SOCIETY OF NUCLEAR MEDICINE AND MOLECULAR IMAGING
MIRD COMMITTEE

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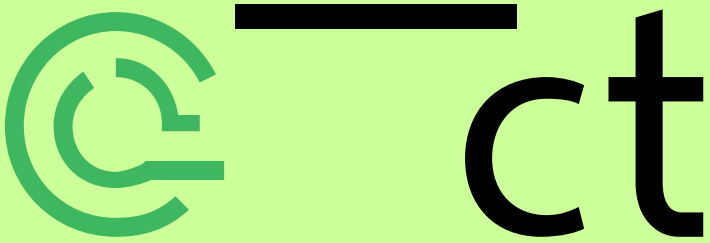

Computed tomography dosimetry software

User Manual

Version 1.0

Memorial Sloan Kettering Cancer Center

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Legal Notice

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2 SOFTWARE OVERVIEW

2.1. MIRDCT

As part of the MIRDsoft.org community software development project, MIRDct has been developed to provide organ model-based CT dosimetry.

The MIRDct software supports easy and fast calculations of effective dose (using ICRP 103 tissue weighting factors) and organ absorbed dose given user provided input of scan parameters [1]. Additionally, as an optional output, the software calculates risk evaluation quantities such as detriment weighted dose [2], lifetime attributable risk [3] and risk index [4].

MIRDct is part of the MIRDsoft radiation dosimetry community platform which has been endorsed by the SNMMMI MIRD committee [5]. The novelty, and accessibility of the tool for model-base CT dosimetry and radiation risk assessment open the space for future innovation and updates.

Users are encouraged to read manual thoroughly. All input parameters can/will affect output dosimetry estimates; therefore, a full understanding of input design is required by the user.

2.2. ACKNOWLEDGEMENTS

MIRDct is part of a grant supported project from the United States National Institute of Biomedical Imaging and Bioengineering, grant U01-EB028234: "MIRDct – A Community Tool for Deriving and Reporting Patient Organ Doses in Nuclear Medicine, Computed Tomography, and Hybrid Imaging". Principle Investigators are: Wesley Bolch (University of Florida) and Adam Kesner (Memorial Sloan Cancer Center).

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We acknowledge guidance and support from the Society of Nuclear Medicine and Molecular Imaging Committee on Medical Internal Radiation Dose (MIRD), and the SNMMI organization.

3 INSTALLATION

3.1. DOWNLOADING

MIRDct is freely available on the MIRDsoft.org website: www.mirdsoft.org

3.2. REQUIREMENTS

The MIRDct software is built within the Microsoft Excel environment and compiled using XLS padlock. MIRDct software requires a windows PC with Microsoft Windows 7 (32- or 64-bit) or later, and Microsoft Office 2013 or later installed.

3.3. INSTALLING

The MIRDct installation file can be downloaded from www.MIRDsoft.org.

To install the software, launch installation file and follow instructions. Software will automatically install to the location "C:\MIRDsoft\MIRDct\MIRDct_v1.0\".

User's may need permissions and firewall exceptions from their site administrators to complete installation.

3.4. UNINSTALLING

To uninstall MIRDct, use the MIRDct uninstaller "C:\MIRDsoft\MIRDct\MIRDct_v1.0\uninstaller.exe"

3.5. TROUBLESHOOTING

We are collecting feedback from users and will post troubleshooting advice as it is collected. These items will be posted on our website:

https://mirdsoft.org/MIRDct-software-use-notes

4 MIRDCT SOFTWARE

4.1. INTRODUCTION

Computed tomography (CT), as an advanced imaging modality, has established itself as a pivotal component in the expansive field of medical imaging. Its significance is further accentuated within the specialized subset of hybrid imaging techniques. In the last couple decades, the prevalence of CT scans has witnessed a remarkable surge on a global scale, bolstered by advancements in medical technology and the expanding scope of clinical applications.

The fundamental use of Computed Tomography (CT) is to create detailed cross-sectional images of the body's internal structures. CT combines X-ray images taken from different angles around the body and uses computer processing to create these cross-sectional (tomographic) images. Because the images are acquired using ionizing radiation the use of CT poses potential health risks due to radiation exposure. Considering this, the development and implementation of robust, reliable, and accessible dosimetric tools are of paramount importance. Such tools are essential in tracking, recording, and optimizing the radiation dose received by patients during CT scanning procedures.

The assessment of radiation dose to individual organs, as well as the effective dose, represents a critical factor of radiological practice. Dosimetry methodologies provide essential quantitative data and serve as key indicators for healthcare professionals. These indicators are not merely numerical values but are instrumental in guiding the responsible management of CT technology. They enable clinicians to balance diagnostic efficacy with patient safety, ensuring that the benefits of imaging outweigh potential risks.

Furthermore, these dosimetric evaluations support the standardization across the healthcare industry, fostering the development and optimization of CT imaging protocols. Standardization is crucial, ensuring that patients receive the highest quality care irrespective of the facility or equipment used. It also propels forward the development of new protocols that maximize diagnostic yield while minimizing radiation exposure.

In addition, the metrics garnered from dosimetric tools are essential for the assessment of radiation risks. These risk evaluations are imperative when considering the long-term use and widespread application of CT technology. They inform policy makers, guide regulatory bodies, and shape the protocols that govern the safe use of medical imaging technologies. Hence, dosimetry plays an indispensable role in the conscientious deployment of computed tomography, fortifying its status as a vital tool in modern medicine while safeguarding patient health.

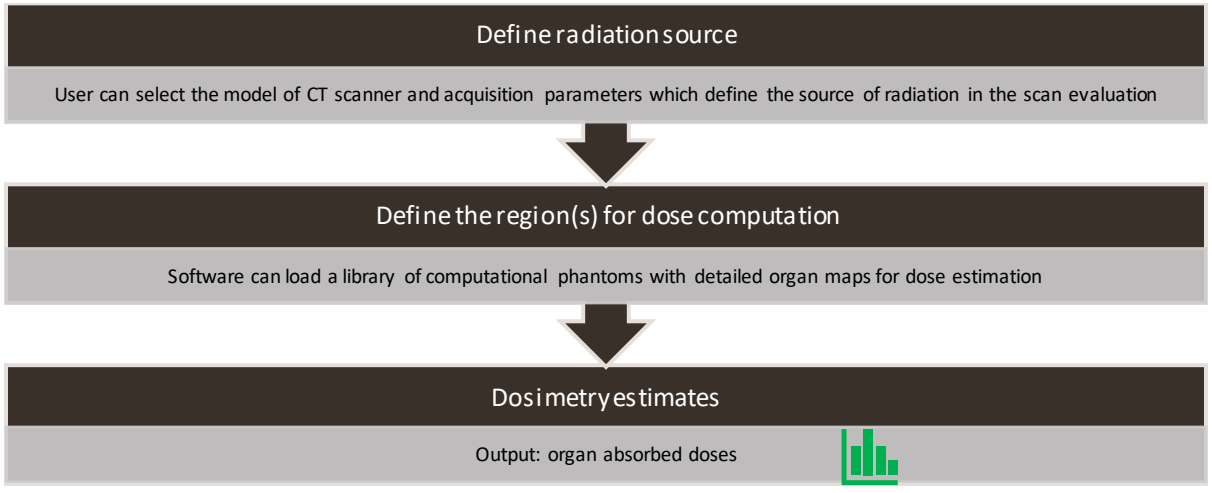
4.1 INTENDED USE

In MIRDct, absorbed dose estimations are calculated based on user input parameters. The intended uses of MIRDct include:

- Evaluation of organ doses for CT dosimetry in research.
- Evaluation of effective dose and other metrics as key indicator and survey evaluation.
- Optimization of CT protocols, techniques, and procedures.
- Comparison of CT techniques, procedures, technologies in terms of radiation dose.
- Evaluation of radiation-induced risk of patients for optimization and risk communication.
- To support the establishment of diagnostic reference levels (DRLs).
- As an educational tool for healthcare professionals and students.

