IMIE

Individual Monitoring of the Internal Exposure Computer code

User's Guide

Kiev, 2013

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1 GENERAL DESCRIPTION

Individual Monitoring of the Internal Exposure (IMIE) computer code is developed for the purposes of the retrospective dosimetry. It gives to the user the sophisticated engine for the analysis and interpretation of bioassay measurements. The IMIE code helps the user to make estimations about a history of intakes and associated doses on the basis of individual monitoring data.

1.1 Minimum system requirements

Personal computer with
CPU : Intel Pentium 100 or higher;
RAM : 64 MB or more;
Video : 1024x768 or higher, 16K colours or more;
Hard Disk: 100 MB of free space (excluding size of databases, which will be filled during exploitation) or more;
Operating system: Microsoft Windows XP, Windows 7 environment;
CD drive;
Mouse or other pointing device;
Network installation: not supported.

1.2 Installation of the program

To install the IMIE program, insert the installation CD-ROM into a CD-ROM drive. Run the Setup.exe. The *Setup* program will prompt you to select the destination folder, where the program files will be copied. An *RPI* group will be created in your Windows *Start* menu. To start the IMIE program selects the *IMIE* item in the *RPI* group of the *Start* menu.

1.3 Structure of the folders

During the installation the IMIE.exe file is placed to the destination folder and the following subfolders are created:

- **Curves** – contains all available response functions and corresponding dose values in tabulated binary form. These functions are used in approximation during the analysis;
- **Data** – contains the radionuclides database with energy spectra;
- **DB** – contains the database with personal information and measurements;
- **ICRP-66** – contains files with standard lung deposition fractions from ICRP Publication 66;
- **Mix** – contains descriptions of user defined mixed intakes (fractions of paths of intake, fractions of Types of Material and AMADs etc.) in binary form;
- **Results** – contains the results of the analysis in a binary form.

The structure of program folders can be changed in the *Preference* window of the IMIE program (see section 8) but this action is not recommended.

1.4 Available parameters and modes

Detailed list of parameters and modes, which are available in the IMIE, is given in Annex E.

1.5 Essential notes

The main aim of the IMIE program is the reconstruction of multiple intakes on the base of the body counter or bioassay data and known exposure conditions, such as date of exposure, route of intake, AMAD and Type of Materials (in the inhalation case). Moreover, the program allows the user to estimate unknown exposure conditions: date of intake, AMAD and Type of

Materials of inhaled aerosols. In that case unknown conditions can be set out as supposed ranges. The program will analyse all combinations of parameters from the selected ranges and will find the set of exposure conditions, which gives the best fit to the analysed measurement series.

The solution in that case is often ambiguous, because several approximation results usually are close enough to the points of the measurement series. The wider are ranges of unknown parameters the more ambiguous is the result. The user must pay a great attention to obtained results. The final selection of the best result is responsibility of user. The IMIE program cannot give the "absolutely true" solution, it is only a tool, which helps to a skilled user to analyse and quantitatively compare all possible combinations of exposure conditions.

The reconstruction of date of intake is most reliable if other conditions of the exposure are known (AMAD and Type of Materials). Due to similarity of slopes of biokinetic response functions for different AMADs, the precise reconstruction of AMAD is usually problematic even if lung measurements are used. The significant difference between approximation results can be seen only for AMADs, which differ in orders. Usually the user can estimate that the AMAD was of 0.001 μm order, 0.1 μm order or 10 μm order only. The detailed set of AMADs is available in the program for cases when the AMAD is known *a priori*. A reliable answer is problematic if all exposure conditions are unknown.

One more obvious problem, which makes the analysis harder and the results more ambiguous, is the lack of data (measurements) and the large time periods between the intake and first measurements. The single measurement is an extreme case, when the intake value only can be estimated and other exposure conditions must be supposed.

A more detailed discussion of these subjects can be found in the Annex D 'Reconstruction of the intake with an arbitrary shape in the time'.

The program provides three main modes of the analysis (*ICRP78 mode*, *Semi-Automated mode* and *Manual mode*) and additional *Smart mode*. The *ICRP78 mode* supports the full-automated analysis based on the ICRP Publication 78. The *Semi-Automated mode*, the *Manual mode* and the *Smart mode* implement the new intake reconstruction method. The *Smart mode* is full automated (like *ICRP78 mode*) and gives the quickest results. The *Semi-Automated mode* provides more interaction with the user. The *Manual mode* is appropriate for the experienced user. This mode provides to the user a possibility to participate in the selection of a 'best fit' curve on the each step of the analysis. The *Accident mode* is a modification of the *Manual mode* useful for analysis of accidental cases.

2 *MAIN* WINDOW OF THE IMIE

Figure 1 shows the *Main* window of the IMIE as it appears after a first start of the program. The *Main* window includes 6 basic components:

1. *Main* menu (see callout 1 on the Figure 1);
2. *Toolbar* (see callout 2 on the Figure 1);
3. *Data* panel with all controls, for the management of the data analysis (see callout 3 on the Figure 1);
4. *Graph* panel, which displays data measurements, results of approximation and used for interactive defining of the time intervals for the analysis (see callout 4 on the Figure 1);
5. *Status* bar, which displays a current mode, an approximation method and a progress of the analysis (see callout 5 on the Figure 1);
6. *Splitter* – the thin mouse-sensitive vertical line, which separates the *Data* panel from the *Graph* panel (see callout 6 on the Figure 1). User can change the width of these elements by dragging the *Splitter* to the left or to the right. Also, user can set the minimal or maximal width of the *Data* panel by double click with the left mouse button on the *Splitter*.

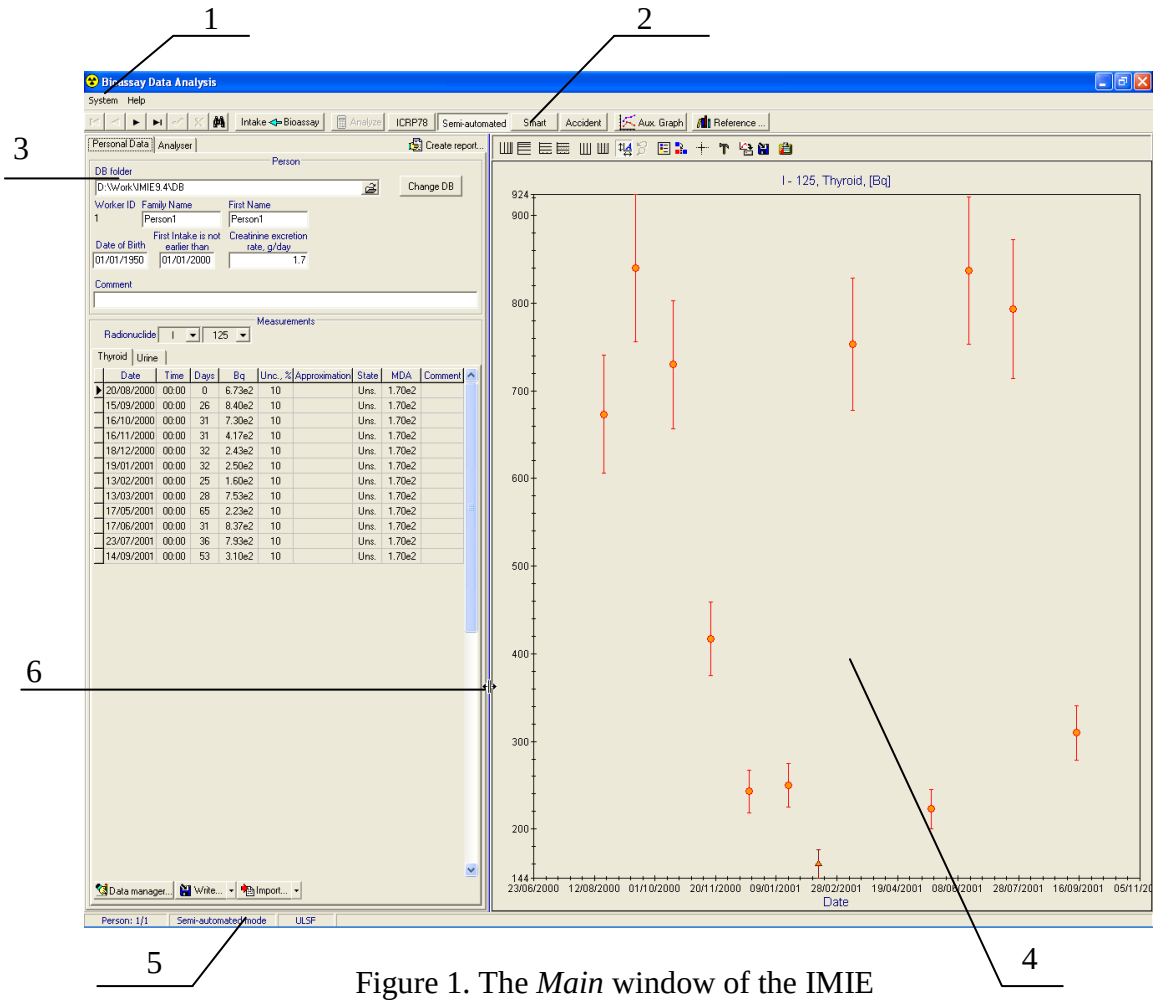


Figure 1. The *Main* window of the IMIE
(see description of callouts in the list above)

2.1 *Main* menu

The *Main* menu contains following items:

- *System* item:
  - *Analyse* item – execution of the analysis step (see subsection 3.1.1). This action is identical to the action of the corresponding *Toolbar* button (see subsection 2.2);
  - *Data manager* item – shows the *Data manager* window (see section 5), which allows to add/edit/delete personal information and measurement data;
  - *Preference* item – shows the *Preference* window (see section 8), which allows setting the working folders of the program, mode and global parameters of analysis (user can also set the mode with the *Semi-Automated mode* button, the *Smart mode* button, the *Accident mode* button or the *ICRP78 mode* button on the *Toolbar* – see subsection 2.2);
  - *Exit* item – exit the program.
- *Help* item:
  - *Reference window* item – shows the *Reference* window (see section 8), which is designed for obtaining the graphical and numerical reference information on decay chains and dose spectrums of radionuclides;
  - *IMIE Help* item – calls the help system for the IMIE program;
  - *About* item – information about program version and authors.

2.2 *Toolbar*

Figure 2 shows the *Toolbar* of the *Main* window.

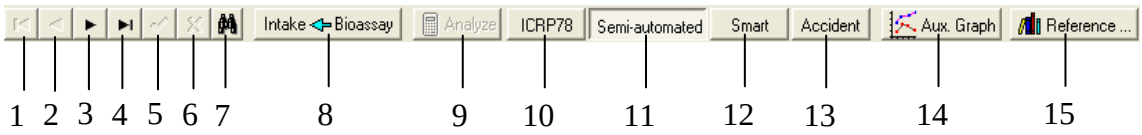


Figure 2. *Toolbar* of the *Main* window

Buttons placed on the *Toolbar* perform following actions:

1. Select first record of the *Persons* database;
2. Select previous record of the *Persons* database;
3. Select next record of the *Persons* database;
4. Select last record of the *Persons* database;
5. Accept changes of the personal data;
6. Reject changes of the personal data;
7. Calls *Search* window (see section 7), which allows to find a record in the *Persons* database;
8. Switch between *Retrospective* and *Prospective modes* of analysis. The *Retrospective mode* of analysis allows calculating the intake and dose analyzing available bioassay data (see subsection 3.1). The *Prospective mode* of analysis allows calculating the radionuclide retention or excretion from the known intake value (see subsection 3.2);
9. Performs the analysis step (see subsection 3.1.1). This action is identical to the action of the corresponding *Main* menu item (see subsection 2.1);

10 – 13: All of these buttons set on/off status for the selected mode (*ICRP78 mode*, *Semi-Automated mode*, *Smart mode*). Only one button among three can be down. When all enumerated buttons are up the *Manual* mode (see subsection 3.1.2) is active. A message about a currently active mode is displayed in the *Status* bar;

10. Sets on/off status of the *ICRP78 mode* (see subsection 3.1.3). When this button is down the *ICRP78 mode* is active;
11. Sets on/off status of the *Semi-Automated mode* (see subsection 3.1.1). When this button is down the *Semi-Automated mode* is active;
12. Sets on/off status of the *Smart mode* (see subsection 3.1.5). When this button is down the *Smart mode* is active;
13. Sets on/off status of the *Accident mode* (see subsection 3.1.3). When this button is down the *Accident mode* is active;
14. Turns on/off the *Auxiliary* graph (see section 6);
15. Calls the *Reference* window, which is designed for obtaining the graphical and numerical reference information on decay chains and dose spectrums of radionuclides (see section 10).

2.3 *Data* panel

The *Data* panel consists of two pages:

- *Personal Data* page;
- *Analyser* page.

The *Data* panel also contains the *Create report* button, which allows saving a report file with current results of the analysis. This file can be saved in the Text Format or in the Rich Text Format (rtf). Annex F

2.3.1 *Personal Data* page

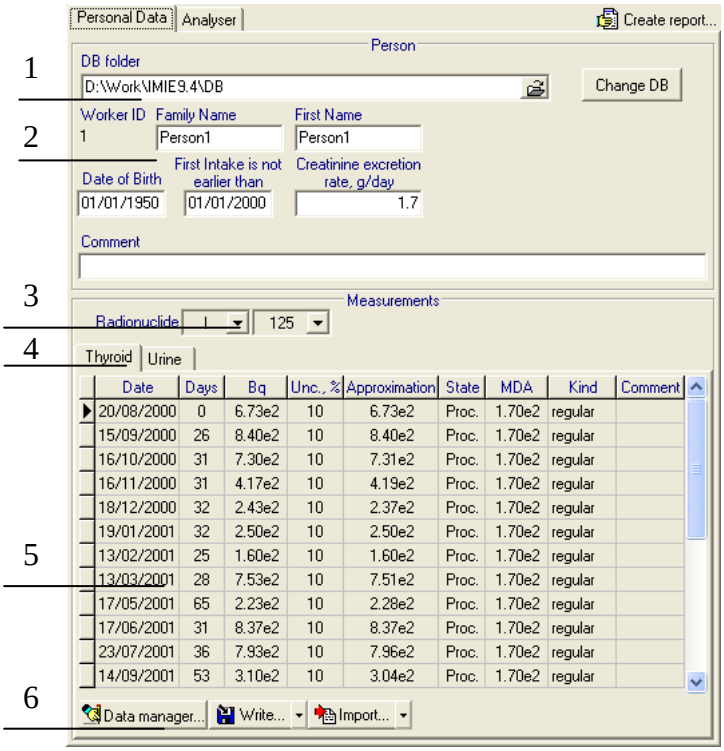


Figure 3. The *Personal Data* page

Personal Data page contains the following elements (see Figure 3):

1. *DB folder* edit box and *Change DB* button designed for selection of *Measurements* database and results folders. For selection of the *Measurements* database enter its full path to the *DB folder* edit box and press the *Change DB* button. The program will check presence of necessary database files in the selected folder and open the database. The analysis results will be placed to the *Results* subfolder of the selected *DB* folder. The *Results* folder value of the *Preference* window will be implicitly set to this subfolder. If the *Results* subfolder does not exist it will be created automatically. Paths to the working database and results folders can be changed also in the *Preference* window (see section 8).
2. *Personal information*:
   - *Worker ID* – the unique personal code;
   - *Family name*;
   - *First name*;
   - *Date of Birth*;
   - *First intake is not earlier than* – the supposed date of the first possible intake;
   - *Creatinine excretion rate* – the daily creatinine excretion rate for the person (if unknown the default value of 1.7 g per day is accepted);
   - *Comment* – any necessary comments (not obligatory).
3. *Radionuclide* – drop-down lists, which allows selecting the measurement series from available sets of measurements for the selected person.
4. Tabs, designed to select the measurement series for the selected person and radionuclide (i.e. Thyroid measurements, urine measurements, etc.).
5. *Table of the measurements* – displays the selected measurement series. The set of columns in this table is different for urine measurements and other measurement series. For all measurement series except urine measurements it contains following columns:
   - *Date* – date of the measurement;
   - *Time* – time of the measurement (displayed if *Use time* mode is checked in the *Preference* window – see section 8);
   - *Days* – time in days since the date of the previous measurement;
   - Measurement value in units of activity or daily excretion selected in the *Preference* window;
   - *Unc., %* – measurement uncertainty in percents. These values may be used as weighting factors in the analysis (see the equation 4 in the Annex B). If at least one of these values is zero or *ULSF* or *WLSF-EV* weighting method is set in *Preference* window (see section 8) then uncertainty values are not used in the analysis of the measurement set. If uncertainty values are unknown they must be set to zero;

– *Approximation* – approximation value for the measurement, calculated in analysis process. Approximation values are displayed in units selected in the *Preference* window;
– *State* – indicates the state of the measurement record in the measurement series. It contains one of three values: *Uns.* (unselected), *Sel.* (selected for the analysis) or *Proc.* (processed; it means that the record has been used on previous steps of the analysis). The state of measurement points is also indicated on the *Graph* panel by different colours;
– *MDA* – value of the minimal detectable activity for the measurement. MDA values are displayed in units selected in the *Preference* window;
– *Kind* – the kind of measurement. This value indicates the monitoring program within the framework of which the measurement was done (regular monitoring, special monitoring). For each kind of measurement the highlighting colour for the *Table of measurements* can be selected (see section 8);
– *Comment* – notes for the particular measurement (not required).

For urine measurements the *Table of measurements* displays following columns (see Figure 4):

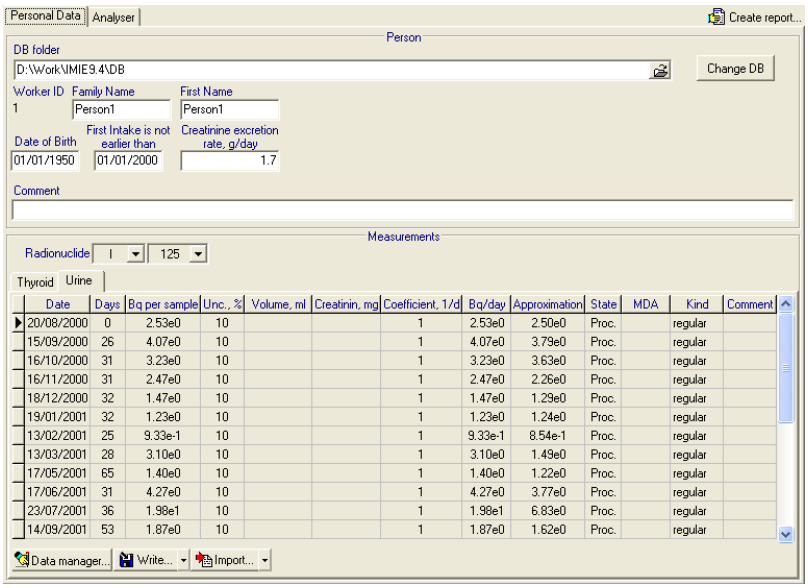


Figure 4. The *Personal Data* page with *Table of measurements* for urine measurements

– *Date* – date of the measurement;
– *Time* – time of the measurement (displayed if *Use Time* mode is checked in the *Preference* window – see section 8);
– *Days* – time in days since the date of the previous measurement;
– Measurement value in per urine sample in units selected in the *Preference* window;
– *Unc.,%* – measurement uncertainty in percents. These values may be used as weighting factors in the analysis (see the equation 4 in the Annex B). If at least one of these values is zero or *ULSF* or *WLSF-EV* weighting method is set in *Preference* window (see section 8) then uncertainty values are not used in the analysis of the measurement set. If uncertainty values are unknown they must be set to zero.
– *Volume, ml* – the volume of the urine sample in ml;
– *Creatinine, mg* – the creatinine content in urine sample in mg;
– *Coefficient, 1/d* – the coefficient for calculation of the daily radionuclide excretion with urine on the base of *Activity per sample* value. This coefficient is calculated automatically or can be entered manually (see section 5);
– Calculated value of the daily radionuclide excretion with urine in units selected in the *Preference* window. In accordance with ICRP-78 the urinary excretion data for tritiated water must be given in term Activity/litre (NOT in terms of the daily excretion rate)! The urinary excretion data for organically bound tritium must be given in terms of the daily excretion rate. The program automatically calculates these values and shows for tritiated water the Activity/litre value in this column.
Rest of columns is the same as for other measurement series.

6. Set of buttons:
   – *Data manager…* – shows the *Data manager* window (see section 5), designed to add/edit/delete personal information and measurement data;
   – *Write…* – allows to save the personal information and measurement data to the file in comma delimited, tab delimited text format or in rich text format;
   – *Import…* – allows importing personal and measurement data from the text file (see section 9).

2.3.2 *Analyser* page

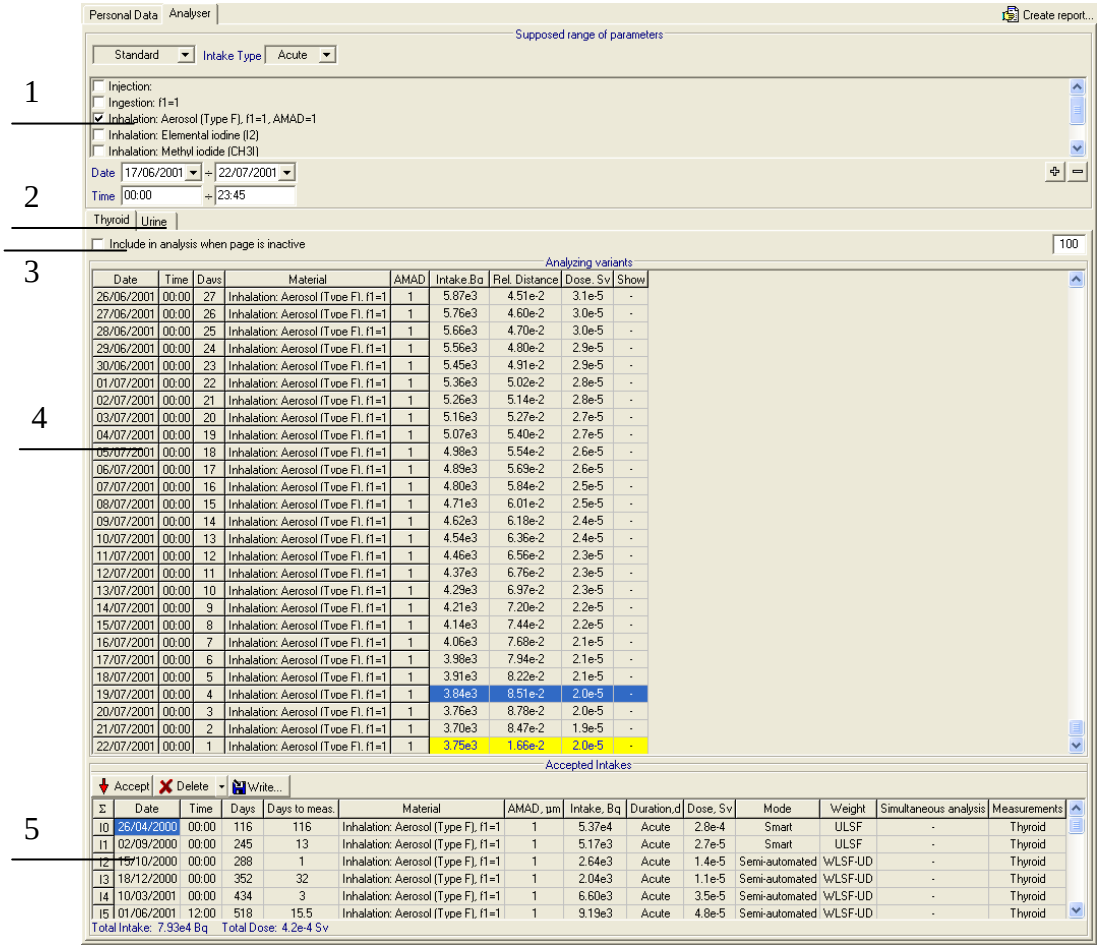


Figure 5. The *Analyser* page

The *Analyser* page contains the following elements (see Figure 5):

1. *Supposed range of parameters.* This section allows selection of intake variants and supposed ranges of their parameters for the current step of analysis. Elements of this section are (see Figure 6):
   1.1. *Standard/Mixture* combo box allows switching the list of intakes between standard set of intakes and set of mixed intakes. For information about creation of mixed intakes see section 4.
   1.2. *Intake path* checklist box shows available set of standard or mixed intakes. It is designed for selection of the subset of

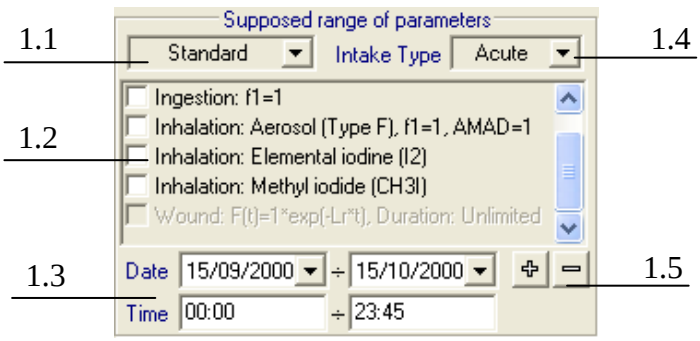


Figure 6. The *Supposed range of parameters* section

intakes for analysis with appropriate check boxes. For standard inhalation intakes of the aerosol the range of available AMADs can be selected for analysis. The available range is 0.001÷20 μm. To select the range of AMADs click on the name of the corresponding intake with the right mouse button. The popup window will appear which allows entering the range of AMADs. Selected range of AMADs will be displayed in the name of the intake.

Wound intakes (or mixed intakes, which include wound intake) are available in this list box in the *Accident mode* only. For standard wound intake a wound retention function and duration of retention (e.g. if contaminated tissues in wound were rejected) can be defined. To define these parameters click on the name of the corresponding intake with the right mouse button. The popup dialog window will appear which is designed for defining the parameters of wound intake (see Figure 7). The *Wound intake* dialog allows to set up to 5 exponents to define the wound retention function of the following view: $F(t) = \sum_{i=1}^{5} C_i \, e^{-(\lambda_i + \lambda_r)t}$, where λ_r is a radioactive decay constant of the analysed radionuclide. The *Wound intake* dialog also allows setting the duration of retention. If the unlimited duration is selected, then defined in the *Preference* window (see section 8) value of duration substitutes into the description of the wound intake. Specified retention function and duration of retention will be displayed in the name of the intake.

Figure 7. The *Wound intake* dialog

To add/edit/delete mixed intakes click with the right mouse button on the list of mixed intakes. This action calls the dialog for managing the complex mixed intakes (see section 4). The list of mixed intakes is displayed when the *Mixture* item is selected in the check box above (see callout 1.1).

1.3. *Date* and *Time* edit boxes. They set the supposed range of dates and/or time when the intake (currently analysed) may occur. The format of date is dd/MM/yyyy (note that the year must be given by four digits – i.e. 22/10/2001), the format of time is hh:mm. *Time* edit box is available if the *Use Time* mode is checked in the *Preference* window (see section 8).

1.4. *Intake type* (*acute* or *chronic*).
When the *Intake type* is chronic the supposed range of dates (see above) defines a start and a finish of the chronic intake. To change chronic intake parameters, click on the *Intake type* combo box with the right mouse button. This action opens a small dialog window (see Figure 8). In this window a user can set a necessary chronic intake type (constant or exponential) and λ value (for exponential chronic only).

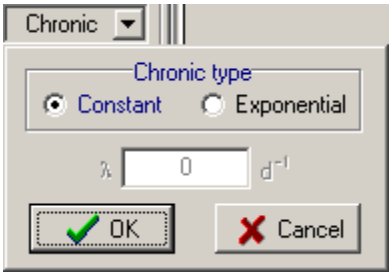


Figure 8. The *Chronic type* popup window

1.5. *Plus/Minus* buttons allow to show or to hide all plots of the analyzing variants on the *Graph* panel (see the description of the callout 4 below).

2. *Tabs*, designed to select the measurement series (i.e. Whole body measurements, urine measurements, etc.) and radionuclide.

3. *Include in analysis when page is inactive* – check box, which allows selection of several measurement sets for simultaneous analysis. Check this box for each measurement set (represented by the *Tabs* (callout 2)), which have to be involved in the analysis. Graphs for each checked measurement series will be displayed simultaneously on the *Graph* panel. If the *Minimal distance* mode of the simultaneous analysis is selected in the *Preference* window

(see section 8) the weight for each checked measurement series may be set in the edit box to the right of the *Include in analysis when page is inactive* check box.

4. *Table of analyzing variants*. It contains the full set of combinations of intake parameters from the *Supposed range of parameters* group as well as results for the current step of analysis. Each row of the table contains the description of the intake with unique combination of parameters and corresponding results:
   - *Date* – date of intake from the *Supposed range of parameters* group;
   - *Time* – time of intake (available only if the *Use Time* mode is checked in the *Preference* window (see section 8));
   - *Days* – time in days between the calculated intake date and the date of the first measurement that is considered in that intake calculation;
   - *Material* – the description of the intake;
   - *AMAD* – AMAD value for the intake variant, which is described by the current row of the table;
   - *Intake* – value of reconstructed intake in activity units, selected in the *Preference* window (see section 8);
   - *Distance* – the average deviation of the approximation from the measurement data points. This column is invisible by default. To make it visible use the popup menu, which could be called by click of the right mouse button on the table. Value *Distance* is calculated as:

$$D = \frac{1}{j_2 - j_1}\sqrt{\sum_{k=j_1}^{j_2}\left(\sum_{i=1}^{n} I_i\, R_i(t_k - \tau_i) - M(t_k)\right)^2},$$

     where
     - k = index of the measurement of the radionuclide $M(t_k)$ at time t_k;
     - i = index of the time interval, on which a single response can fit the selected subset of measurement series;
     - n = current step number in the iterative analysis process;
     - τ_i = shift in the time of the i^{th} acute intake; the shift τ_n for the last term of the sum is a required time, when the currently reconstructed intake occurs;
     - $R_i(t)$ = response of the biokinetic model (response function) on a unit delta-impulse (radionuclide content in the body, organs or in bioassay probes after a unit acute intake at t=0 predicted by the model at time t), which was used during step i of the analysis;
     - I_i = reconstructed intake on the step;
     - j_1, j_2 = index of the extreme left and right points of data series $M(t_k)$ included into the current interval of approximation n;
   - *Rel. Distance* – the average relative deviation of the approximation from the measurement data points:

$$D^r = \frac{1}{j_2 - j_1}\sqrt{\sum_{k=j_1}^{j_2}\left(\sum_{i=1}^{n} I_i\, R_i(t_k - \tau_i) - M(t_k)\right)^2 W_k},$$

     where
     - k = index of the measurement of the radionuclide $M(t_k)$ at time t_k;
     - i = index of the time interval, on which a single response can fit the selected subset of measurement series;
     - n = current step number in the iterative analysis process;
     - τ_i = shift in the time of the i^{th} acute intake; the shift τ_n for the last term of the sum is a required time, when the currently reconstructed intake occurs;
     - $R_i(t)$ = response of the biokinetic model (response function) on a unit delta-impulse (radionuclide content in the body, organs or in bioassay probes after a unit acute

intake at t=0 predicted by the model at time t), which was used during step i of the analysis;

W_k = weighting factor for the measurement k, corresponding to the *Weighting method* selected in the *Preference window* (see section 8). If the *ULSF* weighting method is selected, W_k=1 and D^r=D;

I_i = reconstructed intake on the step i;

j_1, j_2 = index of the extreme left and right points of data series $M(t_k)$ included into the current interval of approximation n;

– *Dose* – the committed effective dose from the reconstructed intake, Sv. The double click on the dose value in the table calls the *Committed equivalent doses* window (see Figure 9) which displays corresponding committed equivalent doses to organs and tissues;

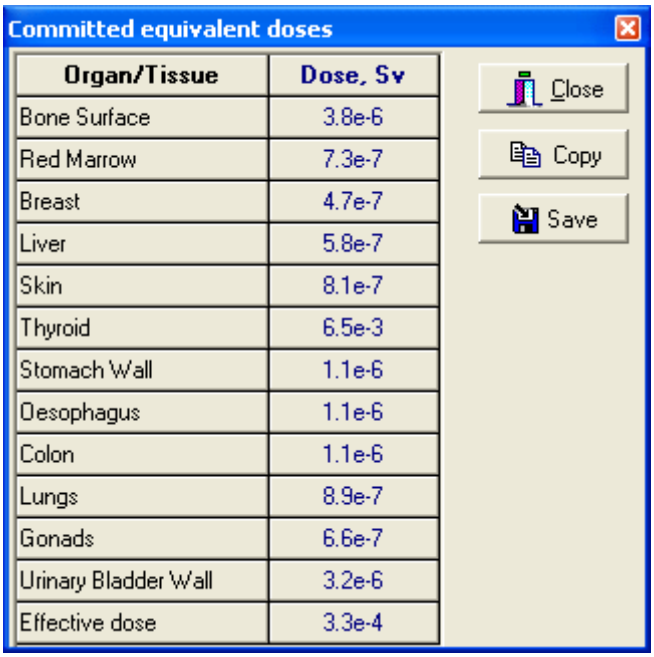


Figure 9 *Committed equivalent doses* dialog

– *Show* – reflects the state of the graph of the function $R(t) = \sum_{i=1}^{n} I_i \, R_i(t - \tau_i)$ on the *Graph* panel. Function $R(t)$ represents the linear combination of biokinetic responses to acute intakes reconstructed during n steps of the analysis, where n is a number of the current step. Signs "+"/"-" indicate that the plot of the function $R(t)$ is shown/hidden. The double click on the table row with the left mouse button visualises the plot. To show all plots press button. This action is not recommended because too many curves may be displayed. To hide all plots press button.

The "best result" row (the row with the minimal value in the *Rel. Distance* column) is marked with the yellow background colour. The focus in the table is automatically placed to that row. The combinations of parameters which cannot be analysed (usually due to the incorrect supposed intake date) are marked with the red background in the table. If several measurement sets are checked for the simultaneous analysis then the row "best result" of the simultaneous analysis is marked with the green background colour. The focus in the table is automatically placed to that row instead of the yellow row, which represents the "best result" of analysis of single measurement series. The "best result" of the simultaneous analysis is searched accordingly to the selected in the *Preference* window mode of the simultaneous analysis (*Closest intakes mode* or *Minimal distance mode* – see section 8). If the *Closest intakes mode* is selected the "best result" of the simultaneous analysis is searched as a minimal relative distance between intakes, reconstructed on the base of each checked measurement series (see formula (6) of the Annex B). If the *Minimal distance mode* is selected the "best result" of the simultaneous analysis is searched as minimal relative distance between measurements and approximation functions, constructed on the base of analysis of all checked measurement series (see formula (8) of the Annex B).

5. *Accepted intakes* group contains the *Intakes* table (table with final results accepted by the user) and buttons for managing the table content:
   – *Date* – the date, when reconstructed intake occurs;

- *Days* – the reconstructed time in days since the date of the first possible intake. The date of the first possible intake is pointed out in the *First intake is not earlier than* field of the *Personal information*;
- *Days to meas.* – time in days between the calculated intake date and the date of the first measurement that is considered in that intake calculation;
- *Material* – the description of the response function;
- *AMAD* – the reconstructed AMAD (μm);
- *Intake* – the reconstructed intake in activity units selected in the *Preference* window (see section 8);
- *Duration* – the duration of intake (days) (for chronic intakes only);
- *Dose* – the committed effective dose associated with the reconstructed intake (Sv). The double click on the dose value in the table calls the *Committed equivalent doses* window (see Figure 9) which displays corresponding committed equivalent doses to organs and tissues;
- *Mode* – the mode of analysis (see section 3) which was used in reconstruction of the intake;
- *Weight* – weighting method (see section 8 and Annex B) which was selected for analysis;
- *Simultaneous analysis* – the selected mode of "best fit" search in simultaneous analysis of several data sources;
- *Measurements* – list of data sources which were used in reconstruction of intake. If the *Minimal distance mode* of the simultaneous analysis is used, weighting factors for each data source are displayed.

At the bottom of the *Accepted intakes* group the total accepted intake and total dose are displayed. The double click on the dose value calls the *Committed equivalent doses* window (see Figure 9) which displays corresponding committed equivalent doses to organs and tissues.

The set of columns in the *Intakes* table can be chosen in the popup menu, which can be called with the right mouse button click on the *Intakes* table (see Figure 10). Each column, listed on the right side of the popup menu may be shown or hidden with the click on the corresponding checkbox. Also, the predetermined set of visible columns may be selected by selection *Maximum columns* item or *Minimum columns* item on the left side of the popup menu. The *Maximum columns* item shows all described columns of the table. The *Minimum columns* item hides all columns except *Date*, *Time*, *Intake* and *Dose* columns.

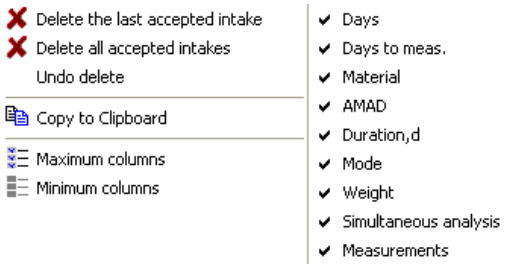


Figure 10 Popup menu of the *Intakes* table

The content of the *Intakes* table can be copied to the Clipboard by selection the *Copy to Clipboard* item. User can delete the last reconstructed intake or all intakes from the table by selection *Delete the last accepted intake* item or *Delete all accepted intakes* item. Also, the user can abolish one or several last delete actions by selection of the *Undo delete* item. The actions of *Delete* and *Undo delete* items are the same as for *Delete* button, described below.

The leftmost upper cell of the *Intakes* table is marked with Σ sign and is used like button. The user can open the *Annual doses* dialog by pressing this cell (see the Figure 11). This dialog provides saving of annual doses in a text file (with tabulation as separator) or copying theirs to clipboard. The saved text file can be opened by Microsoft Excel. A data copied to clipboard can be inserted in a Microsoft Excel document too. If the wound intake was used at any step of analysis the calculation of annual committed doses is not performed in the current IMIE version.

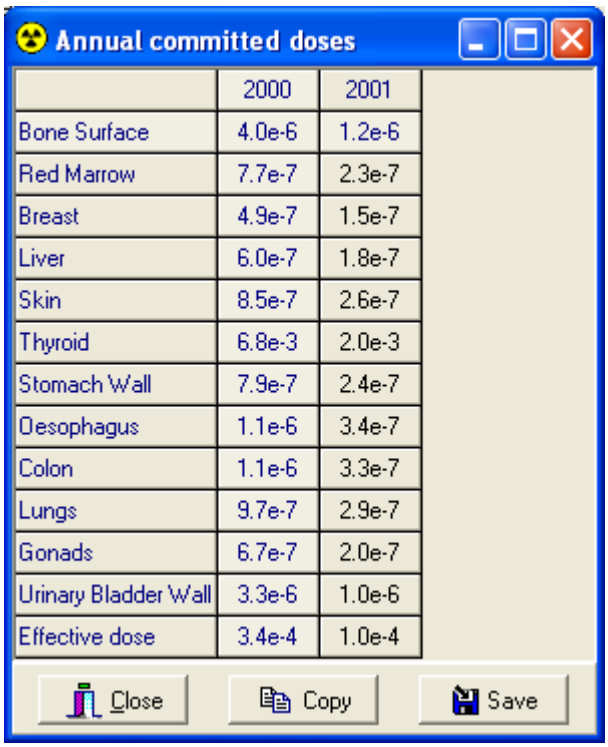


Figure 11. The *Annual committed* dialog

The *Accepted intakes* group also contains following buttons (see Figure 12):

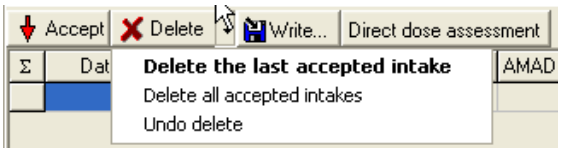


Figure 12. Buttons of the *Accepted intakes* group

- The *Accept* button adds the record about reconstructed intake selected in *Table of analyzing variants* to the *Intakes* table. This button is available only in the *Manual mode* or in the *Accident mode* of the *Retrospective* analysis or in the *Prospective* analysis. In the *Semi-Automated mode* or in the *Smart mode* the best result in *Table of analyzing variants* (record with the minimal value of *Rel. Distance*) is automatically added to the *Intakes* table.
- *Delete* button. By default this button deletes the last row in the *Intakes* table, corresponded to the last completed step of the analysis. The measurement points, which were analysed during that step, will be marked as unselected. The user can also clear all *Intakes* table with *Delete all accepted intakes* item of the dropdown menu of the *Delete* button (see Figure 12). If do so, all measurement points in the selected series will be marked as unselected. The user can abolish one or several last delete actions by selection of the *Undo delete* item. When selecting this menu item the last deleted row of the *Intakes* table is restored and measurement points, which were analysed during restored step, will be marked as processed. The *Undo delete* item is available after delete actions while any new step of analysis is not performed.
- *Write* button saves the set of reconstructed intakes as a text file (with tabulation as separator). The saved text file can be opened by Microsoft Excel.
- *Direct dose assessment* button is available for tritium and whole body measurements of caesium only. This button calls the *Direct method of dose calculation* window (Figure 13). The *Direct method of dose calculation* estimates the integral decays in the body by integration of the available measurements and the corresponding effective dose by multiplying the integral decays in the body by the corresponding SEE (specific effective energy) value.

