625E+05	Real	1.800E+00	LOGNORM
3.150E+02	3.415125E+06	Real	1.800E+00	LOGNORM
3.220E+02	8.32125E+05	Real	1.800E+00	LOGNORM
3.360E+02	3.04500E+05	Real	1.800E+00	LOGNORM
3.430E+02	2.52000E+05	Real	1.800E+00	LOGNORM

Figure 4.107. ASCII text file of input data for tritium urinalysis case.

In this example, we will:

- Use the whole dataset to determine individual intake events - and the resulting effective doses. This is the way that IMBA Professional Plus is used for most radionuclides.
- 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.

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 directly (from the HTO urinalysis data) using the routine tritium urinalysis "tool".

Setting up the HTO Models

Figure 4.108 shows the Main Screen of IMBA Professional Plus **as set up to analyze the** input data**. The setup steps are:**

- Select **"**H(i)-3**" as the** Indicator Nuclide **-** i.e.**, 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**.**
- Click **the "**Load ICRP DEFS**" button - this loads the "**Std H(i)**" bioassay model (Figure 4.109) defining retention of HTO in the "**bioassay quantity**" (**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.**

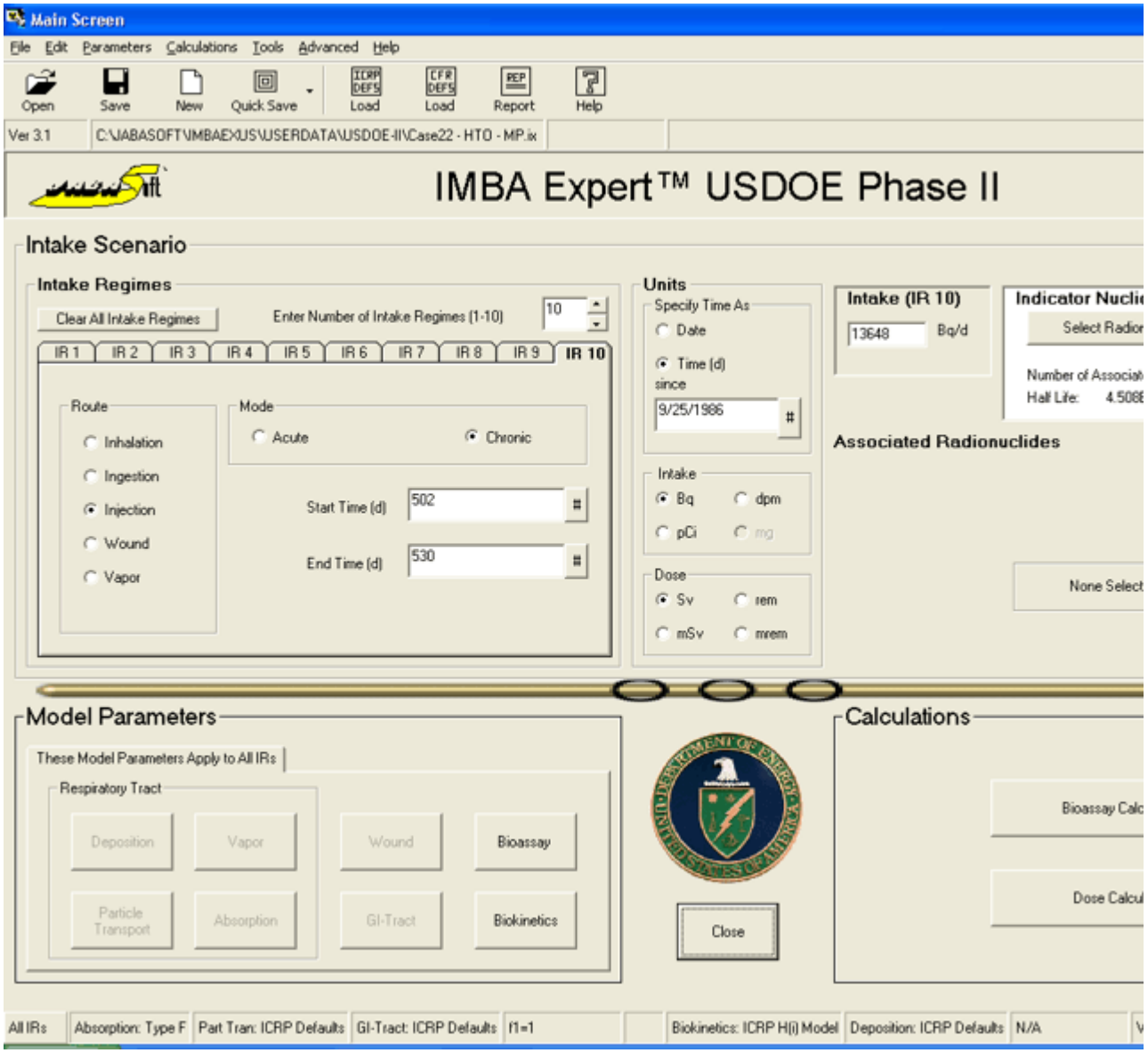


Figure 4.108. Main Screen setup for analysis of 10 discrete intakes of inorganic tritium vapor (HTO).

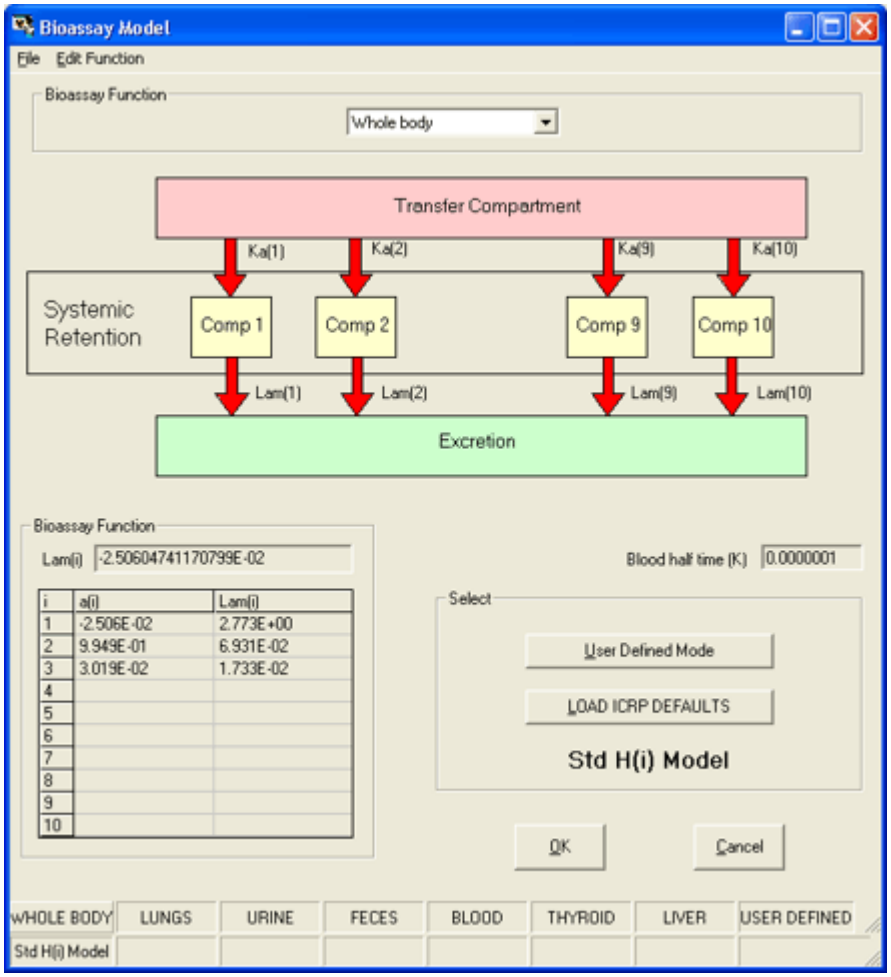


Figure 4.109. ICRP's "Standard H(i) Model" for HTO bioassay (Whole Body retention).

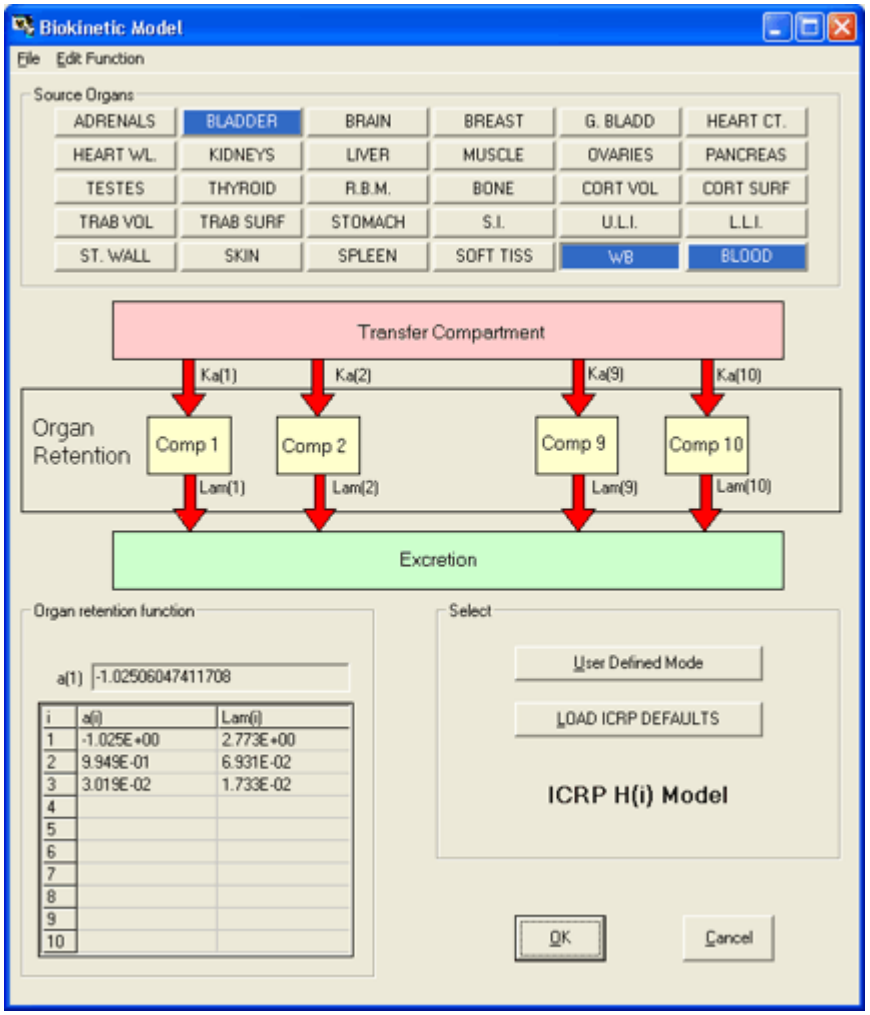


Figure 4.110. Default "ICRP H(i) Model" for HTO biokinetics.

- Proceed to the next step in this example case.
- Return to the case description.

Fitting Discrete HTO Intake Events

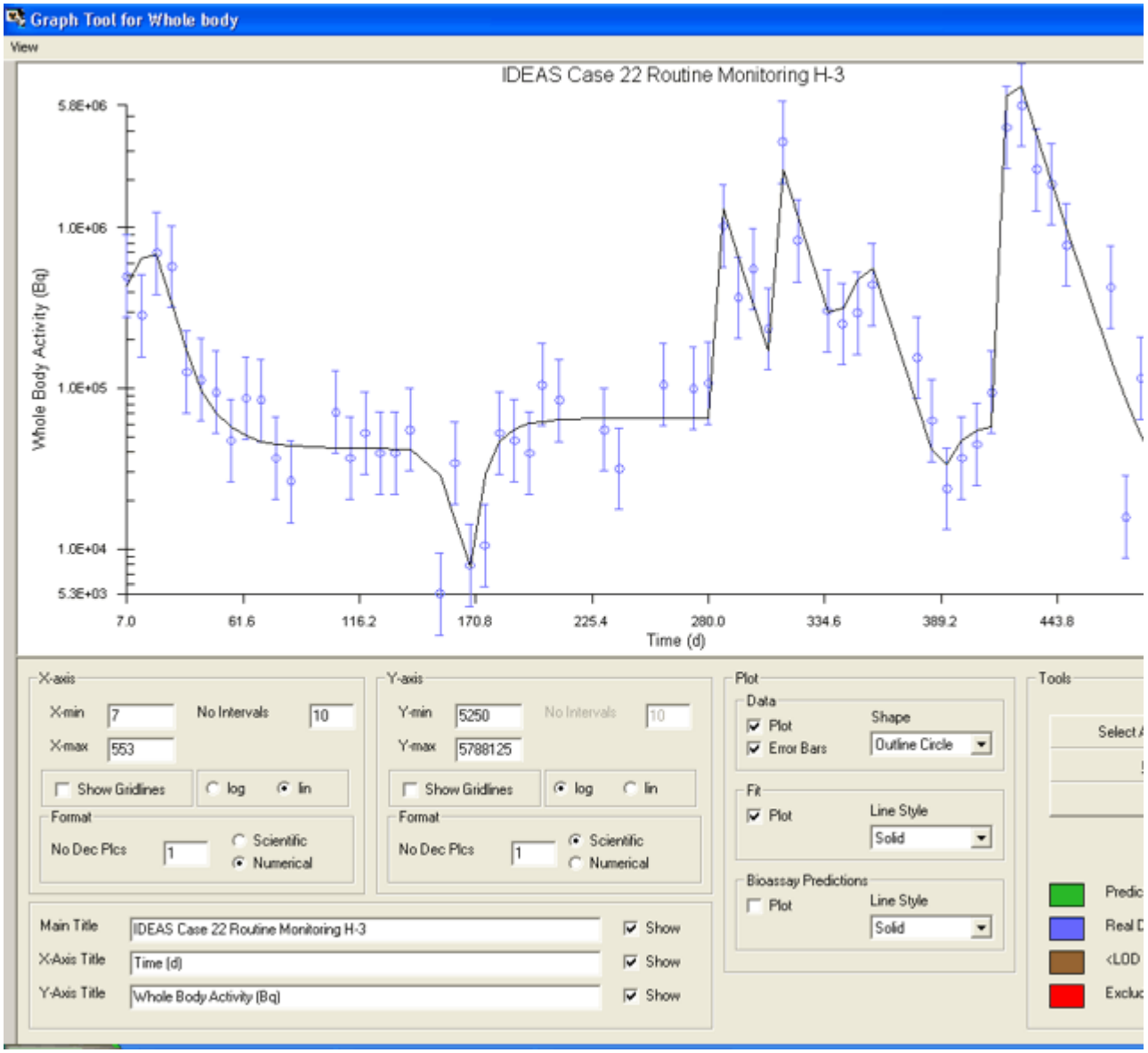


Figure 4.111. Routine tritium urinalysis data together with 'fit' obtained by assuming 10 separate intake events.

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 IDEAS Project (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, i.e., equal to, that in urine. IMBA Professional Plus **allows up to 10 discrete intakes to be defined. In this case, it was necessary to use all 10 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 Appendix A: Assumed Metabolism of Tritiated 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 iteratively - 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 undefined) - 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 automatically **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.

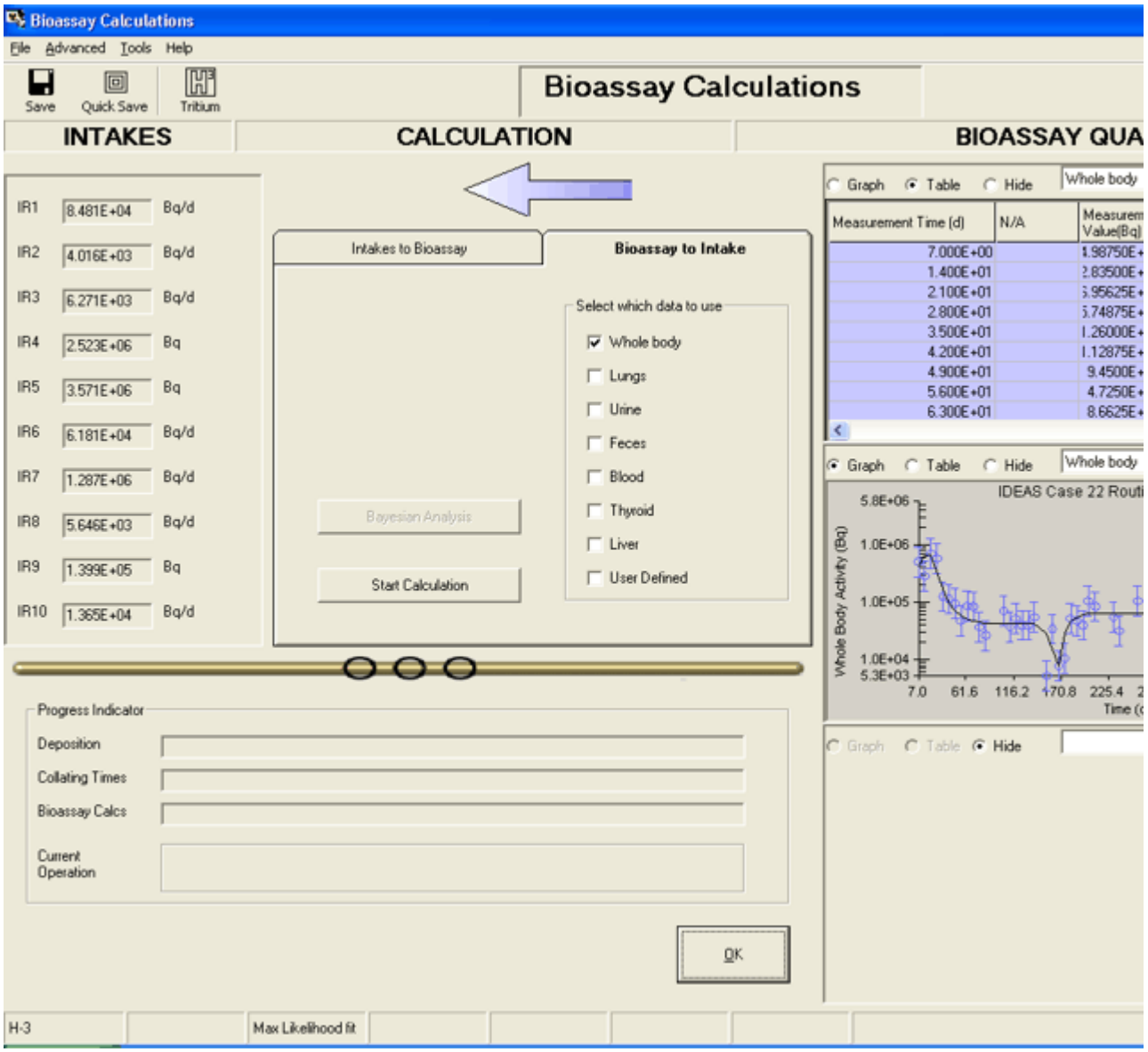


Figure 4.112. Calculated intakes (IR1 through IR10) for tritium urinalysis case.

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.**

Intake regime	Assumed timing	Intake amount/rate (Bq/Bq d-1)
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 yourself - from "scratch" - using the raw input data (by importing the text file [Install Drv]:\JABASOFT\IMBAEXUS\UserData1\Demo\Case_22_Tritium.txt **into the** Table Tool**).** 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

Dose Tool : Effective Doses (H-3)

File Edit Help

Target Organs	Cont. to Eff Dose (Sv) IR(1)	Cont. to Eff Dose (Sv) IR(2)	Cont. to Eff Dose (Sv) IR(3)	Cont. to Eff Dose (Sv) IR(4)	Cont. to Eff Dose (Sv) IR(5)	Cont. to Eff Dose (Sv) IR(6)	Cont. to Eff Dose (Sv) IR(7)	Cont. to Eff Dose (Sv) IR(8)	Cont. to E (Sv) IR(9)
Adrenals	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	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	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	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	0.00E+00	0.00E+00	0.00E+00	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	0.00E+00	0.00E+00	0.00E+00	0.00E+00	
Kidneys	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	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	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	
Ovaries	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	
Pancreas	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	
Testes	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	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	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	
U.L.I.	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	
L.L.I.	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	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	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	
Thymus	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	
Uterus	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	
ET	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	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	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	
ET2	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	
LN(ET)	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	
BBsec	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	
BBbas	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	
bb	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	
AI	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	
LN(TH)	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	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	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	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 Dose Calculations screen, in this example (Figure 4.114) by:

- Selecting the "ICRP Default" radiation weighting factors (wR).
- Selecting the "ICRP68" tissue weighting factors (wT).

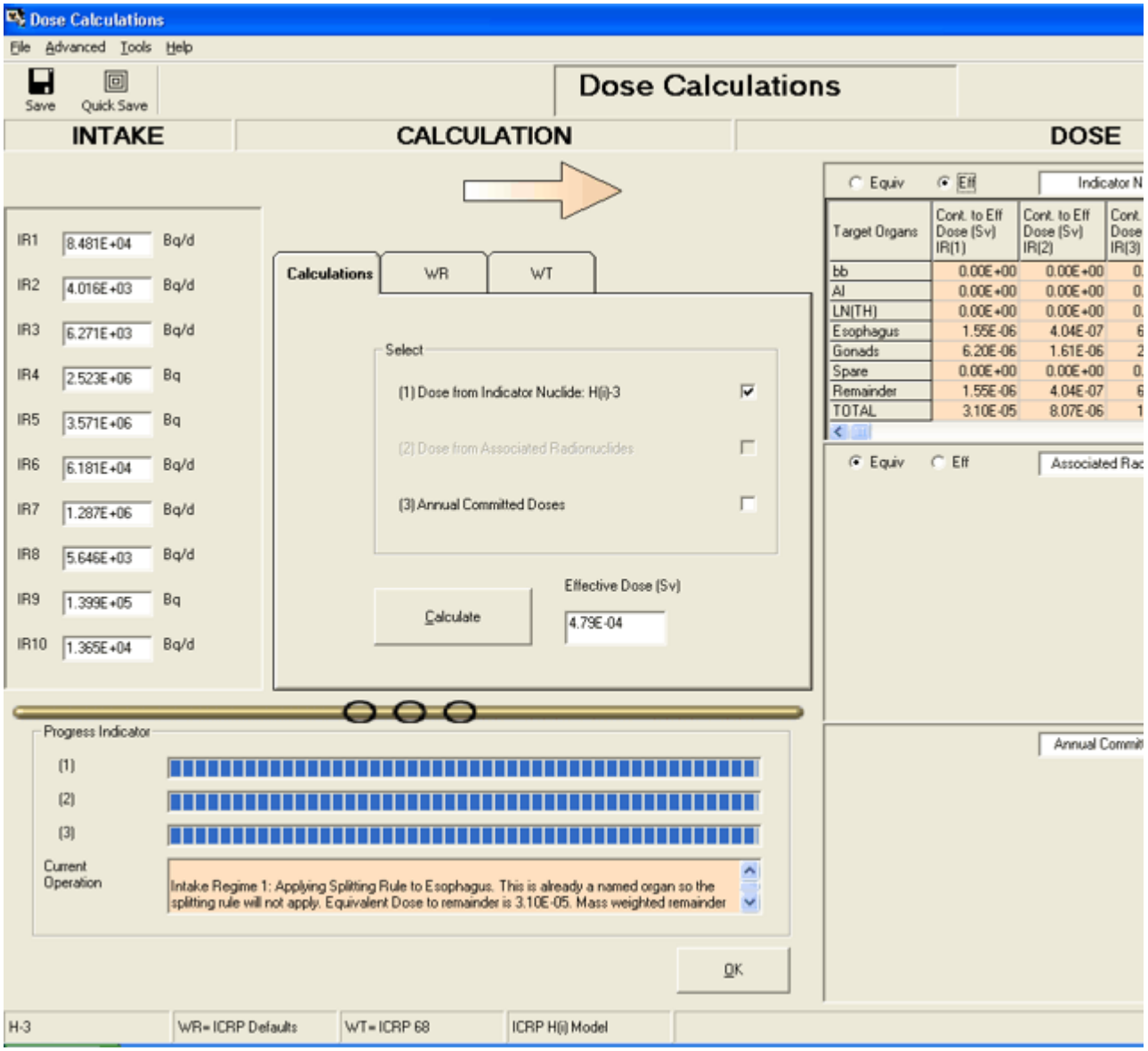


Figure 4.114. Calculating and displaying both the contributions to effective dose from each HTO intake and the effective doses committed each year.

Note: In this example, the TOTAL (committed) effective dose is 4.79 ´ 10-4 Sv (479 µSv).

- Proceed to the next step in this example case.
- Return to the case description.

Dose Committed During HTO Monitoring Periods

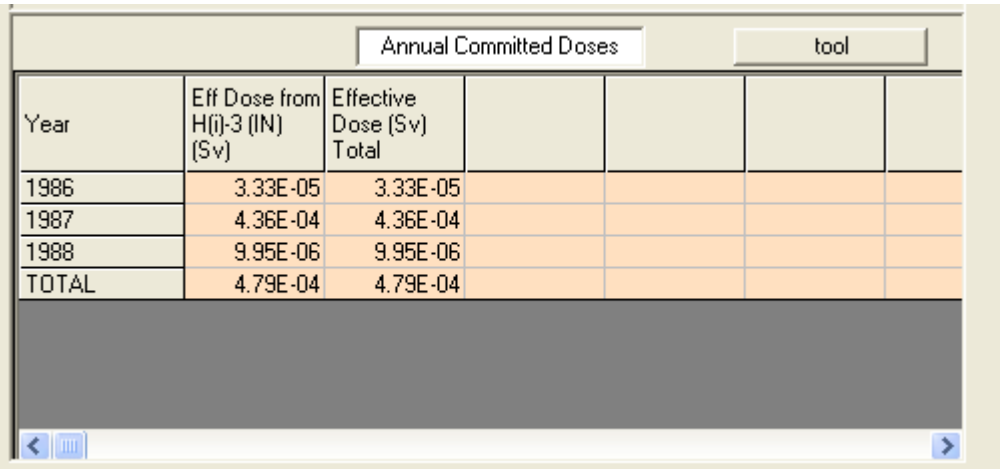
The next section (Using the Routine Tritium Urinalysis "Tool"), describes how to calculate committed doses directly from the tritium urinalysis data - without having first to determine

(by manual fitting) the amounts of each discrete tritium intake. The urinalysis "tool" analyses up to 10 sequential urinalysis results - and calculates automatically the total effective dose committed over this whole monitoring period.

In this example, we can use the special feature provided in IMBA Professional Plus to calculate the Annual Committed Doses resulting from a series of intakes - to generate "benchmark" values of dose for comparison with the results obtained using the Urinalysis "Tool". The "Tool" analyses a sequence of up to 10 routine monitoring results. In this example, the first 10 monitoring results covered the period from day "0" to day "70" (Figure 4.107). In this example, we can calculate the total dose committed over just this initial 70-day period, by simply:

- Changing the "Start Date" (in the Main Screen) to [December 31st, 1986 - 70 d] = October 22nd, 1986.
- Re-calculating the "Annual Committed Doses".

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 µSv) corresponds to the effective dose committed during the first 70-d monitoring period.



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 µSv (from IR1) and 30/110 ´ 8.1 µSv (from IR2) = 33.2 µSv (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 previous section. 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:

- Setting up the Tritium Tool.

Setting up the Tritium Tool

After clicking the "**New**" button - or opening IMBA Professional Plus from its desktop icon - you first:

- Select "H(i)-3" - "inorganic tritium (HTO)" - as the Indicator Nuclide.
- Click the "ICRP DEFS Load" button.
- Click the "Bioassay Calculations" button.
- Select "Whole Body" as the bioassay data to use.
- Click the "H3 Tritium" button - top-left-corner of the Bioassay Calculations screen.

This will open the "Tritium Routine Monitoring Tool" window (Figure 4.116).

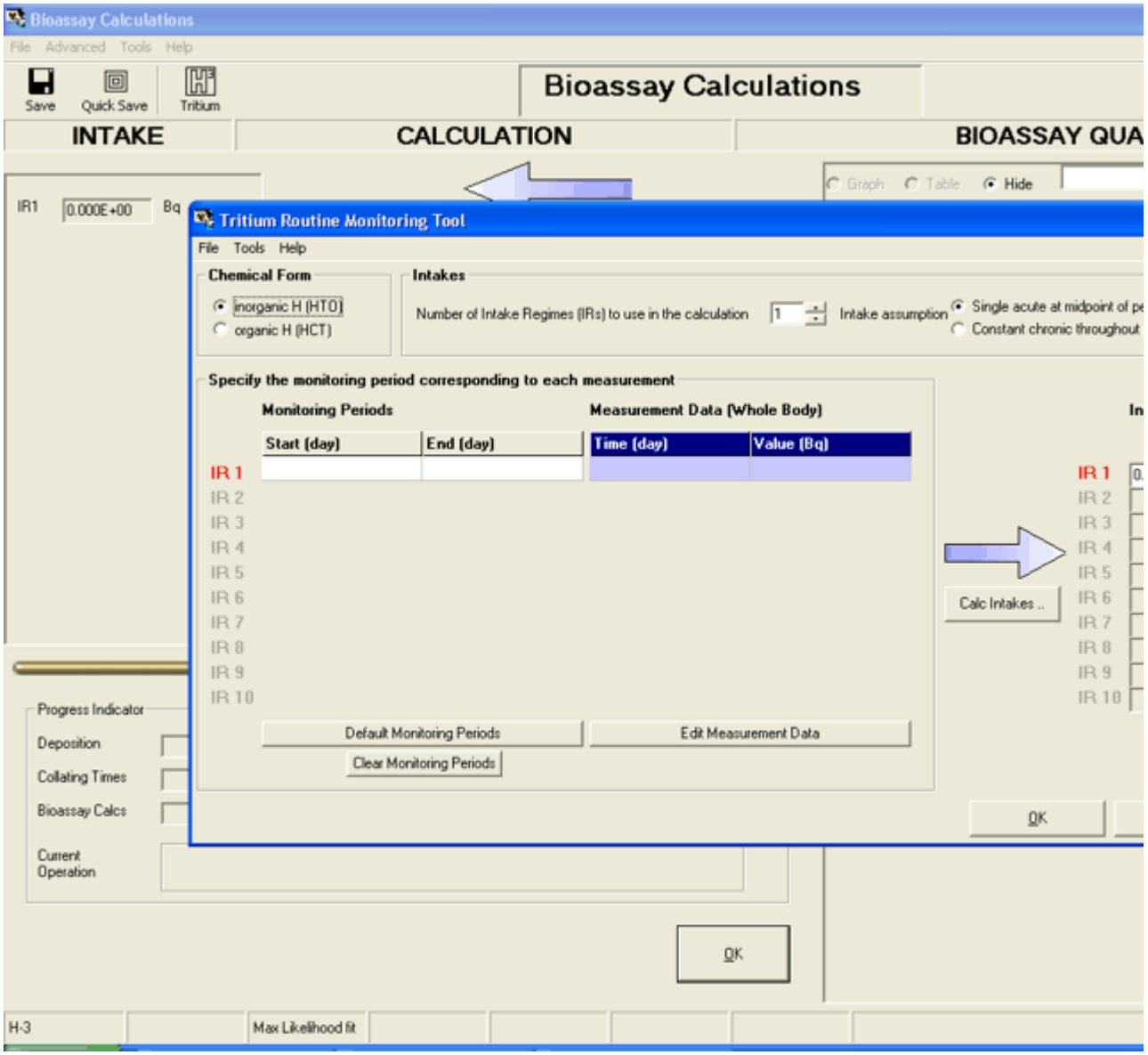


Figure 4.116. Opening the **Tritium Routine Monitoring Tool**.

Note #1: This example considers only intakes of "**inorganic H (HTO)**" - for which the bioassay quantity is automatically set as "**Measurement Data (Whole Body)**". However, you also have the option to select "**organic H (HCT)**" from the Tritium Routine Monitoring Tool. In that case, the bioassay quantity will automatically be set as "**Measurement Data (Urine)**" - in the Tritium Routine Monitoring Tool, and "**Urine Data**" in the Table Tool.

Note #2: The Tritium Routine Monitoring Tool works independently of the **Indicator Nuclide** (which is selected in the **Main Screen**). None of the options selected in the "Tritium Tool" affect settings in the **Main Screen**.

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

follows:

- Using "pre-loaded" bioassay data - from the **Table Tool**.
- Using the "Import Wizard".