4.2. GENERAL OVERVIEW OF SOFTWARE USE

MIRDct is an organ level dosimetry software for computed tomography, designed to be used independently for diagnostic radiology or as a complementary tool to the MIRDcalc nuclear medicine dosimetry software. It shares some similarities with other available dosimetry programs – the general workflow consists of a few basic steps:



4.3. MIRDCT INNOVATIONS

MIRDct was built with an aim of providing an advanced, free, and user-friendly organ level dosimetry tool for computed tomography. Organ absorbed dose estimation and other metrics are calculated based on user selection appropriate input, the software supports consideration of uncertainty in dose estimation. Several notable features include:

- Realistic anatomical models: State-of-art refence models, with 24 ICRP mesh-type family phantoms, 12 with the arms down and 12 with the arms up. Additional non-reference phantoms are currently being generated.
- Graphical user interface: a single-screen, user-friendly and intuitive interface provides the functionality required for dosimetry evaluations.
- Dosimetric models: Dose engine and Tube Current Modulation (TCM) is included.
- Uncertainty evaluation: Software can optionally propagate uncertainties into the absorbed dose calculational results, if desired.
- CT dosimetry database: CT-slice-specific organ dose coefficients, CT manufacturer, model, collimations, kVp, and bowtie filters.
- Quality control measures
- Data archiving

4.4. MIRDCT QUICK-STEP INSTRUCTIONS FOR USE

A quick overview of steps required for dose estimation in computed tomography is provided below:

MIRDct Quick-Step Usage Summary

1. Select ***Scanner model:***
   - Vendor
   - Model
   - Filter
   - kVp
   - Collimation
   - TCM (Tube current modulation)
2. Select a ***Phantom*** model:
   - Computational phantom sex
   - Reference phantom age
   - Reference phantom model
3. Enter **CT parameters**:
   - mAs, Pitch, CTDIvol
   - Case ID (optional)
4. **Protocol** selection
   - By body region (name)
   - By region and length
   - By manual selection (start/end slice)
5. Uncertainty propagation (Optional)
6. Get dosimetry estimates
7. (Optional) copy/save the dosimetry output results

In MIRDct all processing is available for review to users in spreadsheet format (i.e. open source). All the calculations are transparent and can be used for quality assurance and/or education. MIRDct can ideally be utilized by students, educators, and professionals in the field.

Note - An elemental understanding of the fundamentals of dosimetry is strongly encouraged for proper use of this software.

5 DETAILED INSTRUCTIONS FOR ABSORBED DOSE CALCULATIONS

5.1. GENERAL INPUT INSTRUCTIONS

MIRDct has two types of input fields: multiple choice slicers and text fields.

Slicers – the MS Excel platform supports multiple choice selections via slicers. The user may select presented fields from the slicers by clicking the fields.

Text fields – all "light blue" fields on the interface are editable.

MIRDct has three main panels: Input parameters, graphics and output, shown in Figure 1.

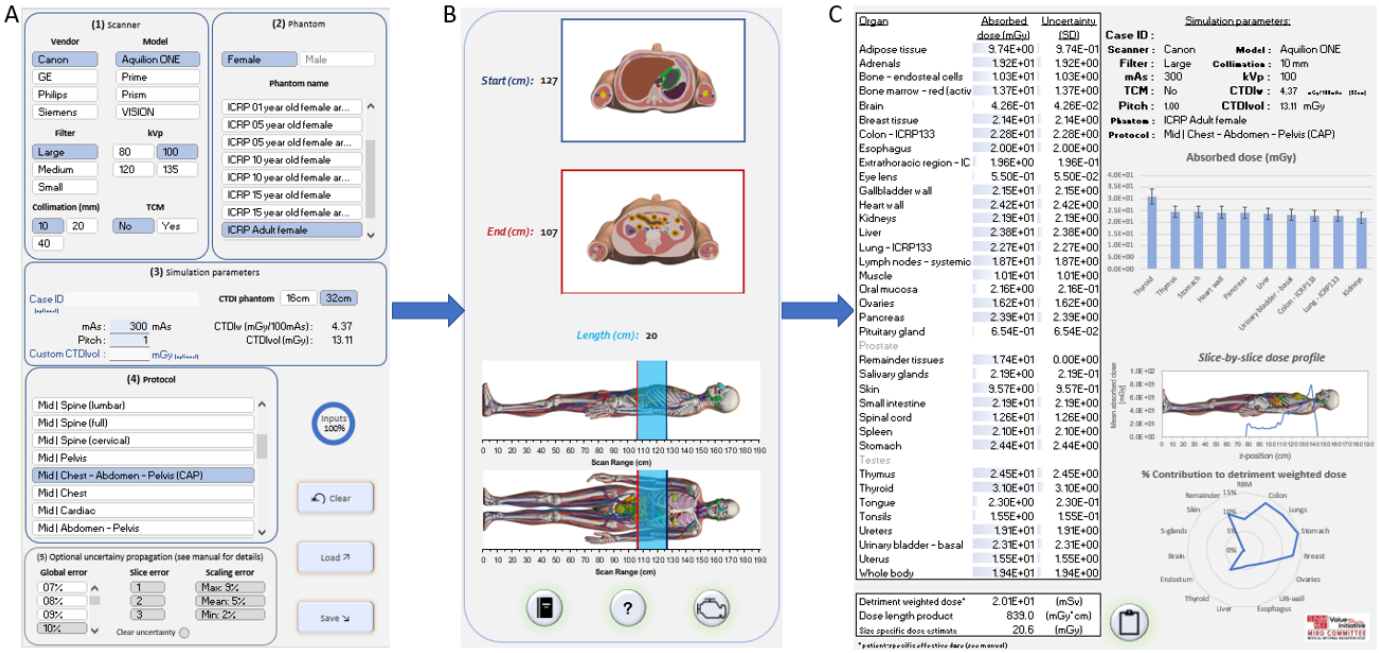


Figure 1 – MIRDct main panels. A) Input parameters. B) Images and interface. C) Numerical and graphical output.

5.2. INPUTS (FOR ABSORBED DOSE CALCULATION)

MIRDct evaluations works by calculating the absorbed doses in the computational phantoms from a pre-computed adsorbed dose library. The computations are dependent on user-selected scenarios. The scenario selection fields include scanner model, phantom model, CT parameters and protocol – the

protocol defines the start and end slices of the scan. Once these variables are selected the program extract required data from library and compute the expected organ doses for the given scenario.

The process for generating CT imaging dosimetry scenario include:

5.2.1. Scanner parameters

This portion of generating a scanning scenario includes the selection of vendor, model, filter, kVp, collimation and TCM (tube current modulation).

5.2.2. Phantom selection

Phantom selection allows the software to load the appropriate dosimetry database. MIRDct has pre-loaded region lists for each of the International Commission on Radiological Protection (ICRP) reference phantoms. These are the same digital phantoms models available in the MIRDcalc nuclear medicine dosimetry software (note MIRDcalc uses voxel type phantoms, MIRDct uses mesh-type versions of the same phantoms) [6].

In MIRDct version 1.0 twelve reference MESH-type computational phantoms, from the ICRP, are available for user selection (see figure 2). The main morphological characteristics of these model are presented in the table 1. At this stage of selection, a user should select the phantom that most closely models the scanning subject to be simulated. Additionally, users have the opportunity to select these phantoms with arms down or modified arms up position, as can be visualized in the Figure 3.

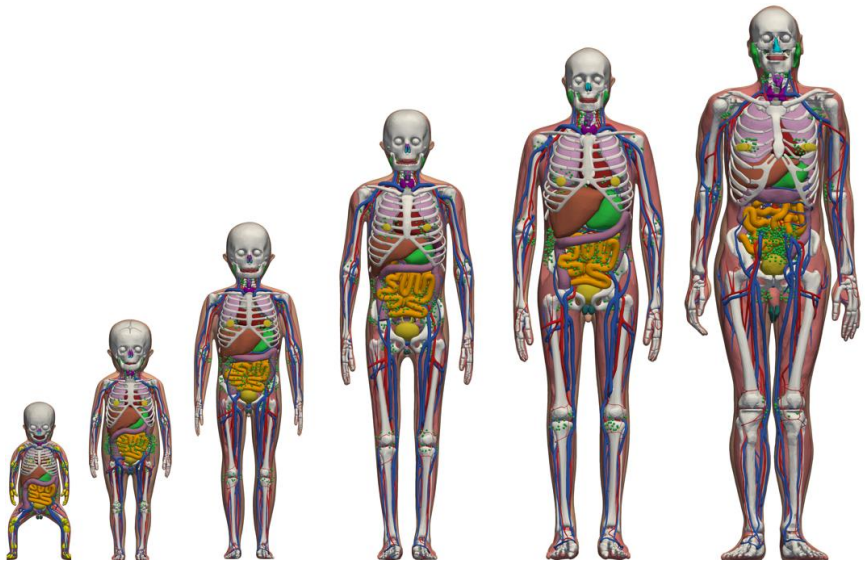


Figure 2 – Male computational phantom available in MIRDct with the arms Down. From left to right: Newborn, 1y, 5y, 10y, 15y and adult. [7,8]

