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PCXMC v 1.5

USER'S GUIDE

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General

PCXMC is a Monte Carlo program that is intended to be used for the calculation of the patient's doses in x-ray examinations. For a more thorough explanation of the program, see report STUK-A139¹ or the web-pages of the program <http://www.stuk.fi/pcxmc>. This manual concentrates only on the use of the program.

PCXMC version 1.5 runs under Microsoft Windows 32 bit operating systems (Windows95/98/NT/2000/XP). A PC equipped with at least 64 MB of RAM and a processor of at least 120 MHz clock frequency is recommended for the use of the program. The program files require approximately 2.5 MB of free disk space; additionally, you should have at least 1-2 MB free disk space for the Monte Carlo data that you will generate. The present version also requires a sufficiently large display matrix size: the examination data input form needs a desktop area of at least 1024 x 768 to be fully visible; if the user's PC cannot be used with this desktop size, we recommend the use of PCXMC version 1.4.1.

PCXMC 1.5 differs from the previous version 1.4.1 in a few respects: (1) The examination data input form has been improved, and now shows also the phantom and radiograph images. The form also simplifies the specification of the FSD by providing an FSD calculator. (2) The user can now estimate the doses as based on the x-ray tube current time product (mAs), without performing actual dose or dose-area product measurements as was required in the previous program versions. For the accuracy of specifying exposure by the x-ray tube current time product, see later text. (3) The small errors that were present in PCXMC version 1.4 were corrected already in version 1.4.1.

All data files calculated with the various PCXMC versions are compatible: you do not need to simulate your old examinations again, unless recalculation is necessary because of the errors in the previous versions. If these errors are not critical in the calculation, you can use your old data directly in the new version as well.

This manual, the plain text version of this manual, and a software order form can be found in the directory \PCXMC\Manuals.

¹ Tapiovaara M, Lakkisto M and Servomaa A: PCXMC - A PC-based Monte Carlo program for calculating patient doses in medical x-ray examinations, Finnish Centre for Radiation and Nuclear Safety (STUK), Helsinki, 1997.

Program installation on hard disk

If you have PCXMC 1.4 or 1.4.1 installed on your hard disk, you can install PCXMC by running the Setup program in the PCXMC 1.5 Update Diskette. Before the installation, check where PCXMC14.exe was installed, and then use the same directory (X:\PCXMC, where X is the hard disk drive letter) for the installation of PCXMC 1.5.

If you do not have a previous version of PCXMC installed in your PC, or if you wish to install PCXMC 1.5 in a different folder, you need a copy of the PCXMC 1.5 Installation Diskette. Follow the instructions below to install the program in your PC:

- Set the PCXMC 1.5 Installation Diskette in the diskette drive of your PC.
- Press the “Start” button on the Task Bar, select the option “Run...” from the appearing menu, and type: a:\setup. This will start the installation program, which will guide you through the rest of the installation procedure. The installation program will suggest Program Files\PCXMC as the folder where the program and data will be put. If you wish, you can install the program also to whatever folder you choose.

The installation program will also ask you about the start menu program group where PCXMC is to be located. You can accept the suggested group ‘pcxmc’ (simply by choosing ‘Next’ at that stage), or you can place the program in another program group.

- If you wish to add a short-cut to the program on your desktop when the installation is complete, first locate the pcxmc15.exe file in your hard disk using the 'My Computer'-program, drag the pcxmc-icon to your desktop with the right mouse button pressed, and then choose 'Create Shortcut here', (or see your Windows operating manual to learn how to create the shortcut). Check in the 'properties'-display of the shortcut that the 'Start in'-folder is set to the MCRUNS folder which is a sub-folder in the same folder where PCXMC15.exe is located (For example, if PCXMC15.exe is installed in C:\PCXMC, The start in -folder should be set to C:\PCXMC\MCRUNS.)
- For best graphics quality, set the display mode of your PC to use at least 16 bit colour depth (65536 colours); in the 8-bit display mode the graphics in the program will be of poor quality due to the small number of available colors. The desktop size must be at least 1024 x 768.