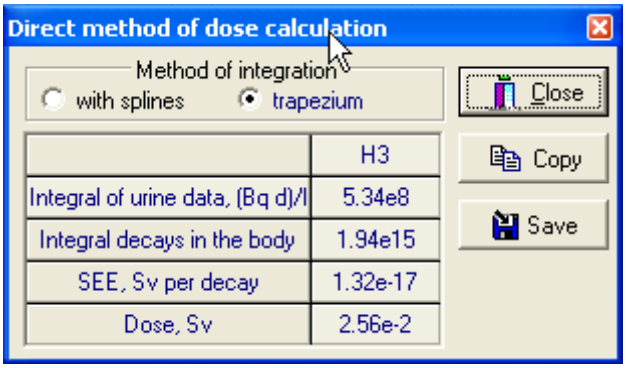


Figure 13 *Direct method of dose calculation* window

Such estimation will be correct only if there are sufficient available measurements.

2.4 *Graph* panel

The *Graph* panel is designed for a graphical presentation of the one or several selected measurement series and resulting approximation curves. Second important purpose of the *Graph* panel is a graphical selection of the measurement points on the each step of the analysis. The *Graph* panel contains following elements (see Figure 14):

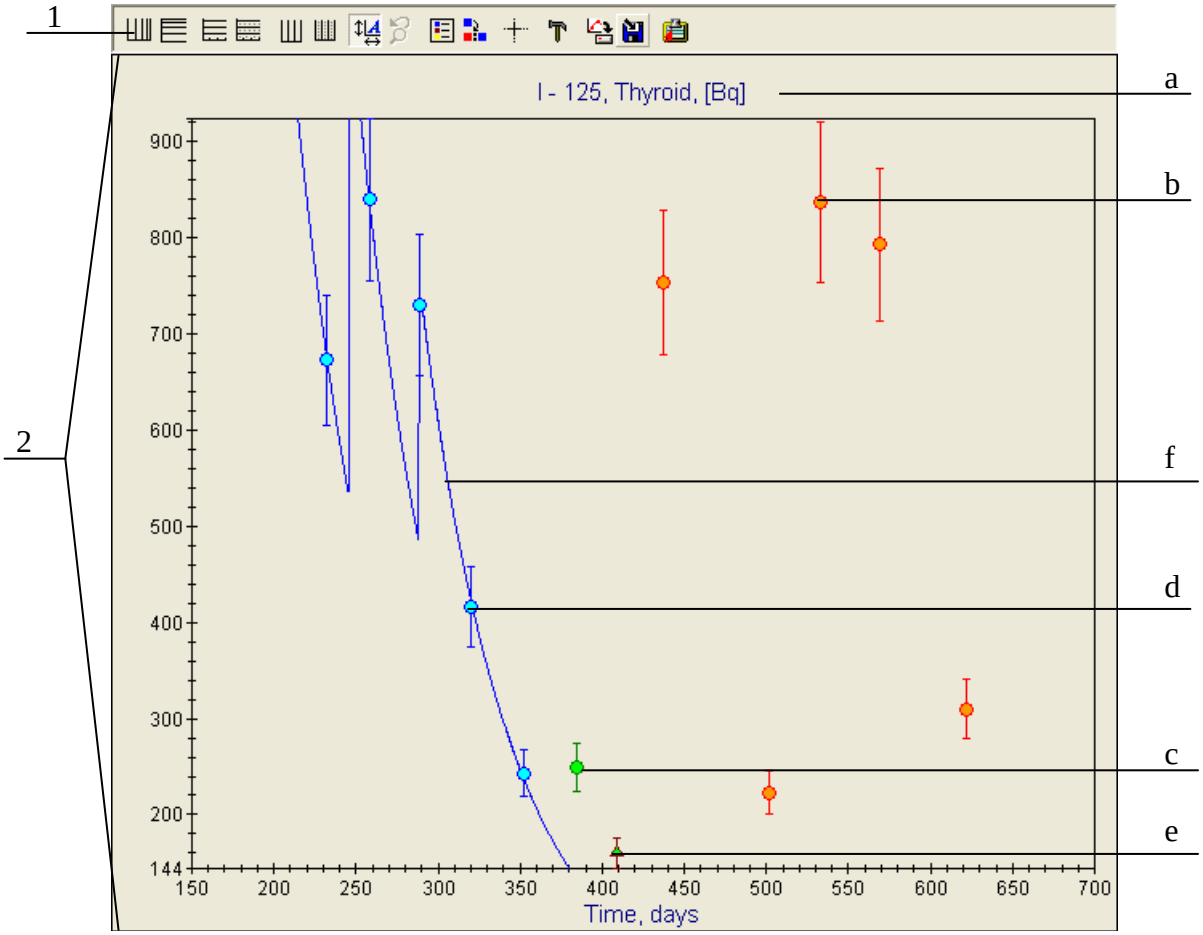


Figure 14 *Graph panel* of the *Main* window

1. *Toolbar* – the set of buttons for managing the plots. If the *Toolbar* is hidden use the *Show Toolbar* command of the popup menu, which can be called with the right mouse click on the *Graph* panel.
2. *Plot area* – the area where all measurement and approximation curves are drawn. The following elements are usually displayed in the plot area:
   a) Graph title; contains the name of selected radionuclide and subject of measurement;
   b) Measurement points, which have not been selected (coloured in red). These measurement points neither have been processed on previous steps of the analysis nor have been selected for the analysis on current step (may be analysed on the next steps);
   c) Measurement points selected for the current step of the analysis (coloured in green);
   d) The measurement points already processed on previous steps of the analysis (coloured in blue);
   e) The measurement point lies under MDA (triangle shape and brown frame);

f) The approximation curve $R(t) = \sum_{i=1}^{n} I_i \, R_i(t - \tau_i)$. It represents the linear combination of biokinetic responses, corresponded to the reconstructed intakes. The *n* value is the number of rows in the *Intakes* table; the I_i values are intake values from the *Intakes* table (see the description of the *Accepted intakes* group of the *Analyser* page). This curve is displayed automatically during fill out of the *Intakes* table.

The X-axis of the plot area shows time in days since first possible intake, which is pointed out in the *First intake is not earlier than* field of the *Personal Data* page. The Y-axis of the plot area shows the units of measurements (Bq or Bq/day).

The X-axis of the *Plot area* in dependence of the *Preference* window setting (see section 8) shows time in days since first possible intake, which is pointed out in the *First intake is not earlier than* field of the *Personal Data* page, or absolute dates. The Y-axis of the *Plot area* shows the units of measurements (by default – Bq or Bq/day). The output units may be changed on the *Input/Output* page of the *Preference* window (see section 8).

The *Toolbar* of the *Graph* panel contains the following buttons (see Figure 15):

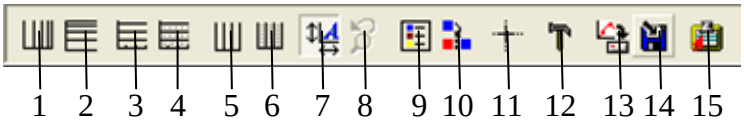


Figure 15. The *Toolbar* of the *Graph* panel

1. Set the logarithmic/linear scaling of the X-axis;
2. Set the logarithmic/ linear scaling of the Y-axis;
3. Show/hide the major horizontal gridlines;
4. Show/hide the major and minor horizontal gridlines;
5. Show/hide the major vertical gridlines;
6. Show/hide the major and minor vertical gridlines;
7. Set the auto-scaling mode. In this mode axes are scaling so that all measurement point become visible;
8. Undo the zoom operation. To enlarge the region ("zooming") of the *Plot area* select this region with the mouse holding the right mouse button;
9. Show/hide the legend;
10. Switch the long/short legend format;
11. Turn on/off the "sight" mode. In this mode user can scan any position in the plot area by clicking the left mouse button on it. The (x, y) coordinates of the selected position will be displayed at the bottom of the *Graph* panel;
12. Call the *Chart options* dialog of the *Graph* panel;
13. Call the *Save chart to a file* dialog. Plot can be saved in the format of Windows Metafile(*.wmf), Windows Enhanced Metafile (*.emf) or Windows Bitmap (*.bmp);
14. Call *Save data to a file* dialog. It is designed for saving of all underlying data of the graph in a text file (with tabulation as separator). The saved text file can be opened by Microsoft Excel (this text file contains some additional information in a header for internal purpose that may be ignored);
15. Copy the plot to the clipboard in the format of Windows Metafile, Windows Enhanced Metafile or Windows Bitmap. A chart saved to file or copied to clipboard can be inserted in any document (for example, Microsoft Word document).

When the user points to the data point with the mouse, the hint with (x, y) coordinates of the selected data point is displayed.

To enlarge the region of the plot area, select this region with the mouse, holding the right mouse button.

To select (unselect) measurement points for the next step of the analysis select the region which contains desired points. Selecting of such region can be performed with the mouse (press

the left mouse button at the beginning of the region and move the mouse, holding the button, to the end of the region). The selected region will be painted in darker colours during selection. After the selection all measurement points within the region (except of processed points) become selected (unselected) and change their colour to green (red). This action is enabled only when the "sight" mode is off.

User can design the view of the plot area with the mouse. Axes can be moved with the mouse. Legend and title can be moved with the mouse while *Ctrl* key is pressed.

2.5 *Status* bar

The *Status* bar displays the current position in the personal database, the current modes and the progress of the analysis. Modes of analysis can be switched with the left mouse button double click on the corresponded fields of the status bar.

3 MODES OF THE ANALYSIS

3.1 *Retrospective mode*

The *Retrospective mode* of analysis is set on by default in the IMIE program. It can be switched to the *Prospective mode* by pressing the button 

(see subsection 3.2).

Five *Retrospective modes* of the analysis are available in the program:

- *Manual mode*;
- *Semi-Automated mode*;
- *ICRP78 mode*;
- *Smart mode*;
- *Accident mode*.

The *ICRP78 mode* is based on the classical interpretation scheme for individual monitoring, which has been recommended by the ICRP Publication 54 and by the ICRP Publication 78. The detailed description of the classical ICRP scheme of intake reconstruction is given in the Annex A.

Manual, *Semi-Automated*, *Smart* and *Accident mode*s are based on the same new method of intake reconstruction, described in the Annex B. The only difference between these modes is the level of automation. The *Manual* and *Accident mode*s of analysis have low level of automation. The *Semi-Automated mode* has the higher level of automation but the user has lower influence on the analysis process. The user can switch between these three modes on any step of the analysis. The *Smart mode* is a full automatic mode of analysis.

The simultaneous analysis of several different measurement sets is available in *Manual*, *Accident* and *Semi-Automated modes*.

3.1.1 Interactive *Semi-Automated mode*

Semi-Automated mode implements an iteration process of the data interpretation. For data point's approximation the linear combination of biokinetic responses is built in the course of a multi-step optimisation process. The *Semi-Automated mode* of data fitting helps the user to achieve the most reliable results. A subset of the observed series of measurements is used on each step. Detailed description of this method of intake reconstruction is given in the Annex B.

All figures and examples in this section will be given for the case of inhalation of the particulate aerosol. Figures and examples are given for two cases of *Semi-Automated mode* of analysis usage:

1. Analysis of one measurement set (figures marked with letter a),
2. Simultaneous analysis of two measurement sets with selected *Minimal distance mode* of the simultaneous analysis, weight for faecal measurements is 10%, for thyroid measurements – 100% (figures marked with letter b).

To turn on this mode select the *Semi-Automated* button on the *Toolbar*. Before a first step of the analysis user have to (see Figures 16a):

1. select one or more measurement sets with the tabs and check boxes (see callout 1 on the Figures 16a, 16b). All selected measurement sets are displayed in the *Graph* panel,
2. select the supposed intake variants (see callout 2 on the Figures 16a),
3. clear all previously reconstructed intakes with the *Delete all accepted intakes* item of the dropdown menu of  button (see callout 3 on the Figure 16a).

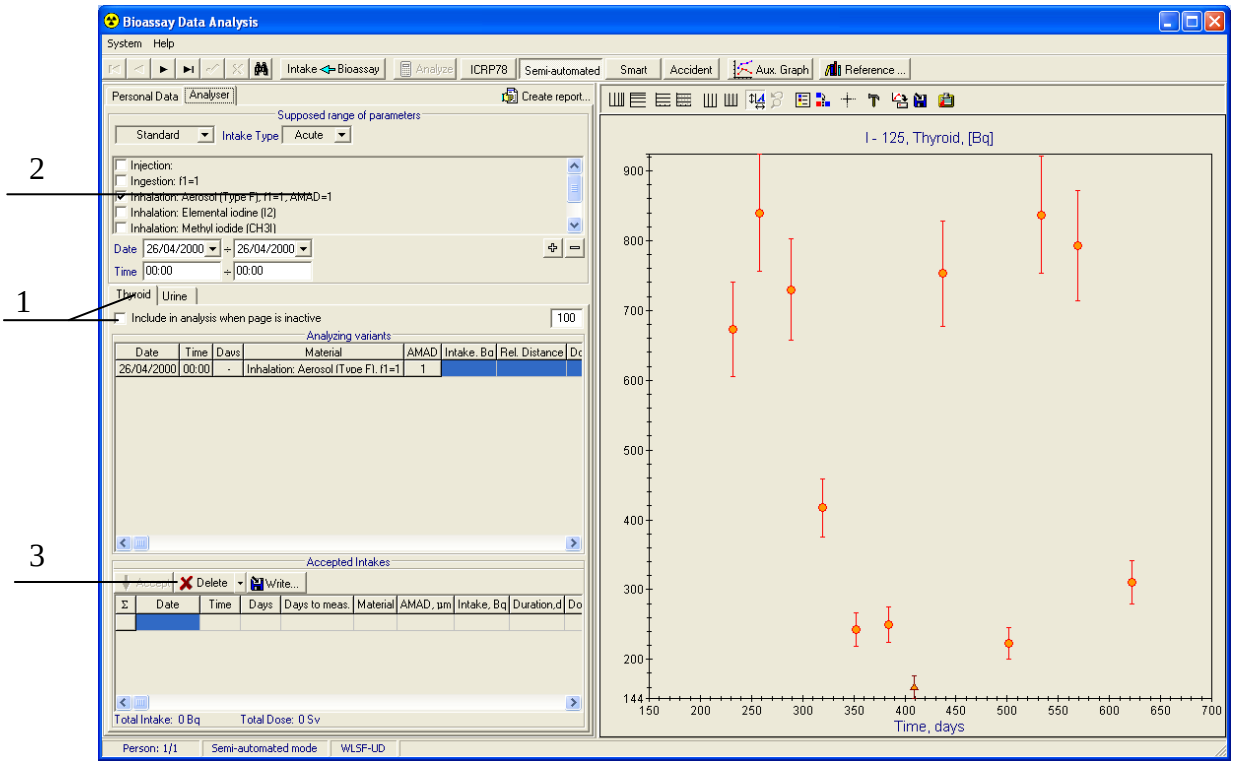


Figure 16a. Initialisation of the *Semi-Automated mode*
(analysis of one measurement set)

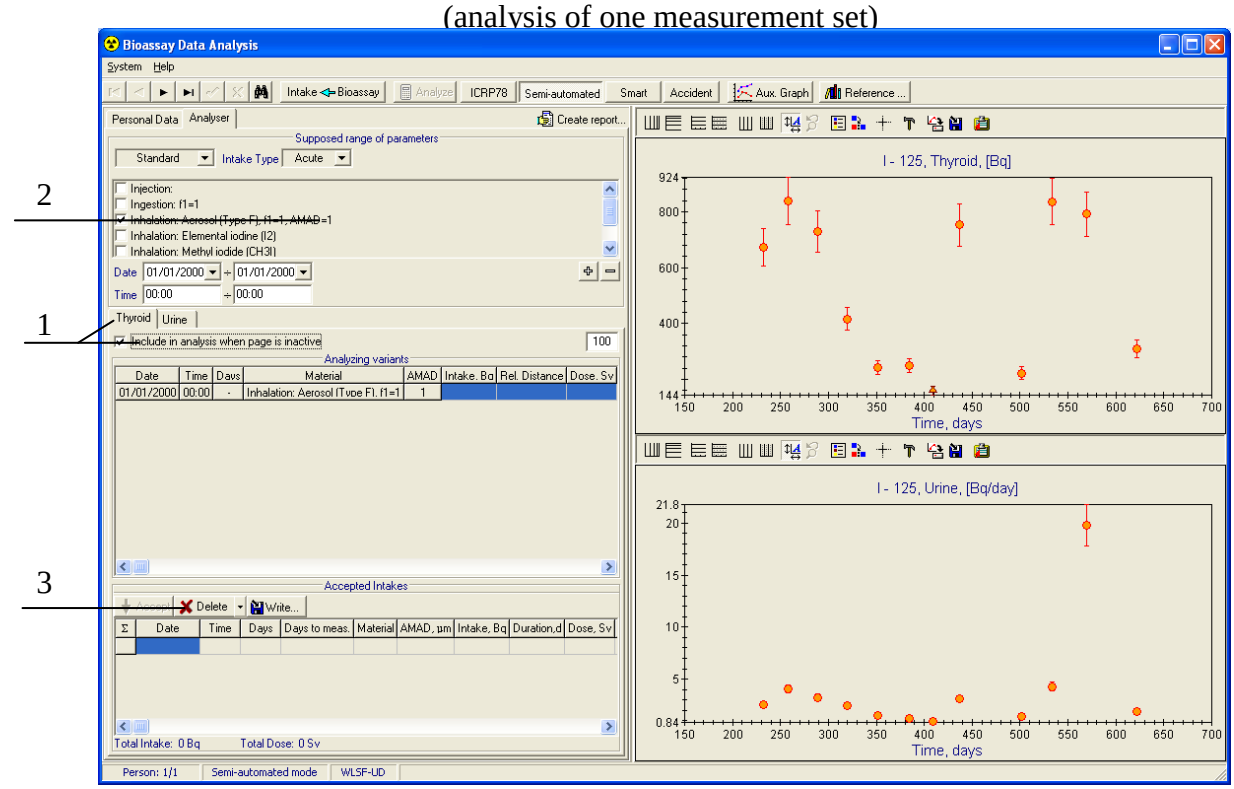


Figure 16b. Initialisation of the *Semi-Automated mode*
(simultaneous analysis of two measurement sets – *Minimal distance mode*)

From that moment the program is ready to start the first iteration step of the consecutive automatic analysis. To perform the data analysis:

User action	Program response
1. Select the first time interval of the analysis, on which biokinetic response to the acute intake can fit the selected subset of the measurement series. One or several data points can be included into selected time interval (see Figures 17a, 17b). 1.2 Move mouse to the start of the time interval on the graph; 1.3 Press the left mouse button; 1.4 Move the mouse with the pressed left button to the end of the time interval; 1.5 Release the left mouse button. 2. If the calculated results on the current step are not satisfactory (for example due to incorrect selection time interval) the undo process is available: 2.2 Delete the last calculated intake with  button of *Accepted intakes* group; 2.3 Reselect measurements for the current step. 3. Repeat step 1 consecutively for next data points (see Figures 19a, 19b, 21a, 21b). 4. The analysis process finishes when all measurement values are analysed (see Figures 23a, 23b).	Selected measurement points change colour from red to green. The program automatically (see Figures 18a, 18b, 20a, 20b, 22a, 22b): a) Generates the supposed range for the *Intake date* (see callout (a) on the Figures 18a, 18b, 20a, 20b, 22a, 22b); b) Calculates the intake for all possible combinations of date, AMAD and Types of Materials (see callout (b) on the Figures 18a, 18b, 20a, 20b, 22a, 22b). Processed measurement points change colour from green to blue; c) Chooses a "best fit" result. Puts the corresponding intake into *Intakes* table (see callout (c) on the Figures 18a, 18b, 20a, 20b, 22a, 22b).

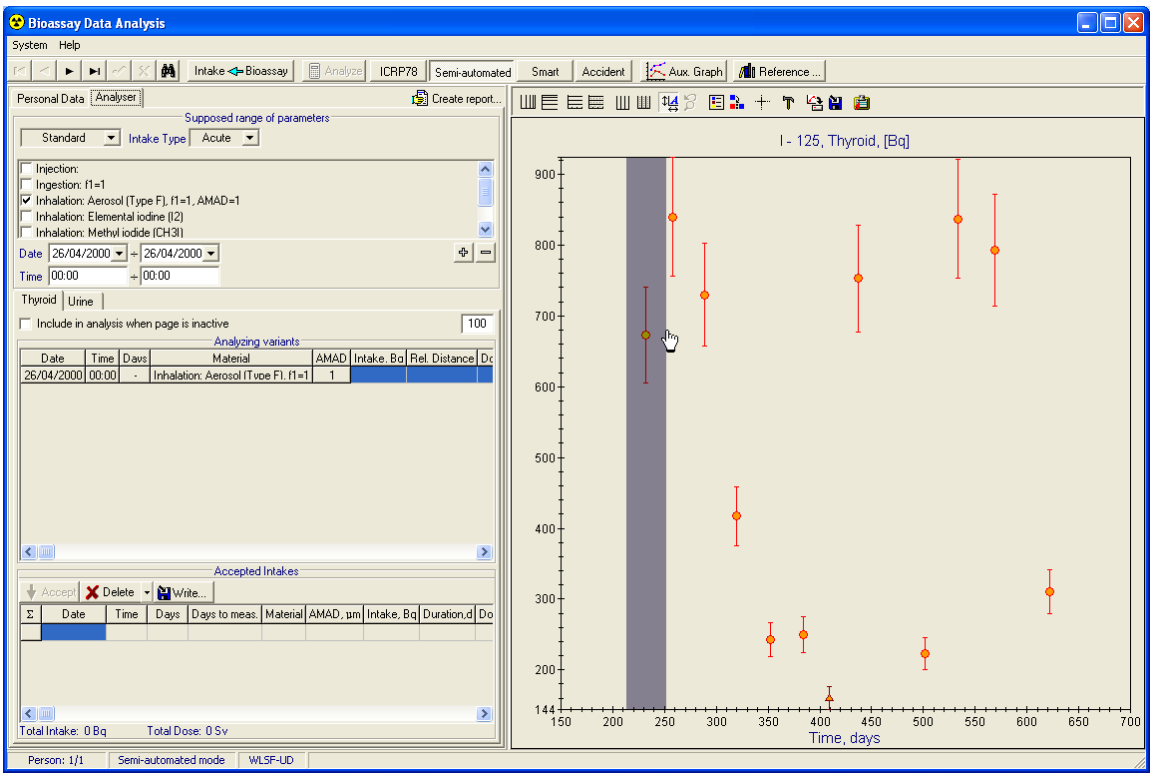


Figure 17a *Semi-Automated mode* (Iteration step 1)
(analysis of one measurement set)

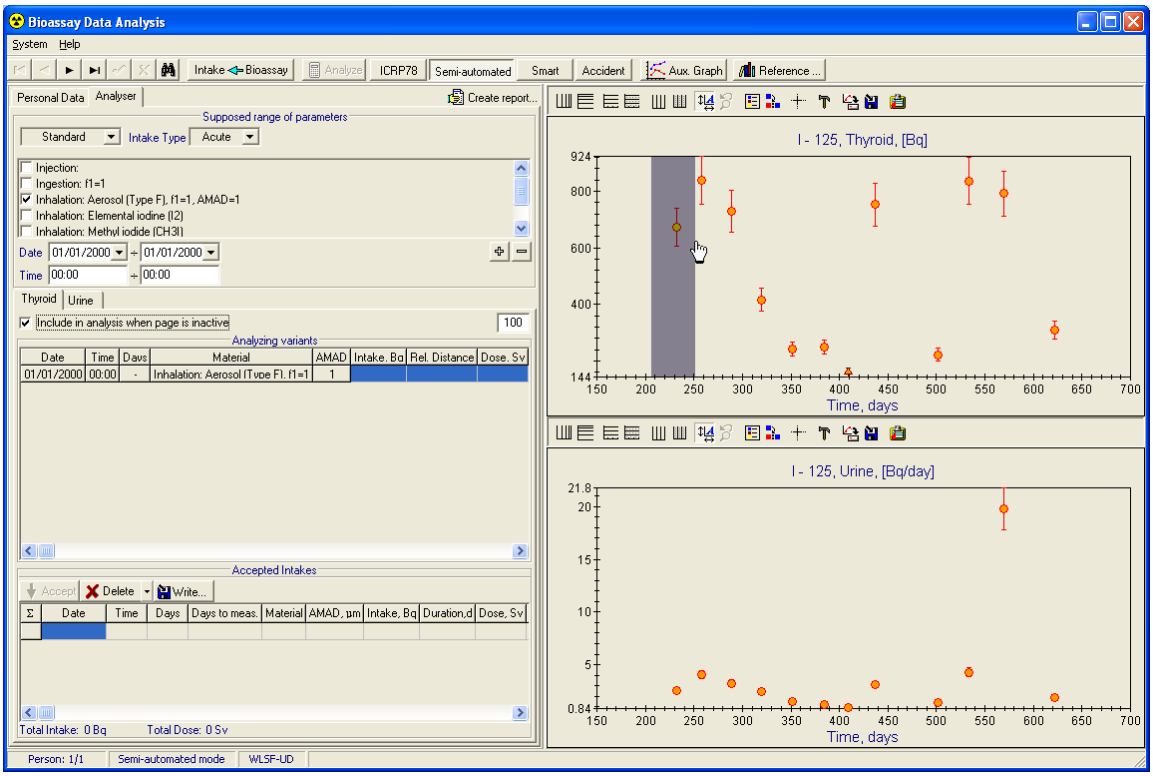


Figure 17b *Semi-Automated mode* (Iteration step 1)
(simultaneous analysis of two measurement sets – *Minimal distance mode*)

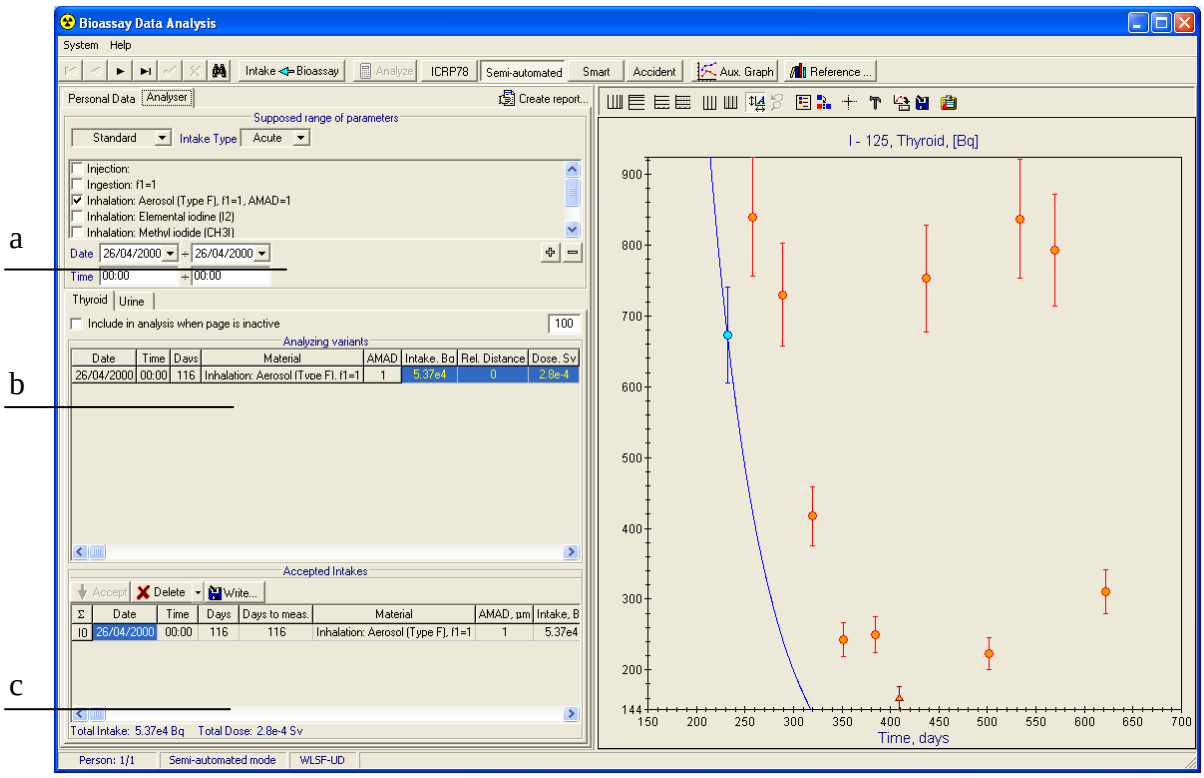


Figure 18a *Semi-Automated mode* (Results of the iteration step 1)
(analysis of one measurement set)

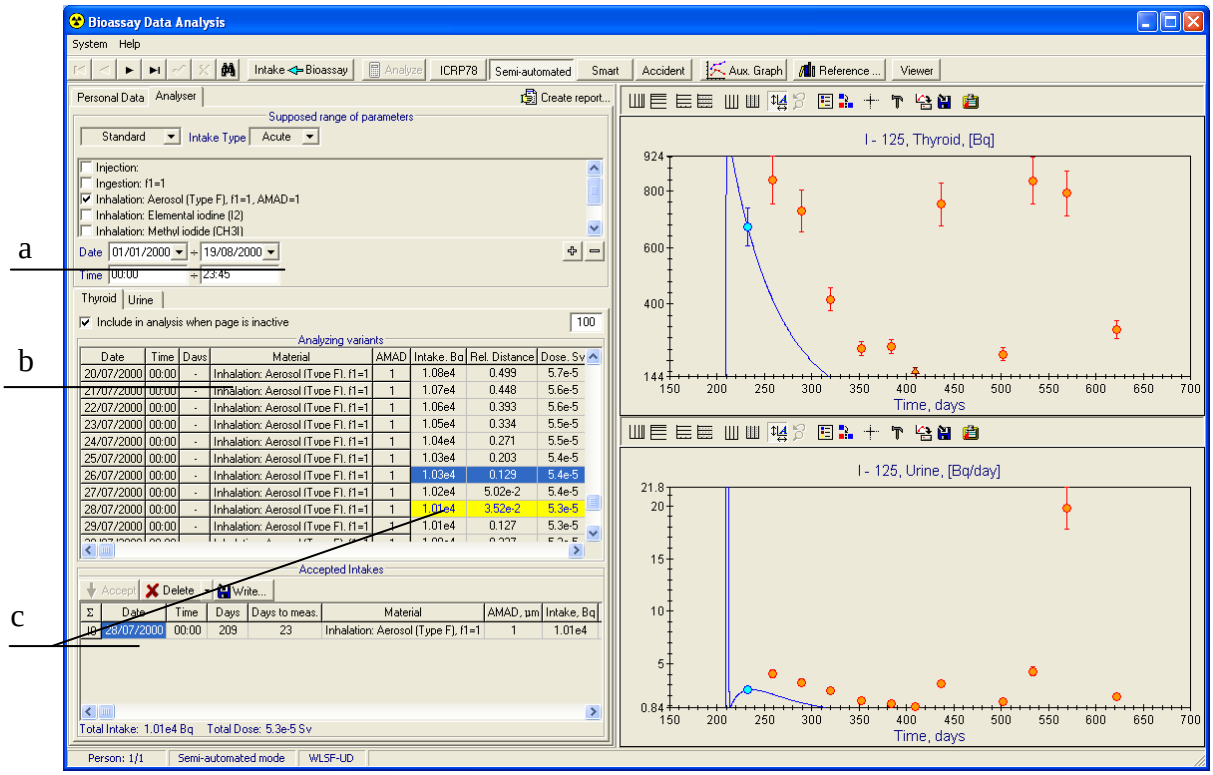


Figure 18b *Semi-Automated mode* (Results of the iteration step 1)
(simultaneous analysis of two measurement sets – *Minimal distance mode*)

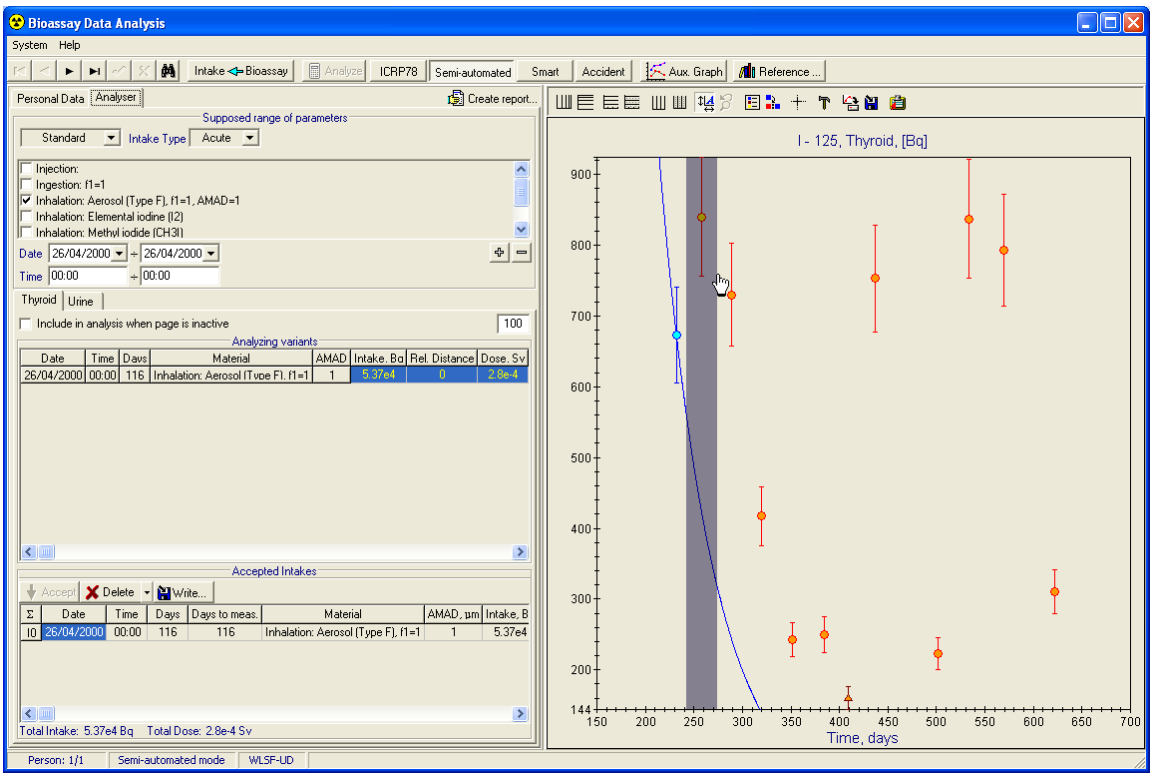


Figure 19a *Semi-Automated mode* (Iteration step 2)
(analysis of one measurement set)

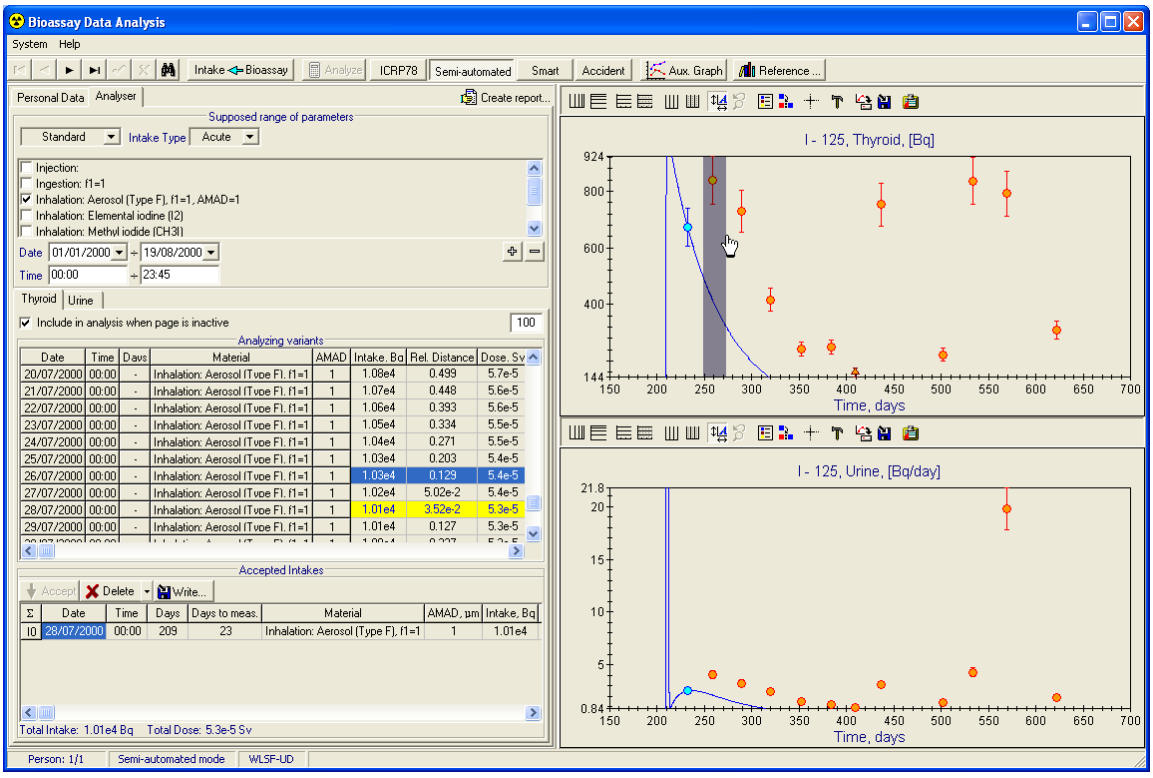


Figure 19b *Semi-Automated mode* (Iteration step 2)
(simultaneous analysis of two measurement sets – *Minimal distance mode*)

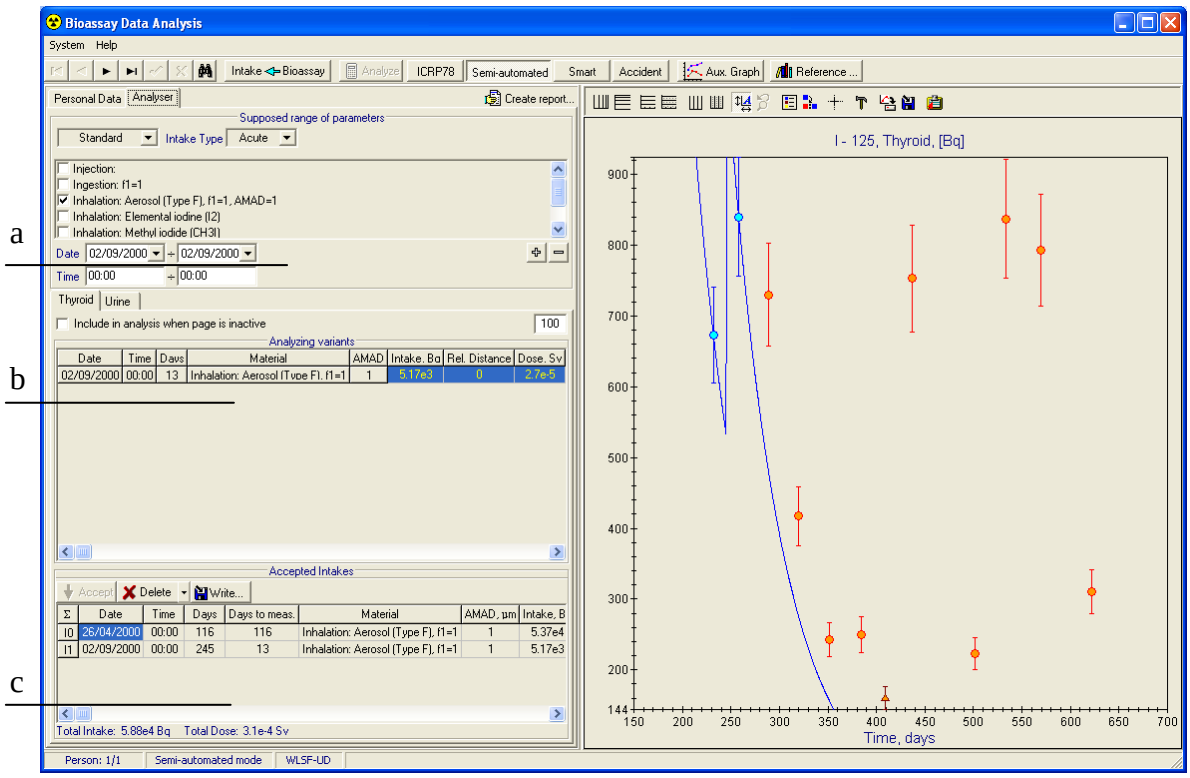


Figure 20a *Semi-Automated mode* (Results of the iteration step 2)
(analysis of one measurement set)