Loading Tritium Data Already in the Table Tool

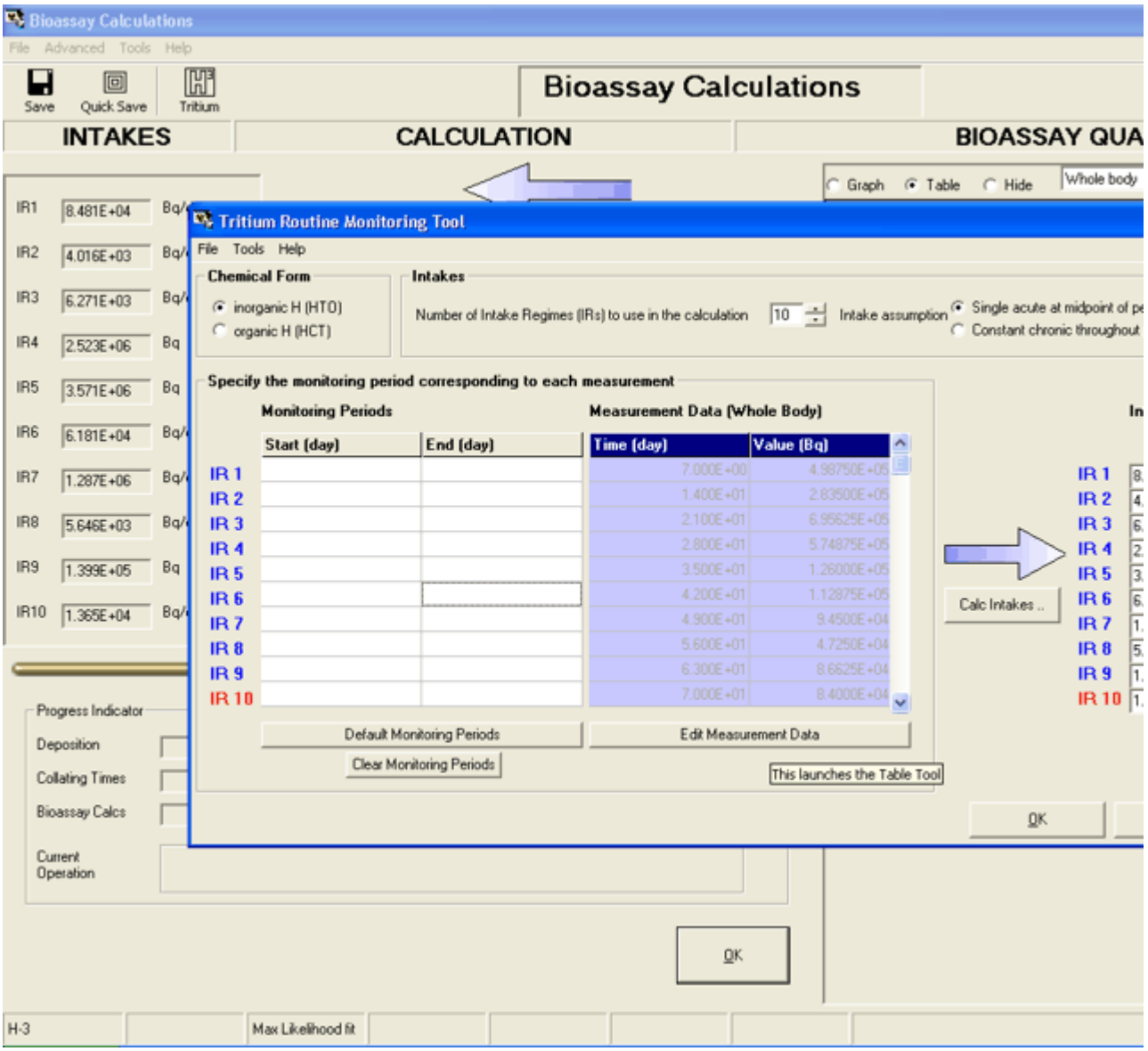


Figure 4.117. Opening the Tritium Routine Monitoring Tool with "Whole Body" data already in the Table Tool - from "Case22 - HTO - MP.ix".

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 (IR1 through IR10) - 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".

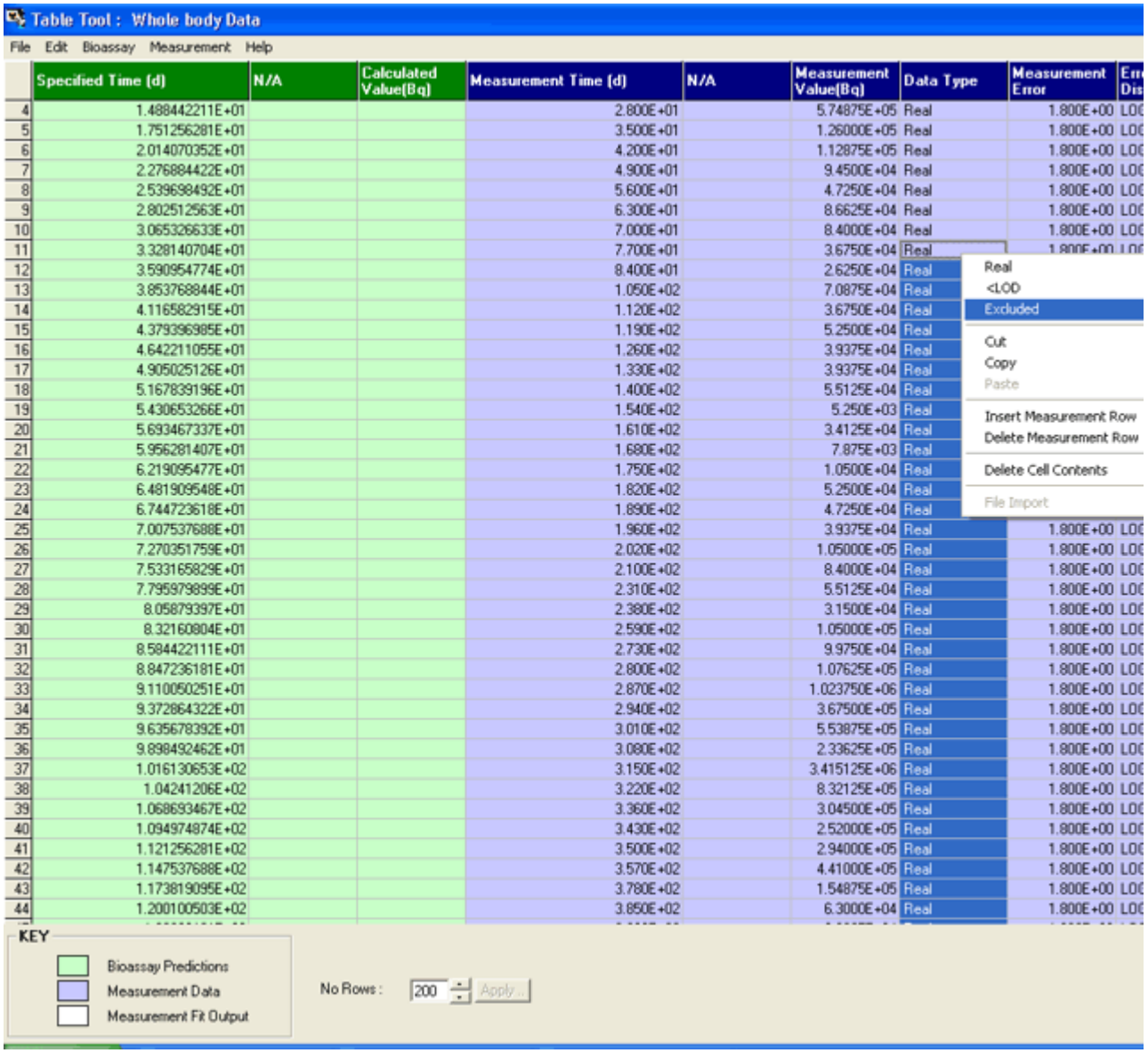


Figure 4.118. Excluding all data in rows 11 and below in the Table Tool.

This will change the color of all data entries in row 11 and below to red, and also change the color of the corresponding data points plotted in the Bioassay Quantity graph (Figure 4.119).

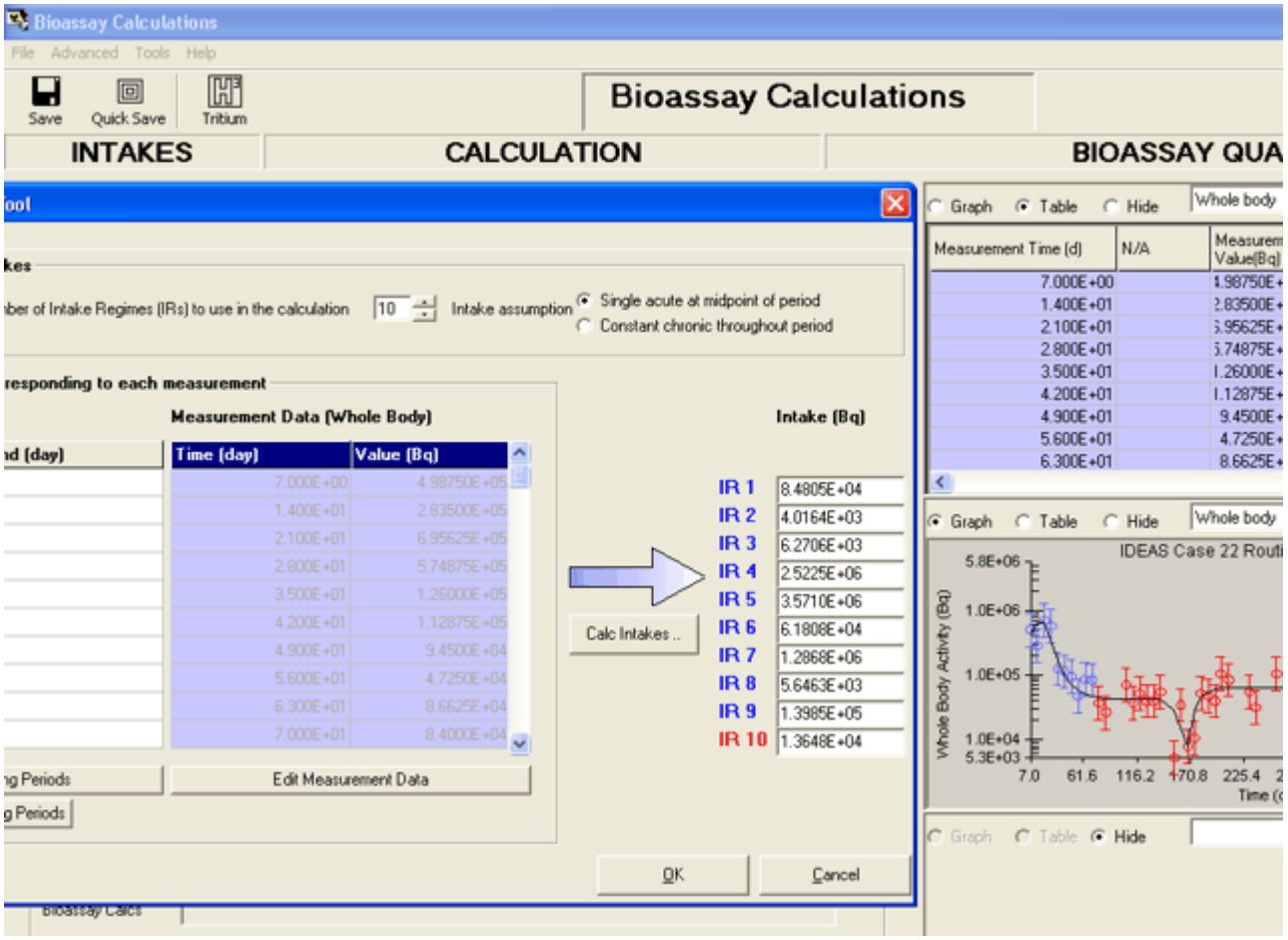


Figure 4.119. Excluding the 11th and all further data points from analysis by the tritium tool.

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).

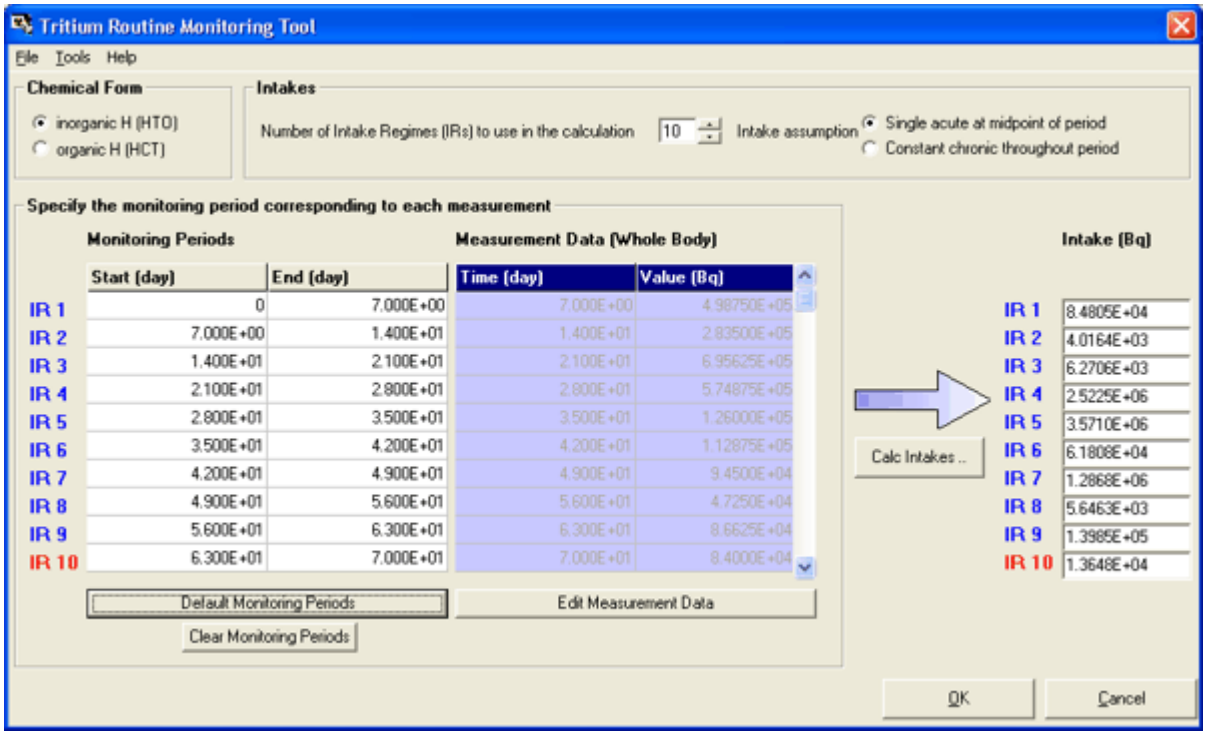


Figure 4.120. Specifying the monitoring periods automatically.

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.

Warning: By default, the Tritium Routine Monitoring Tool assumes a "Start (day)" value of "0" - since the actual value is not included in the imported data. If "0" is incorrect, you will have to enter the appropriate value yourself. This is generally the "End (day)" of previous (most recent) set of monitoring data.

Note: You can select ANY sub-set of contiguous data rows (up to a maximum of 10 rows) from the Table Tool - for automatic importation into the Tritium Routine Monitoring Tool.

This completes the step of loading a sub-set of the bioassay data into the Tritium Routine Monitoring Tool - directly from the Table Tool.

- Proceed to Using the Tritium 'Tool' to Calculate Intakes Automatically.

Loading Tritium Data with the Import Wizard

Clicking the "Edit Measurement Data" button in the Tritium Routine Monitoring Tool opens the Table Tool. You can then import the required bioassay data (Figure 4.117A).

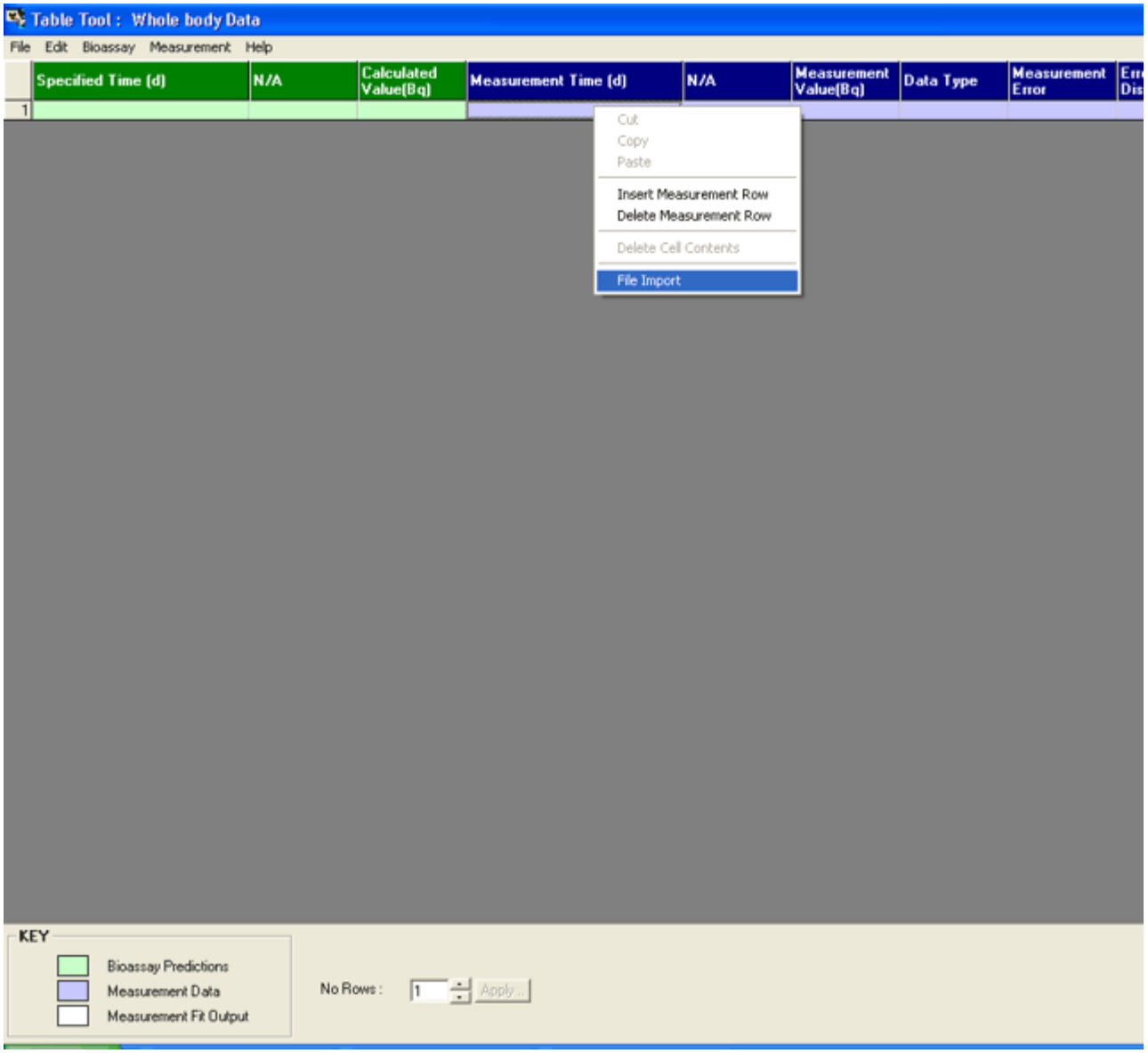


Figure 4.117A. Blank Table Tool ready to import a file of whole body bioassay data.

In the Table Tool, right-click on the empty cell under the "Measurement Time (d)" heading (Figure 4.117A). From the drop-down menu, select "File Import" (as in Figure 4.117A). This will open the "ASCII file import wizard" (Figure 4.118A).

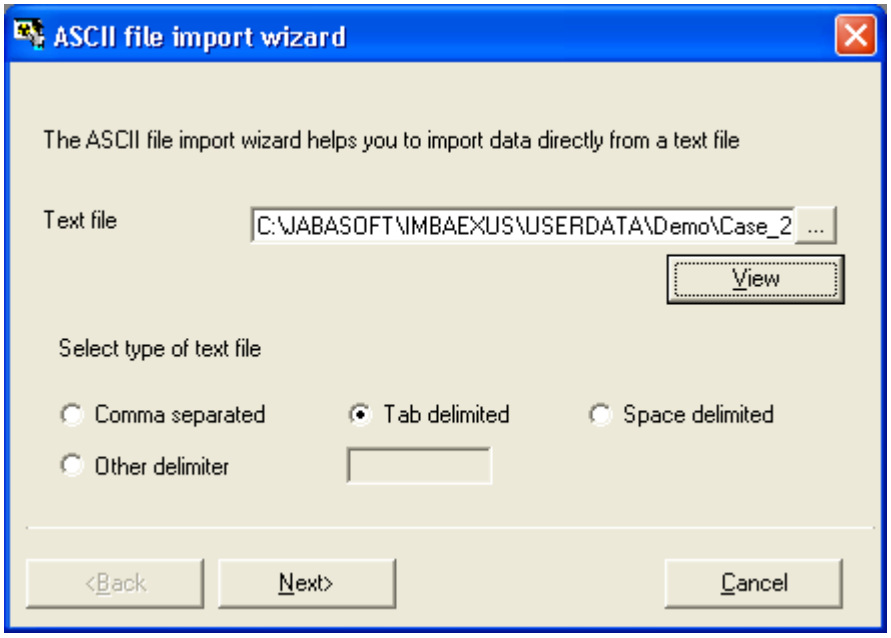


Figure 4.118A. The ASCII file import wizard.

In the ASCII file import wizard, browse to the folder [Install Drv]:\\JABASOFT\IMBAEXUS\UserData1\Demo\ and select the file "Case_22_Tritium.txt" data file, and click View (Figure 4.118A). This will open the file in NotePad® (Figure 4.119A).

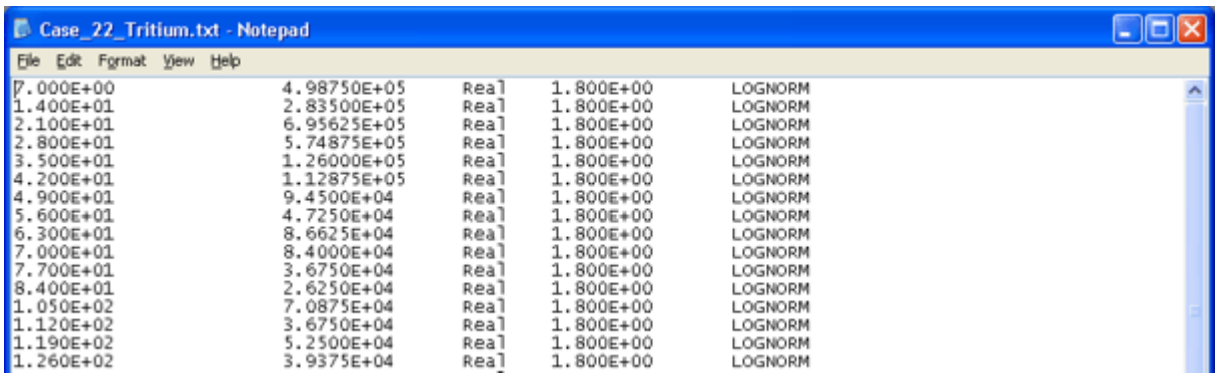


Figure 4.119A. First part of the "Case_22_Tritium.txt" data file - viewed in NotePad®.

This file is "tab delimited" - and so you need to click the "Tab delimited" button (Figure 4.118A) before clicking Next. The whole file will then be imported (into rows and columns) in the ASCII file import wizard (Figure 4.120A).

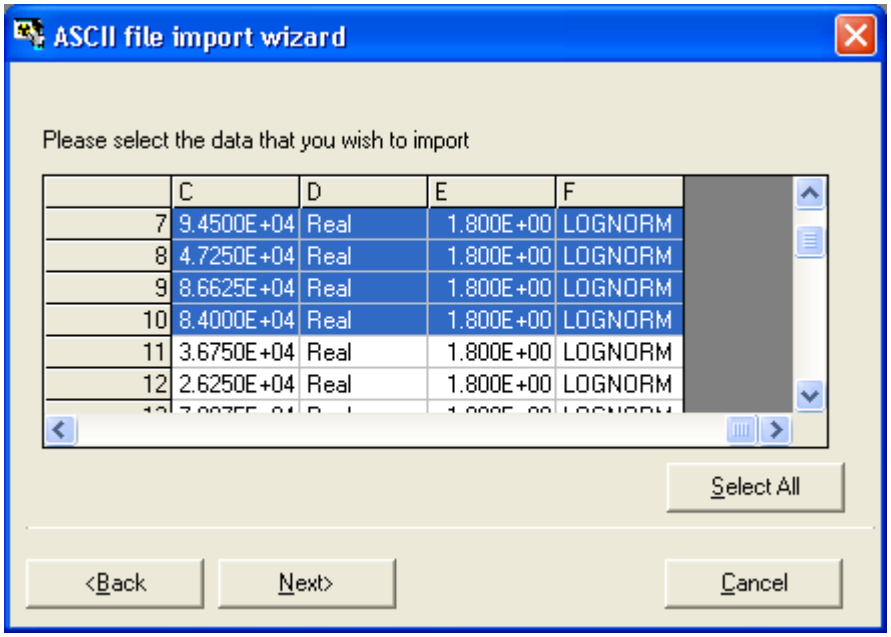


Figure 4.120A. Selecting the first 10 rows of data.

The Tritium Routine Monitoring Tool analyzes the bioassay data a maximum of 10 rows (i.e., 10 data points) at a time. Therefore, you should highlight just 10 rows of data in the import wizard - before clicking the Next button. The highlighted 10 rows are then automatically loaded into the Table Tool (Figure 4.121).

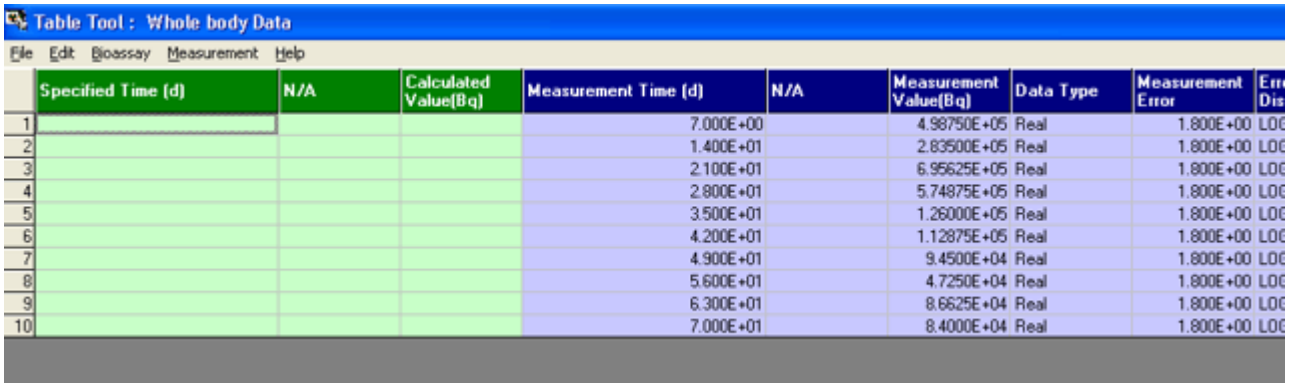


Figure 4.121. 10 rows of bioassay (whole body) data imported into the Table Tool.

Clicking "OK" in the Table Tool returns you to the Bioassay Calculations screen - with the Tritium Routine Monitoring Tool window still open. However, the imported data is now visible (automatically) in this window (figure 4.122).

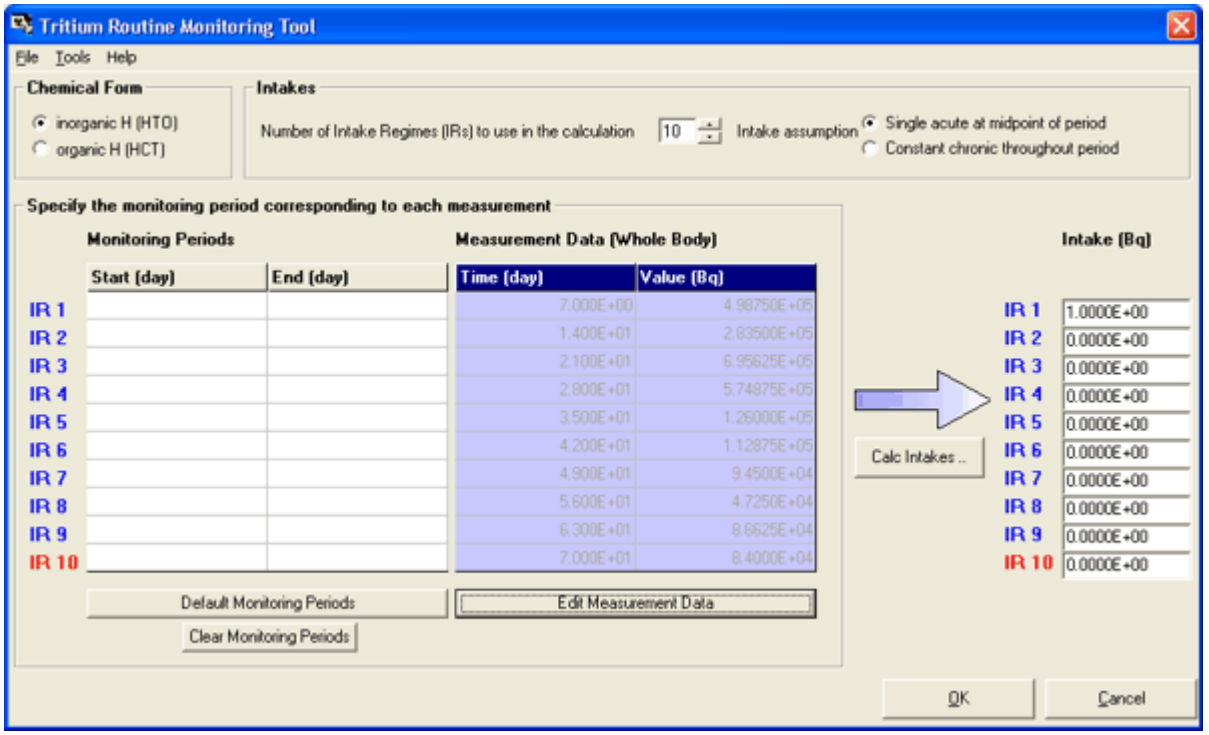


Figure 4.122. Tritium Routine Monitoring Tool window showing 10 rows of imported data.

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 4.123).

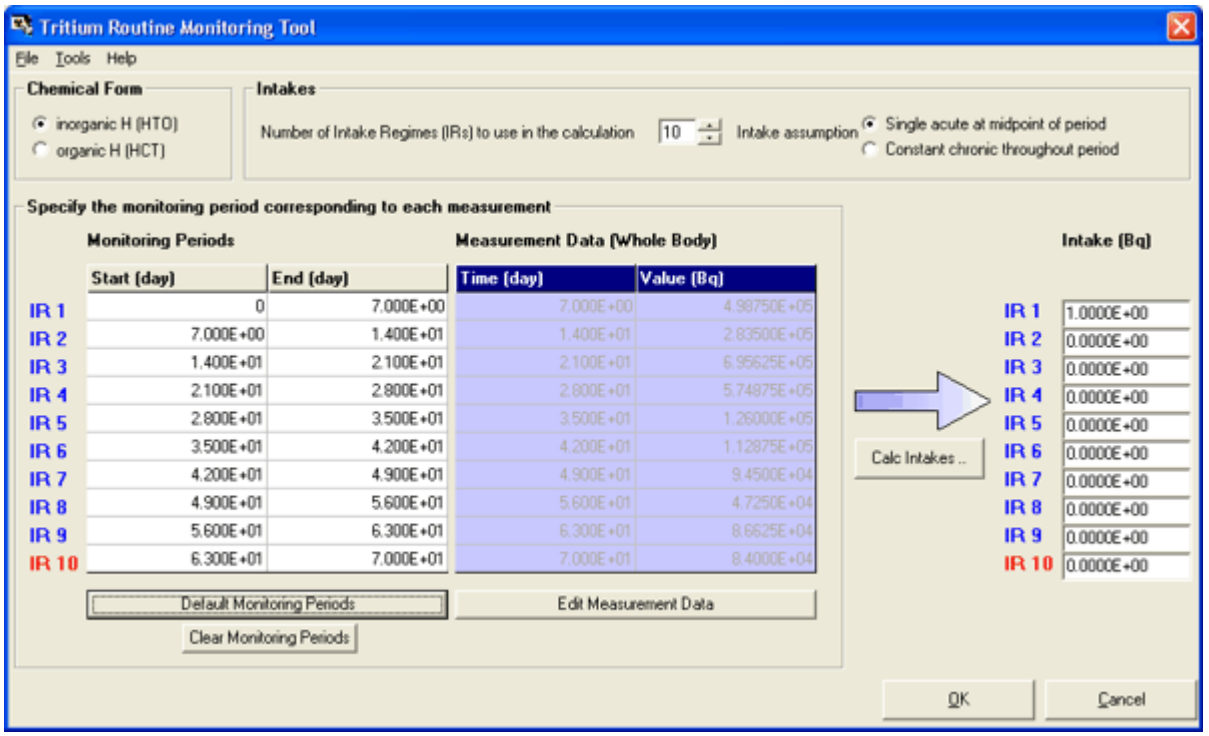


Figure 4.123. Specifying the monitoring periods automatically.

If the monitoring periods are not in fact all contiguous, you can edit any "Start (day)" value directly in the Tritium Routine Monitoring Tool table. Also, clicking the "Edit Measurement Data" button (Figure 4.123) 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 integrated with that of the Table Tool.

Warning: By default, the Tritium Routine Monitoring Tool assumes a "Start (day)" value of "0" - since the actual value is not included in the imported data. If "0" is incorrect, you will have to enter the appropriate value yourself. This is generally the "End (day)" of previous (most recent) set of monitoring data.

This completes the step of loading the bioassay data into the Tritium Routine Monitoring Tool - using the Import Wizard.

- Proceed 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 (i.e., 10 rows in the Measurement Data table) and defined all of the associated Monitoring Periods (as in Figure 4.123), you can use the Tritium Routine Monitoring Tool to calculate automatically a set of discrete Intakes 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 Tritium Routine Monitoring Tool provides two standard (commonly made) assumptions - that are applied automatically to all potential intakes:

- Single Acute intake at the mid-point of each monitoring period - set by default.
- Constant Chronic intake throughout each monitoring period.

For the default setting (Single Acute), the Tritium Routine Monitoring Tool automatically calculates the time value corresponding to each sample mid-point. For the "Constant Chronic" option, the pre-calculated "Start (day)" and "End (day)" values are used to calculate the associated Intake values. In order to "fit" the monitoring data (bioassay values), the Tritium Routine Monitoring Tool uses the maximum likelihood method (as extended to multiple intakes in IMBA Professional Plus) to find the most likely value of the hypothetical intake 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 over-estimate the actual intake during this monitoring period - by the amount of "carry over". However this effect will become smaller for each subsequent intake calculation, i.e., later intakes will be calculated more accurately.