Note: If the display matrix size of the monitor you use is too small, there may

not be enough screen space to show the whole area of each display window. In such cases, horizontal and vertical scroll bars are created on the display window, and these can be used to access the hidden areas. The images on the examination data input form will not be shown properly, however, and using the program becomes cumbersome.

Using the program

To start PCXMC 1.5, double-click its icon on the desktop, or choose PCXMC15 from the Programs folder after pressing the “Start”-button on your task bar. This will open the main window of the program.

The dose calculation for a new examination condition, with changes of patient age, patient size or examination geometry from previously calculated cases, involves three steps, which will be explained in detail below. In summary: these steps require (1) defining the examination conditions, (2) performing the Monte Carlo simulation, and (3) calculating the organ doses for a specified x-ray spectrum and patient input dose. If the patient data (age, weight, height) and the geometric data of the examination are unchanged from a previous calculation, one does not need to perform the first two of the above steps, but the dose calculation is accomplished by performing step (3) only. That is, you do not need to perform the Monte Carlo simulation again, if you just change the x-ray spectrum or the input dose.

The program produces files of different extensions during the operation. The program adds these extensions automatically and keeps track of them. Therefore, **do not use any extensions for the file names that you specify**. Files containing the examination and patient parameters of Monte Carlo simulation (definition files) use the extension '.def', data files produced by the Monte Carlo calculation use the extension '.ene', and final dose results for specific x-ray spectra and input dose use the extension '.mGy'. For a more detailed explanation of the file types, see Appendix A of this manual.

We recommend that all the above files are kept in the directory \PCXMC\MCRUNS or that the user creates new subdirectories in this directory for organising the data. In this version (PCXMC 1.5) there are several readily calculated Monte Carlo data, which are located in a few subfolders of MCRUNS. The data have been organised by the age of the patient and are for typical common projections.

When the user starts PCXMC, the main form is displayed showing five buttons

- *Examination data*
- *Simulate*
- *Compute doses*
- *About*

- *E*xit

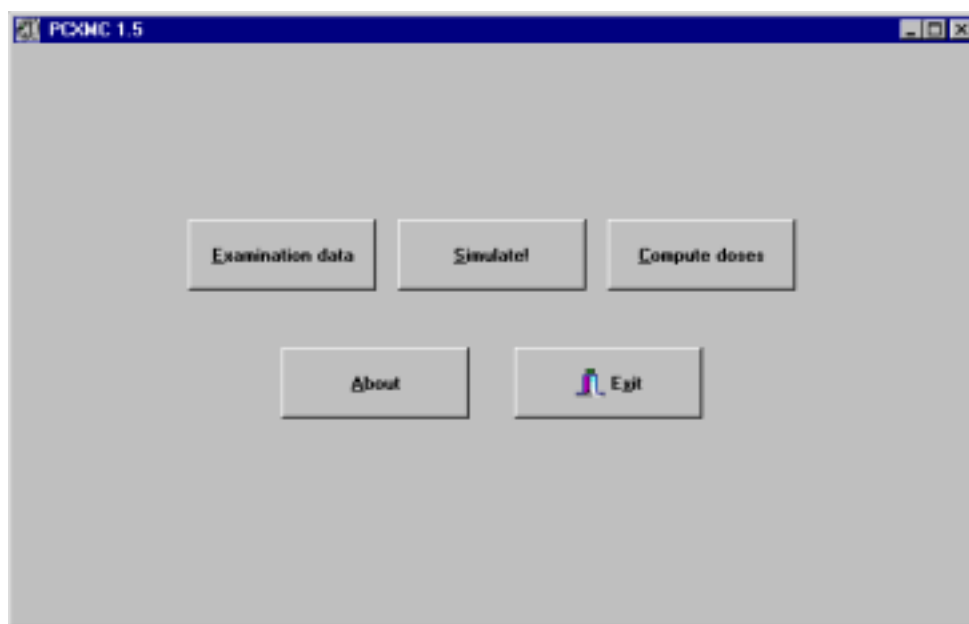


Figure 1. The main form of PCXMC.