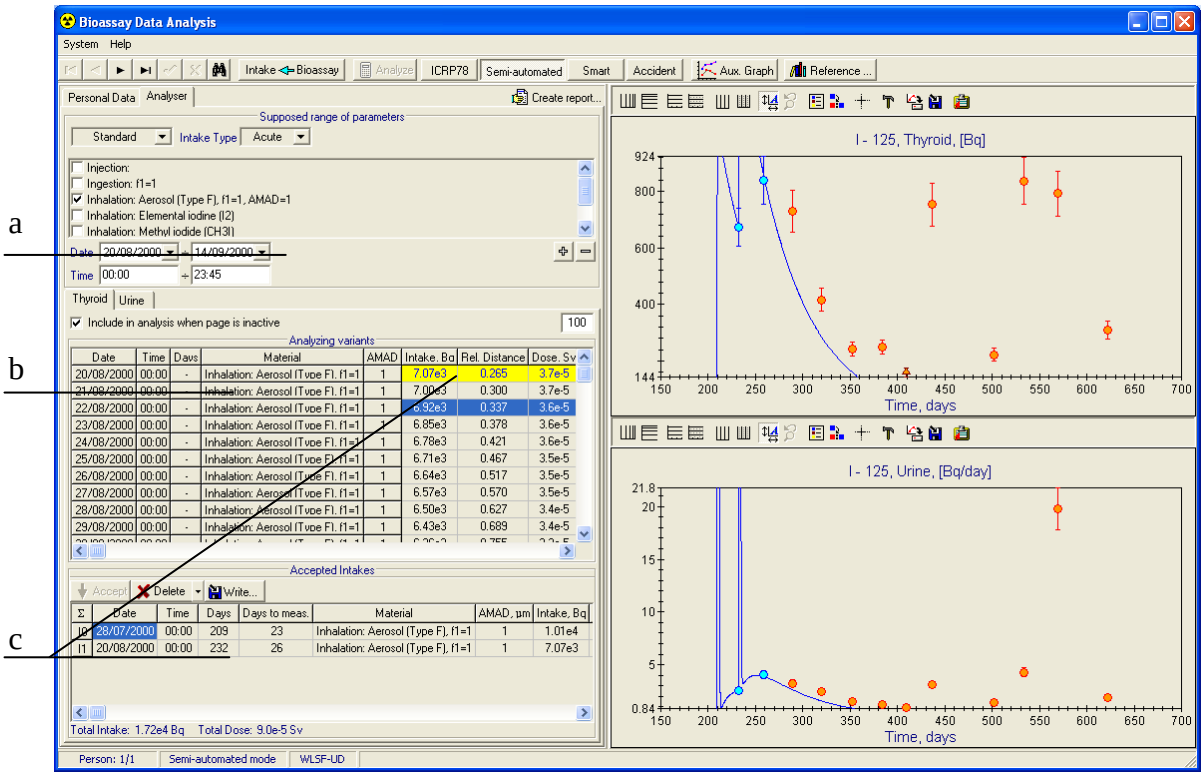


Figure 20b *Semi-Automated mode* (Results of the iteration step 2)
(simultaneous analysis of two measurement sets – *Minimal distance mode*)

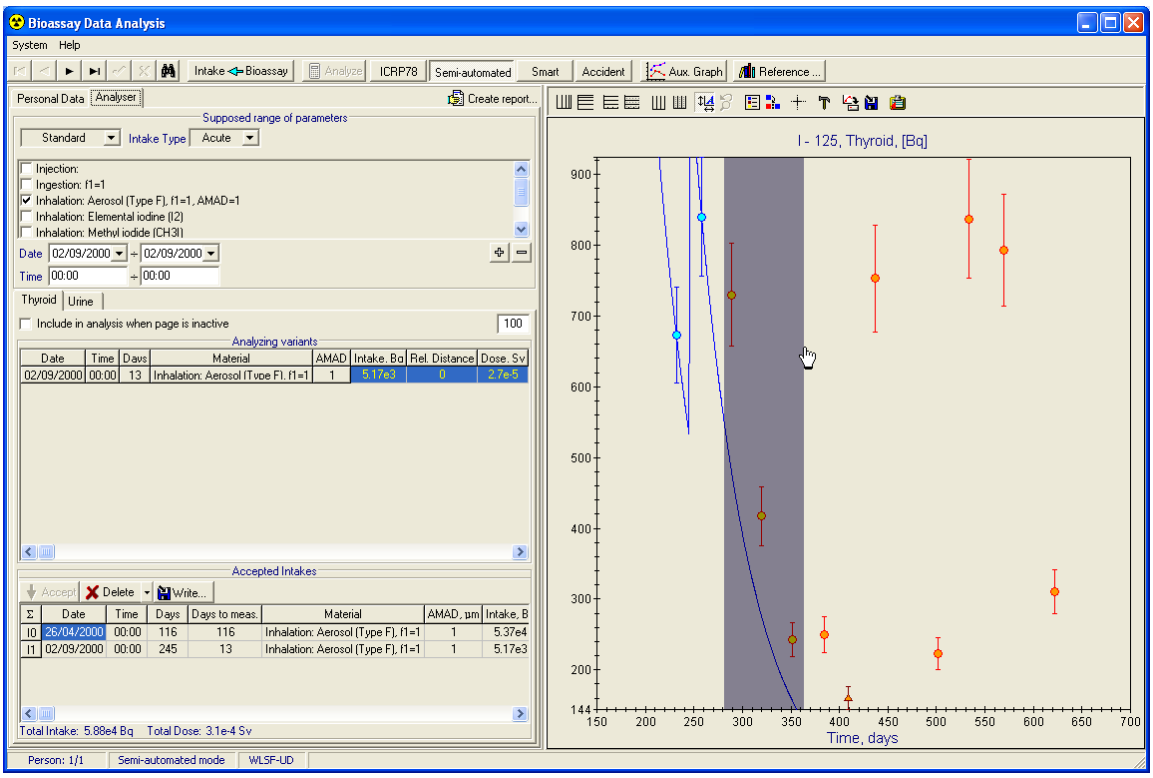


Figure 21a *Semi-Automated mode* (Iteration step 3)
(analysis of one measurement set)

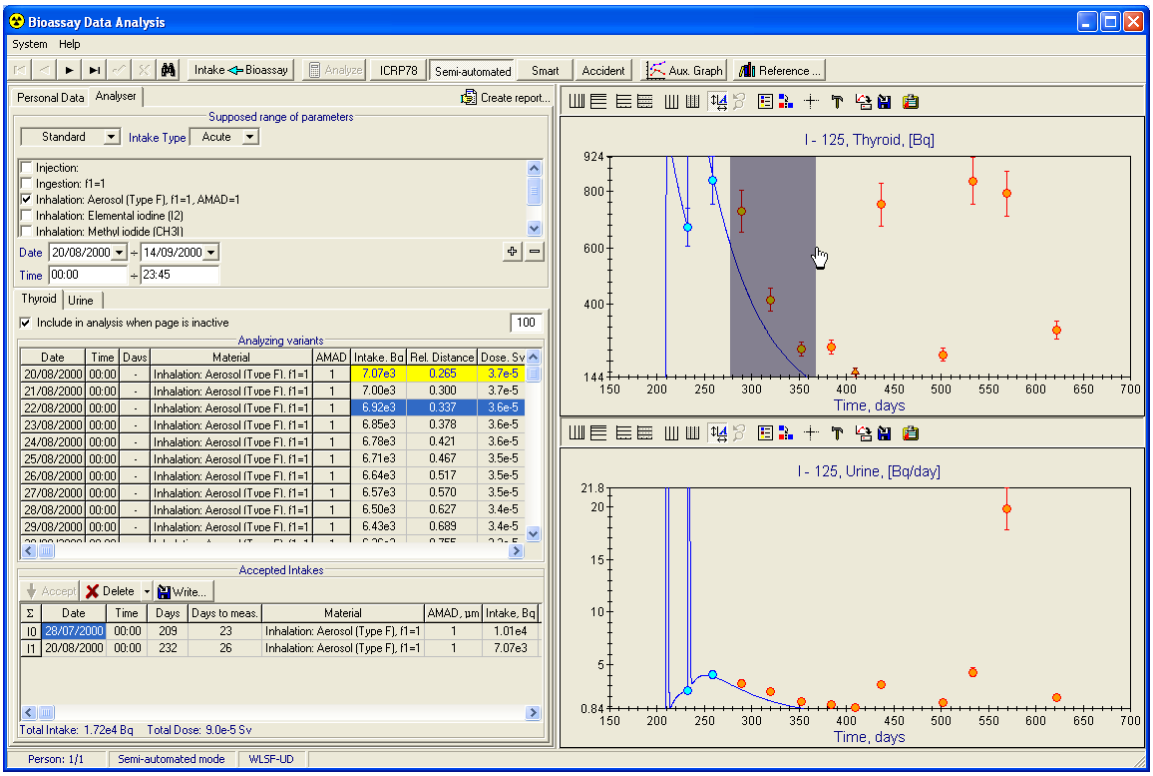


Figure 21b *Semi-Automated mode* (Iteration step 3)
(simultaneous analysis of two measurement sets – *Minimal distance mode*)

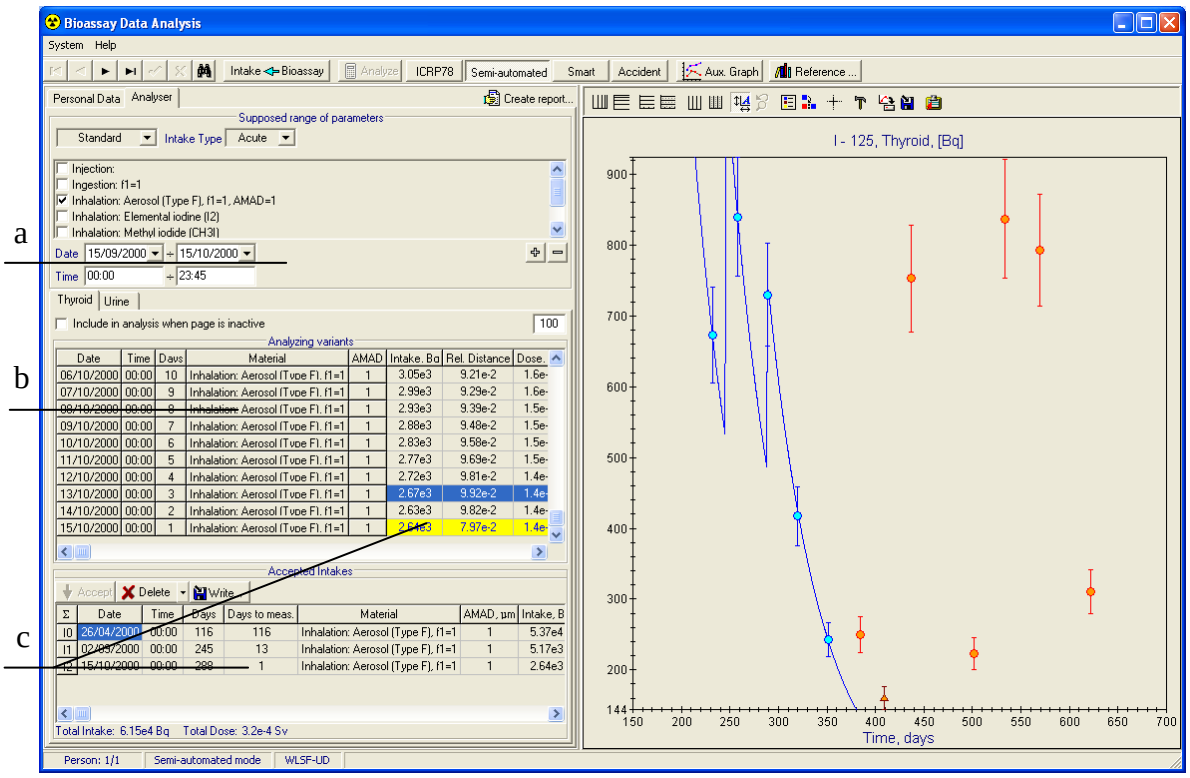


Figure 22a *Semi-Automated mode* (Results of the iteration step 3)
(analysis of one measurement set)

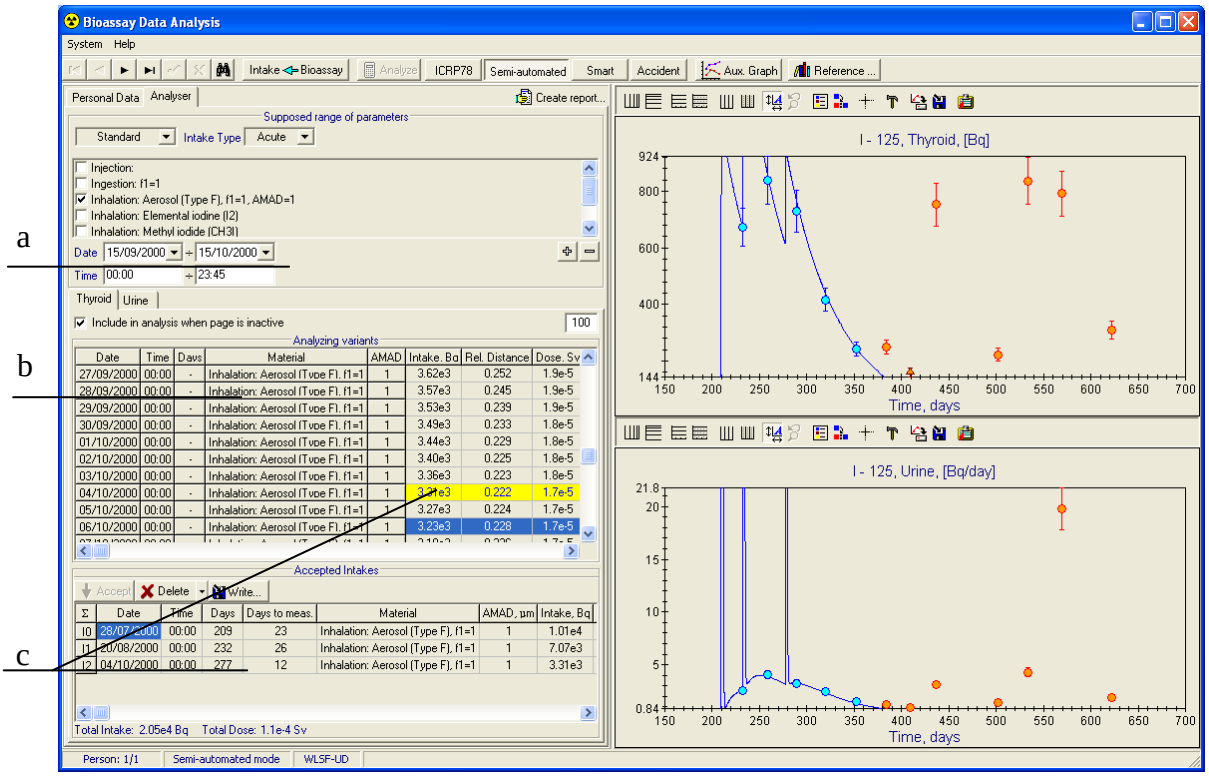


Figure 22b *Semi-Automated mode* (Results of the iteration step 3)
(simultaneous analysis of two measurement sets – *Minimal distance mode*)

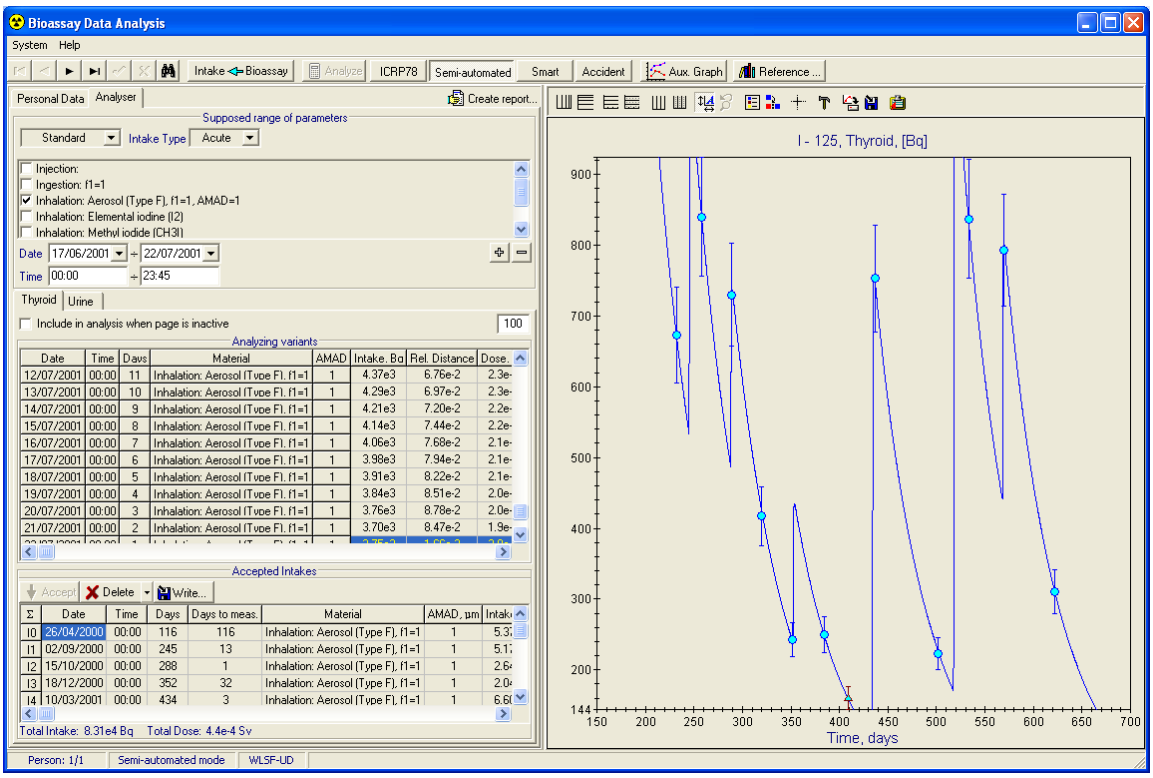


Figure 23a *Semi-Automated mode* (Final results)
(analysis of one measurement set)

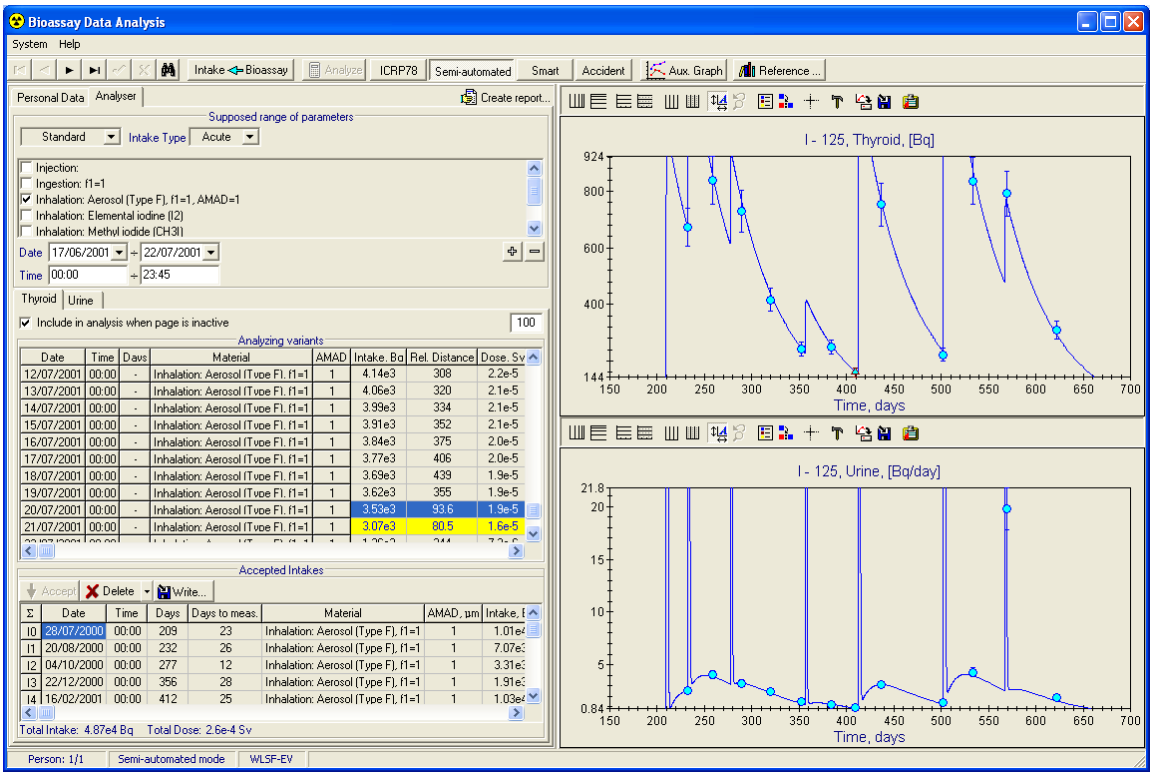


Figure 23b *Semi-Automated mode* (Final results)
(simultaneous analysis of two measurement sets – *Minimal distance mode*)

3.1.2 *Manual mode*

To turn on the *Manual mode* deselect the *ICRP78*, *Semi-automated*, *Accident* and *Smart* buttons on the *Toolbar* or select this mode in the *Preference* dialog (*System* menu).

The *Manual mode* implements the iteration process, which is similar to the *Semi-Automated mode*. It has the following peculiarities (see Figure 24):

1. After a selection of the time interval the analysis does not start automatically. At that moment user can check the supposed range of the *Intake date* and correct it. To start press the *Analyse* button on the *Toolbar* (see callout 1 on the Figure 24) (features that accessible by dropdown menu described in the subsection 3.1.5).
2. The "best fit" result is not automatically included into *Intakes* table. All calculated intakes are displayed in the *Table of analyzing variants*. The best-fit approximation is displayed as blue text on the yellow background (see callout 2 on the Figure 24). User can reselect the best-fit line.
3. To add the selected intake to the *Intakes* table press Accept button (see callout 3 on the Figure 24).

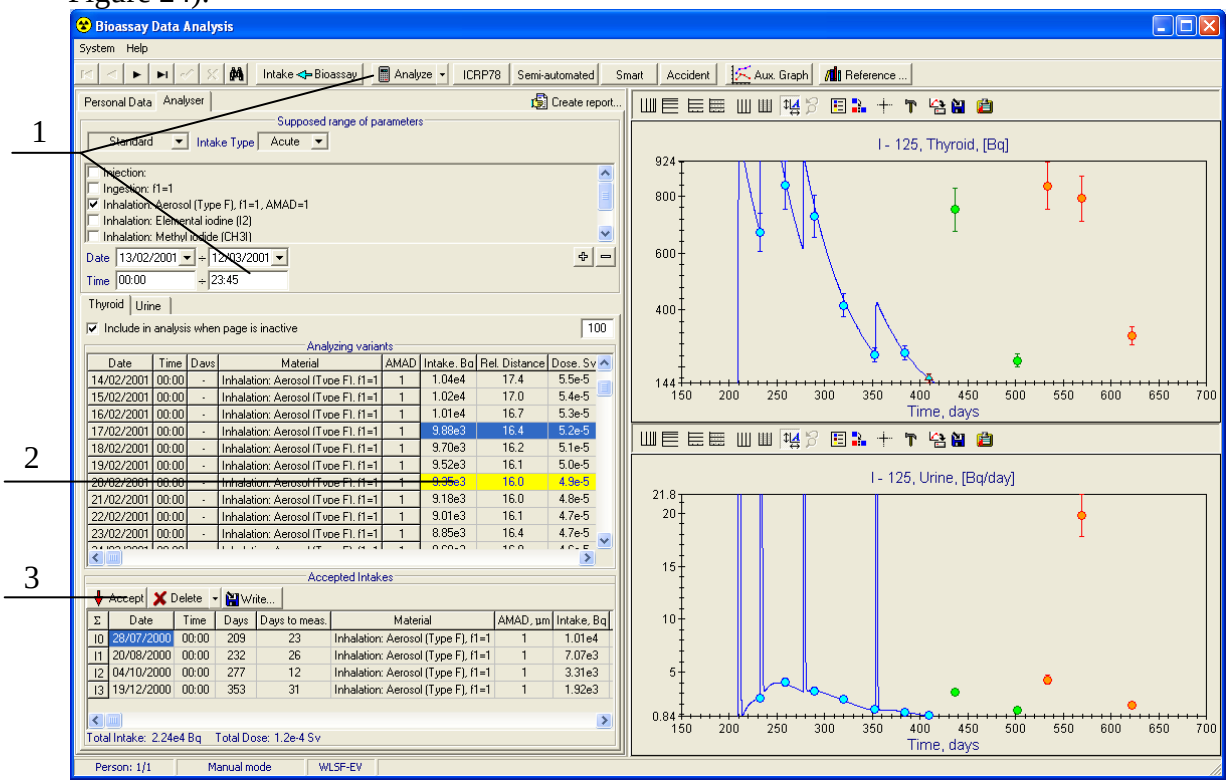


Figure 24. *Manual mode* (see description of callouts in the list above)

3.1.3 *Accident mode*

The *Accident mode* can be selected with the *Accident* button on the *Toolbar*. This mode is useful for analysis of accidental cases, when the date of intake is known. The functionality of this mode is the same as in the *Manual mode*, except that the search of the "best fit" by date of intake is not performed. Instead of the time range of the supposed dates of intake the known date of the accident must be set in the *Date* field of the *Supposed range of parameters* group. The analysis of wound intakes is available in this mode only (see subsection 2.3.2).

3.1.4 *ICRP78 mode*

The *ICRP78 mode* can be selected with the *ICRP78* button on the *Toolbar*. To start an analysis in the *ICRP78 mode*, select the set of measurements (i.e. daily urine excretion measurements or measurements of thyroid content), select (press) the *ICRP78* button on the *Toolbar* and press the *Analyse* button. Results of the approximation process will be shown on the

graph and reconstructed intakes and doses will be collected in the *Intakes* table on the *Analyser* page of the *Data* panel (see Figure 25). It must be noted that in this mode any region (points) selections in the *Graph* panel (as it is described in subsection 2.4) have no effect. The analysis process can be started only with the *Analyse* button and all points in the selected series are always analysed.

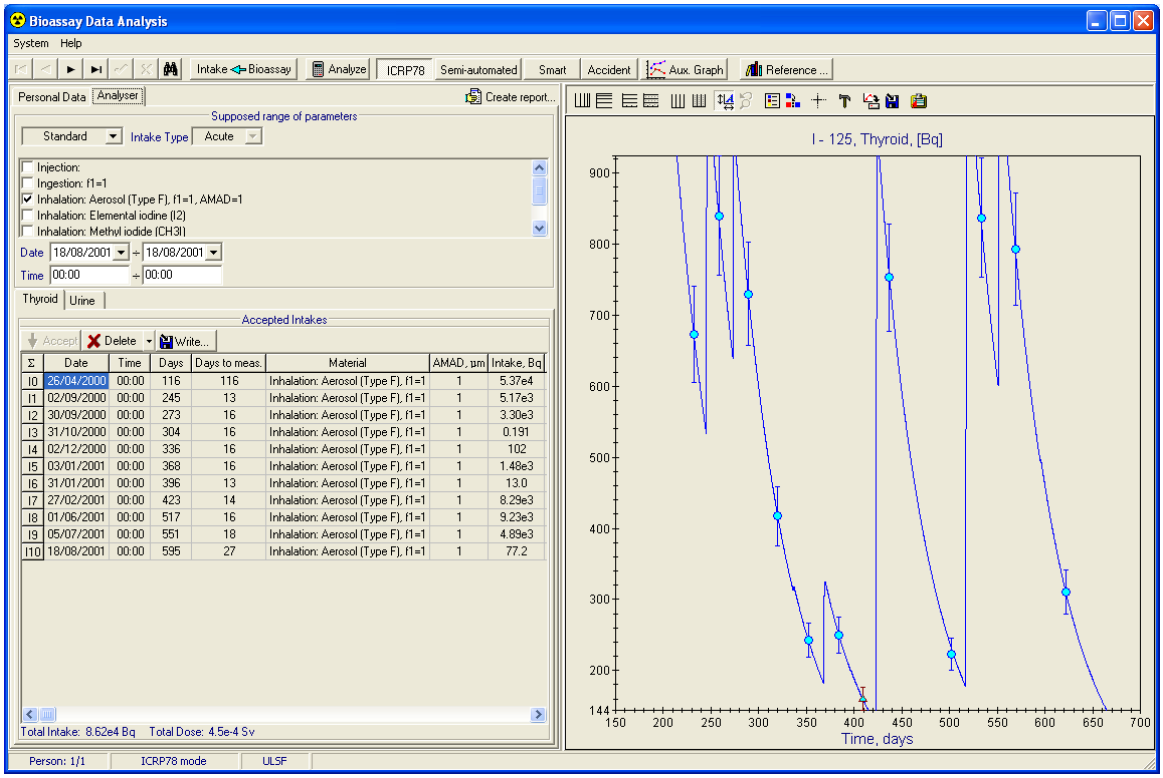


Figure 25. Results of the *ICRP78 mode*

3.1.5 *Smart mode*

The *Smart mode* is based on the new method of intake reconstruction, described in the Annex B (like the *Semi-automated* and *Manual modes*). The *Smart mode* can be selected with the *Smart* button on the *Toolbar*. To start an analysis in the *Smart mode*, select the set of measurements (i.e. daily urine excretion measurements or measurements of thyroid content), select (press) the *Smart* button on the *Toolbar* and set parameters using by the *Set parameters of the Smart mode…* command in a dropdown menu of the *Analyse* button. This command opens a dialog showed on the Figure 26. The *Smart mode* tries to incorporate several measurements as a result of one intake by using criteria enumerated on the Figure 26.

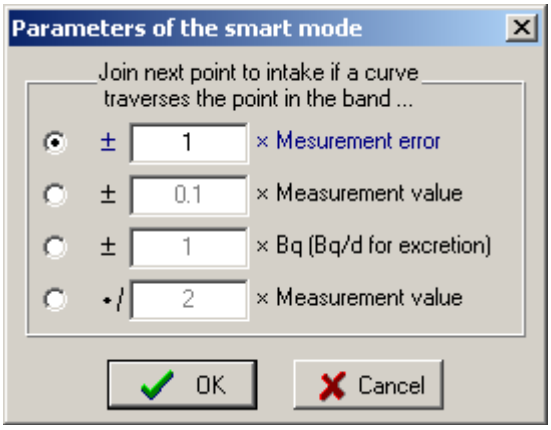


Figure 26. *Parameters of the Smart mode* window

To start an analysis process in the *Smart mode*, press the *Analyse* button. Results of the approximation process will be shown on the graph and reconstructed intakes and doses will be collected in the *Intakes* table on the *Analyser* page of the *Data* panel (see Figures 27 - 28).

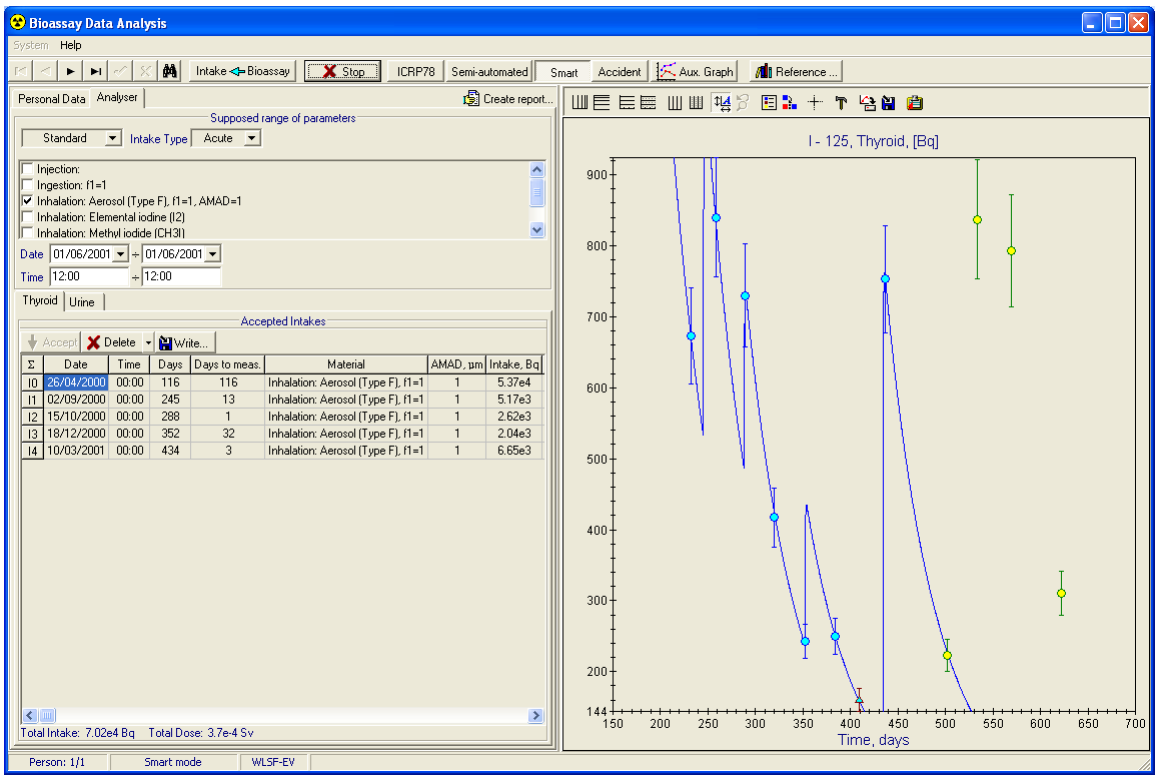


Figure 27. Progress of the *Smart mode*

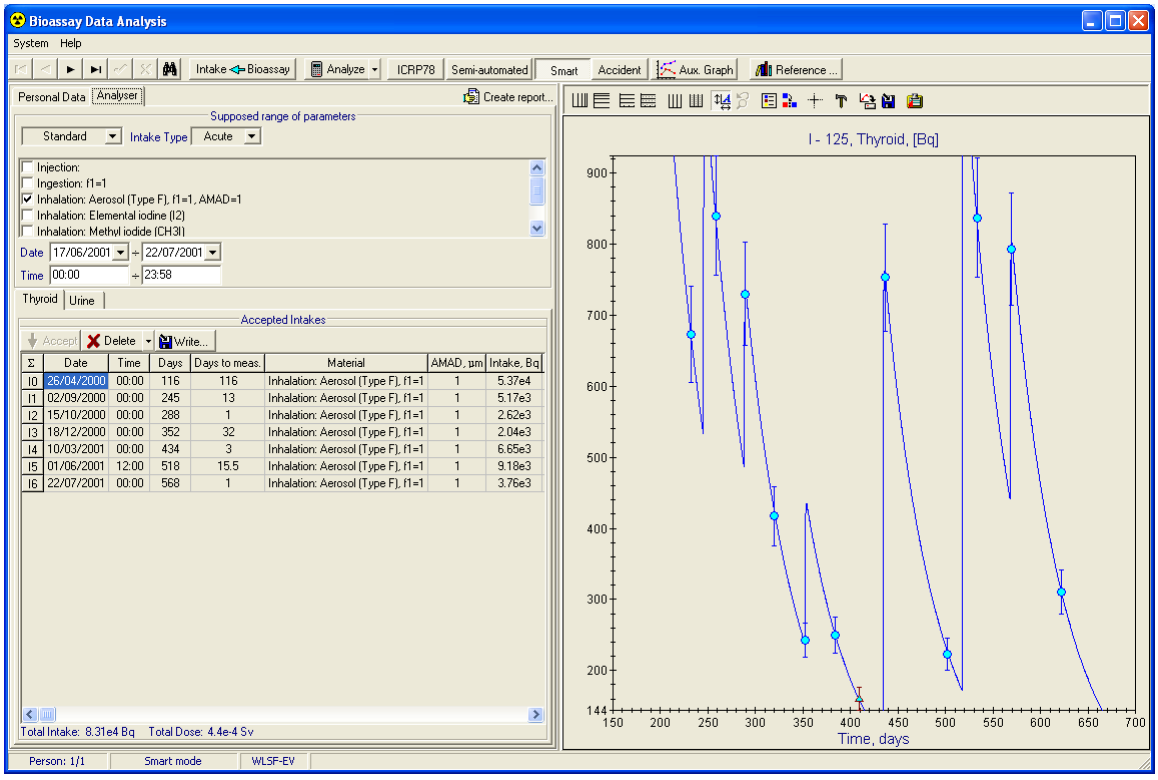


Figure 28. Results of the *Smart mode*

The analysis process can be started only with the *Analyse* button and all points in the selected series are always analysed (like in the *ICRP78 mode*).

The *Manual mode* has advanced features of the *Smart mode* accessed via *Smart analyse* command and *Smart test* command in a dropdown menu of the *Analyse* button. These commands allow performing a *Smart analysis* and *Smart testing* for selected points only.

3.2 Prospective analysis

The *Prospective mode* of analysis allows to calculate the dose from the known intake. The *Prospective mode* may be set on by pressing the Intake Bioassay button of the *Toolbar*. The arrow on the button changes its direction indicating that the *Prospective* analysis is on (see callout 1 on the Figure 29). To return to the *Retrospective mode* of analysis press the Intake Bioassay button again. When the *Prospective mode* is on the *Intake* field is displayed in the *Supposed range of parameters* group (see callout 2 on the Figure 29). It allows to enter the known intake value in units selected in the *Preference* window.

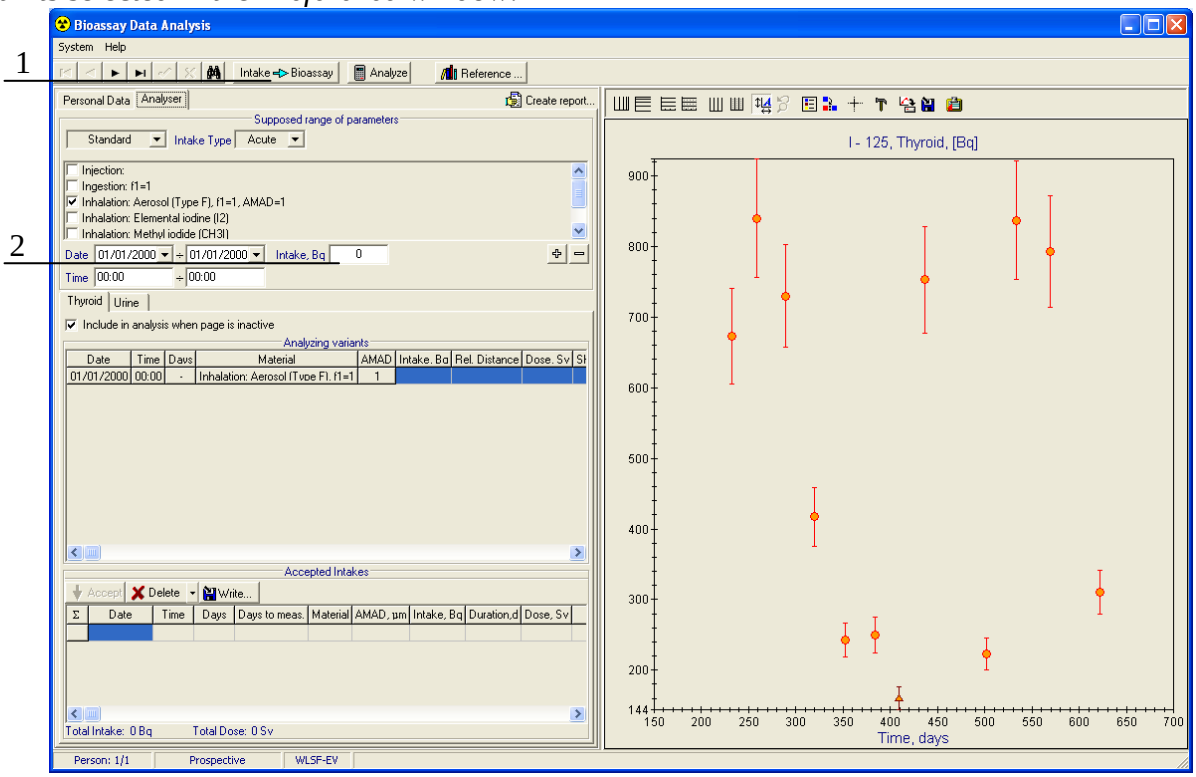


Figure 29. *Main* window in *Prospective mode* of analysis

To perform the *Prospective* calculation:

1. Select one or more measurement sets with the tabs and checkboxes (see callout 1 on the Figure 30). All selected measurement sets are displayed in the *Graph Panel*.
2. Select the supposed intake variants and intake value (see callout 2 on the Figure 30).
3. To start calculation, press the *Analyse* button on the *Toolbar* (see callout 3 on the Figure 30).
4. All calculated doses are displayed in the *Table of analyzing variants* (see callout 4 on the Figure 30). Corresponding retention and excretion functions may be displayed on the graphs by double clicking on the "-" sign of last column of the *Table of analyzing variants*.
5. User can select one of results and add it to the *Intakes* table by pressing the Accept button (see callout 5 on the Figure 30).

