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Abbreviations

3D	Three-dimensional
AP	Anterior posterior
API	Application Programming Interface
ATCM	Automatic Tube Current Modulation
CBCT	Cone Beam Computed Tomography
CPU	Central Processing unit - processor
CT	Computed Tomography
CTDI	Computed Tomography Dose Index
DICOM	Digital Imaging and Communication in Medicine
DR	Digital Radiography
FOV	Field of View
FTC	Fixed Tube Current
GPU	Graphics Processing Unit
GUI	Graphical User Interface
HU	Hounsfield (scale) Unit
IGRT	Image Guided Radiation Therapy
kV	kilovoltage
LAT	Lateral (projection)
MC	Monte Carlo
MC	Monte Carlo
MV	Megavoltage
NAS	Network Attached Storage
PA	Posterior-Anterior
PACS	Picture Archiving and Communications System
ReLU	Rectified Linear Unit activation function
TCM	Tube Current Modulation
TPS	Treatment Planning System
WED	Water Equivalent Diameter

1. Development of a method to estimate patient organ dose from radiological examinations involved in cancer diagnosis, treatment, and follow-up

Lymphoma and brain tumor patients, with multiple exposures in radiology, nuclear medicine, and radiation therapy, face risks of radiation-induced malignancies, especially children and young adults [1-4]. The objective of Tasks 2.1 and 2.4 by UoC was to propose accurate methods, considering patient size and exposure characteristics utilizing computational MC and AI models, for estimating radiation dose to organ structures during the diagnosis and radiotherapy of tumors.

The proposed method combines Monte Carlo (MC) computational techniques and patient CT scans in five steps: (a) collecting suitable patient CT scans; (b) determining examinations' parameters; (c) conducting MC dosimetric computations; (d) obtaining three-dimensional (3D) patient-specific dose distribution output; and (e) establishing correlations between dose and patient characteristics. These 3D dose distributions will form the foundation for AI and ML algorithms to derive organ doses from the 3D dose-volume during or immediately after a radiological examination by modeling the patient-specific dose-response relationship.

2. Data Collection

Images from 226 pediatric and 308 adult lymphoma and brain tumor patients were included in this task. All images and exposure were selected and extracted from the local Picture Archiving and Communication System (PACS) database following specific data protection guidelines as proposed by the SINFONIA Data Management Board to ensure data privacy and security.

Data Privacy and Security

Data was collected on-site, using a local secure network through PACS Digital Imaging and Communication in Medicine (DICOM) protocol. Before delineation and MC simulations, all CT images collected were anonymized and patient and exams id were kept in a different password protected archive, so as images' identifiers were all limited to alphanumeric characters with no direct connection to patient personal data.

Anonymization

Proper handling is essential for maintaining patient privacy when dealing with sensitive patient data. [5]. There are mainly two methods to de-identify patient-related information through a DICOM header strategy [6]. The first method is anonymization which removes information carried by header elements or replaces the information with random data such that the remaining information cannot be used to reveal the patient identity at all. Another method, pseudo-anonymization, is implemented by replacing these fields using artificial identifiers that could be used to track down the real identity of the patient in case of clinical analysis. An in-house developed application was used to access and pseudo-anonymize DICOM Metadata.

3. Monte Carlo based dosimetric calculations: Software parametrization

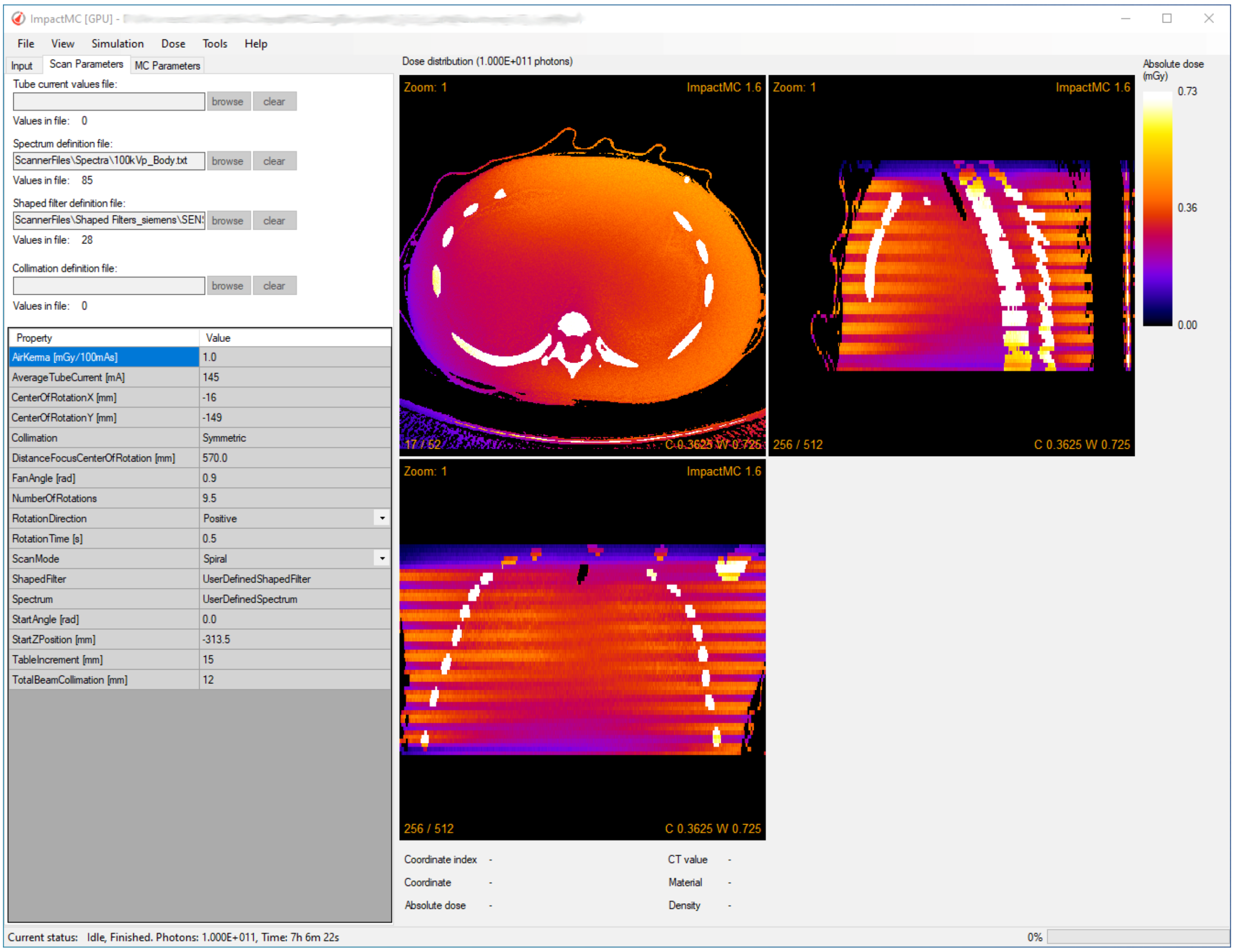
Monte Carlo software for dosimetric computations

The MC software selected for dosimetric computations was ImpactMC (version 1.6, CT Imaging© GMBH, Erlangen, Germany). ImpactMC is a software package providing fast calculation of 3D dose distributions for CT scans using MC algorithms [7-9].

Based on volumetric data as input, an individualized voxelized MC simulation is performed to calculate the dose deposited. Dose is calculated on a per image voxel basis, considering all available physical interactions. ImpactMC's output comprises of parametric dose images in which every voxel carries the normalized dose (to Computed Tomography Dose Index- CTDI) of the initial image grid.

The generated 3D dose distributions are useful to estimate organ doses and to calculate effective dose of individual scans. Figure 1 demonstrates the graphical user interface (GUI). The GUI consists of two main panels - one for parameter input and one for visualization. At the bottom of the image viewer a panel gives information on dose, density and material for the voxel selected with the mouse cursor.

ImpactMC utilizes any available Nvidia graphics processing unit (GPU) to accelerate computations. In conjunction with high-speed parallel processing within the GPU, higher GPU memory bandwidth facilitates greater compute efficiency compared to CPU-only intensive calculations.



Tube current values file:
Values in file: 0

Spectrum definition file: ScannerFiles\Spectra\100kVp_Body.txt
Values in file: 85

Shaped filter definition file: ScannerFiles\Shaped Filters_siemens\SEN
Values in file: 28

Collimation definition file:
Values in file: 0

Property	Value
AirKerma [mGy/100mAs]	1.0
AverageTubeCurrent [mA]	145
CenterOfRotationX [mm]	-16
CenterOfRotationY [mm]	-149
Collimation	Symmetric
DistanceFocusCenterOfRotation [mm]	570.0
FanAngle [rad]	0.9
NumberOfRotations	9.5
RotationDirection	Positive
RotationTime [s]	0.5
ScanMode	Spiral
ShapedFilter	UserDefinedShapedFilter
Spectrum	UserDefinedSpectrum
StartAngle [rad]	0.0
StartZPosition [mm]	-313.5
TableIncrement [mm]	15
TotalBeamCollimation [mm]	12

Dose distribution (1.000E+011 photons)

Coordinate index -
Coordinate -
Absolute dose -
CT value -
Material -
Density -

Current status: Idle, Finished. Photons: 1.000E+011, Time: 7h 6m 22s
0%

Figure 1: The graphical user interface of ImpactMC.

Each estimation of the dose distribution in a CT volume starts with setting up an ImpactMC project.

Figure 2 provides an overview of the project structure. The following input data were required by the software to start the dose computation procedure:

1. Input volume: The input volume represents the scanned patient or phantom; a set of CT reconstructed images from one examination, in DICOM format.
2. Scan parameters: Data for beam spectrum, filtration, and geometrical specifications
3. Simulation parameters: The number of x-rays depositing energy in the input volume was selected.

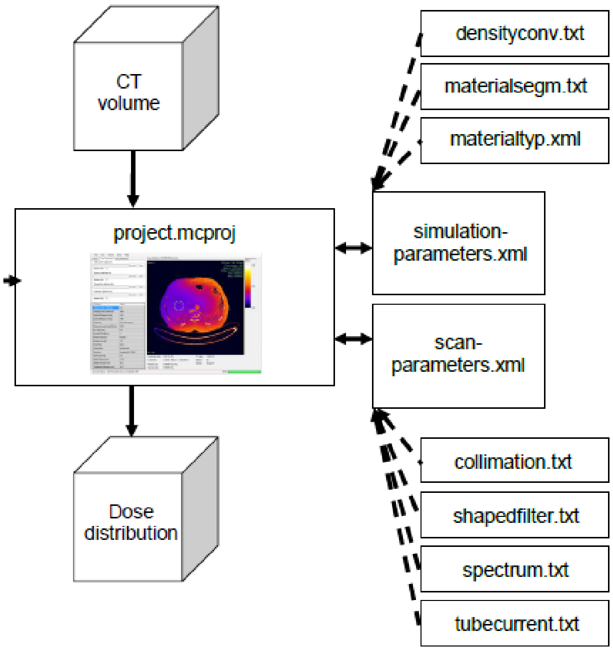

CT volume
project.mcproj
Dose distribution
densityconv.txt
materialsegm.txt
materialtyp.xml
simulation-parameters.xml
scan-parameters.xml
collimation.txt
shapedfilter.txt
spectrum.txt
tubecurrent.txt

Figure 2: ImpactMC project structure.

4. Monte Carlo based dosimetric calculations: Simulations

Diagnostic CT scans simulations

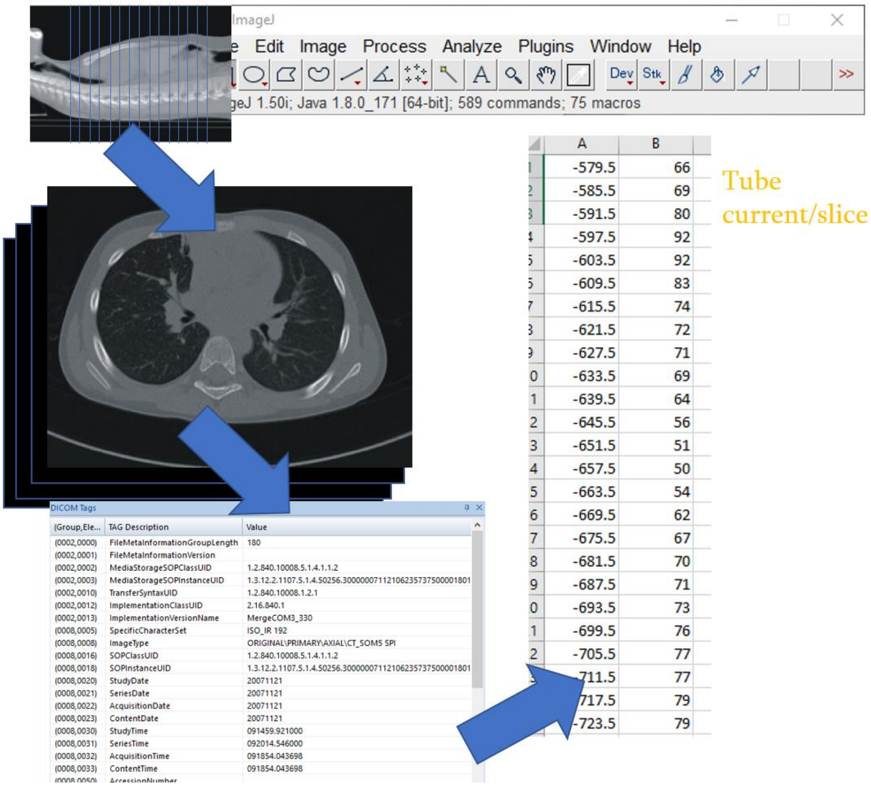
Scanner-specific dose computations required the parameterization of the MC software according to operating and physical characteristics of each CT scanner [10]. The scanner model used was based on the scanner used in our institution (GE GSI Revolution 64). Data for x-ray beam spectra, beam shaping devices (bow-tie filters) and geometrical specifications were provided by the manufacturer (Table I) and converted to input parameters suitable for the Monte Carlo software.

Focus to Isocenter (mm)	Fan Angle (deg)	Beam collimation (mm)	Beam shaping devices
539	58	20.0	Small, Medium, Large

Table 1: Scanner geometric parameters used to model the GE GSI Revolution 64 behavior.

Simulation of CT Scanner tube current modulation

The DICOM header of each reconstructed image (z) included a unique mAz value along with the corresponding table location. Each mAz value is the average of the angularly and longitudinally modulated values applied over the gantry rotation used to reconstruct this z-th image. mAz profile values were retrieved from the DICOM header of the image data using ImageJ manipulation software and used as a custom tube current file for the MC simulation software (Figure 3).


ImageJ
e Edit Image Process Analyze Plugins Window Help
Dev Stk >>
geJ 1.50i; Java 1.8.0_171 [64-bit]; 589 commands; 75 macros
Tube current/slice
DICOM Tags

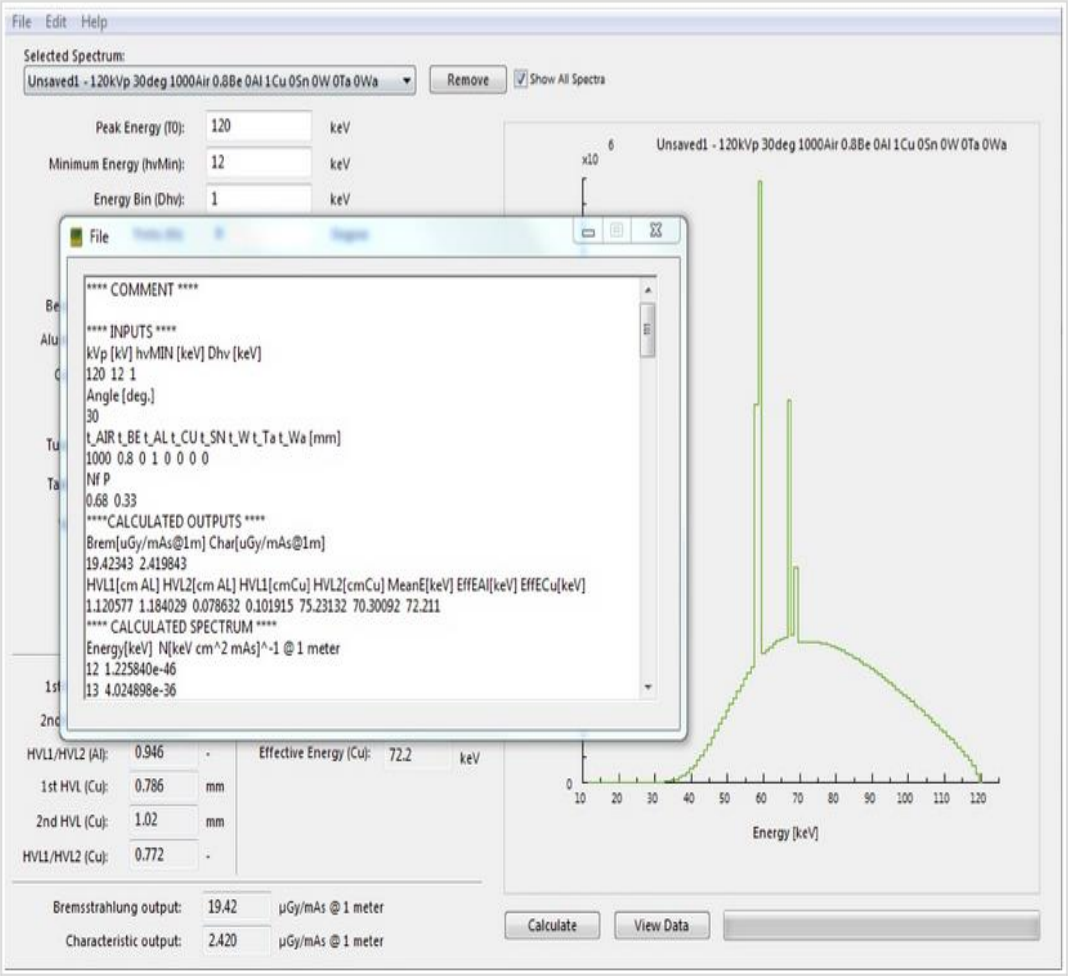
(Group,Ele...	TAG Description	Value
(0002,0000)	FileMetaInformationGroupLength	180
(0002,0001)	FileMetaInformationVersion	
(0002,0002)	MediaStorageSOPClassUID	1.2.840.10008.5.1.4.1.1.2
(0002,0003)	MediaStorageSOPInstanceUID	1.3.12.2.1107.5.1.4.50256.30000007112106235737500001801
(0002,0010)	TransferSyntaxUID	1.2.840.10008.1.2.1
(0002,0012)	ImplementationClassUID	2.16.840.1
(0002,0013)	ImplementationVersionName	MergeCOM3_330
(0008,0005)	SpecificCharacterSet	ISO_IR 192
(0008,0008)	ImageType	ORIGINAL\PRIMARY\AXIAL\CT_SOM5 SPI
(0008,0016)	SOPClassUID	1.2.840.10008.5.1.4.1.1.2
(0008,0018)	SOPInstanceUID	1.3.12.2.1107.5.1.4.50256.30000007112106235737500001801
(0008,0020)	StudyDate	20071121
(0008,0021)	SeriesDate	20071121
(0008,0022)	AcquisitionDate	20071121
(0008,0023)	ContentDate	20071121
(0008,0030)	StudyTime	091459.921000
(0008,0031)	SeriesTime	092014.546000
(0008,0032)	AcquisitionTime	091854.043698
(0008,0033)	ContentTime	091854.043698
(0008,0050)	AccessionNumber	

A	B
-579.5	66
-585.5	69
-591.5	80
-597.5	92
-603.5	92
-609.5	83
-615.5	74
-621.5	72
-627.5	71
-633.5	69
-639.5	64
-645.5	56
-651.5	51
-657.5	50
-663.5	54
-669.5	62
-675.5	67
-681.5	70
-687.5	71
-693.5	73
-699.5	76
-705.5	77
711.5	77
717.5	79
-723.5	79

Figure 3: Graphical representation of extraction of longitudinally modulated tube current from DICOM header. Columns A and B represent z-axis position and tube current, respectively.

Determination of scanner parameters – Spectral characteristics

Beam spectra for various modes of operation, were produced for each modality using SpekCalc spectrum calculation program [11]. SpekCalc allows the user to calculate and display the x-ray spectra emitted from tungsten-anode x-ray tubes. The underlying theoretical description for the bremsstrahlung and characteristic x-ray production was taken from a recently published model [12]. The user can select tube potential in kVp, the take-off angle and the amount of filtration. The resulting spectrum can be calculated, displayed, and saved/exported for later use. Beam quality parameters such as the half-value-layer, in mm of aluminum and copper, and the mean beam energy, in keV, can also be considered as depicted in Figure 4. Filtration can be selected in mm, for 7 materials (e.g., Al, Co, Zn, etc.).