Clicking these buttons with the left button of the mouse (or pressing the <Alt>-key and the underlined letter) activates different subprograms of PCXMC. The function of these buttons is explained in the following chapters.

- **Main form button: Examination data**

Clicking this button opens a new window (see Fig 2), and allows the user to define the x-ray examination conditions and phantom model which will be used in the Monte Carlo simulation. Examination data (definition files) are saved by the name that the user specifies, with the standard extension '.def'. Do not explicitly type the extension, the program will add it automatically.

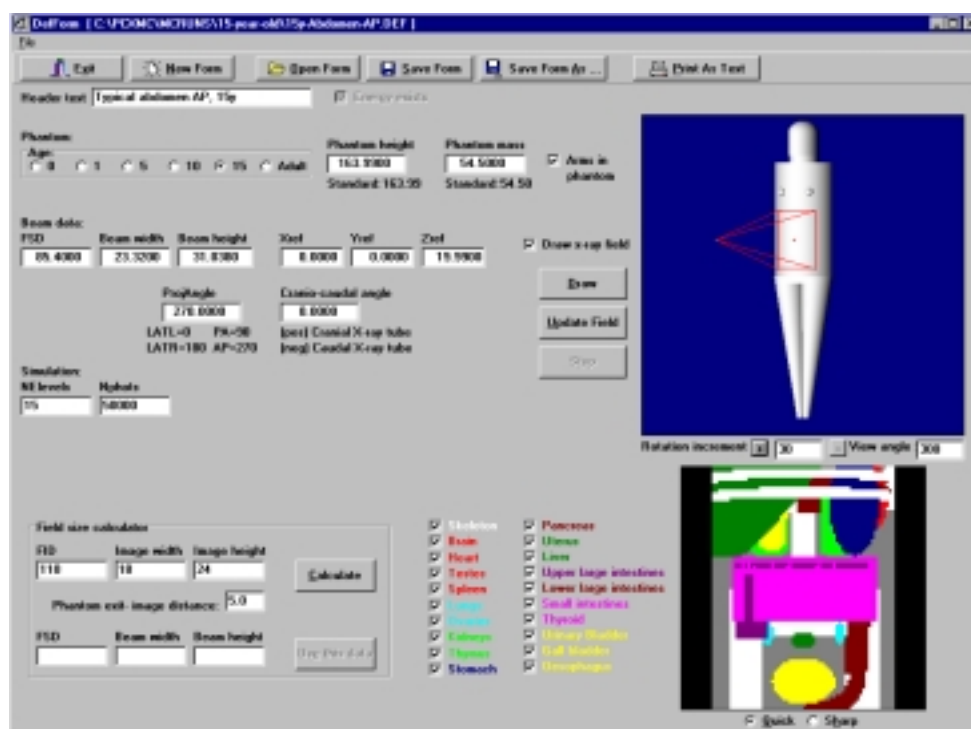


Figure 2. The x-ray examination data input form of PCXMC.

The *form caption* (at the top of the form) shows the file name and full path of the definition file chosen. If no file has been specified there is no text between the brackets.

On the first data row there is an *EditBox* displaying the '*header*'. This datafield can be used for a short user-typed text to further explain the simulation conditions. On the same row there is a check-box named '*Energy exists*'. If this box is checked, the user must save the data using another definition file name after editing the data. Renaming will be prompted when the user will try to save the changed definition file or exit the examination data input form. Otherwise, if the check-box is not checked, editing will affect the datafile shown in the form caption, unless the edited data are saved by the *Save As...*-button.

The next row of data is for specifying patient data: *age*, *height* and *weight*. The age is chosen by checking the proper radio button. The age-dependent standard height and weight of each phantom are obtained either by entering their proper values (in cm and kg) or the value 0.0 in the fields of these data. Instead of the standard values, actual patient measures can be used for height and weight data as well.