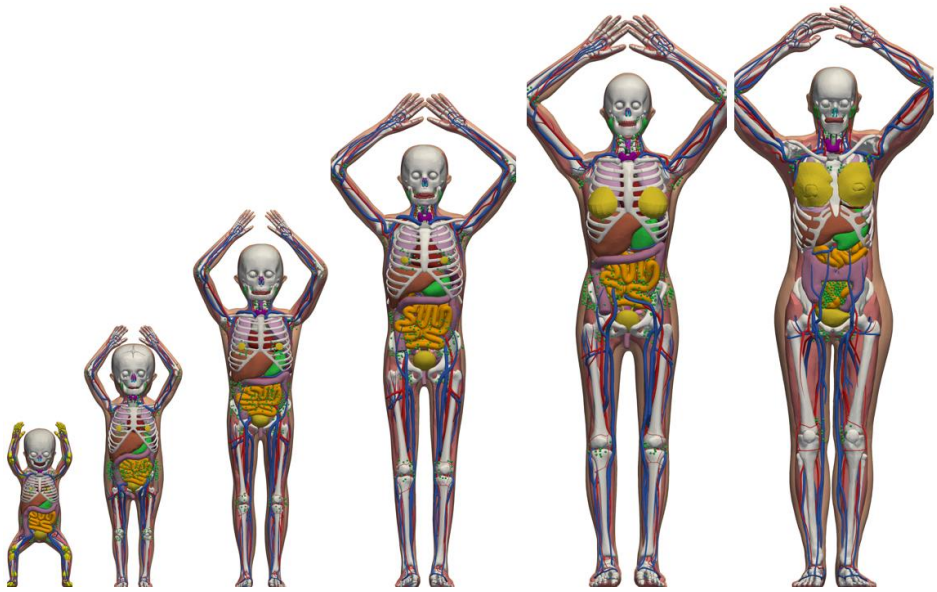


Figure 3 – Female computational phantom available in MIRDct with the arms Up. From left to right: Newborn, 1y, 5y, 10y, 15y and adult.

Table 1. Anatomical reference values for the ICRP computational phantoms.

	Height (cm)		**Mass (kg)**	
Age	Male	Female	Male	Female
Newborn	51	51	3.5	3.5
1 year	76	76	10	10
5 years	109	109	19	19
10 years	138	138	32	32
15 years	167	161	56	53
Adult	176	163	73	60

5.2.3. CT evaluation parameters

The user must select the specific combination of manufacturer, model, kVp, filter and collimation. Other acquisition parameters are required for the calculation like mAs, pitch, etc. The user may also assign a name to the file (case ID).

5.2.4. Protocol selection

The acquisition protocol defines the start and end slice of the simulated CT acquisition. This is important because the scanning range will determine which organs are directly irradiated and to what extent. MIRDct protocols are labelled starting with a "Upper", "Mid" and "Lower" prefix to indication the portion of the body the protocol correlated to.

MIRDct provides three main categories for protocol selection:

1. Region-based protocol: here the start and end point of the acquisition are fixed and defined by the protocols available in MIRDct. A region-based protocol can be loaded by selecting the appropriate option in the protocol selection slicer menu (Fig 4A). For example: "Mid | Abdomen".
2. Length-based: For these protocols, a default start end slice is loaded and defined with a pivot point at the start, end or middle of the field of view. The user can specify/modify the axial length of the protocol, then the start and end points are calculated accordingly to the pivot (caudal, cranial and central). The user must specify the length (in increments of 1 cm) in the central panel. A length-based protocol can be loaded by selecting the appropriate option in the protocol selection slicer menu (Fig 4B). These protocols are indicated with a "*" prefix. For example: "*Mid | Chest-Pivot-Cranial". Table 2 contains information for the placement and direction of length increase for this type of input.
3. Manual-based: The user has the option to manually define the start and end slice of the simulated acquisition using the manual-based protocol selection. Once selected, the user can set the start and end slice using the scroll bars at the bottom of the axial images located in the central panel (Figure 4C).

Table 2. Protocols names, Anatomical markers, and pivot placement for the length-based input.

Protocol parameters					***Placement of Reported Scan Length***		
#	***Body section***	***Protocol Name***	***Anatomical Start*** *(Cranial)*	***Anatomical End*** *(Caudal)*	*Center*	*Pivot - Cranial*	*Pivot - Caudal*
1	Upper	Head/Brain	Skull vertex	Skull Base/Mid oral cavity		X	
2	Upper	Maxillofacial/Sinus	Above frontal sinus	Through mandible	X		
3	Upper	Temporal Bone	Above sella	Through Hard palate	X		
4	Upper	Neck	Mid oral cavity	Through Carina		X	
5	Upper	Head/Brain/Neck	Skull vertex	Through Carina		X	
6	Mid	C-Spine	Sella	T3	X		
7	Mid	T-Spine	C7	L1	X		
8	Mid	L-Spine	T11-T12	Tip of coccyx			X
9	Mid	Full Spine	Sella	Tip of coccyx			X
10	Mid	Chest	Thoracic Inlet	Top of Kidneys		X	
11	Mid	Cardiac	Carina	Base of Heart	X		
12	Mid	Abdomen & Pelvis	Above dome of Diaphragm	Lesser Trochanter			X
13	Mid	Abdomen	Above dome of Diaphragm	Below iliac crest	X		
14	Mid	Pelvis	Top of Iliac crest	Lesser Trochanter			X
15	Mid	Chest-Abdomen-Pelvis (CAP)	Thoracic Inlet	Lesser Trochanter	X		
16	Lower	Lower Extremity - Thigh	Lesser Trochanter	Patellae			X
17	Lower	Lower Extremity - Knees to Foot	Patellae	Base of Feet			X
18	Whole	Whole body	Eyes	Thighs		X	
19	Whole	Total body	Skull vertex	Base of Feet		X	

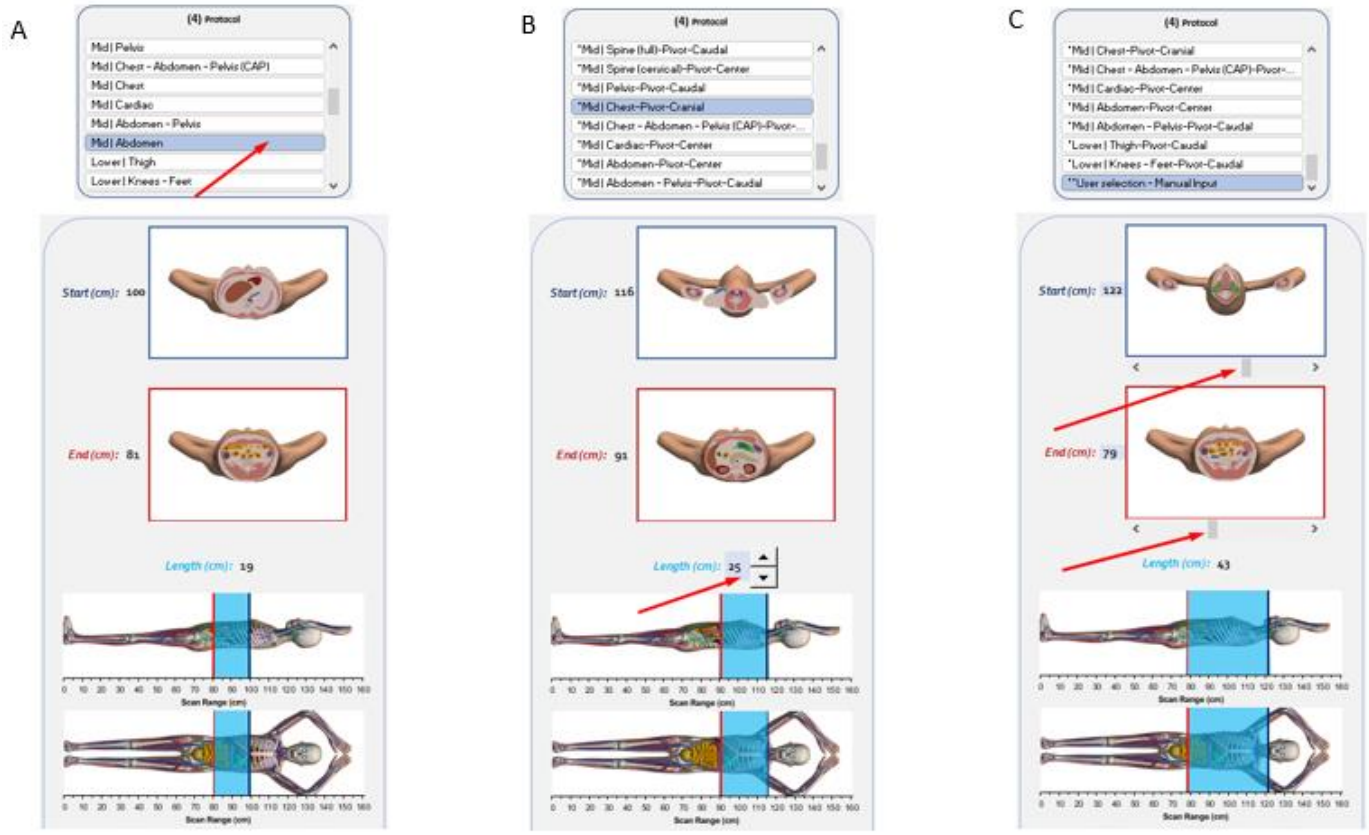


Figure 4 – Types of protocol selection. The red arrow shows the input interface. A) fixed protocol. B) by-Length. C) By user specification.