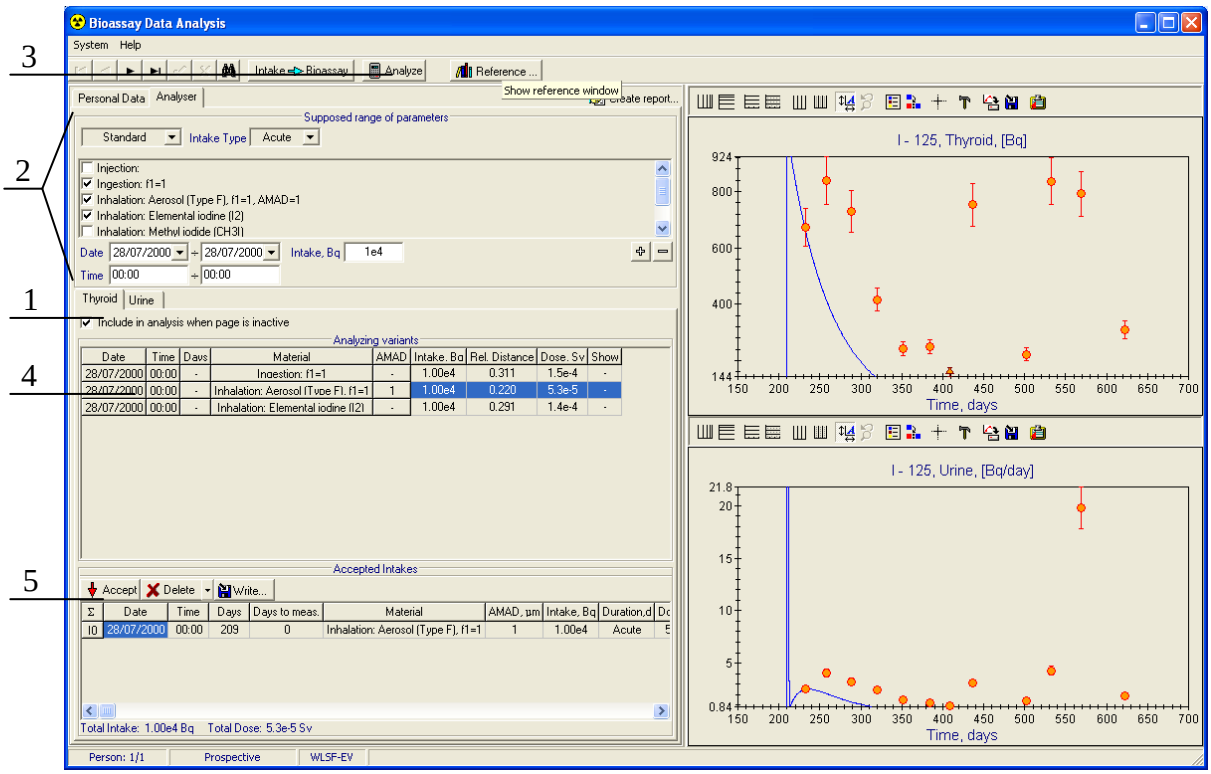


Figure 30 Result of the *Prospective* calculation

4 *MIXED INTAKES* WINDOW

The *Mixed intakes* window designed to create/edit complex mixed intake descriptions for the radionuclide, which measurements are currently analyzed. The *Mixed intake* window is shown on the Figure 31.

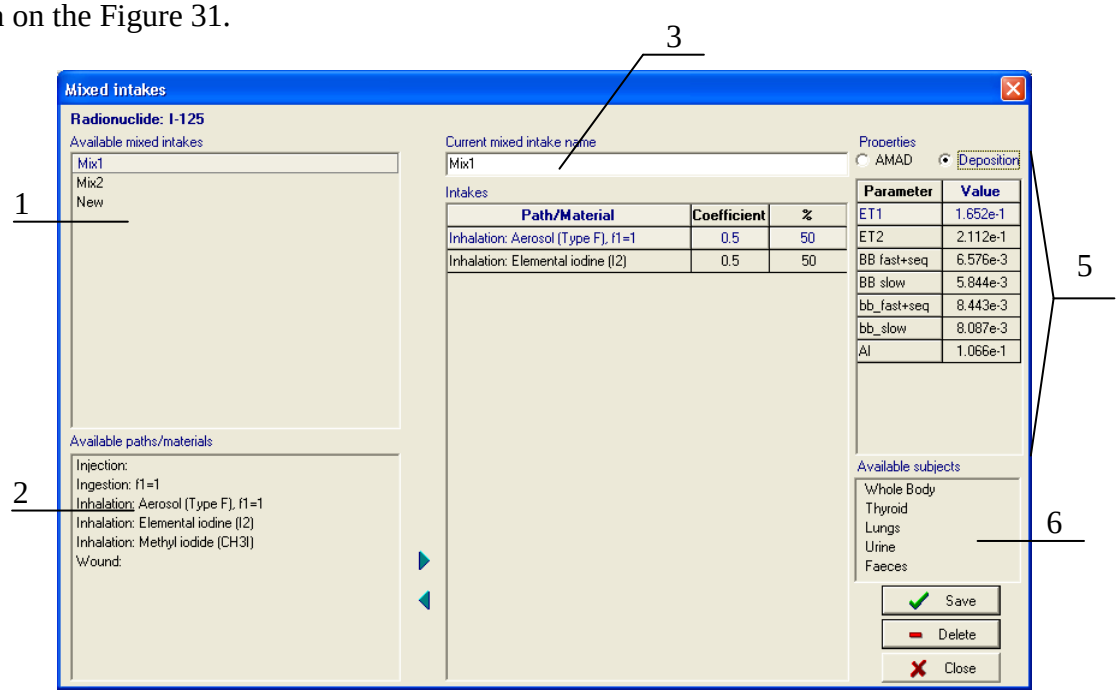


Figure 31. The *Mixed intakes* window

Mixed intake is a combination of the standard intakes, weighted accordingly to the supposed amounts of radioactive material incorporated into the human body by them. Standard intake means one of the:

– Injection;

- Ingestion of the radioactive material with the specified absorption fraction;
- Inhalation of the radioactive aerosol with the specified Type of Material and AMAD;
- Inhalation of the radioactive vapour or gas;
- Wound intake with the specified wound retention function and duration of retention in wound.

The *Mixed intakes* window contains following elements:

1. *Available mixed intakes* list displays the set of saved mixed intakes available for the current radionuclide. It allows the selection of one of already created mixed intakes for modification. The creation of a new mixed intake may be performed by selection of the *New* item in the list.
2. *Available paths/materials* list contains the set of available standard intake descriptions. The user can build the mixed intake combining the standard descriptions. To add the new standard intake to the description of the mixed intake, currently selected in the *Available mixed intakes* list, select this intake in *Available paths/materials* list and drag it to the *Intakes* table (see description of the callout 4) or press  button.
3. *Current mixed intake name* edit box displays the name of the currently edited mixed intake and may be used to enter the name of the newly created mixed intake.
4. *Intakes* table contains the description of the currently edited mixed intake. Each row of this table contains the name of the standard intake and its weight in the total mixed intake. To add the new standard intake to the description of the mixed intake select it in the *Available paths/materials* list and drag it to the *Intakes* table (see description of the callout 2) or press  button. To remove the standard intake from the description of mixed intake, select it in the *Intakes* table and drag somewhere out of the table or press  button. To change the weight of the standard intake, double click with the left mouse button on the corresponding cell in the *Coefficient* column.
5. *Properties* group of controls designed for setting the parameters of inhalation or wound intakes. For the inhalation the AMAD or regional deposition values can be set. For the wound intake the wound retention function and duration of retention in wound can be defined. To view or change properties of an inhalation or wound intake select it in the *Intakes* table.
6. *Available subjects* list displays the subjects of measurement for which the response functions on the currently selected mixed intake are available. Subjects with unavailable response functions are grey.

To save the created or modified description of the mixed intake press the *Save* button. To remove a description of the mixed intake select its name in the list of *Available mixed intakes* (see callout 1 on the Figure 31) and press the *Delete* button. The description of the selected mixed intake will be deleted after confirmation. Be sure that the deleted description of the mixed intake is not longer needed and no results of the analysis are based on that description of intake.

5 *DATA MANAGER* WINDOW

The *Data manager* window is designed to add/modify/delete all the data in the program database. It divides into three parts (see Figure 32):

1. *Personal information* group;
2. *Sets of measurements* group;
3. *Measurement values* group.

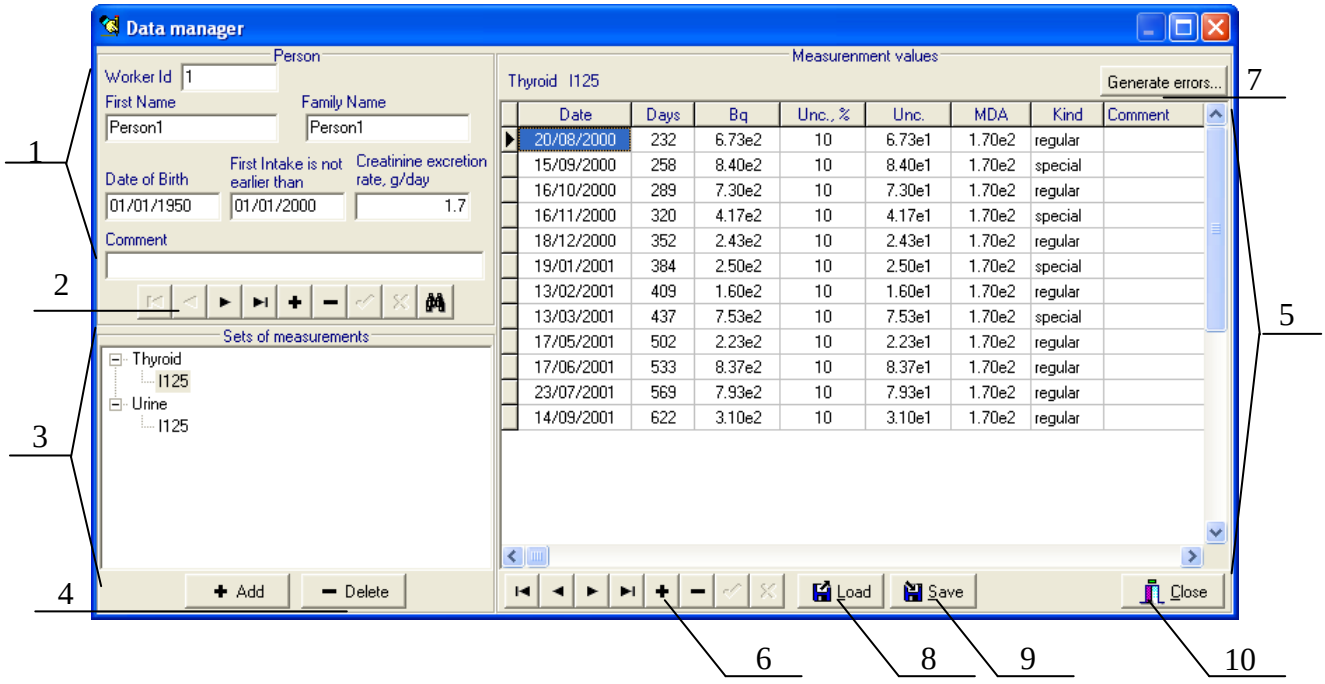


Figure 32. The *Data manager* window

5.1 *Personal information* group

The *Personal information* group contains following elements (see Figure 32):

1. Edit boxes for enter/modification of personal information for the selected person (see callout 1).
2. Set of navigation and management buttons (see callout 2).

   Use [+] button to create a new empty record for the new person. To save the new record to the database press [✓] button. To reject this action press [✕] button.

   [−] button deletes the current personal record and all corresponding measurements from the database.

   All other buttons perform the same actions as the identical buttons on the *Toolbar* of the *Main* window.

5.2 *Sets of measurements* group

The *Sets of measurements* group contains following elements (see Figure 32):

1. *Sets of measurements* list (see callout 3) shows the expanded list of measurement sets, which the database contain for the selected person. The list includes the names of the subjects of measurement (organ or tissue, whole body, excretion products). For each subject the list of measured radionuclides is shown. For the tritium the list of chemical forms is displayed (tritium water or organically bound tritium). The *Sets of measurements* list allows to select the set of measurements, which will be displayed in the *Table of measurement values*. All operations in the *Measurement values* part of the window will work with the measurement set selected in this list.

2. Buttons for managing the sets of measurements (see callout 4 on the Figure 32).

Use  button to add the new set of measurements to the list for the selected person.

Use  button to delete the selected set of measurements from the list for the selected person.

5.3 *Measurement values* group

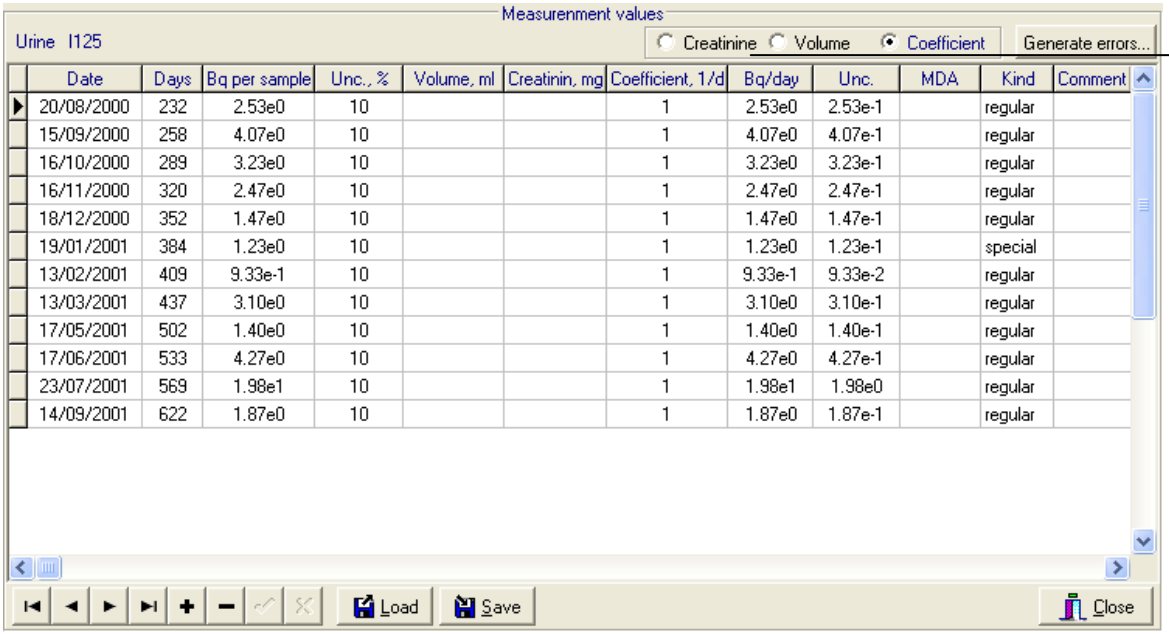
Measurement values group contains (see Figure 32):

1. *Table of measurement values* (see callout 5) is designed to enter new or to modify existing measurement records. To add the new measurement record click with the left mouse button anywhere in the last row of the table (select the last row) and press the down (down arrow) button or the *Insert* button on the keyboard. This action also may be performed with  button of the *Measurement values* group. The new empty row will appear in the table. Now it is possible to fill the new measurement record. The new or modified record will be saved automatically when the user moves the cursor to another row of the table or when *Ctrl+End* keys are pressed simultaneously. It is also could be done with  button of the *Measurement values* group. To delete the measurement record it is necessary to select it (click with the left mouse button anywhere in the corresponding row) and press *Ctrl+Delete* keys simultaneously. This action also may be performed with  button of the *Measurement values* group. The confirmation dialog will be displayed and after confirmation the record will be deleted.

The set of columns described the measurement is different for urine measurements and for other measurements. For all measurement series except urine measurements it contains following columns:

- *Date* – date of the measurement;
- *Time* – time of the measurement (displayed if *Use time* mode is checked in the *Preference* window – see section 8);
- *Days* – time in days since the date of the first possible intake. The date of the first possible intake is pointed out in the *First intake is not earlier than* field of the *Personal information* group;
- *Measurement value* in units, selected in the *Preference* window;
- *Unc.,%* – measurement uncertainty in percents. These values may be used as weighting factors in the analysis (see the Equation 4 in the Annex B). If at least one of these values is zero then *ULSF* weighting method is used in the analysis of the measurement set (see the Equation 3 in the Annex B). If uncertainty values are unknown they must be set to zero;
- *Unc* – absolute measurement uncertainties. They are automatically calculated on the base of Measurement value and *Unc, %* values;
- *MDA* – value of the minimal detectable activity for the measurement in units, selected in the *Preference* window;
- *Kind* – the kind of measurement. This value indicates the monitoring program within the framework of which the measurement was done (regular monitoring, special monitoring). The value in this field can be entered from drop-down list, which appears while editing;
- *Comment* – notes for the particular measurement (not required). These values are not currently used in analysis.

If the urine measurement series is selected in the *Sets of measurements* list the following columns set is displayed in the *Table of measurement values* (see Figure 33):



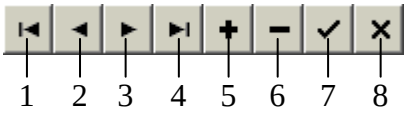
Date	Days	Bq per sample	Unc., %	Volume, ml	Creatinin, mg	Coefficient, 1/d	Bq/day	Unc.	MDA	Kind	Comment
20/08/2000	232	2.53e0	10			1	2.53e0	2.53e-1		regular	
15/09/2000	258	4.07e0	10			1	4.07e0	4.07e-1		regular	
16/10/2000	289	3.23e0	10			1	3.23e0	3.23e-1		regular	
16/11/2000	320	2.47e0	10			1	2.47e0	2.47e-1		regular	
18/12/2000	352	1.47e0	10			1	1.47e0	1.47e-1		regular	
19/01/2001	384	1.23e0	10			1	1.23e0	1.23e-1		special	
13/02/2001	409	9.33e-1	10			1	9.33e-1	9.33e-2		regular	
13/03/2001	437	3.10e0	10			1	3.10e0	3.10e-1		regular	
17/05/2001	502	1.40e0	10			1	1.40e0	1.40e-1		regular	
17/06/2001	533	4.27e0	10			1	4.27e0	4.27e-1		regular	
23/07/2001	569	1.98e1	10			1	1.98e1	1.98e0		regular	
14/09/2001	622	1.87e0	10			1	1.87e0	1.87e-1		regular	

Figure 33. *Measurement values* group for the urine measurement series

- *Date* – the same as for other measurement series;
- *Time* – the same as for other measurement series;
- *Days* – the same as for other measurement series;
- *Activity per sample* – measurement value in *Activity per urine sample* units. The activity units can be selected in the *Preference* window;
- *Unc.,%* – the same as for other measurement series;
- *Volume, ml* – the volume of the urine sample in ml (not required if not involved in calculations);
- *Creatinine, mg* – the creatinine content in urine sample in mg (not required if not involved in calculations);
- *Coefficient, 1/d* – the coefficient for calculation of the daily radionuclide excretion with urine on the base of *Activity per sample* value. This coefficient is calculated automatically if the *Creatinine* or *Volume* item of the *Measurement calculation switch* (see callout 1 of the Figure 33) is checked. If the *Creatinine* item is checked, then the *Coefficient* is calculated as ratio between person's daily creatinine excretion rate and the *Creatinine* content in the sample. If the *Volume* item is checked, then the *Coefficient* is calculated as ratio between the standard value of daily urine excretion (1.6 litres per day) and the sample *Volume*. If the *Coefficient* item is checked, then the *Coefficient* value must be entered manually;
- *Activity/day* – calculated value of the daily radionuclide excretion with urine in *Activity per day* units. The activity units can be selected in the *Preference* window. This value is calculated as the product of the measured radionuclide content in the sample (*Activity per sample*) and the *Coefficient*. In accordance with ICRP-78 the urinary excretion data for tritiated water must be given in term *Activity/litre* (NOT in terms of the daily excretion rate). The urinary excretion data for organically bound tritium must be given in terms of the daily excretion rate. The program automatically calculates this value for tritiated water as the ratio between the measured radionuclide content in the sample (*Activity per sample*) and the *Volume* of the sample and shows for the *Activity/litre* value in this column.

Rest of columns is the same as for other measurement series.

2. Set of navigation and management buttons (see callout 6 on the Figure 32).



These buttons perform following actions:

1. Select first measurement record in the *Table of measurement values*;
2. Select previous measurement record;
3. Select next measurement record;
4. Select last measurement record;
5. Add new measurement record to the *Table of measurement values*;
6. Delete selected measurement record from the *Table of measurement values*;
7. Accept changes of the measurement record;
8. Reject changes of the measurement record.

3. *Generate errors* button (see callout 7 on the Figure 32) calls the *Generate errors* dialog (see Figure 34), which allows to set measurement uncertainty values automatically. Use the *Uniform Absolute* item to set the absolute measurement uncertainties (relative uncertainties in percents will recalculate automatically). Use the *Uniform Relative (%)* item to set relative measurement uncertainty values (absolute measurement uncertainties will recalculate automatically). Use the *Square Root* item to set absolute measurement uncertainties equal to values of square roots of corresponding measurement values multiplied by the coefficient entered in the *Value* field (relative uncertainties in percents will recalculate automatically). If the *Apply to all* check box is checked, then all uncertainties in the *Table of measurement values* will be changed. Otherwise, uncertainty will be set only for the currently selected measurement in the *Table of measurement values*.

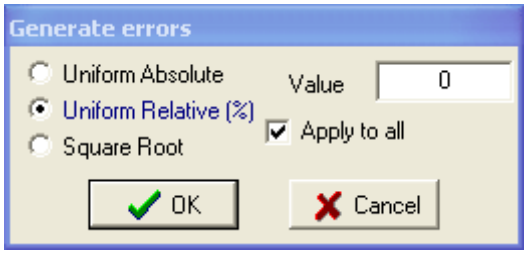


Figure 34. The *Generate errors* dialog

4. *Load* button (see callout 8 on the Figure 32) loads a measurement series for the currently selected person from the file. User must select the corresponding measurement set in the *Sets of measurements* list (see the description of the *Sets of measurements* group) before loading. In the file each measurement must be described in the separate string. Whole Body, Thyroid, Lungs and Faecal measurements in the following order:

– *Date of the measurement* – date in the format dd/MM/yyyy with the four-digit year;
– *Time of the measurement* – time in the format hh:mm. If the *Use Time* checkbox of the *Preference* window (see section 8) is not checked, this field must be omitted;
– *Measurement value* in Activity or Activity /day units. The Activity units can be selected in a popup window before load starts;
– *Measurement error* in percents;
– *MDA* value in units, which can be selected in a popup window before load starts;
– *Kind of measurement* – the index of the measurement kind (0 for regular measurement, 1 for special measurement).

Values in strings must be separated with commas.

For example:

File Pu239.csv (*Use Time* checkbox is not checked)

```
31/01/1995,1.66E-04,10, 1E-05, 0
27/02/1995,1.14E-04,5, 1E-05, 1
28/03/1995,1.37E-04,10, 1E-05, 0
29/04/1995,1.37E-04,10, 1E-05, 0
```

File Pu239.csv (*Use Time* checkbox is checked)

```
31/01/1995,12:00,1.66E-04,10, 1E-05, 0
27/02/1995,13:10,1.14E-04,5, 1E-05, 1
28/03/1995,12:30,1.37E-04,10, 1E-05, 0
29/04/1995,14:00,1.37E-04,10, 1E-05, 0
```

Urine measurements must be described in the following order:

- *Date of the measurement* – date in the format dd/MM/yyyy with the four-digit year;
- *Time of the measurement* – time in the format hh:mm. If the *Use Time* checkbox of the *Preference* window (see section 8) is not checked, this field must be omitted;
- *Measurement calculation flag* – the integer value that defines the way of the radionuclides daily excretion calculation (is similar to the *Measurement calculation switch*). 0 value corresponds to the *Creatinine* item, 1 to the *Volume* item, 2 to the *Coefficient* item;
- *Measurements value* in Activity per sample units. The Activity units can be selected in a popup window before load starts;
- *Measurement error* in percents;
- The value of parameter, indicated by the *Measurement calculation flag*. If the *Measurement calculation flag* has 0 value then the creatinine content in mg per sample must be placed here, if 1 – the volume of the sample in ml, if 2 – the value of *Coefficient*. For the tritiated water the value of sample volume must be placed here independently of the value of *Measurement calculation flag*;
- *MDA* value in units, which can be selected in a popup window before load starts;
- *Kind of measurement* – the index of the measurement kind (0 – regular measurement, 1 - special measurement).

For example:

File UrinePu239.csv (*Use Time* checkbox is checked)

```
01/05/2000, 12:00, 0, 1.6E-2, 10, 400, 1E-3, 0
01/05/2000, 12:00, 0, 2.4E-2, 10, 500, 1E-3, 1
01/05/2000, 12:00, 0, 1.1E-2, 10, 840, 1E-3, 0
01/05/2000, 12:00, 0, 8.6E-3, 10, 900, 1E-3, 0
```

5. *Save* button (see callout 9 on the Figure 32) saves a measurement series for the currently selected person to the file. User must select the measurement set in the *Sets of measurements* list (see the description of the *Sets of measurements* group) before saving. The resulting file will have the same format as the described file format for import operation.
6. *Close* button (see callout 10 on the Figure 32) closes the *Data manager* window.

6 *AUXILIARY* GRAPH

The *Auxiliary* graph represents additional XY plots of target functions in an optimisation process (values, which must be optimised during the data approximation). Such graphical presentation can help to examine the form of the target function and to analyse all its local extremes. This graph is essential for analysis of non-trivial cases in the manual mode and for simultaneous analysis of several measurement sets. To turn the *Auxiliary* graph on press the *Aux. Graph* button on the *Toolbar*. The graph appears at the bottom of the *Graph* panel (see callout 1 on the Figure 35).

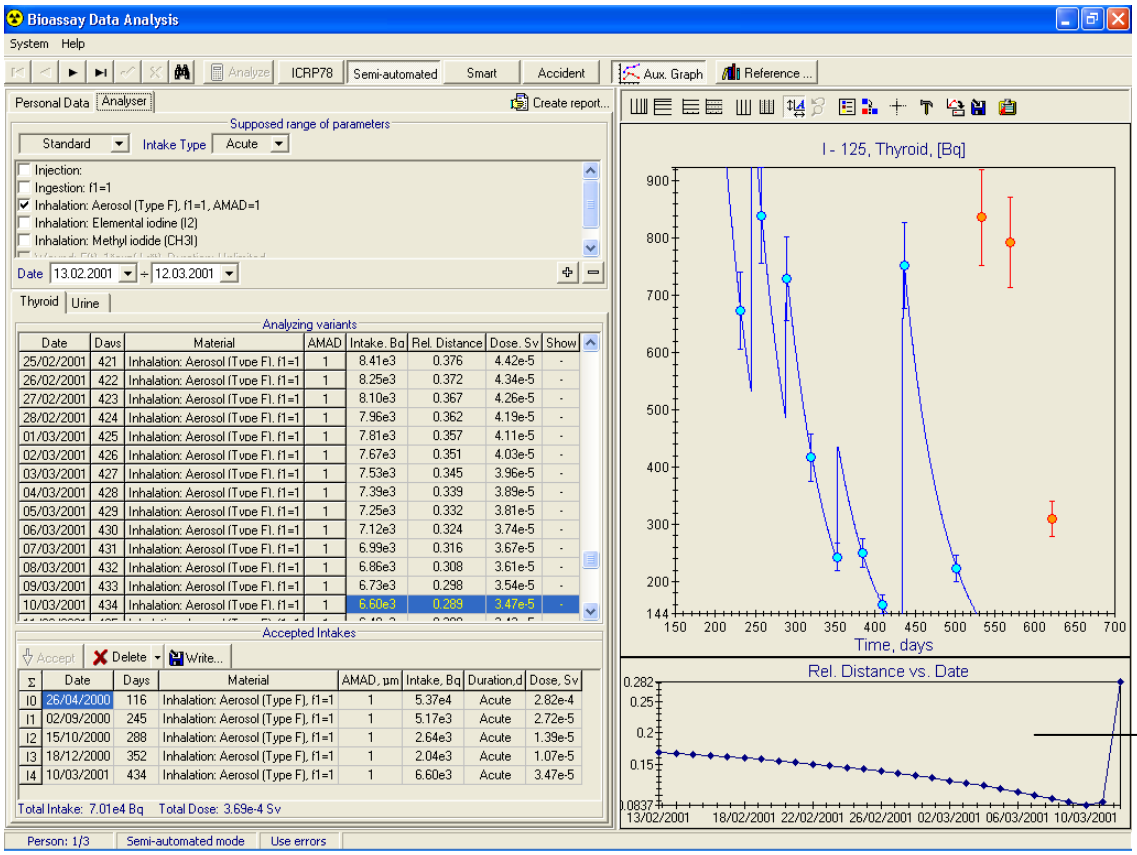


Figure 35. Usage of the *Auxiliary* graph

To select what information to show in the *Auxiliary* graph use the popup menu, which can be called with the right mouse button click on the *Auxiliary* graph (see Figure 36). In the popup menu the *Intake*, *Distance* or *Relative Distance* plots can be chosen. Plotted values are presented in the numerical form in the corresponded columns of the *Table of analysis results*. On the X-axis the supposed date of the analysed intake is displayed.

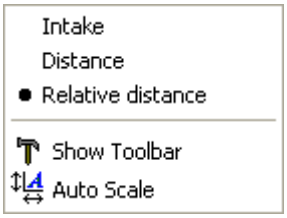


Figure 36. Popup menu of the *Auxiliary* graph

7 *SEARCH* WINDOW

The *Search* window (see Figure 37) can be called with  button of the *Main* window or the *Data Management* window. It allows finding the personal record in the database by the *Last Name* field. At the top of the window the edit box is placed (see callout 1). While typing in this edit box the incremental search will be performed and the record with the most similar the *Last Name* field will be automatically selected in *Table of persons* (see callout 2). *Table of persons* is sorted by the value of the *Last Name* field. If the user presses *OK* button then the selected personal record becomes the active record in the system. If the user presses the *Cancel* button then the active record remains unchanged.

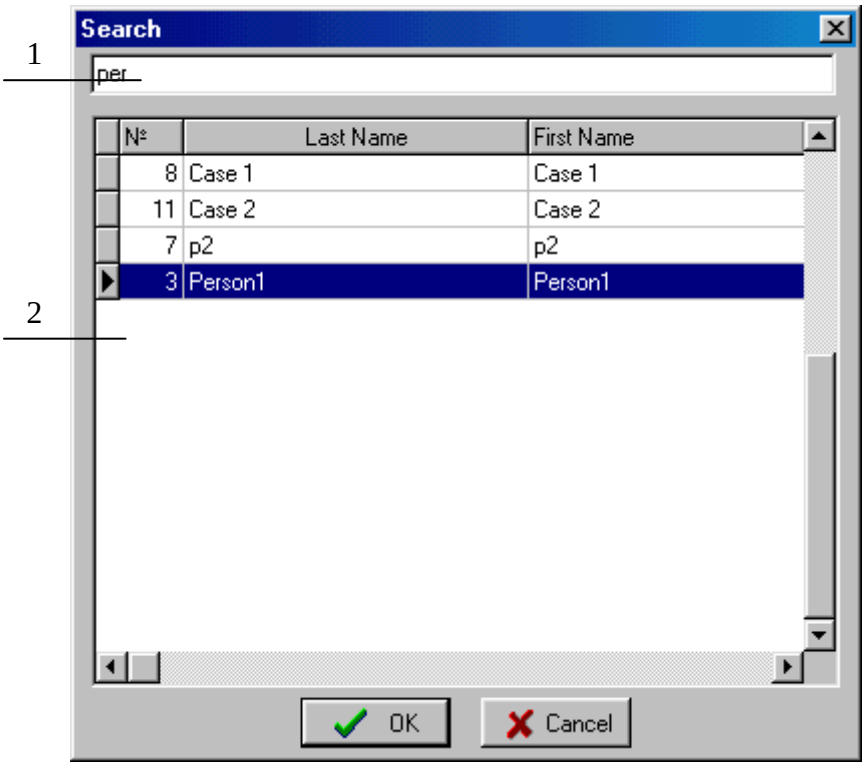


Figure 37. The *Search* window

8 *PREFERENCE* WINDOW

The *Preference* window sets the working folders of the program, a mode of the analysis (user can also set the mode with *ICRP78*, *Semi-Automated*, *Smart* and *Accident* buttons on the *Toolbar* – see subsection 2.2) and other analysis and interface options. It contains three pages. Figure 38 shows the *Directories* page of the preference window, Figure 39 shows the *Options* page, and Figure 40 shows the *Input/Output* page.

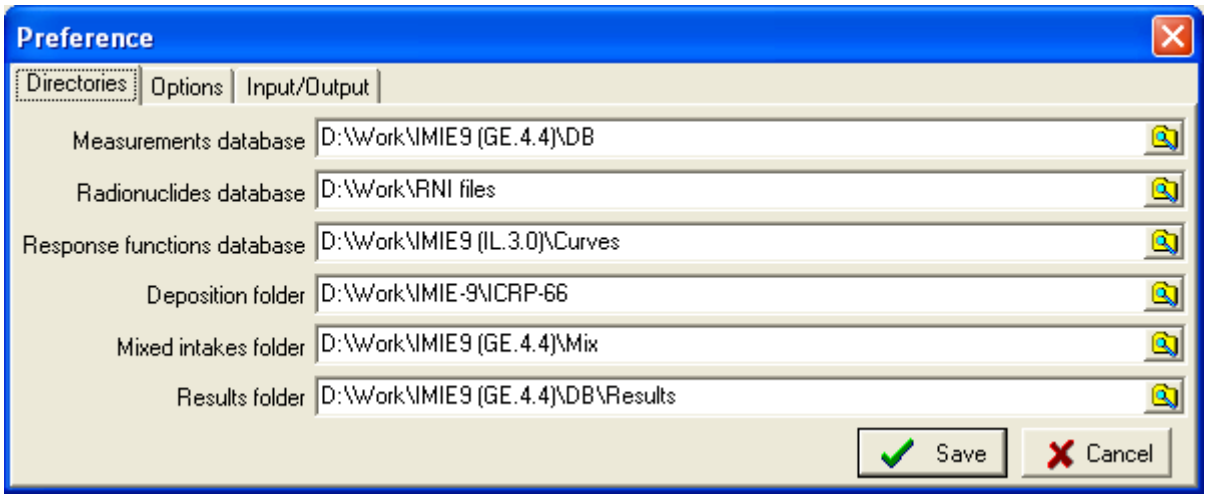


Figure 38. The *Preference* window
(the *Directories* page is selected)

On the *Directories* page user can change:

- the folder with the *Measurements* database (the database with personal data and measurement results). This database is usually placed at the network location for common access. The folder with the Measurements database also can be set on the *Personal data* page of the *Data* panel of the *Main* window (see subsection 2.3.1);
- the folder with the radionuclides database (the folder, which contains radionuclides database with spectrums and dose coefficients);
- the folder with the response functions database (this folder contains all available response functions in binary form. These functions are used in approximation during the analysis);
- the folder with files with standard lung deposition fractions from ICRP Publication 66;
- the folder with files with descriptions of user defined mixed intakes;
- the folder with the results (this folder contains results of the analysis in a binary form). The path to the *Results* folder also can be implicitly set on the *Personal data* page of the *Data* panel of the *Main* window (see subsection 2.3.1) by selection of the path to the *Measurements* database.

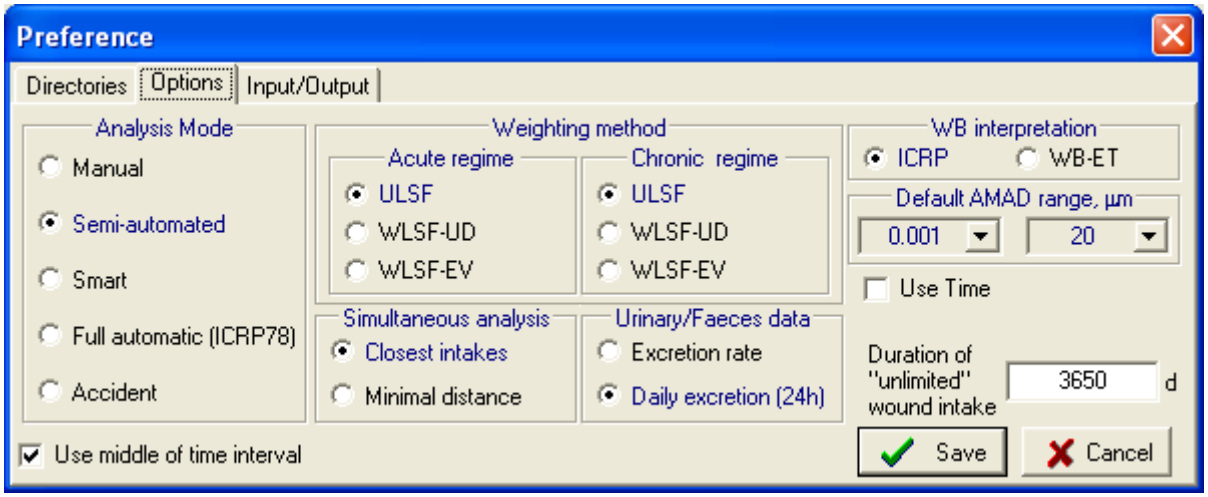


Figure 39. The *Preference* window
(the *Options* page is selected)

The *Options* page is designed for setting a mode of the analysis (see section 3) and permanently saving it. On the next start of the program the analysis mode will be automatically set to the saved value.

The *Weighting method* switches define the fitting procedure for reconstruction of acute or chronic intakes. The *ULSF* method implements the *unweighted least-squares fit* procedure, which is described by Equation (3) of the Annex B. The *WLSF-UD* method implements the *weighted least-squares fit* procedure with weights inversely proportional to the squares of *User Defined* (UD) measurement uncertainties (see Equations (2), (4) of the Annex B). The *WLSF-EV* method implements the *weighted least-squares fit* procedure with weights inversely proportional to the expected measurement values (see Equations (2), (5) of the Annex B).

The *Simultaneous analysis* radio group sets the mode of the simultaneous analysis. The "best result" of the simultaneous analysis is searched accordingly to the selected mode (*Closest intakes* or *Minimal distance*). If the *Closest intakes* mode is selected the "best result" of the simultaneous analysis is searched as a minimal relative distance between intakes, reconstructed on the base of each checked measurement series (see Equation (6) of the Annex B). If the *Minimal distance* mode is selected the "best result" of the simultaneous analysis is searched as minimal relative distance between measurements and approximation functions, constructed on the base of analysis of all checked measurement series (see Equation (8) of the Annex B).

The *Urinary/Faeces data* radio group allows defining how to interpret urine and faeces measurements. Such data may be interpreted as daily excretion values or excretion rate values.

This switch has no influence on the interpretation of measurements of excretion of tritiated water. Urine measurements of tritiated water are always interpreted as concentration of tritium in urine (Activity per litre), not as tritium excretion.

The *Duration of "unlimited" wound intake* field defines the time (in days) which will be substituted to the wound intake duration, when duration of the wound intake is defined as unlimited (see comments to the Figure 7 in subsection 2.3.2).

The *WB interpretation* radio group on the *Options* page allows selecting the definition of the Whole Body. The standard ICRP definition of the Whole Body (*ICRP* radio button) includes the ET (Extrathoracic) region. The *WB interpretation* radio group allows defining the *Whole Body without the ET region* (the *WB-ET* radio button). In some cases, when there is a small emission from the ET region, the standard ICRP definition leads to the underestimation in the dose assessment.

The *Default AMAD range* comboboxes allows to set the range of AMADs which will be used in generation of analysing variants.

The *Use Time* checkbox switch on the processing of fractions of the day (hours, minutes): input, taking into account during analysis, storage in database.

The *Use middle of time interval* check box allows to switch on/off the rule of use the middle of the analysed time interval when only one measurement is analysed. Generally, when only one measurement is analysed the used method of analysis can not reconstruct the time of intake. In such case just the middle of the analysed time interval is used as proposed by the ICRP Publication 78. But if user needs to see all variants of intake reconstruction for each date of analysed time interval, the *Use middle of time interval* check box may be turned off. This is useful in the *Manual mode* of analysis.

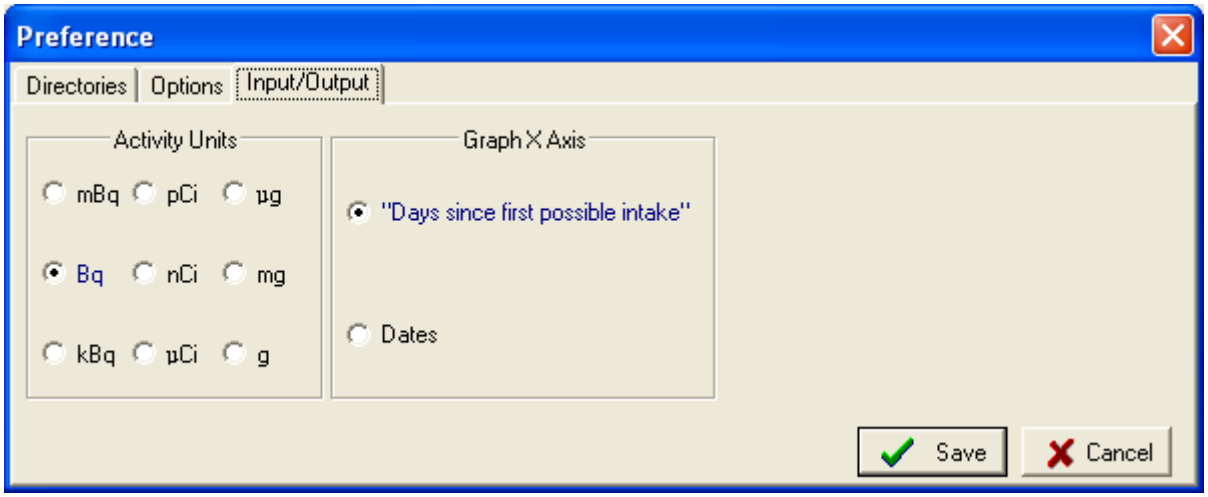


Figure 40. The *Preference* window
(the *Input/Output* page is selected)

The *Input/Output* page is designed for setting input and output parameters of IMIE interface.

The *Activity units* radio group allows selection of the activity units for all input and output procedures of the IMIE. Please, enter the activity data in the *Data manager* window in the units corresponding to this setting (see subsection 5.3).