File
Edit
Help
Remove
☑ Show All Spectra
File
Calculate
View Data
x10
6
Unsaved1 - 120kVp 30deg 1000Air 0.8Be 0Al 1Cu 0Sn 0W 0Ta 0Wa
0
10
20
30
40
50
60
70
80
90
100
110
120
Energy [keV]

Selected Spectrum: Unsaved1 - 120kVp 30deg 1000Air 0.8Be 0Al 1Cu 0Sn 0W 0Ta 0Wa

Peak Energy (T0): 120 keV
Minimum Energy (hvMin): 12 keV
Energy Bin (Dhv): 1 keV

```
**** COMMENT ****

**** INPUTS ****
kVp [kV] hvMIN [keV] Dhv [keV]
120  12  1
Angle [deg.]
30
t_AIR t_BE t_AL t_CU t_SN t_W t_Ta t_Wa [mm]
1000  0.8  0  1  0  0  0  0
Nf P
0.68  0.33
****CALCULATED OUTPUTS ****
Brem[uGy/mAs@1m] Char[uGy/mAs@1m]
19.42343  2.419843
HVL1[cm AL] HVL2[cm AL] HVL1[cmCu] HVL2[cmCu] MeanE[keV] EffEAl[keV] EffECu[keV]
1.120577  1.184029  0.078632  0.101915  75.23132  70.30092  72.211
**** CALCULATED SPECTRUM ****
Energy[keV]  N[keV cm^2 mAs]^-1 @ 1 meter
12  1.225840e-46
13  4.024898e-36
```

HVL1/HVL2 (Al): 0.946 -
1st HVL (Cu): 0.786 mm
2nd HVL (Cu): 1.02 mm
HVL1/HVL2 (Cu): 0.772 -
Effective Energy (Cu): 72.2 keV

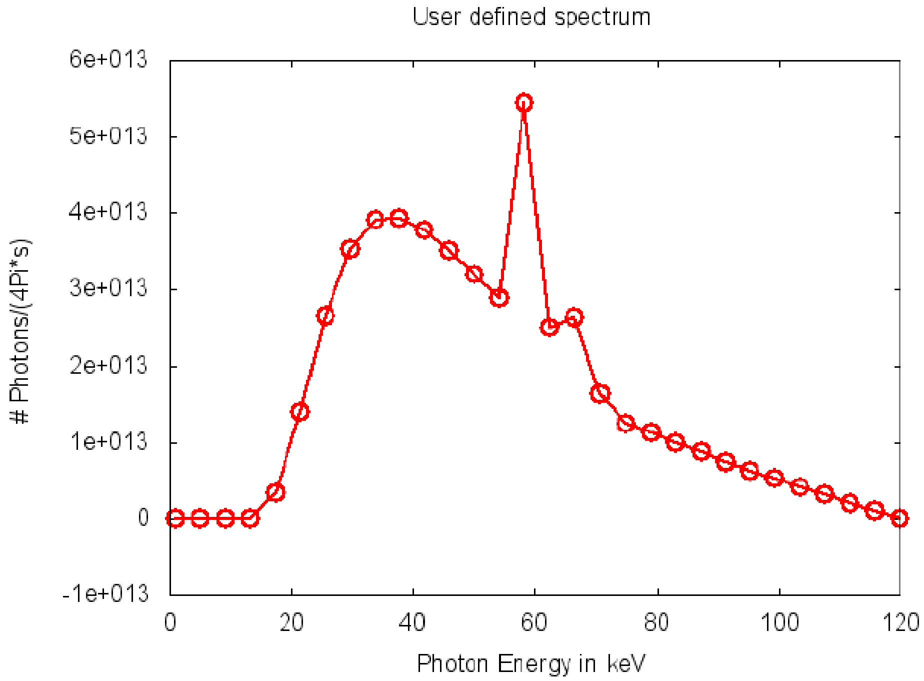
Bremsstrahlung output: 19.42 µGy/mAs @ 1 meter
Characteristic output: 2.420 µGy/mAs @ 1 meter

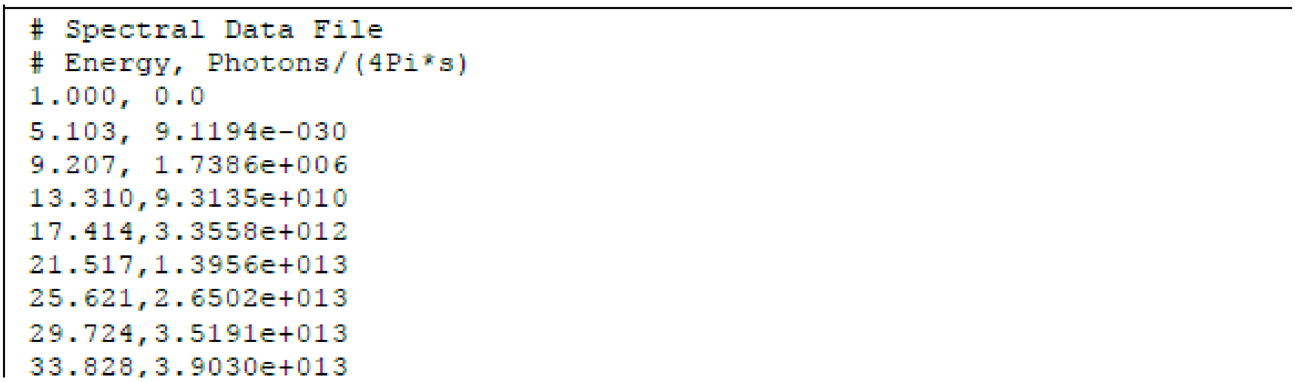
Figure 4: SpekCalc spectrum calculation software GUI.

The structure of IMPACTMC 's spectrum text file consists of several entries, each defining the number of photons at a certain energy level (**Fehler! Verweisquelle konnte nicht gefunden werden.**). Each line has the following syntax:

energy e (in keV), number of photons in the spectrum in energy bin e

The values for e must be positive, monotonically increasing, and equidistant. The number of photons did not have to be normalized because normalization was done by the software, if necessary. This text file was imported using the GUI.





```
# Spectral Data File
# Energy, Photons/(4Pi*s)
1.000, 0.0
5.103, 9.1194e-030
9.207, 1.7386e+006
13.310,9.3135e+010
17.414,3.3558e+012
21.517,1.3956e+013
25.621,2.6502e+013
29.724,3.5191e+013
33.828,3.9030e+013
```

Figure 5: A user defined spectrum and spectral data file.

Determination of scanner parameters – CT shaping filters modelling

In ImpactMC software, the user has the option to include a shaped filter where the thickness of the filter is varying with the fan angle at the x-ray source in the MC simulations. The shaped filter can be switched off and on from the GUI (Figure 6). The user can add a shaped filter from a specification file. In this case the values for filter material and thickness are read from the file according to the following file structure:

line 1: Filter (keyword)

line 2: # Name of the material (mandatory comment line)

line 3: Name of the material, e.g. Al. (software specific name)

line 4: # Density of the material (g/cm^3) (mandatory comment line)

line 5: Density of the material in g per cm3,

line 6: # Angular increment (°) (mandatory comment line)

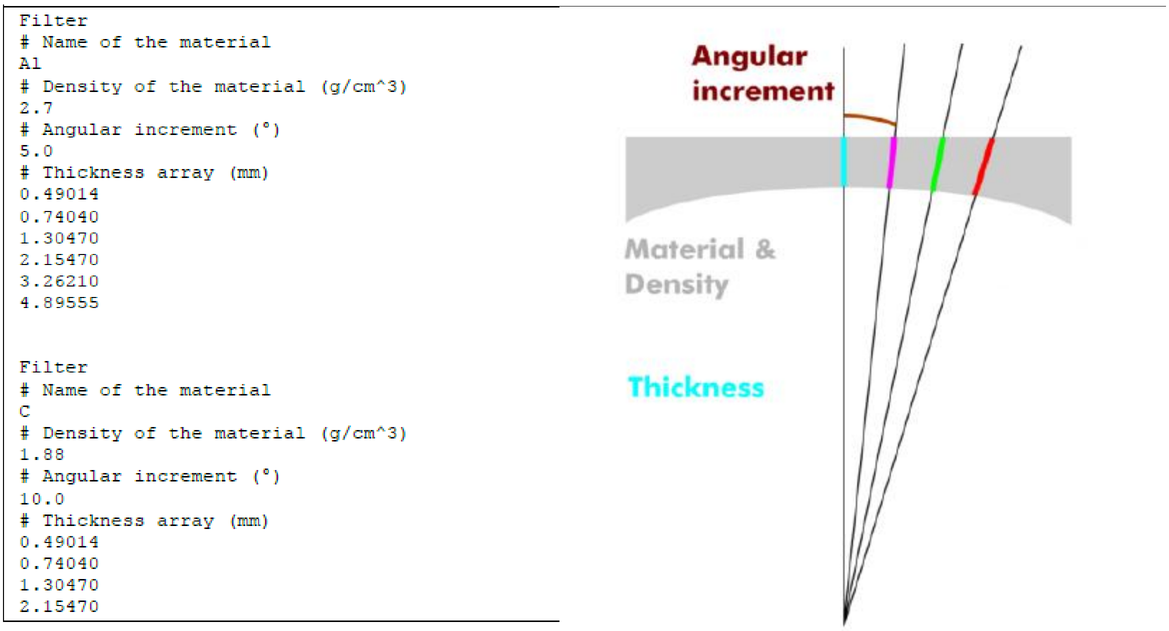
line 7: Angular increment between the given thickness values in degrees.

line 8: # Thickness array (mm) (mandatory comment line)

line 9: thickness of the shaped filter at angle = 0°, i.e. in the middle of the fan beam

line 10: thickness of the shaped filter at angle +/- angular increment

following lines: thickness of the shaped filter at n angle +/- angular increment



```
Filter
# Name of the material
Al
# Density of the material (g/cm^3)
2.7
# Angular increment (°)
5.0
# Thickness array (mm)
0.49014
0.74040
1.30470
2.15470
3.26210
4.89555


Filter
# Name of the material
C
# Density of the material (g/cm^3)
1.88
# Angular increment (°)
10.0
# Thickness array (mm)
0.49014
0.74040
1.30470
2.15470
```

Figure 6: Definition of the shaped filter material and density, angular increment, and thickness (Adapted from ImpactMC user-manual).

Radiotherapy related CT scans simulations – Treatment planning CT

CT imaging is used in radiotherapy treatment planning serves two key purposes: to allow, with high geometric fidelity, the position of the tumor and surrounding tissues along with organs at risk to be accurately identified and to provide a map of the electron density information for the various tissues to be used in the treatment planning system (TPS) dose calculation. Simulating a treatment planning CT requires the same equipment, spectral and protocol parameters as conventional diagnostic CT imaging (Table 2). The modeled scanner was GE GSI Revolution 64.

Patient Population	Anatomical Site	kV	mA modu-lation	Acquisition Type	Filter Type & Collimation (mm)	Pitch
Adult	Head Thorax Abdomen/ Pelvis	120	No	Helical	Large / 40 mm	0.984
Pediatric	Head Thorax Abdomen/ Pelvis	120	No	Helical	Large / 40 mm	0.984

Table 2: CT exposure parameters for Treatment Planning CT scans.

Radiotherapy related pre-treatment scans – CBCT simulations

Cone beam computed tomography (CBCT) is a 3D x-ray imaging technique in which the x-ray beam is transmitted to an object with wide beam geometry producing a 2D image per projection. Due to its faster image acquisition time, wide coverage length per scan, and fewer motion artifacts compared to conventional CT, CBCT systems are becoming popular in diagnostic and therapeutic radiology. In radiation oncology, on gantry-CBCT imaging is utilized for on-line correction of patient's isocenter localization error for image guided radiation therapy (IGRT).

Simulating a pre-treatment CBCT scan requires similar equipment, spectral and protocol parameters as conventional diagnostic CT imaging. However, several alterations must be implemented to MC software to simulate a CBCT scan compared to a conventional CT simulation. These adaptations include definition of a) in-plane fan angle of the x-ray beam (smaller than conventional CT), b) number of rotations (0-1 for a full rotation), and c) starting angle z-position of the x-ray tube. Most prominently, a sequential mode was selected, and a collimation file was implemented according to ImpactMC configuration.

ELEKTA XVI (R5.04) system was modeled [13]. The protocols were supplied by ELEKTA through the XVI interface and are tabulated in Table 3. The Elekta XVI CBCT system does not employ moveable collimators and the field size is specified using lead cassettes with a predefined, fixed, opening. Bow-tie filtration is usually employed in half-fan acquisitions.

Patient Population	Preset protocol/ collimation	Anatomical Site	kV	mAs/per frame	Acquisition Type	Filter Type	Span (deg)	Frames
Adult & Pediatric	M20	Chest	120	0.40	CBCT	F1	360	660
Adult	M20	Pelvis	120	1.60	CBCT	F1	360	660
Adult	L20	Pelvis	120	3.84	CBCT	F1	360	660

Table 3: Exposure parameters for CBCT in-room pre-treatment scans.

In both medium and large FOV, the center of the kV detector panel is offset from the kV center axis in the direction of the beam limiting device (Figure 8, 9). This is to prevent a collision with the touch guard of the MV detector arm when this detector panel is retracted. Off-setting were modeled through different collimations options in IMPACTMC collimation and fan and Z-collimation file options (Figure 7).

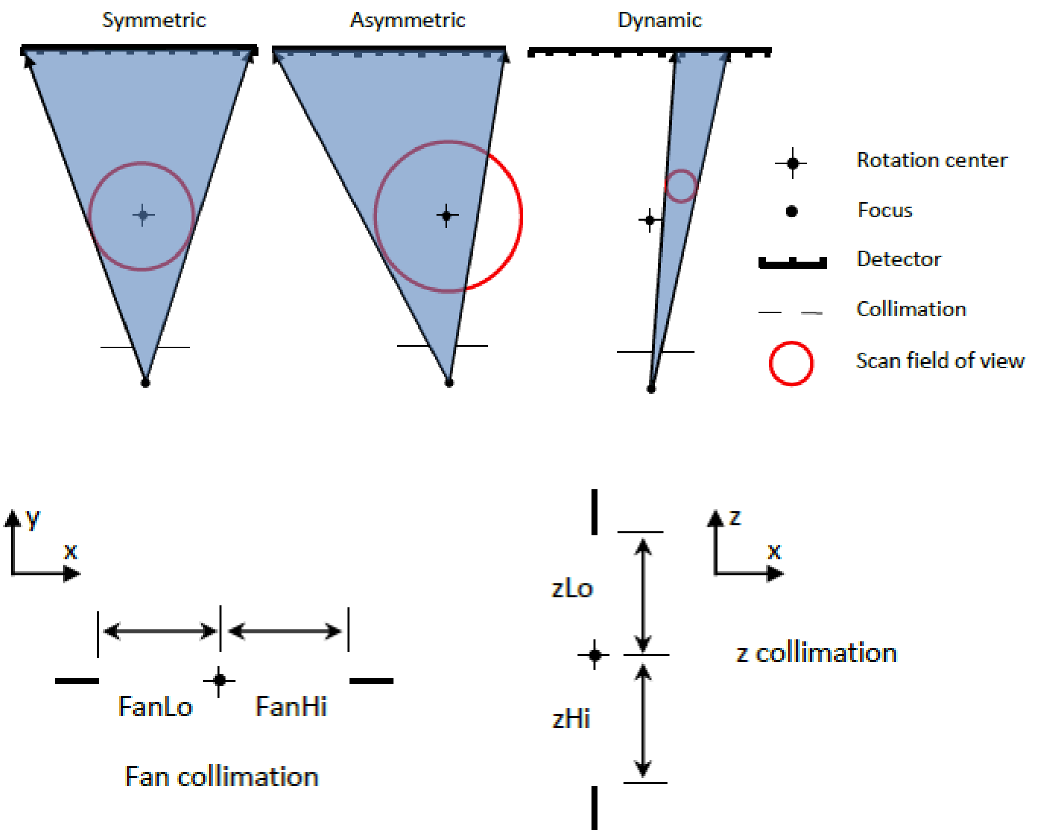
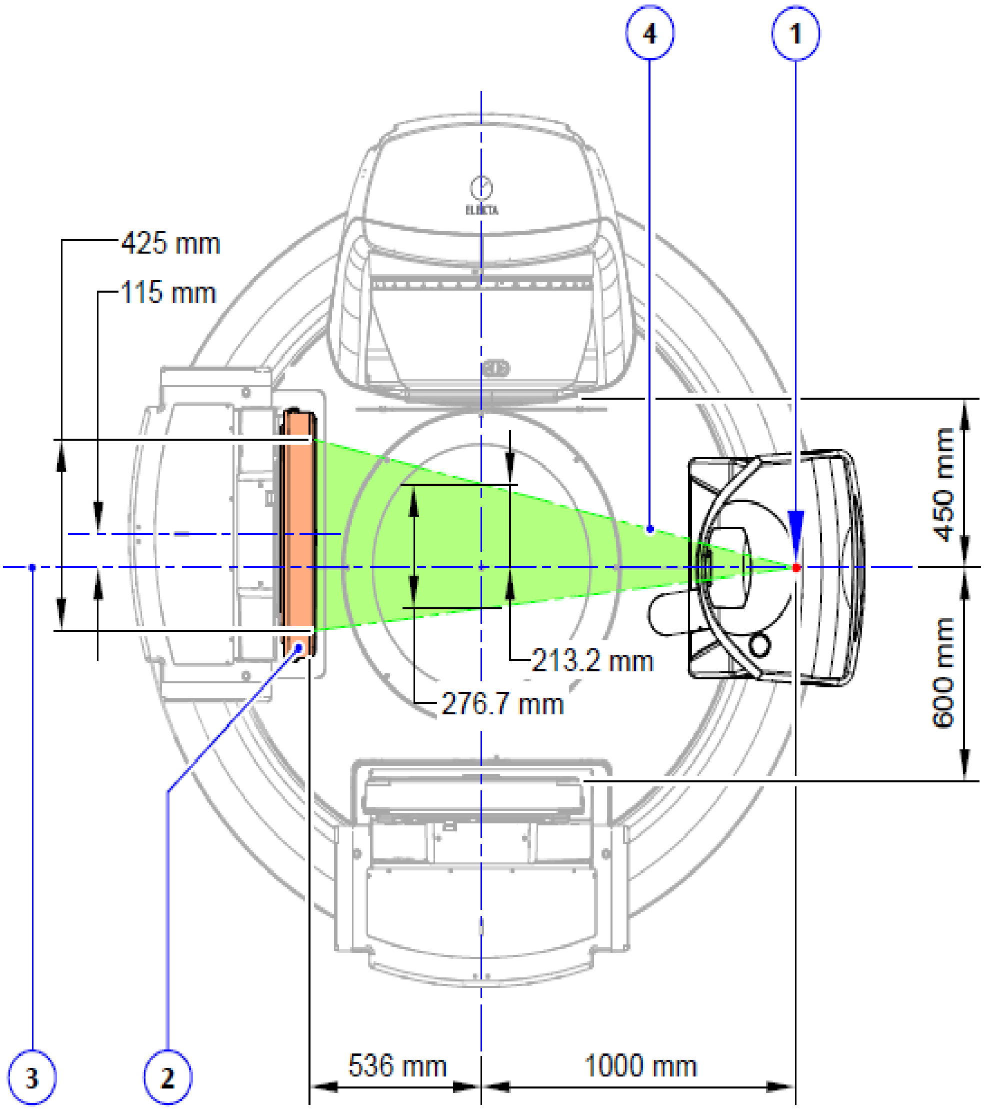

Symmetric
Asymmetric
Dynamic
Rotation center
Focus
Detector
Collimation
Scan field of view
y
x
FanLo
FanHi
Fan collimation
zLo
zHi
z
x
z collimation

Figure 7: Sketch of the different collimation options in IMPACTMC collimation file and definition of the fan and z collimation with respect to the center of rotation.


4
1
ELEKTA
425 mm
115 mm
450 mm
600 mm
213.2 mm
276.7 mm
3
2
536 mm
1000 mm

000155 ©2011 Elekta Limited

Figure 3.10 Medium FOV position

(1) Focal spot of the kV X-ray beam

(2) Image receptor (kV detector panel)

(3) kV X-ray beam reference axis (perpendicular to image receptor plane)

(4) X-ray field projection

Figure 8: Graphical description of the medium FOV position of the kV detector panel (XVI user manual).

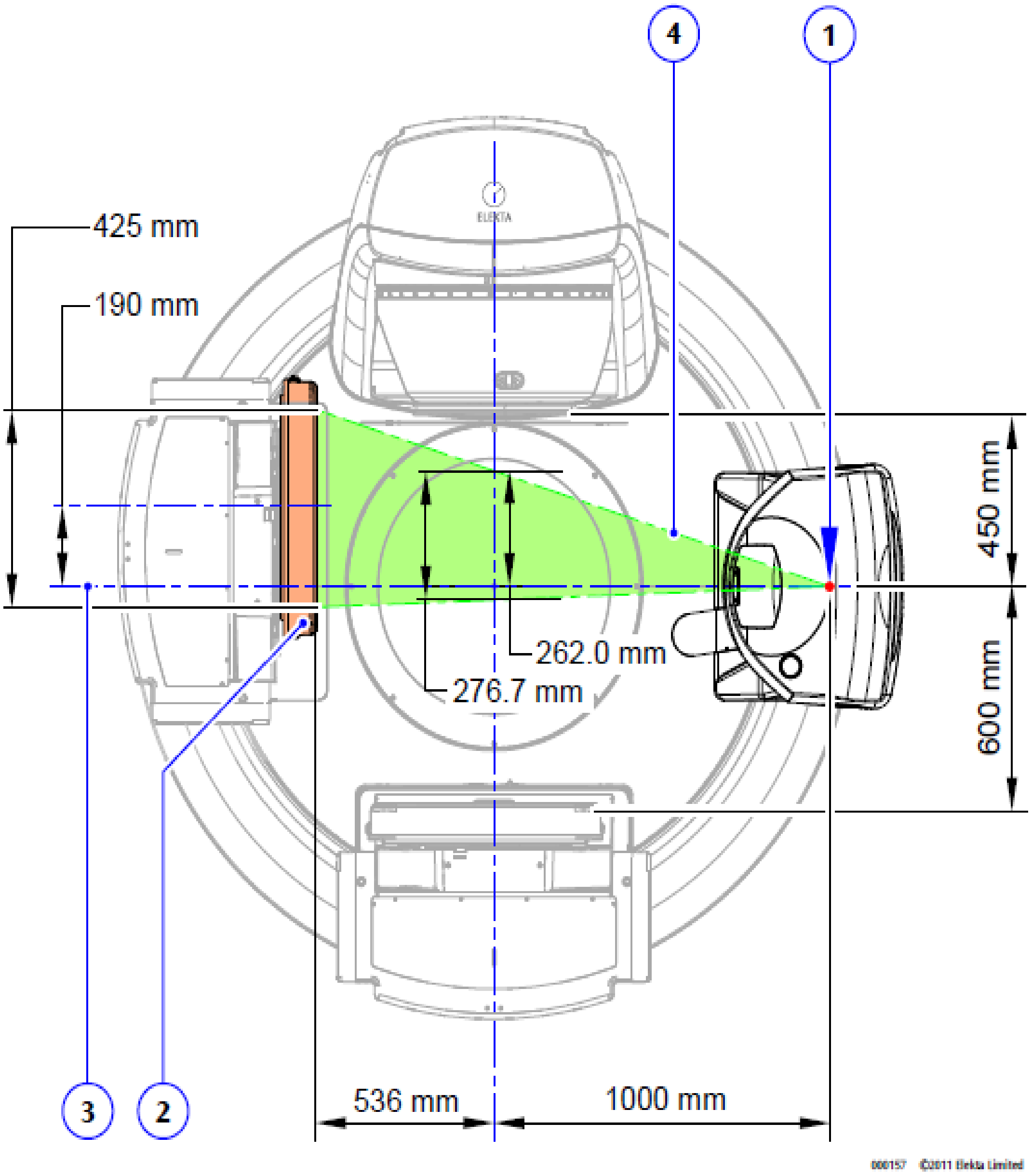


Figure 3.11 Large FOV position

(1) Focal spot of the kV X-ray beam

(2) Image receptor (kV detector panel)

(3) kV X-ray beam reference axis (perpendicular to image receptor plane)

(4) X-ray field projection

Figure 9: Graphical description of the large FOV position of the kV detector panel (XVI user manual).