5.2.5. Optional uncertainty propagation

Optionally, the user may enter/select uncertainties associated with evaluation. Several sources of uncertainties have been identified and can be modelled in MIRDct:

- Global uncertainty: Anatomical discrepancies between the real patient and the selected computational phantom can be accounted for here.
- Slice uncertainty: Accounting for uncertainty in the anatomical start and end point of the protocol.
- Scanner Scaling: This variable takes in consideration the error associated with the CTDI normalization used for extrapolating absorbed doses between different CT scanner and models.

This optional input requires the user to choose values for each of these items using the respective slicers. The uncertainty in each observation may be entered as an absolute standard deviation, a relative standard deviation, or include or dismiss the error input. There are no default values used if no uncertainty entries are supplied.

5.2.6. Workflow

The GUI has a series of slicer that allow arrange and filter input parameter, the typical selection order is: Vendor → Model → Filter → kVp → Collimation → TCM → Phantom Sex → Phantom Name → Scaling model → Protocol. All these selections are required to allow calculation. There is an input quality control indicator that turns at 100% when all required inputs are correctly selected (see interface map).

Additional input variables include mAs, Pitch, and Case ID, while the optional inputs are Errors and Uncertainty Propagation.

5.3 CT DOSE CALCULATION AND CT DOSE LIBRARY

MIRDct calculates absorbed doses based on a pre-populated Monte Carlo based dose library.

The dose library is a large database of normalized dose factors for a specific combination of kVp, filter and collimation, these dose factors were computed for 10 mm slices in each of the computational phantoms.

Once a specific selection is performed, first, the correct library is loaded from the database into MIRDct based on user-supplied input.

The loaded library is then used to calculate dose using equation 1.

$$D = \sum_{i=Z_{start}}^{Z_{end}} D_i * A_i * mAs * \left(\frac{Scan\ Length}{Pitch*collimation*N}\right) \qquad \text{Eq. 1}$$

Where D_i is the normalized dose for the slice i (in mGy/mAs), Z_{start} and Z_{end} are the start and end slice number of the scan, A_i is the attenuation factor for the specific slice i, N is the number of slices in the scan range.

When tube current modulation (TCM) is selected a generic TCM algorithm is employed: A_i is changed from 1.0 in every slice to a new value which represents the attenuation correction factor for the specific slice i then the factor Ai*mAs simulates the correction factor for TCM.

5.3.1 Tube current modulation algorithm

MIRDct use a generic based method to simulate TCM. The algorithm was developed calculating the air kerma to an annulus of air for each z-axis slice of the phantom. For each slice i, the air kerma was determined to be inversely proportional to the total attenuation across both x and y dimensions (resulting in a combination of longitudinal and angular TCM). The resulting set of attenuation correction factors (Ai), generated for a given phantom and technique factor combination, was then normalized by the maximum

value within the set. When TCM is applied, the organ doses for each slice are scaled by this normalized Ai factor to produce the final dose values. This modeling approach is based on first-principles physics, providing a generic representation of TCM rather than mimicking specific commercial TCM algorithms. Ongoing developments aim to refine this algorithm to more closely align with vendor-specific TCM implementations in the future.

5.3.2 Scanner modeling

MIRDct models dosimetry for different scanners using CTDI scaling [9] by normalizing organ absorbed doses by their CTDIvol. MIRDct includes a default library of CTDIvol values for many existing scanners, these values depend on the manufacturer, model, kVp, filter and collimation. Alternatively, the user may also enter their own specific CTDI value to be used for dose scaling, for accommodating site-specific dosimetry calculation. This value could be taken from the CT console or by direct measurements.

$$\frac{Organ\ Dose_{scanner1}}{CTDIvol_{scanner\ 1}} = \frac{Organ\ Dose_{scanner2}}{CTDIvol_{scanner\ 2}} \qquad \text{Eq. 2}$$

5.4 OUTPUT DESCRIPTION

MIRDct display numerical and graphical results of the metrics evaluated, this allows easy readability and interpretation of the results.

5.4.1 Organ absorbed dose

The primary output of MIRDct is organ absorbed dose calculations. These data are automatically presented upon completion of input parameters. The data is displayed in the "CT dosimetry OUTPUT" on the right side of the GUI (figure 5). This panel presents an organ level absorbed dose evaluation for the phantom used in the evaluation. Absorbed dose is presented in units of mGy (SI unit). All major organs absorbed dose calculations are presented in the user interface. However, the digital phantoms used incorporate a large number of evaluated regions. To get a full list of dosimetry in all the regions the user may view them on the "engine tab" or save the MIRDct case to a save file (in .csv format) for further review. Additionally, two graphical displays are shown in the MIRDct interface; the first one displays the 10 highest organ absorbed doses and the second graph presents a slice-by-slice absorbed dose profile.

5.4.2 Detriment-weighted dose

The detriment-weighted dose (E_{DW}) is a risk-related weighted sum of organ absorbed doses. It is calculated using radiation weighting factors and tissue weighting factors described in ICRP Publication 103. The key difference between E_{DW} and E is that the former does not require the input dose estimates to be modelled specifically with a population-averaged ICRP reference phantom. The E_{DW} is more appropriate for users to report a summary dose metric derived from patient-specific organ dose estimates. In the E_{DW}, one may use a broader array of computational human phantoms from a phantom library which includes models at height and weight that differ from reference values. Furthermore, the E_{DW} avoids the need for sex-averaging of the male and female organ doses (absorbed doses or equivalent doses) as is described by the ICRP Publication 103 definition of E. The expression for E_{DW}, as originally given in Kofler et al [10], is as follows:

$$E_{DW}^{S,H,W} = \sum_{T} w_T \sum_{R} w_R D_{T,R}^{S,H,W} \qquad \text{Eq. 3}$$

where the superscripts S, H, and W indicate variations in the sex, height, and weight of the selected computational phantom toward values that more closely match those of a given patient. One can thus interpret this quantity as a "sex-specific non-reference E.". The unit for the detriment-weighted dose is the same as for effective dose, the sievert (Sv).

5.4.3 Dose Length Product (DLP)

Dose Length Product (DLP) is a measure of the total radiation output or exposure from a CT scan. While it is related to the Volume CT Dose Index (CTDIvol), which represents the dose delivered to a single slice of a standardized physical phantom(32 or 16 cm diameter), DLP extends this concept by accounting for the total length of the scan along the z-axis (the long axis of the patient). It is calculated using the following equation expressed in mGy*cm:

$$DLP = CTDIvol \times Scan\ length \quad Eq.4$$

In MIRDct the Scan length can be defined by protocol (fixed length between anatomical landmarks), manual input (user determine the start and end of the scan) or length-based protocol (user define the total length).

5.4.4 Size Specific Dose Estimates (SSDE)

While CTDIvol and DLP are commonly used to estimate radiation exposure during a CT procedure, these values remain constant regardless of patient size. However, patient size significantly influences the actual absorbed dose. Since SSDE could be determined using effective diameter, the anterior-posterior and lateral dimensions were derived from the ICRP mesh phantoms. SSDE is then calculated by applying CTDIvol along with the conversion factors proposed in AAPM TG 204, which are based on the effective diameter.

5.4.5 Saving dosimetry calculations

There are two ways to select or save the dosimetry output:

1. User may copy the dosimetry data to the clipboard by clicking the copy button  . Once copied, the user may paste the tab delimited data in an external document (e.g. notepad, excel, word…).
2. The user may click the ***Save*** button. This creates a comma delimited MIRDct save file automatically saved to "C:\MIRDsoft\MIRDct\MIRDct_v1.0\MIRDct_output\". This file can be reviewed by user and has a more robust accounting of input/output of case. This file can also be used to reload case at a later time (see section 5.3.4).