Important Note #2: This methodology leads to a somewhat conservative estimate of the effective dose committed over the whole monitoring period - although, usually not a serious over-estimate if the whole monitoring period is greater than a month.

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 this example. In this case, we have assumed (by default) that each potential intake would have occurred at the mid-point of each sampling period.

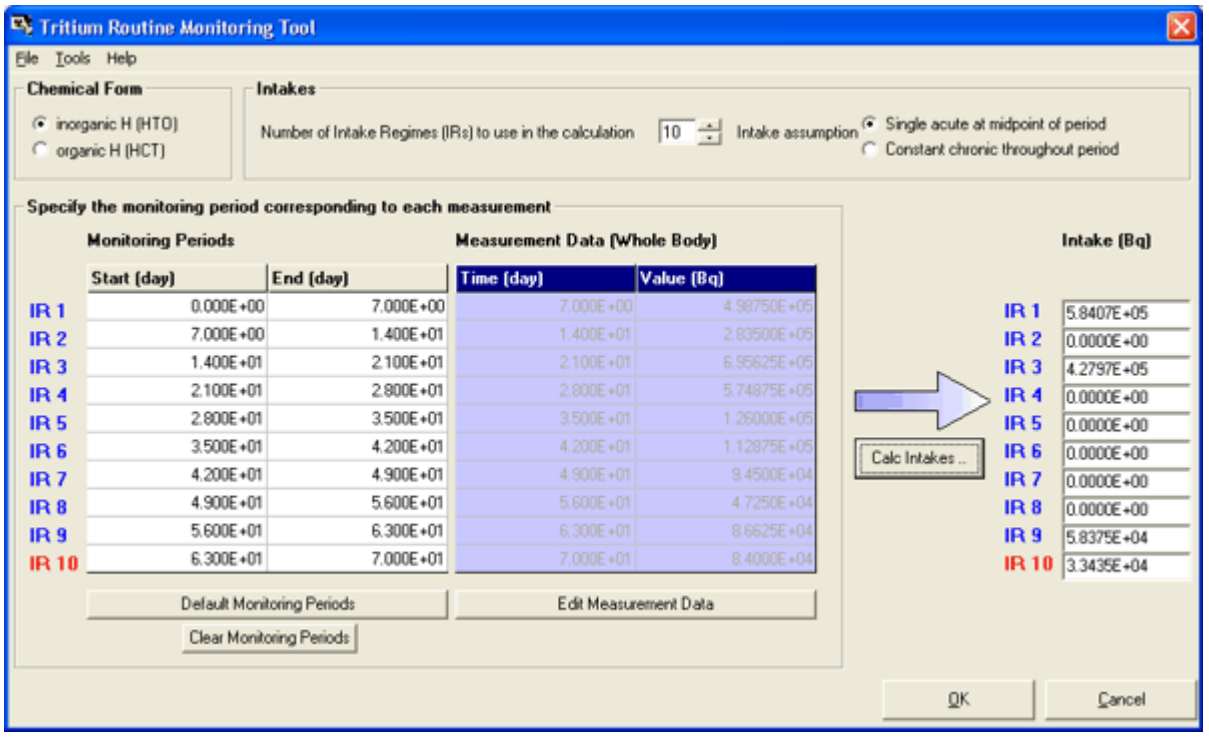
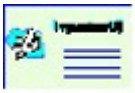


Figure 4.124. Result of clicking the "Calc Intakes .." button in the Tritium Routine Monitoring Tool.



Note: For this set of 10 bioassay values, the Tritium Routine Monitoring Tool calculated 4 finite values of intake (for IR1, IR3, IR9 and IR10). All other potential intakes were calculated to be zero.

Clicking the "OK" buttton in the Tritium Routine Monitoring Tool returns you to the Bioassay Calculations screen (Figure 4.125).

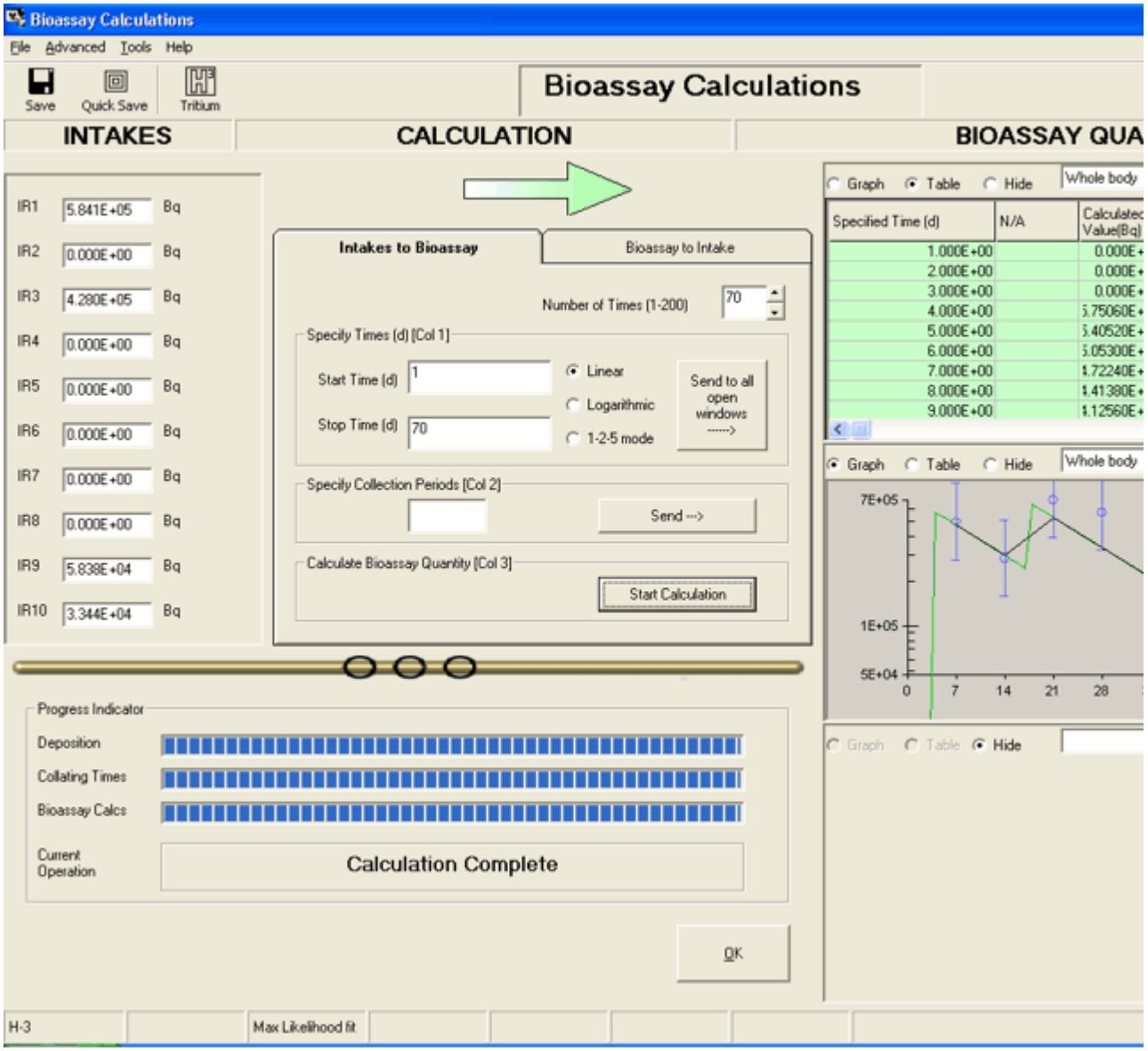


Figure 4.125. The amount of intake calculated to have given rise to each successive bioassay measurement is displayed automatically in the Bioassay Calculations screen.

Tip: If you set up a Graph window for the Bioassay Quantity (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 "Effect of Assumed HTO Intake Pattern".

Clicking "OK" in the Bioassay Calculations screen then returns you to the Main Screen (Figure 4.126).

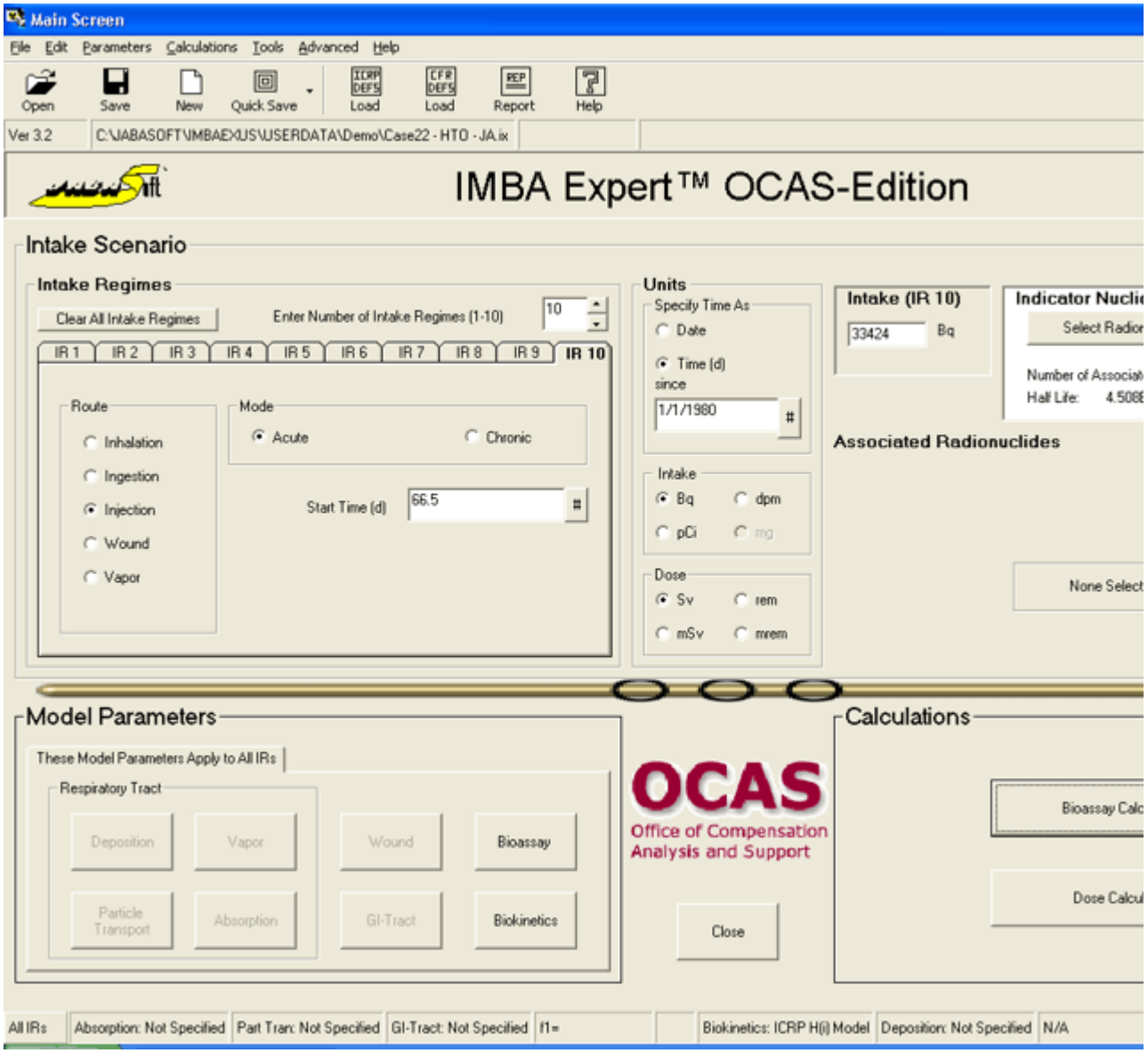


Figure 4.126. Main Screen after returning from the Tritium Routine Monitoring Tool.

Note: The calculated intake values (and the assumed times and durations of the intakes) are automatically displayed in the Main Screen - so that you can proceed directly to the Dose Calculation.

This completes the step of calculating automatically the associated Tritium Intakes:

- Proceed to Using the Tritium 'Tool' to Calculate Doses Automatically.

Automated Tritium Dose Calculation

Clicking the Dose Calculations button in the Main Screen opens the Dose Calculations screen (Figure 4.127). Then, to calculate the resulting values of effective dose, you simply click the "Calculate" button. The results for the whole tritium monitoring period (0 to 70 d) are shown

in Figure 4.127.

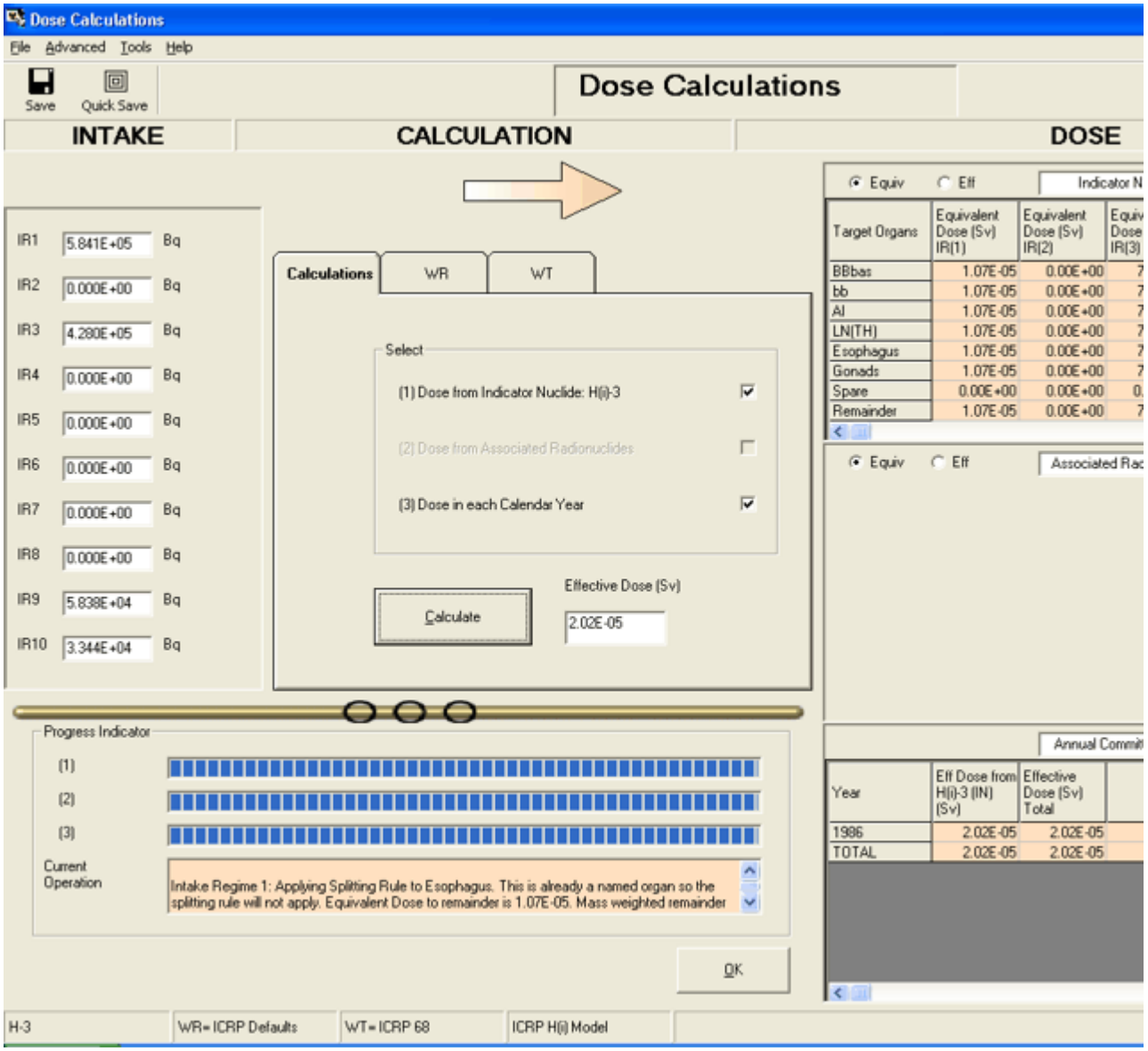


Figure 4.127. Calculating and displaying the resulting committed effective dose.

In this case, the total committed effective dose is 20.2 µSv.

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 "Case_22_Tritium.txt" - gives the calculated values of committed effective dose shown in Table 4.7.

Note: There are 65 rows of data, imported as 6 sets of 10 values with a residual set of 5 values.

Table 4.7. **Total committed effective dose calculated for each monitoring period.**

Monitoring period (d)	Total Committed Effective Dose (µSv)
#1: 0 - 70	**20.2**

#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
Total: 0 - 553	317

Note: These calculated values assume that intakes occurred at the mid-point of the corresponding sampling interval. The total committed effective dose (317 µSv) is substantially lower than the value (479 µSv) calculated earlier - 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 mid-point of the corresponding sampling interval:

- Proceed 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 mid-point of the corresponding sampling period, the Tritium Routine Monitoring Tool gives you the option of assuming that all intakes occur continuously (i.e., are uniform chronic) over the corresponding sampling interval. Figure 4.128 shows the effect of making the uniform chronic assumption on the intakes calculated for the first set of monitoring data (from 0 to 70d).

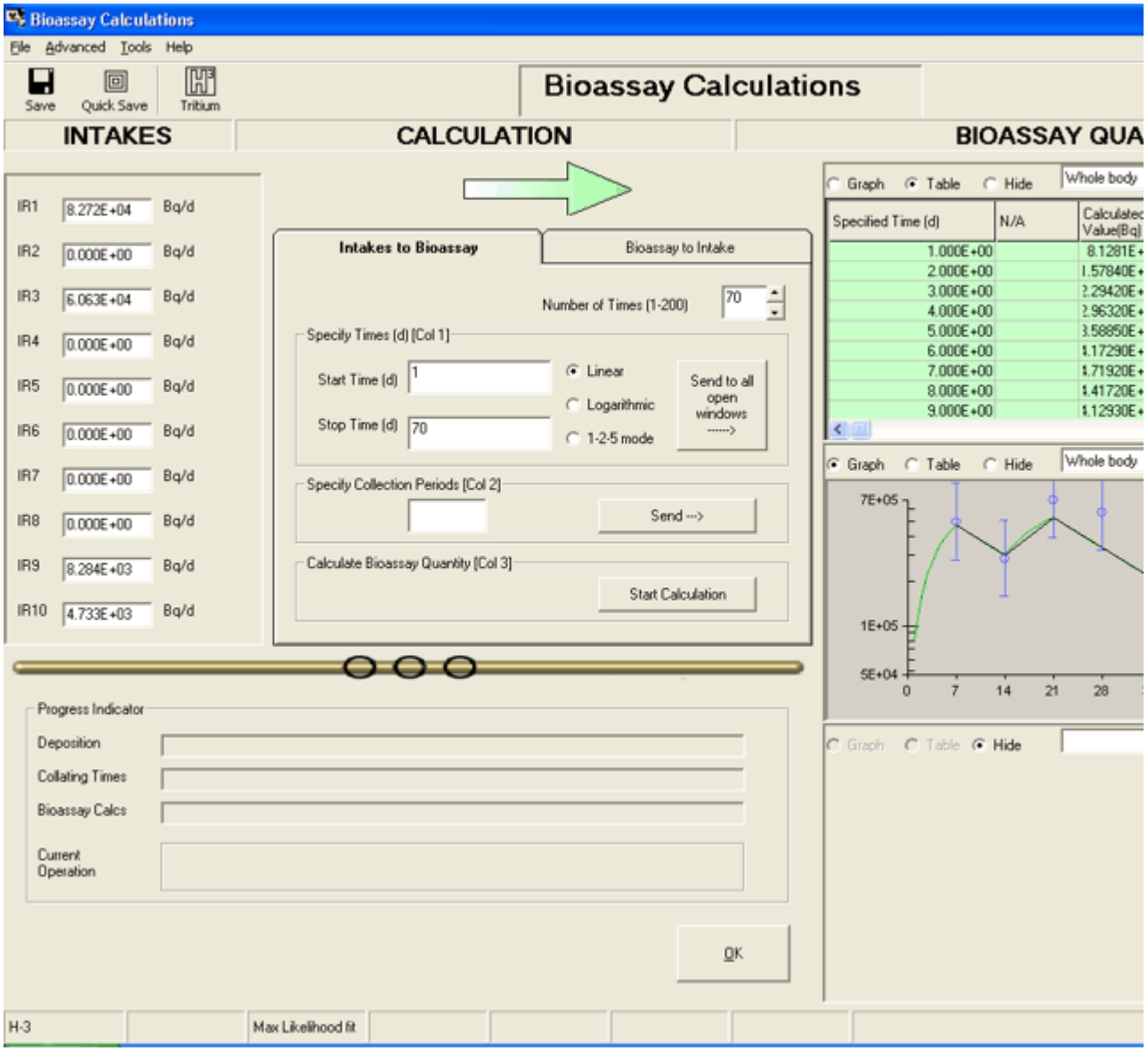


Figure 4.128. The amount of intake calculated to have given rise to each successive bioassay measurement on the assumption of constant chronic intake over the corresponding sampling interval.

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.**

Monitoring period (d)	Total Committed Effective Dose (μSv)
#1: 0 - 70	**20.0**
#2: 70 - 161	**4.5**
#3: 161 - 259	**8.3**
#4: 259 - 343	**57.0**
#5: 343 - 427	**177**
#6: 427 - 518	**43.1**
#7: 518 - 553	**3.4**
Total: 0 - 553	313

Note: These calculated values are very close to (marginally lower 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 µSv) - to be compared with (317 µSv) for the "mid-point" assumption (Table 4.7).

This completes the step of calculating doses automatically - assuming that all intakes occurred continuously over the corresponding sampling interval:

- Proceed 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 "Case22 - HTO - JA.ix" contains a solution to this example case that was obtained (by ACJ & Associates, Inc.) independently of the "Case22 - HTO - MP.ix" solution. This independent solution is shown in Figure 4.129.

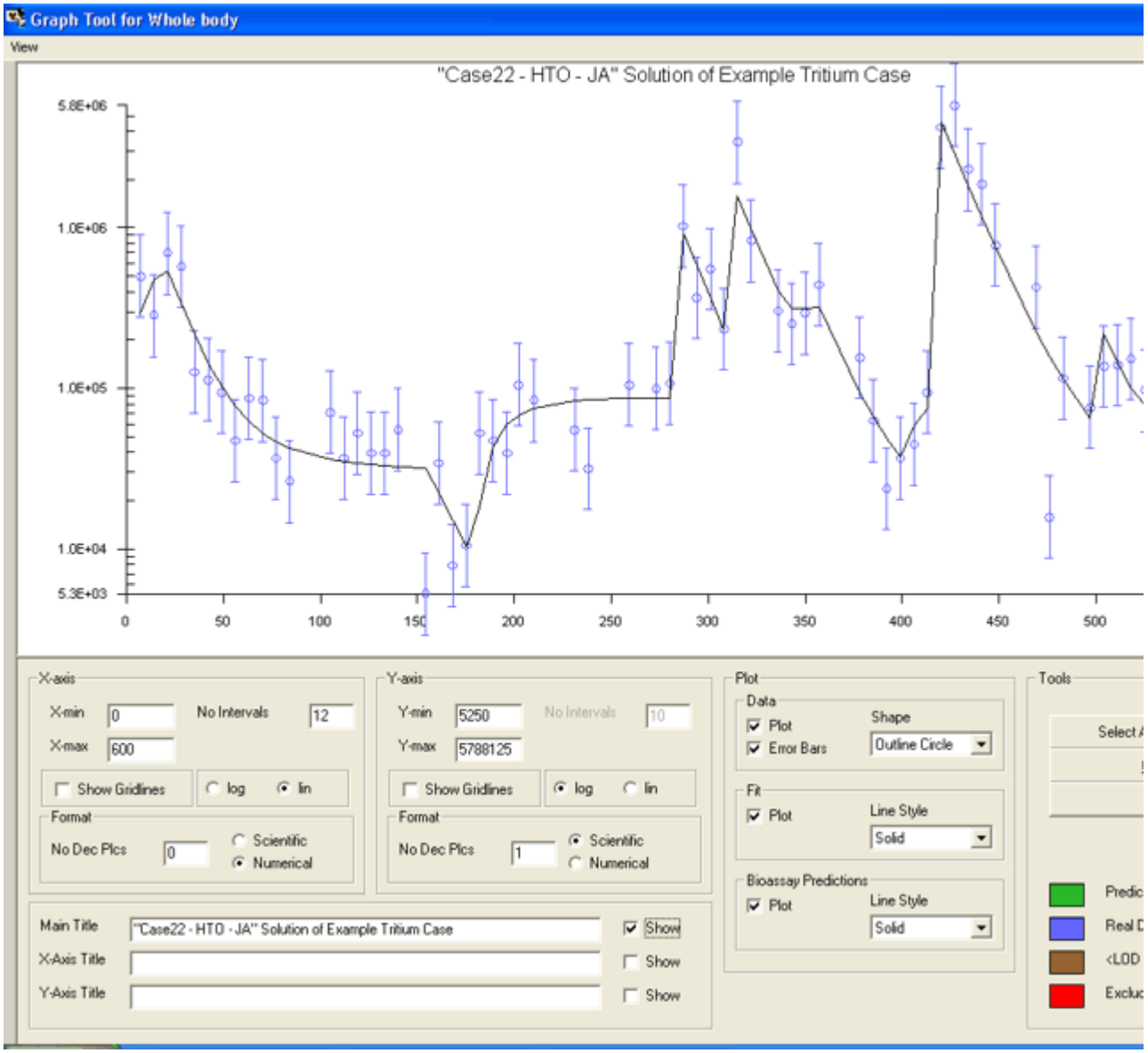


Figure 4.129. A second solution of the tritium routine monitoring example case.

Table 4.8 shows the 10 discrete intakes fitted to the bioassay data - c.f., the results of the earlier solution (Table 4.6).

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 Bq/d**
IR7 - chronic	**400 - 440 d**	**5,837 Bq/d**
IR8 - acute	**418 d**	**4,977,000 Bq**
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 Table 4.6 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 Figure 4.111, respectively.

Figure 4.130 shows the committed effective doses calculated from the estimates of intake given in Table 4.8.

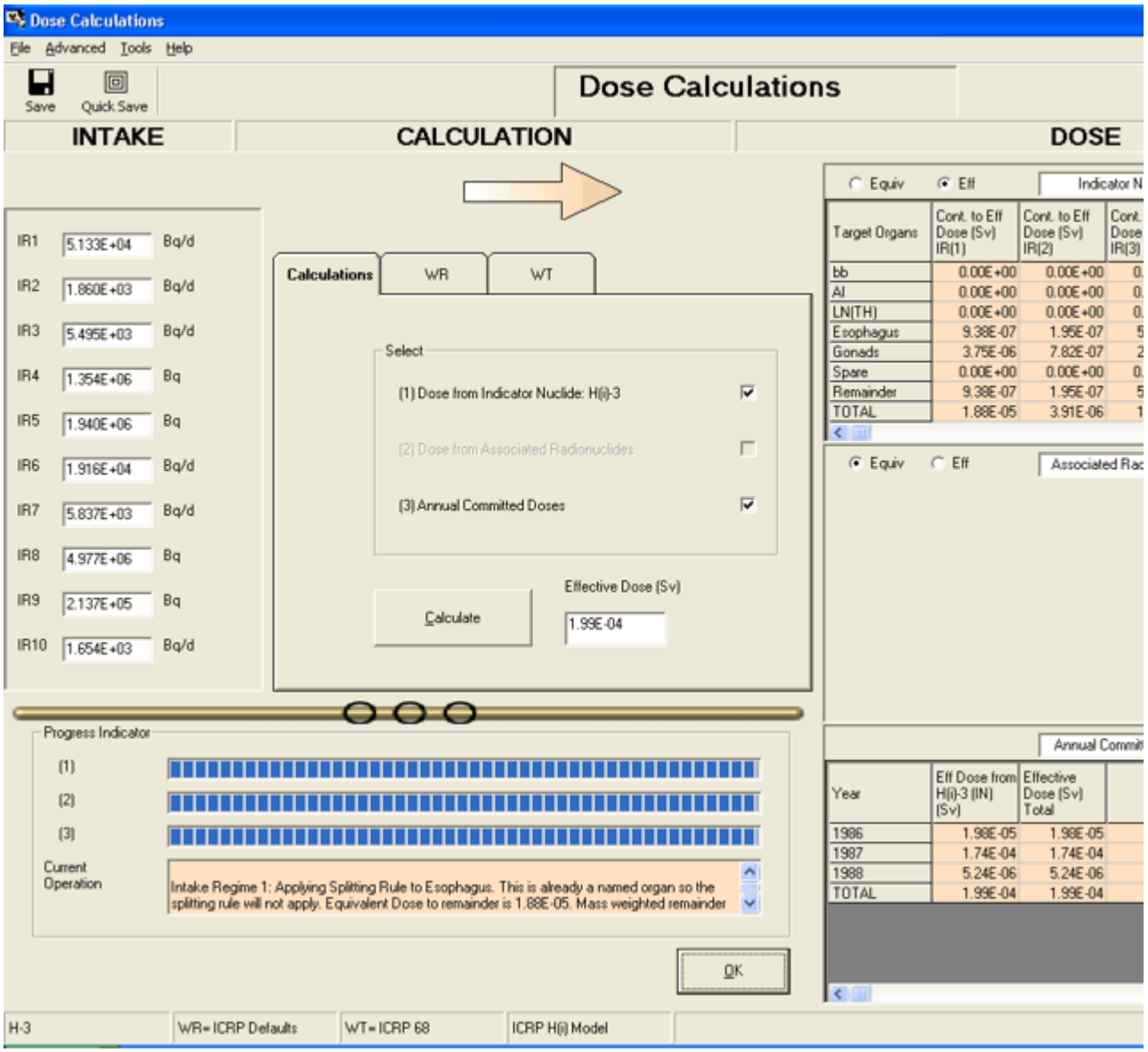


Figure 4.130. Dose calculated from the second solution of the tritium routine monitoring example case.

Note #1: The total committed effective dose calculated in this second solution (199 µSv) is less than half the value (479 µSv) calculated in the earlier solution.

Note #2: However, the average of the two independent estimates of total committed effective dose is 339 µSv (± 198 µSv standard deviation). This is within 8% of the average value (315 µSv) obtained using the "automated" 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 Automated Tritium Intake Estimation (and Dose Calculation) 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 Table 4.7 (where the monitoring period was divided into seven parts). In both cases, it was assumed that intakes occurred at the mid-point of the corresponding sampling interval.

Table 4.9. Total committed effective dose calculated for each monitoring period.

Monitoring period (d)	Total Committed Effective Dose (µSv)
#1: 0 - 35	**19.9**
#2: 35 - 70	**4.7**
#3: 70 - 119	**3.6**
#4: 119 - 161	**1.9**
#5: 161 - 196	**1.9**
#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**
Total: 0 - 553	334

Note #1: The total committed effective dose (334 µSv) shown in Table 4.9 is higher (by 5%) than the value (317 µSv) obtained earlier - when we analyzed larger sets (6 ´ 10 + 1 ´ 5) 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 over-estimate 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 smaller the resulting over-estimate for the set as a whole. 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

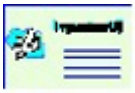
Table 4.10 summarizes the estimates of effective dose committed over the whole (553-d) monitoring period - comparing the results of both manual fitting exercises and both "automated" fits. The table also shows the total value of **c**2 calculated in each case by comparing the "predicted" and "observed" values of the bioassay quantity.

Table 4.10. **Comparison of estimated total committed doses and the associated c**2-sum statistic**.**

Case Analysis: **Intake Assumption**	Estimated Effective Dose (µSv)	**c**2-sum
Manual (Whole Dataset):		
MP	479	56.9
JA	199	55.7
Automated (6´ 10 + 1´ 5):		
"Mid-point"	317	25.2
"Continuous"	313	25.2
Automated (13´ 5):		
"Mid-point"	334	24.4
"Continuous"	331	24.4

The points to note from Table 4.10 are:

- The "Manual" analyses (of the whole dataset) differed only marginally in their "goodness of fit" - i.e., the respective **c**2-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 large 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 **c**2 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 **c**2 statistic.
- The (5% lower) value of total committed dose calculated using bioassay values 10-at-a-time (the maximum number) is likely to be more accurate (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

Note: The case example below is taken from IMBA Expert™ OCAS-Edition. **It relates specifically to the** application of calculated annual tissue doses 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.**

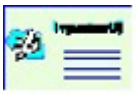
IMBA Expert™ OCAS-Edition **was designed specifically to meet NIOSH's requirements under the Energy Employees' Occupational Illness Compensation Program Act (**EEOICPA**). In particular, the software is customized to do the following:**

1. **Provide all of the capabilities of the** IMBA Expert™ USDOE-Edition (Phase II) **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. Calculate equivalent doses received by specified target organs and tissues in each Calendar Year **- from the start of a claimant's qualifying occupational exposure through to the date(s) of diagnosis of the claimant's qualifying 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** direct **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 60**Co (**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.