For all anatomical sites, the M20 protocol was applied in most of the patients, and the L20 protocol in especially larger patients. The protocols/presets for CBCT imaging in radiotherapy are presented in Table 3, and the MC parameters for the simulations are depicted in Table 4. The F0 filter cassette is a blank filter and has no effect on the X-ray beam. The F1 bowtie filter cassette delivers a lower skin dose, decreases the image saturation of the kV detector panel, and decreases the cupping artifacts across the FOV. This increases the image quality for a range of anatomical sites. F1 cassette is the bowtie filter used by ELEKTA for kV imaging [14].

Parameter	Value
Air Kerma	4.92 mGy/ 100 mAs
Average tube current	20 mA
Number of rotations	1
Rotation time	13.2 s *
Scan mode	Sequential
Start angle	-π
Table increment	0

$$^{*}\left.\begin{matrix}20\ ms/frame\\660\ frames\end{matrix}\right| \Rightarrow 13.2\ s$$

Table 4: ImpactMC simulation/ exposure parameters for CBCT pre-treatment scans (Adapted from Elekta XVI 5.0 user manual).

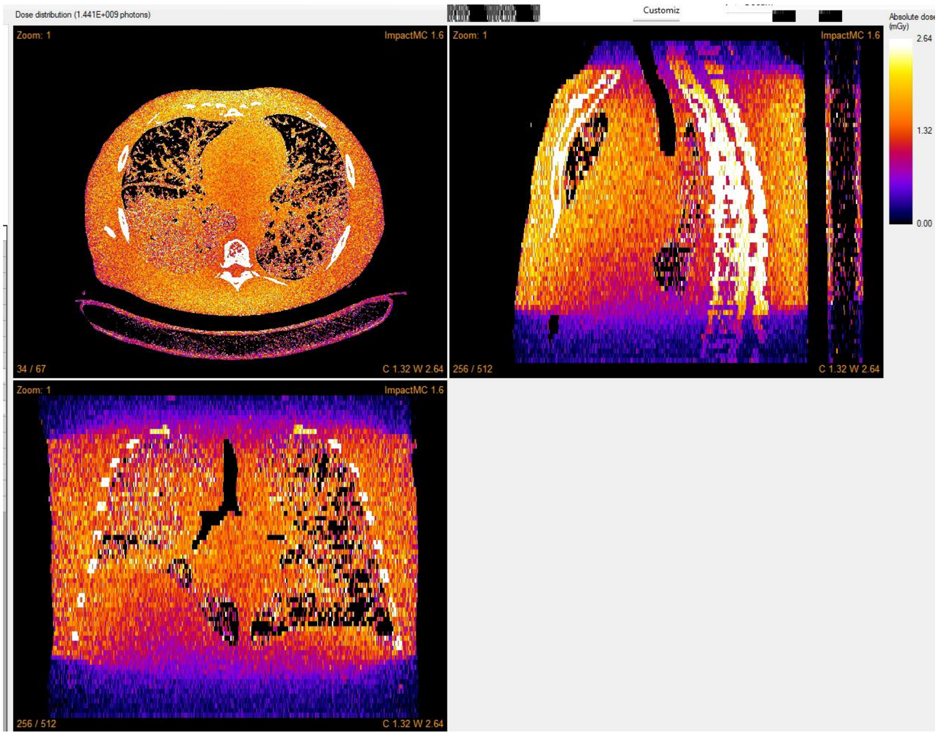

Dose distribution (1.441E+009 photons)
Customiz
Absolute dose (mGy)
2.64
1.32
0.00
Zoom: 1
ImpactMC 1.6
34 / 67
C 1.32 W 2.64
Zoom: 1
ImpactMC 1.6
256 / 512
C 1.32 W 2.64
Zoom: 1
ImpactMC 1.6
256 / 512
C 1.32 W 2.64

Figure 10: ImpactMC simulation of CBCT pre-treatment on-line isocenter correction scan.

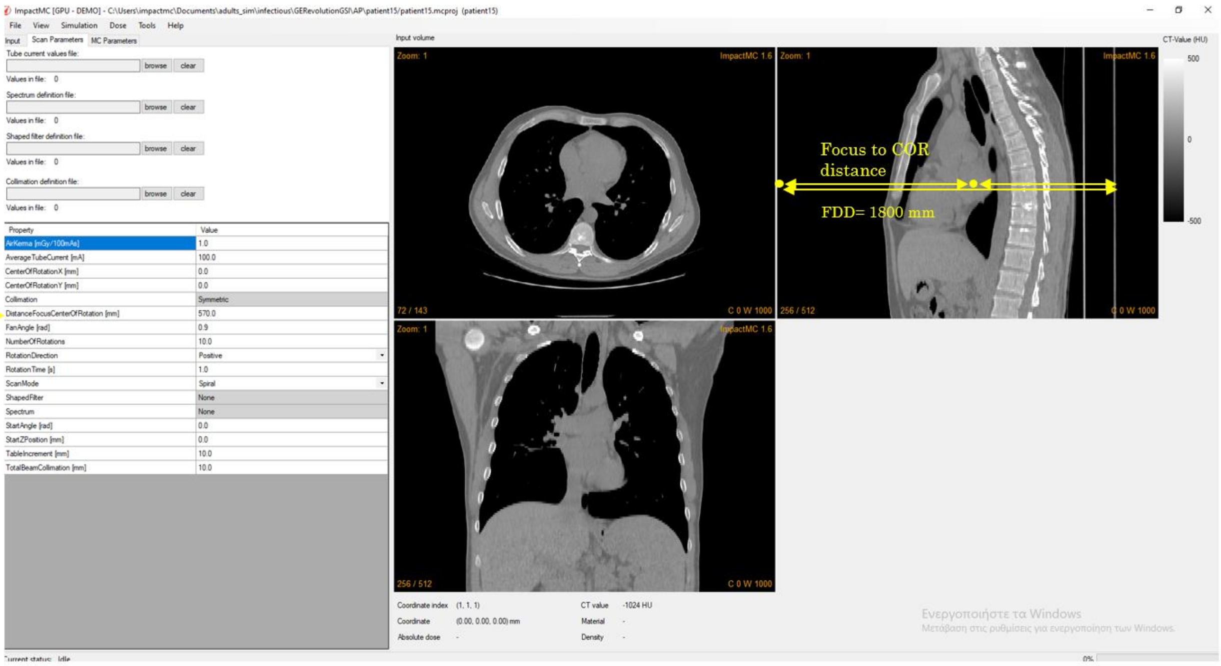
Radiotherapy related imaging – kV-planar IGRT

Simulating a kV-planar radiograph requires the same equipment, spectral and protocol parameters as conventional projection DR radiography. Radiography simulations were performed in lateral (Lat), and Anterior-Posterior (AP) position.

The number of performed simulations was determined by the specified protocol for each modality and anatomical site. Protocol selection for simulation was based on most frequent examinations performed in our institute. The modeled protocols are depicted in Table 5.

Patient Population	Anatomical Site	kV	mAs	Views
Adult	Head	100	0.5	AP, Lat
Adult	Thorax	120	6.25	AP, Lat
Adult	Abdomen	120	5/6.4	AP, Lat
Pediatric	Head	100	0.5	AP, Lat
Pediatric	Thorax	120	6.25	AP, Lat
Pediatric	Abdomen	120	5/6.4	AP, Lat

Table 5: Exposure parameters for diagnostic radiology DR scans.


File
View
Simulation
Dose
Tools
Help
Input
Scan Parameters
MC Parameters
browse
clear
Input volume
Zoom: 1
ImpactMC 1.6
72 / 143
256 / 512
C 0 W 1000
CT-Value (HU)
500
0
-500
Focus to COR distance
FDD= 1800 mm
Ενεργοποιήστε τα Windows
Μετάβαση στις ρυθμίσεις για ενεργοποίηση των Windows.
0%

ImpactMC [GPU - DEMO] - C:\Users\impactmc\Documents\adults_sim\infectious\GERevolutionGSI\AP\patient15/patient15.mcproj (patient15)

Tube current values file:
Values in file: 0
Spectrum definition file:
Values in file: 0
Shaped filter definition file:
Values in file: 0
Collimation definition file:
Values in file: 0

Property	Value
AirKerma [mGy/100mAs]	1.0
AverageTubeCurrent [mA]	100.0
CenterOfRotationX [mm]	0.0
CenterOfRotationY [mm]	0.0
Collimation	Symmetric
DistanceFocusCenterOfRotation [mm]	570.0
FanAngle [rad]	0.9
NumberOfRotations	10.0
RotationDirection	Positive
RotationTime [s]	1.0
ScanMode	Spiral
ShapedFilter	None
Spectrum	None
StartAngle [rad]	0.0
StartZPosition [mm]	0.0
TableIncrement [mm]	10.0
TotalBeamCollimation [mm]	10.0

Coordinate index (1, 1, 1)
Coordinate (0.00, 0.00, 0.00) mm
Absolute dose -
CT value -1024 HU
Material -
Density -

Current status: Idle

Figure 11: Simulation of plain projection radiography with IMPACTMC - Distance focus- center of rotation.

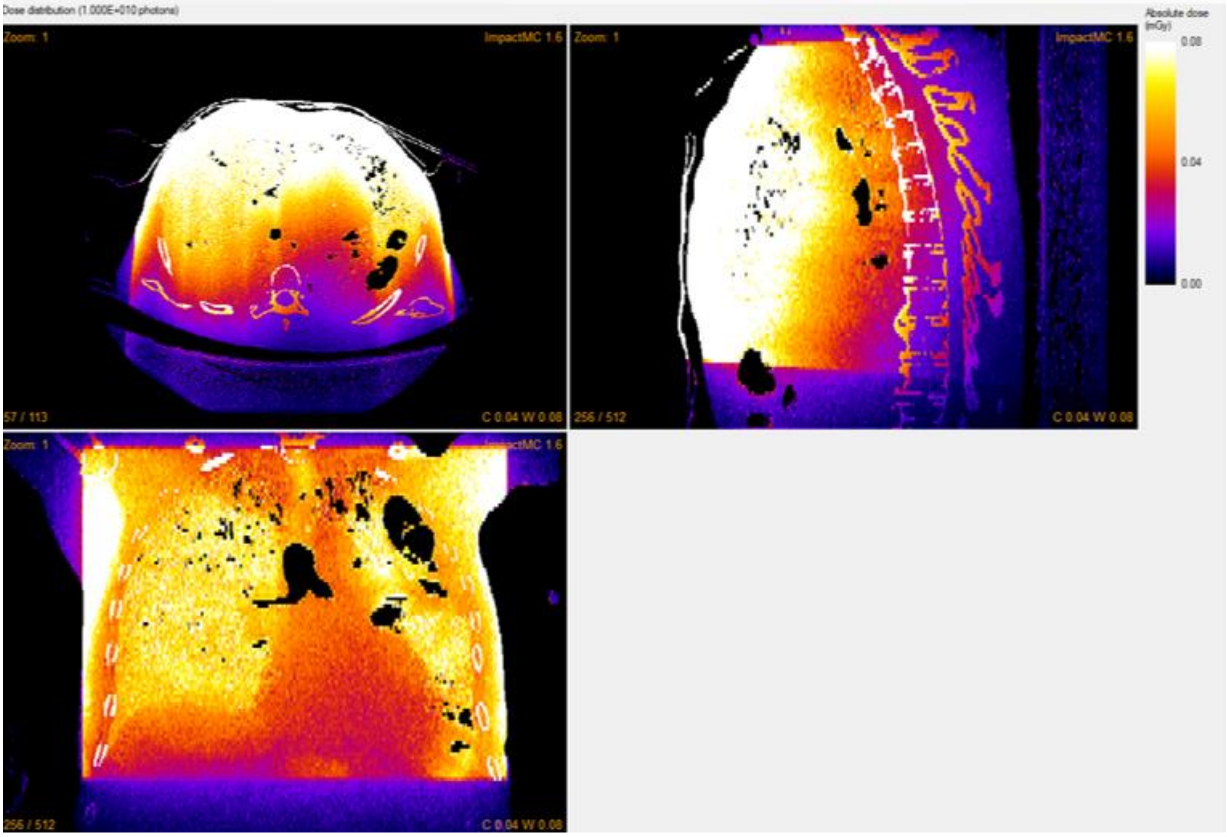

Dose distribution (1.000E+010 photons)
Zoom: 1
ImpactMC 1.6
57 / 113
C 0.04 W 0.08
Zoom: 1
ImpactMC 1.6
256 / 512
C 0.04 W 0.08
Zoom: 1
ImpactMC 1.6
256 / 512
C 0.04 W 0.08
Absolute dose (mGy)
0.08
0.04
0.00

Figure 12: ImpactMC simulation of digital radiography (DR) AP projection.

5. Patient-specific 3D dose distributions

The MC software output after each computation is in the form of a 3D dose distribution (Figures 13 a, b), based on the physical properties (i.e., attenuation, composition, and size) obtained from the patient-specific input. Each slice in the dose volume corresponds to the same slice of patient-input. Each pixel in a specific slice of the input volume has a corresponding dose value in the 3D dose distribution output. The dose distribution was exported in DICOM file format. The unit of dose values in the 3D volume was mGy/mGy per 100mAs. Organ dose information was extracted from 3D dose distributions through appropriate delineation.

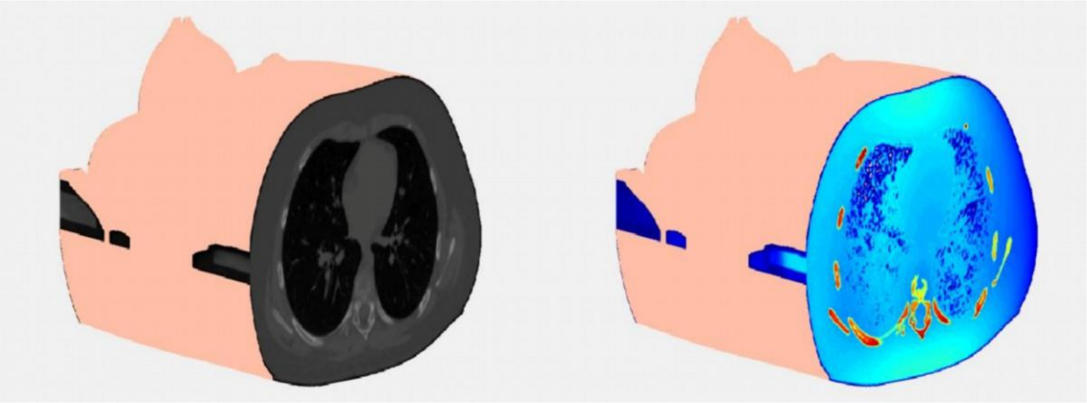


Figure 13: (a) CT image slices and (b) corresponding dose distribution in the thorax region.

The contours of an organ were overlaid on the corresponding slices of the dose distribution (Figure 14) and the respective dose was extracted. The dose over the whole organ was computed as:

$$D = \sum_{i}^{N} D_i \qquad (1)$$

where, D_i is the dose within the contour at slice i, and N the total number of slices that contain contours of a specific organ. The calculated dose (D) was normalized to 100 mA, pitch factor (p) equal to one, and rotation time (t_{rot}) equal to one second using the following formula:

$$D_n = D \times \frac{p \times 100}{t_{rot} \times mA} \qquad (2)$$

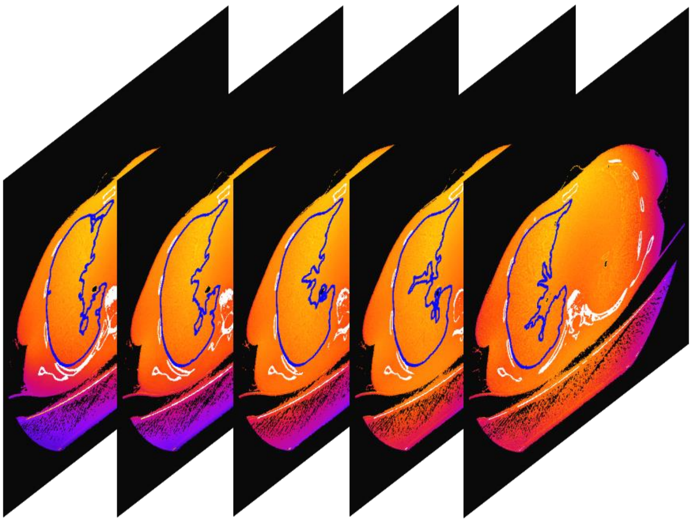


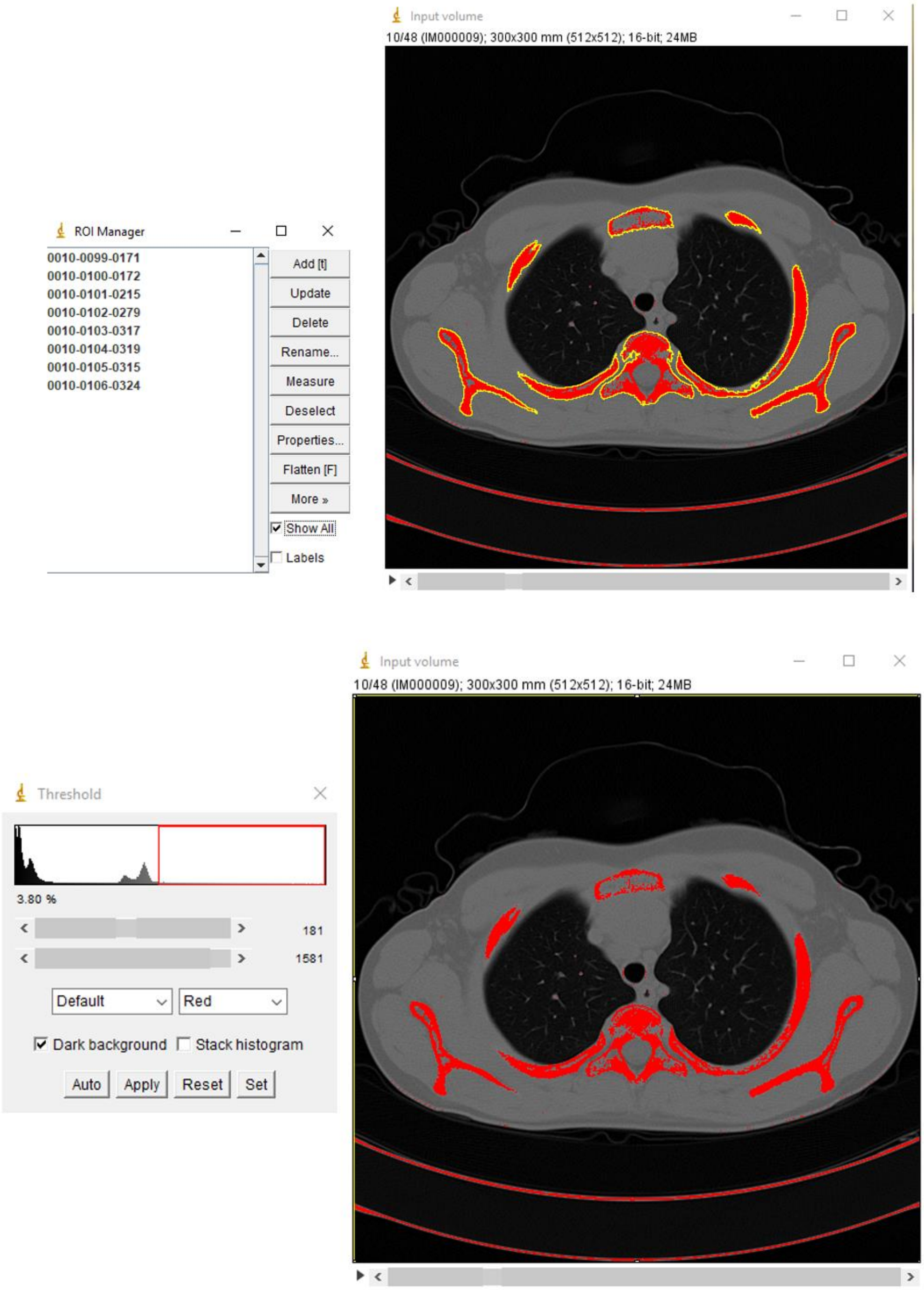
Figure 14: Graphical representation of right lung contours overlaid on corresponding dose slices.