The standard measures are:

Age (y)	Height (cm)	Weight (kg)
Newborn	51.5	3.51
1y	75	9.36
5y	109	19.1
10y	138.6	32.1
15y	164	54.5
Adult	174	71.1

The standard phantom height and weight of the chosen phantom age are also shown below the height and weight edit-boxes.

A cross in the box '*Arms in phantom*' (or the value 1 for '*Arms in phantom*' in the definition file) implies that the arms are included in the phantom during simulation. Arms should be excluded from lateral projections where the arms are positioned outside the x-ray beam in actual practice.

The next rows are for geometric data. All length data are entered using cm as the unit of length. '*FSD*' (focus-skin distance) means the distance between the focal spot of the x-ray tube and the skin entrance point of the central axis of the x-ray beam. If the value 0.0 is used for FSD, the program will interpret the distance to be infinite: this choice may be useful for example, when point scanning x-ray beams are used in the examination. Beam '*width*' and '*height*' refer to the lateral and vertical dimensions of the x-ray beam, as measured at the distance FSD from the focal spot and in the plane that is normal to the central axis of the x-ray beam. It does not refer to the x-ray field size at the image receptor. If only the latter data for beam size is available, one must first calculate the beam size at skin entrance from the image size, focus-image distance and FSD. These calculations can be easily done using the field size calculator at the lower left part of the examination data input form. The use of this calculator is explained in detail in the next section.

X_{ref} , Y_{ref} , and Z_{ref} are the coordinates of an arbitrary point inside the phantom, through which the central axis of the x-ray beam is directed: these data are used for specifying the location of the x-ray beam with respect to the phantom. Choosing any point along the intended beam centre-line will give same calculation results. The origin of the phantom coordinate system is located at the centre of the bottom of the phantom trunk section. The positive z-axis is directed upwards, the positive y-axis to the back of the phantom, and the positive x-axis to the left-hand side of the phantom.

The graphics capabilities of the PCXMC-program and the figure and tables of

Appendix A of report STUK-A139 can be used as guidance in finding proper coordinates for this reference point: Tables A5 - A18 in the above mentioned report describe the location of various organs in the phantoms and Table A19 shows typical reference points for a few common radiographic projections. Note, that the reference point can be most easily edited by *clicking the mouse within either the phantom image or the radiograph*. In the former case the reference point will be put just below the phantom surface at the position of the cursor when the button is clicked, and in the latter case the reference point is put below the surface of the organ clicked.

'ProjAngle' and *'Cranio-caudal angle'* specify the direction of the x-ray beam with respect to the phantom. The first of these angles specifies whether the x-ray beam enters the patient from the front or back-side (or at any other angle), and the latter specifies the tilting of the beam. All angles are given in degrees, and any reasonable numbers can be used. It is suggested that the user checks his/her proper entering of these angles from the *'Phantom image'*.

The check-box *'Draw x-ray field'* is used to control whether the x-ray beam edges are shown in the phantom image. It is useful to keep this box checked; one might wish to leave the image without beam indication only in special occasions.

The next row of data is for simulation details: the maximum quantum energy of interest and the number of quanta in the simulation. The field *NElevels* shows the maximum energy/10 keV: i.e. $NElevels = 9$ corresponds to a maximum x-ray tube potential of 90 kV in subsequent dose calculations. Unless calculation speed is of great concern, we suggest that this value is kept at its maximum, $NElevels = 15$. *Nphots* is a main factor in determining the statistical precision that will be achieved in the Monte Carlo simulation: it represents the number of photon histories that will be generated. For this parameter we recommend a minimum value of 10 000. *Nphots* must be a multiple of 100: lower numbers will result in floating point errors. If all 15 photon energies are chosen for the simulation (field: *NElevels*), the value of 10 000 photons (field: *NPhots*) takes typically about 30 seconds of computation time on a modern (2000) PC with a 500 MHz processor – and of course less with faster processors. The calculation time can be shortened by specifying a lower value for *NElevels* (which then restricts the use of the data for x-ray tube voltages higher than this value times 10 kV), or *NPhots* (which then results in larger stochastic errors in the data), or by using a faster computer. The required precision depends on the intended use of the data.