The *Graph X Axis* radio group allows selection of the output data for the X axis of the *Graph* panel (see subsection 2.4). Dates or time in days since first possible intake, which is pointed out in the *First intake is not earlier than* field of the *Personal Data* page, can be displayed on the X axis.

9 IMPORT DATA

A user can create new personal records in the database and import measurement data from text files with delimiters pressing the *Import* button on the *Personal data* page of the *Main* window. To perform import press the *Import* button and select all text files, which contain measurement data in the opened dialog. After successful import of each file the new personal record is created in the database and all measurement sets are added to this record. Results of import procedure will be shown in a separate window and saved in a file 'IMIEImport.log'. The format of a text file, which can be imported, is described in the subsection 9.1.

User can customize import parameters using the *Options…* command in a dropdown menu of the *Import* button (see Figure 41). This command opens the *Import Options* window (see Figure 42).

Figure 41. Dropdown menu of the *Import* button

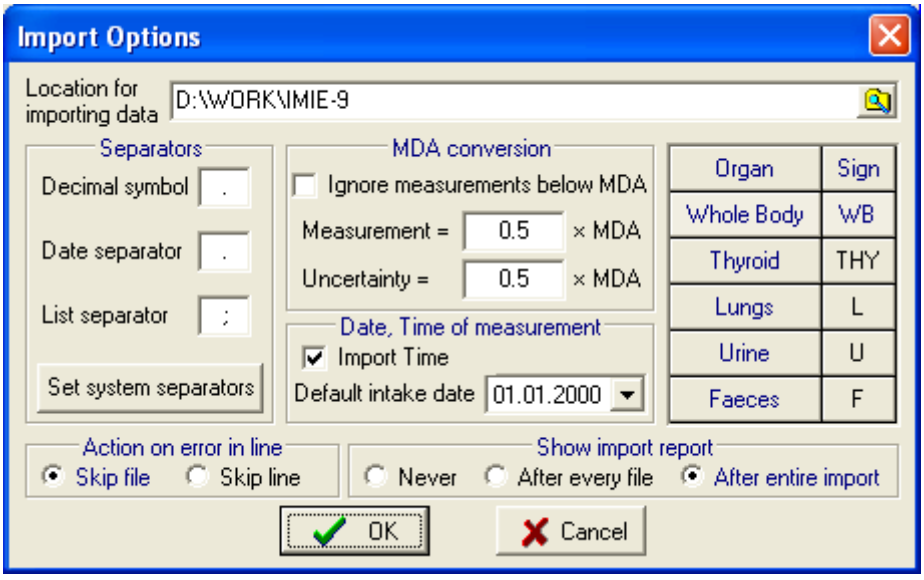


Figure 42. The *Import Options* window

This window is designed to set:

- *Location for importing data* where files are contain in;
- decimal, date and list separators (*Set system separators* button assigns system values to these parameters);
- interpretation of measurements below MDA (if the measurement value is blank): ignore or convert MDA values to measurement and uncertainty values;
- organ signs (default signs represented on the Figure 42);
- intake date (is used as a value of the *First intake is not earlier than* field);
- action on error in data format: skip the file or the line with an error only;
- type of import report: no report, report after every file or entire procedure.

9.1 File format and import example

A text file must have the header and the list of measurement values. The header consists of three lines (see the Example) that contain:

1. *Worker ID, First Name* and *Family Name* separated by list separators;
2. *Date of the first possible intake*;
3. *Daily creatinine excretion rate* (in g per day).

The list of measurement values must contain following fields (columns) separated by list separators: *Type-ID, Date, Time, Radionuclide, Chemical form, Calculation flag, Result,*

Uncertainty, *Parameter*, *MDA*, *Kind of measurement*, *Comment*. Fields in the file must satisfy next conditions:

Type-ID	–	one of organ signs (see Figure 42 for the list of organ signs);
Date	–	date of measurement in format ‘dd/MM/yyyy’ where ‘/’ is a date separator.
Time	–	time of measurement in format hh:mm. Can be blank if *Import Time* is not checked in the *Import Options* window (Figure 42);
Radionuclide	–	radionuclide name in format ‘Ag-110m’;
Chemical form	–	the chemical form of the *Radionuclide*. Significant only for tritium, for other radionuclides is ignored. For tritium the “W” means tritiated water, “O” means organically bound tritium;
Calculation flag	–	the calculation flag is significant only for urine measurements, for other measurements is ignored. It indicates the way of calculation of the radionuclides daily excretion from the value of radionuclide content in the sample. 0 value indicates the calculation with use of creatinine content in the urine sample, 1 – the calculation with use of sample volume, 2 – the calculation with use of coefficient;
Results	–	measurement value as a real number. Field can be blank if the *MDA* field is not blank or the *Ignore measurements below MDA* mode is switched on (see Figure 42). For whole body, thyroid, lungs measurements the value must be in Activity units, for faecal measurements – in Activity per day units, for urine measurements – in Activity per sample units. The Activity units can be selected in the popup window, which is shown before import starts. If *Results* field is blank and the *Ignore measurements below MDA* mode is switched off then both *Results* field and *Uncertainty* field are calculated using the *MDA conversion* rules;
Uncertainty	–	uncertainty value in percents;
Parameter	–	parameter value is significant only for urine measurements, for other measurements it is ignored. For urine measurements this value depends on the value of the *Calculation flag*. If the *Calculation flag* is 0 then the creatinine content in the urine sample must be placed here, if the *Calculation flag* is 1 – the volume of the urine sample, if the *Calculation flag* is 2 – the coefficient value;
MDA	–	MDA value as a real number (can not be blank if *Results* field is blank). The MDA value must be given in units selected in the popup window, which is shown before import starts;
Kind of measurement	–	the index of the measurement kind (0 – regular measurement, 1 – special measurement);
Comment	–	any text.

Example of a text file prepared for import into the IMIE database is represented below (decimal separator is ‘**.**’, date separator is ‘/’, list separator is ‘**;**’).

Case 1:

```
Line                                        Text
   1  Case 1;Nam;Fam
   2  01/01/1983
   3  1.5
   4  U;15/01/1983;01:00;Pu-238;;2;7E-05;;1;;0;Comment 1
   5  U;15/01/1983;01:30;Pu-239;;2;7E-05;;1;;0;
   6  U;17/07/1983;02:05;Pu-239;;2;7E-05;;1;;1;Comment 2
   7  F;15/01/1983;01:00;Pu-238;;;7E-05;;;;0;Comment 3
   8  F;15/01/1983;01:30;Pu-239;;;7E-05;;;;0;
   9  F;22/01/1984;14:30;Pu-238;;;8E-4;10;;;0;
  10  F;26/07/1984;16:00;Pu-238;;;;;;10;1;
```

In accordance with ICRP-78 the urinary excretion data for tritiated water must be given in term Activity/litre (not in terms of the daily excretion rate). The urinary excretion data for organically bound tritium must be given in terms of the daily excretion rate (Activity per day). Therefore 1 as the *Calculation flag* value and the sample volume as the *Parameter* value must be specified for urine measurements of tritiated water.

If file cause a failure during the import procedure the ‘IMIEImport.log’ file, which is displayed after import, contains description of all occurred errors. For example, if the system date separator is “.” the file shown in example above will cause a failure during the import procedure. A file ‘IMIEImport.log’ will look like on Figure 43. A user can read this file by means of any text viewer or IMIE code if the *Show import report* mode is not set to the *Never* status.

```
********************************************************************************

Import parameters:
-------------------------------------------------------------
  Decimal symbol: "."
  Date separator: "."
  List separator: ";"
  MDA conversion:
    Ignore MDA  = "No"
    Measurement = "0.5" * MDA
    Uncertainty = "0.5" * MDA
  Use Time      = "Yes"
  Organ signs:
    Whole Body  : "WB"
    Thyroid     : "THY"
    Lungs       : "L"
    Urine       : "U"
    Faeces      : "F"
  Action on error in line: "Skip file"
  Default intake date: "01.01.2000"
  Default intake time: "00:00"

-------------------------------------------------------------

Start     -  07.08.2004, 19:21.39


-------------------------------------------------------------

File      - "D:\WORK\IMIE-9\Test\IDEASTest.txt"
Total lines count - 15
  Warning - Line 2: "01/01/1983" is not a valid date of the first possible intake
  Error   - Line 4: "15/01/1983" is not a valid date
  Error   - Line 5: "15/01/1983" is not a valid date
  Error   - Line 6: "17/07/1983" is not a valid date
  Error   - Line 7: "17/07/1983" is not a valid date
  Error   - Line 8: "22/01/1984" is not a valid date
  Error   - Line 9: "26/07/1984" is not a valid date
  Error   - Line 10: "15/01/1983" is not a valid date
  Error   - Line 11: "15/01/1983" is not a valid date
  Error   - Line 12: "17/07/1983" is not a valid date
  Error   - Line 13: "17/07/1983" is not a valid date
  Error   - Line 14: "22/01/1984" is not a valid date
  Error   - Line 15: "26/07/1984" is not a valid date
File import failed!
-------------------------------------------------------------

Finish    -  07.08.2004, 19:21.50
********************************************************************************
```

Figure 43. Import ‘log’-file

10 *REFERENCE* WINDOW (VIEWER OF RADIONUCLIDE INFORMATION)

The *Viewer of radionuclide information* is designed for obtaining the graphical and numerical reference information on decay chains, dose spectrums and other information about radionuclides. The viewer uses information kindly provided by Dr. K.F.Eckerman, Chairman of the ICRP Task Group on Dose Calculations. Pressing the *Reference…* button on the *Toolbar* opens the viewer window. This window is shown on the Figure 44. It consists of the following components:

1. *Radionuclide* panel allow selection of the radionuclide (see callout 1 on the Figure 44 and subsection 10.1).
2. *Choice* panel contains three check boxes and allow to show/hide left panel (the *Decay chain* panel) or right panel (the *Spectrum* panel or the *Activity* panel) (see callout 2 on the Figure 44 and subsection 10.2).
3. *Decay chain* panel visualizes the radioactive-decay scheme and displays ancestors of the selected radionuclide (see callout 3 on the Figure 44 and subsection 10.3).
4. *Spectrum* panel displays detailed and summary spectrum characteristics for the selected radionuclide (see callout 6 on the Figure 44 and subsection 10.4).
5. *Activity* panel shows the change of activities for the selected radionuclide and its ancestors as a result of radioactive decay (see callout 5 on the Figure 45 and subsection 10.5).

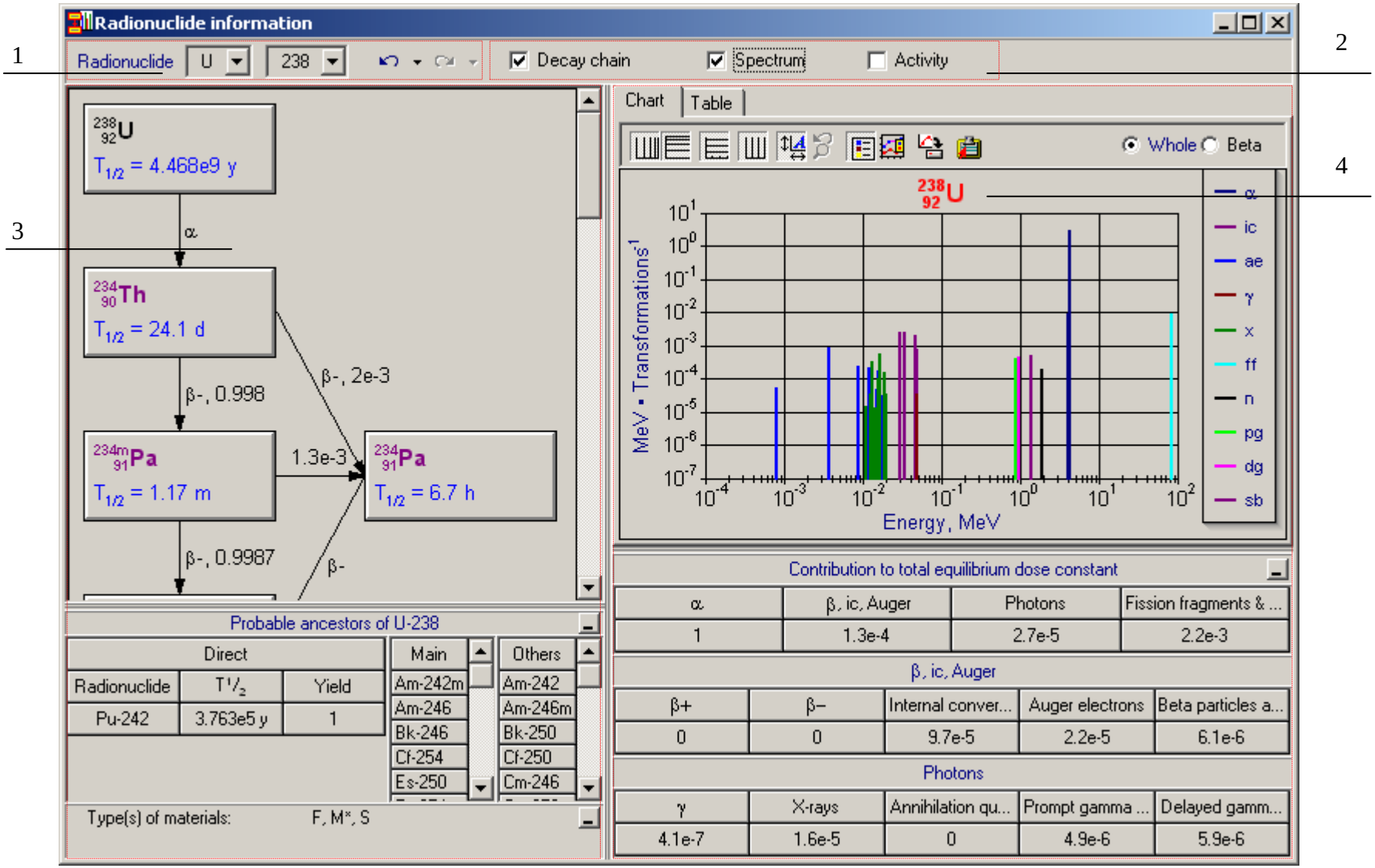


Figure 44. The *Viewer of radionuclide information* – the *Spectrum* panel activated (see description of callouts in the list above)

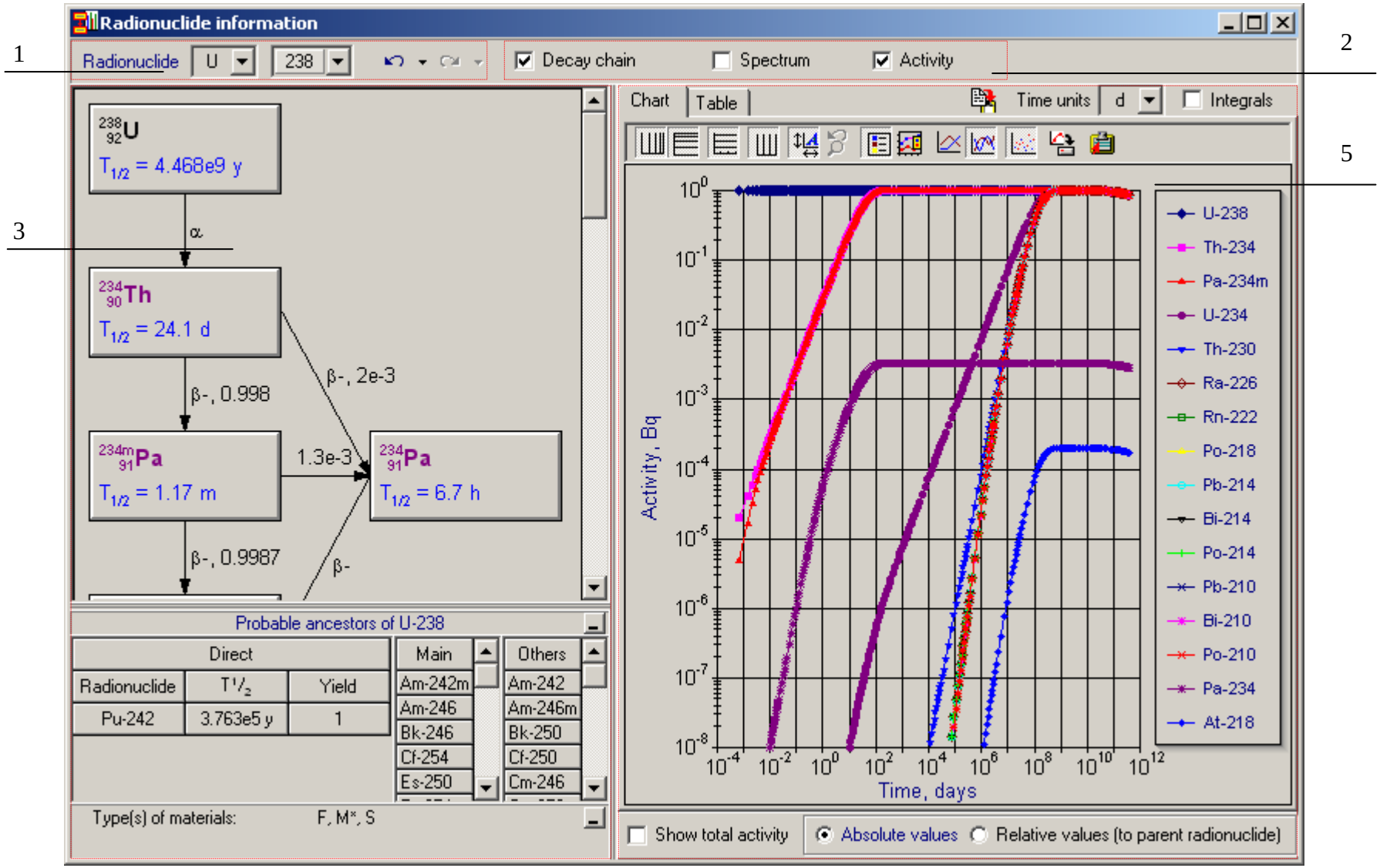


Figure 45. The *Viewer of radionuclide information* – the *Activity* panel activated (see description of callouts in the list above)

10.1 *Radionuclide* panel

The *Radionuclide* panel allows selecting the chemical element on a simple dropdown list or dropdown menu (see Figure 46). The dropdown menu appears when the user press and hold down *Ctrl* key and click left (main) mouse button on the *Chemical element* combo box. The dropdown list enables the selection of which accessible from database.

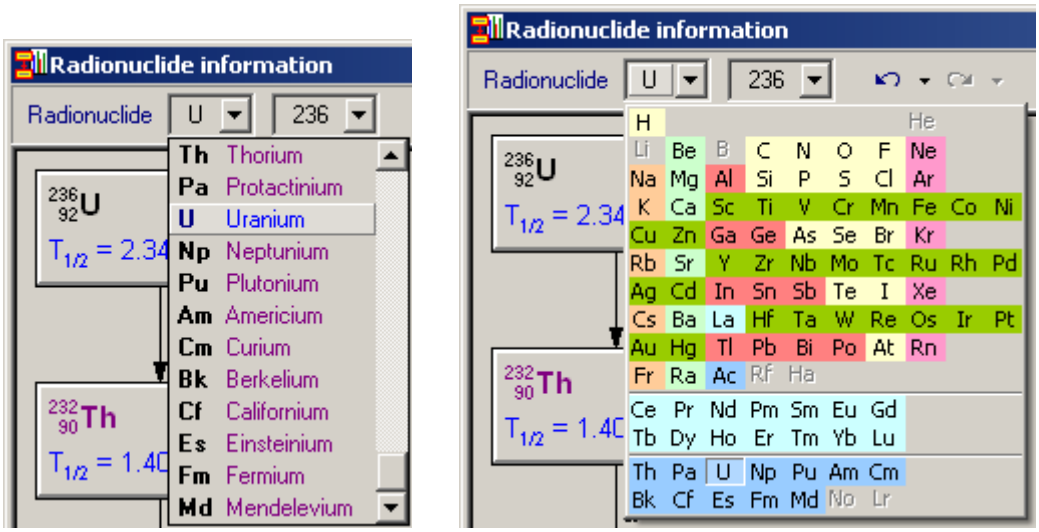


Figure 46. Choice of the chemical element in the *Radionuclide* panel

A popup (context) menu of the *Radionuclide* panel (see Figure 47) allows switching a display type (between *Independent choice of element and atomic mass* and *Radionuclides list* – see Figure 48) and changing a sort type of the chemical elements (by alphabet or by periodic table) and radionuclides (by alphabet, by periodic table or by atomic mass) in dropdown lists.
The *Radionuclide* panel contains *Undo* and *Redo* buttons (see Figure 49) which track the history of selected radionuclides.

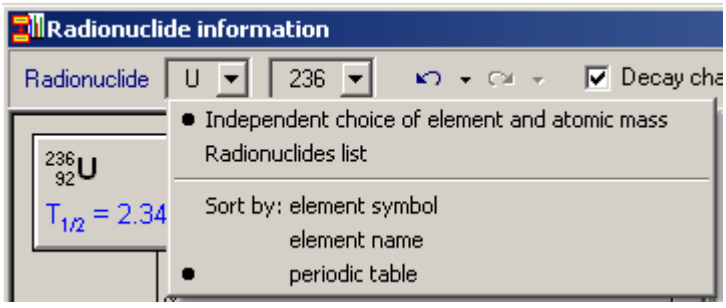


Figure 47. Popup (context) menu of the *Radionuclide* panel

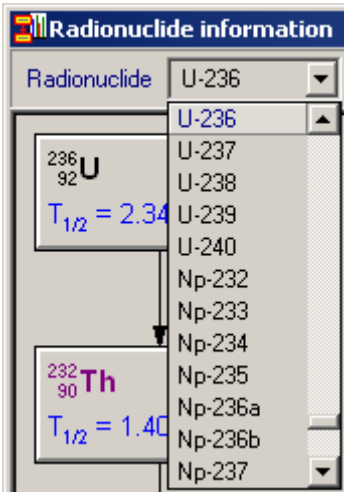


Figure 48. *Radionuclides list* display type of the *Radionuclide* panel

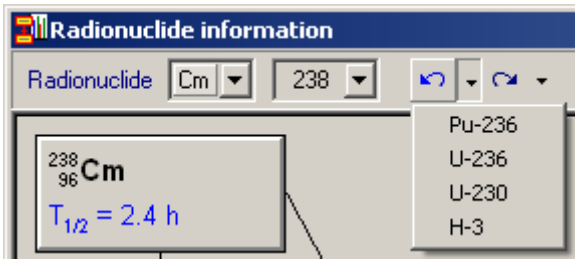


Figure 49. *Undo* and *Redo* popup menus of the *Radionuclide* panel

10.2 *Choice* panel

The *Choice* panel (see callout 2 on the Figure 44) contains three check boxes (*Decay chain*, *Spectrum* and *Activity*), which allow to show/hide left panel (the *Decay chain* panel) or right panel (the *Spectrum* panel or the *Activity* panel). These capabilities allow examining a complex decay chain (see the Figure 50), spectrum (see the Figure 51) or dynamics of activities in radionuclide chain (see the Figure 52).

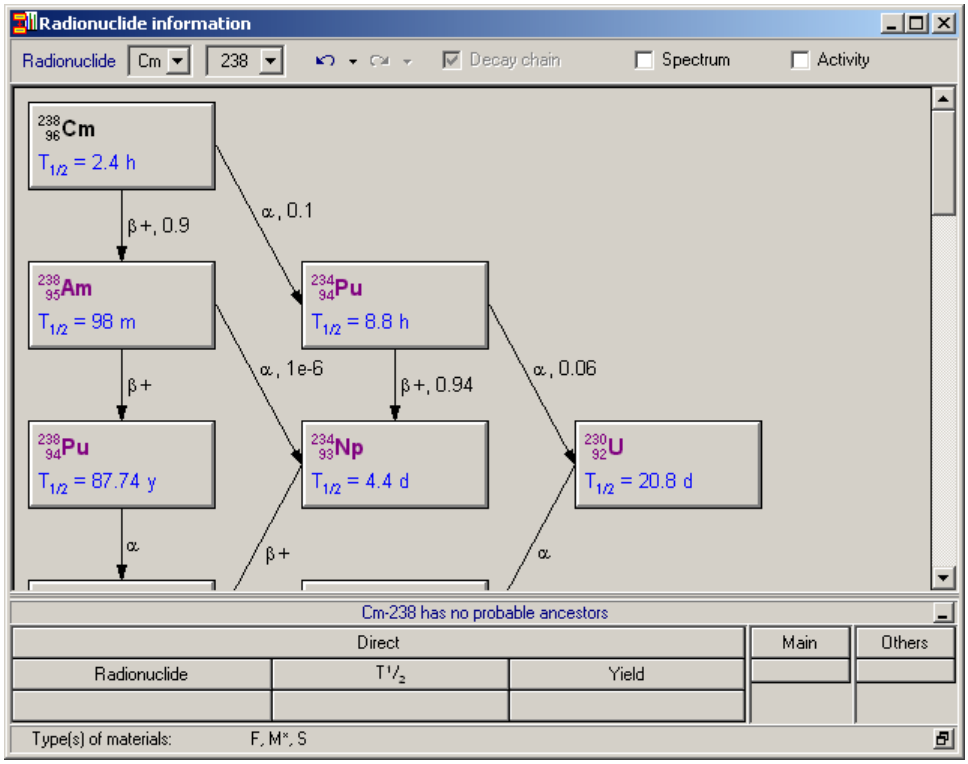


Figure 50. The *Viewer of radionuclide information* (the *Decay chain* panel)

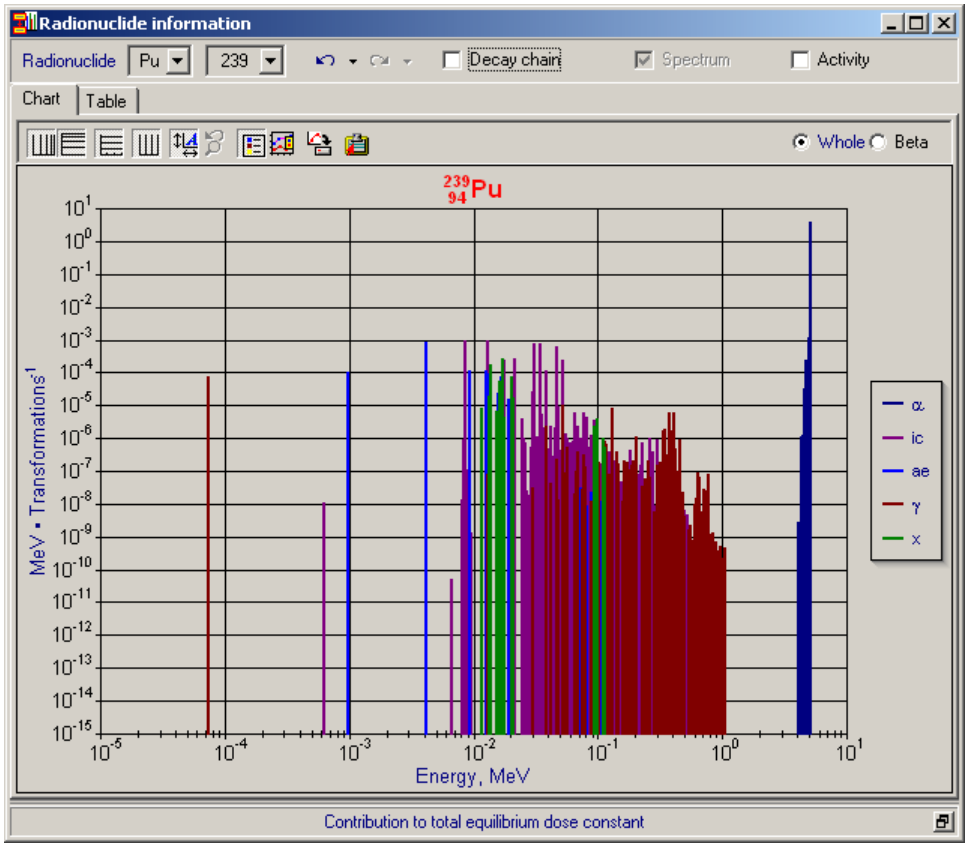


Figure 51. The *Viewer of radionuclide information* (the *Spectrum* panel).

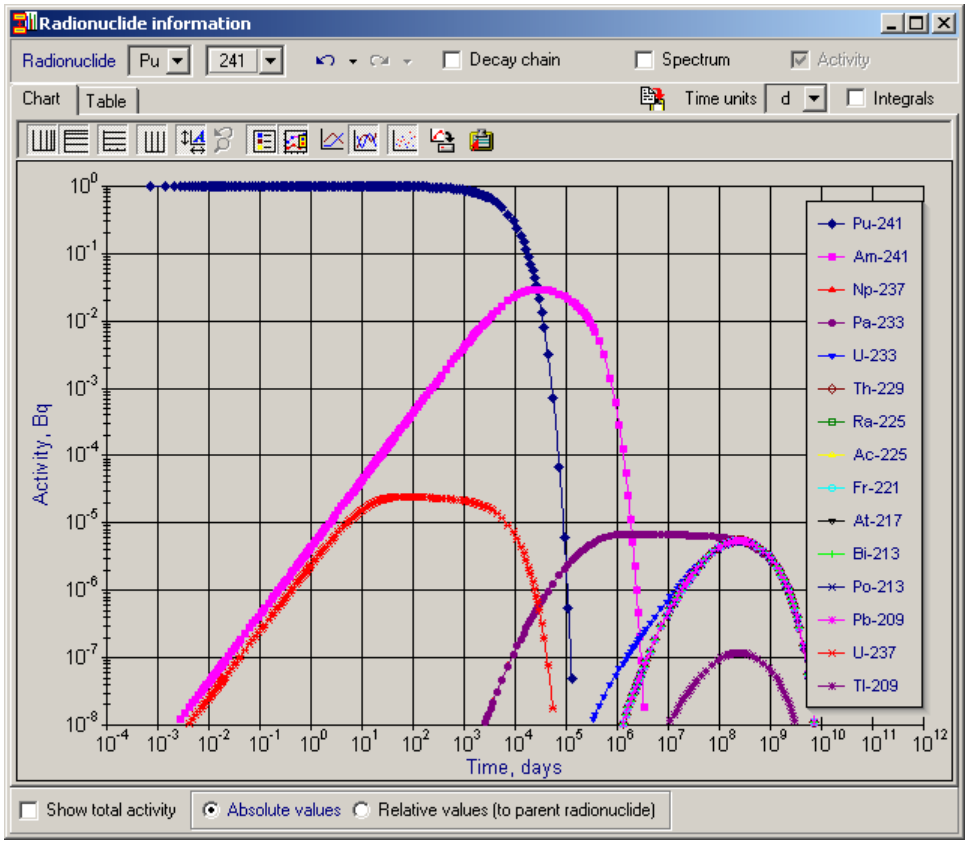


Figure 52. The *Viewer of radionuclide information* (the *Activity* panel).

10.3 *Decay chain* panel

The *Decay chain* panel contains following elements (from top to bottom):

– *Radioactive-decay scheme* panel visualizes the decay chain of the selected radionuclide (see subsection 10.3.1);
– *Probable ancestors* panel displays all ancestors of the selected radionuclide (see subsection 10.3.2);
– *Types of Materials* panel indicates recommended Types of Materials for selected radionuclide (see subsection 10.3.3).

10.3.1 *Radioactive-decay scheme* panel

The *Radioactive-decay scheme* panel visualizes the decay scheme of the selected radionuclide. Any radionuclide in the scheme appears as a box. To select the style of displayed in the *Radioactive-decay scheme* panel use popup (context) menu, which could be called by clicking the right mouse button (see Figure 53):

- 3-dimensional view of the radionuclide boxes (on/off);
- half-life time of radionuclide decay (show/hide);
- yield of radiation per nuclear transformation (show/hide) (only yield values < 1 are displayed);
- mode of decay (α, β-, β+);
- stable nuclides in chain (show/hide);

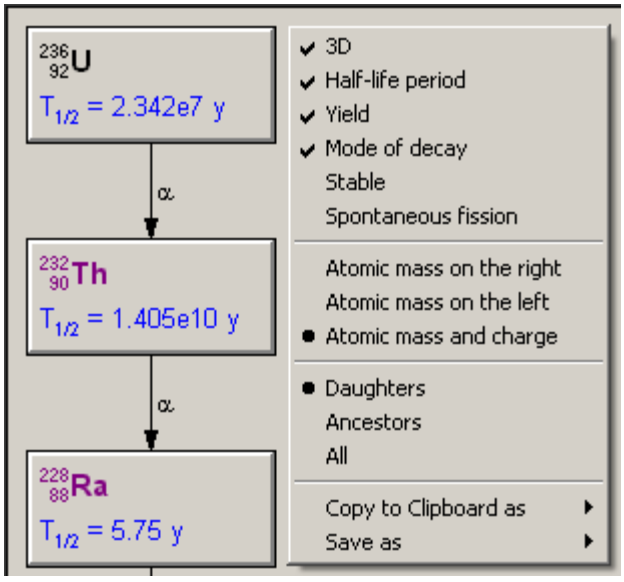


Figure 53. Popup (context) menu of the *Radioactive-decay scheme* panel

- spontaneous fission (show/hide) (see Figure 54);
- radionuclide name presentation (atomic mass on the right (using by dash), on the left (as superscript), atomic mass and charge as indexes; for example: Pu-239, ^{239}Pu or $^{239}_{94}$Pu));
- decay chain presentation type: daughter radionuclides for the selected radionuclide, ancestor radionuclides for the selected radionuclide (chains which goes to the selected radionuclide only), daughter and ancestor radionuclides (see Figure 55).

Any radionuclide box in the *Radioactive-decay scheme* panel could be selected for the dose spectrum depicting (on the *Spectrum* panel) by the mouse click (like a button – see box 'Th-232' on the Figure 56).

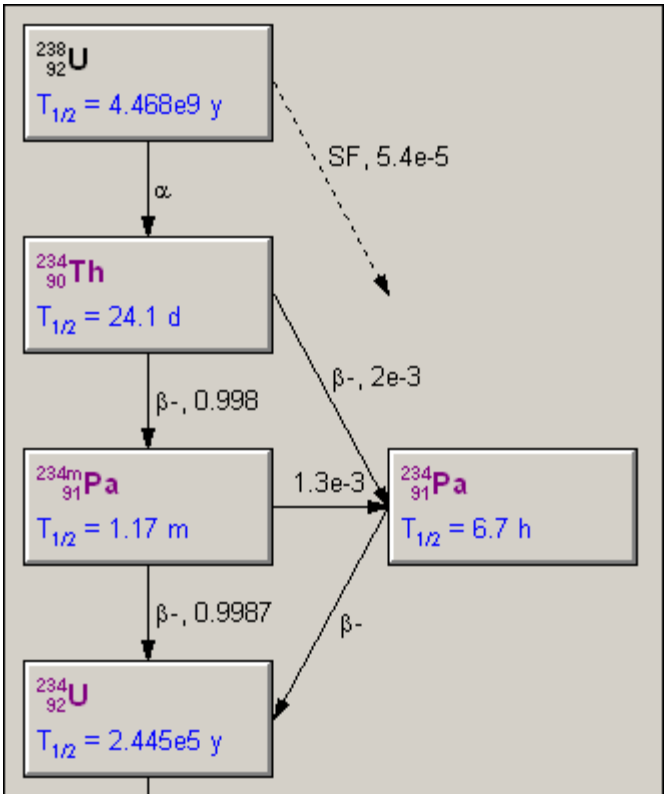


Figure 54. The *Radioactive-decay scheme* panel for the 'U-238' (*Mode of decay* and *Spontaneous fission* items in the context menu are checked)

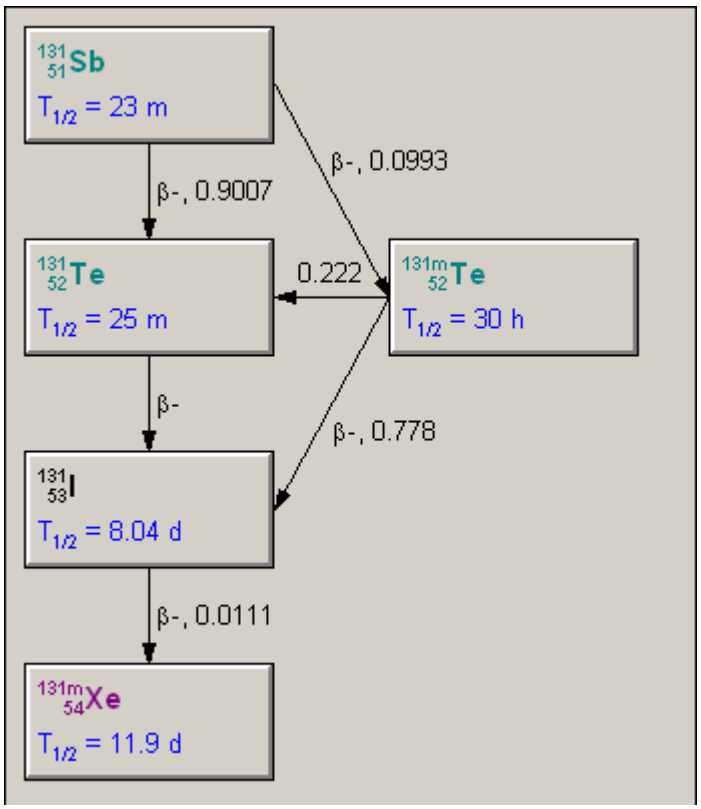


Figure 55. The *Radioactive-decay scheme* panel for the 'I-131' (decay chain presentation type is *All*; ancestors (Sb-131, Te-131, Te-131m) and daughter radionuclides (Xe-131m) are displayed)

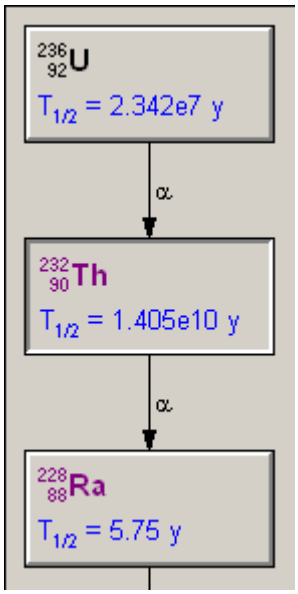


Figure 56. Choice of the 'Th-232' box of the *Radioactive-decay scheme* panel by mouse clicking

10.3.2 *Probable ancestors* panel

The *Probable ancestors* panel displays all ancestors of the selected radionuclide in three different grids: *Direct* (callout 1 on the Figure 57), *Main* (callout 2 on the Figure 57) and *Others* (callout 3 on the Figure 57). The *Direct* grid contains radionuclides that are direct ('immediate') ancestors for the selected radionuclide. A half-life time and yield (of the selected radionuclide) also appear for direct ancestors. The *Main* grid contains radionuclides that are main (root) ancestors for the selected radionuclide (ancestors that have not ancestors). If the direct ancestor is simultaneously a main ancestor, it displays bold-faced. The *Others* grid contains others ancestors (not direct and not main ancestors). All ancestors for the selected radionuclide are displayed if user chose the *Ancestors* item in the *Decay chain* panel context menu.

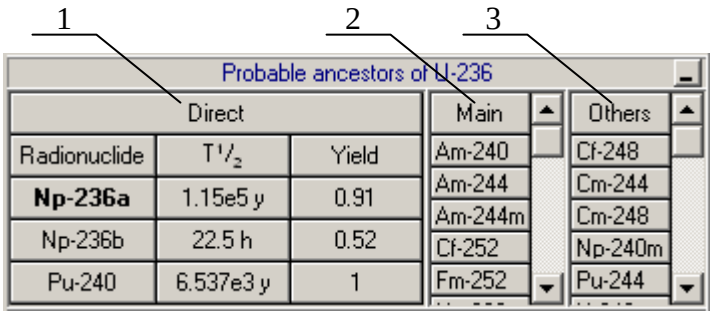


Figure 57. The *Probable ancestors* panel

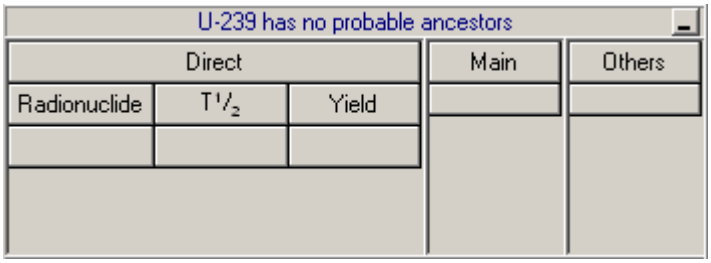


Figure 58. The *Probable ancestors* panel for the U-239

If the selected radionuclide has no probable ancestors the *Probable ancestors* panel look like at the Figure 58.

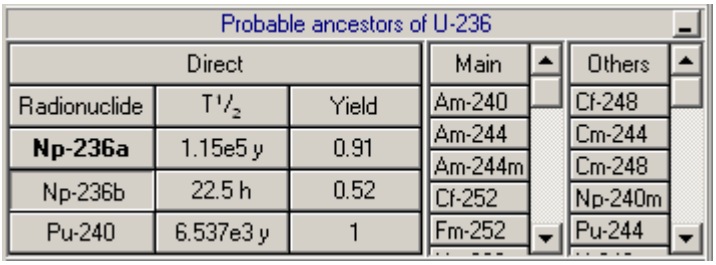


Figure 59. The *Probable ancestors* panel for the U-236 (cell 'Np-236b' is pressed)

Any radionuclide in the *Probable ancestors* panel could be selected for the dose spectrum presentation (on the *Spectrum* panel) by the mouse click (like a button – see cell 'Np-236b' on the Figure 59).