Due to the large number of simulated results organ dose calculation procedure was automated. Relevant in-house algorithms were implemented to provide unsupervised organ dose calculation, WED values and corresponding linear regression outcomes.

6. Delineation of radiosensitive organs within the primary exposed volume

Open-source tools were utilized to delineate radiosensitive organs within the primary exposed volume of all pediatric and adult CT scans. Structures that were automatically delineated were bones, lungs, and the outline of the patient. To segment these structures, thresholding techniques were utilized [14-15]. Lung entities were manually selected after thresholding, and bone structures were automatically assembled using the analyze particles ImageJ tool, which extracts and measures objects in binary or thresholded images. Size and circularity were used to trace particles:

Esophagus, breast, heart, bladder, kidneys, liver, gallbladder, pancreas, stomach and spleen were manually delineated by a radiologist using a Wacom tablet for added accuracy and by adjusting the brightness and contrast of the image to optimum levels ImageJ ROI (Region of Interest) Manager was used for working with multiple selections. Multiple organ selections for each structure were saved as a ZIP file, containing multiple ROIs incorporating complete CT-sequence’s organ assortment.



Input volume

10/48 (IM000009); 300x300 mm (512x512); 16-bit; 24MB

ROI Manager

0010-0099-0171
0010-0100-0172
0010-0101-0215
0010-0102-0279
0010-0103-0317
0010-0104-0319
0010-0105-0315
0010-0106-0324

☑ Show All
☐ Labels

Add [t]
Update
Delete
Rename...
Measure
Deselect
Properties...
Flatten [F]
More »

Threshold

3.80 %

181

1581

Default
Red

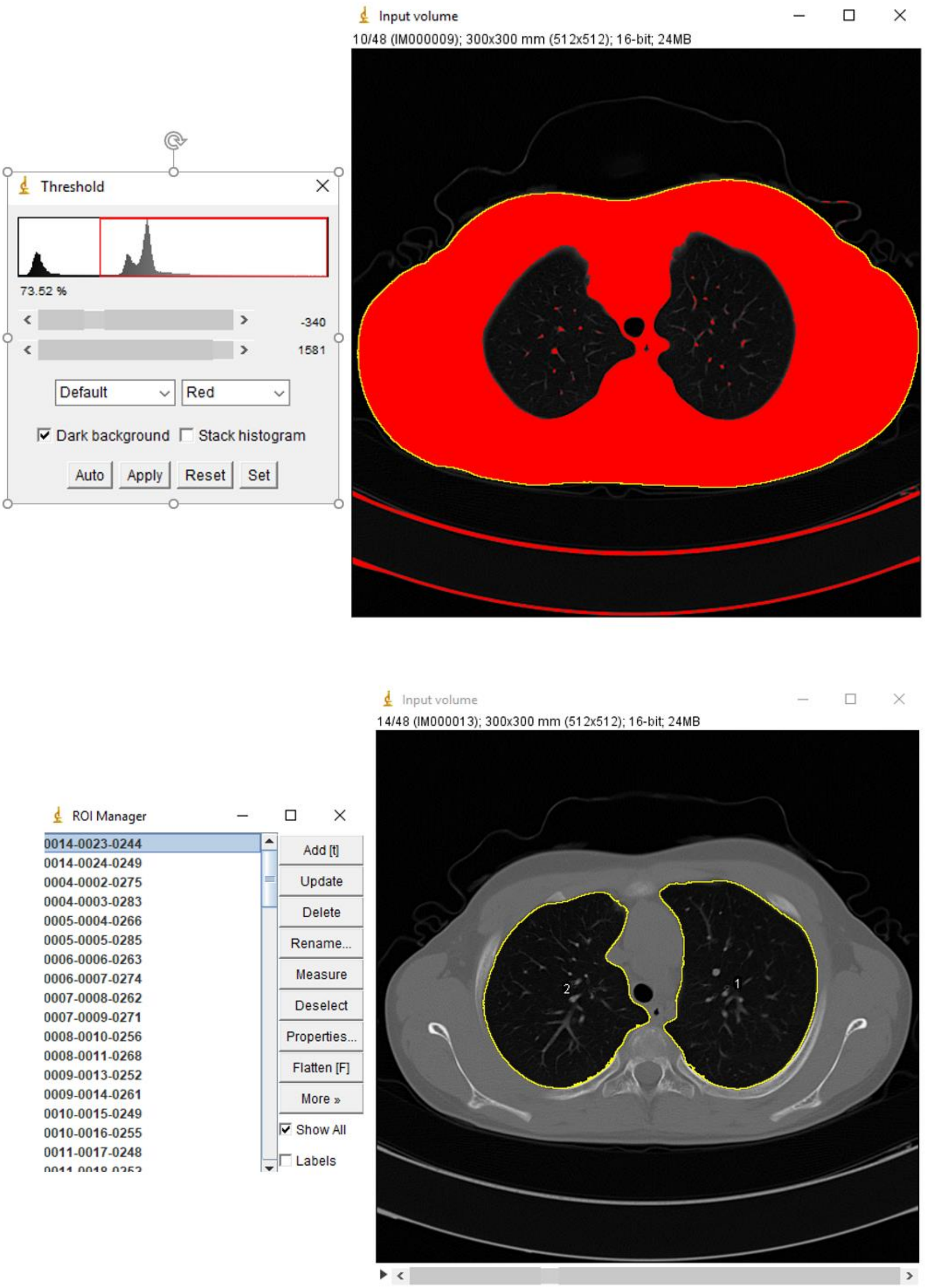
☑ Dark background ☐ Stack histogram

Auto
Apply
Reset
Set

Input volume

10/48 (IM000009); 300x300 mm (512x512); 16-bit; 24MB

Figure 15: Automatic segmentation of bone structures using thresholding techniques.


Threshold
Default
Red
☑ Dark background
☐ Stack histogram
Auto
Apply
Reset
Set
Input volume
ROI Manager
Add [t]
Update
Delete
Rename...
Measure
Deselect
Properties...
Flatten [F]
More »
☑ Show All
☐ Labels
1
2

Threshold: 73.52 %; -340; 1581

Input volume: 10/48 (IM000009); 300x300 mm (512x512); 16-bit; 24MB

Input volume: 14/48 (IM000013); 300x300 mm (512x512); 16-bit; 24MB

ROI Manager:

0014-0023-0244
0014-0024-0249
0004-0002-0275
0004-0003-0283
0005-0004-0266
0005-0005-0285
0006-0006-0263
0006-0007-0274
0007-0008-0262
0007-0009-0271
0008-0010-0256
0008-0011-0268
0009-0013-0252
0009-0014-0261
0010-0015-0249
0010-0016-0255
0011-0017-0248

Figure 16: Automatic segmentation of skin contour and lungs using thresholding techniques.

7. Automatic CT couch/table removal

Accurate patient skin segmentation requires detailed delineation of the patient body outline on the CT slice without including the CT couch/table. In radiation therapy, body, organ and tissue delineation is part of the treatment planning routine, hence, body outline is readily available. In diagnostic radiology, such delineations are not usually provided. Although this task can be performed manually by experts, it is practically cumbersome and time-consuming over many CT scans.

Within the scope of this project, an algorithm to automatically delineate the patient body and remove the couch from each CT slice was developed (body segmentation). The algorithm is based on morphological operations applied on each image slice (Fig. 17a). A square structuring element with heuristically determined size equal to 12 pixels was used to perform morphological opening. This step effectively removed small structures in the vicinity of the body and preserved the body shape and size (Fig. 17b). The next step was conversion of the image to binary using Otsu's method to determine the single HU threshold between background and any other structure [16,17]. During this step, the couch is usually removed from the image without affecting the body size or shape (Fig. 17c).

In addition, since lungs and other low-density tissues are likely to produces empty spaces (holes) in the binarized image within the region defined by the body shape. This empty space was filled by detection of zero value locations that were not connected with the image borders (Fig. 17d). In the final step, non-zero areas that were not connected were identified and the largest area was kept (i.e. the body) as seen in Fig. 17e.

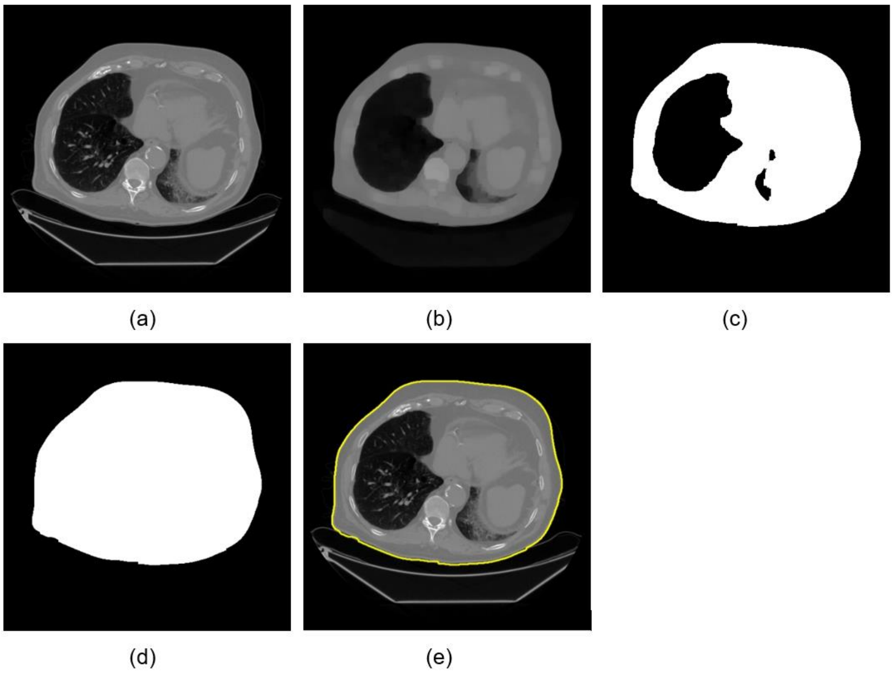


Figure 17: (a) original image slice of patient with pulmonary fibrosis; (b) image after morphological opening; (c) binarization – notice the couch has been already removed; (d) filling the empty space; (e) outline overlaid on original image.

8. Dosimetric results

Correlation of organ doses to Water Equivalent Diameter (WED)

Water Equivalent Diameter (WED) and organ dose correlation was determined through univariate regression analysis. The estimated regression function was of the exponential form:

$$y = a \cdot e^{b \cdot x} \qquad (2)$$

were the independent variable, x, corresponds to the WED value in millimeter (mm) units, estimated per patient as described previously. The WED was measured at the central axial plane crossing the geometrical center of the heart. The variable y, corresponds to the dependent variable, organ dose in mGy/mGy/100mAs (or similar normalized unit). Parameters a and b were estimated for each patient-specific WED at each organ dose computed by the MC software. The coefficient of determination R^2, was used as a measure to assess the strength of correlation between WED and organ dose.

In the following sections tables are demonstrated with the results of regression analysis for all WED and organ dose correlations. Furthermore, representative graphs for exponential fits depicting WED and organ dose correlations are provided. parameters appearing on the tables are explicated as follows:

Organ: The name of the organ (e.g. , bones, breast, esophagus, heart, lungs, etc.)

Scanner: The name of the simulated scanner (GE: GE Revolution GSI 64)

Region: Anatomical Region (Head, Thorax, Abdomen/Pelvis)

kV: The kV beam setting of the computed dose data

AEC: True (1) if TCM was used or False (0) if tube current was fixed

a, b: Fit parameters of $y = ae^{bx}$

Organ dose conversion coefficients: Parametric fits for Radiotherapy Treatment Planning CT Imaging – Adult Patients

Region	Scanner	kV	AEC	Organ	a	b
Head	GE	120	0	Bones	0.03291	-0.006308
Head	GE	120	0	Brain	0.006727	-0.001457
Head	GE	120	0	Eye bulbs	0.00929	-0.001403
Head	GE	120	0	Oral mucosa	0.006774	-0.0007512
Head	GE	120	0	Salivary glands	0.008461	-0.001048

Region	Scanner	kV	AEC	Organ	a	b
Thorax	GE	120	0	lungs	0.01712	-0.005316
Thorax	GE	120	0	heart	0.0203	-0.005254
Thorax	GE	120	0	bone	0.02373	-0.005022
Thorax	GE	120	0	esophagus	0.01444	-0.004972
Thorax	GE	120	0	skin	0.009394	-0.00371
Thorax	GE	120	0	breast	0.006829	-0.005123

Region	Scanner	kV	AEC	Organ	a	b
Abdomen	GE	120	0	bones	0.02756	-5.3470E-03
Abdomen	GE	120	0	gbladder	0.02507	-6.2510E-03
Abdomen	GE	120	0	kidneys	0.02641	-6.6520E-03
Abdomen	GE	120	0	liver	0.01868	-5.5200E-03
Abdomen	GE	120	0	pancreas	0.02286	-6.3250E-03
Abdomen	GE	120	0	spleen	0.02380	-6.3170E-03
Abdomen	GE	120	0	stomach	0.02097	-6.0170E-03

Organ dose conversion coefficients: Parametric fits for Radiotherapy Treatment Planning CT Imaging – Pediatric Patients

Region	Scanner	kV	AEC	Organ	a
Head	GE	120	0	Bones	0.04879
Head	GE	120	0	Brain	0.01491
Head	GE	120	0	Eye bulbs	0.01174
Head	GE	120	0	Eye lens	0.01339
Head	GE	120	0	Oral mucosa	0.09986
Head	GE	120	0	Skin	0.01002

Region	Scanner	kV	AEC	Organ	a
Thorax	GE	120	0	lungs	0.0118
Thorax	GE	120	0	heart	0.01198
Thorax	GE	120	0	bone	0.02703
Thorax	GE	120	0	esophagus	0.01039
Thorax	GE	120	0	skin	0.009099

Region	Scanner	kV	AEC	Organ	a
Abdomen	GE	120	0	Bones	0.024060
Abdomen	GE	120	0	Gallbladder	0.009380
Abdomen	GE	120	0	Kidneys	0.009108
Abdomen	GE	120	0	Liver	0.006694
Abdomen	GE	120	0	Pancreas	0.007304
Abdomen	GE	120	0	Small intestine	0.005761
Abdomen	GE	120	0	Stomach	0.010630

Organ dose conversion coefficients: Parametric fits for Radiotherapy pre-Treatment CBCT Imaging – Adult Patients

Region	Scanner	kV	Organ	a	b
Head	ElektaXVI	100	bones	0.03184	-8.399E-03
Head	ElektaXVI	100	brain	0.01689	-9.376E-03
Head	ElektaXVI	100	eyes	0.03812	-9.452E-03
Head	ElektaXVI	100	oralmucosa	0.006803	-2.886E-03

Region	Scanner	kV	Organ	a	b
Thorax	ElektaXVI	120	lungs	0.02184	-4.6700E-03
Thorax	ElektaXVI	120	heart	0.02279	-4.7480E-03
Thorax	ElektaXVI	120	bone	0.03175	-4.4890E-03
Thorax	ElektaXVI	120	esoph	0.02043	-5.0800E-03
Thorax	ElektaXVI	120	skin	0.004094	-4.2980E-03
Thorax	ElektaXVI	120	breast	0.02079	-4.0460E-03

Region	Scanner	kV	Organ	a	b
Abdomen	ElektaXVI	120	adrenals	0.02752	-6.8420E-03
Abdomen	ElektaXVI	120	bones	0.04492	-7.7080E-03
Abdomen	ElektaXVI	120	esoph	0.02607	-9.4530E-03
Abdomen	ElektaXVI	120	gbladder	0.02600	-5.3810E-03
Abdomen	ElektaXVI	120	kidneys	0.02843	-5.9180E-03
Abdomen	ElektaXVI	120	liver	0.01497	-4.1580E-03
Abdomen	ElektaXVI	120	pancreas	0.02436	-5.8410E-03
Abdomen	ElektaXVI	120	prostate	0.11470	-1.8790E-02
Abdomen	ElektaXVI	120	spleen	0.03315	-6.5250E-03

Organ dose conversion coefficients: Parametric fits for Radiotherapy pre-Treatment CBCT Imaging – Pediatric Patients

Region	Scanner	kV	Organ	a	b
Head	XVI	100	Bones	0.1273	-7.464E-03
Head	XVI	100	Brain	0.0399	-6.424E-03

Region	Scanner	kV	Organ	a	b
Thorax	XVI	120	lungs	0.01632	-4.7120E-03
Thorax	XVI	120	heart	0.01265	-2.6830E-03
Thorax	XVI	120	bone	0.0325	-4.5860E-03
Thorax	XVI	120	esoph	0.01089	-2.4640E-03
Thorax	XVI	120	skin	0.01415	-3.7430E-03
Thorax	XVI	120	breast	0.01524	-4.1350E-03

Region	Scanner	kV	Organ	a	b
Abdomen	XVI	120	Bones	0.04387	-6.678E-03
Abdomen	XVI	120	Gallbladder	0.01371	-3.743E-03
Abdomen	XVI	120	Kidneys	0.01504	-3.922E-03
Abdomen	XVI	120	Liver	0.01335	-3.808E-03
Abdomen	XVI	120	Pancreas	0.01313	-3.550E-03
Abdomen	XVI	120	Spleen	0.01348	-3.706E-03
Abdomen	XVI	120	Adrenal Glands	0.01056	-2.573E-03
Abdomen	XVI	120	Skin	0.01941	-6.420E-03
Abdomen	XVI	120	Small intestine	0.0119	-1.870E-03
Abdomen	XVI	120	Stomach	0.01417	-4.124E-03
Abdomen	XVI	120	Large Intestine	0.01375	-3.001E-03

Organ dose conversion coefficients: Parametric fits for Imaging in Radiotherapy Planar X-ray Imaging – Adult Patients

Region	Scanner	kV	Organ	a	b
Head AP	XVI	100	bone	0.234800	-2.649E-02
Head AP	XVI	100	brain	0.004278	-8.740E-04
Head AP	XVI	100	eyes	0.011850	-1.905E-03
Head AP	XVI	100	oral_mucosa	0.005836	-1.092E-03
Head AP	XVI	100	salivary_glands	0.010990	-4.504E-03

Region	Scanner	kV	Organ	a	b
Thorax AP	XVI	120	bone	0.05872	-6.6730E-03
Thorax AP	XVI	120	breast	0.49250	-1.3390E-02
Thorax AP	XVI	120	esophagus	0.04008	-6.9770E-03
Thorax AP	XVI	120	heart	0.04364	-5.3810E-03
Thorax AP	XVI	120	lungs	0.04931	-6.8750E-03

Region	Scanner	kV	Organ	a	b
Abdomen AP	XVI	120	bladder	0.01468	-7.1650E-03
Abdomen AP	XVI	120	bowel	0.05248	-1.4140E-03
Abdomen AP	XVI	120	kidneys	0.03659	-3.9330E-03
Abdomen AP	XVI	120	liver	0.04995	-2.8540E-03
Abdomen AP	XVI	120	rectum	0.00742	-4.7890E-03
Abdomen AP	XVI	120	spleen	0.03251	-4.1810E-03
Abdomen AP	XVI	120	stomach	0.12010	-3.1560E-03

Region	Scanner	kV	Organ	a	b
Abdomen LAT	XVI	120	bladder	0.12250	-1.9950E-02
Abdomen LAT	XVI	120	bowel	0.12560	-1.3880E-02
Abdomen LAT	XVI	120	kidneys	0.01312	-3.2930E-03
Abdomen LAT	XVI	120	liver	0.00837	-7.6710E-03
Abdomen LAT	XVI	120	rectum	0.06671	-1.8690E-02
Abdomen LAT	XVI	120	spleen	0.01384	-3.7630E-04
Abdomen LAT	XVI	120	stomach	0.25460	-1.4180E-02

Organ dose conversion coefficients: Parametric fits for Imaging in Radiotherapy Planar X-ray Imaging – Pediatric Patients

Region	Scanner	kV	Organ	a	b
Head AP	XVI	100	bone	0.01514	-1.7360E-03
Head AP	XVI	100	brain	0.02760	-7.5070E-03
Head AP	XVI	100	eye_bulbs	0.03336	-1.4030E-03
Head AP	XVI	100	eye_lens	0.02765	-7.3570E-04
Head AP	XVI	100	oral_mucosa	0.04486	-5.8430E-03
Head AP	XVI	100	skin	0.03594	-1.1240E-02
Head AP	XVI	100	bone	0.01514	-1.7360E-03

Region	Scanner	kV	Organ	a	b
Thorax AP	XVI	120	bone	0.15300	-3.6520E-03
Thorax AP	XVI	120	esophagus	0.09021	-5.0390E-03
Thorax AP	XVI	120	heart	0.06585	-3.3860E-04
Thorax AP	XVI	120	lungs	0.07097	-2.4440E-03