5.5 INTERFACE MAP

The full input/output interface is displayed to the user in a single screen. A screenshot with numbered info-points is displayed below along with a tabulated description (*vide infra*):

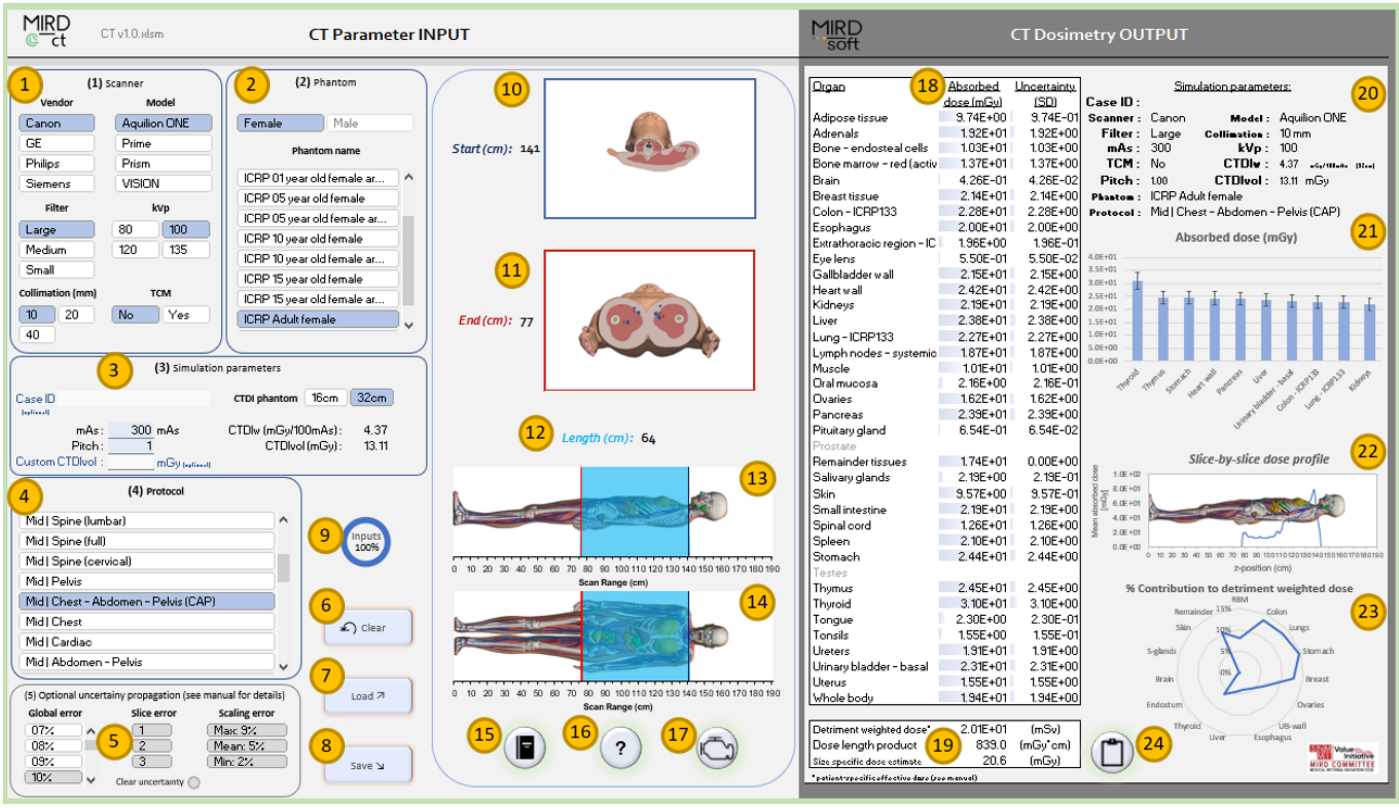


Figure 5 – Screenshot of MIRDct graphical user interface.

Description of Info-points for the Graphical User Interface of MIRDct			
1	Scanner model selection: Vendor and model.	2	Phantom model selection: Sex and computational model name (reference, non-refence phantom, age, arms up/arms down, etc.).
3	Simulation Parameters: mAs, pitch, CTDI phantom (Body: 32 cm, Head:16 cm), CTDIw, CTDIvol, custom CTDIvol, case ID, etc.	4	Protocol selection: By protocol name, *For by protocol/length and ** for Manual input.
5	Optional uncertainty selection: Global Error, slice error, Monte Carlo uncertainty and Scanner scaling error.	6	The Clear button can be used to clear the data entered and reset all the calculations.
7	The load button can be used load a previously saved file (or a modified saved file).	8	The save button should be used to save a dosimetry case. When the button is selected, MIRDct files are written to C:\MIRDsoft\MIRDct\MIRDct_output\.
9	Input quality control indicator, is 100% when all the needed inputs are correctly selected	10	Upper axial image and start point of the acquisition.
11	Inferior axial image and end point of the acquisition	12	Scan length in cm.

13	Sagittal image and graphical indicator of the irradiated anatomy	14	Coronal image and graphical indicator of the irradiated anatomy
15	Manual: the button launches the user manual.pdf	16	Description: the button opens the MIRDct information tab.
17	Engine: the button opens the MIRDct engine tab. Here the user can see and track all the input/output and calculation in MIRDct.	18	Absorbed dose output: numerical and graphical results of the organ absorbed dose calculation in mGy.
19	Detriment-weighted dose (E_{DW}), DLP and SSDE	20	Simulation parameters: This is a quality control feature to double check all the needed input used for the dose evaluation.
21	Organ absorbed dose graphic. Here only the ten highest values are displayed.	22	Slice-by-Slice plot: the profile of absorbed dose is showed over a sagittal image of the selected phantom.
23	Radar map of the contribution to the E_{DW} (sex-specific non-reference effective dose)	24	Clipboard: button (a) copies the displayed dosimetry calculations to the clipboard and (b) opens a text file showing the copied data.

6 ADVANCED FEATURES

6.1 ERROR PROPAGATION

The use of uncertainty propagation in MIRDct dosimetry calculations is optional. Simply leaving uncertainty input slicers no selected will default calculations to zero uncertainty.

MIRDct includes a propagation of uncertainty feature, allowing the user to incorporate the uncertainty in their input to derive an associated uncertainty of their organ absorbed dose output. To utilize this feature, the user can select the uncertainty values from the optional input slicers. (Figure 6).

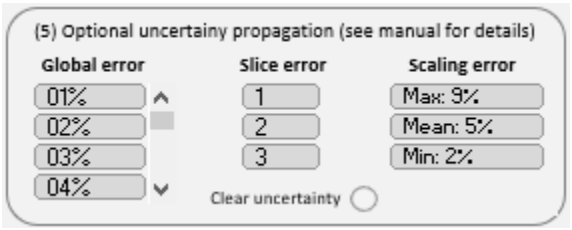


Figure 6. Optional Error and uncertainty propagation inputs in the GUI.

6.2 CASE SAVE/LOAD

To estimate dosimetry in MIRDct, the user needs to load or input case parameters (Scanner, Phantom, CT parameters). This information can be entered manually on the graphical user interface or loaded with a MIRDct input file.

MIRDct output files: When a case is properly entered, the user can click the save button 

to archive case. This saves two files a comma delimited file containing the input and output parameters and a pdf file with a screenshot of the GUI, these files are saved to the default "C:\MIRDsoft\MIRDct\MIRDct_v1.0\MIRDct_output\". MIRDct save files are in .csv format and can be viewed with a text editor (e.g. notepad). The MIRDct save files include by default a CASE LOADING BLOCK and therefore can be used to reload the saved case.