10.3.3 *Types of Materials* panel

This panel displays *Types of Materials* for selected radionuclide and classes for gases/vapours. The recommended default Type (see ICRP Publication 71) for the particulate aerosol (when no specific information is available) is marked by asterisk (Figure 60).

Figure 60. The *Types of Materials* panel for the H-3

Types of Materials and Classes for Gases and Vapours (according to ICRP Publication 66):

Type V	deposited materials that, for dosimetric purposes, are assumed to be instantaneously absorbed into body fluids from the respiratory tract; in this report applied only to certain gases and vapours (Very fast absorption).
Type F	deposited materials that are readily absorbed into body fluids from the respiratory tract (Fast absorption).
Type M	deposited materials that have intermediate rates of absorption into body fluids from the respiratory tract (Moderate absorption).
Type S	deposited materials that are relatively insoluble in the respiratory tract (Slow absorption).
Class SR-1	soluble or reactive. Deposition throughout the respiratory tract, which may be complete or incomplete.
Class SR-2	highly soluble or reactive. Complete deposition in the respiratory tract with instantaneous uptake to body fluids.

10.4 *Spectrum* panel

The *Spectrum* panel contains following items (from top to bottom):

- *Detailed spectrum characteristics* panel displays the spectrum of the selected radionuclide in graphical or tabular form (see subsection 10.4.1);
- *Summary spectrum characteristics* panel displays the contribution of different radiation types to the "equilibrium dose" constant for the selected radionuclide (see subsection 10.4.2).

10.4.1 *Detailed spectrum characteristics* panel

The *Detailed spectrum characteristics* panel displays the spectrum of the selected radionuclide in graphical (see the Figure 61) or tabular (see the Figure 63) form. The *Chart* page contains a graphical presentation of the spectrum. Energy of spectrum line is on the X-axis and an "equilibrium dose" constant for the spectrum line is on the Y-axis of the chart. *Total equilibrium dose constant* (Δ) is calculated as:

$$\Delta = \sum_i E_i \eta_i ,$$

where E_i is a radiation energy, η_i is a yield.

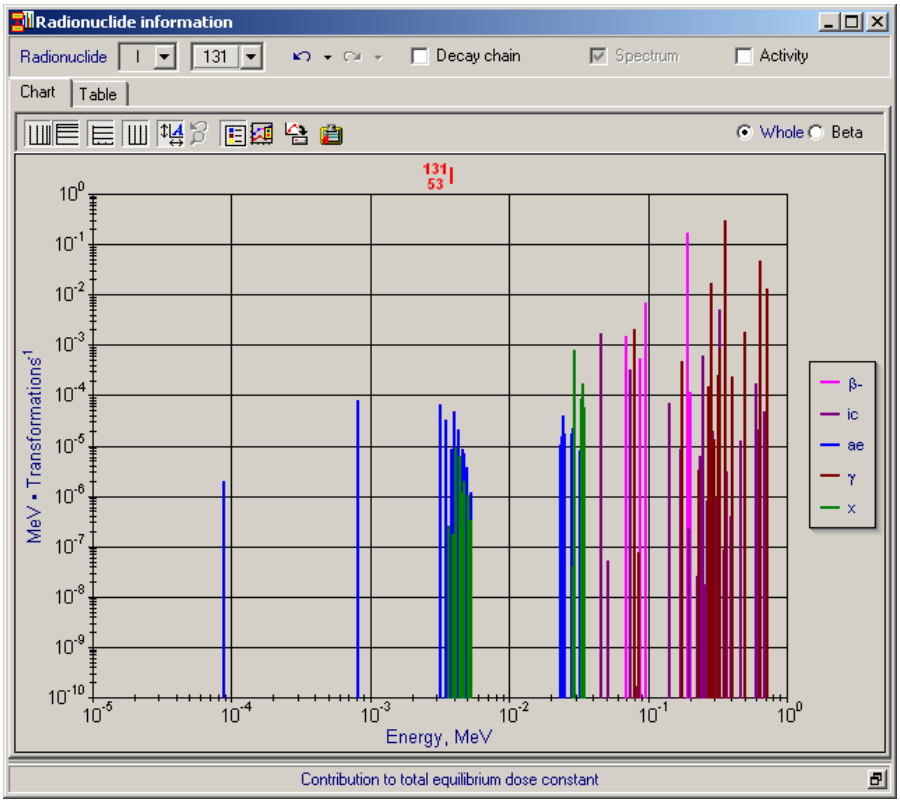


Figure 61. Spectrum of the I-131

A one line is displayed on the chart for radiation with continuous spectrum. This line presents an average value of the equilibrium dose constant. To display continuous beta-spectrum user can select the *Beta* radio item (see the Figure 62).

Most elements on the graph (plot area, titles, legend etc.) are sensitive to mouse manipulations and can be moved or resized using by drag-and-drop technology.

The *Table* page contains a tabular presentation of the dose spectrum (see the Figure 63). Columns of the table are grouped in pairs for radiation type. Energy of spectrum line (in MeV) is displayed in the first column in every pair; an equilibrium dose constant for the spectrum line is displayed in the second column.

Some abbreviations used in the *Detailed spectrum characteristics* panel:

γ	– gamma rays	α *or* a	– alpha particles
x	– X-rays	ff	– fission fragments
aq	– annihilation quanta	n	– neutrons
β+ *or* b+	– beta+ particles	pg	– prompt gamma rays
β- *or* b-	– beta- particles	dg	– delayed gamma rays
ic	– internal conversion electrons	sb	– beta particles associated with spontaneous fission
ae	– Auger electrons		

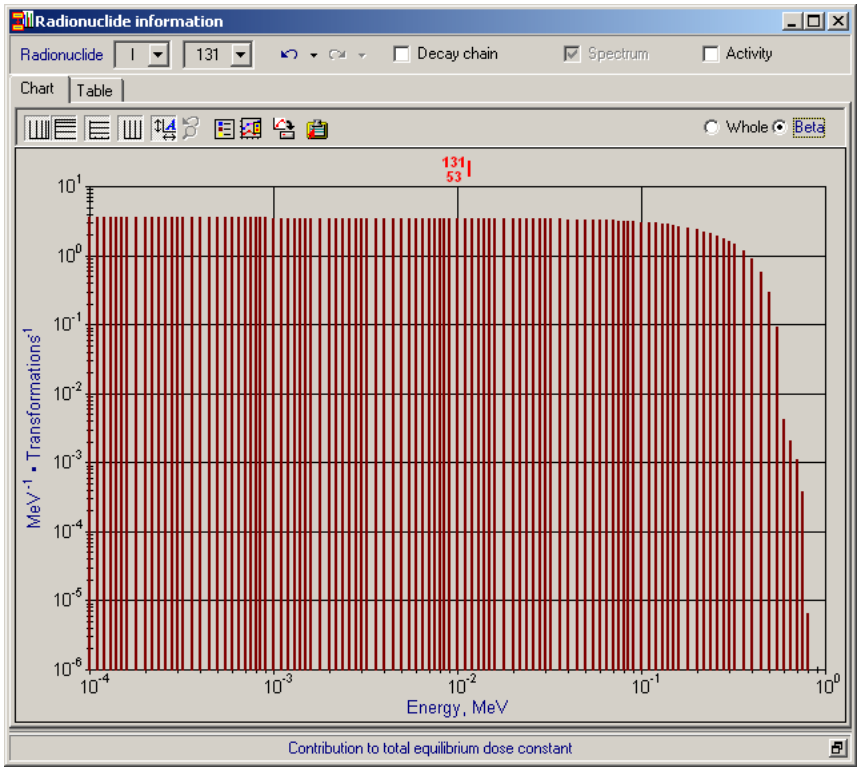
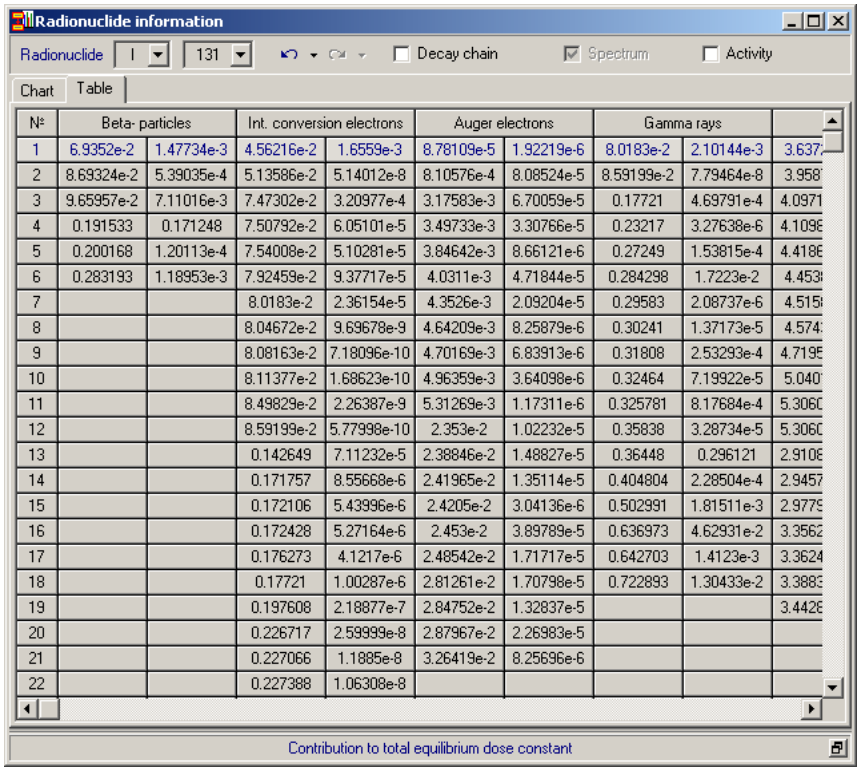


Figure 62. Beta-spectrum of the I-131



№	Beta- particles		Int. conversion electrons		Auger electrons		Gamma rays		
1	6.9352e-2	1.47734e-3	4.56216e-2	1.6559e-3	8.78109e-5	1.92219e-6	8.0183e-2	2.10144e-3	3.637
2	8.69324e-2	5.39035e-4	5.13586e-2	5.14012e-8	8.10576e-4	8.08524e-5	8.59199e-2	7.79464e-8	3.958
3	9.65957e-2	7.11016e-3	7.47302e-2	3.20977e-4	3.17583e-3	6.70059e-5	0.17721	4.69791e-4	4.0971
4	0.191533	0.171248	7.50792e-2	6.05101e-5	3.49733e-3	3.30766e-5	0.23217	3.27638e-6	4.1098
5	0.200168	1.20113e-4	7.54008e-2	5.10281e-5	3.84642e-3	8.66121e-6	0.27249	1.53815e-4	4.4186
6	0.283193	1.18953e-3	7.92459e-2	9.37717e-5	4.0311e-3	4.71844e-5	0.284298	1.7223e-2	4.453
7			8.0183e-2	2.36154e-5	4.3526e-3	2.09204e-5	0.29583	2.08737e-6	4.515
8			8.04672e-2	9.69678e-9	4.64209e-3	8.25879e-6	0.30241	1.37173e-5	4.574
9			8.08163e-2	7.18096e-10	4.70169e-3	6.83913e-6	0.31808	2.53293e-4	4.7195
10			8.11377e-2	1.68623e-10	4.96359e-3	3.64098e-6	0.32464	7.19922e-5	5.040
11			8.49829e-2	2.26387e-9	5.31269e-3	1.17311e-6	0.325781	8.17684e-4	5.3060
12			8.59199e-2	5.77998e-10	2.353e-2	1.02232e-5	0.35838	3.28734e-5	5.3060
13			0.142649	7.11232e-5	2.38846e-2	1.48827e-5	0.36448	0.296121	2.9108
14			0.171757	8.55668e-6	2.41965e-2	1.35114e-5	0.404804	2.28504e-4	2.9457
15			0.172106	5.43996e-6	2.4205e-2	3.04136e-6	0.502991	1.81511e-3	2.9779
16			0.172428	5.27164e-6	2.453e-2	3.89789e-5	0.636973	4.62931e-2	3.3562
17			0.176273	4.1217e-6	2.48542e-2	1.71717e-5	0.642703	1.4123e-3	3.3624
18			0.17721	1.00287e-6	2.81261e-2	1.70798e-5	0.722893	1.30433e-2	3.3883
19			0.197608	2.18877e-7	2.84752e-2	1.32837e-5			3.4428
20			0.226717	2.59999e-8	2.87967e-2	2.26983e-5			
21			0.227066	1.1885e-8	3.26419e-2	8.25696e-6			
22			0.227388	1.06308e-8					

Figure 63. Spectrum of the I-131 in a tabular form

10.4.2 *Summary spectrum characteristics* panel

The *Summary spectrum characteristics* panel can display following information for the selected radionuclide:

- *Contribution to total equilibrium dose constant* (default state, see the Figure 64);
- *Equilibrium dose constants, MeV* (see the Figure 66);
- *Average energies, MeV* (see the Figure 67).

The *Summary spectrum characteristics* panel has a popup (context) menu (see the Figure 65). This menu allows switching between states of the panel. The *Contribution to dose constant* panel contains *Minimize* (and *Restore*) button as the *Probable ancestors* panel.

Equilibrium dose constant for specified radiation type R (Δ_R) is calculated as:

$$\Delta_R = \sum_{i \in R} E_i \eta_i \,,$$

where only spectrum lines for specified radiation type R are included in sum.

Contribution to total equilibrium dose constant (c_R) and *Average energy* (E_R) for radiation type R are calculated as:

$$c_R = \frac{\Delta_R}{\Delta}, \; E_R = \frac{\sum_{i \in R} E_i \eta_i}{\sum_{i \in R} \eta_i} = \frac{\Delta_R}{\sum_{i \in R} \eta_i}.$$

Contribution to total equilibrium dose constant

α	β, ic, Auger	Photons	Fission fragments & neutrons
2.8e-2	0.4	0.57	0

β, ic, Auger

β+	β−	Internal conversion ele...	Auger electrons	Beta particles associat...
0	0	0.34	6.5e-2	0

Photons

γ	X-rays	Annihilation quanta	Prompt gamma rays	Delayed gamma rays
0.21	0.36	0	0	0

Figure 64. The *Summary spectrum characteristics* panel for Am-239

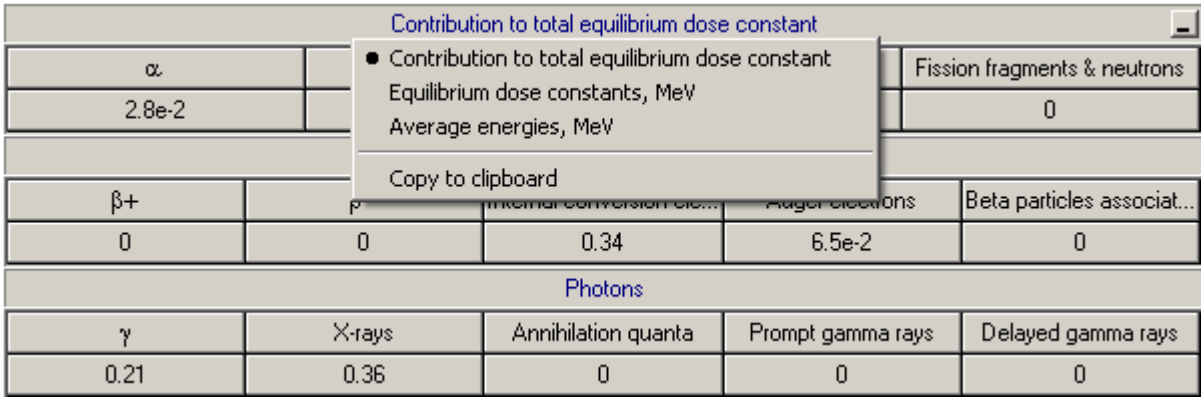


Figure 65. Popup (context) menu for the *Summary spectrum characteristics* panel

Equilibrium dose constants, MeV

α	β, ic, Auger	Photons	Fission fragments & neutrons
5.7691e-4	0.16785	0.23932	0

β, ic, Auger

β+	β−	Internal conversion ele...	Auger electrons	Beta particles associat...
0	0	0.14079	2.7061e-2	0

Photons

γ	X-rays	Annihilation quanta	Prompt gamma rays	Delayed gamma rays
8.7627e-2	0.15169	0	0	0

Figure 66. The *Summary spectrum characteristics* panel for Am-239
(the *Equilibrium dose constants, MeV* item was chosen in the context menu)

Average energies, MeV

α	β, ic, Auger	Photons	Fission fragments & neutrons
5.7691	2.3843e-2	8.8744e-2	0

β, ic, Auger

β+	β−	Internal conversion ele...	Auger electrons	Beta particles associat...
0	0	6.3413e-2	5.6145e-3	0

Photons

γ	X-rays	Annihilation quanta	Prompt gamma rays	Delayed gamma rays
0.24405	6.489e-2	0	0	0

Figure 67. The *Summary spectrum characteristics* panel for Am-239
(the *Average Energies, MeV* item was chosen in the context menu)

10.5 *Activity* panel

The *Activity* panel displays changes of activities for parental radionuclide and its daughter radionuclides with the lapse of time. In initial time, activity of parental radionuclide is equal to 1 Bq, activities of all daughter radionuclides is 0 Bq. The data are represented in graphical (the *Chart* page) and tabular (the *Table* page) forms (see Figures 68 – 69).

Two cut-off levels are used simultaneously: 10^{-8} is used for absolute values, 10^{-7} is used for relative values. If activity of any radionuclide in any point of time is less than 10^{-8}, it is accepted its activity is 0. If the ratio of activity of radionuclide to the maximal activity among all radionuclides in decay chain (for the same point of time) is less than 10^{-7}, it is accepted the activity is 0. The result of cutoff action is shown in the Figure 68 (see Pu-241, Am-241, Np-237).

The range of time from 1 minute till 10^9 years is used. The user can change time units with the *Time units* combo box

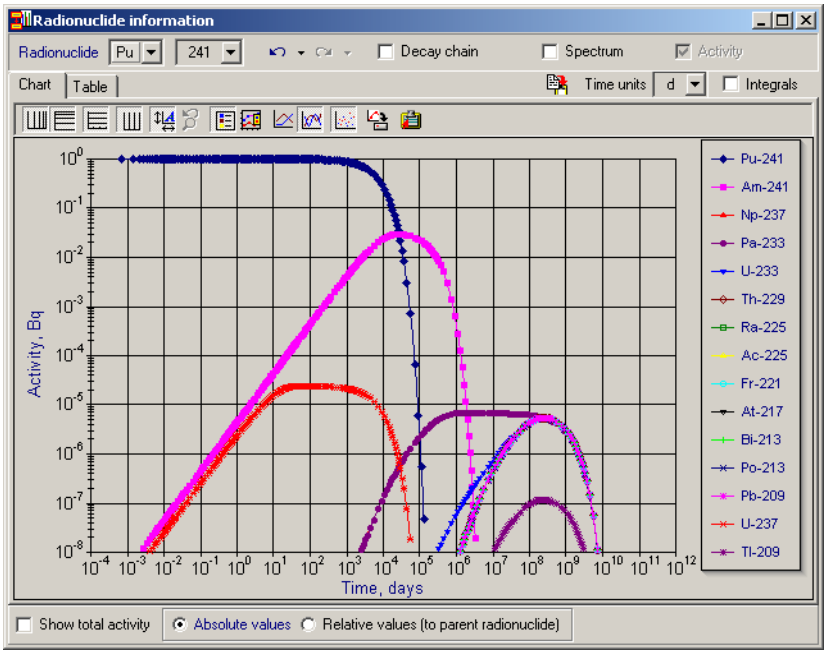


Figure 68. The *Activity* panel for Pu-241
(The *Chart* page is selected)

(see the Figure 70). Available time units are years (y), days (d), hours (h) and minutes (m). The selected time unit is displayed in the *Time units* combo box and in the title of X-axis in the chart.

The *Copy data to clipboard* button (in the Figure 69) allows copying the data from *Table* page to clipboard (with tabulation as a separator). The data copied to clipboard can be inserted into Microsoft Excel document.

The *Integrals* combo box can be used to represent integrated values of activities (see the Figure 70) in the specified time units (e.g., Bq·y or Bq·d).

The *Show total activity* check box allows to show/hide total activity data (the sum of activities of all radionuclides in a point of time). Usage of this check box is shown in Figures 71, 73. Strictly speaking, total activity is a strange value, but display of total activity can be interesting, if *Relative values* radio button is checked (see the Figure 73).

The *Values type* radio group contains two radio buttons:

- *Absolute values* radio button;
- *Relative values* radio button.

If the *Absolute values* radio button is checked (by default) the *Chart* page and the *Table* page contain absolute values of activities (or integrated activities) of radionuclides in the decay chain (see Figures 68 – 71).

There are two appearances of the *Relative values* radio button:

- *Relative values (to parental radionuclide)* (see the Figure 72);
- *Relative values (to total activity)* (see the Figure 73).

The *Relative values* radio button gives a possibility to display ratios of activities of daughter radionuclides to activity of parental radionuclide (or to total activities if the *Show total activity* check box is checked). This feature is useful, for example, to determine time for equilibrium between daughter radionuclide(s) with parental radionuclide.

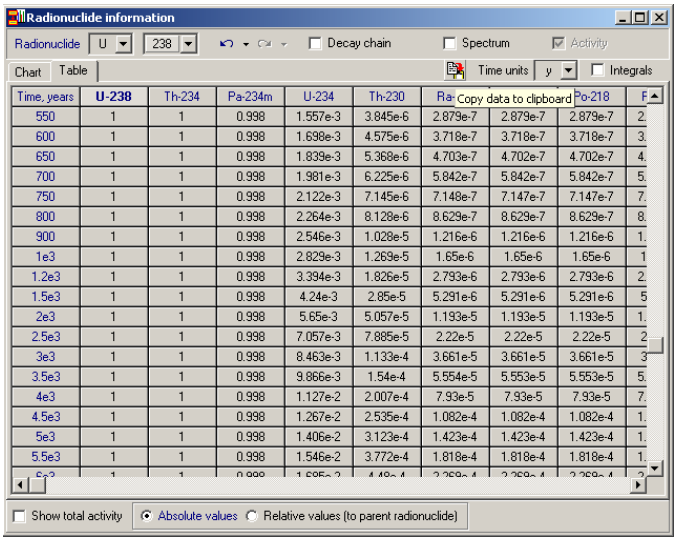


Figure 69. The *Activity* panel for U-238 (the *Table* page is selected; hint for the *Copy data to clipboard* button is displayed)

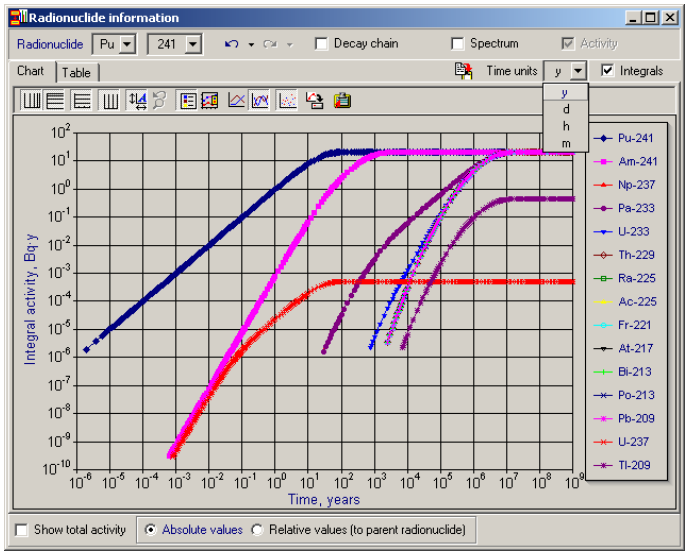


Figure 70. The *Activity* panel for Pu-241 (the *Integrals* check box is switched on; the *Time units* combo box is dropped down)

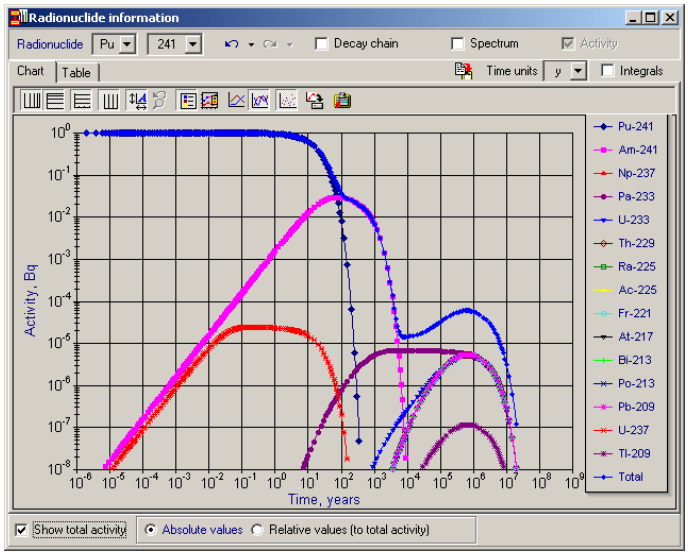


Figure 71. The *Activity* panel for Pu-241 (the *Show total activity* check box is switched on)

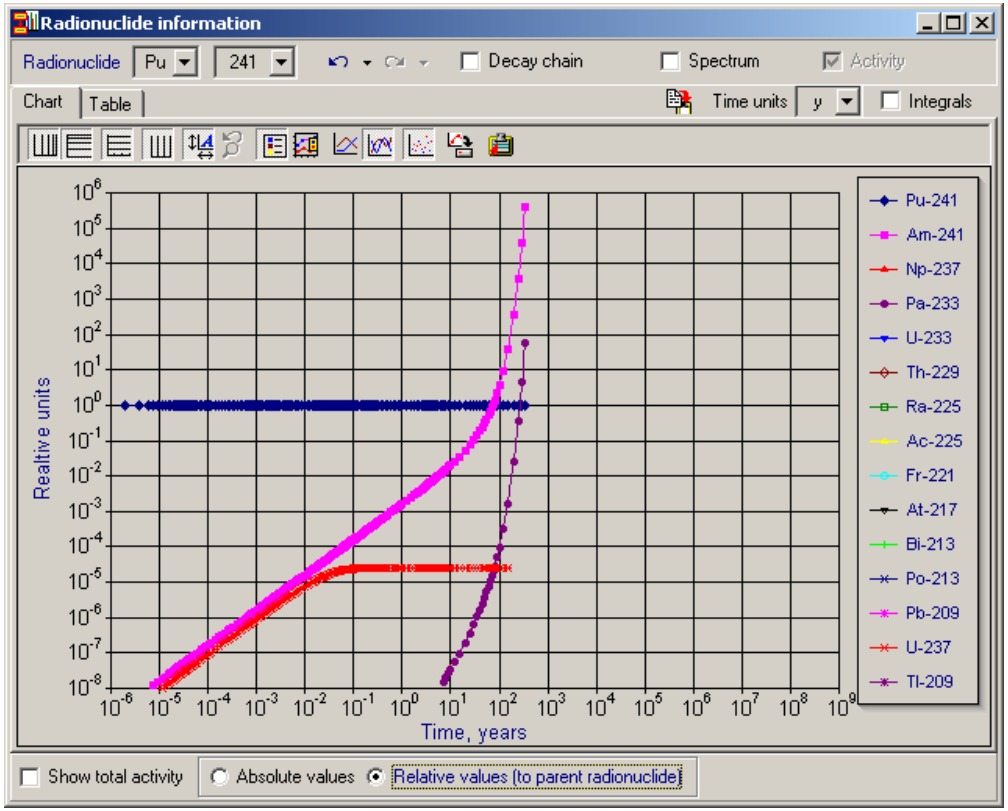


Figure 72. The *Activity* panel for Pu-241
(the *Relative values (to parent radionuclide)* radio button is selected;
the *Show total activity* check box is switched off)

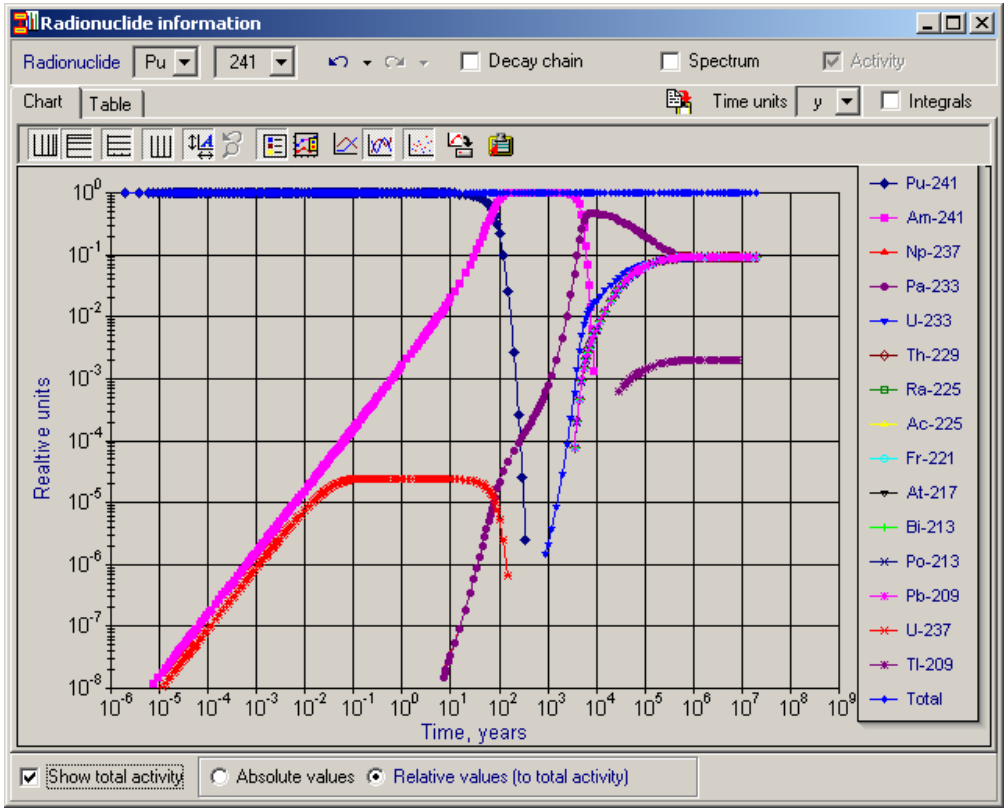


Figure 73. The *Activity* panel for Pu-241
(the *Relative values (to total activity)* radio button is selected;
the *Show total activity* check box is switched on)

10.6 *Advanced radionuclide filter*

The *Advanced radionuclide filter* is designed for selection of radionuclides in concordance with specified characteristics.

The *Advanced radionuclide filter* can be activated using the *Advanced filter…* item in Popup (context) menu of the *Radionuclide* panel (see the Figure 74). The *Advanced radionuclide filter* contains 5 'filter' pages (in top part of window) that corresponded to 5 methods of filtering, and 2 'result' pages (in bottom part of window) that display radionuclides and elements that satisfied the conditions of filtering (see the Figure 75).

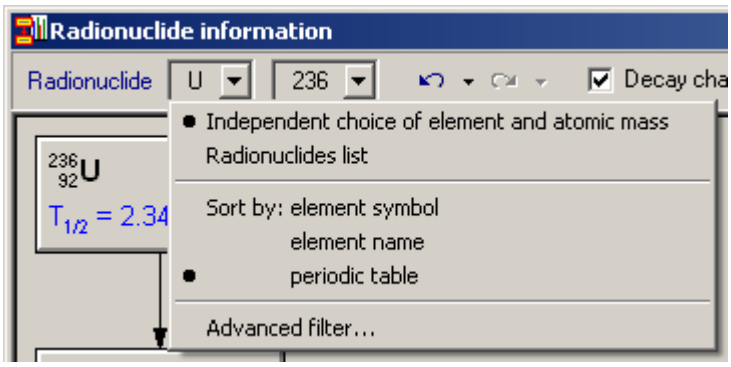
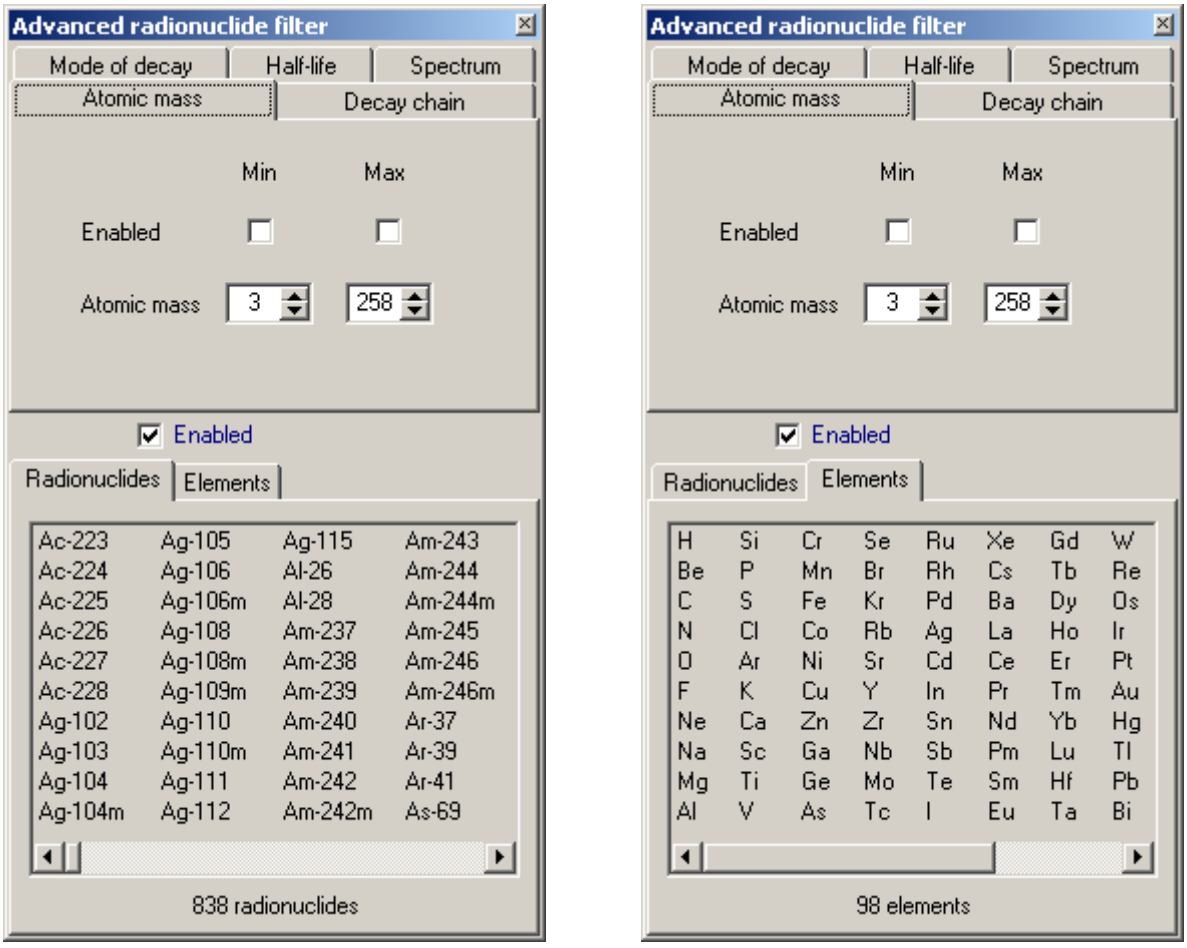


Figure 74. Popup (context) menu of the *Radionuclide* panel with *Advanced filter…* item



a b

Figure 75. The *Advanced radionuclide filter* window
(a – *Radionuclides* page is selected; b – *Elements* page is selected. All filters are disabled)

Each 'filter' page contains one or several *Enabled* check boxes that allow to switch on/off the using of corresponded filter. The *Advanced radionuclide filter* allows using several filters simultaneously (e.g. filters in *Mode of decay* page and *Spectrum* page). Quantity of filtered radionuclides and elements are displayed in the bottom part of the corresponded 'result' page (see the Figure 75). Results of filtering are applied to the *Advanced radionuclide filter* and to the *Radionuclide* panel (see subsection 10.1). Therefore, if the user will specify too many conditions in the *Advanced radionuclide filter*, he will can see empty lists in the *Advanced radionuclide*

filter and also in the *Radionuclide* panel (see the Figure 76). The *Enabled* check box in the central part of the *Advanced radionuclide filter* allows to switch on/off using the *Advanced radionuclide filter*. If 'main' *Enabled* check box is unchecked all 'local' *Enabled* check boxes in 'filter' pages are ignored and filtering is disabled.

The *Advanced radionuclide filter* contains the following 'filter' pages:

1) *Atomic mass* page (see the Figure 77) allows to perform the filtering by atomic mass. The user can specify minimum and/or maximum atomic mass and check corresponded *Enabled* checkbox (es).
2) *Decay chain* page (see the Figure 78) is designed for filtering by quantity of ancestors (one or several values from 0 to 4) and/or daughter radionuclides (one or several values from 0 to 3). 'OR' logical operation is applied to selected values (or corresponded check boxes) inside each group (*Ancestors* group or *Daughters* group). 'AND' logical operation is applied to filter results between groups. Each group contains individual *Enabled* check box.