Clicking the button *'New form'* initializes the input form settings to a standard set. *'Open form'* shows all files with the extension *'.def'* and allows the user to open any of them in order to modify or view the data. After editing the data,

they can be saved by clicking the *'Save'*- or *'Save as'* -buttons. It is reminded that if the data have already been used in simulation (which is indicated by a cross in the field *'Energy exists'*) the definition file must be saved under a new file name if it has been edited.

Clicking the *'Draw'* -button results to the display of the currently specified phantom and examination geometry ('Phantom image', see Fig 2). If the examination data have been modified without clicking this button, there will appear a yellow warning text on the form noting that the images do not anymore correspond to the data on the form. This message text disappears when the draw-button is clicked. The phantom image will also show the edges of the x-ray beam if the box *'Draw x-ray field'* is checked. Those parts of the x-ray field that hit the phantom are indicated in red colour and parts that do not intersect the phantom are shown as green. The background colour of the image is the same as is set for the 'Active Title Bar' in the Windows Control Panel colour settings. You can move the cursor over the phantom image to see the coordinates of the cursor point on phantom surface, and you can rotate the phantom by any angle to see it from different directions (editing of the *rotation angle* increment is allowed). This rotation of the image can be done by pressing the *+ or - buttons*. Your input data are not changed by these operations. You can change the reference point by clicking on the phantom image: the cursor point then becomes the new reference point.

Clicking the *'Update field button'*-button causes the formerly specified beam edges to be colored gray, and the newly specified beam edges to be shown with the colors explained above. The *'Stop'*-button can be used for stopping the draw procedure if a mistake has been made.

After drawing the phantom image, the program draws also a simulated 'radiograph' which shows the organs in the defined x-ray beam as viewed from the x-ray tube focal spot: this picture mimics the x-ray image of the specified examination conditions. Those parts in the 'radiograph' that are outside the phantom or x-ray field are displayed black, parts that belong to the phantom but not to any of the (checked) organs in the organ list are displayed grey. Other colours correspond to the first organ in the path of a photon, and are similar to the colours of the organ names in the list. The user can *check and uncheck organs* to be displayed. The input data are not changed by these choices, they affect only the radiograph image display. The user can choose whether the displayed 'radiograph' is drawn with higher detail or more quickly by choosing the *'Quick'* or *'Sharp'* radio-button. The x-ray beam geometry can be edited similarly as in the 'phantom image', i.e., by clicking on the image in an area depicting a specified organ (color other than black or grey). The clicked cursor position will then be the new x-ray field centre.

The user can save the definition file by clicking the *'Save'*- or *'Save as...'*-buttons and the active definition file can be printed by clicking the *'Print as text'*-button. When ready, the user can return to the main window by clicking the *'Exit'* button.

- ***Examination data input form: Field size calculator***

The field size calculator calculates the *FSD* and the width and height of the x-ray beam at the patient's input plane. To use the calculator, one must know and enter the x-ray beam size at the image plane (i.e. the width and height of the image), the distance between the x-ray tube focal spot and the image receptor (*FID*), and the distance between the patient's exit surface and the image receptor (typically about 5 cm in Bucky tables). In order to calculate the *FSD* and the field size at the patient's entrance, one must further know the patient's thickness. This is automatically calculated by the program, when the user clicks the *'Calculate'*-button. The patient thickness thus obtained corresponds to the phantom and x-ray beam location and direction data specified in their appropriate editboxes on the examination data input form. The calculated *FSD* and beam size data are copied to their editboxes when the user clicks the *'Use this data'*-button.