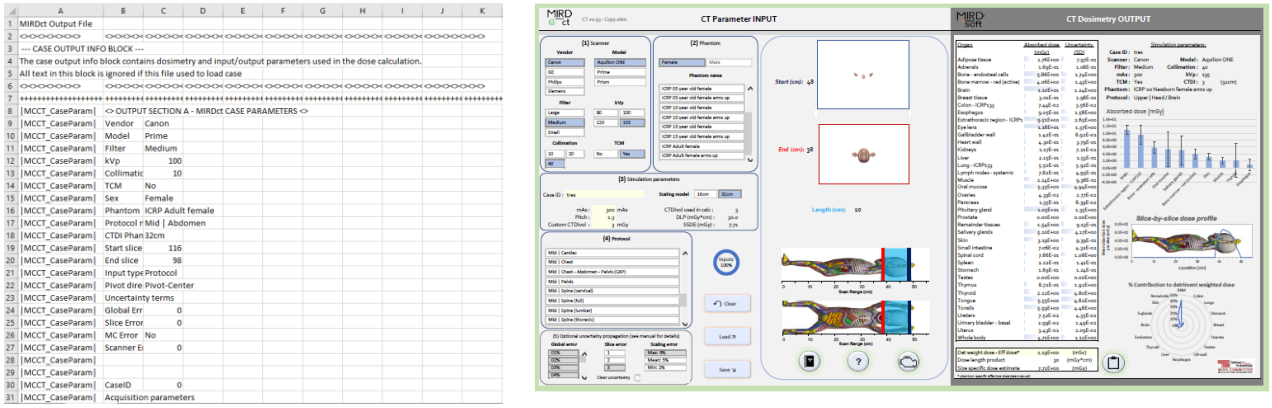


Figure 7. Example of Saved files, MIRDct output file (Left) and GUI screenshot (Right).

MIRDct input files: MIRDct input files are .cvs or .xlsm files that can be stored locally and used to load specific input parameters into the MIRDct spreadsheet. The required format of input files is exemplified in any/all saved output files (under CASE LOADING BLOCK). To manually create a MIRDct input file, we suggest starting with a MIRDct save file, and editing the filename/data as desired. Another way to define an input file is to use the batch processing utility.

6.3 BATCH PROCESSING

MIRDct supports the running of several case dosimetry calculations via the batch processing feature, in which MIRDct run automatically for several input cases.

To use the batch processing feature:

1. Create a .cvs file with the input parameters, using the following order (see figure 8):
   Vendor, Model, Filter, kVp, Collimator (mm), TCM, Sex, Phantom, Scaling, Model, Protocol Name, Global Error (%), Slice Error, Scaling Error, mAs, Pitch, CTDI (custom), Case ID.

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q
1	Vendor	Model	Filter	kVp	Collimato	TCM	Sex	Phantom	Scaling Model	Protocol Name	Global Error (%)	Slice Error	Scaling Error	mAs	Picth	CTDI (custom)	Case ID
2	Canon	Aquilion ONE	Medium	80	10	Yes	Female	ICRP Adult female arms up	32cm	Mid | Chest	10%	1	Min: 2%	100	1.1	1	uno
3	Canon	Aquilion ONE	Large	100	20	No	Male	ICRP 05 year old male	16cm	Mid | Abdomen	20%	2	Mean: 5%	200	1.2	2	dos
4	Canon	Aquilion ONE	Medium	135	40	Yes	Female	ICRP 00 Newborn female arms up	32cm	Upper | Head / Br	30%	3	Max: 9%	300	1.3	3	tres

Figure 8. Example of input file

2. Launch MIRDct.

   When MIRDct is launched, click the Load button 

and select the input file. MIRDct will run in batch mode, line-by-line. Dosimetry output files will be automatically generated for each input line.

6.4 RISK INDEX

MIRDct provides a calculation of Risk Index (RI), found in the output of a case save file. This value is presently used for research and has not been established for use in the field.

Consideration of medical exposures is important for low levels of radiation absorbed doses. When exposure to ionizing radiation occurs, it is essential to be able evaluate how much radiation a patient receives, and to be able to it in context of risk and benefit. Having accurate metrics and quantities to understand those variables is critical in the process of justification and optimization in medical imaging.

Traditionally the effective dose has been used as a risk indicator, and as a value for comparison in medical radiation procedures, even though this application for medical imaging was not the original intended use of this radiation protection quantity. It has been proposed that the risk determination process for medical diagnostic use of ionizing radiation can be adjusted using newer data, more specific modeling, and presented in more refined terms. Using appropriate risk values for the individual tissues at risk, and stratification by age and sex may offer greater insight into understanding individual risk. For this reason, the RI value has been proposed in literature.

The RI is a special and advanced feature included in MIRDct, the aim of this quantity is to provide to specialized users a more clinically relevant alternative to the effective dose for risk assessment and optimization processes for the use of radiopharmaceuticals in nuclear medicine. The RI is recently established in the literature [2] and has been integrated as an output calculation in the MIRDct software.

The RI estimation is defined as a ratio of the estimated added risk of cancer from specific radiation exposure, relative to the estimated natural risk of cancer. For implementation, we estimated the lifetime attributable risk of cancer (LAR) from a given exposure using the National Cancer Institute's Radiation Risk Assessment Tool (RadRAT) [3]. The baseline, the natural incidence of cancer in a population with an absence of exposure, was derived from the SEER database as defined in RadRAT. All risks are extracted on an age and sex basis.

$$Risk\ Index = \frac{\text{Estimate Radiation Induced Cancer Risk}}{\text{Natural Incidence of Cancer}}\ x\ 100$$

Several reports like BEIR VII, EPA, NCI, ICRP provide data and methodologies in order to estimate LAR values from radiation exposure for age, sex. LAR values can be calculated for incidence or mortality of cancer as well for specific organs/tissue cancer sites and for the addition of all types of cancer.

In MIRDct age and sex specific LAR values are estimated from organ absorbed doses using the approach of the NCI for cancer incidence, LAR for specific organs is calculated and summed to obtain the total whole-body LAR.

As an example, a RI of 1.0 would suggest a patient has a 1% higher chance of radiation induced cancer when compared to their natural probability of cancer incidence. Note that the percentage is over the baseline natural risk of cancer.

The user should be aware that the values of LAR are based on the LNT model and that the numerical values are inferences of the extrapolation of that model to low absorbed doses. Numerous publications point out that this model is not suitable for calculating individual risk at low doses. It is therefore not advisable to attribute a LAR or RI value as a risk assessment to any one individual patient.

Ultimately, the RI is presented in MIRDct as a resource for users. The field has yet to come to consensus on its appropriate use. This will likely be in areas of optimization and comparative risk assessments. The RI presents a newly designed variable to help understand and communicate risk associated with diagnostic radiation doses, and can potentially be used as a substitute or complementary measurement of the ED.

Values of LAR ([(case / 100k)]) and RI (%) are provided for ages 0, 5, 10, 15, 20, 30, 40, 50, 60, 70, 80, 90, 100 years old. From the output the user can select the proximal age between the available data ages and then perform the interpolation for the desired age. For pediatric patients the user may run MIRDct for the two close ages and then perform the interpolation.

For traceability of the RI, values used for calculation of LAR and the natural risk of cancer in MIRDct are provided in the following tables. Estimates of Lifetime risk of radiation-related cancer are provided in tables Table 3 and Table 4 for males and females respectively, values are applicable for a particular age of exposure and for a single-acute absorbed dose of 0.1 Gy. Estimates of cancer incidence are shown for several site-specific solid cancers, leukemia, and all types of cancers. Table 5 and Table 6 shows lifetime risks of cancer incidence in the absence of exposure, i.e., the natural Incidence of cancer by age and sex per 100,000 population.

Table 3- Lifetime Attributable Risk of Cancer Incidence by age and site for males (Number of cases per 100,000 persons exposed to a single dose of 0.1 Gy). Derived from RadRAT 4.2.

Cancer Site/Age	0	5	10	15	20	30	40	50	60	70	80
Oral Cavity & Pharynx	83.7	70.3	58.5	48.7	40.6	27.9	24.6	18.4	11.1	5.12	1.61
Esophagus	102	86.5	72.9	61.4	51.8	36.7	35	30	21.3	11.2	3.8
Stomach	256	212	174	142	117	76.8	71.5	62.2	47.7	29.3	12.1
Colon	523	447	379	321	273	195	187	167	129	74.5	26.3
Rectum	52.7	45	38	32.1	27.2	19.1	17.8	14.9	10.4	5.48	1.88
Liver	167	139	115	95	78.8	53.9	51.4	44.3	34.3	21.5	9.49
Gallbladder	0	0	0	0	0	0	0	0	0	0	0
Pancreas	89.1	76.2	64.6	54.8	46.6	33.5	32.2	28.4	21.1	11.7	3.95
Lung	511	428	355	295	246	172	170	159	131	84.2	37.8
Prostate	307	266	229	197	170	128	127	115	75.4	30.3	7.85
Bladder	372	319	271	230	196	142	140	132	108	67.2	26.4
Kidney	122	104	88.8	75.8	64.8	46.6	43	35.5	23.6	11.3	3.31
Nervous System	152	104	79.5	63.1	50.6	32.6	27.6	21.4	14	6.35	1.64
Thyroid	296	197	130	85	55.4	22.6	8.59	3	0.88	0.184	0.0243
Other	1020	851	701	569	460	298	259	212	150	80.5	26.7
Leukemia	364	177	136	115	103	91.5	91.5	94.3	99	95.6	69.5
All cancers	4418	3522	2892	2385	1981	1376	1286	1137	877	534	232

Table 4: Lifetime Attributable Risk of Cancer Incidence by age and site for females (Number of cases per 100,000 persons exposed to a single dose of 0.1 Gy). Derived from RadRAT 4.2.