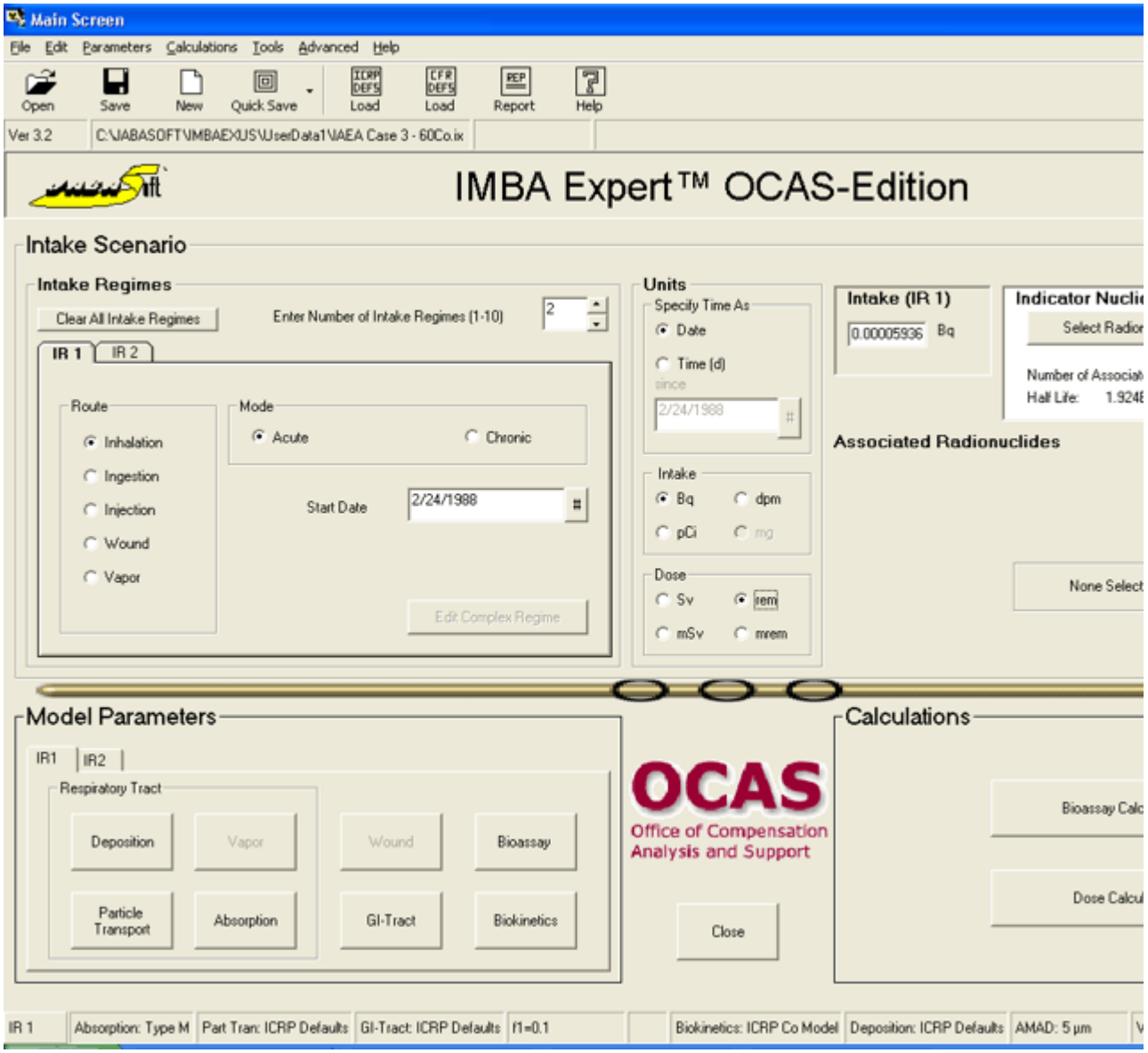


Figure 9.1. Main Screen after opening the parameter file "IAEA Case 3 - 60Co.ix

Important Note: NIOSH-IREP requires calculated annual equivalent doses to be experessed in centi-Sv (cSv), i.e., in the traditional dose unit 'rem'. Therefore, it is IMPORTANT to ensure that you have selected '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-µm AMAD aerosol of 'Type M' 60**Co** on February 24th, 1988. To calculate the annual equivalent doses received by all target organs or tissues:

- click the "Dose Calculations" button - to open the Dose Calculations screen.
- click the "ORG DOSE Calendar" button - to open the 'Equivalent Dose to selected organ received in each calendar year' window (Figure 9.2).

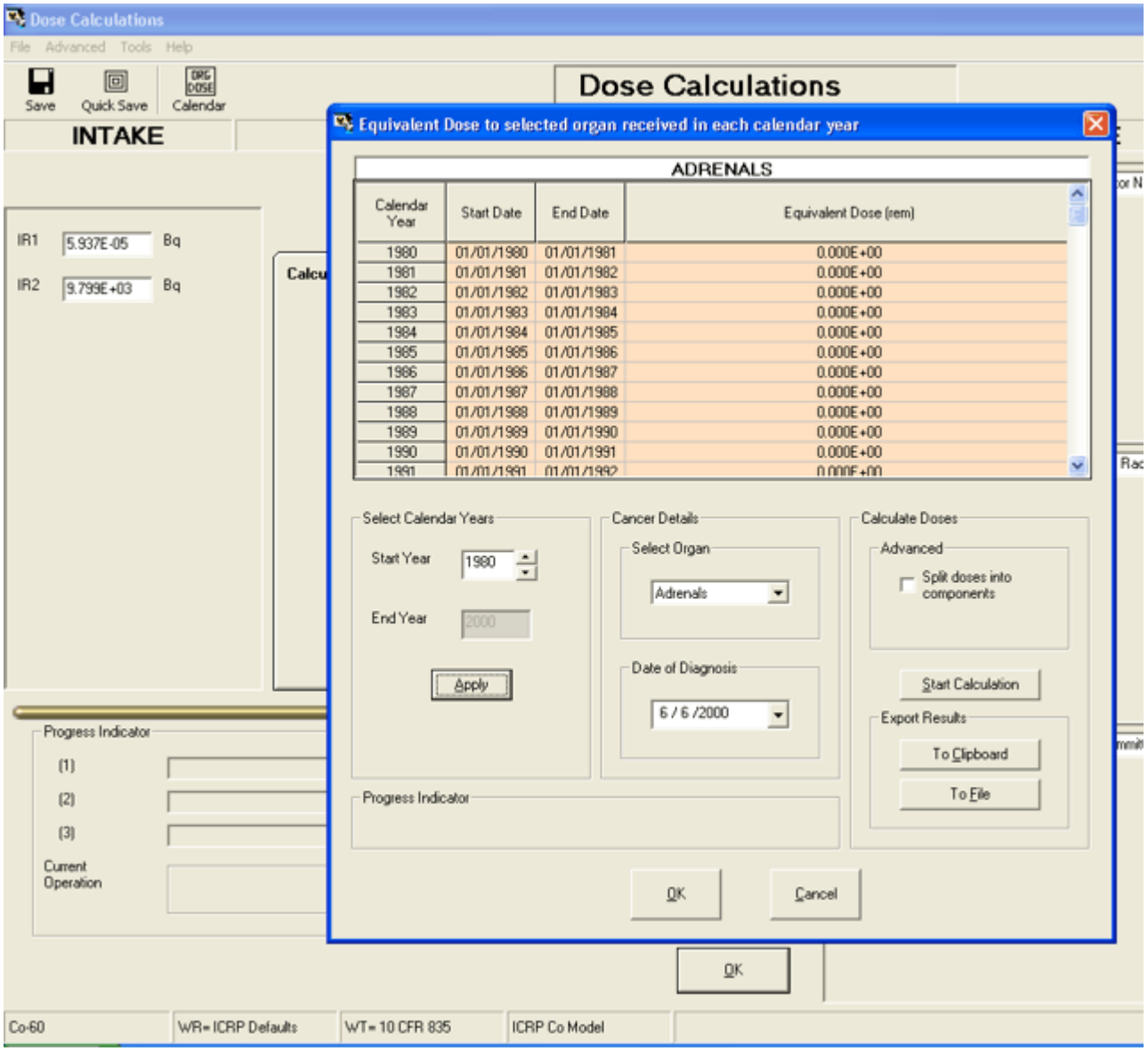


Figure 9.2. Opening the 'Equivalent Dose to selected organ received in each calendar year' window.

Note #1: The 'Equivalent Dose to selected organ received in each calendar year' window opens with the default settings shown in Figure 9.2, i.e., 'Start Year' = 1980; 'Select Organ' = Adrenals; 'Date of Diagnosis' = 6/6/2000; 'Split doses into components' = unchecked.

Note #2: As specified by NIOSH/OCAS, Version 3.2 of IMBA Expert™ OCAS-Edition **enables you to select for display (and to send to the output report file) the calculated annual doses received by ONE designated target organ, as** selected **from a drop-down list. It is anticipated that a future enhanced version of the software will enable you to** select several **target organs (or tissues) for which the calculated annual doses will ALL be tabulated in the output report file. In** Version 3.2**, a separate output report file is needed to pass the calculated annual doses for each additional target organ (or tissue) to '**FeedIREP**'.**

Note #3: Again, as per initial specification, Version 3.2 of IMBA Expert™ OCAS-Edition **enables you to define a time-span of up to 50 years for calculation of the annual doses received by target organs. However, in practice, it has been found that greater time-spans may be needed in some cases. Accordingly, it is anticipated that a future enhance version**

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 'tissue weighting factors' - shown in the 'Status Bar' (Figure 9.2) do NOT affect the calculated values of equivalent dose. These apply ONLY to the calculation of effective dose.

- **Proceed to "** Example Annual Dose Calculation**".**

Example Annual Dose Calculation

We will assume for this example (IAEA Case 3 - 60Co.ix):

- that the (hypothetical) claimant data file defines the diagnosed cancer as "Cancer1=Stomach (151)";
- that the (hypothetical) claimant data file defines the 'Date of Diagnosis' as "Cancer1DiagnosisDate=02/25/1997".

The corresponding data values in the 'Equivalent Dose to selected organ received in each calendar year' are shown in Figure 9.3.

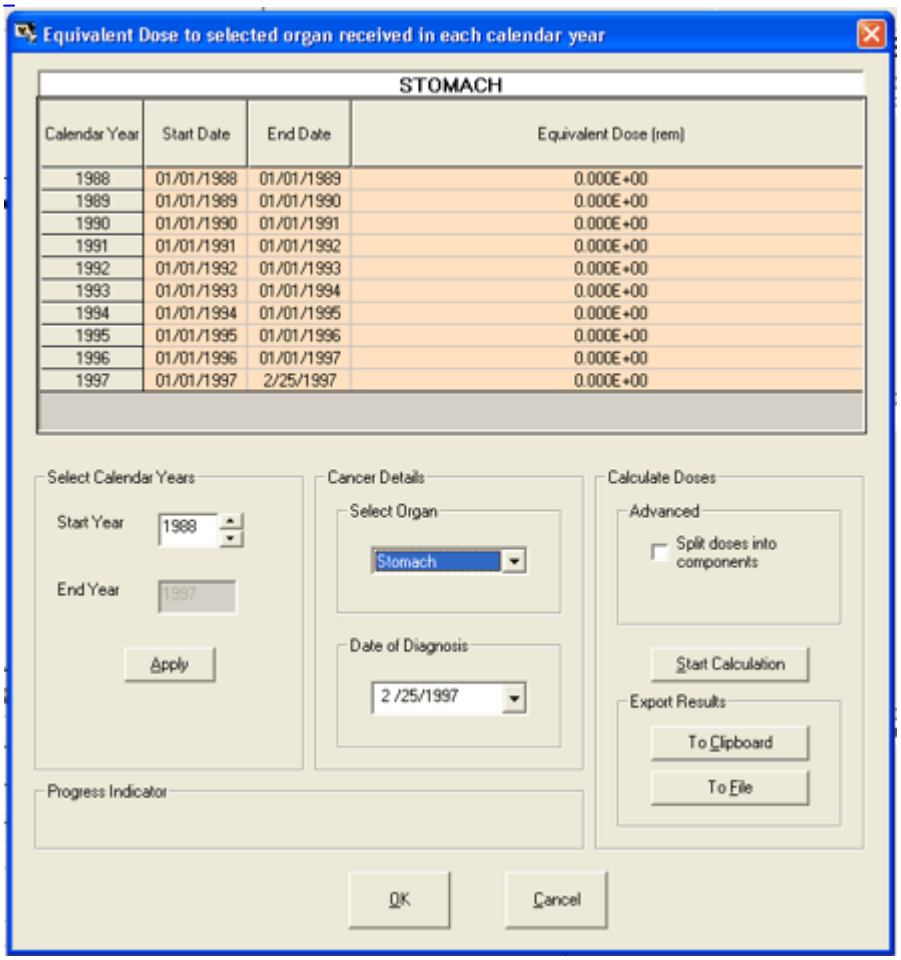


Figure 9.3. Settings of 'Equivalent Dose to selected organ received in each calendar year' window for hypothetical case of stomach cancer.

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.

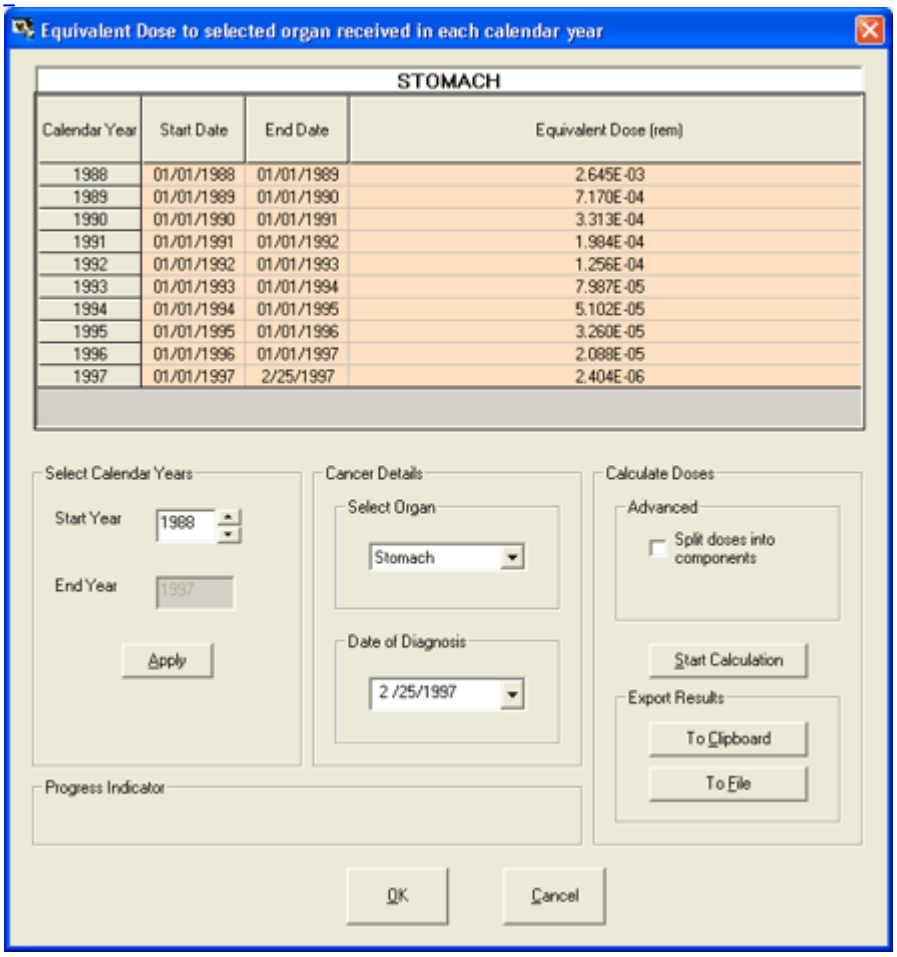


Figure 9.4. Total annual equivalent doses displayed for the stomach wall.

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.

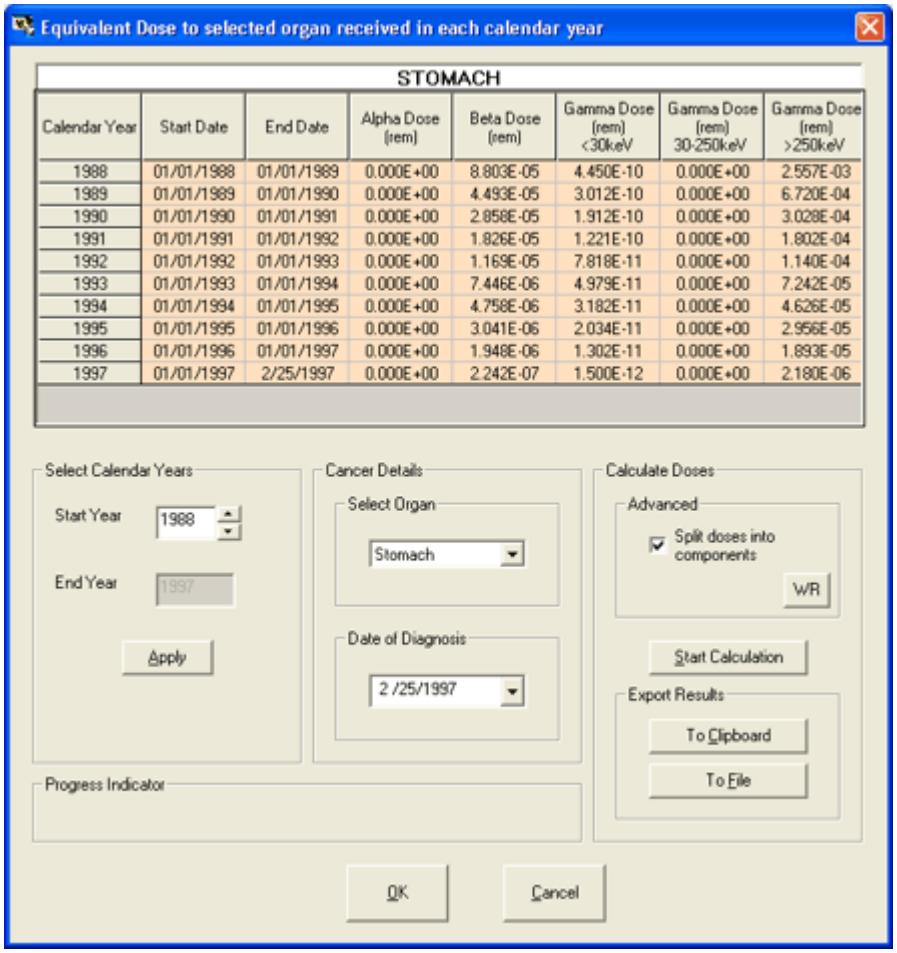


Figure 9.5. 'Split' components of annual equivalent doses displayed for the stomach wall.

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 NIOSH-IREP program automatically applies the required pre-defined 'weighting' distributions (as multipliers) to evaluate the corresponding uncertainty distributions of equivalent dose.

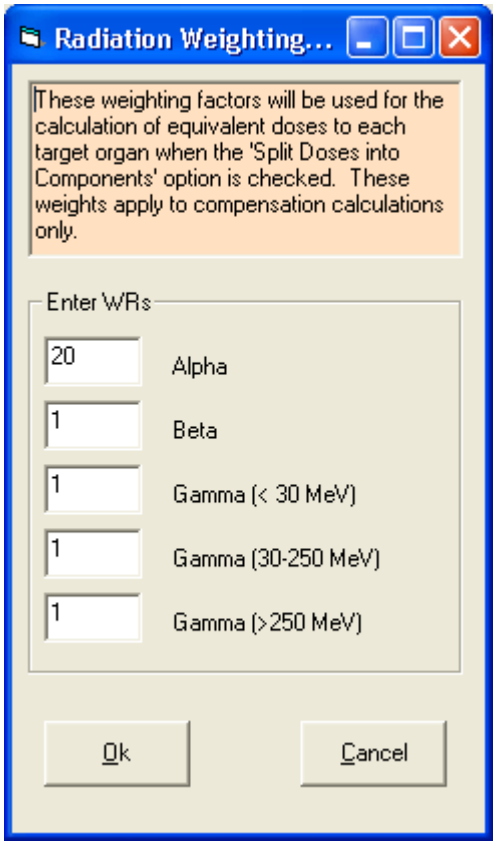


Figure 9.6. Standard values of radiation weighting factor used to calculate 'split' annual equivalent doses.

Important Note: IMBA Expert™ OCAS-Edition (Version 3.2) **calculates annual 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** summed **(year-by-year) before entry into the** NIOSH-IREP program**.**

- See 'Summing Annual Doses from Multiple Radionuclides' - by exporting results to a spreadsheet via the Windows clipboard.
- Proceed to "How to Use the '*.ini' File".

Summing Annual Doses Calculated for Associated Radionuclides

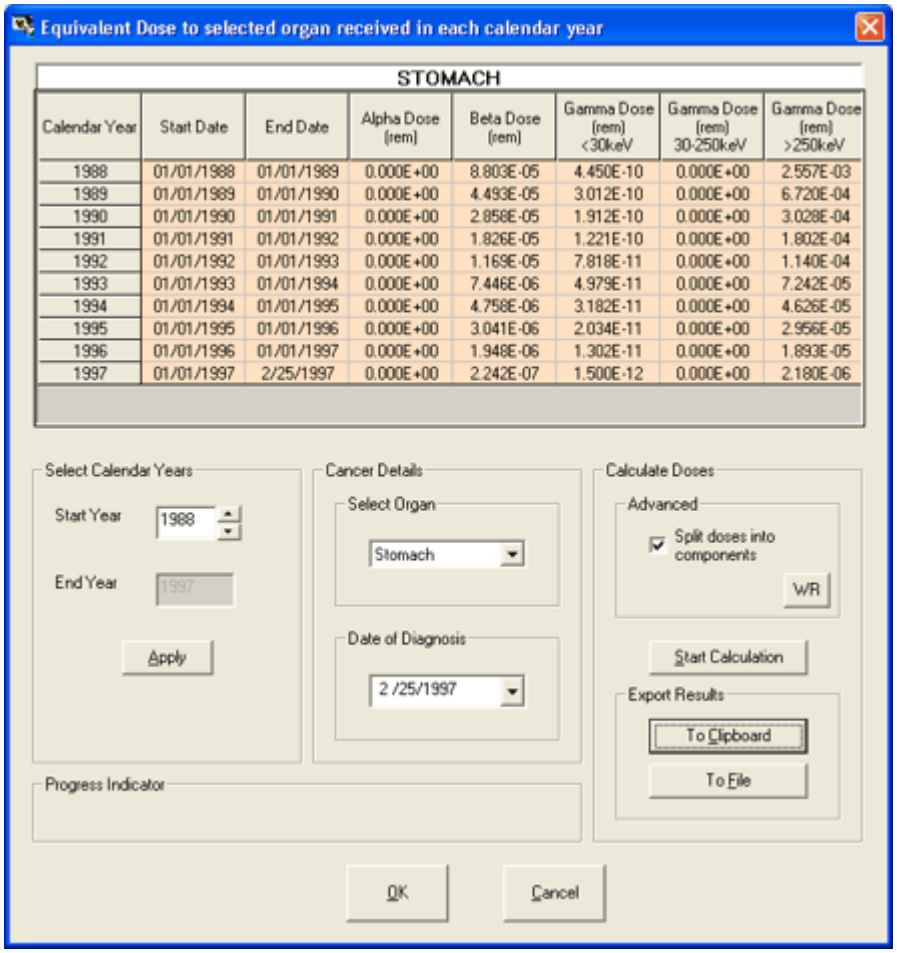
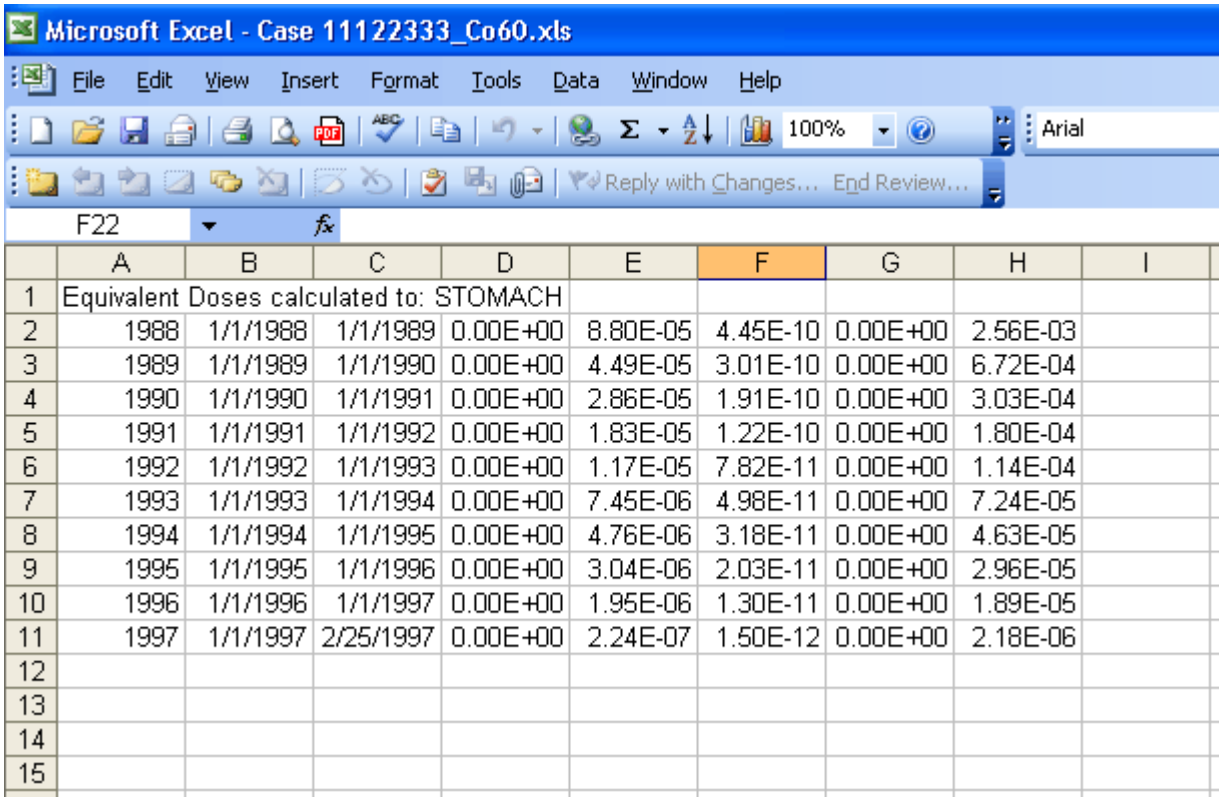


Figure 9.7. The 'Export Results - To Clipboard' button.

Clicking the Export Results - To Clipboard' button (Figure 9.7) copies 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.



	A	B	C	D	E	F	G	H	I
1	Equivalent Doses calculated to: 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 add the annual doses calculated (separately) for ALL Associated Radionuclides. The resulting total annual equivalent doses can then be copied and pasted directly into the NIOSH-IREP input file - by-passing part of the function of 'FeedIREP'.

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

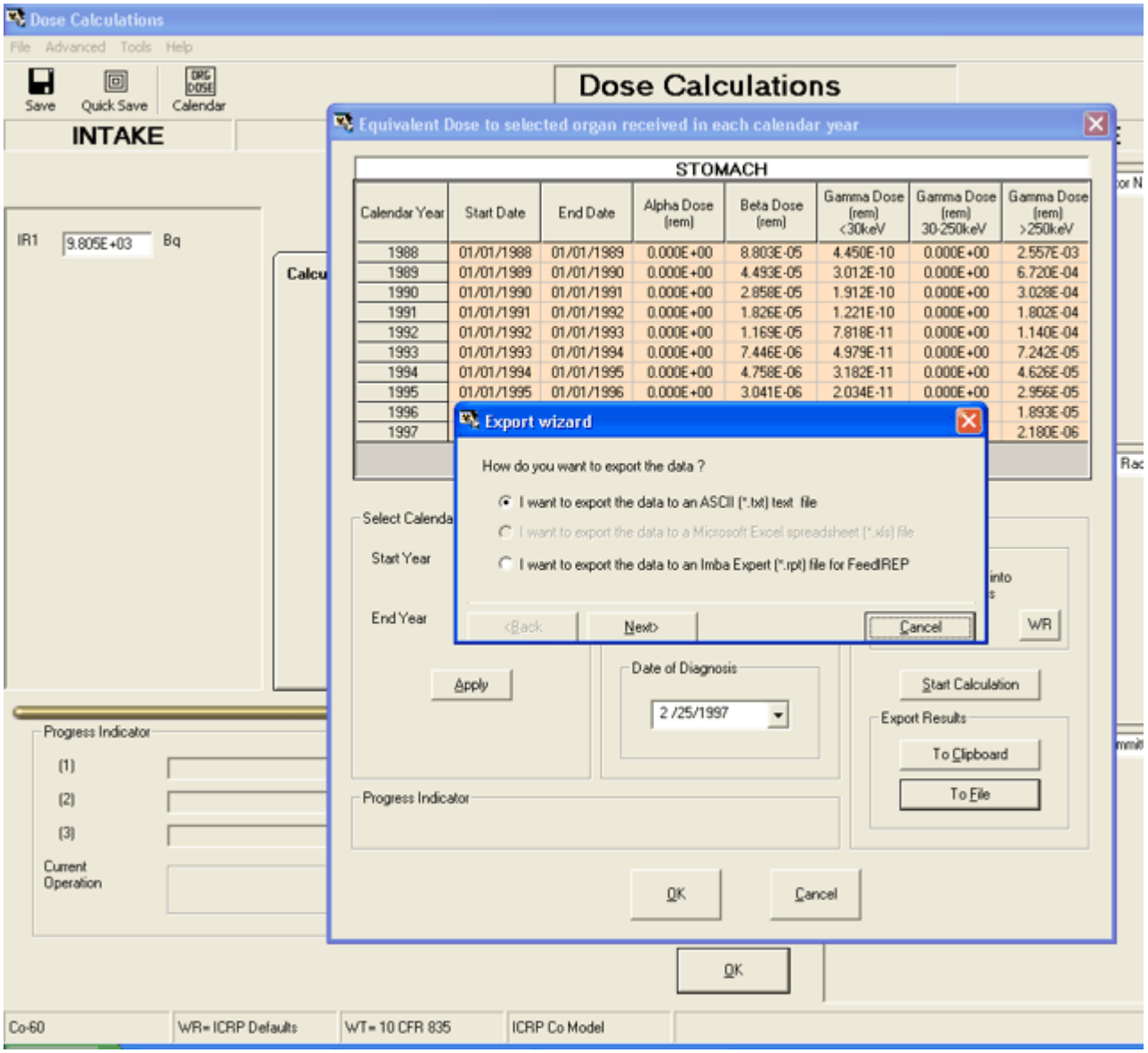


Figure 9.9. Opening the 'Export Wizard'.

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), clicking the 'Next' button opens 'Please specify the name and location of the ASCII file you want to create' browse option in the ' Export Wizard' (Figure 9.10).

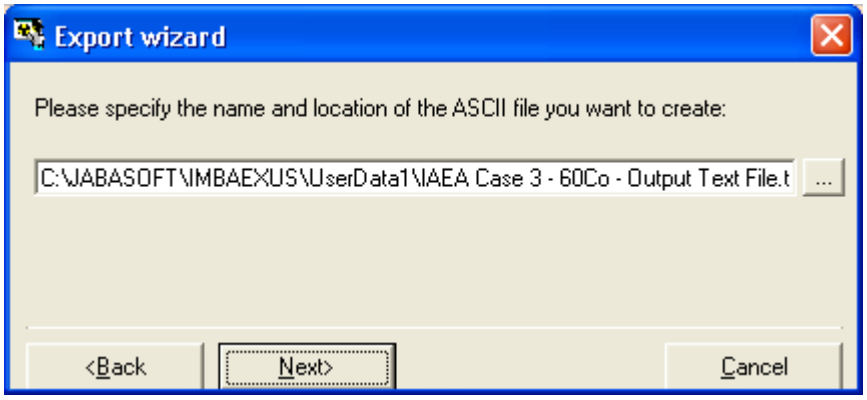


Figure 9.10. Specifying the name and location of the ASCII (*.txt) output text file.

You simply browse to the folder where you want to store the output (*.txt), and name the file. Clicking the 'Next' button enables you to select the type of text delimiter that you want to use (Figure 9.11).

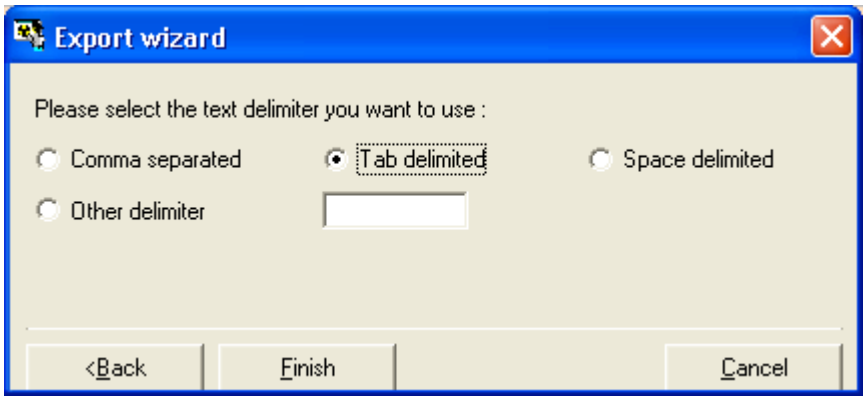


Figure 9.11. Selection of a 'Tab delimited' output (*.txt) file.

In this example we have selected a 'Tab delimited' output file. Clicking the 'Finish' button completes the data export process. Successful export of the data will be confirmed (Figure 9.12), and clicking the 'View File ...' button will display the resulting (*.txt) file (Figure 9.13) in NotePad®.