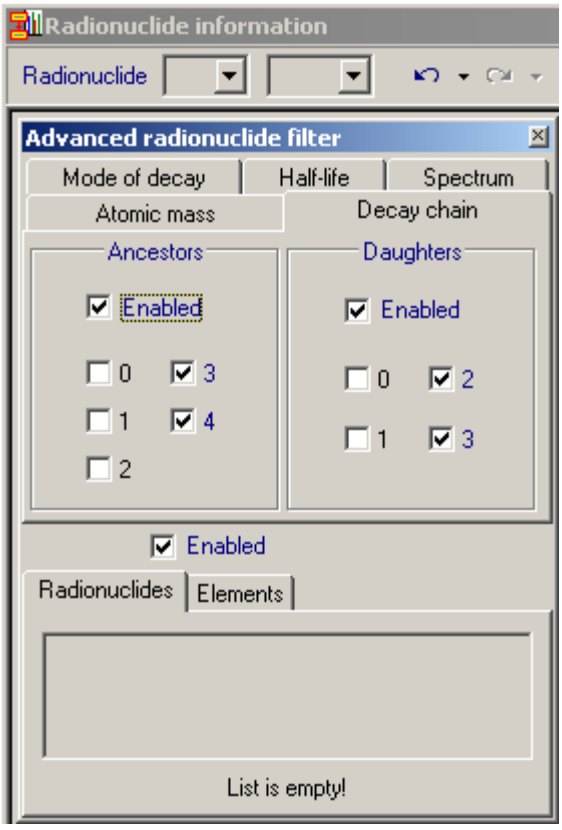


Figure 76. The *Advanced radionuclide filter* and the *Radionuclide* panel with empty lists

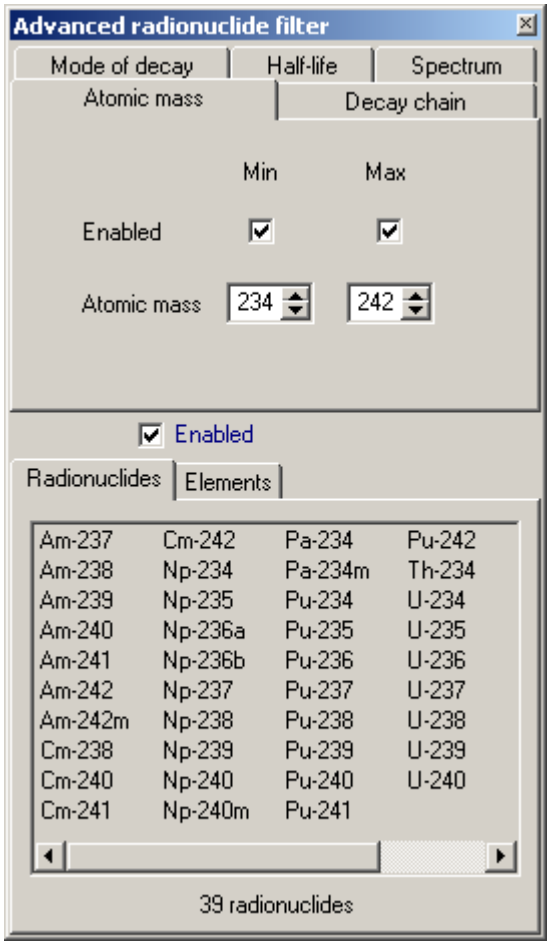


Figure 77. The *Atomic mass* page of *Advanced radionuclide filter*

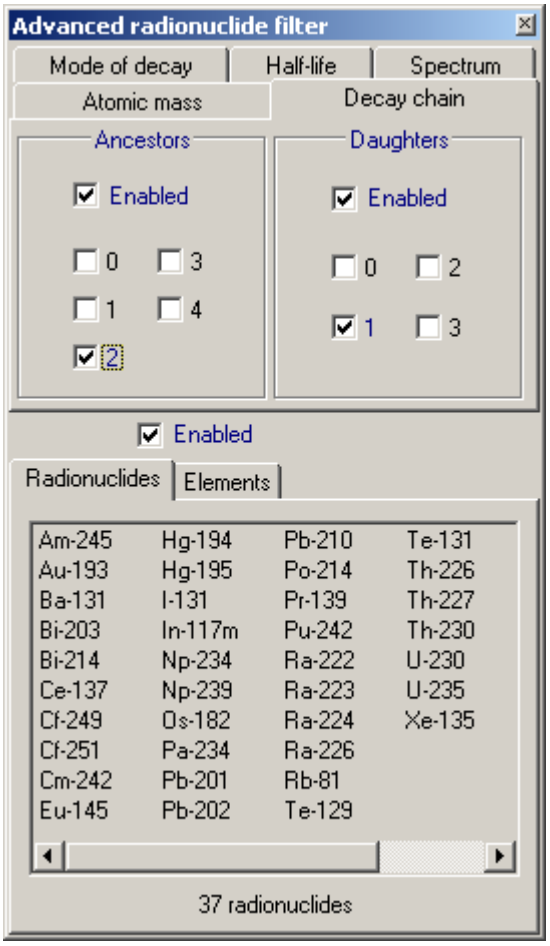
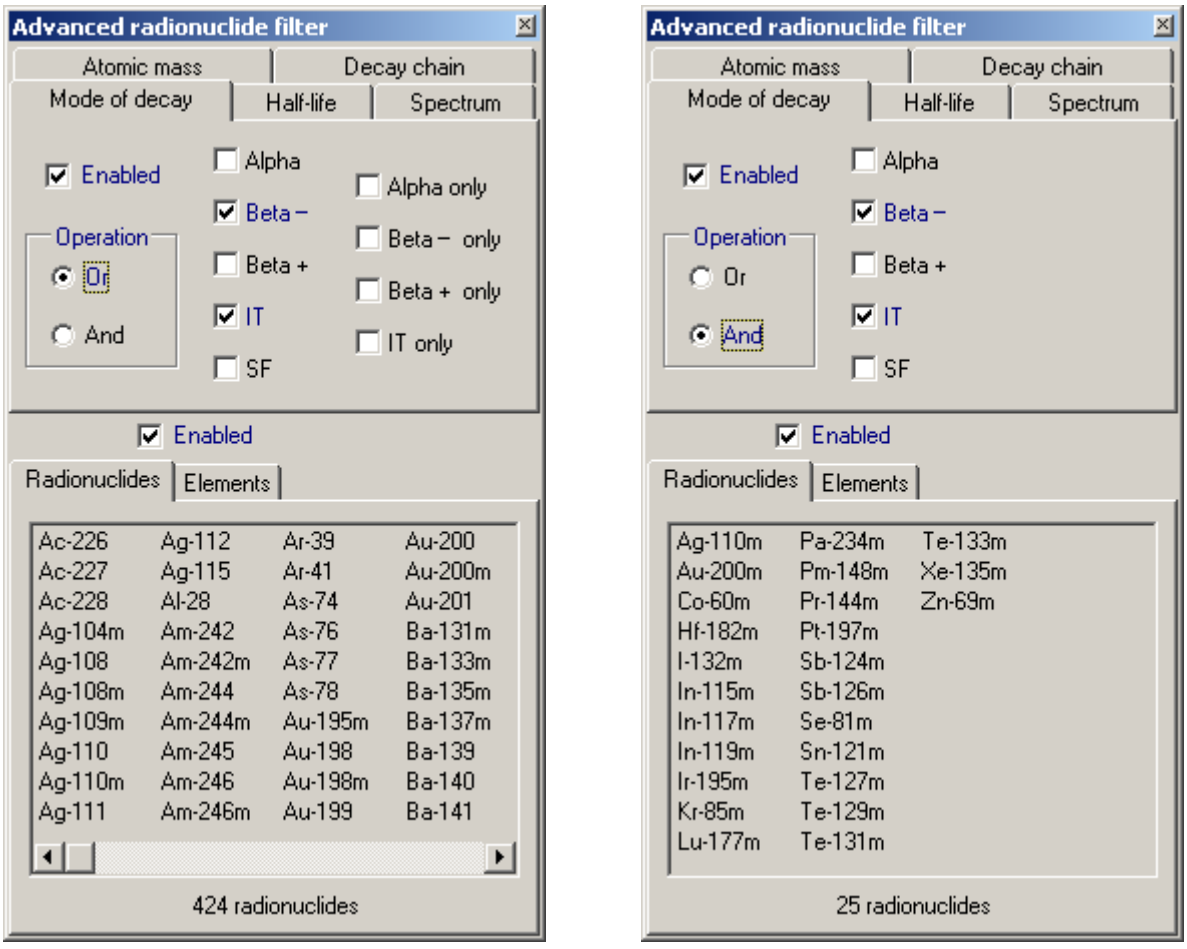


Figure 78. The *Decay chain* page of *Advanced radionuclide filter*

3) *Mode of decay* page (see the Figure 79) is meant for filtering the radionuclides by their modes of decay. The following modes of decay are available for filtering:
   – alpha decay (*Alpha* check box and *Alpha only* check box);
   – beta-negative decay (*Beta* – check box and *Beta – only* check box);
   – beta-positive decay (*Beta* + check box and *Beta + only* check box);
   – internal conversion or internal transition (*IT* check box and *IT only* check box);
   – spontaneous fission (*SF* check box).

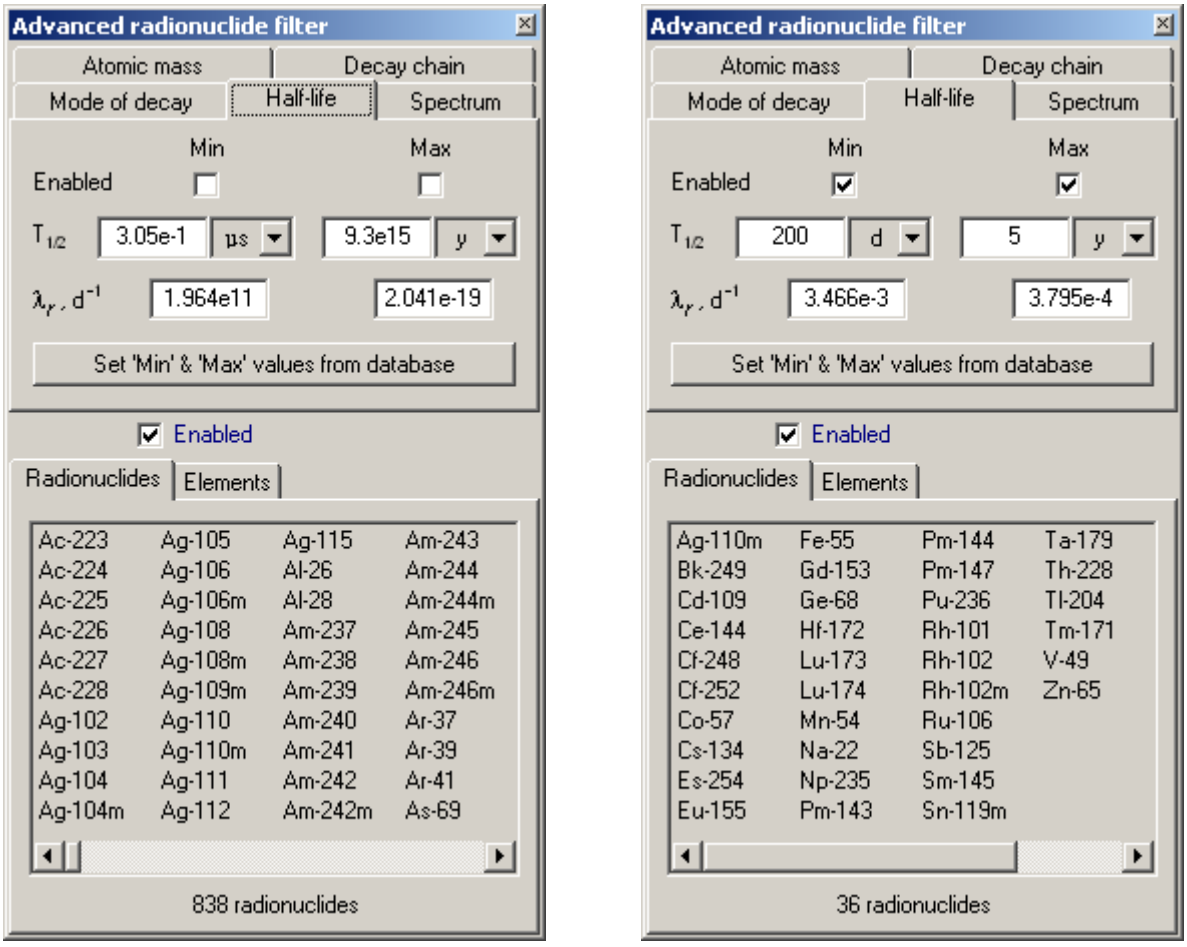
   Electron capture (for purposes of filtering) is included in beta-positive decay.
   The *Operation* radio group gives a possibility to specify a logical operation which will be used for the filtering: OR operation (see the Figure 79a) or AND operation (see the Figure 79b). For example, if the user checks the *Beta* – check box and the *IT* check box when the *Or* radio item is selected, 'result' pages will contains radionuclides for which beta-negative decay or internal conversion are possible (424 radionuclides, see the Figure 79a). If the user checks aforesaid check boxes and selects the *And* radio item, 'result' pages will contains radionuclides for which both beta-negative decay and internal conversion are possible (25 radionuclides, see the Figure 79b).
   Check boxes with 'only' additions are intended for including in the filtering radionuclides for which only one mode of decay is possible (e.g., alpha or beta-negative decay). Since specified check boxes define disjoint sets of radionuclides, they are visible only if *Or* radio item is selected (OR operation is activated).



a b

Figure 79. The *Mode of decay* page of *Advanced radionuclide filter*
(a – *Or* operation is selected; b – *And* operation is selected)

4) *Half-life* page (see the Figure 80) gives a possibility to select radionucludes which half-lives ($T_{1/2}$) or decay constants (λ_r) are in a specified range. The user can set the minimal and/or maximal value for $T_{1/2}$ or λ_r and specify measurement units for $T_{1/2}$ values (from microseconds till years as it is showed in the Figure 80b). λ_r values are displayed always in d^{-1}. When minimal or maximal $T_{1/2}$ value is changed by the user the corresponded λ_r value is automatically synchronized with $T_{1/2}$ value and vice versa. If the user changes measurement units the $T_{1/2}$ value is automatically recalculated (e.g., from 200 days to 4 800 hours).
Initially minimal $T_{1/2}$ value is equal to 0.305 μs (half-life of Po-212), maximal $T_{1/2}$ value is equal to $9.3 \cdot 10^{15}$ years (half-life of Cd-113). Initial $T_{1/2}$ values are displayed in the Figure 80a. If the user changes these values they can be restored by pressing the *Set 'Min' & 'Max' values from database* button.



a b

Figure 80. The *Half-life* page of *Advanced radionuclide filter*
(a – minimal and maximal half-life values are determined from radionuclide database (initial state);
b – result of the filtering: radionuclides with half-lives in range from 200 days to 5 years)

5) *Spectrum* page (see the Figure 81) is intended for the filtering by spectrum characteristics of radionuclides. The following characteristics are used for the filtering:
- *total equilibrium dose constant* (Δ, MeV) which is described in subsection 10.4.1;
- *equilibrium dose constant* for radiation type R (Δ_R, MeV) which is described in subsection 10.4.2. Δ_α, Δ_β, Δ_γ, and Δ_{SF} values are available for the filtering;
- *contribution to total equilibrium dose constant* (c_R, %) for radiation type R which is described in subsection 10.4.2. c_α, c_β, c_γ, and c_{SF} values are available;
- radiation energy for spectrum line of radiation type R ($E_{R,i}$, MeV). $E_{\alpha,i}$, $E_{\beta,i}$, and $E_{\gamma,i}$ are available for the filtering (subscript i means that at least one spectrum line of radionuclide must satisfy to the condition);

– ‘equilibrium dose constant’ for spectrum line of radiation type R ($\Delta_{R,i}$, MeV; actually, for one spectrum line it is equal to product of a radiation energy and a yield, i.e. $\Delta_{R,i} = E_i \cdot \eta_i$). $\Delta_{\alpha,i}$, $\Delta_{\beta,i}$, and $\Delta_{\gamma,i}$ are available for the filtering (subscript i means that that at least one spectrum line of radionuclide must satisfy to the condition).

Above-listed characteristics are combined in one table (see the Figure 81). For editing values in cells of the table the user should double-click or press the *F2* key.

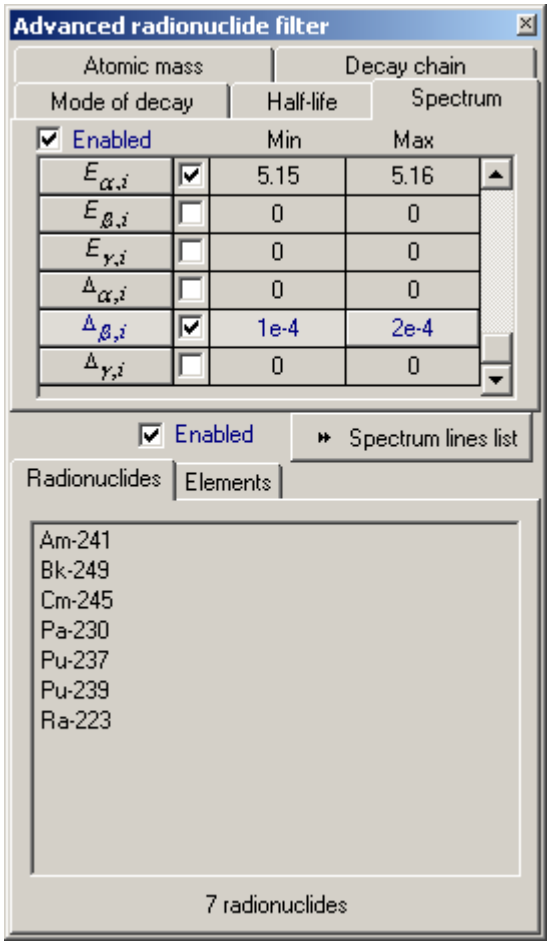


Figure 81. The *Spectrum* page of *Advanced radionuclide filter* (the *Spectrum lines* group is hidden)

In contrast to other ‘filter’ pages the *Spectrum* page contains the *Spectrum lines list* button that allows displaying spectrum lines which are satisfy to the conditions of the filtering. If the user presses the *Spectrum lines list* button, right part of the *Advanced radionuclide filter* with the *Spectrum lines* group becomes visible (see the Figure 83).

The *Spectrum lines* group contains three tables (for alpha, beta, and gamma radiation) which can display corresponded spectrum lines satisfied to specified conditions for Δ, Δ_R, c_R, $E_{R,i}$, and $\Delta_{R,i}$ values. Switching between the tables is performed by means of radio group with 3 corresponded radio items (α, β, γ) in top part of the *Spectrum lines* group. Each table is filled only if a corresponded characteristic ($E_{R,i}$ and/or $\Delta_{R,i}$) is used for the filtering. For example, the table for alpha radiation is filled only if the user includes $E_{\alpha,i}$ and/or $\Delta_{\alpha,i}$ in the filtering (see the Figure 83a). Other characteristics also can effect on the contents of this table, but if neither $E_{\alpha,i}$ nor $\Delta_{\alpha,i}$ does not included in the filtering the table for alpha radiation will be empty.

Each table in the *Spectrum lines* group has a popup (context) menu (see the Figure 82). Menu items of the popup menu give a possibility:

– to sort a table by periodic table, by half-life, by energy, by product of energy and yield;
– to copy a table to the clipboard with tabulation as separator.

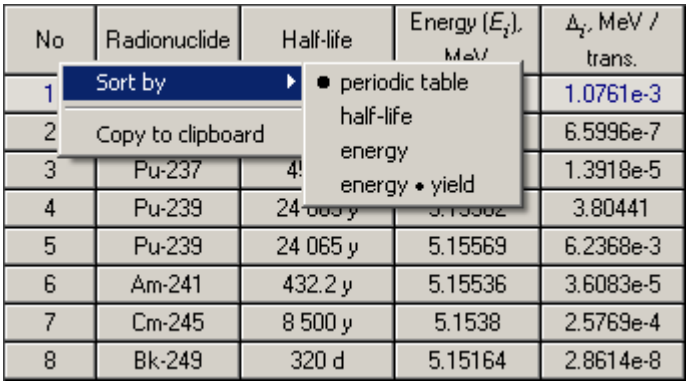
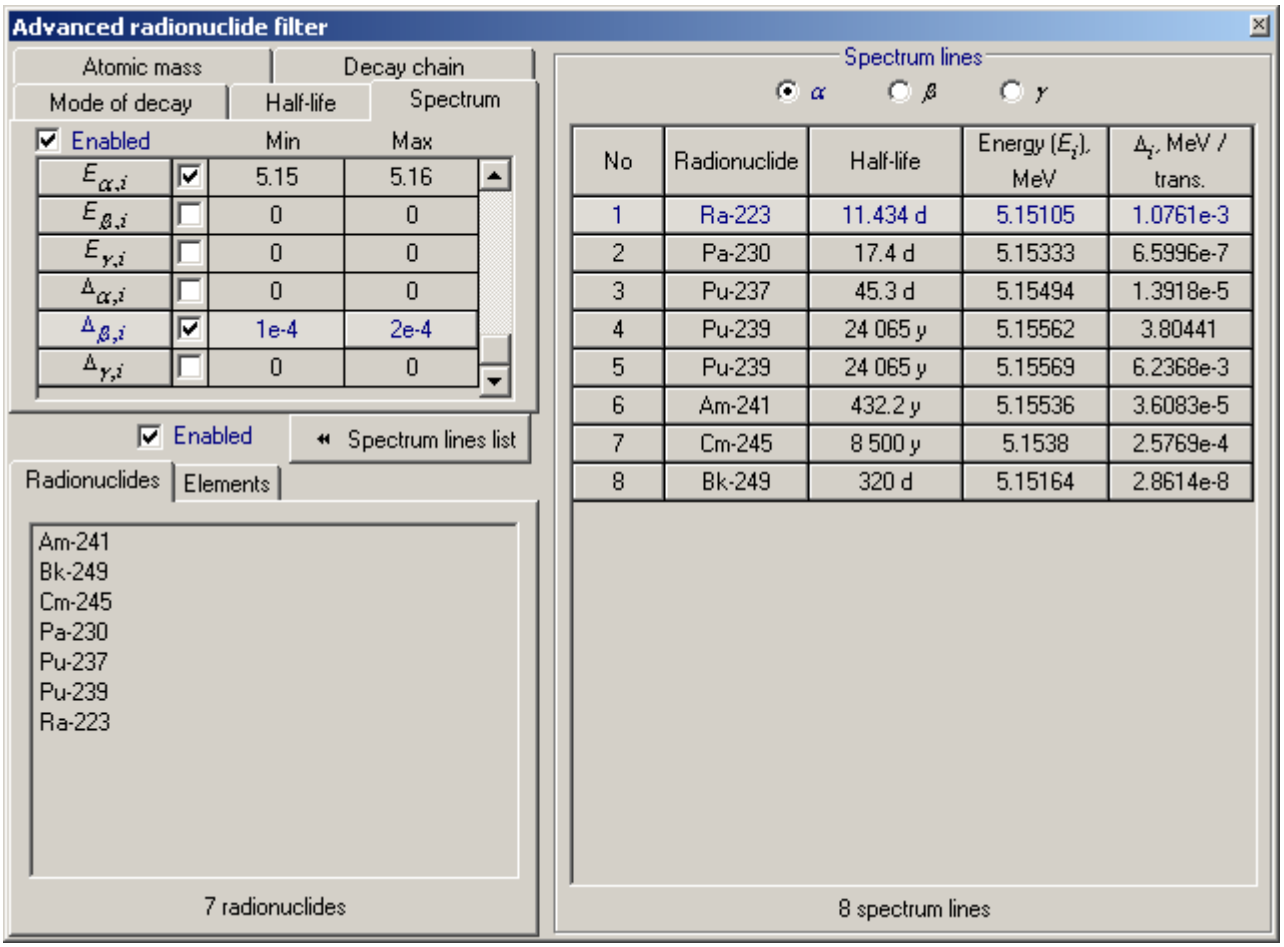


Figure 82. Popup (context) menu of a table in the *Spectrum lines* group

a



b

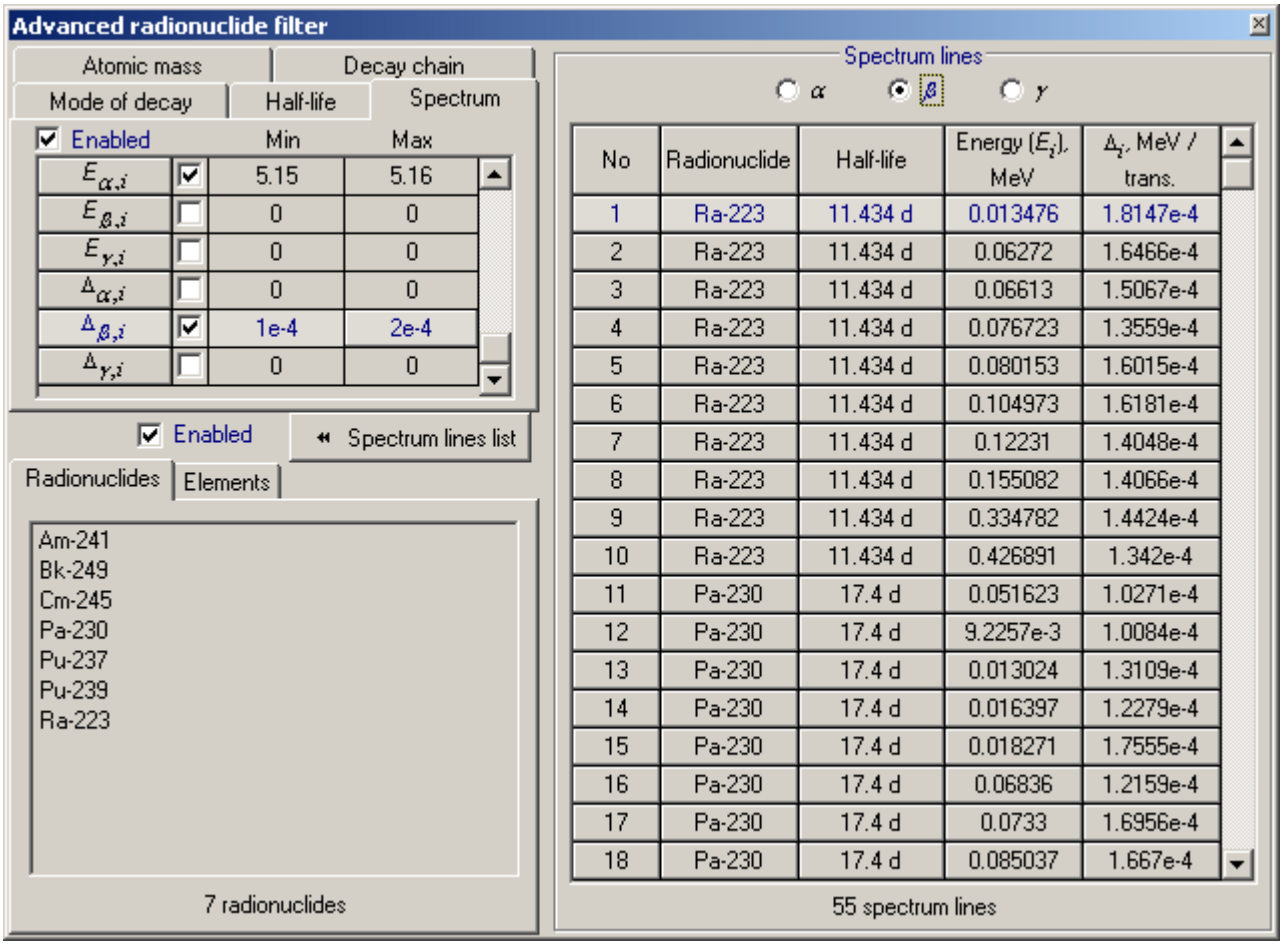


Figure 83. The *Spectrum* page of *Advanced radionuclide filter*
(a – α radio item is selected; b – β radio item is selected)

ANNEX A

Classical ICRP scheme of the intake reconstruction

Classical interpretation schemes for routine, special and task-related individual monitoring have been recommended by the ICRP Publication 54 and by the ICRP Publication 78, which replaced the Publication 54 in 1997. Classical approaches have the following distinguishing features:

(a) Routine monitoring is carried out at regular intervals during normal operation. In data interpretation it is assumed that acute intake occurs at the mid-point of the monitoring interval.

(b) The reconstruction of an intake is usually performed on a basis of a single data point in a time series of measurements. If more than 10% of the actual measured quantity may be attributed to intake in previous monitoring intervals, for which intake have already been assessed, a relevant correction is recommended.

(c) In special and task-related monitoring it is assumed that an acute intake has occurred and the time of intake is known.

(d) In a case of inhalation all types of interpretation schemes demand *a priori* information about the Type of Materials and the aerosol particle size (in the Publication 78 an AMAD of 5 μm is assumed).

This scheme could be used for the analysis of all cases of intakes of radionuclides. In many cases it gives acceptable estimation of the total intake, as far as it could be done at all. But this classical scheme has some substantial limitations, connected with used approaches.

ANNEX B

New method of the intake reconstruction

The new method extends the possibilities of the classical ICRP scheme. The features of this data interpretation method are:

(a) Reconstruction of the intake on a basis of a multi-points approximation of observed trends of measurements;
(b) Possibility to use several data sets simultaneously (e.g. WBC and bioassay data);
(c) Approximation of observed data with the use of a set of tabulated retention and excretion functions, calculated in advance for an assumed range of exposure conditions. Arbitrary intake patterns can be used in such calculations. The line up and scaling of theoretical curves are performed in the interactive mode;
(d) Approximation, which involves an interactive numerical deconvolution and a recurrent optimisation of the data fitting during the deconvolution. The linear combination of time-shifted biokinetic model response (retention or excretion functions following an acute intake of unit amount) is used in this method;
(e) Possibility to assess the date and pattern of intake, the solubility of the aerosol (Types of Materials) and its particle size;
(f) Interactive and automatic modes of data interpretation.

In the approximation the linear combination of biokinetic responses is built in the course of a multi-step optimisation process. The *Manual mode* or *Semi-Automated mode* of data fitting helps the user to achieve the most reliable results. A subset of the observed series of measurements is used on each step.

The required linear combination has the form:

$$F_n(t) = \sum_{i=1}^{n} a_i R(t - \tau_i), \qquad (1)$$

where

$F_n(t)$ = function of time t, which approximates the observed time series of the radionuclide content in the body, organs and bioassay probes;

n = number of intervals constituting a time segment $[0, t]$; in the course of the approximation process n denotes the number of iteration steps;

$R(t)$ = response of the biokinetic model for a unit delta-impulse (radionuclide content in the body, organs or in bioassay probes after a unit acute intake at $t = 0$ predicted by the model at time t);

τ_i = time shift of the acute intake i (the result of the optimising search);

a_i = scaling factor for the response to the acute intake i (the result of the optimising search).

The search for the linear combination is performed from the first point of the observed series of measurements, with involving subsequent measurements into the approximation process. By the time t, n time intervals $\Delta t_i = t_{i+1} - t_i$ are used in the optimisation task. Together they constitute a time segment $[0, t]$: $\sum_{i=0}^{n-1}(t_{i+1} - t_i) = t$. One or several points of measurement series $M(t_j)$ fall on the each of considered time intervals Δt_i, so that $t_i \le t_j < t_{i+1}$.

Either a weighted least-squares fit (*WLSF*)

$$\min \sum_{k=j_1}^{j_2} \left(\sum_{i=1}^{n} a_i R(t_k - \tau_i) - M(t_k) \right)^2 W_k , \tag{2}$$

or an unweighted least-squares fit (*ULSF*)

$$\min \sum_{k=j_1}^{j_2} \left(\sum_{i=1}^{n} a_i R(t_k - \tau_i) - M(t_k) \right)^2 , \tag{3}$$

is used to estimate the value of an intake parameter a_n.

In equations (2) and (3):

k = index of the measurement of the radionuclide $M(t_k)$ at time t_k;

i = index of the time interval, on which a single response can fit the selected subset of measurement series;

n = current step number in the iterative process;

τ_i = shift in time of the i^{th} acute intake; the shift τ_n for the last term of the sum is a required parameter of the current step of the approximation;

$R(t)$ = response of the biokinetic model for a unit delta-impulse (radionuclide content in the body, organs or in bioassay probes after a unit acute intake at $t = 0$ predicted by the model at time t);

a_i = scaling factor for the response function, the factor a_n is the required parameter of the current step of the optimization;

W_k = weighting factor of the measurement k, chosen by a user;

j_1, j_2 = index of the extreme left and right points of data series $M(t_k)$ included into the interval of approximation n.

The *ULSF* procedure is often used to fit bioassay data when it is assumed the constant variance of the measurements. This procedure is implemented in the IMIE as *ULSF weighting method*.

To consider the analytical variance associated with the detection of radionuclides in bioassay samples the *WLSF* procedure is useful with weighting factors

$$W_k = \frac{1}{\sigma_k^2}, \tag{4}$$

where σ_k is an absolute uncertainty of the measurement k. This procedure is implemented in the IMIE as *WLSF-UD weighting method*. If σ_k is treated as standard deviation this method is identical to the maximum likelihood method.

The variance in the measurement data most often is dominated by biological variance as opposed to analytical variance associated with the detection of radionuclides in bioassay samples. In that case the *WLSF* procedure is recommended with weighting factors inversely proportional to the expected measurements:

$$W_k = \frac{1}{\psi\, a_n\, R(t_k - \tau_n)}, \tag{5}$$

where ψ is coefficient of proportion. This procedure is implemented in the IMIE as *WLSF-EV weighting method*.

Several data sets of measurements with non-equal precision can be treated by the described method. For *s* data sets ($m_1..m_s$) the optimisation problem (2) can be formulated as

.

$$\left[\begin{array}{l} \\ \min \sum_{k=j_1}^{j_2}\left(\sum_{i=1}^{n} a_i^{m_1} R^{m_1}(t_k-\tau_i) - M^{m_1}(t_k)\right)^2 W_k^{m_1} \\ t_{n-1} \le t_k < t_n \\ \ldots \\ \min \sum_{l=p_1}^{p_2}\left(\sum_{i=1}^{n} a_i^{m_s} R^{m_s}(t_l-\tau_i) - M^{m_s}(t_l)\right)^2 W_l^{m_s} \\ t_{n-1} \le t_l < t_n \\ 0 \le \tau_{n-1} < \tau_n \\ \min \dfrac{S \cdot \sqrt{\sum_{i=1, j>i}^{s} (a_n^i - a_n^j)^2}}{\sum_{i=1}^{s} a_n^i} \end{array}\right. \qquad (6)$$

Such approach is implemented in the IMIE as the *Closest intakes* method of the simultaneous analysis. Instead of the condition $\min \dfrac{S \cdot \sqrt{\sum_{i=1, j>i}^{s} (a_n^i - a_n^j)^2}}{\sum_{i=1}^{s} a_n^i}$ in (6) an expert's judgment can be used in the interactive mode of approximation.

For example, in the case of intake of plutonium the measurements of the plutonium content in the lungs $M^L(t)$ and in daily urine excretion $M^U(t)$ can be available. In adopting the relative distance method, on the interval *n* of the approximation, the optimisation problem (6) can be formulated as

$$\left[\begin{array}{l} \min \sum_{k=j_1}^{j_2}\left(\sum_{i=1}^{n} a_i^L R^L(t_k-\tau_i) - M^L(t_k)\right)^2 W_k^L \\ t_{n-1} \le t_k < t_n \\ \min \sum_{l=p_1}^{p_2}\left(\sum_{i=1}^{n} a_i^U R^U(t_l-\tau_i) - M^U(t_l)\right)^2 W_l^U \\ t_{n-1} \le t_l < t_n \\ 0 \le \tau_{n-1} < \tau_n \\ \min \dfrac{2 \cdot | a_n^L - a_n^U |}{a_n^L + a_n^U} \end{array}\right. . \qquad (7)$$

To find the "best fit" result in analysis of s data sets of measurements $m_1..m_s$ an alternative optimisation problem can be formulated

$$\begin{cases} \min\left(\sum_{l=1}^{s} \left(C^{m_l} \cdot \sum_{k=j_1^{m_l}}^{j_2^{m_l}} \left(\sum_{i=1}^{n} a_i R^{m_l}(t_k - \tau_i) - M^{m_l}(t_k) \right)^2 W_k^{m_l} \right) \right) \\ t_{n-1} \le t_k < t_n \\ 0 \le \tau_{n-1} < \tau_n \end{cases}, \quad (8)$$

where C^{m_l} = the weight assigned to measurement set m_l by the user. Such approach is implemented in the IMIE as the *Minimal distance* method of the simultaneous analysis. For example, in the above case of intake of plutonium with following measurements of the plutonium content in the lungs $M^L(t)$ and in daily urine excretion $M^U(t)$, the optimisation problem (8) can be formulated as

$$\begin{cases} \min\left(C^L \cdot \sum_{k=j_1}^{j_2} \left(\sum_{i=1}^{n} a_i R^L(t_k - \tau_i) - M^L(t_k) \right)^2 W_k^L + C^U \cdot \sum_{l=p_1}^{p_2} \left(\sum_{i=1}^{n} a_i R^U(t_l - \tau_i) - M^U(t_l) \right)^2 W_l^U \right) \\ t_{n-1} \le t_k < t_n \\ t_{n-1} \le t_l < t_n \\ 0 \le \tau_{n-1} < \tau_n \end{cases}, \quad (9)$$

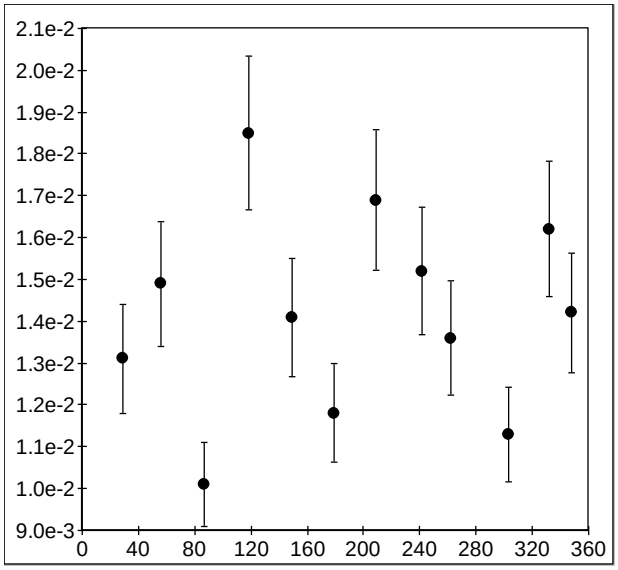
where C^L and C^U = the weights assigned to lungs and urine measurement sets by the user.

In the case of supposed chronic intake the modification of described algorithm is used: assumption on big number of consecutive acute intakes on each monitoring interval is applied.

Figure 84 illustrates the steps in the consecutive data approximation. The artificially generated data set (Figure 84a, 84h) for the case of ^{241}Am multiple inhalation has been sampled every month (points on the graphs). The approximation algorithm works in the following order:

1. The user selects a first time interval of the approximation, on which a single response can fit the selected subset of the measurement series.
   1.1. Taking into account the subject's anamnesis the user inputs the supposed date of the first intake. In the absence of information, and in the automatic mode, the centre of the uncertainty interval can be used.
   1.2. The user chooses the last point of the first data subset. One or several data points can fall on the chosen first interval.
2. Perform the data approximation on the selected interval (Figure 84b).
   2.1. If one data point falls on the selected interval the computer code calculates the scaling factor a_n without a re-assessment of the date of intake and other conditions of exposure.
   2.2. If two or more data points fall on the selected interval the re-assessment of the date of intake and exposure conditions is possible (Figures 84c, 84d, 84f, 84g). The time shift τ_n of the response function is being determined by the 'best fit' search.
   2.3. If the approximation on the Step 2.2 is not satisfactory, the initially selected data subset can be adjusted.
3. Select the next time interval. The left end of a new interval coincides with the right end of the previous interval. The right end of the new interval is chosen as in Step 1.2.
4. Execute Step 2 for the new time interval (Figure 84c).
5. Execute Steps 3 and 4 for successive data points (Figure 84d, 84e, 84f, 84g).

Figure 84h gives the "true" value of the excretion rates.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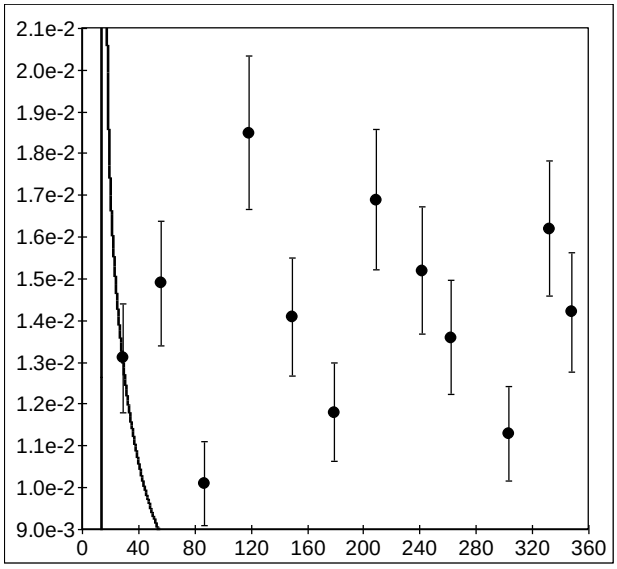
1.8e-2
1.7e-2
1.6e-2
1.5e-2
1.4e-2
1.3e-2
1.2e-2
1.1e-2
1.0e-2
9.0e-3
0 40 80 120 160 200 240 280 320 360

a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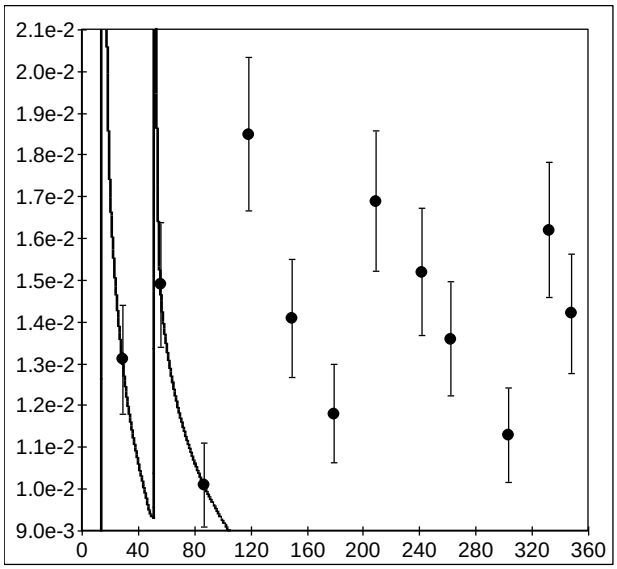
b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1.0e-2
9.0e-3
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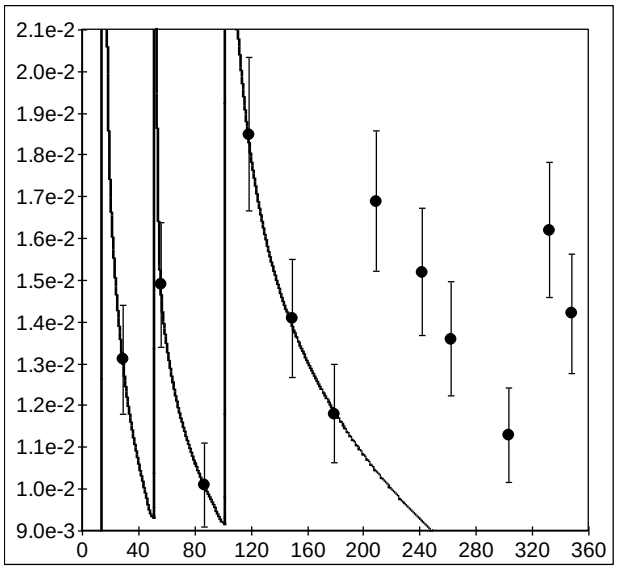
c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1.1e-2
1.0e-2
9.0e-3
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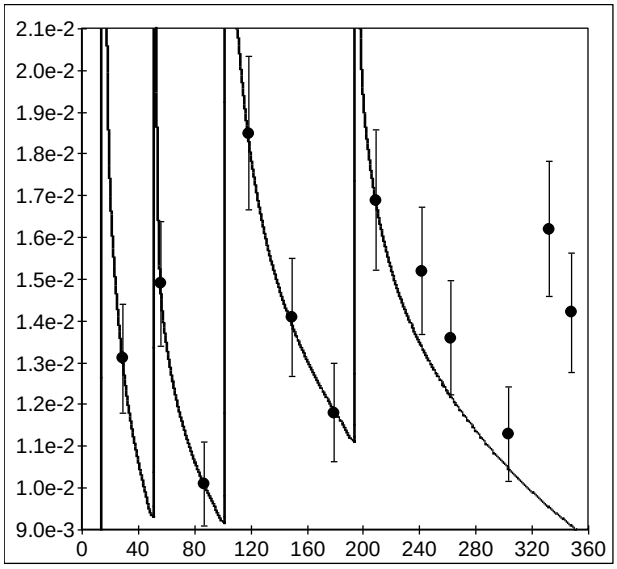
d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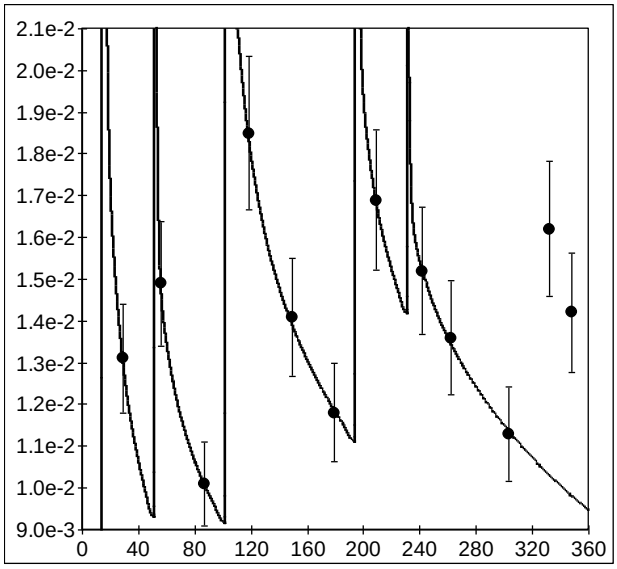
e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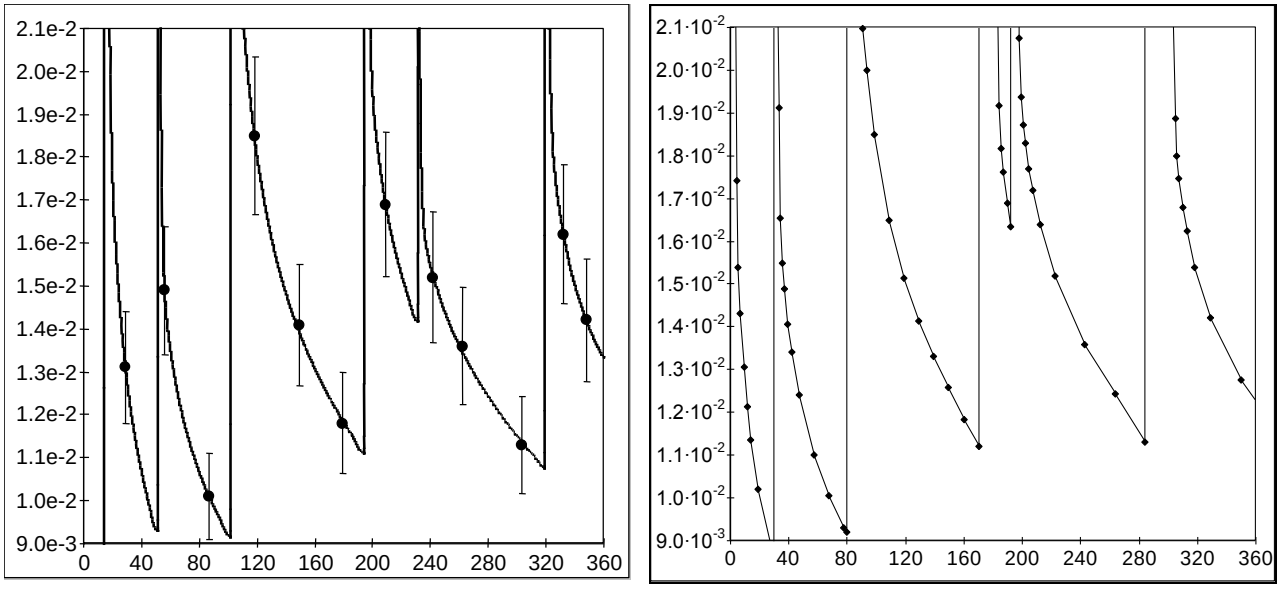
1.1e-2
1.0e-2
9.0e-3
0 40 80 120 160 200 240 280 320 360

f



g h

Figure 84. Scheme of the approximation algorithm work

On vertical axis is daily excretion rate (Bq/day) of ^{241}Am.
On horizontal axis is the time (days).
g – results of approximation
h – "true" curve.