Cancer Site/Age	0	5	10	15	20	30	40	50	60	70	80
Oral Cavity & Pharynx	83.7	70.2	58.5	48.6	40.2	27.2	24.2	19.5	13.6	7.25	2.53
Esophagus	42.4	36.3	30.9	26.3	22.4	16.1	15.5	14	10.7	6.15	2.35
Stomach	307	254	208	171	139	91.6	85.6	75.5	60.1	39.3	17.7
Colon	350	299	254	215	182	130	124	112	89.9	57.7	23
Rectum	48.2	40.9	34.4	28.9	24.3	16.8	15.5	13.1	9.77	5.86	2.36
Liver	95.4	78.8	64.8	53.3	43.9	29.6	28.6	26.1	21.5	14.5	6.89
Gallbladder	0	0	0	0	0	0	0	0	0	0	0
Pancreas	89.9	76.6	64.9	55	46.6	33.2	32	29	23	14.3	5.65
Lung	1210	1020	849	711	596	418	408	378	303	190	86.9
Breast	1810	1420	1100	857	663	386	209	101	43	15.2	3.76
Ovary	164	138	115	95.5	79.6	54.6	48.8	39.1	27	15.1	5.54
Uterus	93.4	78	64.8	53.6	44	28.7	25.9	21.4	15.4	9.25	3.95
Bladder	365	313	266	226	193	139	136	125	102	65.4	27.5
Kidney	79.6	66.7	56.5	47.8	40.4	28.4	26.1	21.9	15.6	8.25	2.76
Nervous System	42.9	28.6	21.6	17	13.5	8.58	7.3	5.76	3.9	1.94	0.585
Thyroid	1650	1100	720	468	298	112	37.8	11.5	3.08	0.63	0.0851
Other	622	515	424	347	281	181	152	119	83	45.8	16.5
Leukemia	329	148	105	88.9	81.1	71.6	72.3	74.1	76.1	73.3	55.4
All cancers	7383	5683	4437	3510	2788	1772	1449	1186	901	570	263

Table 5: Baseline Lifetime Risk estimates of cancer incidence for males, number of cases per 100,000 persons in the absence of exposure – SEER data base (RadRAT 4.2).

Cancer Site/Age	0	5	10	15	20	30	40	50	60	70	80	90	100
Oral Cavity & Pharynx	1430	1440	1440	1440	1450	1460	1460	1380	1140	795	478	269	153
Esophagus	757	764	765	766	770	779	789	789	727	570	351	184	105
Stomach	1100	1110	1110	1110	1110	1120	1130	1120	1080	941	695	395	225
Colon	4080	4120	4120	4120	4140	4190	4230	4260	4130	3660	2710	1590	903
Rectum	1840	1850	1860	1860	1870	1890	1890	1850	1670	1310	833	458	260
Liver	833	837	837	837	841	849	856	821	681	508	286	147	84
Gallbladder	286	288	288	289	290	294	297	299	295	269	211	126	72
Pancreas	1260	1270	1270	1280	1280	1300	1310	1320	1260	1070	747	414	235
Lung	7930	8000	8010	8020	8060	8160	8290	8410	8200	6800	4030	2010	1140
Prostate	16400	16500	16500	16600	16600	16900	17200	17600	16700	12100	6110	3110	1760
Bladder	3690	3720	3730	3730	3750	3790	3840	3910	3880	3530	2610	1510	856
Kidney	1770	1780	1780	1780	1790	1800	1810	1760	1570	1180	701	359	204
Nervous System	661	646	630	617	609	590	561	518	448	344	195	98	55
Thyroid	376	380	380	379	378	366	332	285	220	138	66	30	17
Other & Ill-defined Sites	4970	4980	4980	4960	4940	4810	4600	4330	3890	3160	2160	1210	685
Leukemia	939	903	883	868	854	837	816	793	759	685	524	307	175
All cancers	48322	48588	48583	48656	48732	49135	49411	49445	46650	37060	22707	12216	6928

Table 6: Baseline Lifetime Risk estimates of cancer incidence for females, number of cases per 100,000 persons in the absence of exposure – SEER data base (RadRAT 4.2).

Cancer Site/Age	0	5	10	15	20	30	40	50	60	70	80	90	100
Oral Cavity & Pharynx	683	688	688	687	687	681	669	635	562	442	284	157	84
Esophagus	247	249	249	249	249	250	252	250	239	201	136	78	42
Stomach	683	688	689	689	690	691	685	670	637	571	433	258	138
Colon	4200	4230	4230	4240	4240	4260	4260	4230	4060	3620	2770	1610	863
Rectum	1460	1470	1470	1480	1480	1480	1470	1410	1260	1020	695	392	210
Liver	349	349	349	349	349	349	349	343	319	257	156	78	42
Gallbladder	369	372	372	372	373	374	375	373	359	312	234	133	71
Pancreas	1300	1310	1310	1310	1310	1320	1320	1320	1280	1120	817	472	253
Lung	6330	6370	6380	6380	6390	6420	6460	6420	6050	4720	2530	1160	621
Breast	13200	13300	13300	13300	13300	13300	13000	11800	9600	6710	3780	1870	999
Ovary	1440	1460	1460	1450	1450	1440	1410	1310	1110	831	519	265	142
Uterus	3240	3270	3270	3270	3280	3250	3100	2830	2260	1460	789	383	205
Bladder	1190	1200	1200	1200	1200	1210	1210	1210	1160	1010	737	419	224
Kidney	1050	1050	1050	1050	1050	1050	1040	1000	891	684	401	194	104
Nervous System	537	522	507	496	487	466	440	407	351	268	157	79	42
Thyroid	1070	1080	1080	1070	1060	964	794	592	398	231	100	45	24
Other	3180	3170	3170	3150	3130	3040	2870	2600	2230	1730	1130	617	331
Leukemia	722	691	673	660	650	634	613	585	543	474	355	208	112
All cancers	41250	41469	41447	41402	41375	41179	40317	37985	33309	25661	16023	8418	4507

7 ADDITIONAL ITEMS

7.1 OPERATING SYSTEM

Only PCs running Microsoft Windows 7 or later, with Microsoft Office installed are supported. Please make sure to use the correct installation file based on your Excel version (32-bit or 64-bit).

MIRDct is not supported in Mac environments/virtual machines.

7.2 USAGE QUIRKS

MIRDct is built using the "." decimal separator. If you're using a (European) decimal, i.e. writing pi as "3,14", the settings will be changed during MIRDct use to use the ".", and on closing it will be changed back to the system preference (recorded at MIRDct opening).

7.3 FEEDBACK

MIRDct is built as a community tool. We welcome cooperation and interest to make it better.

We are hoping our MIRDct tool is useful to users throughout the community. Any and all feedback is welcome and will be taken under consideration for future development. Please email any comments or suggestions to contact@mirdsoft.org.