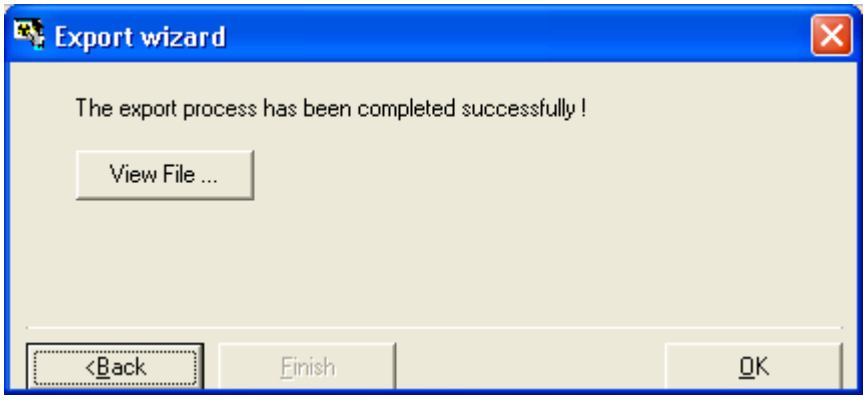
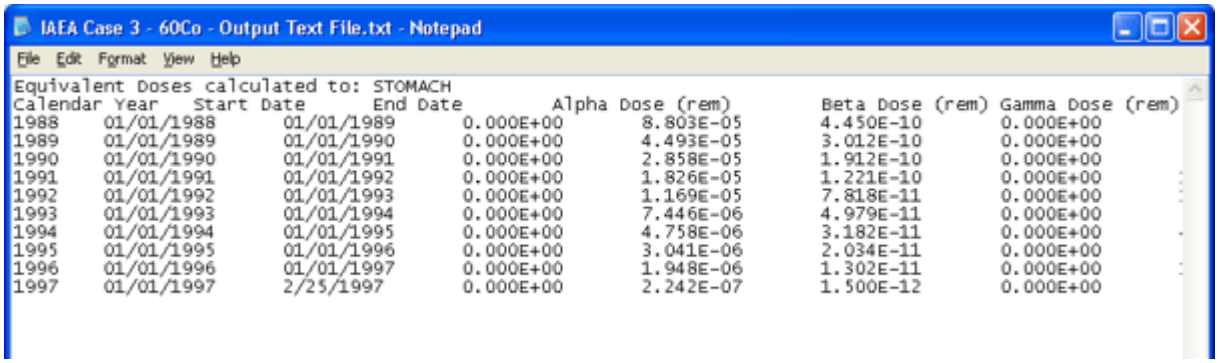


Figure 9.12. Confirmation of successful data export to a (*.txt) file.



IAEA Case 3 - 60Co - Output Text File.txt - Notepad

File Edit Format View Help

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
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
1992	01/01/1992	01/01/1993	0.000E+00	1.169E-05	7.818E-11	0.000E+00
1993	01/01/1993	01/01/1994	0.000E+00	7.446E-06	4.979E-11	0.000E+00
1994	01/01/1994	01/01/1995	0.000E+00	4.758E-06	3.182E-11	0.000E+00
1995	01/01/1995	01/01/1996	0.000E+00	3.041E-06	2.034E-11	0.000E+00
1996	01/01/1996	01/01/1997	0.000E+00	1.948E-06	1.302E-11	0.000E+00
1997	01/01/1997	2/25/1997	0.000E+00	2.242E-07	1.500E-12	0.000E+00