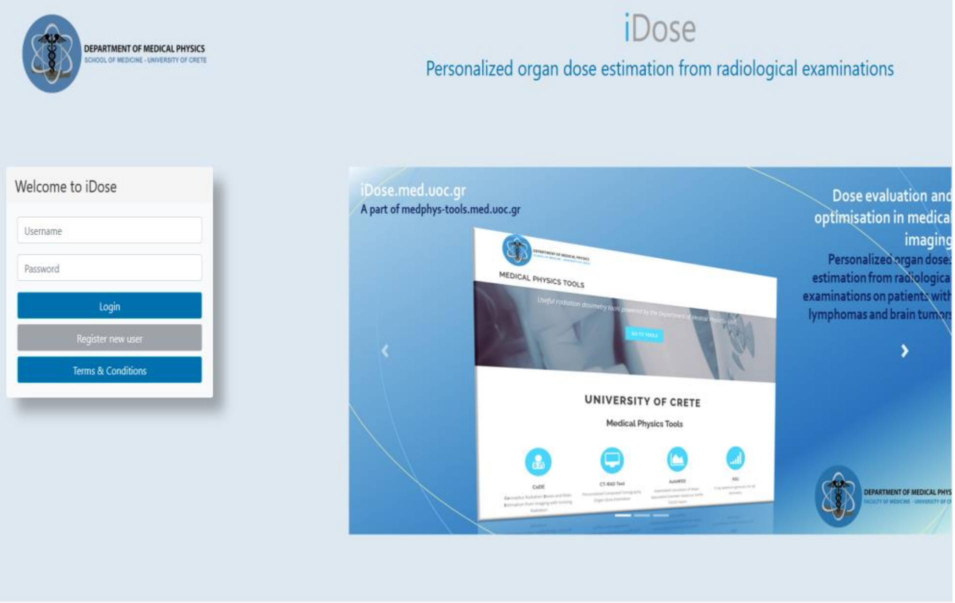
Region	Scanner	kV	Organ	a	b
Thorax LAT	XVI	120	bone	0.15630	-4.5750E-03
Thorax LAT	XVI	120	esophagus	0.07307	-5.3450E-03
Thorax LAT	XVI	120	heart	0.05690	-1.6840E-03
Thorax LAT	XVI	120	lungs	0.05900	-3.1160E-03

Region	Scanner	kV	Organ	a	b
Abdomen AP	XVI	120	bladder	0.14810	-6.2650E-03
Abdomen AP	XVI	120	bone	0.21190	-6.6220E-03
Abdomen AP	XVI	120	kidneys	0.07861	-5.6660E-03
Abdomen AP	XVI	120	liver	0.09920	-5.1710E-03
Abdomen AP	XVI	120	pancreas	0.11320	-5.0270E-03
Abdomen AP	XVI	120	spleen	0.09580	-6.6570E-03

9. Software development – iDose web calculation tool

The server-side (backend) of the calculation tool was developed using Python Django. The client-side (frontend) was implemented using HTML5, pure JavaScript, jQuery, AJAX JavaScript libraries, and Bootstrap for the CSS. jQuery is a JavaScript library designed to simplify HTML DOM tree traversal and manipulation, as well as event handling, CSS animation, and Ajax. Bootstrap is a free and open-source CSS framework directed at responsive, mobile-first front-end web development. It contains CSS- and optionally JavaScript-based design templates for forms, buttons, navigation, and other GUI components. In addition, since XML was not suitable to handle all database entries and possible future data implementations, MySQL was employed.

iDose (Abbrev.) – a tool for personalized organ doses estimation from radiological examinations on patients with lymphomas and brain tumors – is installed at http://medphys-tools.med.uoc.gr and is available upon free user registration (Figure 18).


iDose

Personalized organ dose estimation from radiological examinations

iDose.med.uoc.gr

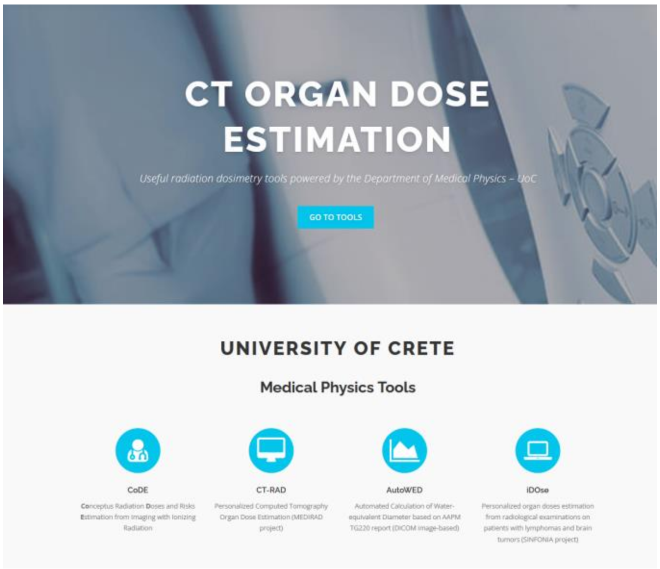
A part of medphys-tools.med.uoc.gr

Dose evaluation and optimisation in medical imaging

Personalized organ doses estimation from radiological examinations on patients with lymphomas and brain tumors

DEPARTMENT OF MEDICAL PHYSICS
SCHOOL OF MEDICINE - UNIVERSITY OF CRETE
Welcome to iDose
Username
Password
Login
Register new user
Terms & Conditions
MEDICAL PHYSICS TOOLS
UNIVERSITY OF CRETE
Medical Physics Tools
DEPARTMENT OF MEDICAL PHYS

http://medphys-tools.uoc.gr and http://idose.med.uoc.gr


CT ORGAN DOSE ESTIMATION

Useful radiation dosimetry tools powered by the Department of Medical Physics – UoC

UNIVERSITY OF CRETE

Medical Physics Tools

CoDE: Conceptus Radiation Doses and Risks Estimation from Imaging with Ionizing Radiation

CT-RAD: Personalized Computed Tomography Organ Dose Estimation (MEDIRAD project)

AutoWED: Automated Calculation of Water-equivalent Diameter based on AAPM TG220 report (DICOM image-based)

iDOse: Personalized organ doses estimation from radiological examinations on patients with lymphomas and brain tumors (SINFONIA project)

Figure 18: UoC Medical Physics tools web site and login page of iDose organ dose estimation tool, which will be located at http://medphys-tools.uoc.gr and idose.med.uoc.gr.

Following the submission of the current deliverable report (D2.1), the dose tools will undergo continuous refinement and development throughout the project's duration. This process will be driven by users' feedback, encompassing input from UoC staff and consortium members. The aim is to address errors, enhance visuals, and improve functionality based on their valuable suggestions. Moreover, further measurements and calculations are planned to validate the precision of results from the iDose tools.

10. iDose web tool calculation interface

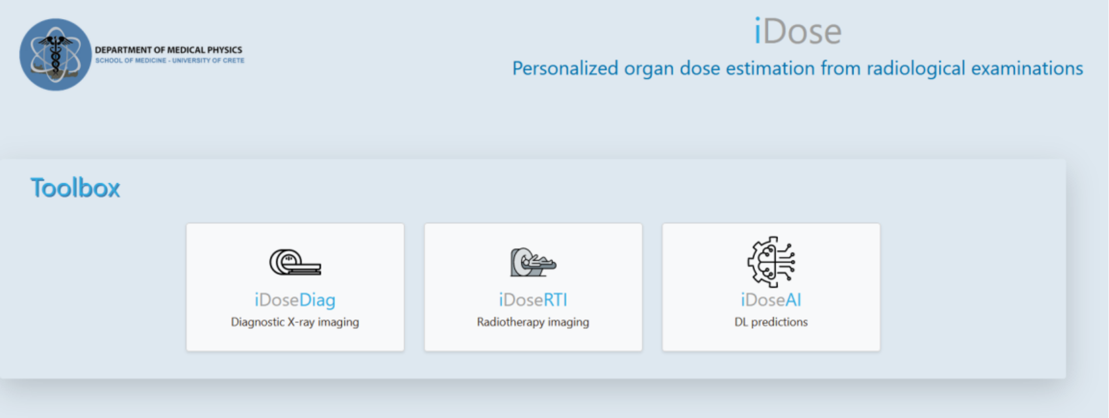
iDose Landing Page Navigation Panel

The web-tool dose calculation code is implemented using Javascript on the client side. This reduces load from server-side requests and improve dose calculation time and web-site responsiveness. After login, the user is presented with a sleek, simple three-option integration of personalized dosimetry tools (Figure 19):

1. **iDoseDiag**: Personalized dosimetry tool for organ doses estimation from radiological examinations on patients with lymphomas and brain tumours (as described here, in Deliverable 2.1).

2. **iDoseRTI**: Personalized dosimetry tool for organ doses estimation from imaging in radiotherapy on patients with lymphomas and brain tumours (as described in Deliverable 2.4).

3. **iDoseAI**: A dosimetric tool which incorporates all ML/AI algorithms from D2.1 and D2.4 for personalized dosimetry tool for organ doses prediction from examinations on patients in diagnostic radiology and radiotherapy imaging (as described in Deliverables 2.1 and 2.4).


DEPARTMENT OF MEDICAL PHYSICS
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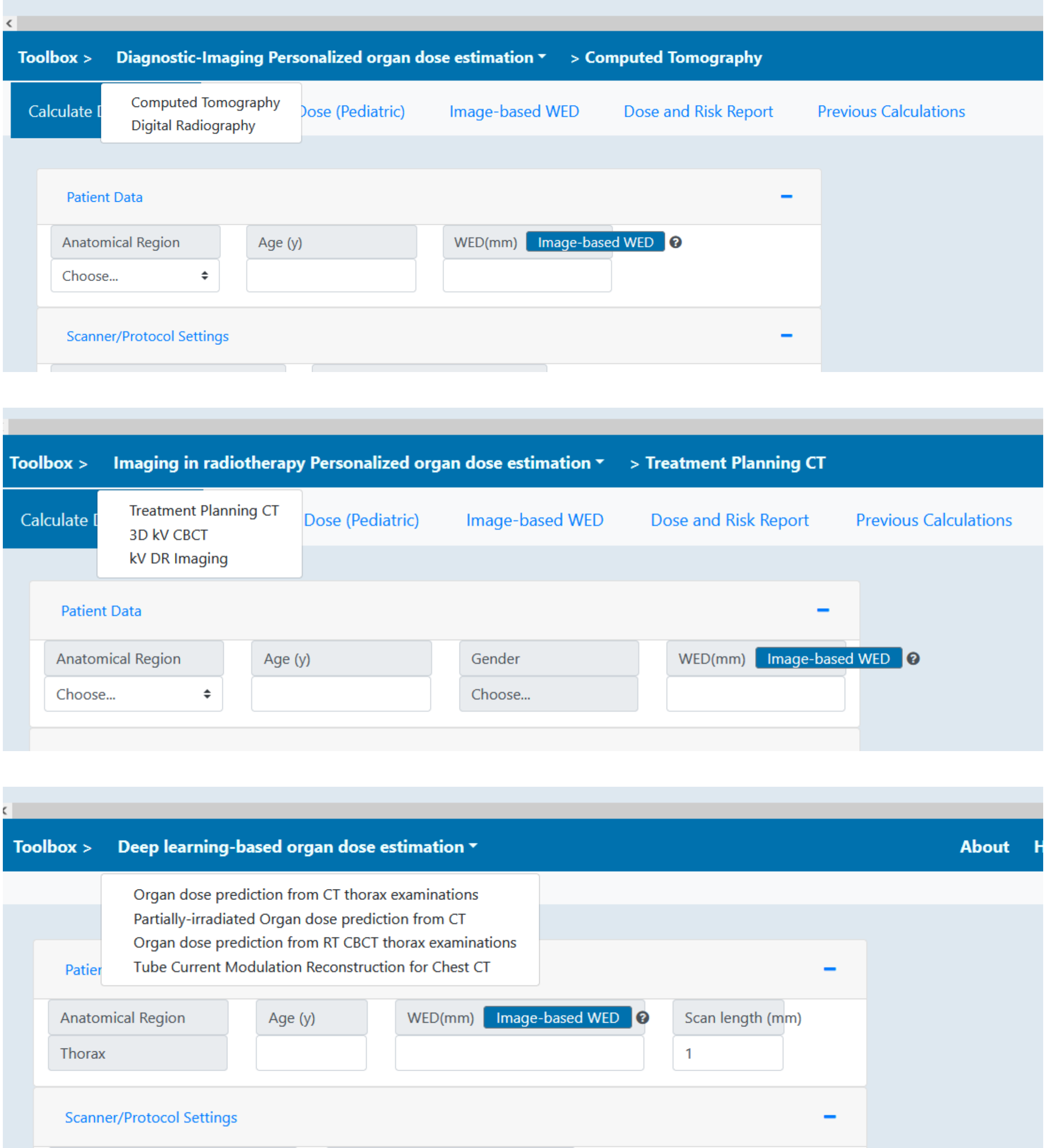
iDose
Personalized organ dose estimation from radiological examinations
Toolbox
iDoseDiag
Diagnostic X-ray imaging
iDoseRTI
Radiotherapy imaging
iDoseAI
DL predictions

Figure 19: iDose organ dose estimation tool initial landing page and selection of personalized dosimetry tools.

After the user leaves the iDose Landing Page, having selected the module to use, a panel is displayed encompassing all the links for access all tools according to a hierarchical structure (Figure 20). The arrangement and appearance of the panel was carefully designed for easy access to all tools, without having to move to the iDose landing page. However, the user can access these pages directly from the browser address bar, by typing:

1. idose.med.uoc.gr/links – for the landing page
2. idose.med.uoc.gr/idosediag – for the iDoseDiag diagnostic calculation page

3. idose.med.uoc.gr/idoserti – for the iDoseRTI imaging in radiotherapy page
4. idose.med.uoc.gr/idoseai – for the iDoseAI ML/AI algorithms calculation page


Toolbox >
Diagnostic-Imaging Personalized organ dose estimation
> Computed Tomography
Calculate D
Computed Tomography
Digital Radiography
Dose (Pediatric)
Image-based WED
Dose and Risk Report
Previous Calculations
Patient Data
Anatomical Region
Choose...
Age (y)
WED(mm)
Image-based WED
Scanner/Protocol Settings
Toolbox >
Imaging in radiotherapy Personalized organ dose estimation
> Treatment Planning CT
Calculate D
Treatment Planning CT
3D kV CBCT
kV DR Imaging
Dose (Pediatric)
Image-based WED
Dose and Risk Report
Previous Calculations
Patient Data
Anatomical Region
Choose...
Age (y)
Gender
Choose...
WED(mm)
Image-based WED
Toolbox >
Deep learning-based organ dose estimation
About
Organ dose prediction from CT thorax examinations
Partially-irradiated Organ dose prediction from CT
Organ dose prediction from RT CBCT thorax examinations
Tube Current Modulation Reconstruction for Chest CT
Patien
WED(mm)
Image-based WED
Scanner/Protocol Settings

Anatomical Region: Thorax
Age (y):
Scan length (mm): 1

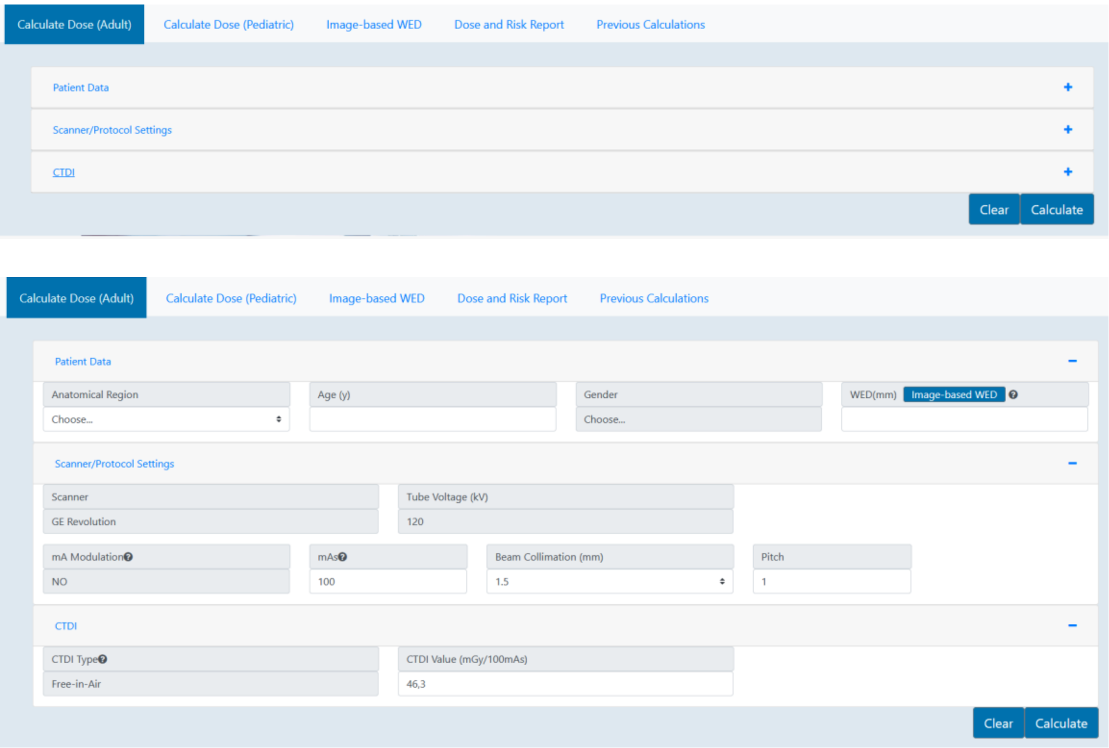
Figure 20: iDose organ dose estimation tool navigation panels for hierarchical selection of dosimetry tools.

11. iDose Radiotherapy Imaging Module – Radiotherapy Treatment Planning CT

In iDoseRTI imaging in radiotherapy module, organ doses from radiotherapy treatment planning CT scans can be estimated using the fitting parameters and dosimetric methodology explained in sections 3 to 8 (Figure 21). Each group can appear or disappear on the screen based on the preference of the user ("accordion" implementation).

User input fields are organized into three groups:

- The 'Patient Data' group requires basic demographic input (i.e., age and gender), CT scan region (currently thorax is the only available choice), and WED, which can either be directly inserted as a number or calculated using the automatic WED calculation tool.
- In the 'Scanner/Protocol Settings' group, users will select the CT scanner model (three models currently available) and corresponding exposure settings (i.e., kV, mA, current modulation, beam collimation, pitch, and rotation time). Users will also select the clinical indication for the CT scan.
- In the 'CTDI Group', users enter the CTDI type and value they for their corresponding scanner.

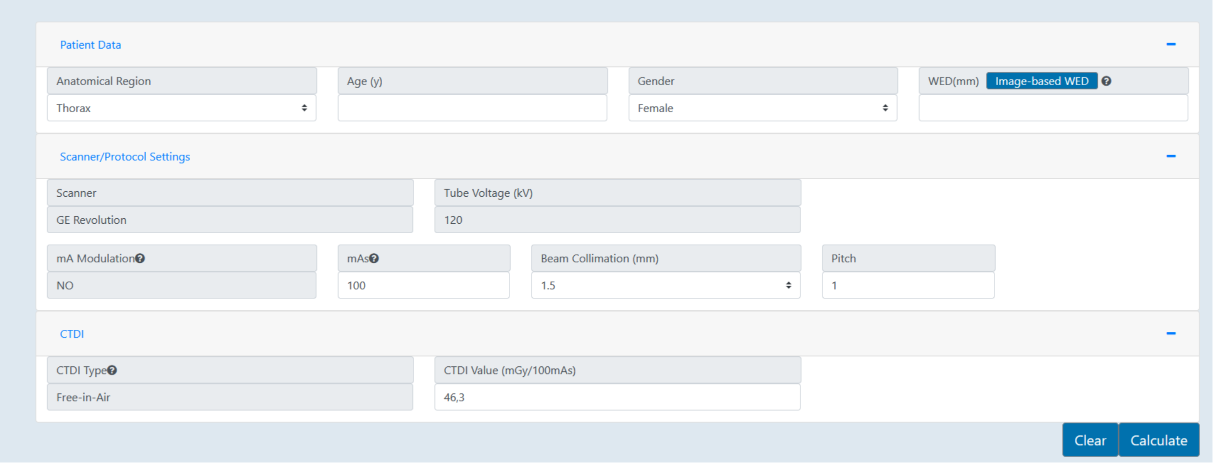


Anatomical Region: Choose...
Age (y):
Gender: Choose...
WED(mm):
Scanner: GE Revolution
Tube Voltage (kV): 120
mA Modulation: NO
mAs: 100
Beam Collimation (mm): 1.5
Pitch: 1
CTDI Type: Free-in-Air
CTDI Value (mGy/100mAs): 46,3

Figure 21: iDoseRTI web calculation tool interface accordion implementation overview.

Both adult and pediatric calculation tabs provide dose estimates for organs in the head/thorax/abdomen/pelvic region for patients undergoing CT examinations for various exposure settings (i.e., kV, mA, current modulation, beam collimation, pitch, and rotation time).

Patient Group submenu requires demographic data such as gender and age to be entered. This data is required for organ dosimetry and risk estimation. Water equivalent diameter is needed for correlation absorbed organ dose and patient size characteristics. WED is given in millimeters and can be entered as a value or calculated from user-uploaded CT data utilizing Image-based WEB tab.



Patient Data

Anatomical Region
Thorax

Age (y)

Gender
Female

WED(mm)

Scanner/Protocol Settings

Scanner
GE Revolution

Tube Voltage (kV)
120

mA Modulation
NO

mAs
100

Beam Collimation (mm)
1.5

Pitch
1

CTDI

CTDI Type
Free-in-Air

CTDI Value (mGy/100mAs)
46,3

Figure 22: iDoseRTI organ dose calculation tool - main calculation tab - adults.

Scanner Group submenu requires:

- Selection of CT scanner; Currently only one scanner is available: GE Revolution.
- Tube Voltage: Currently there is one kV selectable, 120 kV.
- mA modulation: User can select if tube current modulation (TCM) or fixed tube current (NO) will be utilized or not for organ dose calculation. For the radiotherapy imaging module, mA modulation is set to NO (fixed current), for all calculations.
- mAs: User can manually enter the mAs of the examination. For Siemens scanners, effective mAs reading from CT console should be used.
- Beam Collimation: Beam collimation in millimeters. In MDCT the actual beam collimation is not directly correlated with slice thickness. It is the length of the individual detector (or linked detector elements) acquiring data for each of the simultaneously acquired slices that limits the width of the x-ray beam contributing to that slice, this length is often referred to as detector collimation. Beam collimation depends on CT scanner and detectors configuration.
- Pitch: User can select pitch of the examination.
- Rotation time: User can specify time (in seconds) in which a full gantry rotation is performed.