8 REFERENCES

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APPENDIX A: SUMMARY OF MIRDCT ORGAN TARGET REGIONS

	MIRDct	ICRP133	ICRP133
MC order	MC name	Short name	Long name
1	Adipose tissue	Adipose	Adipose tissue
2	Adrenals	Adrenals	Adrenals
3	Bone - endosteal cells	Endost-BS	Endosteal cells
4	Bone marrow - red (active)	R-marrow	Red (active) marrow
5	Brain	Brain	Brain
6	Breast tissue	Breast	Breast
7	Bronchial basal cells	Bronch-bas	Bronchi basal cells
8	Bronchial secretory cells	Bronch-sec	Bronchi secretory cells
9	Bronchiolar secretory cells	Bchiol-sec	Bronchiolar secretory cells
10	Colon - ICRP133	-	-
11	Colon - left	LC-stem	Left colon
12	Colon - rectosigmoid	RS-stem	Rectosigmoid Colon
13	Colon - right	RC-stem	Right colon
14	Esophagus	Oesophagus	Oesophagus
15	ET1 airway basal cells	ET1-bas	ET1 basal cells
16	ET2 airway basal cells	ET2-bas	ET2 basal cells
17	Extrathoracic region - ICRP133	-	-
18	Eye lens	Eye-lens	Lens of eye
19	Gallbladder wall	GB-wall	Gall bladder
20	Heart wall	Ht-wall	Heart wall
21	Kidneys	Kidneys	Kidneys
22	Liver	Liver	Liver
23	Lung - ICRP133	-	-
24	Lungs (AI)	AI	Alveolar-interstitial
25	Lymph nodes - extrathoracic	LN-ET	Extrathoracic lymph nodes
26	Lymph nodes - systemic	LN-Sys	Systemic lymph nodes
27	Lymph nodes - thoracic	LN-Th	Thoracic lymph nodes
28	Lymphatic nodes - ICRP133	-	-
29	Muscle	Muscle	Muscle
30	Oral mucosa	O-mucosa	Oral Mucosa
31	Ovaries	Ovaries	Ovaries
32	Pancreas	Pancreas	Pancreas
33	Pituitary gland	P-gland	Pituitary gland
34	Prostate	Prostate	Prostate

35	Salivary glands	S-glands	Salivary glands
36	Skin	Skin	Skin
37	Small intestine	SI-stem	Small intestine
38	Spleen	Spleen	Spleen
39	Stomach	St-stem	Stomach
40	Testes	Testes	Testes
41	Thymus	Thymus	Thymus
42	Thyroid	Thyroid	Thyroid
43	Tongue	Tongue	Tongue
44	Tonsils	Tonsils	Tonsils
45	Ureters	Ureters	Ureters
46	Urinary bladder wall	UB-wall	Urinary bladder
47	Uterus	Uterus	Uterus
48	Whole body target	-	-

APPENDIX B: PROTOCOL PARAMETERS

B.1 Protocols for the ICRP Newborn Phantoms

	female		male	
Protocol Name	**Start Slice**	**End Slice**	**Start Slice**	**End Slice**
Lower | Knees - Feet	16	0	14	0
Lower | Thigh	24	16	25	14
Mid | Abdomen	37	30	38	30
Mid | Abdomen - Pelvis	37	24	38	25
Mid | Cardiac	41	37	41	37
Mid | Chest	44	36	43	36
Mid | Chest - Abdomen - Pelvis (CAP)	44	24	43	25
Mid | Pelvis	31	24	31	25
Mid | Spine (cervical)	48	42	48	42
Mid | Spine (full)	48	30	48	30
Mid | Spine (lumbar)	36	30	36	30
Mid | Spine (thoracic)	44	35	43	34
Upper | Head - Brain - Neck	51	41	51	41
Upper | Head / Brain	51	46	51	46
Upper | Maxillofacial / Sinus	48	44	49	44
Upper | Neck / Neck	46	41	46	41
Upper | Temporal bone	48	46	48	46
Whole | All	51	0	51	0
Whole | Body (Cranium - knees)	48	22	48	20

B.2 Protocols for the ICRP 01-year-old Phantoms

	female		male	
Protocol Name	**Start Slice**	**End Slice**	**Start Slice**	**End Slice**
Lower | Knees - Feet	23	0	21	0
Lower | Thigh	35	23	37	21
Mid | Abdomen	55	45	57	45
Mid | Abdomen - Pelvis	55	35	57	37
Mid | Cardiac	61	55	61	55
Mid | Chest	65	53	63	53
Mid | Chest - Abdomen - Pelvis (CAP)	65	35	64	37

Mid | Pelvis	46	35	46	37
Mid | Spine (cervical)	72	62	72	62
Mid | Spine (full)	72	44	72	44
Mid | Spine (lumbar)	54	44	53	44
Mid | Spine (thoracic)	65	52	65	51
Upper | Head - Brain - Neck	76	61	76	61
Upper | Head / Brain	76	69	76	69
Upper | Maxillofacial / Sinus	72	66	73	66
Upper | Neck / Neck	69	61	69	61
Upper | Temporal bone	72	69	72	69
Whole | All	76	0	76	0
Whole | Body (Cranium - knees)	71	33	72	29

B.3 Protocols for the ICRP 05-year-old Phantoms

	female		**male**	
Protocol Name	**Start Slice**	**End Slice**	**Start Slice**	**End Slice**
Lower | Knees - Feet	33	0	30	0
Lower | Thigh	51	33	53	30
Mid | Abdomen	79	64	82	65
Mid | Abdomen - Pelvis	79	51	82	53
Mid | Cardiac	87	80	87	79
Mid | Chest	94	76	91	76
Mid | Chest - Abdomen - Pelvis (CAP)	94	51	92	53
Mid | Pelvis	66	51	66	53
Mid | Spine (cervical)	103	89	103	89
Mid | Spine (full)	103	64	103	64
Mid | Spine (lumbar)	77	64	76	64
Mid | Spine (thoracic)	94	75	93	73
Upper | Head - Brain - Neck	109	87	109	87
Upper | Head / Brain	109	98	109	98
Upper | Maxillofacial / Sinus	104	95	104	95
Upper | Neck / Neck	98	87	98	87
Upper | Temporal bone	103	99	103	99
Whole | All	109	0	109	0
Whole | Body (Cranium - knees)	102	47	103	42

B.4 Protocols for the ICRP 10 years old Phantoms

	female		male	
Protocol Name	**Start Slice**	**End Slice**	**Start Slice**	**End Slice**
Lower | Knees - Feet	42	0	38	0
Lower | Thigh	64	42	67	38
Mid | Abdomen	100	81	104	82
Mid | Abdomen - Pelvis	100	64	104	67
Mid | Cardiac	110	101	111	100
Mid | Chest	119	97	115	96
Mid | Chest - Abdomen - Pelvis (CAP)	119	64	116	67
Mid | Pelvis	83	64	84	67
Mid | Spine (cervical)	130	113	131	113
Mid | Spine (full)	130	80	131	81
Mid | Spine (lumbar)	97	80	96	81
Mid | Spine (thoracic)	119	95	118	93
Upper | Head - Brain - Neck	138	110	138	111
Upper | Head / Brain	138	124	138	125
Upper | Maxillofacial / Sinus	131	120	132	120
Upper | Neck / Neck	124	110	125	111
Upper | Temporal bone	130	125	131	125
Whole | All	138	0	138	0
Whole | Body (Cranium - knees)	129	59	130	53

B.5 Protocols for the ICRP 15 years old Phantoms

	female		male	
Protocol Name	**Start Slice**	**End Slice**	**Start Slice**	**End Slice**
Lower | Knees - Feet	49	0	46	0
Lower | Thigh	75	49	81	46
Mid | Abdomen	117	95	125	100
Mid | Abdomen - Pelvis	117	75	125	81
Mid | Cardiac	128	118	134	121
Mid | Chest	138	113	139	117
Mid | Chest - Abdomen - Pelvis (CAP)	138	75	140	81
Mid | Pelvis	97	75	102	81
Mid | Spine (cervical)	152	131	158	137
Mid | Spine (full)	152	94	158	98

Mid | Spine (lumbar)	114	94	117	98
Mid | Spine (thoracic)	138	111	142	112
Upper | Head - Brain - Neck	161	128	167	134
Upper | Head / Brain	161	145	167	151
Upper | Maxillofacial / Sinus	153	140	159	145
Upper | Neck / Neck	145	128	151	134
Upper | Temporal bone	152	146	158	152
Whole | All	161	0	167	0
Whole | Body (Cranium - knees)	150	69	158	65

B.6 Protocols for the ICRP Adults phantoms

	female		**male**	
Protocol Name	**Start Slice**	**End Slice**	**Start Slice**	**End Slice**
Lower | Knees - Feet	50	0	49	0
Lower | Thigh	76	50	85	49
Mid | Abdomen	118	96	132	105
Mid | Abdomen - Pelvis	118	76	132	85
Mid | Cardiac	130	119	141	128
Mid | Chest	140	114	147	123
Mid | Chest - Abdomen - Pelvis (CAP)	140	76	148	85
Mid | Pelvis	98	76	107	85
Mid | Spine (cervical)	154	133	167	144
Mid | Spine (full)	154	95	167	103
Mid | Spine (lumbar)	115	95	123	103
Mid | Spine (thoracic)	140	112	150	118
Upper | Head - Brain - Neck	163	130	176	141
Upper | Head / Brain	163	147	176	159
Upper | Maxillofacial / Sinus	155	142	168	153
Upper | Neck / Neck	147	130	159	141
Upper | Temporal bone	154	148	167	160
Whole | All	163	0	176	0
Whole | Body (Cranium - knees)	152	70	166	68