Figure 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 add other information, such as the identity of the indicator nuclide, 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

```
; 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
Cancer1=Stomach (151)
Cancer1DiagnosisDate=02/25/1997
Cancer1Rank=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 NIOSH-IREP program.

Figure 9.14 shows the general layout of the '*.INI' file. We describe here how to import this file into IMBA Professional Plus.

Important Notice: The information contained in the '*.INI' 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.

Note: The example "*.INI" files used here are purely for the purpose of illustrating the operation of IMBA Professional Plus. **They utilize previously published bioassay data. They contain NO personal information - and are NOT associated in any way with any identified individual claimant. The identifying file names are arbitrary.**

- Proceed to "Incorporating the '*.ini' File Data".

Incorporating the '*.ini' File Data

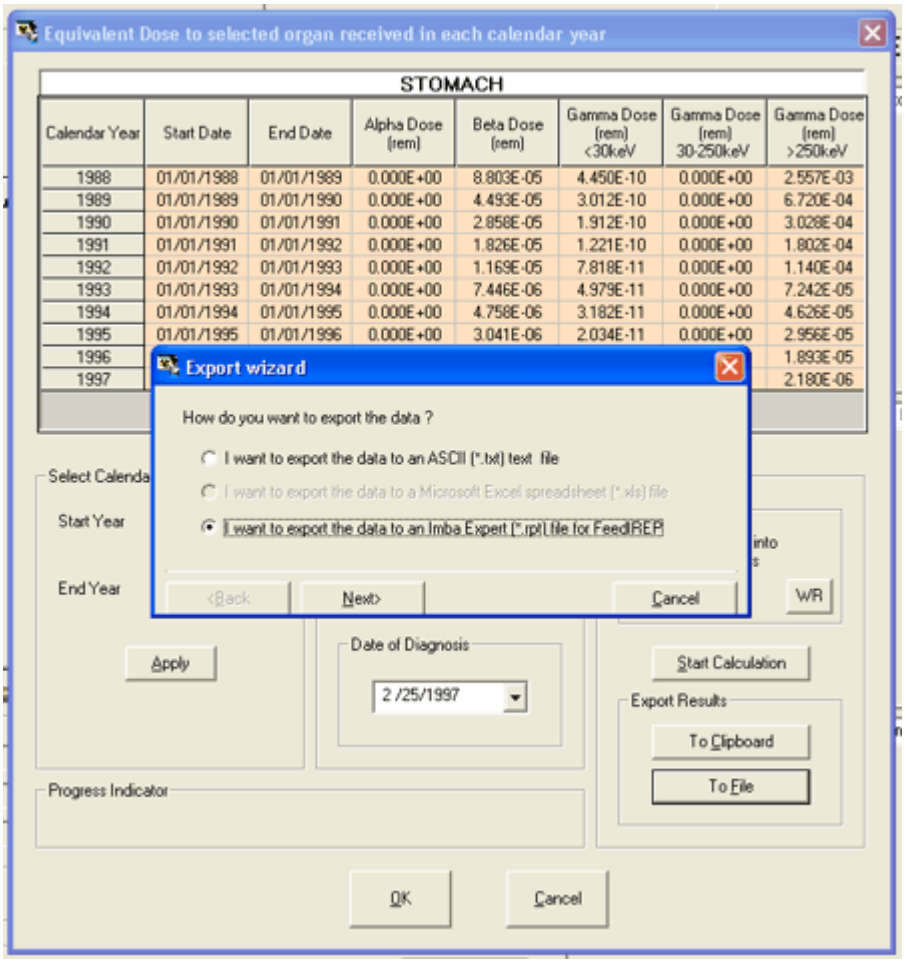


Figure 9.15. Using the 'Export Wizard' to export data directly to a (*.rpt) file - formatted for 'FeedIREP'.

The 'Export Wizard' enables you to export calculated annual equivalent doses to a (*.rpt) file that is formatted for direct input into 'FeedIREP' (Figure 9.15). This method of exporting the calculated results has two advantages:

1. Personal information about the claimant (from the approved standard format Initiation file - '*.ini') is automatically 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.

Checking the 'I want to export the data to an IMBA Expert (*.rpt) file for FeedIREP' and clicking the ' Next ' 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".

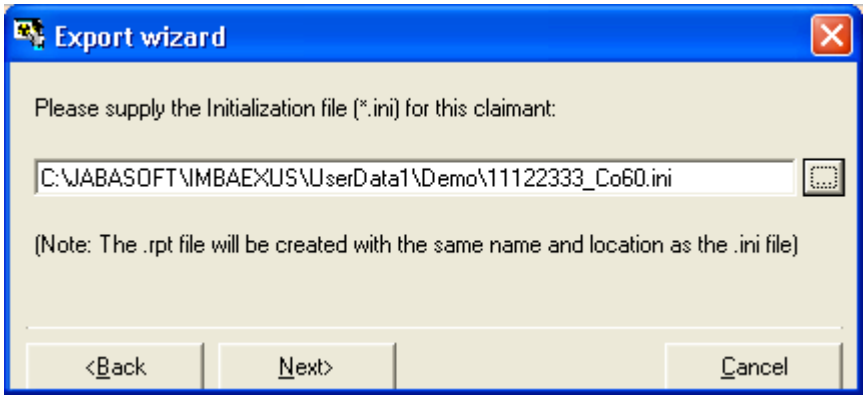


Figure 9.16. Browsing to locate the Initiation file (*.ini).

Note: In ORAU's Energy Employees Occupational Illness Compensation Program Dose Reconstruction Project, the name of the Initiation file is composed of two parts (1) the NIOSH Claim number - full 6 digits with leading zeros, and (2) the file extension '.ini'. For example, '000251.ini' is a valid file name.

Once you have located the '*.ini' file, clicking 'Next' in the 'Export Wizard' will ask you "How do you want to configure the *.rpt file?" (Figure 9.17). The default option is "Automatically" - and this is RECOMMENDED for compatibility with 'FeedIREP'.

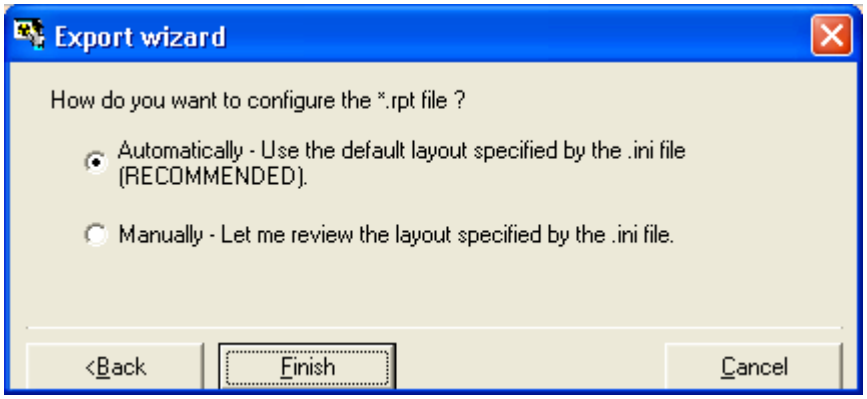


Figure 9.17. Default option for "Automatically" configuring the '*.rpt' file.

Clicking 'Finish' will complete the export process. The resulting '*.rpt' file can be viewed by clicking the 'View File ...' button (Figure 9.18.).

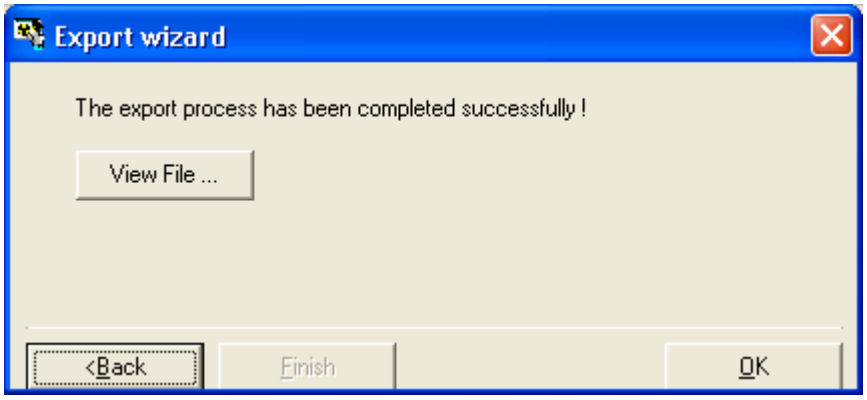


Figure 9.18. Confirmation of successful export of a '*.rpt' file.

Note #1: The output '*.rpt' file is automatically saved in the same folder as the input '*.ini' file.

Note #2: The resulting '*.rpt' file is shown in "Output to 'FeedIREP'".

Standard-format Output to 'FeedIREP'

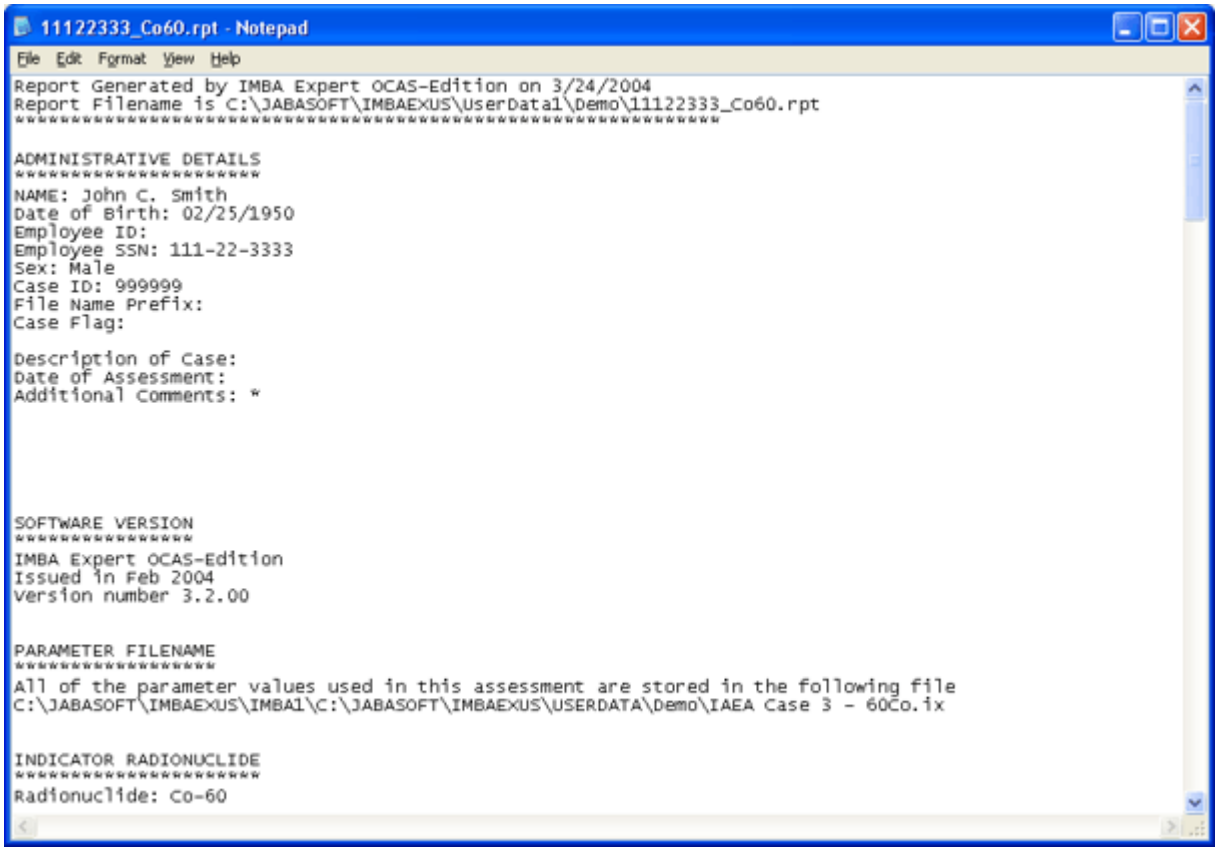


Figure 9.19. '11122333_Co60.rpt' file produced for the example case - as viwed in NotePad®.

The complete '11122333_Co60.rpt' 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 µm
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= 0.005
Fb=0
Sb=0

Particle transport parameters were ICRP Defaults
AI1 to bb1 = 0.02
AI2 to bb1 = 0.001
AI3 to bb1 = 0.0001
AI3 to LNTH = 0.00002
bb1 to BB1 = 2
bb2 to BB1 = 0.03
bbseq to LNTH = 0.01
BB1 to ET2 = 10
BB2 to ET2 = 0.03
BBseq to LNTH = 0.01
ET2 tO GI = 100
ETseq to LNET = 0.001
ET1 out 1

Initial deposition partitioning
ETseq/ET2 = 0.0005
BBseq/BB = 0.007
bbseq/bb = 0.007
AI2/AI = 0.6
AI3/AI = 0.1

GI-tract parameters were ICRP Defaults
Stomach (ST) = 24
Small intestine (SI) = 6
Upper Large Intestine (ULI) = 1.8
Lower Large Intestine (LLI) = 1
Absorption to Blood (f1) = 0.1

Biokinetic model parameters were ICRP Co Model
Organ/tissue retention functions were as follows:

LIVER
a(i), lam(i)
-5.281760000000000E-02, 1.386290000000000E+00
3.272730000000000E-02, 1.155250000000000E-01
1.008400000000000E-02, 1.155250000000000E-02
1.000630000000000E-02, 8.664340000000000E-04
Fraction to urine 8.571430000000000E-01

SOFT TISS
a(i), lam(i)
-4.753576000000000E-01, 1.386290000000000E+00
2.945450000000000E-01, 1.155250000000000E-01
9.075630000000000E-02, 1.155250000000000E-02
9.005630000000000E-02, 8.664340000000000E-04
Fraction to urine 8.571430000000000E-01

BLOOD

a(i), lam(i)
1.000000000000000E+00, 1.386290000000000E+00
Fraction to urine 8.571430000000000E-01

Bioassay function for Whole body was Std Co Model
a(i), lam(i)
5.301073120979730E-01, 1.000000000000000E+00
3.397310000000000E-01, 1.155250000000000E-01
-3.019360000000000E-01, 1.386290000000000E+00
2.864620000000000E-01, 1.800000000000000E+00
1.011860000000000E-01, 1.155250000000000E-02
1.000880000000000E-01, 8.664340000000000E-04
-5.563920000000000E-02, 1.200000000000000E+01
Blood retention: 1.0000E-07

Bioassay function for Urine was Std Co Model
a(i), lam(i)
-6.676703004002170E-01, 1.200000000000000E+01
6.338750000000000E-01, 1.386290000000000E+00
3.272190000000000E-02, 1.155250000000000E-01
9.994940000000000E-04, 1.155250000000000E-02
7.431760000000000E-05, 8.664340000000000E-04
Blood retention: 1.0000E-07

Bioassay function for Feces was Std Co Model
a(i), lam(i)
-1.052446700679250E+00, 1.386290000000000E+00
5.301070000000000E-01, 1.000000000000000E+00
5.156320000000000E-01, 1.800000000000000E+00
6.525410000000000E-03, 1.155250000000000E-01
1.694540000000000E-04, 1.155250000000000E-02
1.240210000000000E-05, 8.664340000000000E-04
Blood retention: 1.0000E-07

MEASUREMENT DATA
****
Whole body data
1. , , 2720 , Real , 272 , NORM , 3334.2
6. , , 1150 , Real , 115 , NORM , 1195.9
16. , , 1010 , Real , 101 , NORM , 1007.7
33. , , 790 , Real , 79 , NORM , 828.3
82. , , 482 , Real , 48.2 , NORM , 555.59
169. , , 358 , Real , 35.8 , NORM , 338.12
1009. , , 78 , Real , 7.8 , NORM , 37.122
1456. , , 35 , Real , 3.5 , NORM , 20.779

During the fitting procedure, the following data were used:

BIOASSAY RESULTS
****
Whole body results
Time, N/A, Value
d, , Bq
1 , , 3334.2
1.4671759259254 , , 2683.8
2.1526041666657 , , 2032.1

3.15825231481358 , , 1540
4.63370370370467 , , 1278.4
6.79846064814774 , , 1169.2
9.97454861110964 , , 1101.1
14.6344097222209 , , 1026.9
21.4712499999987 , , 939.97
31.5021064814828 , , 841.05
46.2191319444428 , , 731.49
67.8115972222222 , , 614.57
99.4915393518531 , , 495.85
145.971585648149 , , 380.5
214.165983796298 , , 272.57
314.219155092593 , , 178.78
461.014768518518 , , 108.29
676.389756944445 , , 63.956
992.382731481484 , , 38
1456 , , 20.779

INTAKES
****
Intake 1 was 9804.8 Bq

EQUIVALENT DOSE to Stomach (Sv) from the Indicator Radionuclide (Co-60) in each calendar year
****

year,	alpha,	beta,	gamma1,	gamma2,	gamma3,
1988,	0.000E+00,	8.803E-07,	4.450E-12,	0.000E+00,	2.557E-05,
1989,	0.000E+00,	4.493E-07,	3.012E-12,	0.000E+00,	6.720E-06,
1990,	0.000E+00,	2.858E-07,	1.912E-12,	0.000E+00,	3.028E-06,
1991,	0.000E+00,	1.826E-07,	1.221E-12,	0.000E+00,	1.802E-06,
1992,	0.000E+00,	1.169E-07,	7.818E-13,	0.000E+00,	1.140E-06,
1993,	0.000E+00,	7.446E-08,	4.979E-13,	0.000E+00,	7.242E-07,
1994,	0.000E+00,	4.758E-08,	3.182E-13,	0.000E+00,	4.626E-07,
1995,	0.000E+00,	3.041E-08,	2.034E-13,	0.000E+00,	2.956E-07,
1996,	0.000E+00,	1.948E-08,	1.302E-13,	0.000E+00,	1.893E-07,
1997,	0.000E+00,	2.242E-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

Note: Consult the approved operating procedure documentation for ORAU's Energy Employees Occupational Illness Compensation Program Dose Reconstruction Project for instructions on how to use 'FeedIREP' to read the '*.rpt' file formatted by IMBA Professional Plus **- and also the** 'User's Guide' **to** run NIOSH-IREP**.**

Case of ^{241}Am 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 Bihl et al (1988), with a longer-term "follow-up" reported by Carbaugh et al (1991). 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 241**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 http://bidug.pnl.gov/references/Carbaugh_PNNL_%20Plutonium_%20Reality_%20Show_s.pdf. 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 isotopic composition of the inhaled material (% by atom) - from mass spectrometry.**
- **Measured** 241Am-in-lung activity in vivo **- from the first through 6,639**th **day (18-y follow-up).**
- **Measured** 241Am-in-liver activity in-vivo **- measurable from about 6,000 d.**
- **Measured** 241Am-in-skeleton activity in-vivo **- also measurable from about 6,000 d.**