- ***Main form button: Simulate***

Clicking this button on the main form opens a new window to initiate the actual Monte Carlo simulation (see Fig. 3). Clicking the *'Start'* button opens a window that allows the user to choose a definition file for simulation. Several files can be chosen at once by keeping the <Ctrl>-button pressed while clicking the names of definition files, or by keeping the <Shift>-button pressed while selecting the last from a range of files. The program will then simulate these conditions one after another automatically, without user interference. For example, the program can be left simulating several conditions overnight. When the *'OK'* button is clicked, the simulation starts and the fields of the window show data and progress of the calculation. The message window shows the header text of the definition file, the field 'Energy level' shows the photon energy under calculation (the energy is 10 times the value in the display), 'Lot' shows the number (1 to 10) of the batch, and 'Photons' shows the number of photons simulated at the present energy level in the present batch.

The simulation can be stopped at any stage by clicking the *'Halt'* button, but then all simulation data of the present run are lost. The calculation is ready when a message window with text 'Done' is displayed. The user can then return to the main window by clicking the *'Exit'* button.

The results of the simulation are stored under the same name as the definition

file of the simulation conditions, but the extension '.def' is replaced by '.ene'. This file is then used for calculating the organ doses for any x-ray spectrum or input dose that the user is interested in, without the need to make new simulations, as long as all other examination parameters are kept unchanged.

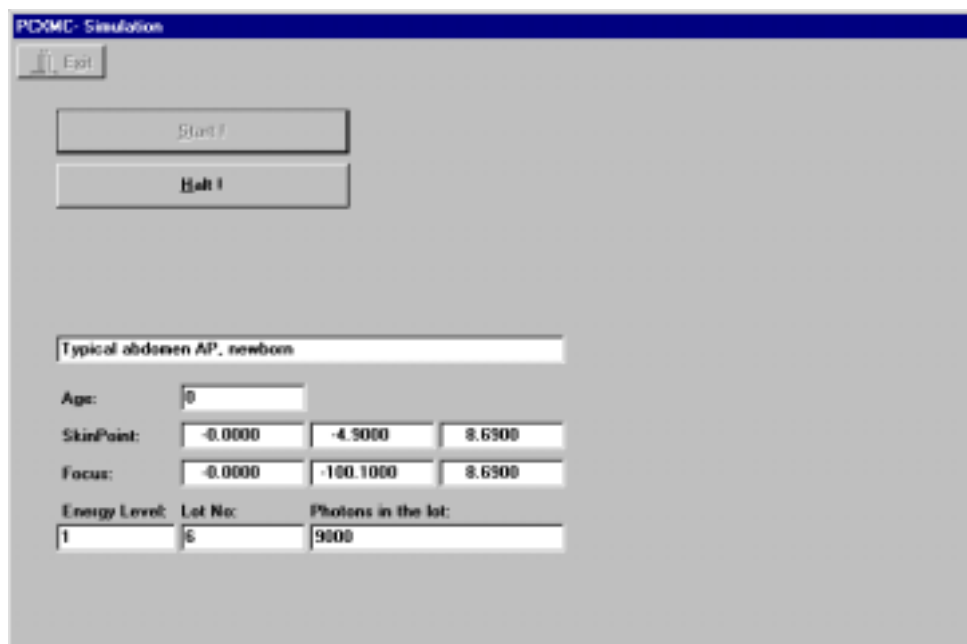


Figure 3. The Monte Carlo simulation window of PCXMC.

Note that when the program is used for the first time for calculating doses in a phantom of the specified age, it automatically creates additional data in the directory \PCXMC\MCINDATA\GRIDS and may prompt the user to wait for the completion of this operation. This operation is not done in later simulations.

- **Main form button: Compute doses**

Clicking this button on the main form opens a window (see Fig 4) for calculating doses in x-ray examinations. It is required that the Monte Carlo simulation part (the previous item) of that examination has been performed earlier.

The data for the presently loaded spectrum (kV, x-ray tube anode angle, filtration) is shown on the window. If this data corresponds to the spectrum that the user wishes to use, the user can proceed directly to calculating the doses. If the spectrum needs to be changed, the following operation needs to be done. Click the '*Update spectrum*' button to start the x-ray spectrum calculation subroutine. Then define the x-ray tube voltage, target angle, and filtration in the form that appears.

Sometimes the actual x-ray tube target angle is not known: in this case, for example, 13° can be used. You should avoid using very small target angles: our experience shows that the program may overestimate the hardness of spectra that are generated with target angles less than 10° .