CTDI Group submenu requires the user to enter CTDI type and value they for their corresponding scanner. CTDI values can be entered in their CTDI-free-in-air form (Figure 22).

12. iDose Radiotherapy Imaging Module – Radiotherapy 3D kV CBCT

In iDoseRTI imaging in radiotherapy module, organ doses from radiotherapy pre-treatment on-board imaging CBCT scans can be estimated using the fitting parameters and dosimetric methodology explained in sections 3 to 8.

User input fields are organized into three groups:

- The ‘Patient Data’ group requires basic demographic input (i.e., age and gender), CT scan region (currently thorax is the only available choice), and WED, which can either be directly inserted as a number or calculated using the automatic WED calculation tool.
- In the ‘Protocol Settings’ group, users will select the on-board imaging device (currently only Elekta XVI only available) and corresponding exposure settings (i.e., kV, mAs/frame, frames/rotation, beam collimation options).
- In the ‘CTDI Group’, users enter the CTDI type and value for their corresponding scanner.

Each group can appear or disappear on the screen based on the preference of the user (“accordion” implementation).

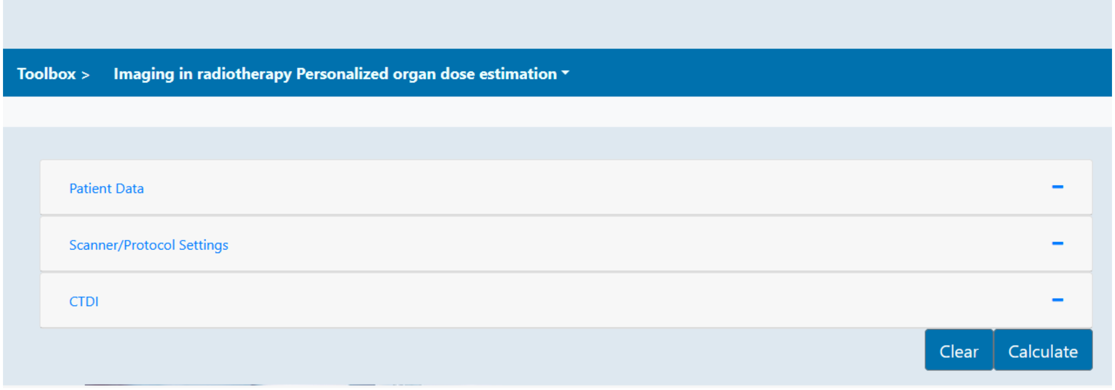
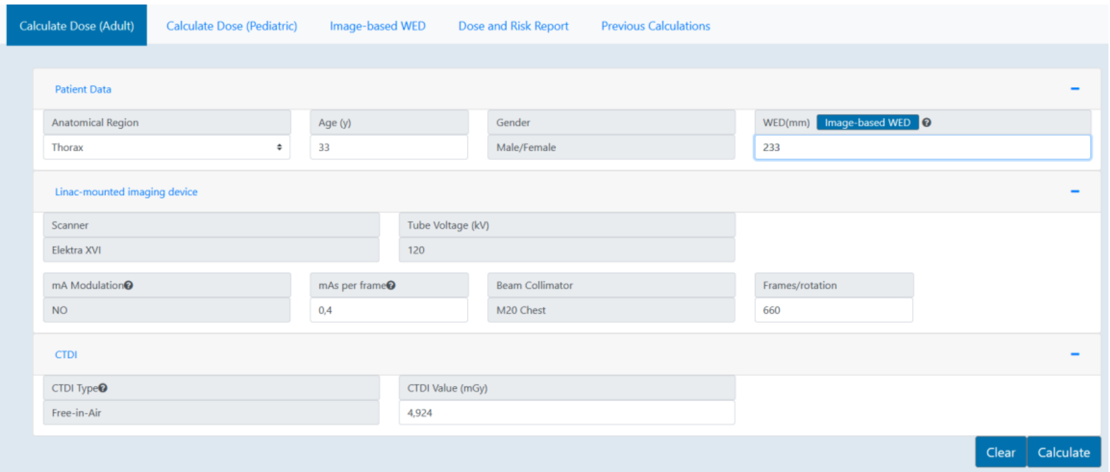

Toolbox >
Imaging in radiotherapy Personalized organ dose estimation
Patient Data
Scanner/Protocol Settings
CTDI
Clear
Calculate

Figure 23: iDoseRTI web calculation tool interface accordion implementation overview.

Both adult and pediatric calculation tabs provide dose estimates for organs in the head/thorax/abdomen/pelvic region for patients undergoing CBCT examinations for various exposure settings (i.e., kV, mAs/frame, frames/rotation, beam collimation options).

Patient Group submenu requires demographic data such as gender and age to be entered. This data is required for organ dosimetry and risk estimation. Water equivalent diameter is needed for correlation absorbed organ dose and patient size characteristics. WED is given in millimeters and can be entered as a value or calculated from user-uploaded CT data utilizing Image-based WEB tab.



Anatomical Region: Thorax
Age (y): 33
Gender: Male/Female
WED(mm): 233
Scanner: Elektra XVI
Tube Voltage (kV): 120
mA Modulation: NO
mAs per frame: 0,4
Beam Collimator: M20 Chest
Frames/rotation: 660
CTDI Type: Free-in-Air
CTDI Value (mGy): 4,924

Figure 24: iDoseRTI organ dose calculation tool - main calculation tab - adults.

Scanner Group submenu requires:

- Selection of CT scanner; Currently only one linac-mounted imaging device is available: Elekta XVI
- Tube Voltage: 100kV is selected for head CBCT and 120 kV for thorax/abdomen/pelvic CBCT scans.
- mA modulation: For the radiotherapy imaging module, mA modulation is set to NO (fixed current), for all calculations.
- mAs/frame: User can manually enter the mAs/frame of the examination. For Elekta XVI, predefined values are provided according to table 5.
- Beam Collimation:
- Frames/roatation: User can specify the number of acquired frames per revolution. For Elekta XVI, predefined values are provided according to table 5.

CTDI Group submenu requires the user to enter CTDI type and value they for their corresponding scanner. CTDI values can be entered in their CTDI-free-in-air form. For Elekta XVI, predefined CTDI values are provided according to manufacturer specifications.

13. iDoseRTI Imaging in Radiotherapy Module – DR Planar Imaging

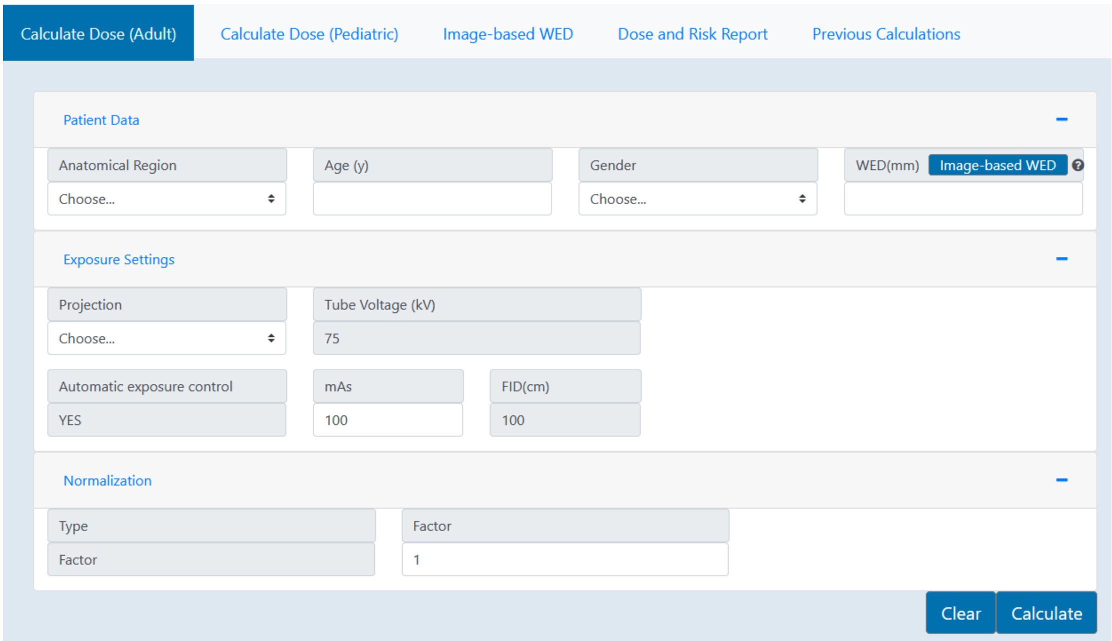
In iDose Radiotherapy Planar Imaging module, organ doses from conventional planar imaging prior to radiotherapy treatment can be estimated using the fitting parameters and dosimetric methodology explained in sections 3 to 8.

Both adult and pediatric calculation tabs provide dose estimates for organs in the head/thorax/abdomen-pelvic region for patients undergoing planar examinations for various predefined exposure settings.

Patient Group submenu requires demographic data such as gender and age to be entered. This data is required for organ dosimetry and risk estimation. Water equivalent diameter is needed for correlation absorbed organ dose and patient size characteristics. WED is given in millimeters and can be entered as a value or calculated from user-uploaded CT data utilizing Image-based WEB tab. In addition, the tool will suggest a value for WED according to patient's BMI, if no image is available for WED calculations.

Exposure settings submenu requires:

- Selection of anatomical region: Head, Thorax, abdomen pelvis
- Tube Voltage: Tube voltage is fixed for each radiological examination (eg 100 kVp for thorax, 100 kVp for head.
- mAs: tube load is fixed for each radiological examination and represents the most commonly mAs used with AEC; however, user can alter tube load to calculate organ dose for different exposure setting used
- FID: Fous-to-Image Receptor-Distance is fixed and represents mostly used distance for each radiological examination



Patient Data

Anatomical Region: Choose...
Age (y):
Gender: Choose...
WED(mm):

Exposure Settings

Projection: Choose...
Tube Voltage (kV): 75
Automatic exposure control: YES
mAs: 100
FID(cm): 100

Normalization

Type: Factor
Factor: 1

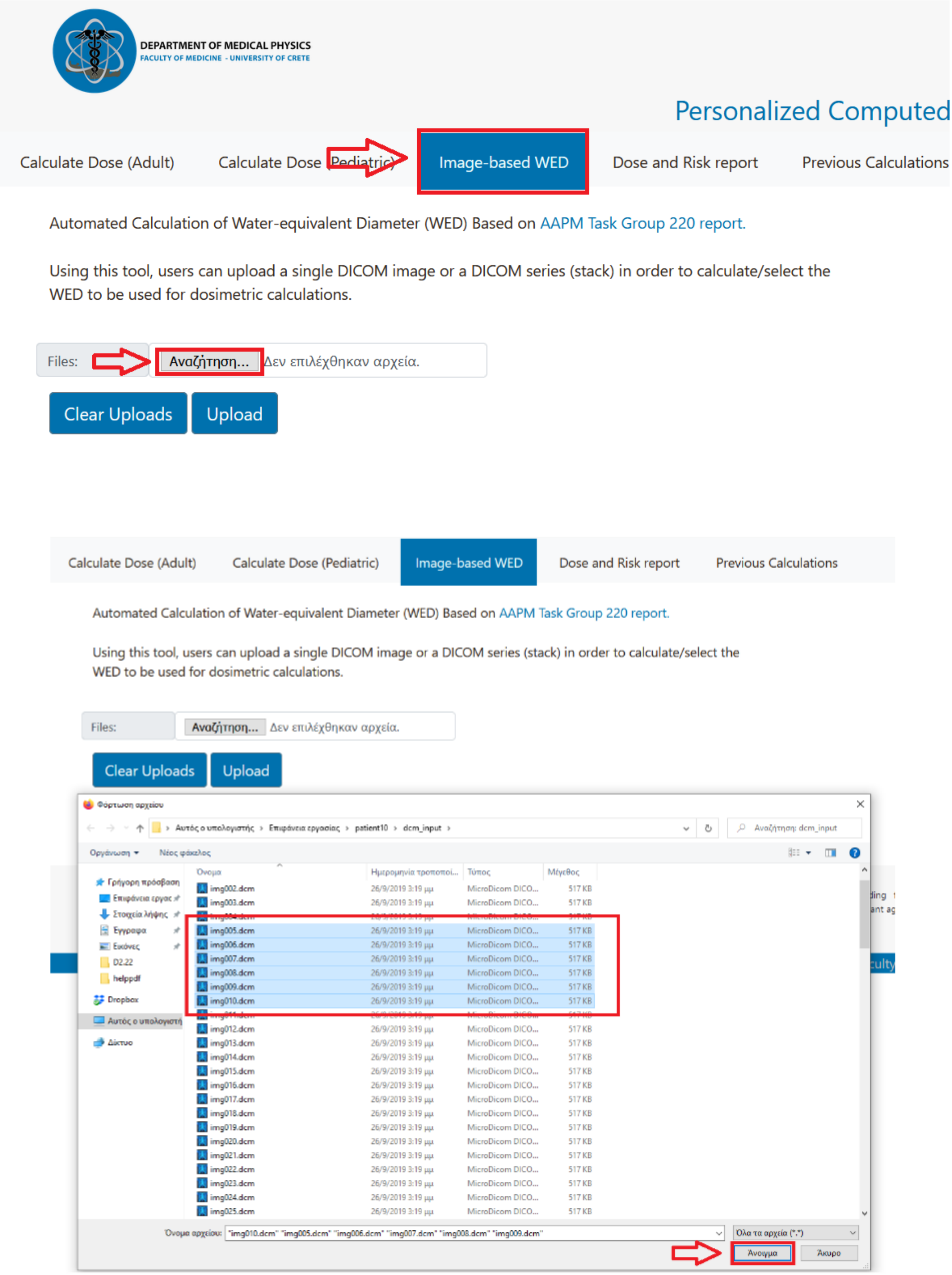
Figure 25: iDose organ dose calculation tool - main calculation tab - adults.

14. Automatic Imaged-Based Water-equivalent diameter (WED) calculation module

Accurate WED determination requires detailed delineation of the patient body outline on the CT slice without including the CT couch/table. Within iDose, an automatic module for calculation of WED based on user-uploaded CT scans was developed. The algorithm is based on morphological operations applied on each image slice. A square structuring element with heuristically determined size equal to 12 pixels was used to perform morphological opening. This step effectively removed small structures in the vicinity of the body and preserved the body shape and size. The next step was conversion of the image to binary using Otsu's method to determine the single HU threshold between background and any other structure [16, 17]. During this step, the couch is usually removed from the image without affecting the body size or shape. Lungs and other low-density tissues are likely to produce empty space (holes) in the binarized image within the region defined by the body shape. This empty space was filled by detection of zero value locations that were not connected with the image borders. In the final step, non-zero areas that were not connected were identified and the largest area was kept.

For imaged-based WED calculation, the user is prompted with an interface to upload a single DICOM image or a DICOM series as a group of images for the WED calculation (of each image/slice) to AAPM TG220 formulation. No images and DICOM header information are stored after exiting the Imaged-Based calculation tab, so there is no risk of sharing sensitive patient data.

WED and tube current values for each uploaded DICOM image are presented and the user can select which WED value will be used/transferred in the organ dose calculation tab. Users can use average, median, or WED value for a specific slice in this tool.


DEPARTMENT OF MEDICAL PHYSICS
FACULTY OF MEDICINE - UNIVERSITY OF CRETE
Personalized Computed
Calculate Dose (Adult)
Calculate Dose (Pediatric)
Image-based WED
Dose and Risk report
Previous Calculations
Files:
Αναζήτηση...
Δεν επιλέχθηκαν αρχεία.
Clear Uploads
Upload
Φόρτωση αρχείου
Αυτός ο υπολογιστής › Επιφάνεια εργασίας › patient10 › dcm_input
Αναζήτηση: dcm_input
Οργάνωση
Νέος φάκελος
Γρήγορη πρόσβαση
Επιφάνεια εργας
Στοιχεία λήψης
Έγγραφα
Εικόνες
D2.22
helppdf
Dropbox
Αυτός ο υπολογιστή
Δίκτυο
Όλα τα αρχεία (*.*)
Άνοιγμα
Άκυρο

Automated Calculation of Water-equivalent Diameter (WED) Based on AAPM Task Group 220 report.

Using this tool, users can upload a single DICOM image or a DICOM series (stack) in order to calculate/select the WED to be used for dosimetric calculations.

Όνομα	Ημερομηνία τροποποί...	Τύπος	Μέγεθος
img002.dcm	26/9/2019 3:19 μμ	MicroDicom DICO...	517 KB
img003.dcm	26/9/2019 3:19 μμ	MicroDicom DICO...	517 KB
[illegible]	[illegible]	[illegible]	[illegible]
img005.dcm	26/9/2019 3:19 μμ	MicroDicom DICO...	517 KB
img006.dcm	26/9/2019 3:19 μμ	MicroDicom DICO...	517 KB
img007.dcm	26/9/2019 3:19 μμ	MicroDicom DICO...	517 KB
img008.dcm	26/9/2019 3:19 μμ	MicroDicom DICO...	517 KB
img009.dcm	26/9/2019 3:19 μμ	MicroDicom DICO...	517 KB
img010.dcm	26/9/2019 3:19 μμ	MicroDicom DICO...	517 KB
[illegible]	[illegible]	[illegible]	[illegible]
img012.dcm	26/9/2019 3:19 μμ	MicroDicom DICO...	517 KB
img013.dcm	26/9/2019 3:19 μμ	MicroDicom DICO...	517 KB
img014.dcm	26/9/2019 3:19 μμ	MicroDicom DICO...	517 KB
img015.dcm	26/9/2019 3:19 μμ	MicroDicom DICO...	517 KB
img016.dcm	26/9/2019 3:19 μμ	MicroDicom DICO...	517 KB
img017.dcm	26/9/2019 3:19 μμ	MicroDicom DICO...	517 KB
img018.dcm	26/9/2019 3:19 μμ	MicroDicom DICO...	517 KB
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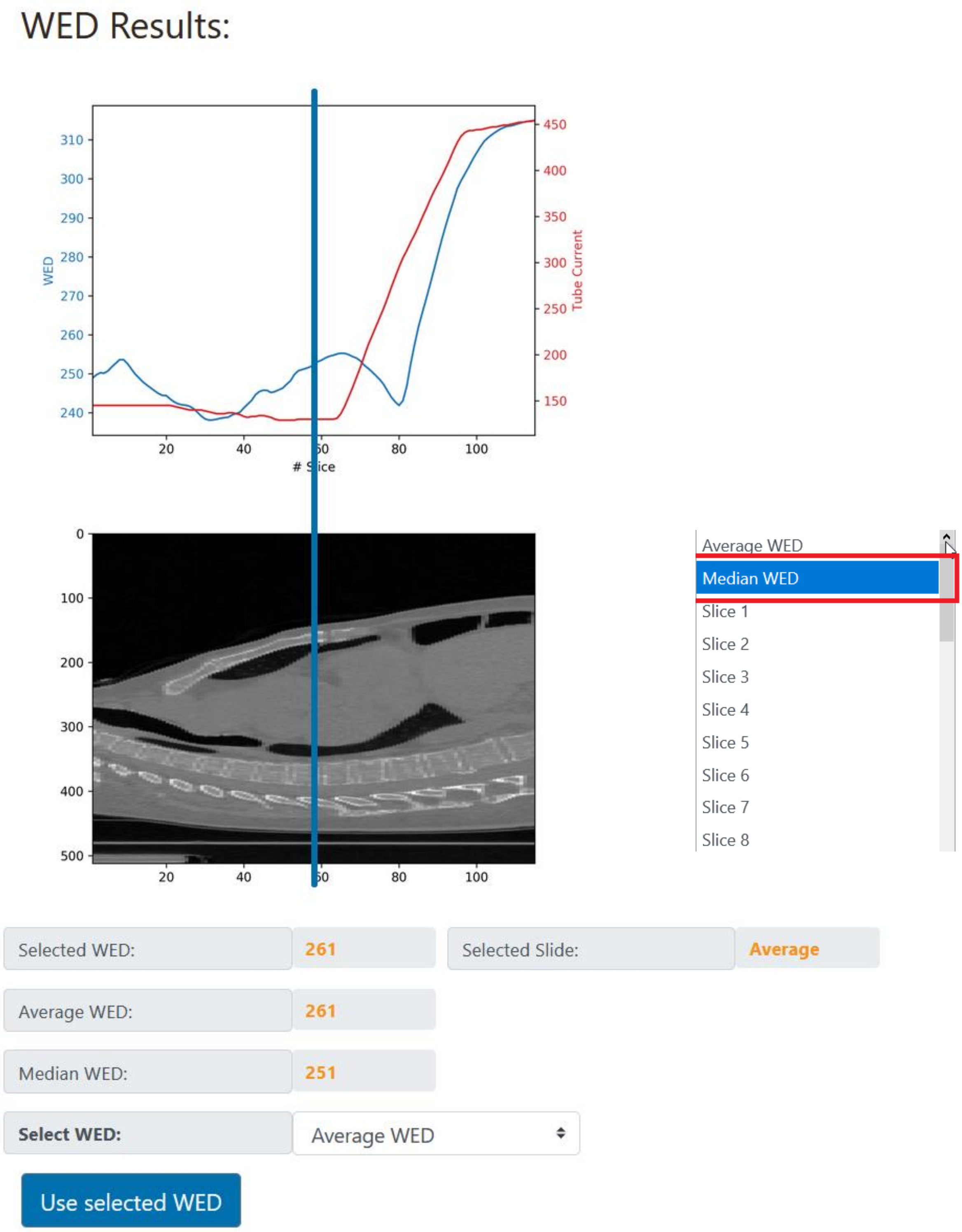
img020.dcm	26/9/2019 3:19 μμ	MicroDicom DICO...	517 KB
img021.dcm	26/9/2019 3:19 μμ	MicroDicom DICO...	517 KB
img022.dcm	26/9/2019 3:19 μμ	MicroDicom DICO...	517 KB
img023.dcm	26/9/2019 3:19 μμ	MicroDicom DICO...	517 KB
img024.dcm	26/9/2019 3:19 μμ	MicroDicom DICO...	517 KB
img025.dcm	26/9/2019 3:19 μμ	MicroDicom DICO...	517 KB

Όνομα αρχείου: "img010.dcm" "img005.dcm" "img006.dcm" "img007.dcm" "img008.dcm" "img009.dcm"

Figure 26: Image-based WED tool inside iDose organ dose calculation tool with user image upload capability.