- **Measured** 239/240Pu excretion rate in urine **- measurable from about 1,800 d onwards.**

See Input Data for Am-241 in Lung Case**.**

Input Data - ^{241}Am in Lung Case

1. Isotopic Composition

Table 4.11. Isotopic composition of plutonium oxide material inhaled in HAN-1.

Radionuclide	% by Number of atoms	% By Activity

241Am	0.25	0.56
238Pu	0.065	0.71
239Pu	86.4	3.46
240Pu	11.6	1.71
241Pu	1.4	93.6
242Pu	0.24	6 ´ 10-4

Clearly, from Table 4.11:

- 239/240Pu 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 259 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
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
12/4/92 12:00 AM	3375
1/8/93 12:00 AM	3050
2/12/93 12:00 AM	2930
3/12/93 12:00 AM	2810
4/12/93 12:00 PM	3050
5/14/93 12:00 AM	3105
6/7/93 12:00 PM	3085
7/5/93 12:00 PM	2855
8/23/93 12:00 PM	3325
10/8/93 12:00 AM	3160
11/24/93 12:00 PM	3455
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

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** 241Am activity in the liver.

Date of Measurement	Measured 241Am Activity (nCi)	Minimum Detectable 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	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. In vivo **measurements of** 241Am activity in the skeleton.

Date of Measurement	Measured 241Am Activity (nCi)	Minimum Detectable 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 241Am 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** 239Pu.

Date of Measurement	Measured Excretion Rate (pCi d-1)	Estimated Error (pCi d-1)
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

- Proceed **to** Analysis of 241Am Retention in the Lungs - Using ICRP Default HRTM Parameter Values.

Analysis of ^{241}Am-in-lung Data - using ICRP Defaults

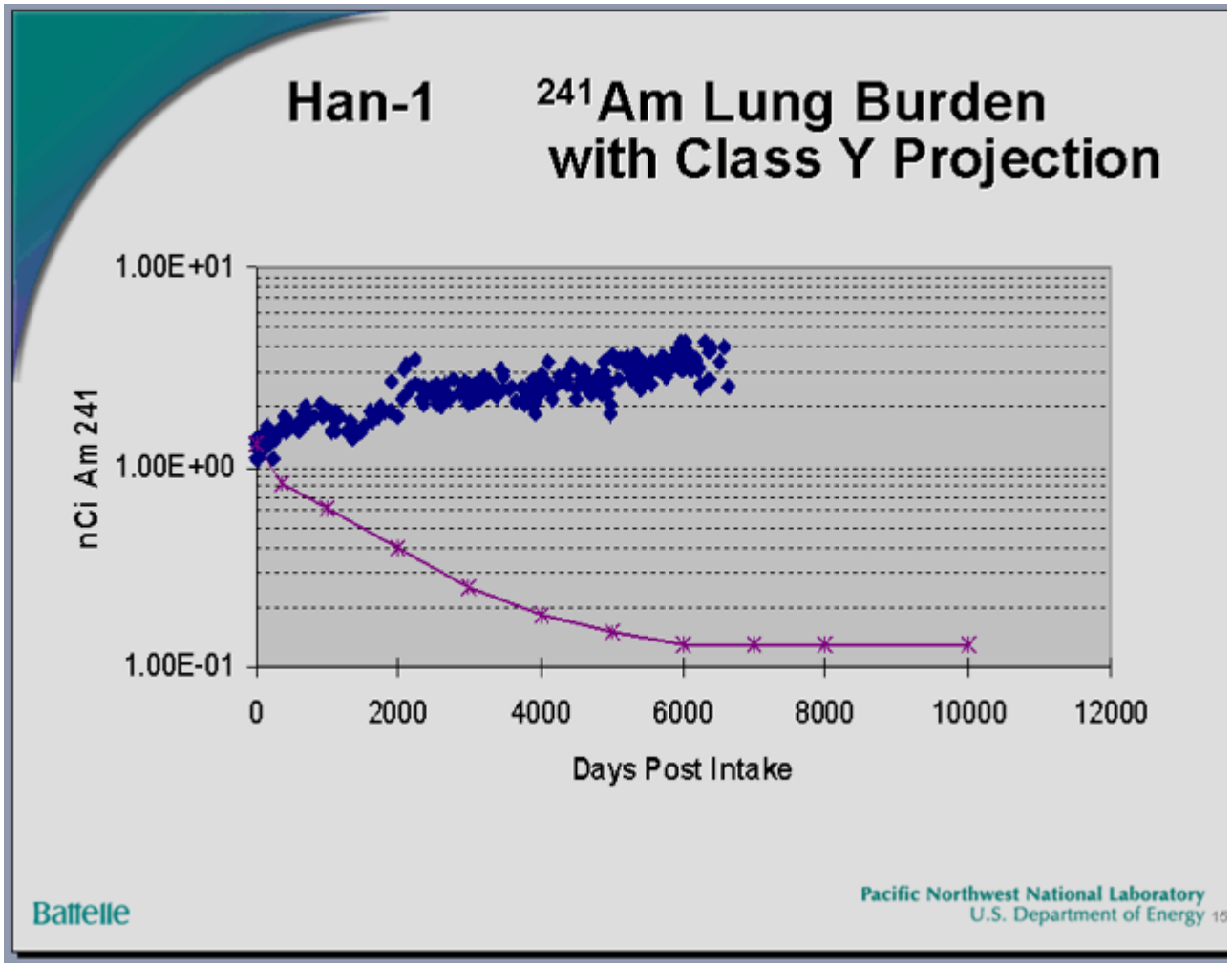


Figure 4.131. Comparison of 241**Am-in-lung data with ICRP30 Class 'Y' prediction (from** Carbaugh 2004**).**

Figure 4.131 shows Gene Carbaugh's updated summary of the 241**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** 241**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** 241**Am activity in the** Liver **and** Skeleton **with the** in vivo **measurements.**

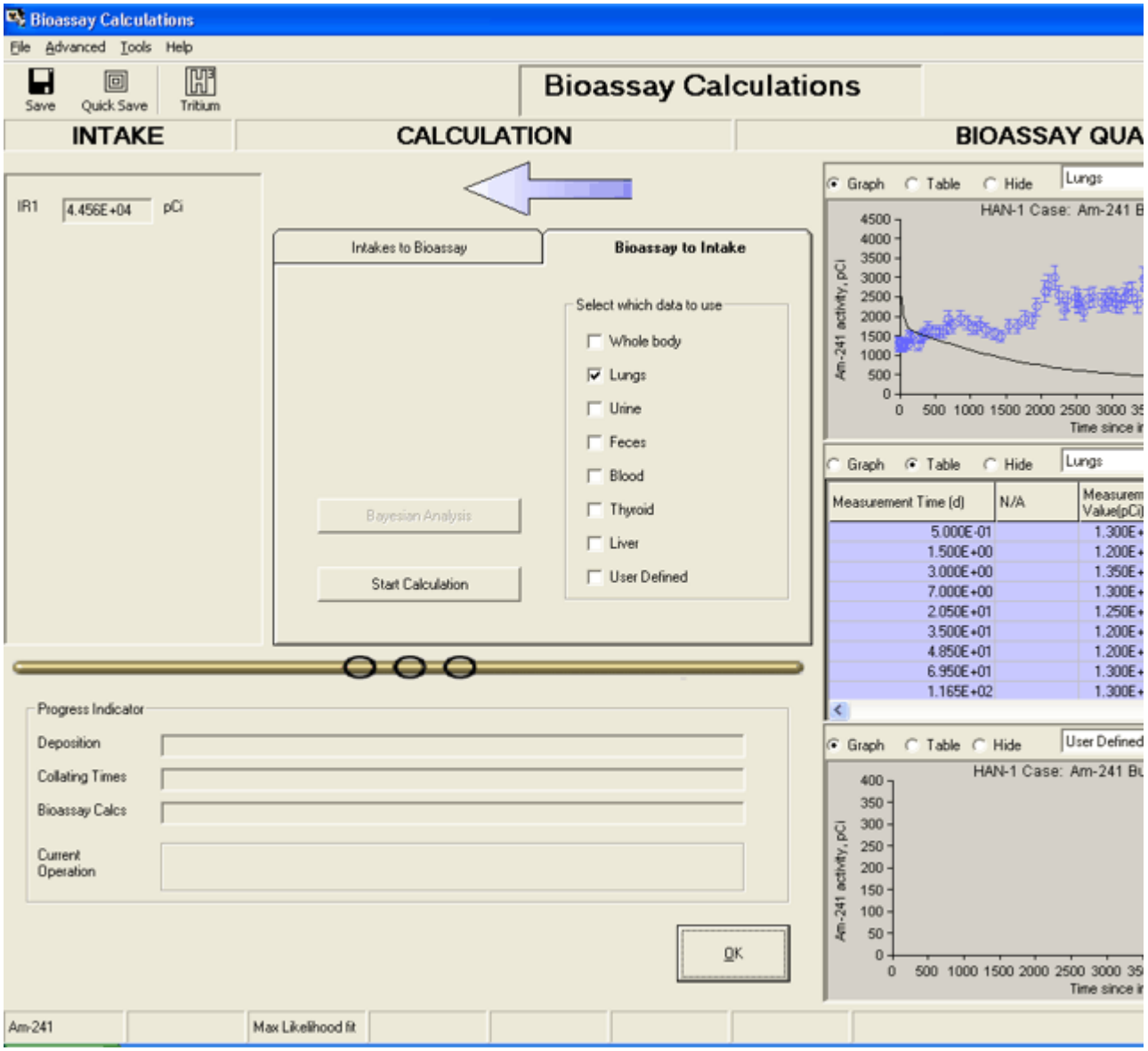


Figure 4.132. Most likely "fit" to HAN-1 ^{241}Am-in-lung data assuming ICRP default HRTM parameter values (Type 'S').

Note: The predicted monotonic decrease of ^{241}Am activity in the lung includes the calculated "in-growth" of ^{241}Am activity into that of the parent ^{241}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 Isotopic 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 Associated Radionuclides of ^{241}Am (the Indicator Nuclide) - see Figure 4.133.

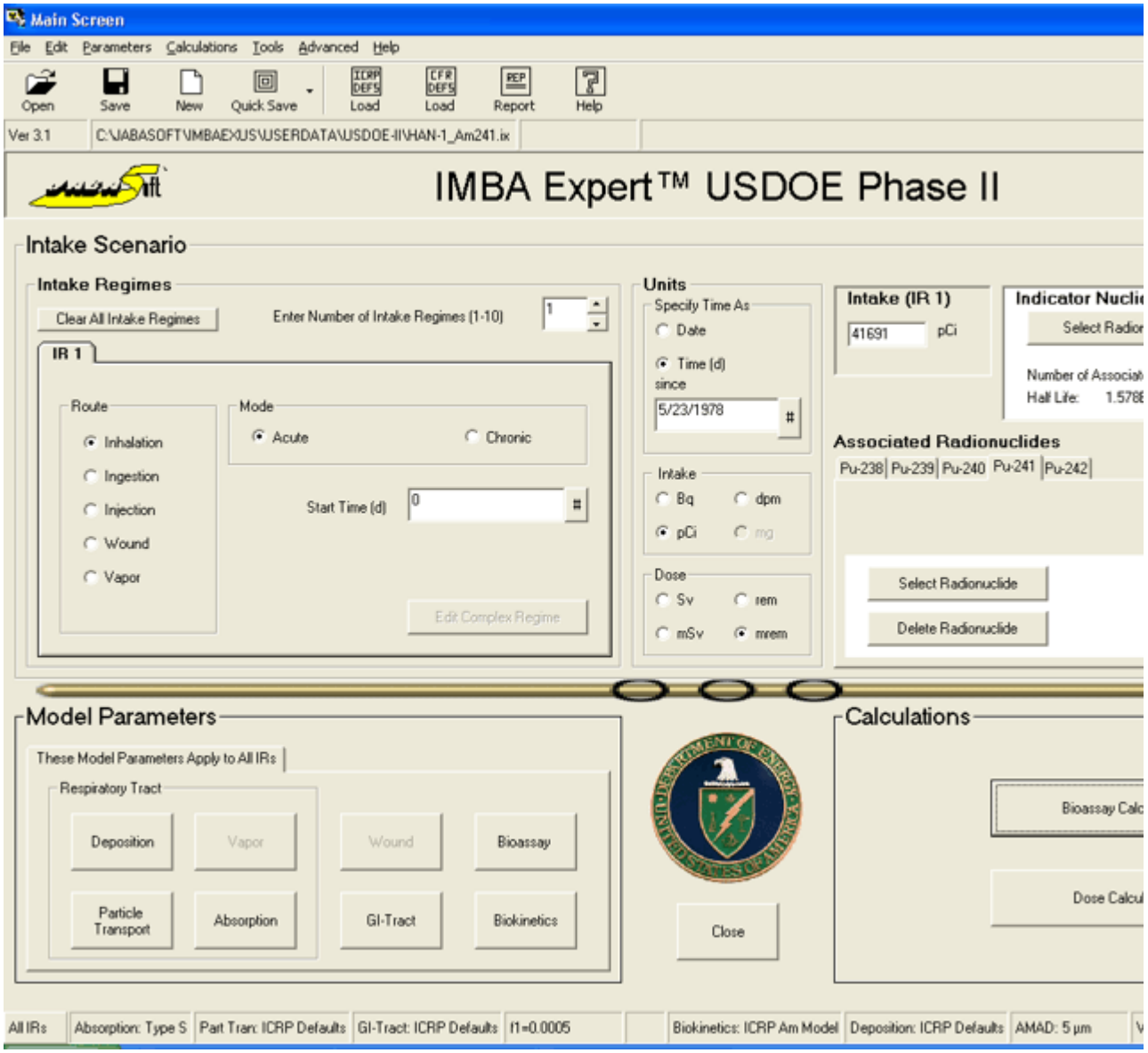


Figure 4.133. **Setting up plutonium isotopes as Associated Radionuclides.**

Figure 4.133 shows the 5 associated plutonium isotopes - ^{238}Pu, ^{239}Pu, ^{240}Pu, ^{241}Pu and ^{242}Pu. Note that the "Abundance" of ^{241}Pu is very high (16,813% - relative to the ^{241}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}Pu intake by comparing the predicted excretion rate in urine with that actually measured (Table 4.15). To do this, however, we have to set up a second "case" in IMBA Professional Plus - with ^{239}Pu as the Indicator Nuclide, and the amount of intake set at 258,900 pCi. The resulting "predicted" urinary excretion rate is shown in Figure 4.134.

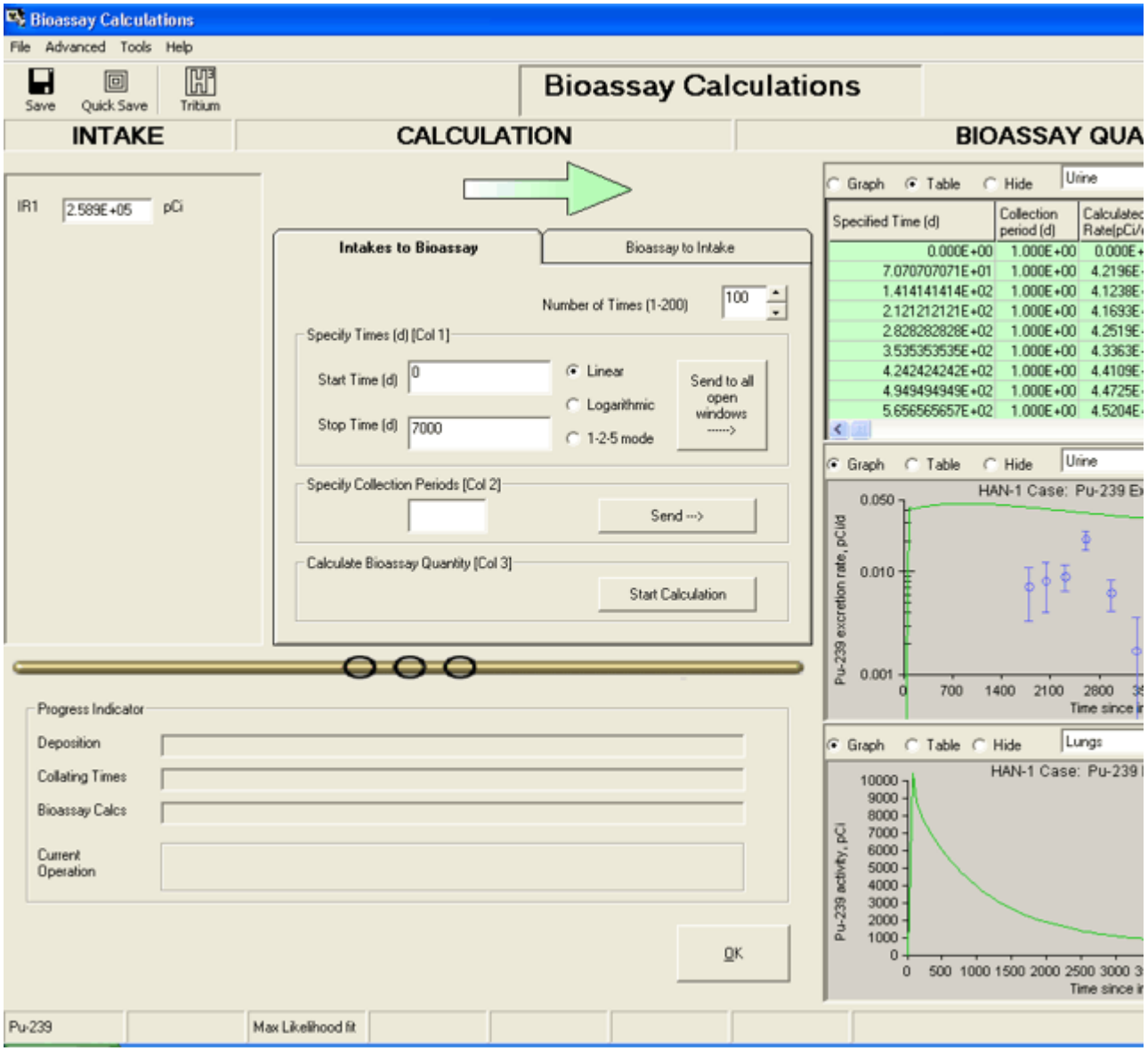


Figure 4.134. **Urinary excretion rate and lung retention predicted for Type 'S' plutonium.**

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):

1. **The the measured** 241Am **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 alveolar-interstitial (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** 241Am **activity in the lungs was observed**

to increase **markedly - whereas, for Type 'S' plutonium it should have** decreased **approximately 10-fold (Figure 4.132).**

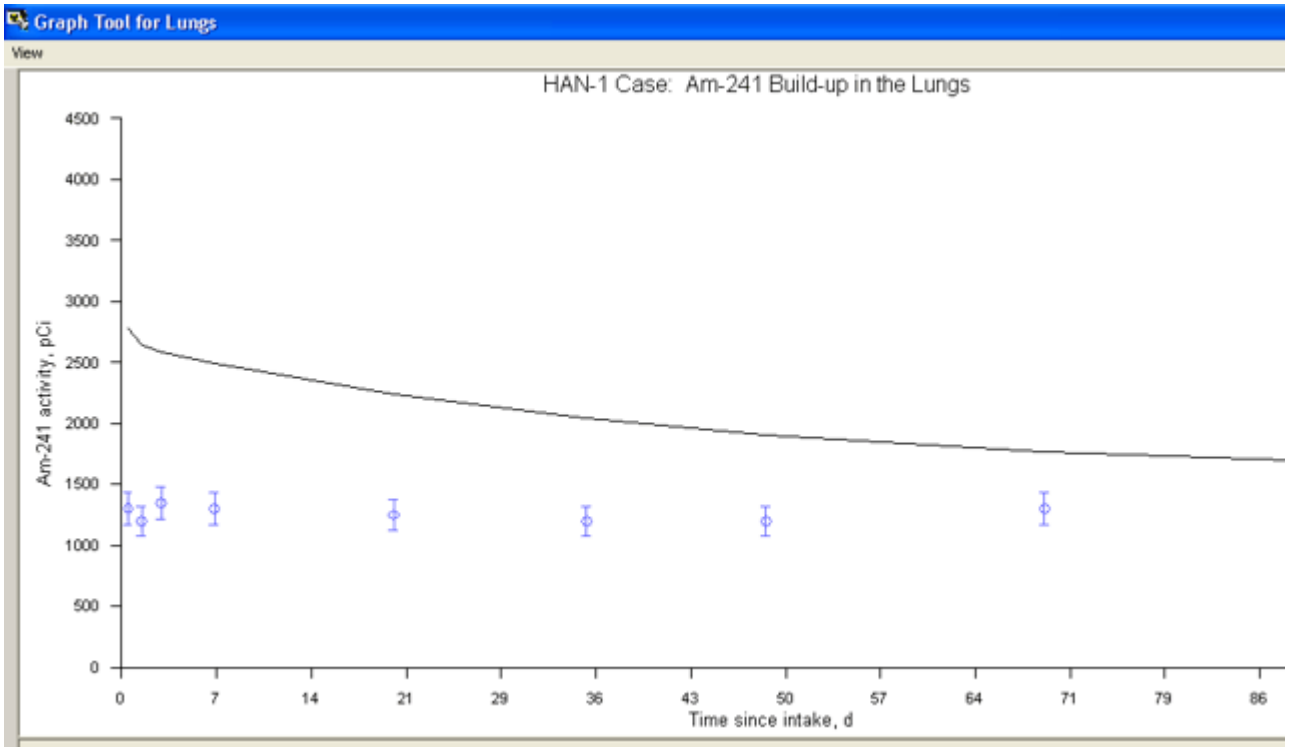


Figure 4.135. **Comparison of predicted and measured early changes in 241Am activity in the lungs.**

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** default **values.**

Note: ICRP has recommended that Default parameter values should be used in 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 rates of transport to the bronchioles (compartments bb1) from BOTH compartments **AI**1 and **AI**2 (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.

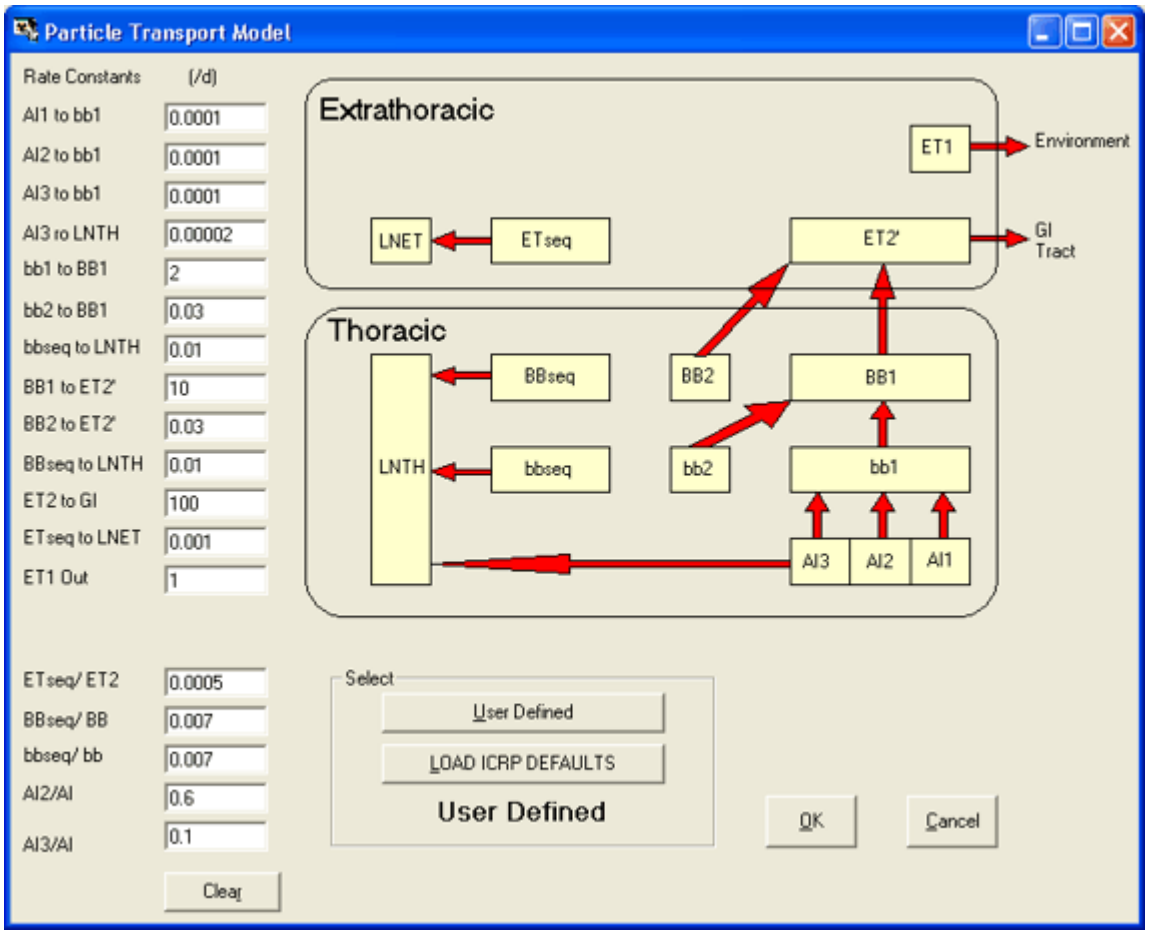


Figure 4.136. User Defined values of the Rate Constants "AI1 to bb1" and "AI2 to bb2" - from their default values of "0.02 d-1" and "0.001 d-1", respectively.

These changes to the transport rates out of compartments **AI**1 and **AI**2 are equivalent to eliminating 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 (ICRP 1994a) - and is not uncommon in cigarette smokers.

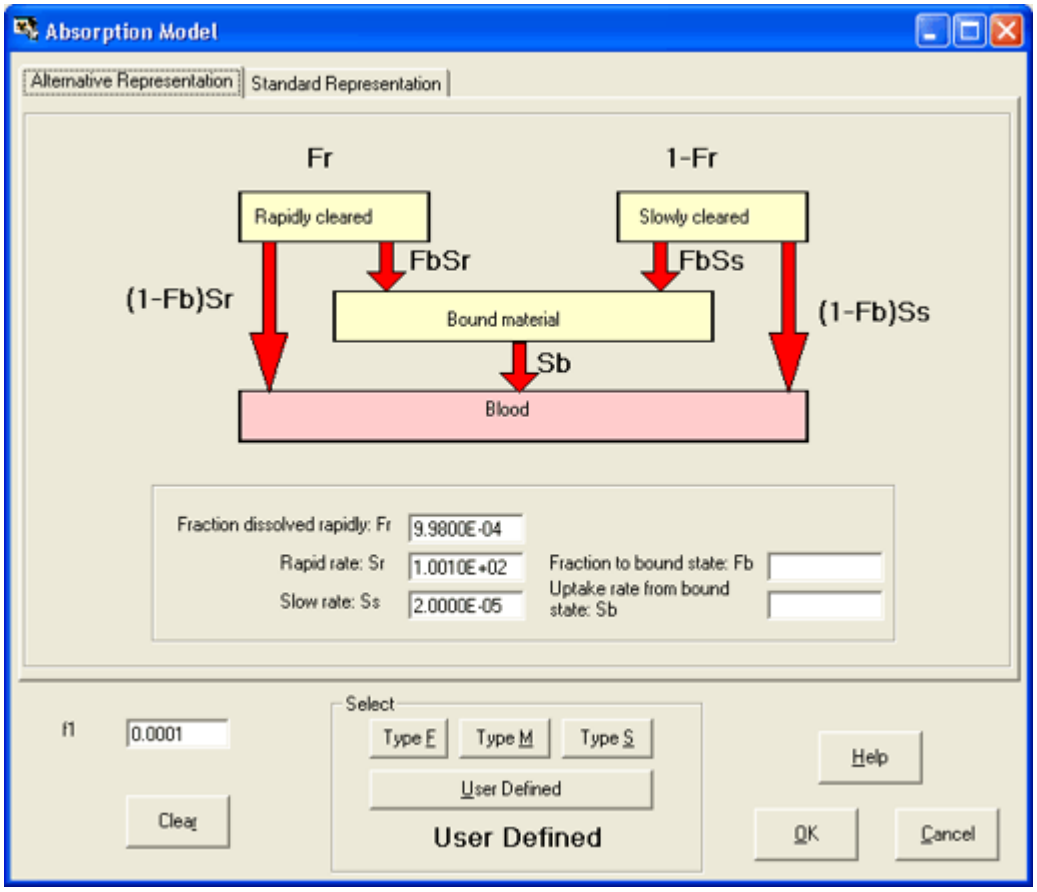


Figure 4.137. User Defined value of the "Slow" absorption rate (Ss) - from the default value of 0.0001 d-1 for Type 'S'.

This changed "slow" absorption rate (Ss) represents a five-fold reduction from the Type 'S' default values (0.0001 d-1).

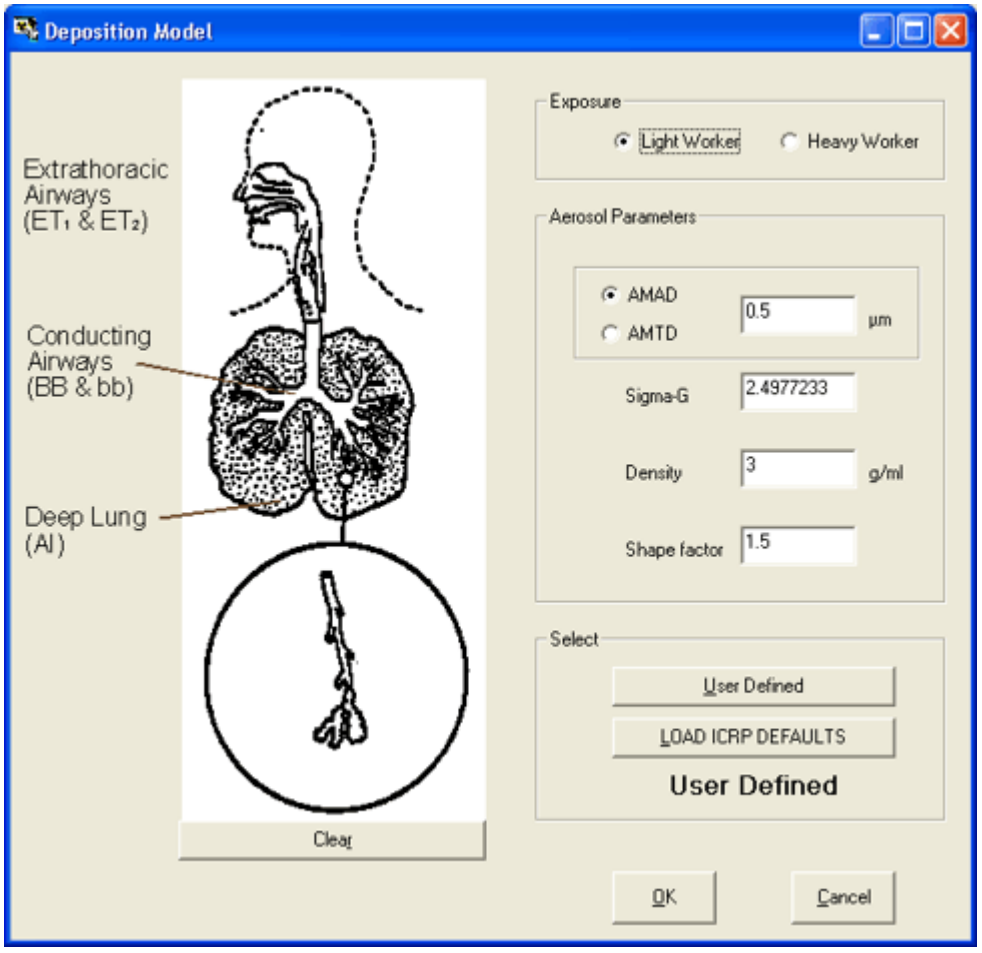


Figure 4.138. User Defined value of the aerosol AMAD (0.5 µm).

- 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 ^{241}**Am and** ^{239}**Pu** 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 ^{241}**Am activity in the lungs. Furthermore, Figure 4.140 shows that the very much improved "fit" to the observed early "constancy" of the** ^{241}**Am activity in the lungs.**

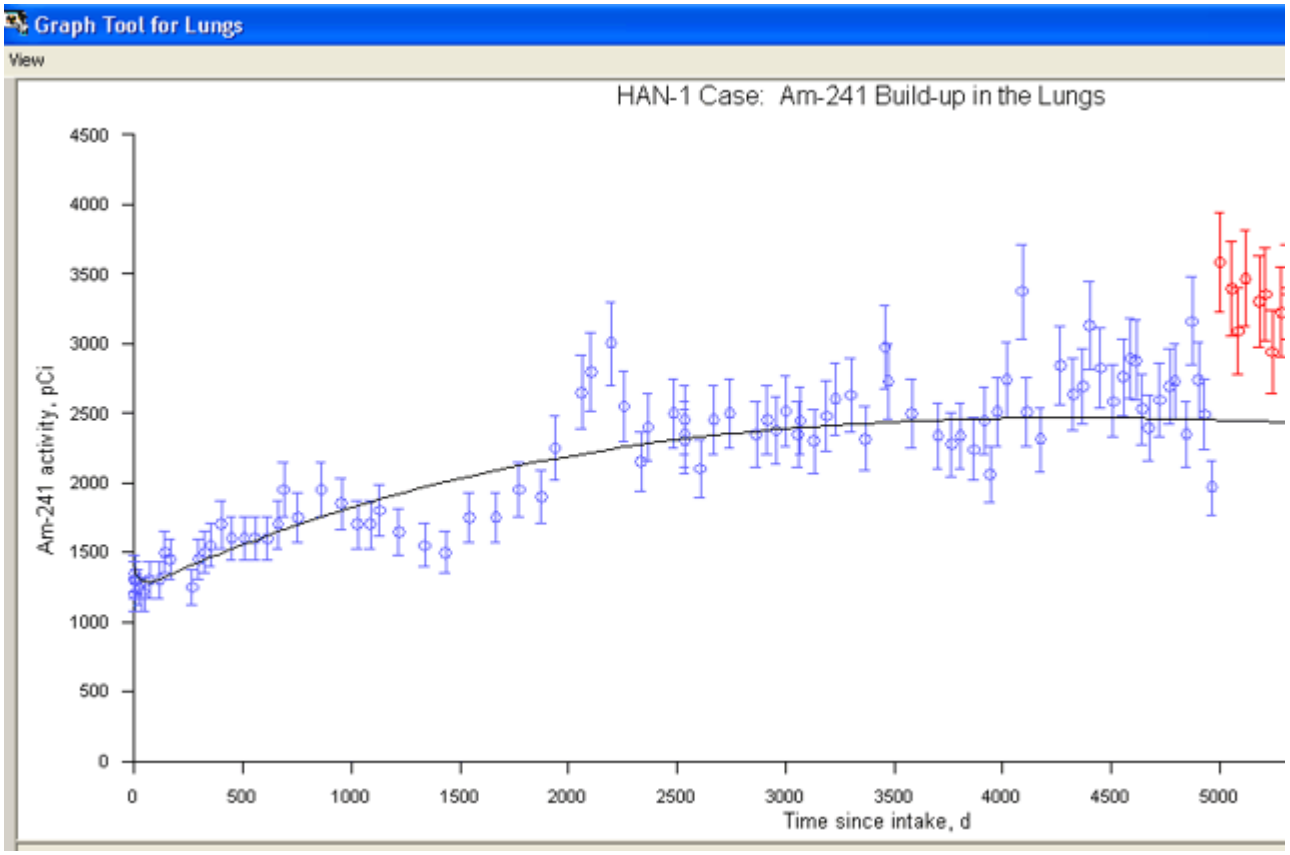


Figure 4.139. **Improved "fit" to the** measured build-up of 241**Am activity in the lungs.**

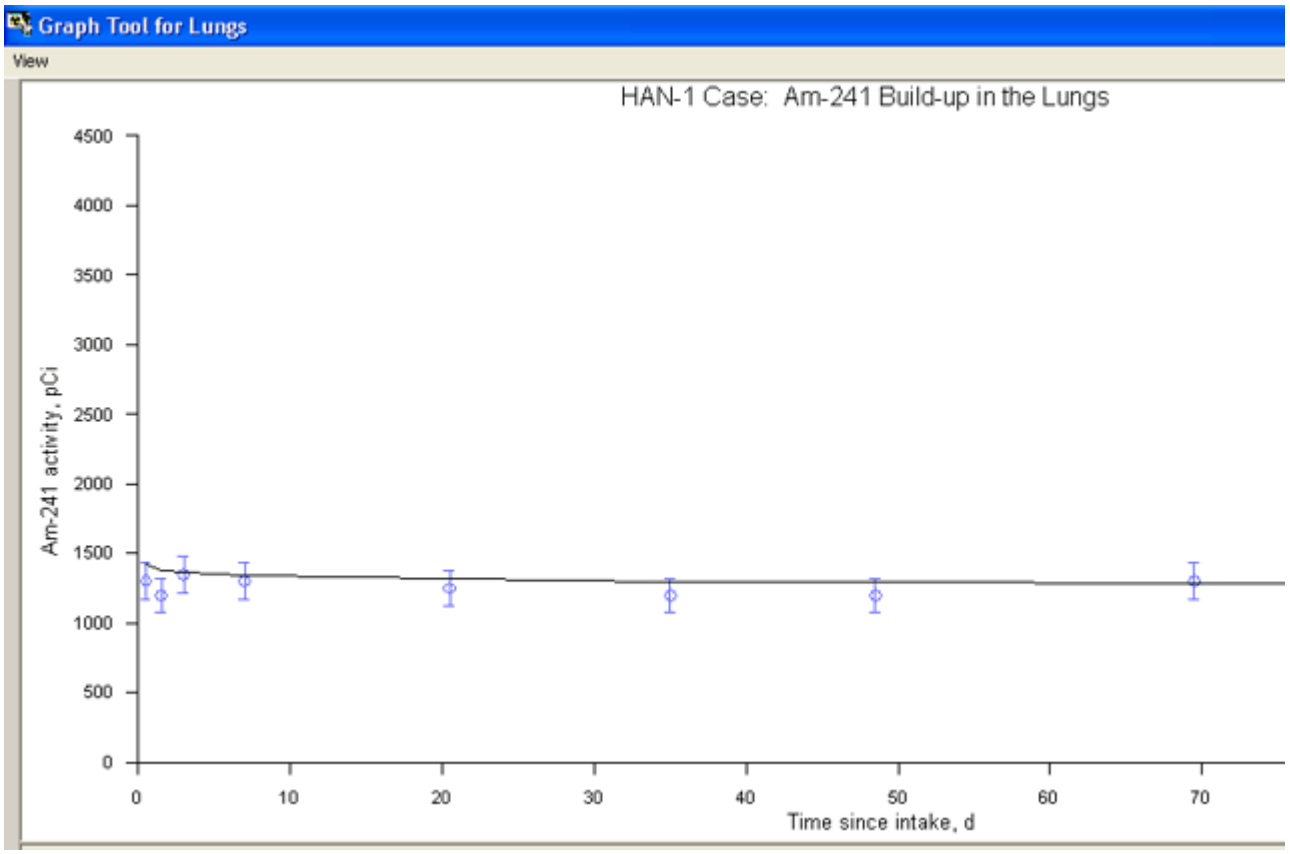


Figure 4.140. Resulting "fit" to the constant 241**Am activity in the lungs maesured over the first 70 d.**

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".

Tip: See for yourself how inclusion/exclusion 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 ^{241}**Am activity in the** Liver **and** Skeleton**.**

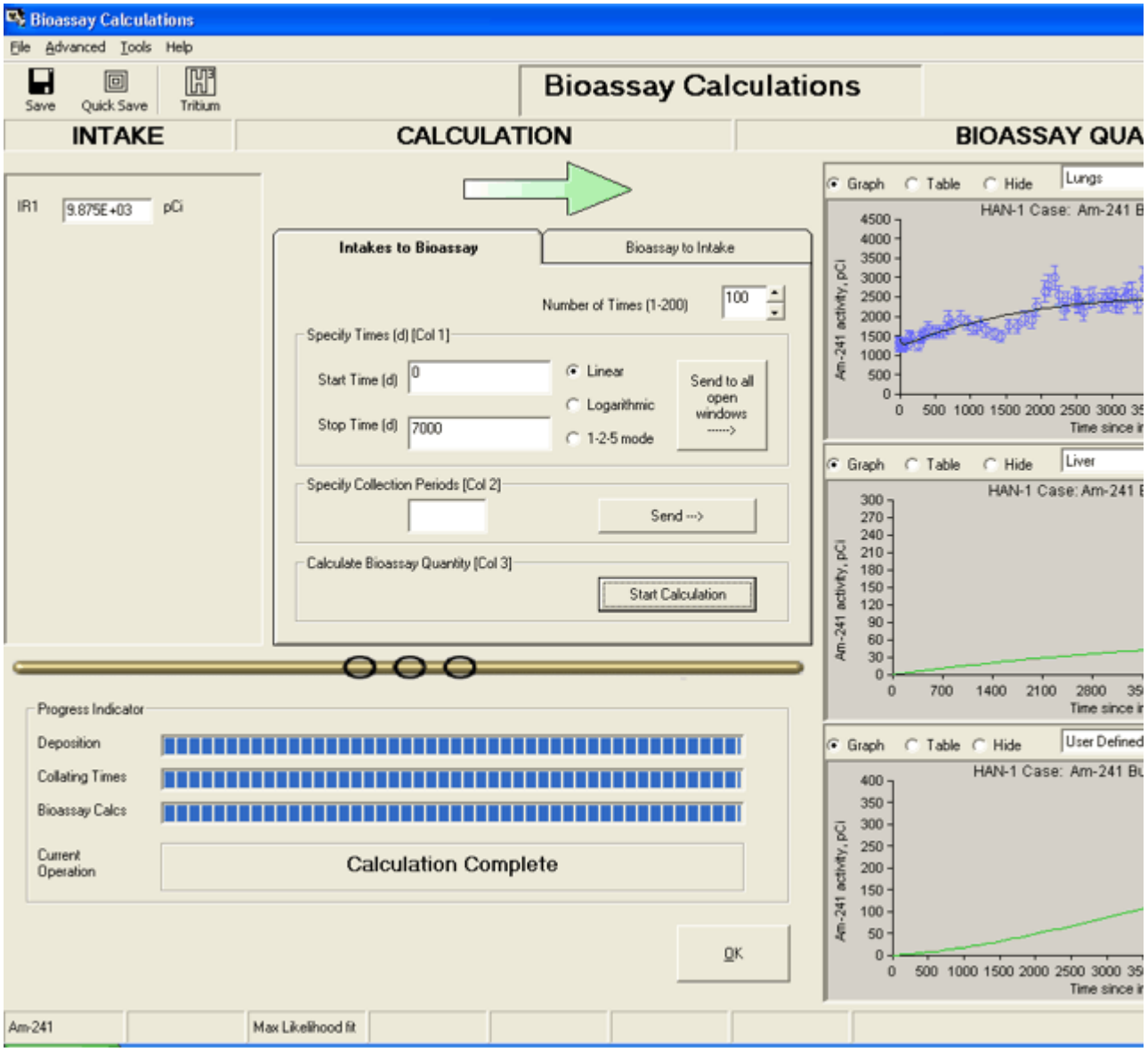


Figure 4.141. **Improved overall "fit" to the HAN-1 data obtained by modifying parameter values in the HRTM.**

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**

plutonium "bulk" material. For the Associated Radionuclides **in body organs, including** 241**Pu, progeny "in-growth" 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 239**Pu 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**).**

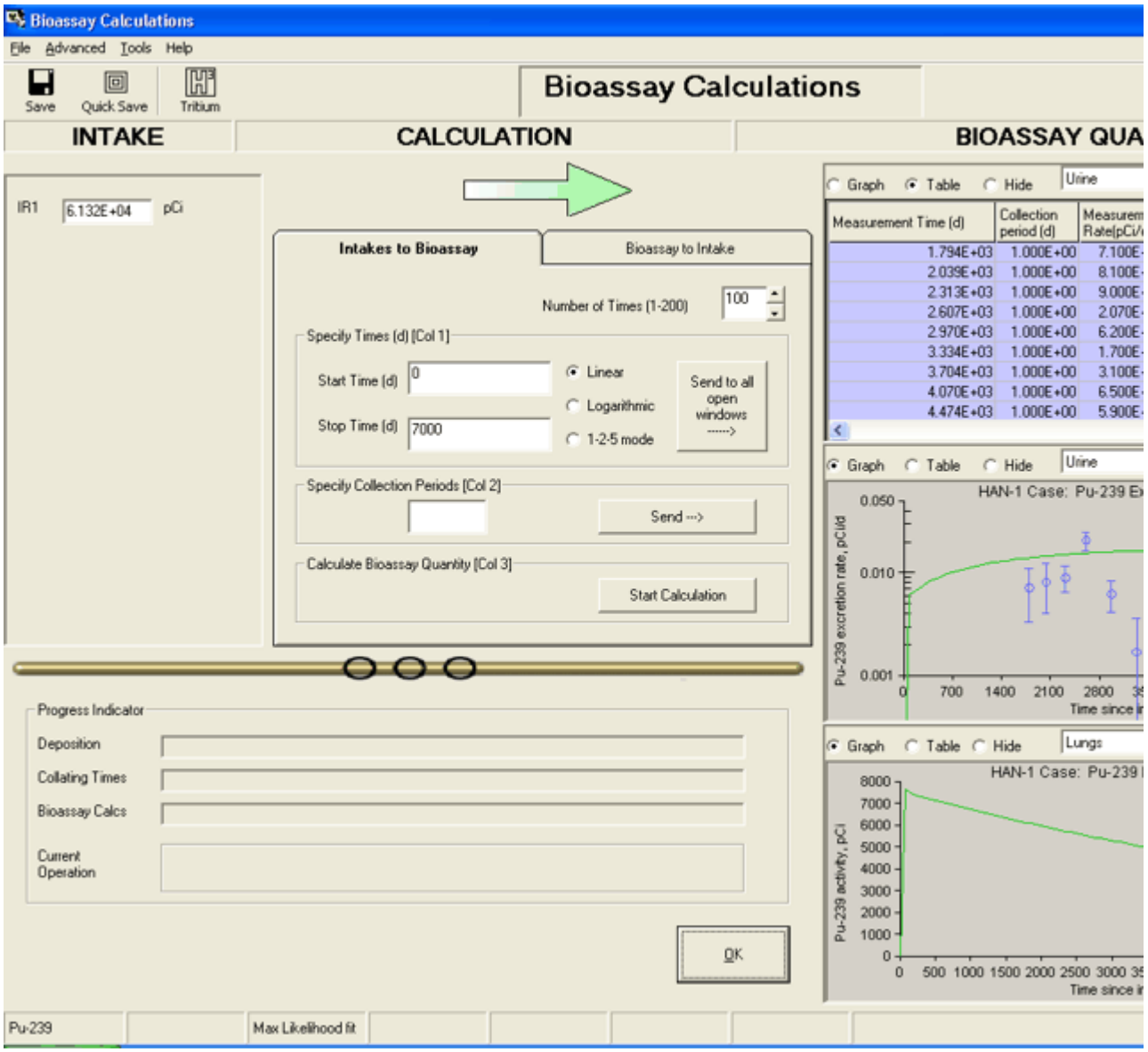


Figure 4.142. **Predicted** 239**Pu urinary excretion rate and lung retention.**

Note: As with the other example cases "solved" in this User Manual, the "solutions" offered are NOT intended to be scientifically definitive. They are

> presented ONLY to demonstrate the scope and flexibility of the IMBA Professional Plus. More thorough review of the specific health physics information relating to each case may well indicate revised modeling assumptions.

- Proceed **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 10CFR835 tissue weighting factors.

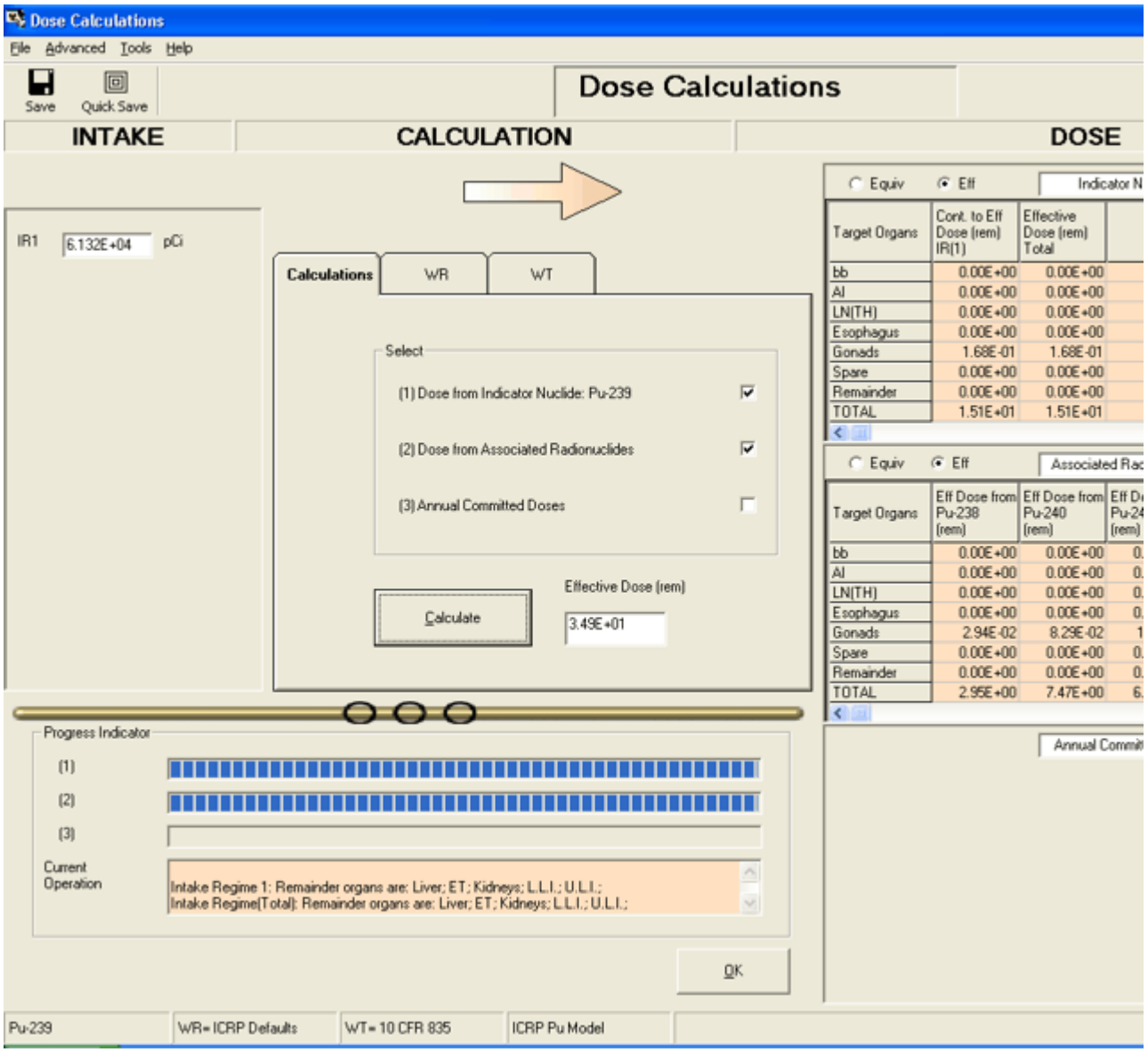


Figure 4.143. Effective doses calculated using 239Pu **as the** Indicator Nuclide**.**

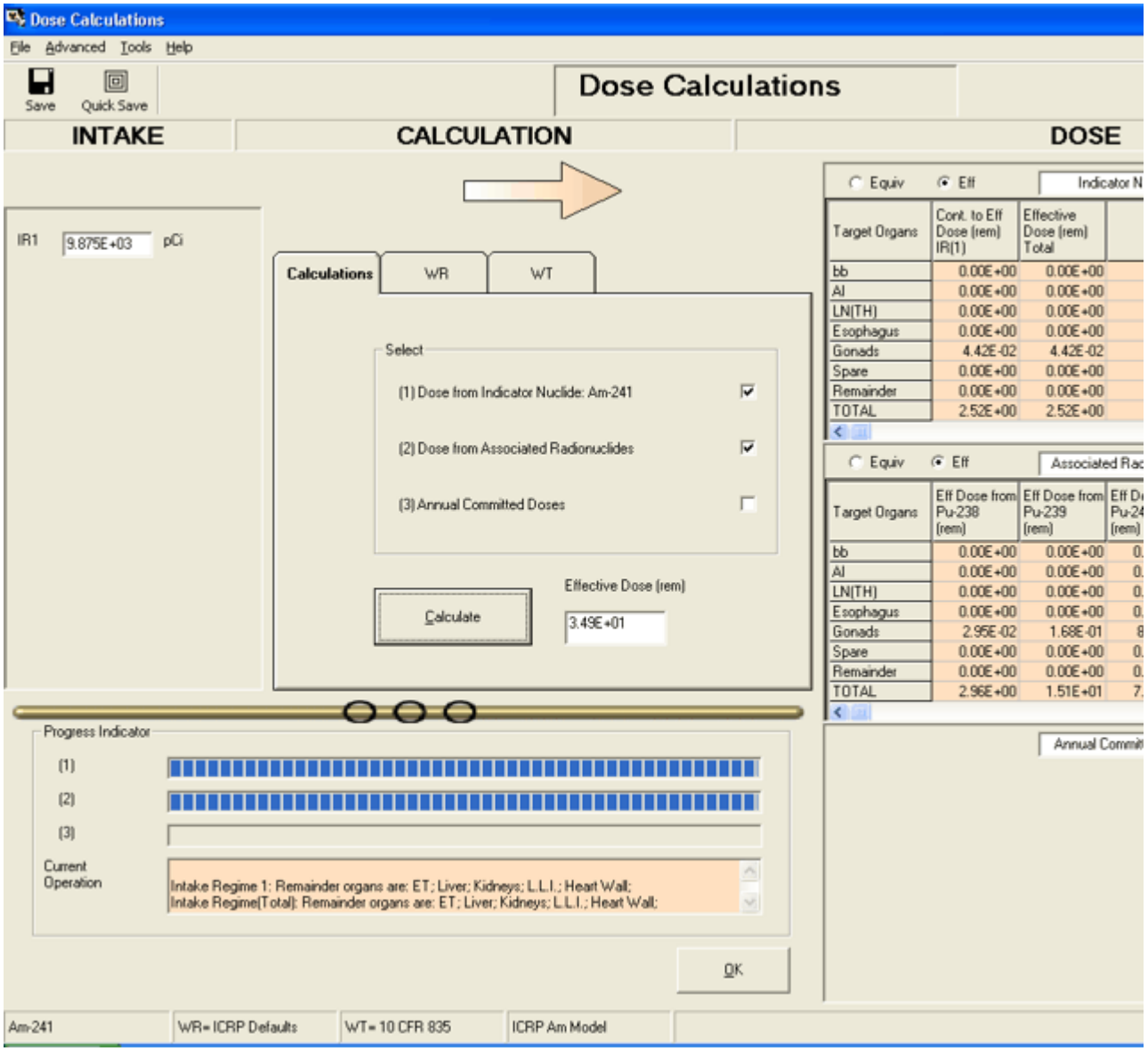


Figure 4.144. Effective doses calculated using 241Am **as the** Indicator Nuclide**.**

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.**

Table 4.16. Contributions to effective dose (in rem and %).

Contribution from:	Optimized Parameter Values - with 239Pu as the Indicator Nuclide	Optimized Parameter Values - with 241Am as the Indicator Nuclide	ICRP Default Parameter Values – Type 'S' Plutonium
238Pu	2.95	2.96	3.05
239Pu	15.1	15.1	14.9

240Pu	7.47	7.48	7.30
241Pu	6.82	6.82	3.93
242Pu	0.00256	0.00252	0.00247
241Am	2.52	2.52	2.44
Total from All Nuclides	34.9 (100%)	34.9 (100%)	31.5 (100%)
Total from Lungs	27.7 (79%)	27.7 (79%)	10.9 (39%)

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%).

Case Using Statistics Package - Requires Add-On 11

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 ^{241}Am 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 Bihl et al (1988), with a longer-term "follow-up" reported by Carbaugh et al (1991). 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 ^{241}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 http://bidug.pnl.gov/references/Carbaugh_PNNL_%20Plutonium_%20Reality_%20Show_s.pdf. 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 isotopic composition of the inhaled material (% by atom) - from mass spectrometry.