In PCXMC, x-ray tube filtration is specified by two different filters of arbitrary elemental materials. These elements are chosen by entering their atomic number or chemical symbol in their proper fields. Note that when entering either of these data, the other is updated simultaneously. If the chemical symbol is used, the program requires that it is typed with the proper upper- and lower-case letters. If only one filter material is used, the atomic number of filter #2 should be set equal to 0, or the chemical symbol of it should be cleared. The filter thickness must be input in units of mm. The program automatically calculates the areal thickness of the filter in units of g/cm^2 according to the filter material and thickness. The user cannot edit this field, but it can be used as guidance if filtration is specified in terms of the areal thickness. The new spectrum is stored and used (until the user specifies a new spectrum) when the user clicks the '*Exit:Generate this spectrum*'-button.

Clicking the '*Calculate doses*' button prompts for the selection of a (previously calculated, see previous chapter) *.ene file. Choose the file whose name corresponds to the examination situation you wish to calculate results for, and click the '*Open*'-button. A new window is displayed prompting you to specify the input dose. This datum can be input in one of five different quantities: (i) air kerma at the phantom entrance point in the middle of the x-ray beam (mGy, free-in-air) (ii) exposure at the phantom entrance point in the middle of the x-ray beam (mR, free-in-air), (iii) [air]kerma-area product (mGycm^2), (iv) exposure-area product (Rcm^2), or x-ray tube beam current time product (mAs, the accuracy of specifying the input dose by mAs is considered in the next section). The program converts the input dose quantity to phantom entrance air kerma in milligray for the further use as the input dose value. When the OK-button is clicked, the calculated organ doses and other dose quantities are displayed (in milligray, or equivalently, in millisievert) along with their estimated precision. Statistical precision is shown in percents, and the symbol NA (not applicable) is used when the precision estimate could not be done because the dose is nil or very close to it.

It should be noted that the accuracy of both the dose estimate and its statistical error depend on the number of simulated interactions in the organ. The number of interactions may be low even for a large number of photon histories, if the dose in the organ is low and/or the organ small. It should also be noted that when the number of interactions is small, which is indicated by a high value of the statistical error, the estimate has a skewed non-normal distribution and the

actual statistical errors may be higher than expected on the basis of the standard deviation.

Organs	Dose (mGy)	Error (%)	Organs	Dose (mGy)	Error (%)
Lungs	0,161050	0,3	Pancreas	0,091285	1,3
Skull	0,007303	1,6	Small intestine	0,005236	1,7
Upper spine	0,073021	1,4	Gall bladder	0,033934	2,9
Middle spine	0,392875	0,4	Upper large intestine	0,006857	2,3
Lower spine	0,091904	1,2	Lower large intestine	0,001163	7,3
Ribs	0,366916	0,3	Urinary bladder	0,000304	19,5
Scapulae	0,513513	0,5	Uterus	0,000980	13,0
Clavicles	0,075725	2,2	Adrenals	0,197249	2,1
Upper arm bones	0,040599	1,6	Thymus	0,038840	4,6
Middle arm bones	0,047491	1,3	Oesophagus	0,091919	1,9
Lower arm bones	0,007927	3,3	Thyroid	0,021290	4,1
Upper leg bones	0,000030	23,4	Brain	0,001296	3,8
Middle leg bones	0,000001	58,5	Testes	0,000051	52,2
Lower leg bones	0,000000	NA	Ovaries	0,001463	26,9
Pelvis	0,002576	2,6	Skin	0,031125	0,3
Heart	0,069302	1,1	Remainder (muscle)	0,035695	0,1
Breasts	0,039429	1,3	Total Body	0,046416	0,1
Liver	0,083379	0,5	Active bone marrow	0,094777	0,2
Stomach	0,048790	1,6	Skeleton	0,094586	0,2
Spleen	0,156807	1,1	Effective dose	0,051320	0,4
Kidneys	0,118056	0,8	Abs fraction (%)	59,436452	

Figure 4. The dose calculation window of PCXMC.