ANNEX C

Fractional absorption (f_1) values used for calculations of response functions and effective dose

Element	Ingestion	Inhalation		
		F	M	S
Ag	0.05	0.05	0.05	0.05
Am	5e-4		5e-4	5e-4
Ba	0.1	0.1		
Ce	5e-4		5e-4	5e-4
Co	0.1		0.1	0.05
Cr	0.1	0.1	0.1	0.1
Cs	1	1		
Fe	0.1	0.1	0.1	
H	1			
I	1	1		
Mn	0.1	0.1	0.1	
Nb	0.01		0.01	0.01
Np	5e-4		5e-4	
P	0.8	0.8	0.8	
Pb	0.2	0.2		
Po	0.1	0.1	0.1	
Pu	5e-4		5e-4	1e-5
Ra	0.2		0.2	
Ru	0.05	0.05	0.05	0.05
S	0.8	0.8	0.8	
Sr	0.3	0.3		0.01
Tc	0.8	0.8	0.8	
Te	0.3	0.3	0.3	
Th	5e-4		5e-4	2e-4
Tl	1	1		
U	0.02	0.02	0.02	2e-3
Zn	0.5			0.5
Zr	2e-3	2e-3	2e-3	2e-3

ANNEX D

Reconstruction of the intake with an arbitrary shape in the time

Mathematical nature of the problem

The *in vivo*/bioassay data interpretation belongs to the class of so named ‘inverse’ mathematical problems, in which known parameters (e.g. the measured activity in the body or organs) is a result of integration of required in the problem parameters (intakes). More precisely, the observed activity in the body is the convolution of the intake function with the retention function. In a common case such problems have not a unique solution and required additional assumptions.

A simple example of the inverse problem is: using the known result of summation of two arbitrary numbers it is required to identify both of them. It is clear, that user shell to make additional assumptions, e.g. that both unknown numbers are equal.

Discretization of the intake

Both the ICRP-78 and the new IMIE methods use a common mathematical basis for the data interpretation. An initial assumption of both methods is that the intake function with an arbitrary shape can be approximated by a limited set of acute intakes. Such assumption is based on the fact that the final required value in the *in vivo*/bioassay data interpretation is the dose; and the dose is connected with the integral of intakes, but not with their instantaneous values. An error in the estimated dose, caused by the discretization of the intake, is substantially mitigated due to the process of integration.

There are additional practical reasons, why the discussed discrete approximation can be treated as more realistic, than an assumption of the ‘pure’ uniform (constant) intake. On the workplace the main pathway is an inhalation. Intakes are happening, as a rule, sporadically, as a result of the non-normal operation with open sources. In a case of the prolonged environmental exposure of the population a typical dominated path of intake is the ingestion. The intake of the contaminated food occurs also sporadically or, at least, periodically. A main conclusion from these examples is that the constant intake is, first of all, an analytical abstraction, rather a realistic model. The discretization gives to us the possibility to simulate a reality.

It should be noted that the monitoring interval must comply the recommendations of the ICRP Publication 78. The shorter is the monitoring interval, the more correct are the reconstructed total intake and the effective dose.

Examples

Two intake scenarios demonstrate the influence of the monitoring interval on the value of reconstructed intake and on the assessed effective dose.

Scenario 1: chronic intake of 1 Bq per day during 360 days.

Scenario 2: chronic intakes of 1 Bq per day during 1–90 days and 181-270 days (no intake from 91 till 180 days).

Both scenarios suppose the inhalation of aerosols with AMAD 1 μm (type F) by the adult. Described scenarios were used for simulation of the Cs-137 and I-131 intake. The IMIE reconstructed the total intake and dose assessment in these scenarios with different monitoring intervals.

Intake of Cs-137

Scenario 1

Figure 85 shows results of the reconstruction of the Cs-137 activity in the 'Whole body' when the monitoring interval is equal to 10 days.

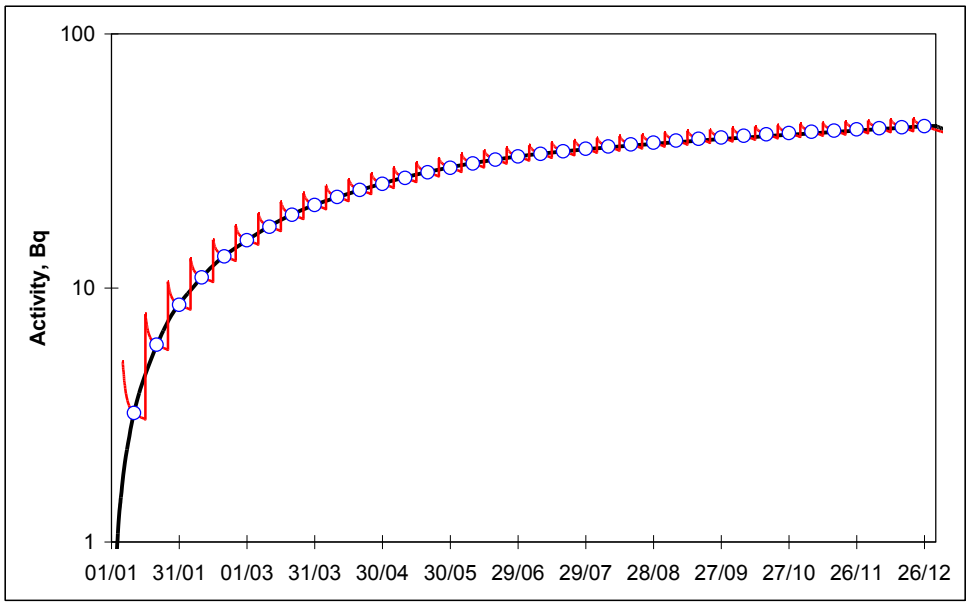


Figure 85. The 'true' and the reconstructed Cs-137 activity in the 'Whole body' (monitoring interval is 10 days)

Black line is the 'true' curve; blue points are measurements with the monitoring interval 10 days; red line is the reconstructed curve.

In this case the reconstructed activity well reproduces the 'true' curve.

Figure 86 shows reconstruction results when the monitoring interval is increased from 10 days till 180 days.

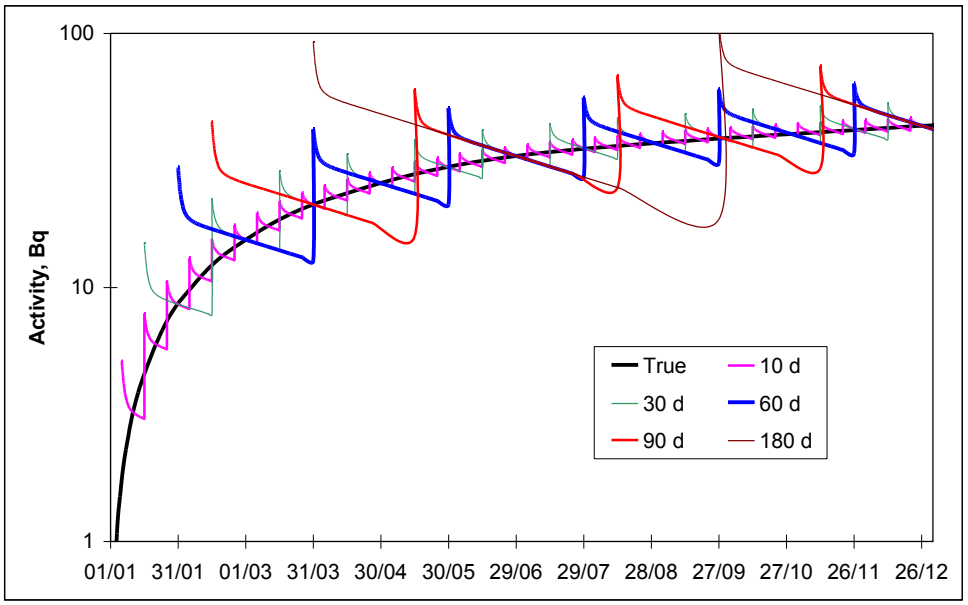


Figure 86. The 'true' and the reconstructed Cs-137 activity in the 'Whole body' (monitoring intervals: 10, 30, 60, 90 and 180 days).

Though big differences between reconstructed activities curves and the ‘true’ activity curve (the longer monitoring interval, the more differences), the discrepancy between the reconstructed intake (and effective doses, respectively) and the ‘true’ total intake is still small (see Table 1).

Table 1. The ‘true’ and the reconstructed intake of Cs–137 and the assessed effective doses (scenario 1)

		Total intake, Bq	Effective dose, μSv
‘True’ value		360	1.66
Monitoring interval, days	10	359	1.65
	30	360	1.66
	60	362	1.67
	90	365	1.68
	180	380	1.75

Scenario 2

Similar to the scenario 1, in a case of the small monitoring interval (10 days), the reconstructed Cs-137 activity in the ‘Whole body’ is practically identical to the ‘true’ value (see Figure 87).

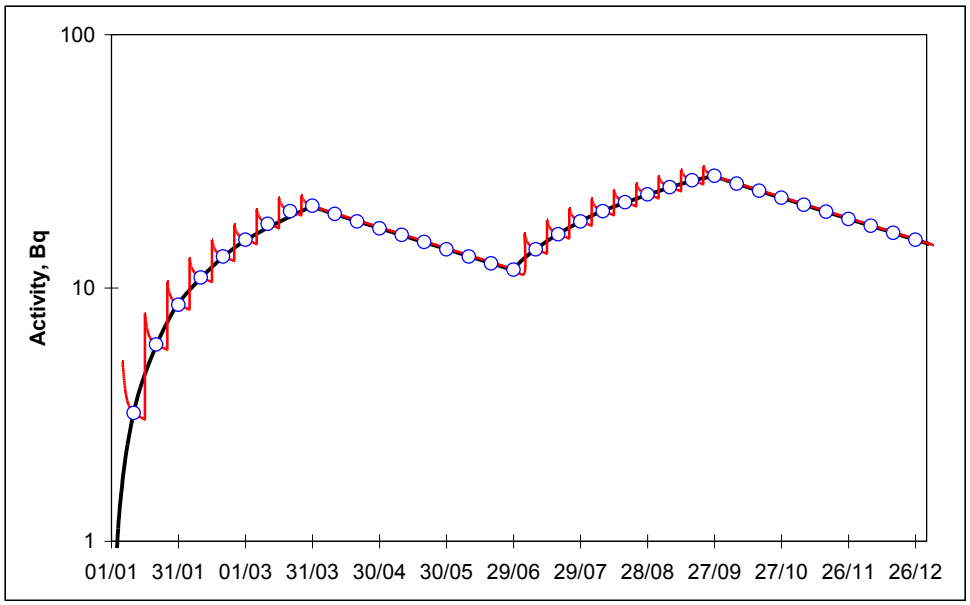


Figure 87. The ‘true’ and the reconstructed Cs-137 activity in the ‘Whole body’ (monitoring interval is 10 days)

Black line is the ‘true’ curve; blue points are measurements with monitoring interval 10 days; red line is the reconstructed curve.

Figure 88 combines results of the reconstruction for different monitoring intervals.

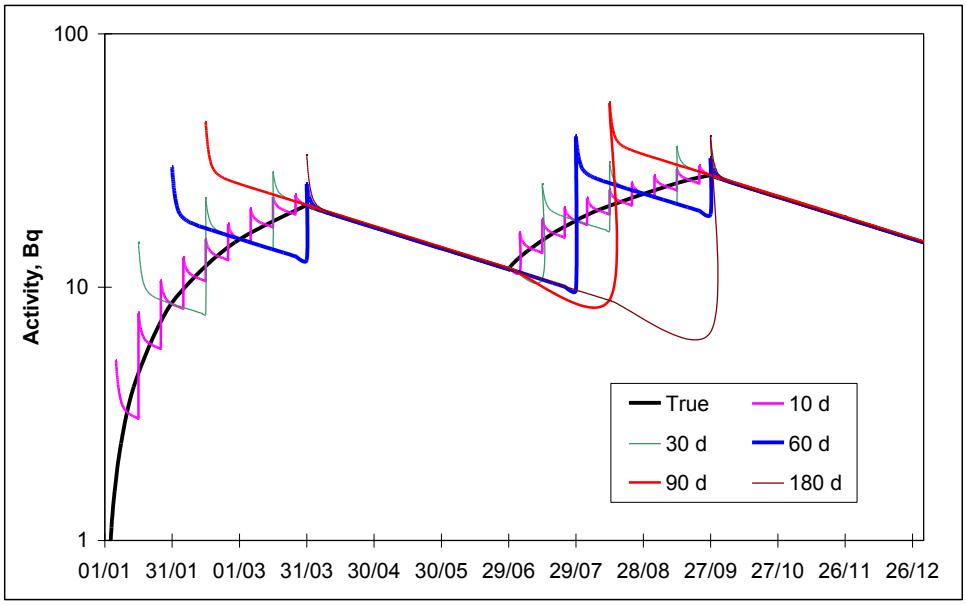


Figure 88. The 'true' reconstructed Cs-137 activity in the 'Whole body' (monitoring intervals: 10, 30, 60, 90 and 180 days)

Monitoring intervals, shorter than 180 days allow receiving an acceptable accuracy (see Table 2).

Table 2. The 'true' and the reconstructed intake of Cs-137 and the effective doses (intake scenario 2)

		Total intake, Bq	Effective dose, μSv
'True' value		180	0.828
Monitoring interval, days	10	181	0.83
	30	181	0.833
	60	175	0.805
	90	183	0.842
	180	136	0.626

Intake of I-131

Scenario 1

Figure 89 contains the result of the reconstruction of the I-131 activity in the 'Thyroid' when the monitoring interval is equal to 10 days.

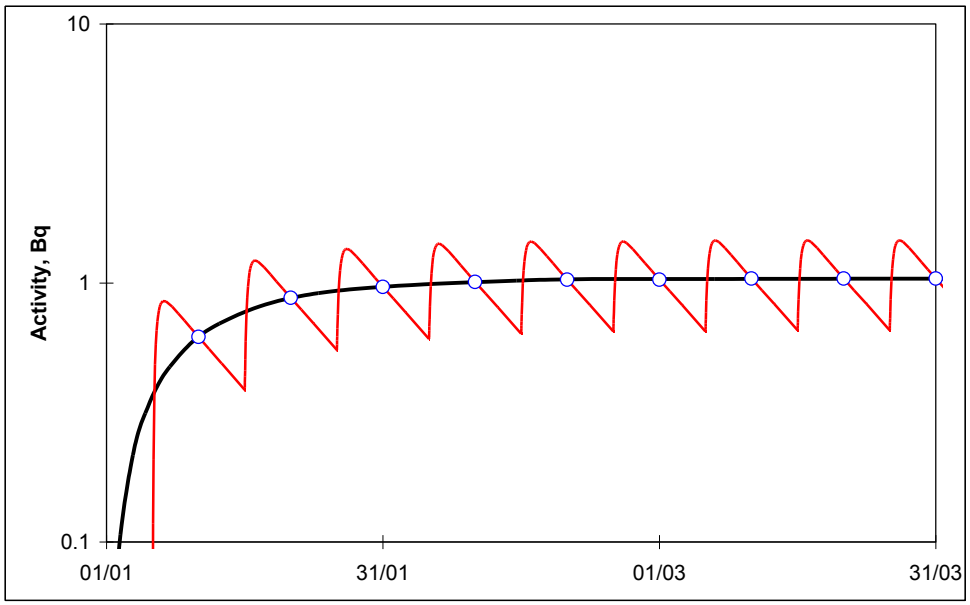


Figure 89. The 'true' and the reconstructed I-131 activity in the 'Thyroid' (monitoring interval is 10 days).

Black line is the 'true' curve; blue points are measurements with monitoring interval 10 days; red line is the reconstructed curve.

Figure 90 shows results of the reconstruction of I-131 activity in the 'Thyroid' for monitoring intervals 10, 30 and 60 days.

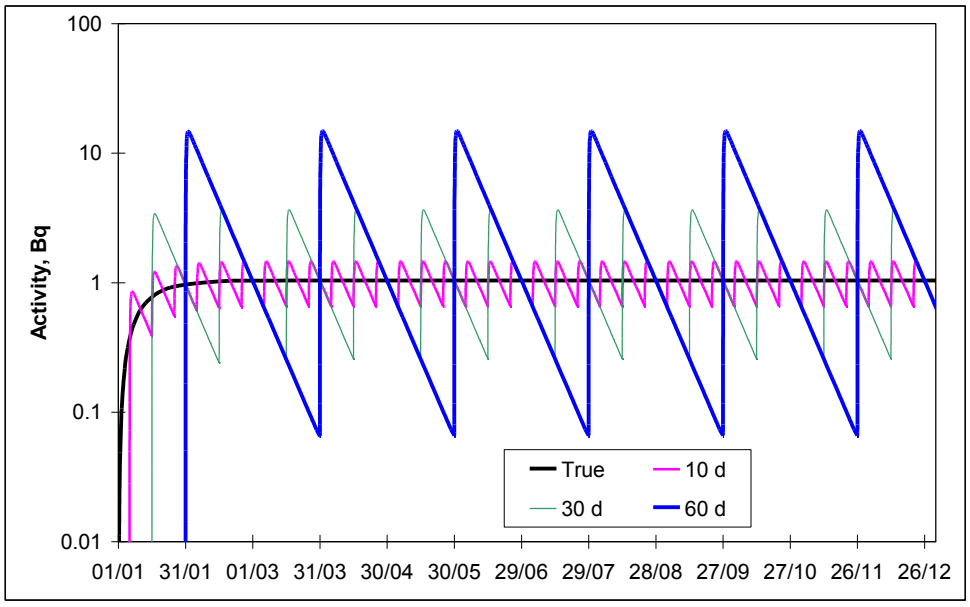


Figure 90. The 'true' curve and reconstructed curves of I-131 activities in the 'Thyroid' (monitoring intervals: 10, 30 and 60 days)

The discussed intake case is similar to the case of Cs-137 (the longer monitoring interval, the more deviation between the reconstructed activity and the 'true' activity curve), but there is

one important difference. The monitoring interval 10 d only (for activity of I-131 in the 'Thyroid') complies the requirements of the ICRP Publication 78. The total intake and the effective dose are assessed with an acceptable accuracy for this monitoring interval only (see Table 3).

Table 3. The 'true' and the reconstructed intake values of I-131 and the assessed effective doses (scenario 1)

		Total intake, Bq	Effective dose, μSv
'True' value		360	2.66
Monitoring interval, days	10	359	2.65
	30	471	3.49
	60	1010	7.49

Scenario 2

Figures 91, 92 demonstrate results of the reconstruction for the intake I-131 by the scenario 2.

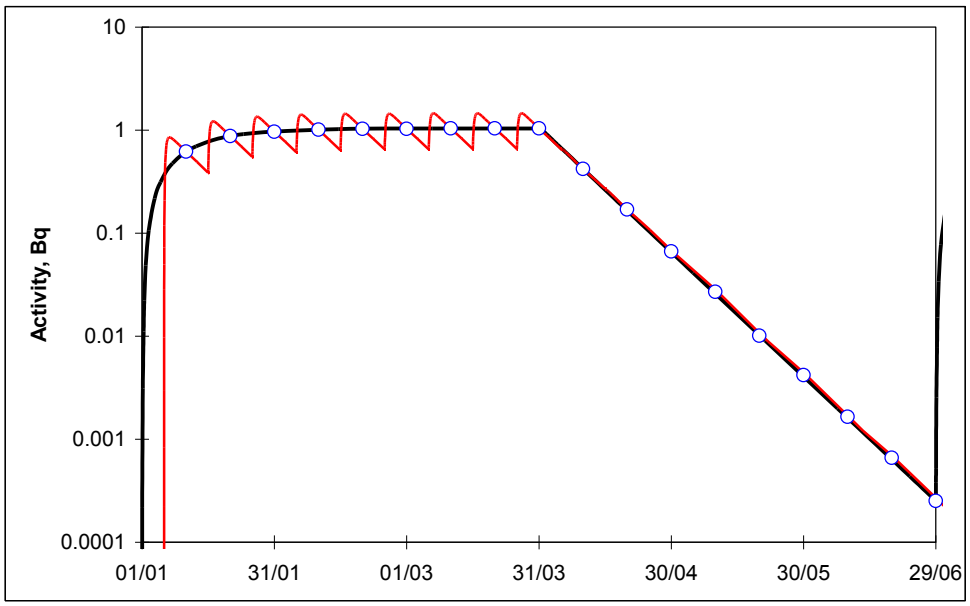


Figure 91. The 'true' and reconstructed curves of the I-131 activity in the 'Thyroid' (monitoring interval is 10 days) (first 180 days only)

Black line is the 'true' curve; blue points are measurements with monitoring interval 10 days; red line is the reconstructed curve.

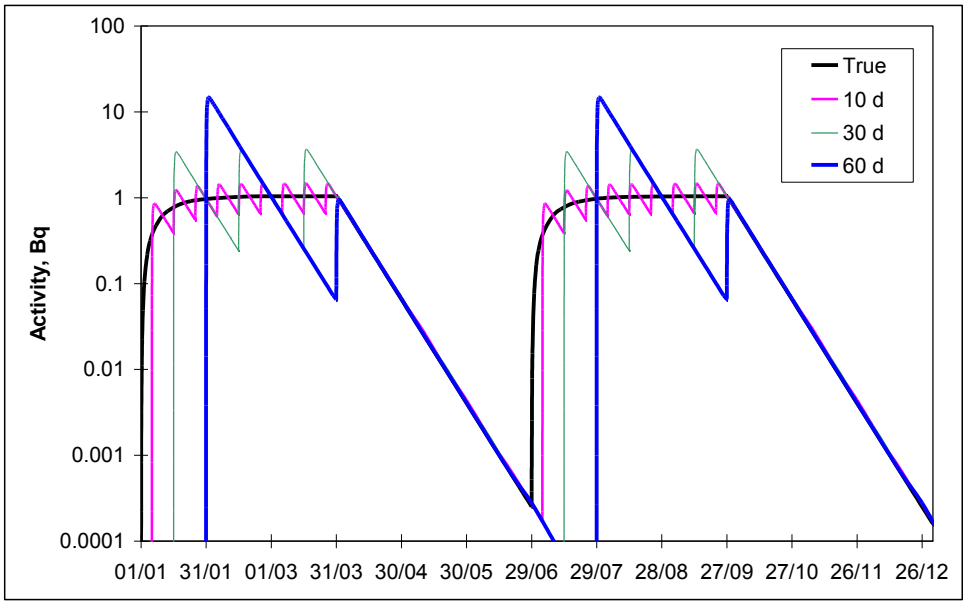


Figure 92. The ‘true’ curve and reconstructed curves of I-131 activities in the ‘Thyroid’ (monitoring intervals: 10, 30 and 60 days)

Table 4. The ‘true’ and the reconstructed intake values of I-131 and assessed effective doses (scenario 2)

		Total intake, Bq	Effective dose, μSv
‘True’ value		180	1.33
Monitoring interval, days	10	179	1.33
	30	235	1.74
	60	356	2.64

Monitoring intervals 30 d and 60 d (for the I-131 activity in the ‘Thyroid’) do not comply with requirements of the ICRP Publication 78 and the total intake and the effective dose did not reconstructed with the acceptable accuracy.

ANNEX E

Available parameters and modes

1. INPUT PARAMETERS AND INTERNAL DATA

Personal data: The information, entered into fields of the IMIE Personal Database (Worker ID, Family Name, First Name, Date of birth, Date of a first possible intake, Comment) will be automatically stored.
Number of database records: no program limitations, limited by the available RAM and hard disk space only.

Data sources: Data of WBC (activity content in the whole body), Thyroid counter (activity content in the thyroid), Lung counter (activity content in the thoracic region of the respiratory tract), Bioassay data (urine and faecal excretion rate) will be stored in a specialized IMIE database for each person recorded in the Personal Database.
Number of database records: no program limitations, limited by available RAM and hard disk space only.

Route of radionuclide intake:
- Inhalation,
- Ingestion,
- Injection,
- Wound,
- Arbitrary mixture of routs of intake.

Regime of Intake:
- *"Multiple Consecutive Acute Intakes"* in all modes of the data analysis,
- *"Chronic Intake"* (constant rate of intake on a single monitoring interval) in *Manual*, *Semi-Automated* and *Smart modes*.

Supposed exposure conditions: Interval of intake dates, Range of AMADs (0.001..20 μm), Set of Types of Materials F, M and S (if applicable) can be specified for searching of the 'best fit'.

Available radionuclides: ^{3}H, ^{32}P, ^{33}P, ^{35}S, ^{51}Cr, ^{54}Mn, ^{59}Fe, ^{58}Co, ^{60}Co, ^{65}Zn, ^{89}Sr, ^{90}Sr, ^{95}Zr, ^{95}Nb, ^{99}Tc, ^{99m}Tc, ^{103}Ru, ^{106}Ru, ^{110m}Ag, ^{132}Te, ^{123}I, ^{125}I, ^{131}I, ^{132}I, ^{134}Cs, ^{137}Cs, ^{140}Ba, ^{141}Ce, ^{144}Ce, ^{201}Tl, ^{202}Tl, ^{210}Pb, ^{210}Po, ^{226}Ra, ^{228}Th, ^{232}Th, ^{234}U, ^{235}U, ^{238}U, ^{237}Np, ^{238}Pu, ^{239}Pu, ^{240}Pu, ^{241}Pu, ^{241}Am, ^{243}Am.

Library of Response functions: Binary library of biokinetic response to the acute intake of radionuclides (activity in the whole body, in the thyroid (for iodine), in the thoracic region of the respiratory tract and the instantaneous/daily excretion rate of activity with urine and faeces) for AMTD/AMAD in the range 0.001..20 μm, and Types of Materials F, M and S (if applicable), calculated by means of

biokinetic models described in ICRP Publications 30 (GI Tract, Cr, Mn, P and Tl), 66 (Respiratory Tract), 67, 68, 69, 71 (other radionuclides) and 78 (tritium urinary excretion). Biokinetic parameters for Adult workers have been used. Response functions for inhalation of type S americium are added, calculated with biokinetic parameters for adult members of public.

Library of Dose Coefficients: Binary library of committed effective doses for the acute intake of radionuclides (see the list above) for AMTD/AMAD in the range 0.001..20 μm, and Types of Materials F, M and S (if applicable), calculated on the basis of the dosimetric models described in the ICRP Publications.

2. OUTPUT PARAMETERS

- Original (fitted) data points (in the table and on the XY plot);
- Fitting curve (XY plot and tabulated values – can be stored in a file);
- Pattern of the reconstructed intake(s) (date and amplitude in the table);
- Assessed Type of Materials and AMAD for each reconstructed intake (for inhalation only; in the table);
- Committed equivalent doses to organs and tissues associated with each reconstructed intake(in the separate window);
- Committed effective dose associated with each reconstructed intake(in the table);
- Annual doses to organs and tissues from all accepted intakes (in the separate window);
- Total committed equivalent doses to organs and tissues associated with each reconstructed intake(in the separate window);
- Total committed effective dose (in the table).

3. USER'S INTERFACE

Mode of interaction with User: Interactive. Microsoft Windows-style. Extended graphical tools for the data presentation and analysis.

Mode of Data analysis:

a) Full automatic *ICRP-78 mode* for interpretation of routine monitoring data, which is compatible with the procedure, described in the ICRP Publication 78 (single type of data source in the analysis; method assumes acute intakes at the middle of monitoring intervals, AMAD and Types of Materials must be assumed by user);

b) Interactive *Semi-Automated mode* permits to find the "best fit" for the given data set in conditions of unknown time of intake, AMAD and Type of Materials;

c) Extended *Manual mode* (with features of the *Smart mode*) is a most powerful tool for interactive data analysis and comparison of different assumptions about characteristic and mode of intake. It gives full control on the process of dose reconstruction;

d) *Accident mode* is a modification of the *Manual mode* adopted for the analysis of accidental cases. It permits to find the "best fit" for the given data set in conditions of unknown AMAD and Type of Material and to analyse wound intakes;

e) Full automatic *Smart mode* is designed to find the "best fit" for the given data set in conditions of unknown time of intake, AMAD and Type of Material;
f) A 'chronic intake' assumption can be used for the data analysis;
g) Simultaneous analysis of several sets of data from different data sources (e.g. WBC and Urine) in *Semi-Automated*, *Manual* and *Accident modes*.

Mode of data input/output: Time trends of measurements (activity content/exertion rate) can be entered into spreadsheet forms or loaded from a text file with delimiters (import from other application).
The clipboard tools for the export of data to Microsoft Windows applications (such as Microsoft Excel or Microsoft Word) are provided.

Multifunctional interactive XY plot window:
– graphical selection of time intervals for analysis by means of the mouse-oriented 'drug-and-drop' technology;
– both linear and logarithmic scales;
– auto-scaling;
– mouse (like 'drug-and-drop' technology) zooming of XY plot fragments;
– 'right mouse button' quick menu;
– customised pattern of the graph, axes, grid, titles etc.;
– data export to other applications (curves: flat text file; graphics: metafile '.WMF', '.EMF' and bitmap '.BMP').

Additional Tools:
a) *Reference system on radionuclide information* allows obtaining the graphical and numerical reference information on decay chains, energy spectrum and other information about radionuclides (838 radionuclides);

b) The additional *XY plot of target functions* in an optimisation process (values, which must be optimised during the data approximation). The graphical presentation will help to achieve the absolute extreme of the target function (in contrast to the local extreme). This auxiliary tool is essential for non-trivial cases as well as for *Several data sources mode*.

ANNEX F

Documenting of the analysis results

Basic report can be generated by pressing the *Create report* button of the *Data* panel (see subsection 2.3). The example of such report is given below.

Personal Data

Worker ID	1
Family Name (ID-Case)	Person1
First Name (ID-Case)	Person1
Date of Birth	01/01/1950
First Intake is not earlier than	01/01/2000
Creatinine excretion rate, g/day	1.7
Comment	

Measurements

Radionuclide I-125

Thyroid

Include in analysis when page is inactive False

Date	Time	Days	Value (Bq)	Unc. (%)	Approximation	State	MDA (Bq)	Kind	Comment
20/08/2000	00:00	232	6.73e2	10	6.73e2	Proc.	1.70e2	regular	
15/09/2000	00:00	258	8.40e2	10	8.40e2	Proc.	1.70e2	regular	
16/10/2000	00:00	289	7.30e2	10	7.31e2	Proc.	1.70e2	regular	
16/11/2000	00:00	320	4.17e2	10	4.19e2	Proc.	1.70e2	regular	
18/12/2000	00:00	352	2.43e2	10	2.37e2	Proc.	1.70e2	regular	
19/01/2001	00:00	384	2.50e2	10	2.50e2	Proc.	1.70e2	regular	
13/02/2001	00:00	409	1.60e2	10	1.60e2	Proc.	1.70e2	regular	
13/03/2001	00:00	437	7.53e2	10	7.51e2	Proc.	1.70e2	regular	
17/05/2001	00:00	502	2.23e2	10	2.28e2	Proc.	1.70e2	regular	
17/06/2001	00:00	533	8.37e2	10	8.37e2	Proc.	1.70e2	regular	
23/07/2001	00:00	569	7.93e2	10	7.96e2	Proc.	1.70e2	regular	
14/09/2001	00:00	622	3.10e2	10	3.04e2	Proc.	1.70e2	regular	

Urine

Include in analysis when page is inactive False

Date	Time	Days	Value (Bq per sample)	Unc. (%)	Volume (ml)	Creatinine (mg)	Coefficient (1/day)	Excretion (Bq/day)	Approximation	State	MDA (Bq/day)	Kind	Comment
20/08/2000	00:00	232	2.53e0	10	-	-	1.00e0	2.53e0	2.50e0	Proc.		regular	
15/09/2000	00:00	258	4.07e0	10	-	-	1.00e0	4.07e0	3.79e0	Proc.		regular	
16/10/2000	00:00	289	3.23e0	10	-	-	1.00e0	3.23e0	3.63e0	Proc.		regular	
16/11/2000	00:00	320	2.47e0	10	-	-	1.00e0	2.47e0	2.26e0	Proc.		regular	
18/12/2000	00:00	352	1.47e0	10	-	-	1.00e0	1.47e0	1.29e0	Proc.		regular	
19/01/2001	00:00	384	1.23e0	10	-	-	1.00e0	1.23e0	1.24e0	Proc.		regular	
13/02/2001	00:00	409	9.33e-1	10	-	-	1.00e0	9.33e-1	8.54e-1	Proc.		regular	
13/03/2001	00:00	437	3.10e0	10	-	-	1.00e0	3.10e0	1.49e0	Proc.		regular	
17/05/2001	00:00	502	1.40e0	10	-	-	1.00e0	1.40e0	1.22e0	Proc.		regular	
17/06/2001	00:00	533	4.27e0	10	-	-	1.00e0	4.27e0	3.77e0	Proc.		regular	
23/07/2001	00:00	569	1.98e1	10	-	-	1.00e0	1.98e1	6.83e0	Proc.		regular	
14/09/2001	00:00	622	1.87e0	10	-	-	1.00e0	1.87e0	1.62e0	Proc.		regular	

IMIE results

Based on Thyroid measurements

	Date	Time	Days	Days to meas.	Material	AMAD, µm	Intake, Bq	Duration, d	Dose, Sv	Mode	Weight	Simultaneous analysis	Measurements
I0	28/07/2000		209	23	Inhalation: Aerosol (Type F), f1=1	1	1.01e4	Acute	5.3e-5	Semi-automated	ULSF	Minimal distance	Thyroid (100), Urine (100)
I1	20/08/2000		232	26	Inhalation: Aerosol (Type F), f1=1	1	6.66e3	Acute	3.5e-5	Semi-automated	ULSF	Minimal distance	Thyroid (100), Urine (100)
I2	15/09/2000		258	31	Inhalation: Aerosol (Type F), f1=1	1	4.35e3	Acute	2.3e-5	Semi-automated	ULSF	Minimal distance	Thyroid (100), Urine (100)

I3	18/12/2000		352	32	Inhalation: Aerosol (Type F), f1=1	1	2.06e3	Acute	1.1e-5	Semi-automated	ULSF	Minimal distance	Thyroid (100), Urine (100)
I4	09/03/2001		433	4	Inhalation: Aerosol (Type F), f1=1	1	6.81e3	Acute	3.6e-5	Semi-automated	ULSF	Minimal distance	Thyroid (100), Urine (100)
I5	17/05/2001		502	31	Inhalation: Aerosol (Type F), f1=1	1	1.22e4	Acute	6.4e-5	Semi-automated	ULSF	Minimal distance	Thyroid (100), Urine (100)
I6	20/07/2001		566	3	Inhalation: Aerosol (Type F), f1=1	1	3.65e3	Acute	1.9e-5	Semi-automated	ULSF	Minimal distance	Thyroid (100), Urine (100)
Total							**4.58e4**		**2.4e-4**				

Based on Urine measurements

	Date	**Time**	**Days**	**Days to meas.**	**Material**	**AMAD, µm**	**Intake, Bq**	**Duration, d**	**Dose, Sv**	**Mode**	**Weight**	**Simultaneous analysis**	**Measurements**
I0	28/07/2000		209	23	Inhalation: Aerosol (Type F), f1=1	1	1.01e4	Acute	5.3e-5	Semi-automated	ULSF	Minimal distance	Thyroid (100), Urine (100)
I1	20/08/2000		232	26	Inhalation: Aerosol (Type F), f1=1	1	6.66e3	Acute	3.5e-5	Semi-automated	ULSF	Minimal distance	Thyroid (100), Urine (100)
I2	15/09/2000		258	31	Inhalation: Aerosol (Type F), f1=1	1	4.35e3	Acute	2.3e-5	Semi-automated	ULSF	Minimal distance	Thyroid (100), Urine (100)
I3	18/12/2000		352	32	Inhalation: Aerosol (Type F), f1=1	1	2.06e3	Acute	1.1e-5	Semi-automated	ULSF	Minimal distance	Thyroid (100), Urine (100)
I4	09/03/2001		433	4	Inhalation: Aerosol (Type F), f1=1	1	6.81e3	Acute	3.6e-5	Semi-automated	ULSF	Minimal distance	Thyroid (100), Urine (100)
I5	17/05/2001		502	31	Inhalation: Aerosol (Type F), f1=1	1	1.22e4	Acute	6.4e-5	Semi-automated	ULSF	Minimal distance	Thyroid (100), Urine (100)
I6	20/07/2001		566	3	Inhalation: Aerosol (Type F), f1=1	1	3.65e3	Acute	1.9e-5	Semi-automated	ULSF	Minimal distance	Thyroid (100), Urine (100)
Total							**4.58e4**		**2.4e-4**				

To save the plots of the *Graph* panel use the buttons on the tool bar of the *Graph* panel. For description of the buttons see subsection 2.4. Stored graphical files can be inserted to basic report file.

For documenting the steps of analysis and final result it is recommending to use the following technology:

- to save the initial state of the analysis save the “screenshots” of the
  1. IMIE *Main* window with the active *Personal data* page of the *Data* panel (to make a “screenshot” press the *Print Screen* key when needed window is active, then switch to the text processor (Microsoft Word for example) and past the picture using the *Edit->Past* menu command);
  2. Preference window with the active *Options* page;
- on each step of analysis make a “screenshot” of the IMIE *Main* window with the active *Analyser* page of the *Data* panel;
- if *Smart mode* is used, make a “screenshot” of the *Parameters of the smart mode* window;
- if mixed intakes is used in the analysis, make a “screenshots” of the *Mixed intakes* window with selected mixed intakes, used in analysis;
- when analysis finished save the IMIE basic report pressing the *Create report* button on the *Data* panel (see the example of the IMIE basic report file below) and copy collected screenshots to this report file.