WED Results:

WED
310
300
290
280
270
260
250
240
450
400
350
300
250
200
150
Tube Current
20
40
60
80
100
# Slice
0
100
200
300
400
500
20
40
60
80
100
Average WED
Median WED
Slice 1
Slice 2
Slice 3
Slice 4
Slice 5
Slice 6
Slice 7
Slice 8

Selected WED: 261

Selected Slide: Average

Average WED: 261

Median WED: 251

Select WED: Average WED

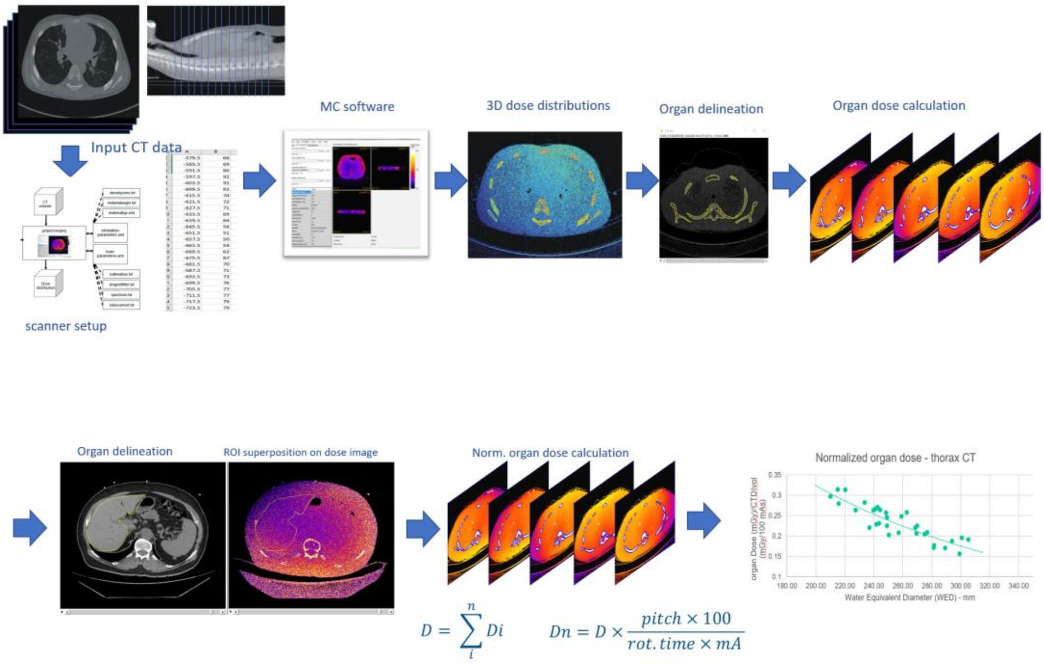
Use selected WED

Figure 27: Image-based WED calculation from user-supplied DICOM series inside iDose organ calculation tool.

15. AI algorithm development – Rapid estimation of patient-specific organ doses from thoracic CBCT examinations using a deep learning network

Various approaches have been adopted over the past decades for the estimation of organ doses such as direct measurements with different kinds of dosimeters, anthropomorphic phantoms and calculations using Monte Carlo methods combined with computational human phantoms. Methods for scanner-specific and patient-specific, organ-dose estimation are based on a procedure that combines MC computational techniques and patient CT scans. The procedure is usually composed of five steps: (a) collection of suitable patient CT scans; (b) determination of scanner parameters; (c) Monte Carlo dosimetric computations; (d) three-dimensional (3D) patient-specific dose distribution output and (e) correlation between dose and patient characteristics.

Time consuming dose computations are based on scanner-specific data for x-ray beam spectra, beam shaping devices (bow-tie filters) and geometrical specifications. Dose is calculated on a per image voxel basis and output comprises of parametric dose images in which every voxel carries the dose normalized to CTDI. Moreover, organ dose information must be extracted from 3D dose distributions through laborious delineation and segmentation of specific organ/tissue structures (Figure 28).


Input CT data
scanner setup
MC software
3D dose distributions
Organ delineation
Organ dose calculation
Organ delineation
ROI superposition on dose image
Norm. organ dose calculation
Normalized organ dose - thorax CT
organ Dose (mGy/CTDIvol (mGy/100 mAs))
Water Equivalent Diameter (WED) - mm
0.35
0.3
0.25
0.2
0.15
0.1
180.00
200.00
220.00
240.00
260.00
280.00
300.00
320.00
340.00

$$D = \sum_{i}^{n} Di \qquad Dn = D \times \frac{pitch \times 100}{rot. time \times mA}$$

Figure 28: Schematic representation of a MC-based organ estimation methodology.

The dataset included 113 adult patients (44 males and 69 females) who underwent radiotherapy treatment planning CT imaging in the thorax region using a 64-slice GE Revolution CT scanner. Delineated contours were generated for bones, esophagus, breast (for female patients), heart, skin, and lungs. CBCT acquisition was performed using the Elekta XVI R5.0.4. CBCT system, capable of producing spectra within the range of 80 to 140 kV. The CBCT system does not employ moveable collimators and the field size is specified using lead cassettes with a predefined, fixed, opening. All patients treated in the thoracic area, were imaged using the M20 protocol, with the bow-tie filter implemented. Specifically, the CBCT acquisition was performed with a voltage of 120 kV and a tube current of 20 mA for 13.2 s. The ImpactMC Monte Carlo software, a well-validated software for dosimetric simulations was employed in this study. A 3D dose distribution for each patient was generated by the ImpactMC after each simulation.

For each organ of interest, a separate dataset was generated consisting of a set of five independent variables and one dependent variable. An artificial neural network, which functions as a regression model, was developed, and optimized, to predict organ doses based on selected features. The independent variables were the patient sex, the left-right and anterior-posterior body dimensions on the axial plane, the organ volume, and the WED. Data preprocessing and splitting was applied for optimization and testing purposes. Each dataset was divided into two parts: the training set (70% of the dataset) and the test set (30% of the dataset). The validation of the model was performed using k-fold cross-validation. The metrics used to determine training convergence and performance was accuracy (defined as 1-validation loss). The networks were trained for 200 epochs using early stopping before reaching the specified maximum number of epochs to avoid overfitting to the data, thus improving the network generalization.

Optimization strategies

Hyperparameters are configurations that determine the structure of machine learning models and control their learning processes. They shouldn't be confused with the model's parameters (such as the bias) whose optimal values are determined during training. Hyperparameter optimization is an integral part of deep learning as a machine learning project is crucially dependent on the choice of good hyperparameters (Figure 29).

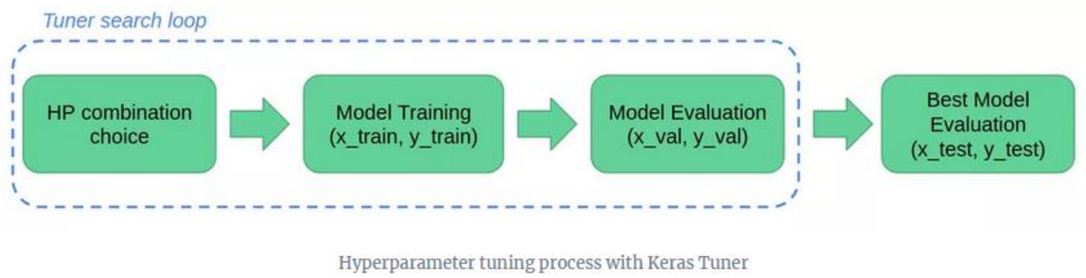

Tuner search loop
HP combination choice
Model Training (x_train, y_train)
Model Evaluation (x_val, y_val)
Best Model Evaluation (x_test, y_test)
Hyperparameter tuning process with Keras Tuner

Figure 29: Optimization strategy of a neural network architecture.

The two main types of hyperparameters are the model hyperparameters (such as the number and units of layers) which determine the structure of the model and the algorithm hyperparameters (such as the optimization algorithm and learning rate), which influences and controls the learning process. Standard hyperparameters for training neural nets include:

1. Number of hidden layers

2. Number of units for hidden layers

3. The dropout rate - A single model can be used to simulate having many different network architectures by randomly dropping out nodes during training.

4. Activation function (Relu, Sigmoid, Tanh) - defines the output of that node given an input or set of inputs.

5. Optimization algorithm (Stochastic Gradient descent, Adam Optimizer, RMSprop, e.tc.) - tools for updating model parameters and minimizing the value of the loss function, as evaluated on the training set.

6. Loss function - a measurement of how good your model is in terms of predicting the expected outcome.

7. Learning rate - controls how much to change the model in response to the estimated error each time the model weights are updated.

8. Number of training iterations (epochs) - the number times that the learning algorithm will work through the entire training dataset.

9. Batch size - this hyperparameter of gradient descent that controls the number of training samples to work through before the model's internal parameters are updated.

Depending on the performance of the model after initial training, these values are repeatedly adjusted to improve the model, until a combination of values that produces the best results is chosen. The process of adjusting hyperparameters to obtain the right set of values that optimizes the performance of machine learning models is known as Hyperparameter Tuning. Tuning hyperparameters could be challenging in deep learning. This is mainly due to the different configurations that need to be rightly set, several trials of re-adjusting these values to improve the performance and the poor results that arise from setting sub-optimal values for the hyperparameters. Manually fine-tuning hyperparameters is often laborious, time-consuming, sub-optimal and inefficient for managing computing resources. An alternative approach is to utilize scalable hyperparameter search algorithms such as Bayesian optimization, Random Search, and Hyperband (Figure 30). Keras Tuner is a scalable Keras framework that provides these algorithms built-in for hyperparameter optimization of deep learning models ([16], also see Appendix A for parametrization).

Random Search Optimization Algorithm

The algorithm sets up a grid of hyperparameter values and selects *random* combinations to train the model where the number of search iterations is set based on time and resources. Random search is much more efficient than grid search, where all the possible combinations from the grid are tried until the best combination is found. Although grid search finds the optimal values of hyperparameters, the random search usually considers a good enough combination in far fewer iterations (Figure 31).

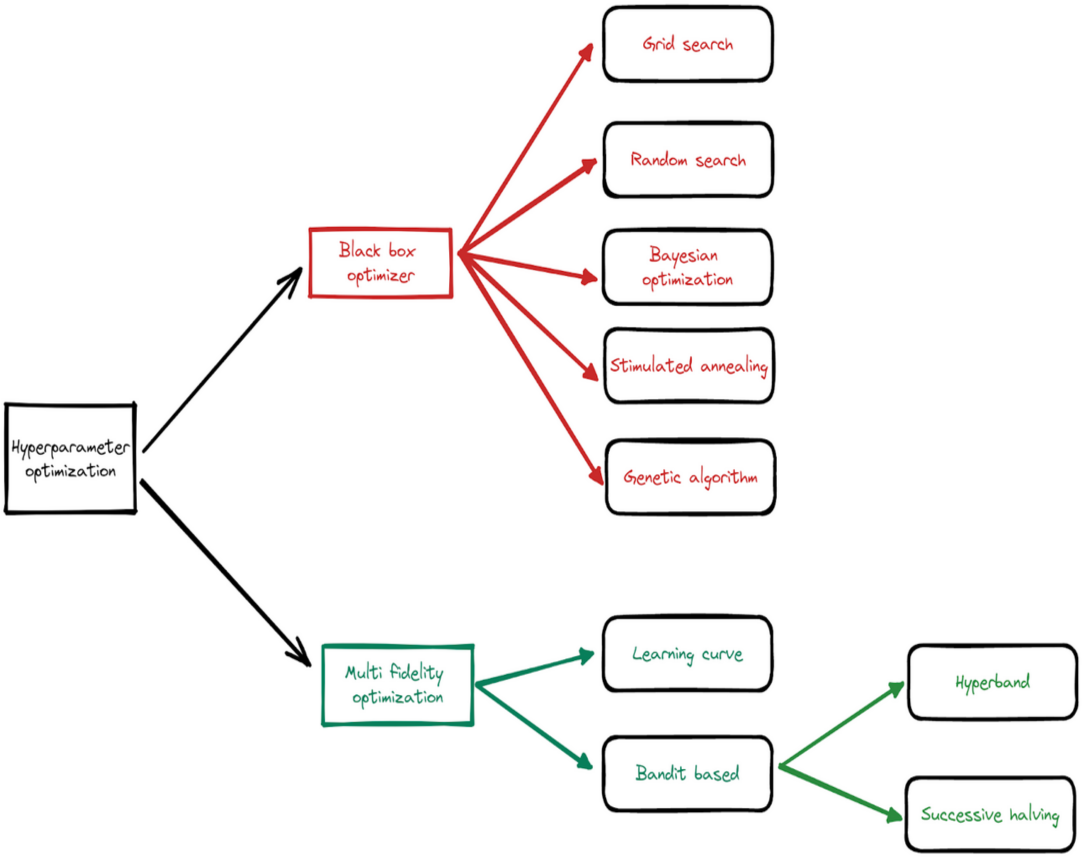

Hyperparameter optimization
Black box optimizer
Grid search
Random search
Bayesian optimization
Stimulated annealing
Genetic algorithm
Multi fidelity optimization
Learning curve
Bandit based
Hyperband
Successive halving

Figure 30: Hyperparameter tuning optimization algorithms.

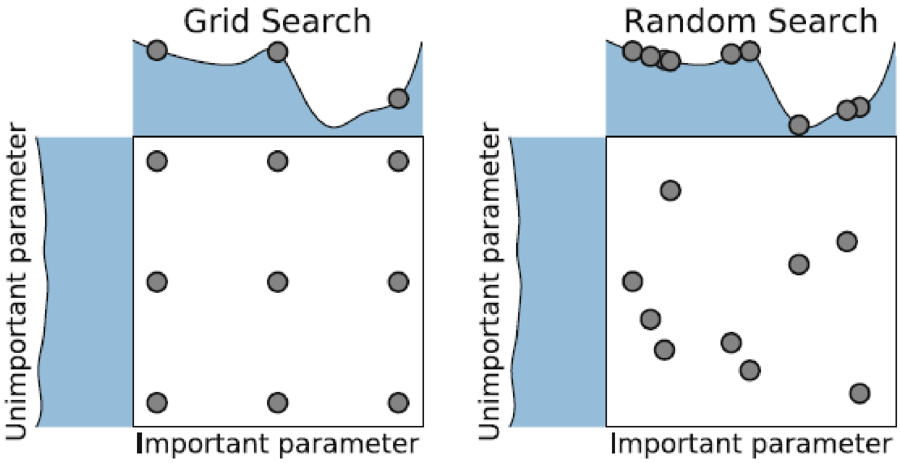


Figure 31: Comparison of grid search and random search for minimizing a function with one important and one unimportant parameter (adapted from [17]).

Bayesian Optimization Algorithm

Bayesian optimization is an iterative algorithm with two key ingredients: probabilistic surrogate model and an acquisition function to decide which point to evaluate next. In each iteration, the surrogate model is fitted to all observations. of the target function made so far. Then the acquisition function, which uses the predictive distribution of the probabilistic model, determines the utility of different candidate points, trading off exploration and exploitation. Bayesian optimization aims to become less wrong with more data inputs done by continually updating the surrogate probability model after each objective function's evaluation epoch. The algorithm builds a surrogate probability model of the objective function and finds the hyperparameters that perform best on the surrogate. The hyperparameters acquired are applied to the actual objective function, and the algorithm is run till the desired results are not achieved.

Hyperband Optimization Algorithm

Hyperband is an optimized variation of random search which uses early stopping to speed up the process. The underlying principle of the procedure exploits the idea that if a hyperparameter configuration is expected to be the best after a considerable number of iterations, it is more likely to perform after a small number of iterations. It allocates resources using a logical early-stopping technique, allowing it to test orders of magnitude more configurations than black-box processes such as Bayesian optimization methods.

The capacity of Hyperband to adapt to unknown convergence rates and the behavior of validation losses as a function of the hyperparameters was proved by the developers in the theoretical study. Furthermore, for a range of deep-learning and kernel-based learning issues, Hyperband is 5 to 30 times quicker than typical Bayesian optimization techniques. In the non-stochastic environment, Hyperband is one solution with properties like the pure-exploration, infinite-armed bandit issue.

To develop more efficient search methods, Bayesian optimization approaches that focus on optimizing hyperparameter configuration selection have lately dominated the subject of hyperparameter optimization. By picking configurations in an adaptive way, these approaches seek to discover good configurations faster than typical baselines such as random search. The goal of an orthogonal approach to hyperparameter optimization is to accelerate configuration evaluation. These methods are computationally adaptive, providing greater resources to promising hyperparameter combinations while swiftly removing bad ones. The size of the training set, the number of features, or the number of iterations for iterative algorithms are all examples of resources.

These techniques seek to analyze orders of magnitude more hyperparameter configurations than approaches that evenly train all configurations to completion, hence discovering appropriate hyperparameters rapidly. The hyperband is designed to accelerate the random search by providing a simple and theoretically sound starting point.

Bayesian optimization	**Hyperband**
A probability-based model	A bandit-based model
Learns an expensive objective function by past observation.	In each given situation, the goal is to reduce the simple regret, defined as the distance from the best choice, as rapidly as feasible.
Bayesian optimization is only applicable to continuous hyperparameters, not categorical ones.	Hyperband can work for both continuous and categorical hyperparameters

Table 6: Bayesian optimization vs Hyperband optimization algorithm properties.

Data preprocessing and data splitting for training and validation purposes

```
#standard data preprocessing for data normanilization
min_max_scaler = preprocessing.MinMaxScaler()
X_scale = min_max_scaler.fit_transform(X)
X_train, X_val_and_test, Y_train, Y_val_and_test = train_test_split(X_scale, 
Y, test_size=0.3)
```

Hyperband Hyperparameters optimization/tuning:

```
def build_model(hp):
  model = tf.keras.Sequential()


  for i in range(hp.Int('layers', 3, 6)):
    model.add(tf.keras.layers.Dense(units=hp.Int('units_' + str(i), 16, 512, 
step=16),
                                    activation=hp.Choice('act_' + str(i), 
['relu','selu'])))

  model.add(Dense(1, kernel_initializer='normal', activation='linear'))
  hp_learning_rate = hp.Choice('learning_rate', values=[1e-2, 1e-3, 1e-4])

    optimizer = hp.Choice('optimizer', ['adam', 'sgd', 'rmsprop'])
  model.compile(optimizer=optimizer,loss=msle,metrics=[msle])

  return model

nEpochs = 40

tuner = kt.Hyperband(build_model,
    max_epochs=nEpochs,
    objective='val_loss',
    directory='keras_tuner',
    project_name='keras_tuner_1',
    #max_trials=15,
    overwrite = 'false'
)

tuner.search(X_train, Y_train, epochs=nEpochs, batch_size=2,
validation_data=(X_val, Y_val))
```

Another problem with training neural networks is in the choice of the number of training epochs to use. Too many epochs can lead to overfitting of the training dataset, whereas too few may result in an underfit model. The model loss v/s Epochs graph shows how the Training loss get reduced with increase in the number of Epochs. The losses reduced as the Epochs increases, but they become saturated after a number of epochs and a further reduction in loss are negligible. An early stopping method which monitors val_loss was used (Figures 32-34).

However, the first sign of no improvement may not be the best time to stop training. This is because the model may get slightly worse before getting much better. We can account for this by adding a delay to the trigger in terms of the number of epochs on which we would like to see no improvement. This can be done by setting the "*patience*" argument.

```
#evaluation of the best model (model with optimal parameters)

stop_early = tf.keras.callbacks.EarlyStopping(monitor='val_loss',
patience=50)
hist = best_model.fit(X_train, Y_train, batch_size=1, epochs=200,
validation_data=(X_val_and_test, Y_val_and_test), verbose=1,
callbacks=[stop_early])
```

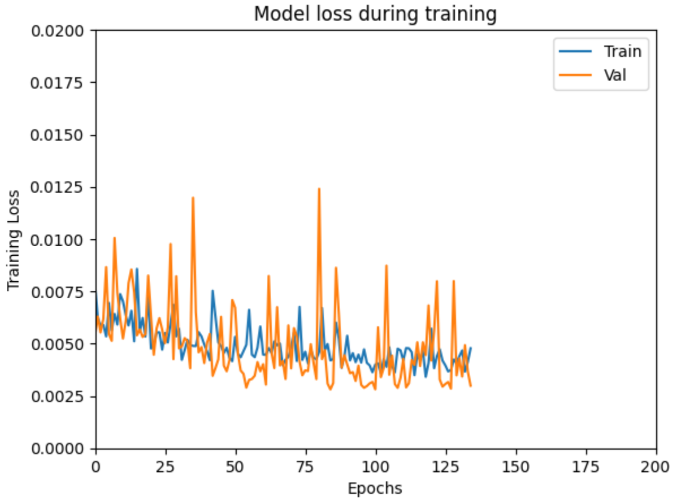


Figure 32: Training model loss v/s Epochs graph (bone model).