'Save as' saves the dose data in a file by the name that the user supplies (these files are saved using the default extension '.mGy'). 'Print' is used for printing the dose data on paper. In version 1.5 the statistical precision is given in percents, whereas the former versions of PCXMC expressed the errors in mGy. Again, clicking 'Exit' takes the user back to the main window.

The operations can also be activated from the 'File' or 'Run' menus. The 'File' menu also enables the user to print existing definition and energy (Monte Carlo data) files.

- **Dose calculation as based on mAs**

The program can evaluate the patient's entrance input dose when mAs is

specified. All other data needed for the evaluation (kV, total filtration and FSD) have already been specified in the examination's input data. In practice, the x-ray tube output varies from one unit to the next, however, and one cannot expect an exact agreement between calculated and measured doses. Variability between x-ray tubes is caused at least by differences in the following factors

- x-ray tube voltage waveform (PCXMC assumes a constant potential or low-ripple high-voltage generator)
- x-ray tube anode angle (not used in the output calculation in PCXMC, although the datum would be available),
- smoothness of the x-ray tube anode surface,
- actual filter materials in the beam path (in spite of matching filtration equivalence, the attenuation of the actual filter (including glass and oil) may differ from the attenuation of an aluminum filter),
- differences in off-focal radiation and its removal by collimation,
- the error between actual and displayed values of the kV, mAs and filtration
- accuracy and precision of the dosimeter used.

The x-ray tube output calculation of PCXMC is largely based on x-ray tube output measurements from diagnostic x-ray tubes. The basic data have been obtained from 46 different x-ray tubes and/or filter choices. The average of these measurements agree with the value calculated with PCXMC, and the standard error between individual measured and calculated results is 16%. Therefore, one can expect the calculated output dose to be within about 30% (2 S.E.) of the correct value.

The ratio of calculated and measured results is typically constant for a given x-ray tube; the ratio stays the same although x-ray tube voltage or filtration is varied. This can be used to improve the accuracy of mAs-based dose calculations: by making x-ray tube output measurements for a given x-ray system and comparing these with the output values calculated by PCXMC one will get an effective 'mAs calibration factor' for that x-ray tube, and it can be used at all kV's and filter choices. By doing such a normalisation for each of the 46 x-ray tubes above, the standard error between individual measured and calculated results dropped to 5%, and the accuracy of the calculation can then be taken as 10%.

- ***Main form button: About***
shows data on the PCXMC program, and
- ***Main form button: Exit***
stops the execution of the program.

Appendix A:

File types of PCXMC

The program produces files of different extensions during the operation. The program adds these extensions automatically and keeps track of them. Therefore, **do not use any extensions for the file names that you specify**. Files containing the examination and patient parameters of Monte Carlo simulation use the extension '.def', data files produced by the Monte Carlo calculation use the extension '.ene', and final dose calculation results for a specific x-ray spectrum and input dose use the extension '.mGy'.

The energy files (.ene) show the examination data, the absorbed energy per photon (in keV), and the statistical error estimated for this energy (one standard deviation, in percent) for each organ of interest.

A new x-ray spectrum is calculated each time the user changes it, and is stored in directory PCXMC\MCINDATA\SPECTRA as an ASCII file 'SPECTRUM.TXT'. Fourteen first lines are used for storing some parameters (like x-ray tube potential, anode angle and filtration). After these lines the relative photon fluence spectrum is given in 1 keV bins, the first bin spanning the energy range 0,5 – 1,5 keV. The same spectral data is used for all dose calculations until the user specifies a new spectrum.

When first used for a given phantom 'age', PCXMC generates data files in the directory \PCXMC\MCINDATA\GRIDS. These files consist of file pairs GparXY.asc and GridXY.bin, where XY denotes phantom 'age'. These files are used in subsequent Monte Carlo simulations. If any of these files becomes corrupted or is accidentally deleted, you should delete both the corrupted file and its companion file – the program will generate them again when run for a phantom of the given age.