- Measured 241Am-in-lung activity *in vivo* - from the first through 6,639th day (18-y follow-up).
- Measured 241Am-in-liver activity *in-vivo* - measurable from about 6,000 d.
- Measured 241Am-in-skeleton activity *in-vivo* - also measurable from about 6,000 d.
- Measured 239/240Pu excretion rate in urine - measurable from about 1,800 d onwards.

See Input Data for Am-241 in Lung Case.

Input Data - ^{241}Am in Lung Case

1. Isotopic Composition

Table 4.11. Isotopic composition of plutonium oxide material inhaled in HAN-1.

Radionuclide	% by Number of atoms	% By Activity

241Am	0.25	0.56
^{238}Pu	0.065	0.71
^{239}Pu	86.4	3.46
^{240}Pu	11.6	1.71
241Pu	1.4	93.6
^{242}Pu	0.24	6×10^{-4}

Clearly, from Table 4.11:

- $^{239/240}Pu$ dominates by number of atoms.
- ^{241}Pu dominates by activity.
- ^{241}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 259 *in vivo* measurements of ^{241}Am 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 ^{241}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
12/4/92 12:00 AM	3375
1/8/93 12:00 AM	3050
2/12/93 12:00 AM	2930
3/12/93 12:00 AM	2810
4/12/93 12:00 PM	3050
5/14/93 12:00 AM	3105
6/7/93 12:00 PM	3085
7/5/93 12:00 PM	2855
8/23/93 12:00 PM	3325
10/8/93 12:00 AM	3160
11/24/93 12:00 PM	3455
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
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. ^{241}Am in the Liver

Table 4.13. *In vivo* measurements of ^{241}Am activity in the liver.

Date of Measurement	Measured ^{241}Am Activity (nCi)	Minimum Detectable 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	0.06

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 of Measurement	Measured 241Am Activity (nCi)	Minimum Detectable 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 ^{241}Am 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 ^{239}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 of Measurement	Measured Excretion Rate (pCi d-1)	Estimated Error (pCi d-1)
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

- Proceed to Analysis of 241Am Retention in the Lungs - Using ICRP Default HRTM Parameter Values.

Analysis of ^{241}Am-in-lung Data - using ICRP Defaults

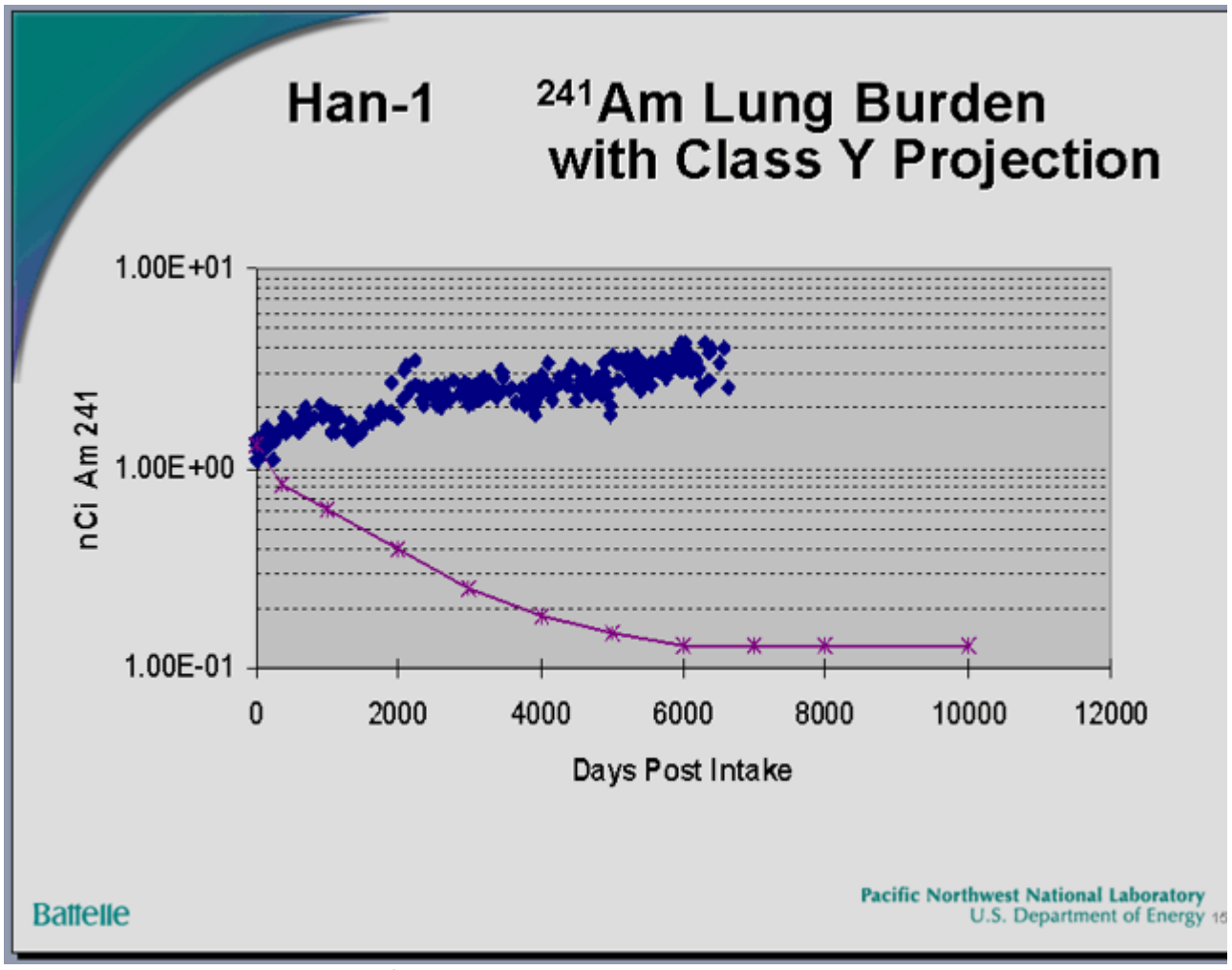


Figure 4.131. Comparison of ^{241}Am-in-lung data with ICRP30 Class 'Y' prediction (from Carbaugh 2004).

Figure 4.131 shows Gene Carbaugh's updated summary of the ^{241}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 ^{241}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 ^{241}Am activity in the Liver and Skeleton with the *in vivo* measurements.

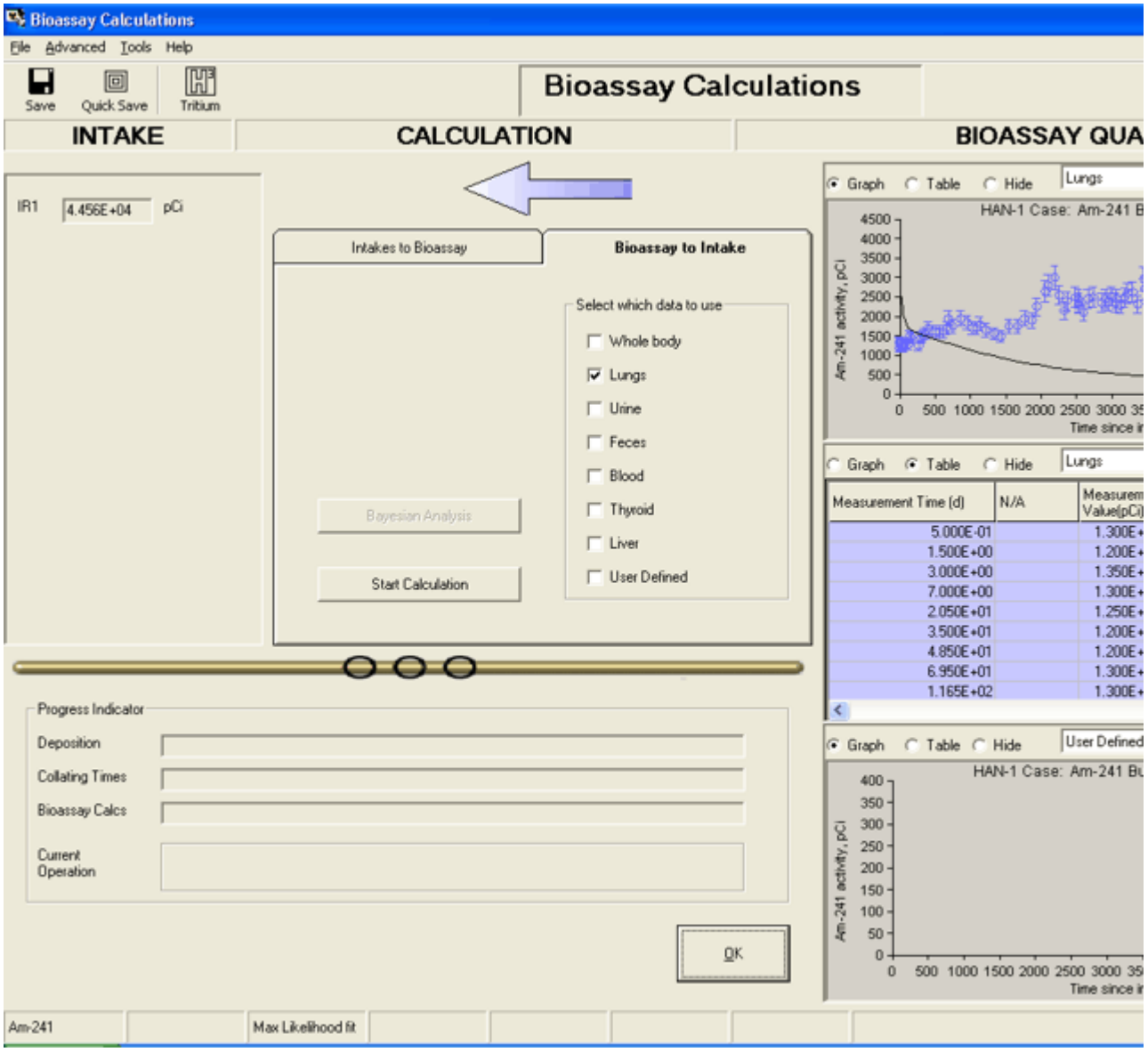


Figure 4.132. Most likely "fit" to HAN-1 ^{241}Am-in-lung data assuming ICRP default HRTM parameter values (Type 'S').

Note: The predicted monotonic decrease of ^{241}Am activity in the lung includes the calculated "in-growth" of ^{241}Am activity into that of the parent ^{241}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 Isotopic 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 Associated Radionuclides of ^{241}Am (the Indicator Nuclide) - see Figure 4.133.

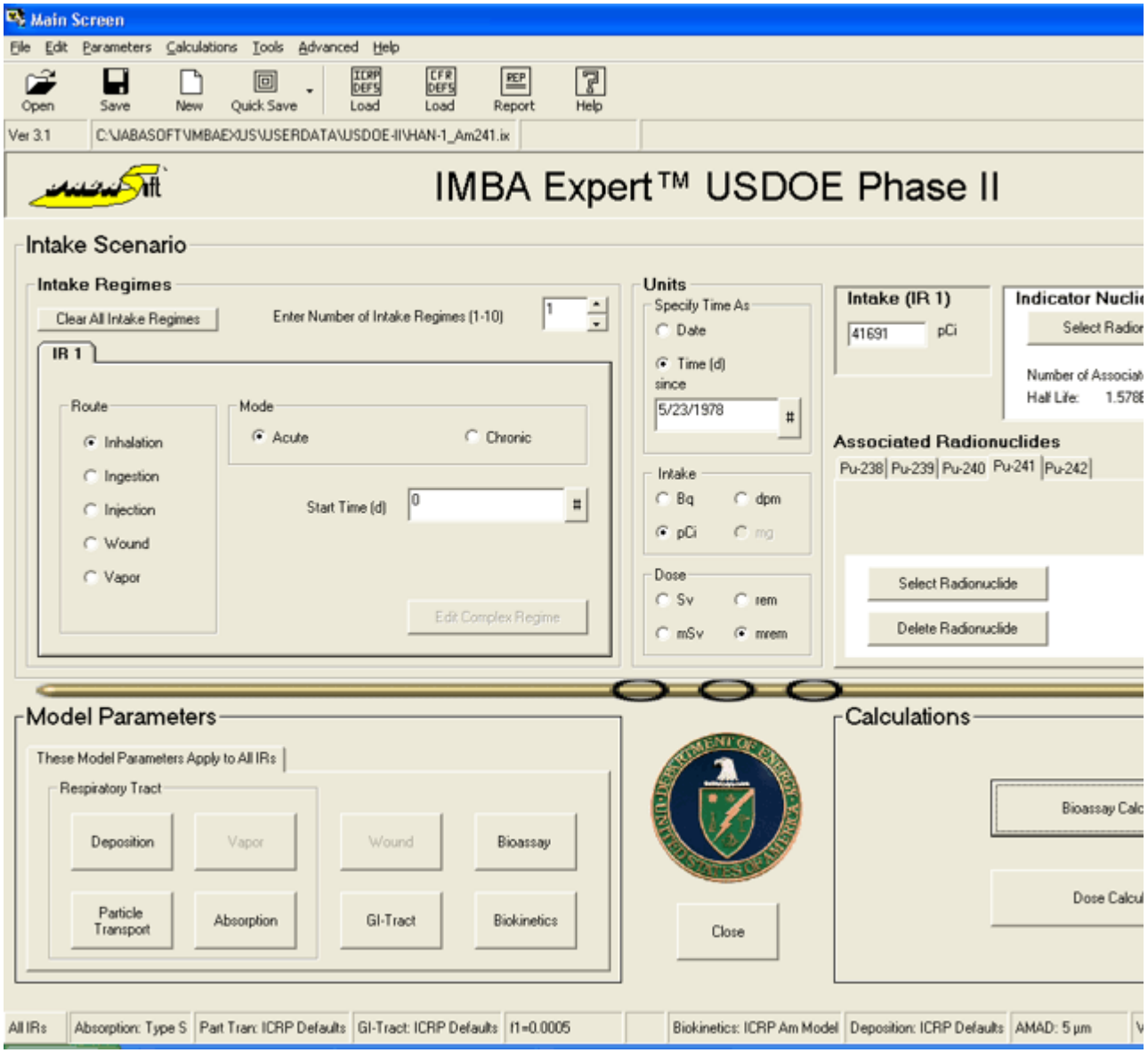


Figure 4.133. Setting up plutonium isotopes as Associated Radionuclides.

Figure 4.133 shows the 5 associated plutonium isotopes - ^{238}Pu, ^{239}Pu, ^{240}Pu, 241Pu and ^{242}Pu. Note that the "Abundance" of 241Pu is *very high* (16,813% - relative to the ^{241}Am activity).

The calculated amount of 241Am intake was 41,691 pCi - on the assumption that the inhaled plutonium oxide (particle matrix) had Type 'S' absorption behavior. The relative abundance of 239Pu was 621% (Table 4.11). Therefore, the associated intake of 239Pu would have been 258,900 pCi (258.9 nCi).

We can test this estimate of the 239Pu intake by comparing the predicted excretion rate in urine with that actually measured (Table 4.15). To do this, however, we have to set up a second "case" in IMBA Professional Plus - with 239Pu as the Indicator Nuclide, and the amount of intake set at 258,900 pCi. The resulting "predicted" urinary excretion rate is shown in Figure 4.134.

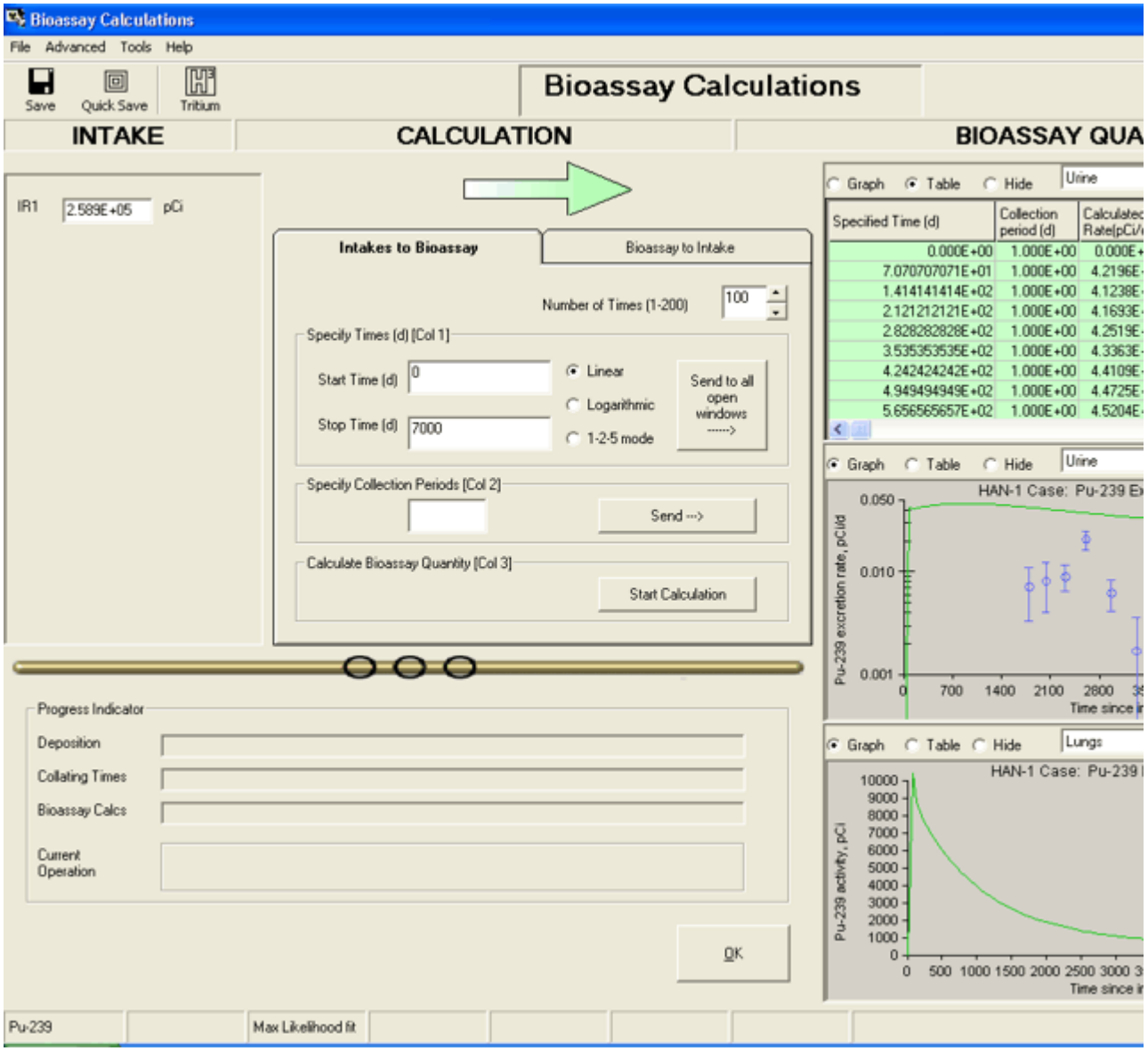


Figure 4.134. Urinary excretion rate and lung retention predicted for Type 'S' plutonium.

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):

1. The the measured 241Am 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 alveolar-interstitial (AI) region predicted a marked *decrease* of activity over this initial period (Figure 4.135). Note that the effect of "in-growth" of ^{241}Am activity as a result of ^{241}Pu decay over this period is *negligible*.

2. Over the long term (18 y) the 241Am activity in the lungs was observed to *increase* markedly - whereas, for Type 'S' plutonium it should

have *decreased* approximately 10-fold (Figure 4.132).

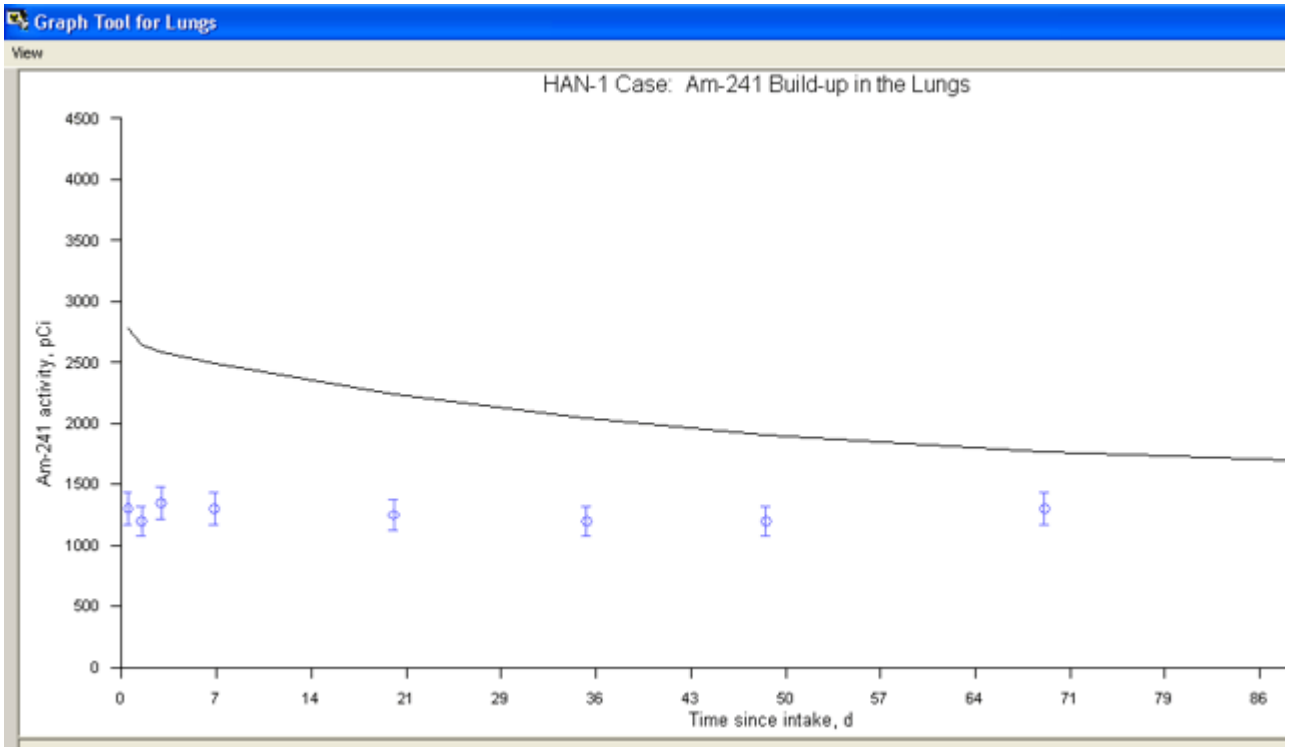


Figure 4.135. Comparison of predicted and measured early changes in ^{241}Am activity in the lungs.

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 Default parameter values should be used in 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 rates of transport to the bronchioles (compartments bb^1) from BOTH compartments AI^1 and AI^2 (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.

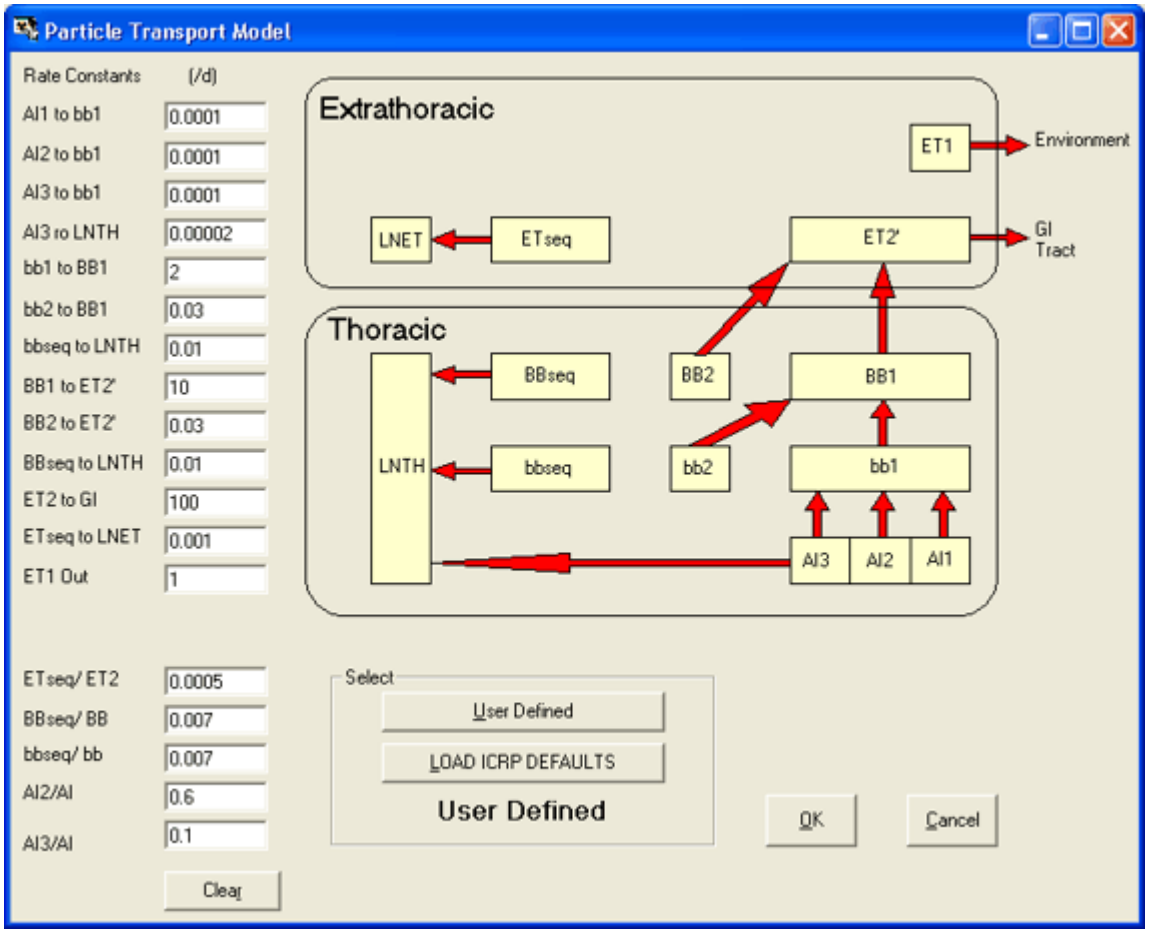


Figure 4.136. User Defined values of the *Rate Constants* "AI1 to bb1" and "AI2 to bb2" - from their default values of "0.02 d-1" and "0.001 d-1", respectively.

These changes to the transport rates out of compartments AI^1 and AI^2 are equivalent to eliminating 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 (ICRP 1994a) - and is not uncommon in cigarette smokers.

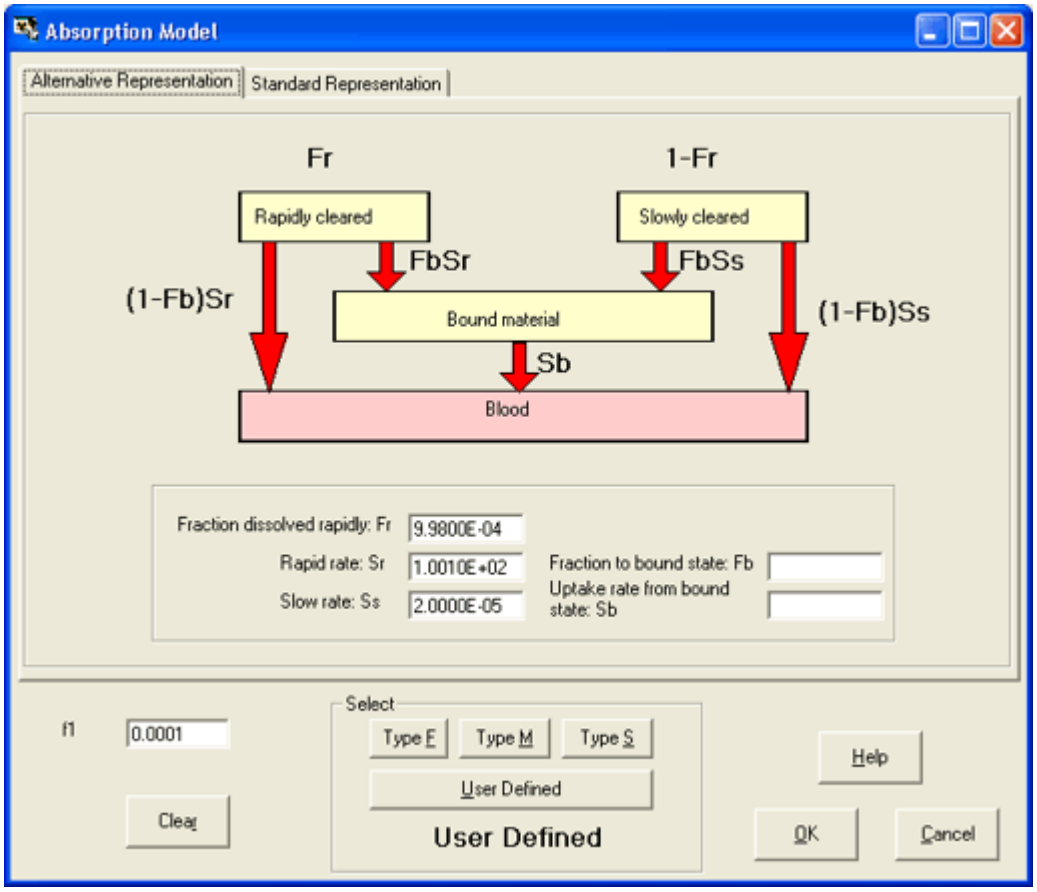


Figure 4.137. User Defined value of the *"Slow" absorption rate* (S^S) - from the default value of 0.0001 d-1 for Type 'S'.

This changed "slow" absorption rate (S^S) represents a five-fold reduction from the Type 'S' default values (0.0001 d-1).

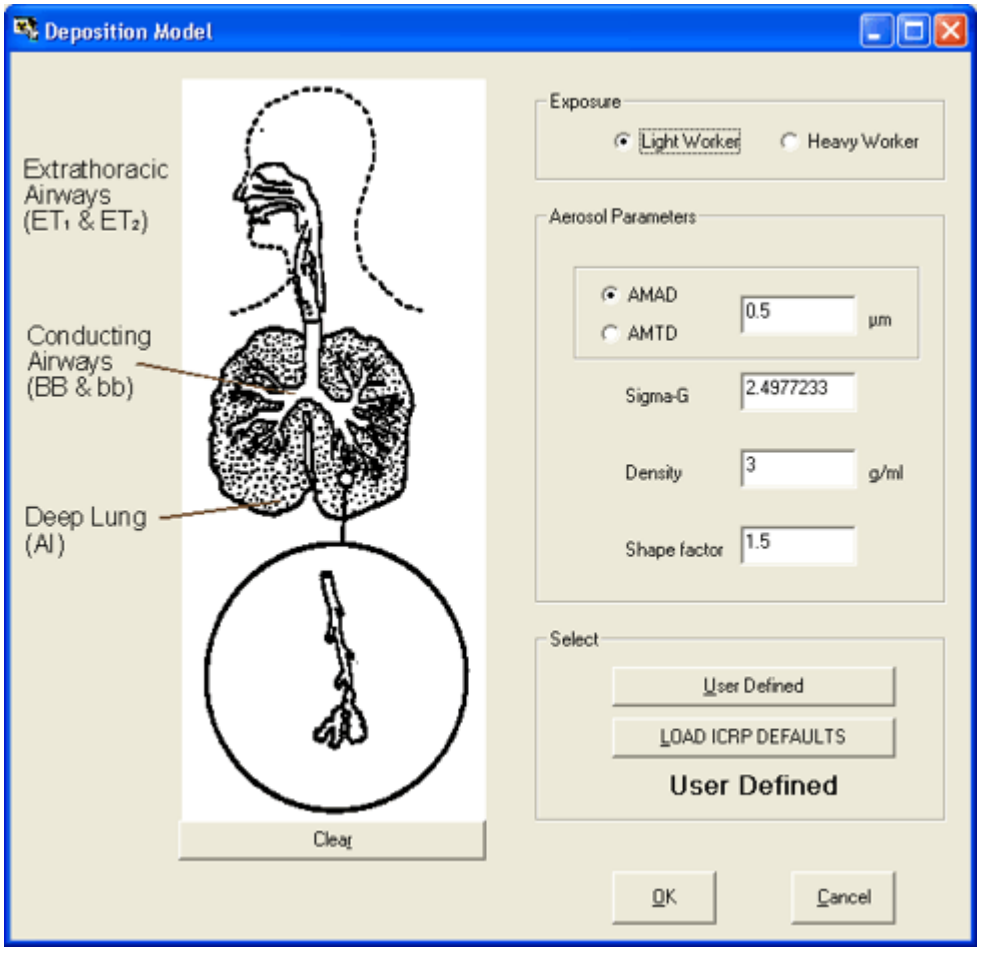


Figure 4.138. User Defined value of the aerosol *AMAD* (0.5 µm).

- 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.

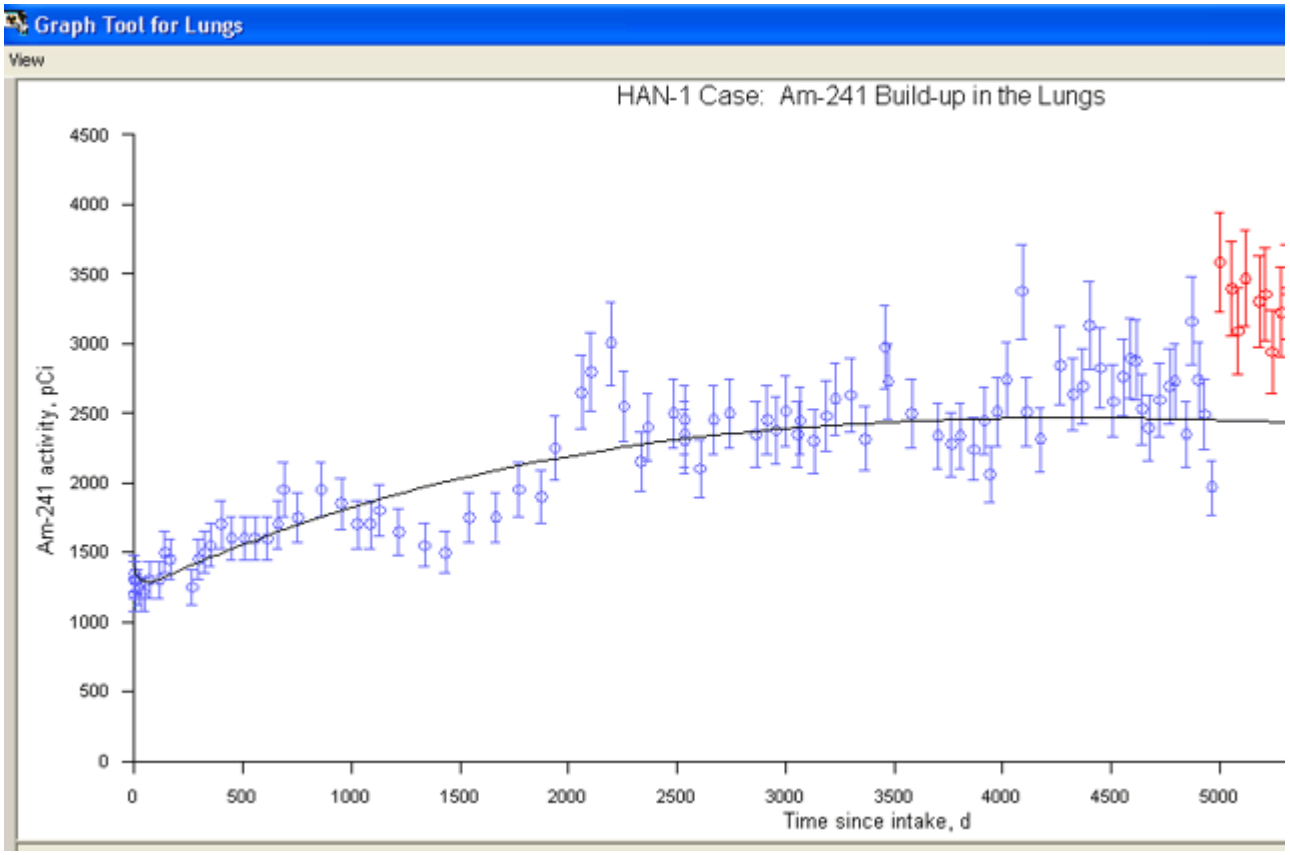


Figure 4.139. Improved "fit" to the measured $^{build\text{-}up}$ of ^{241}Am activity in the lungs.

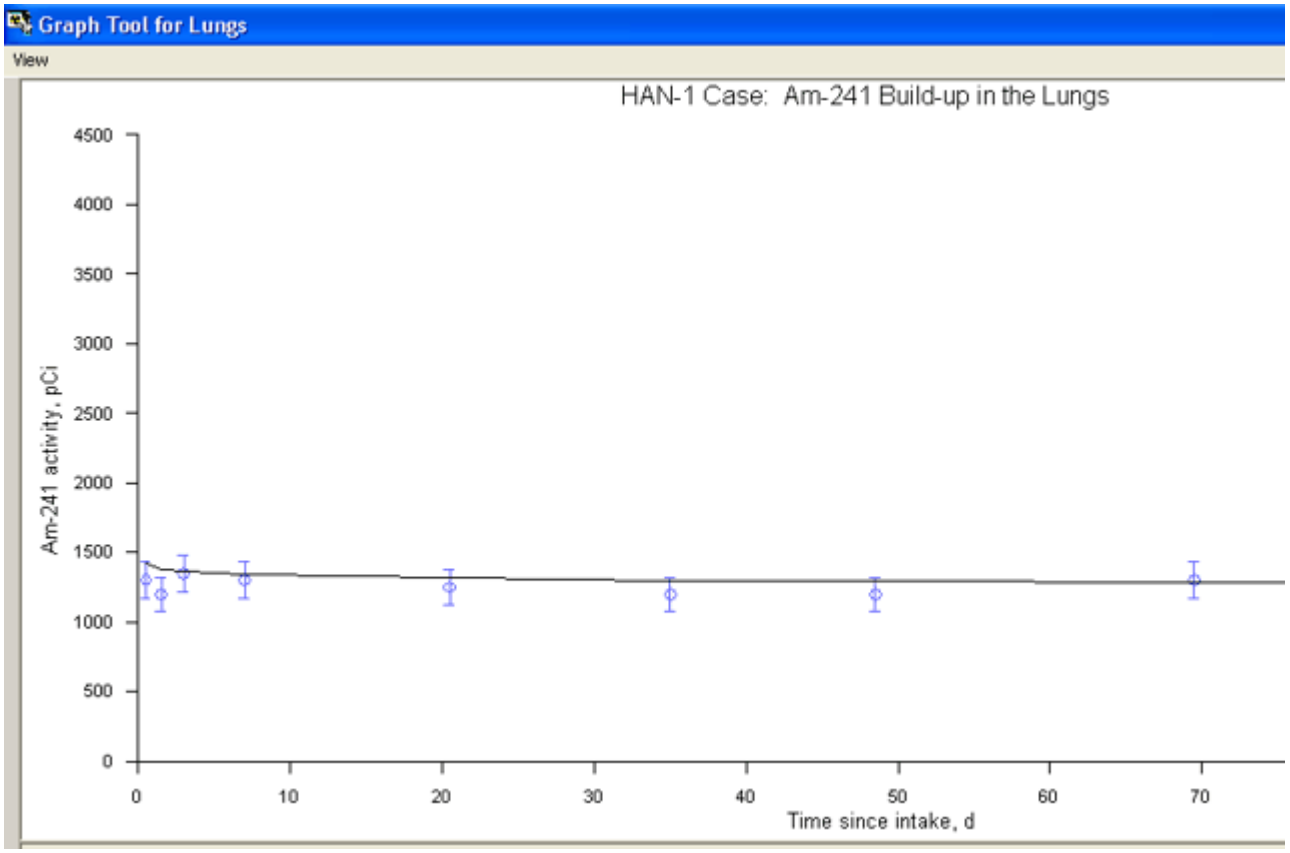


Figure 4.140. Resulting "fit" to the constant ^{241}Am activity in the lungs maesured over the first 70 d.

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".

Tip: See for yourself how inclusion/exclusion 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*.

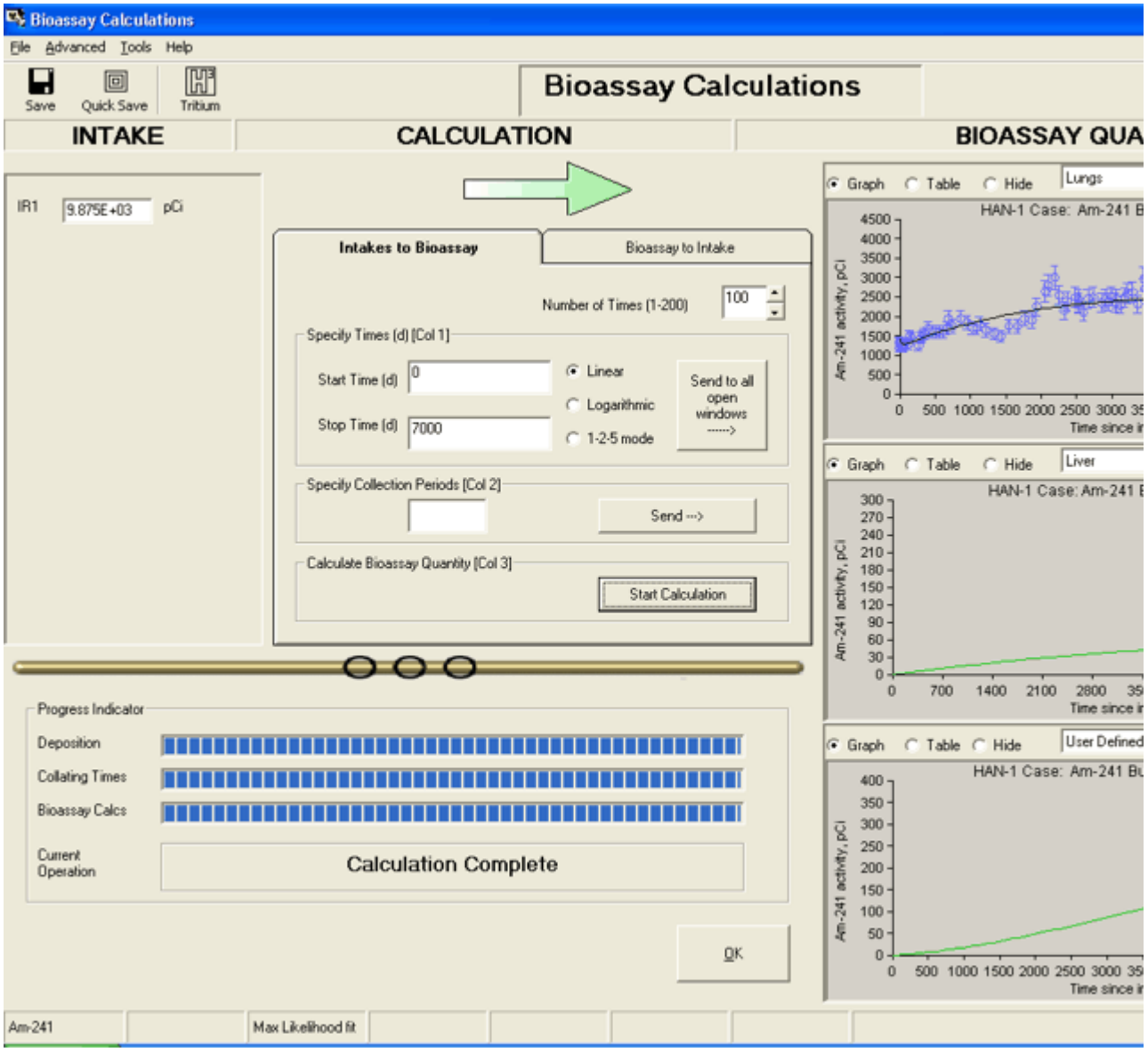


Figure 4.141. Improved overall "fit" to the HAN-1 data obtained by modifying parameter values in the HRTM.

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 241Pu in the particle matrix remains with the plutonium "bulk" material. For the *Associated Radionuclides* in body organs, including 241Pu, progeny "in-growth" 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).

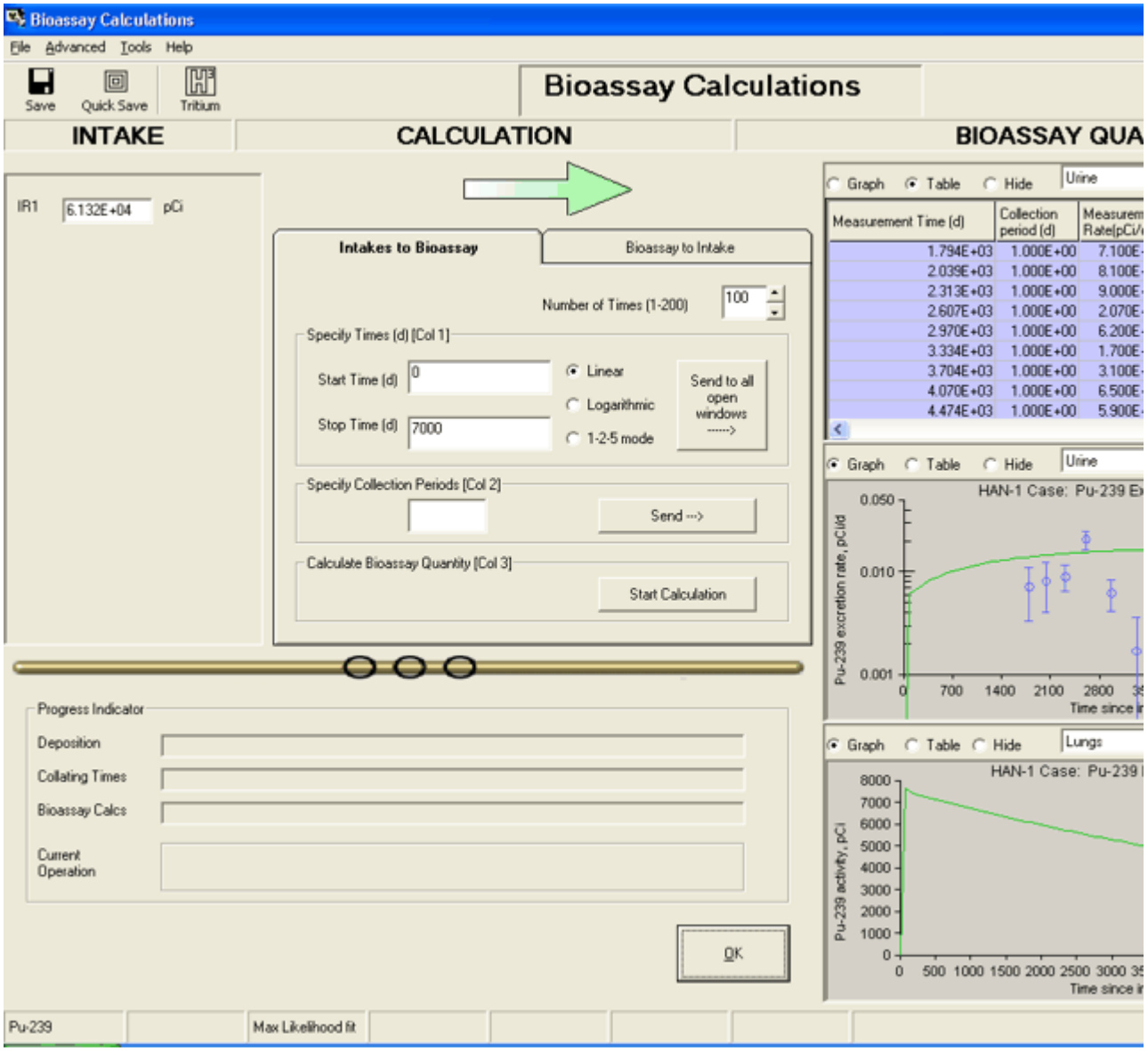


Figure 4.142. Predicted 239Pu urinary excretion rate and lung retention.

Note: As with the other example cases "solved" in this User Manual, the "solutions" offered are NOT intended to be scientifically definitive. They are

presented ONLY to demonstrate the scope and flexibility of the IMBA Professional Plus. More thorough review of the specific health physics information relating to each case may well indicate revised modeling assumptions.

- Proceed 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 10CFR835 tissue weighting factors.

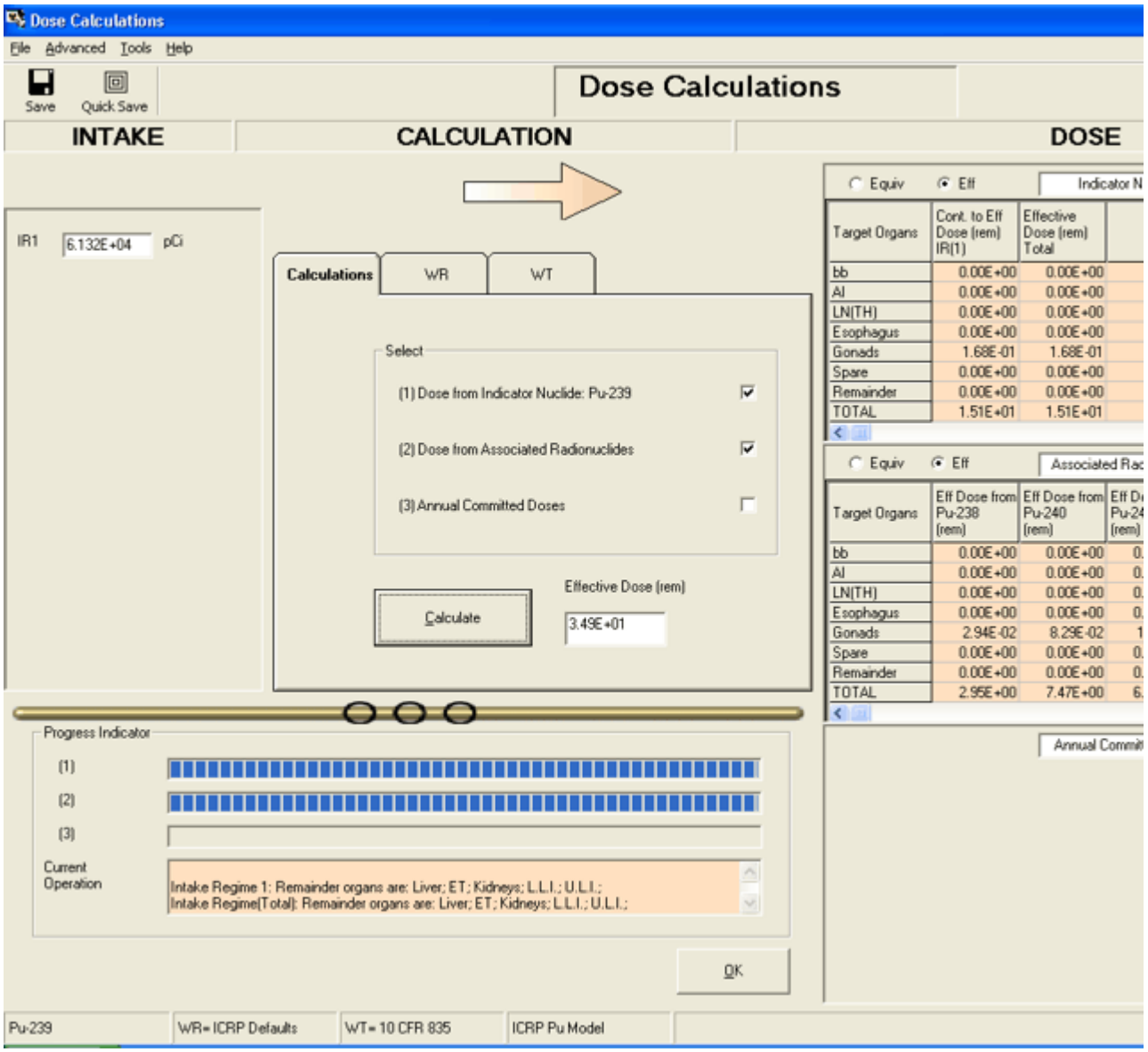


Figure 4.143. Effective doses calculated using ^{239}Pu as the Indicator Nuclide.

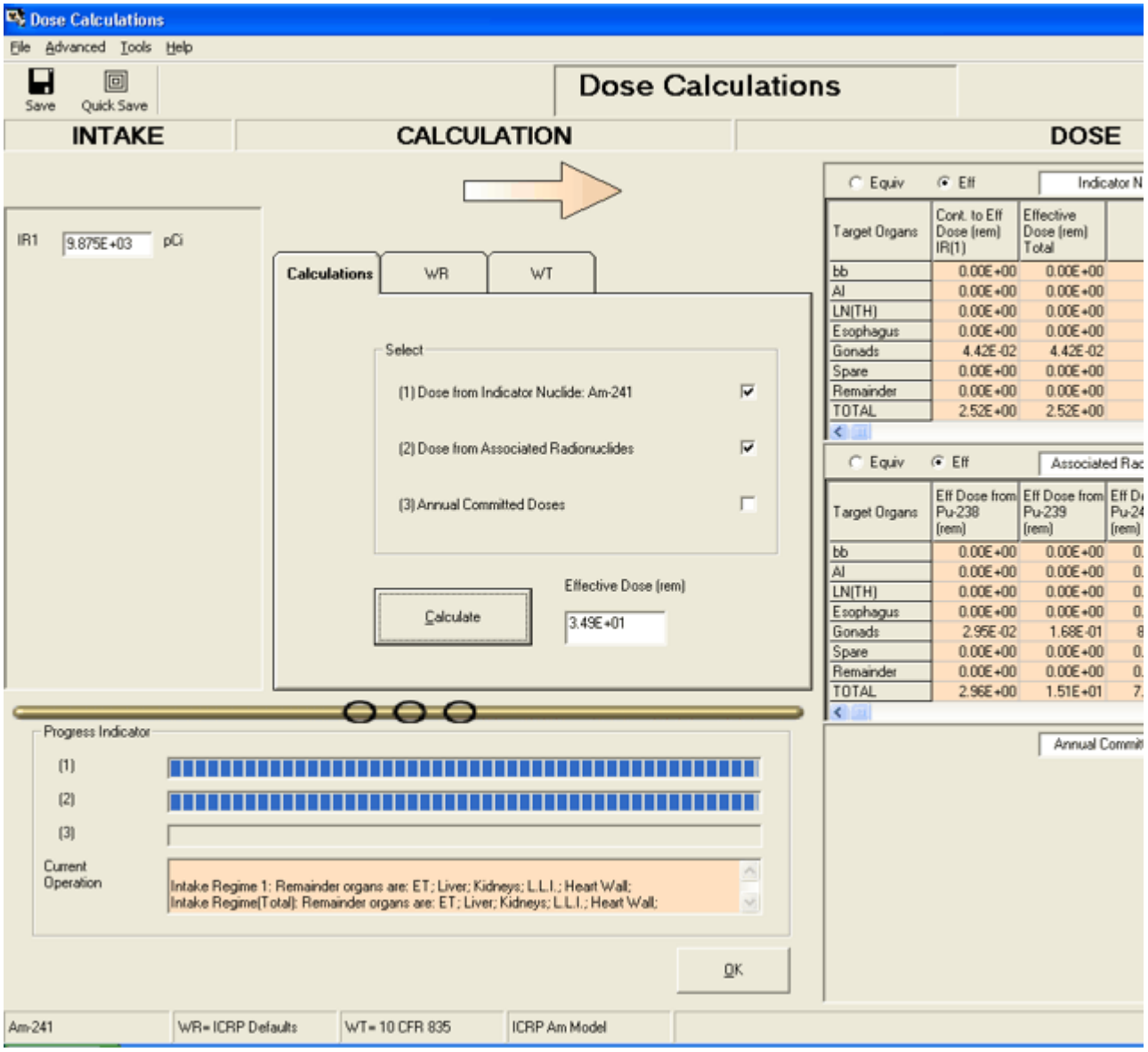


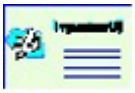
Figure 4.144. Effective doses calculated using ^{241}Am as the Indicator Nuclide.

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.

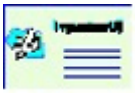
Table 4.16. Contributions to effective dose (in rem and %).

Contribution from:	Optimized Parameter Values - with 239Pu as the Indicator Nuclide	Optimized Parameter Values - with 241Am as the Indicator Nuclide	ICRP Default Parameter Values – Type 'S' Plutonium
238Pu	2.95	2.96	3.05
239Pu	15.1	15.1	14.9
240Pu	7.47	7.48	7.30
241Pu	6.82	6.82	3.93

242Pu	0.00256	0.00252	0.00247
241Am	2.52	2.52	2.44
Total from All Nuclides	34.9 (100%)	34.9 (100%)	31.5 (100%)
Total from Lungs	27.7 (79%)	27.7 (79%)	10.9 (39%)



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%)*.