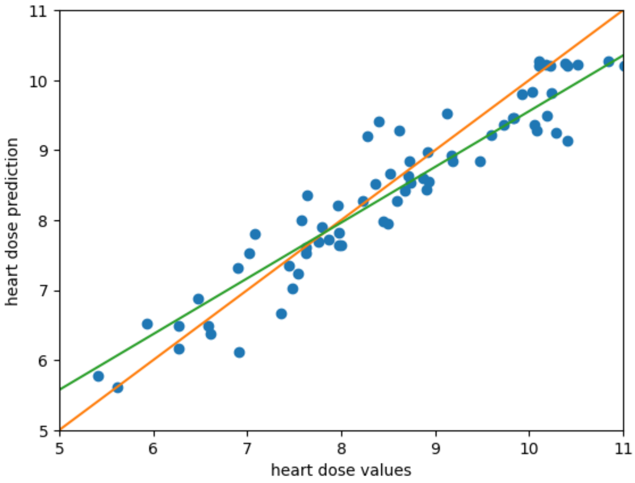


Figure 33: Prediction on the train dataset based on the best model (bone model).

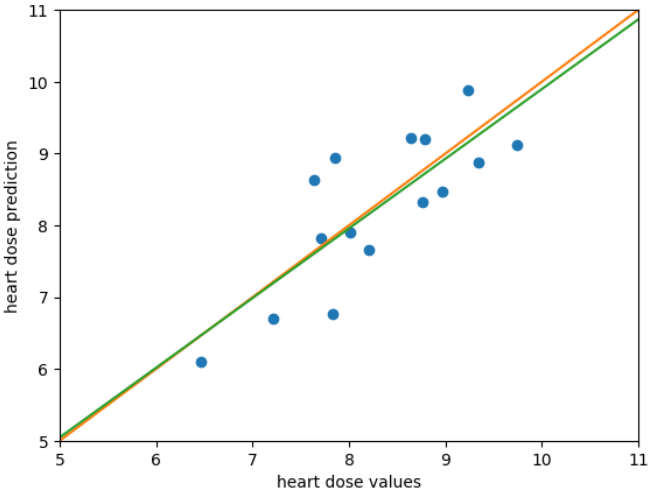
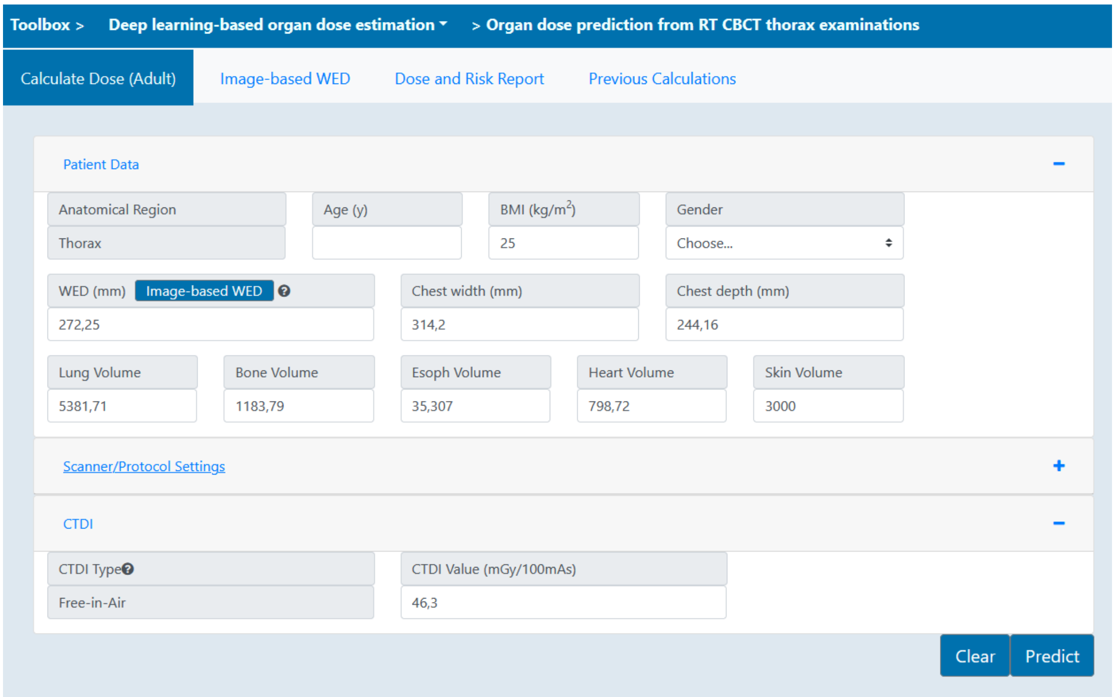


Figure 34: Prediction on the test dataset based on the best model (bone model).

16. iDoseAI organ dose prediction module – Prediction of patient-specific organ doses from thoracic CBCT examinations

In this iDoseAI module, organ doses from CBCT thoracic scans can be predicted using the fitting parameters and dosimetric methodology explained in section 15.


Toolbox > Deep learning-based organ dose estimation > Organ dose prediction from RT CBCT thorax examinations
Calculate Dose (Adult)
Image-based WED
Dose and Risk Report
Previous Calculations
Patient Data
Image-based WED
Scanner/Protocol Settings
CTDI
Clear
Predict

Anatomical Region: Thorax
Age (y):
BMI (kg/m^2): 25
Gender: Choose...
WED (mm): 272,25
Chest width (mm): 314,2
Chest depth (mm): 244,16
Lung Volume: 5381,71
Bone Volume: 1183,79
Esoph Volume: 35,307
Heart Volume: 798,72
Skin Volume: 3000
CTDI Type: Free-in-Air
CTDI Value (mGy/100mAs): 46,3

Figure 35: iDoseAI organ dose estimation tool navigation panels for AI/ML organ prediction module from radiotherapy thoracic CBCT scans.

User input fields are organized into three groups:

- The ‘Patient Data’ group requires basic demographic input (i.e., age and gender), CT scan region (thorax is the only available choice for this AI module), scanning length and WED, which can either be directly inserted as a number or calculated using the automatic WED calculation tool. The user is presented with default organ volume values for AI model independent variables needed, according to patient’s editable BMI value (default BMI value=25).
- In the ‘Scanner/Protocol Settings’ group, users will select the CBCT scanner model (only Elekta XVI available) and corresponding exposure settings (i.e., kV, mAs,). Users will also select the clinical indication for the CT scan.
- In the ‘CTDI Group’, users enter the CTDI type and value for their corresponding scanner.

Each group can appear or disappear on the screen as an “accordion” implementation based on the preference of the user (Figures 30, 31).

Patient Group submenu requires demographic data such as gender and age to be entered. This data is required for organ dosimetry and risk estimation. Water equivalent diameter is needed for correlation absorbed organ dose and patient size characteristics. WED is given in millimeters and can be entered as a value or calculated from user-uploaded CT data utilizing Image-based WEB tab.

Scanner Group submenu requires:

- Selection of CT scanner; Currently only one scanner is available: GE Revolution.
- Tube Voltage: Currently there is one kV selectable, 120 kV.
- mA modulation: For the radiotherapy imaging module, mA modulation is set to NO (fixed current), for all calculations.
- mAs/frame: User can manually enter the mAs/frame of the examination. For Elekta XVI, predefined values are provided according to table 5.
- Beam Collimation:

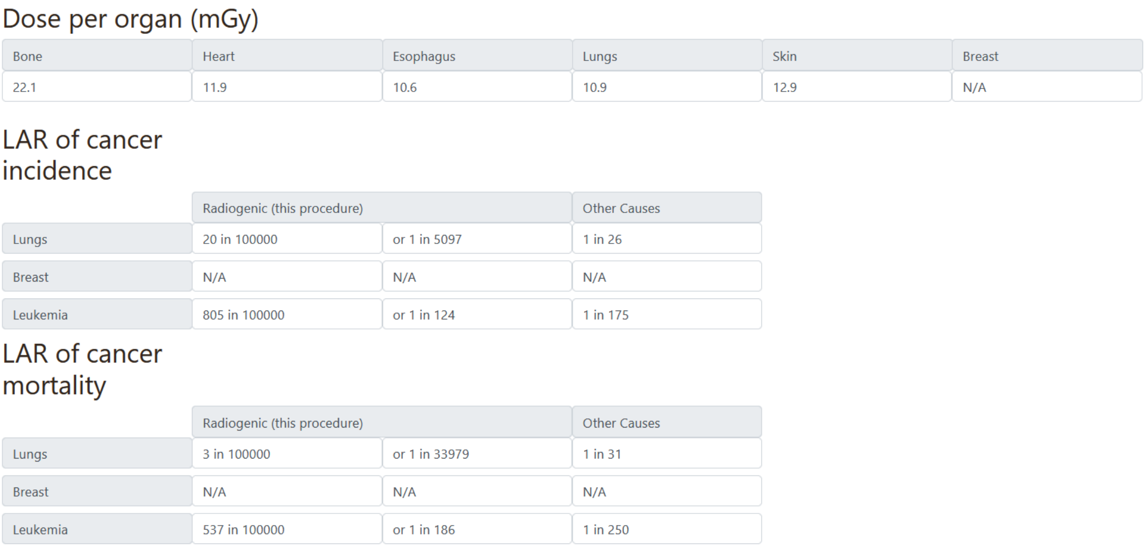
- Frames/roatation: User can specify the number of acquired frames per revolution. For Elekta XVI, predefined values are provided according to table 5.

CTDI Group submenu requires the user to enter CTDI type and value they for their corresponding scanner. CTDI values can be entered in their CTDI-free-in-air form.

17. Dose and Risk report tab

Calculated organ doses from all iDose modules (x-ray imaging, Imaging in Radiotherapy and AI-based predictions) can be used for the assessment of the risk of exposure-induced cancer. The risk estimates are based on the combined absolute and relative risk models of BEIR VII committee (BEIR 2006). The models consider the cancer site, sex, age at the exposure and attained age. Age-dependent mortality rates are used for subsequent assessment of lifetime cancer risk. Risk models are presented for leukaemia and solid cancers in organs that radiation absorbed dose is provided. iDose calculates the risk of exposure-induced death (cancer mortality) for leukaemia and solid cancer for those organs. Also, the user may use the risk calculation module for estimating the cancer risk (cancer incidence) resulting from a predefined single CT exposure.

Many factors, e.g., limitations in epidemiologic data for radiation-induced cancer, contribute to the uncertainty of risk estimation. The BEIR VII committee suggests that the risk estimates should be regarded with a healthy scepticism, placing more emphasis on the magnitude of the risk. The committee estimates that the excess cancer mortality due to radiation can be estimated within a factor of two (at 95% confidence level). For leukaemia the corresponding factor is four. For individual solid cancer sites, the risk estimation may have large uncertainties, up to an order of magnitude or more (BEIR 2006). BEIR VII committee assumes that solid cancers have a latency period of 5 years. For leukaemia the latency period is 2 years.



Dose per organ (mGy)

Bone	Heart	Esophagus	Lungs	Skin	Breast
22.1	11.9	10.6	10.9	12.9	N/A

LAR of cancer incidence

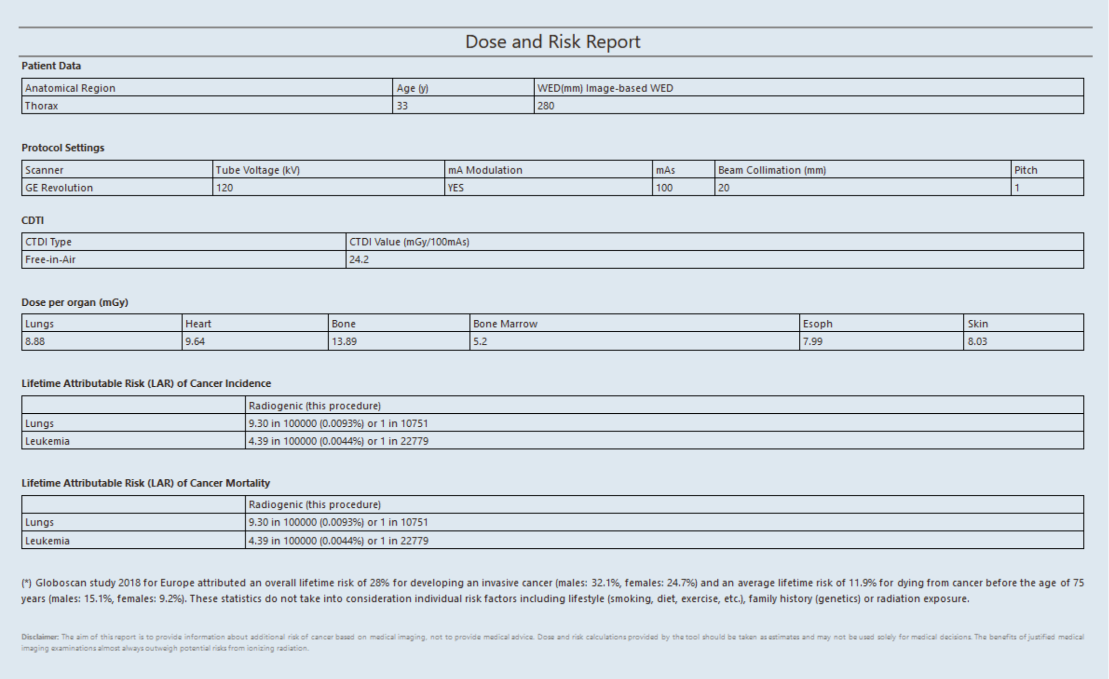
	Radiogenic (this procedure)		Other Causes
Lungs	20 in 100000	or 1 in 5097	1 in 26
Breast	N/A	N/A	N/A
Leukemia	805 in 100000	or 1 in 124	1 in 175

LAR of cancer mortality

	Radiogenic (this procedure)		Other Causes
Lungs	3 in 100000	or 1 in 33979	1 in 31
Breast	N/A	N/A	N/A
Leukemia	537 in 100000	or 1 in 186	1 in 250

Figure 36: iDose organ dose calculation tool - Dose and risk report calculation tab.

iDose software dose and risk report tab provides a summary of the absorbed dose per organ in mGy for each primarily irradiated thorax organ, as well as values of lifetime attributable risk for exposure-induced death (LAR for Lifetime cancer mortality) and lifetime attributable risk for cancer incidence (LAR for Lifetime cancer incidence). In addition to the radiogenic risks provided for the specific CT exposures, the software provides the corresponding LARs for cancer incidence and mortality for all causes (including radiogenic) as presented for the 40 countries in the four United Nations-defined areas of Europe and for Europe and the European Union (Ferlay, 2018).



Dose and Risk Report

Patient Data

Anatomical Region	Age (y)	WED(mm) Image-based WED
Thorax	33	280

Protocol Settings

Scanner	Tube Voltage (kV)	mA Modulation	mAs	Beam Collimation (mm)	Pitch
GE Revolution	120	YES	100	20	1

CDTI

CTDI Type	CTDI Value (mGy/100mAs)
Free-in-Air	24.2

Dose per organ (mGy)

Lungs	Heart	Bone	Bone Marrow	Esoph	Skin
8.88	9.64	13.89	5.2	7.99	8.03

Lifetime Attributable Risk (LAR) of Cancer Incidence

	Radiogenic (this procedure)
Lungs	9.30 in 100000 (0.0093%) or 1 in 10751
Leukemia	4.39 in 100000 (0.0044%) or 1 in 22779

Lifetime Attributable Risk (LAR) of Cancer Mortality

	Radiogenic (this procedure)
Lungs	9.30 in 100000 (0.0093%) or 1 in 10751
Leukemia	4.39 in 100000 (0.0044%) or 1 in 22779

(*) Globoscan study 2018 for Europe attributed an overall lifetime risk of 28% for developing an invasive cancer (males: 32.1%, females: 24.7%) and an average lifetime risk of 11.9% for dying from cancer before the age of 75 years (males: 15.1%, females: 9.2%). These statistics do not take into consideration individual risk factors including lifestyle (smoking, diet, exercise, etc.), family history (genetics) or radiation exposure.

Disclaimer: The aim of this report is to provide information about additional risk of cancer based on medical imaging, not to provide medical advice. Dose and risk calculations provided by the tool should be taken as estimates and may not be used solely for medical decisions. The benefits of justified medical imaging examinations almost always outweigh potential risks from ionizing radiation.

Figure 37: iDose Dose and Risk Report example.

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19. Appendix - Hyperparameters Optimization Algorithms parametrization

Random Search Algorithm – model constructor parameters

kerastuner.tuners.randomsearch.RandomSearch(hypermodel, objective, max_trials, seed=None,

hyperparameters=None, tune_new_entries=True, allow_new_entries=True, **kwargs)

- • The hypermodel parameter accepts an instance of the HyperModel class or a callable that takes hyperparameters and returns a compiled model. An example callable has been created above, which will be provided to this parameter. Alternatively, a class can be created that extends the HyperModel class and has a build() method that functions similarly to the callable mentioned earlier (taking hyperparameters and returning a compiled model). An instance of that class can then be passed to this parameter.
- • The objective parameter accepts either a string value representing an Objective instance that specifies the objective function to optimize, or an instance of the Objective class itself. When a string value is provided, the Keras tuner will infer whether to minimize or maximize the objective function. For example, if 'accuracy' is given as the value, the tuner will attempt to maximize training accuracy, while 'val_loss' will be minimized. Any string metric or loss name can be used for this parameter, such as 'val_loss', 'loss', 'mean_squared_error', etc. However, when using a custom metric or loss and the tuner cannot determine whether to minimize or maximize it automatically, an instance of Objective should be provided. The Objective() constructor requires two arguments:

  name: The name of the metric to monitor.

  direction: A string specifying the direction of optimization, where 'min' indicates minimizing and 'max' indicates maximizing.
- The max_trials parameter accepts an integer value that specifies the number of different hyperparameter settings to try during the optimization process.
- The seed parameter is a random seed that can be set to reproduce the same results.
- The hyperparameters parameter is optional and accepts instances of HyperParameters. It can be used to override the default settings when creating a function that builds the network. More information on its usage will be explained later.
- The optimizer parameter is optional and allows for the use of optimizers that override the one specified in the model creation method.
- The loss parameter is optional and accepts a loss function that can override the one already specified in the model creation method.
- The metrics parameter is optional and accepts a list of metrics that can override the ones already specified in the model creation method.
- The directory parameter accepts a relative path specifying where the work should be saved when the tuner explores various hyperparameter settings. By default, it is set to the current directory.
- The project_name parameter specifies the name of the project. A folder with this name will be created, and all progress during the optimization process will be stored there. If multiple

optimizations are being performed simultaneously, a different value should be provided for each tuner to ensure separate project folders. Unique names have been given to all our tuners.

- The overwrite parameter is optional and accepts a boolean value that determines whether to reload an existing project with the same name if one exists. The default value is False.

Bayesian Optimisation Algorithm - model constructor parameters

kerastuner.tuners.bayesian.BayesianOptimization(hypermodel, objective, max_trials,
num_initial_points=2, seed=None,

hyperparameters=None, tune_new_entries=True, allow_new_entries=True, **kwargs)

- hypermodel: Instance of HyperModel class (or callable that takes hyperparameters and returns a Model instance).
- objective: String. Name of model metric to minimize or maximize, e.g. "val_accuracy".
- max_trials: Int. Total number of trials (model configurations) to test at most. Note that the oracle may interrupt the search before max_trial models have been tested if the search space has been exhausted.
- num_initial_points: Int. The number of randomly generated samples as initial training data for Bayesian optimization.
- alpha: Float or array-like. Value added to the diagonal of the kernel matrix during fitting.
- beta: Float. The balancing factor of exploration and exploitation. The larger it is, the more explorative it is.
- seed: Int. Random seed.
- hyperparameters: HyperParameters class instance. Used to override (or register in advance) hyperparamters in the search space.
- tune_new_entries: Whether hyperparameter entries that are requested by the hypermodel but that were not specified in hyperparameters should be added to the search space, or not. If not, then the default value for these parameters will be used.
- allow_new_entries: Whether the hypermodel is allowed to request hyperparameter entries not listed in hyperparameters.

**kwargs: Keyword arguments relevant to all Tuner subclasses. Please see the docstring for Tuner.

Hyperband Optimization Algorithm - model constructor parameters

kerastuner.tuners.hyperband.Hyperband(hypermodel, objective, max_epochs, factor=3,
hyperband_iterations=1, seed=None,

hyperparameters=None, tune_new_entries=True, allow_new_entries=True, **kwargs)

- hypermodel: Keras tuner class that allows you to create and develop models using a searchable space.
- objective: It is the loss function for the model described in the hypermodel, such as 'mse' or 'val_loss'. It has the data type string. If the parameter is a string, the optimization direction (minimum or maximum) will be inferred. If we have a list of objectives, we will minimize the sum of all the objectives to minimize while maximizing the total of all the objectives to maximize.
- max_epochs: The number of epochs required to train a single model. Setting this to a value somewhat greater than the estimated epochs to convergence for your biggest Model and using early halting during training is advised. The default value is 100.
- factor: Integer, the reduction factor for the number of epochs and number of models for each bracket. Defaults to 3.
- hyperband_iterations: The number of times the Hyperband algorithm is iterated over. Across all trials, one iteration will run about max epochs * (math.log(max epochs, factor) ** 2) cumulative epochs. Set this to the highest figure that fits within your resource budget. The default value is 1.
- seed: An optional integer that serves as the random seed.
- hyperparameters: HyperParameters instance that is optional. Can be used to override (or pre-register) search space hyperparameters.
- tune new entries: Boolean indicating whether or not hyperparameter entries required by the hypermodel but not defined in hyperparameters should be included in the search space. If this is not the case, the default values for these parameters will be utilized. True is the default value.
- allow new entries: The hypermodel is permitted to request hyperparameter entries that are not mentioned in hyperparameters. True is the default value.