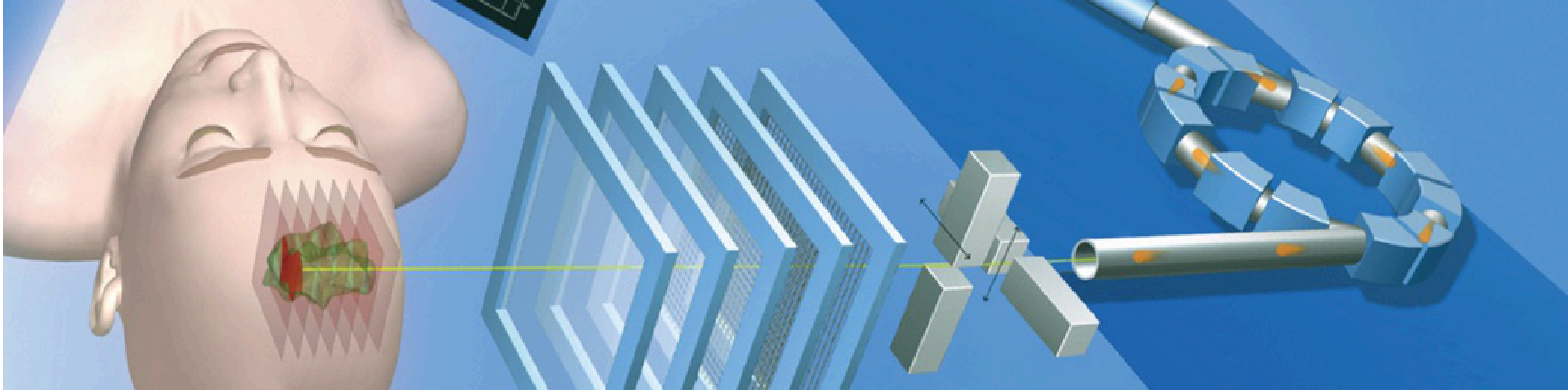


MATRAD

Riccardo.Ridolfi@bo.infn.it

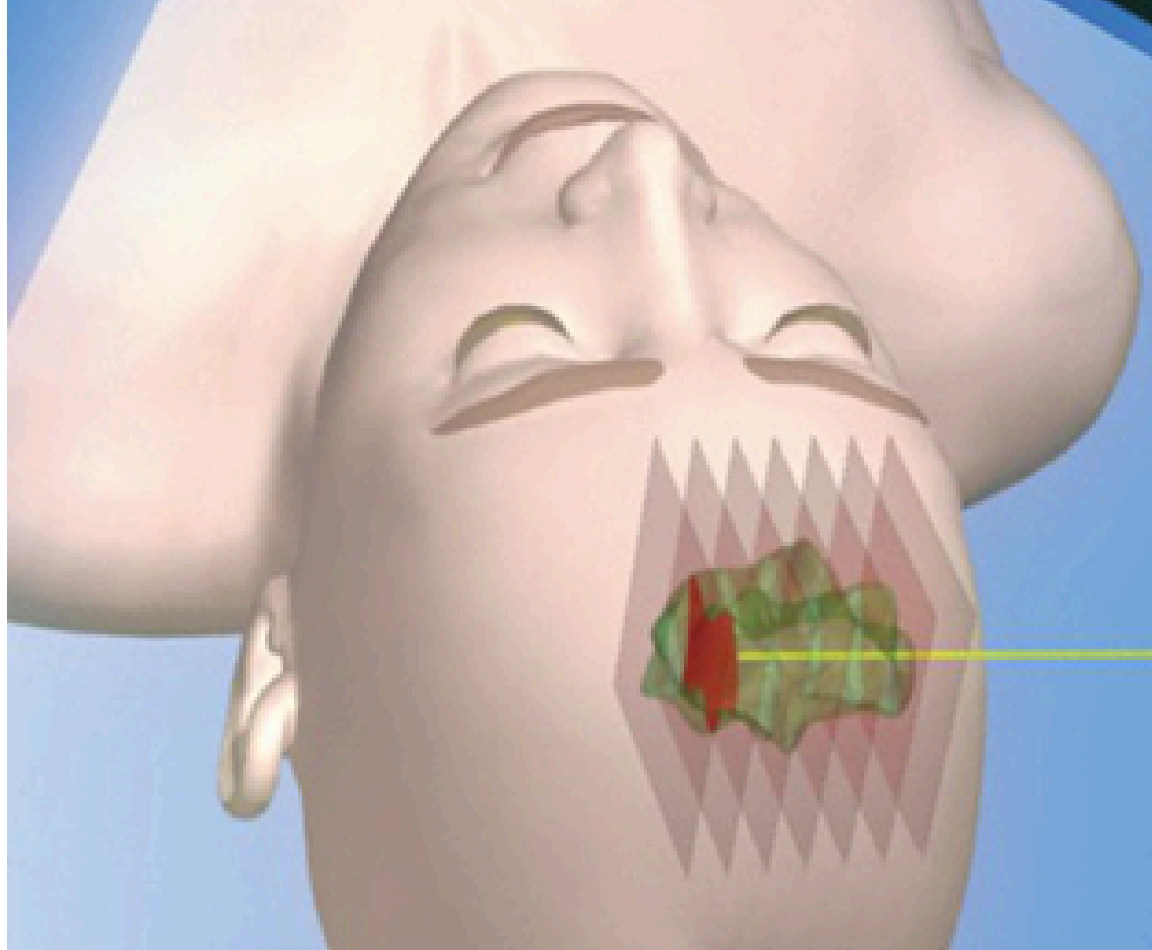




MATRAD is an open source software simulating a *treatment planning system* written in MATLAB

DKFZ is its main developer

Not used in clinical practice but very reliable



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A few keywords before starting...

GTV

TUMOUR VOLUME VISIBLE
FROM CT/MRI

PTV

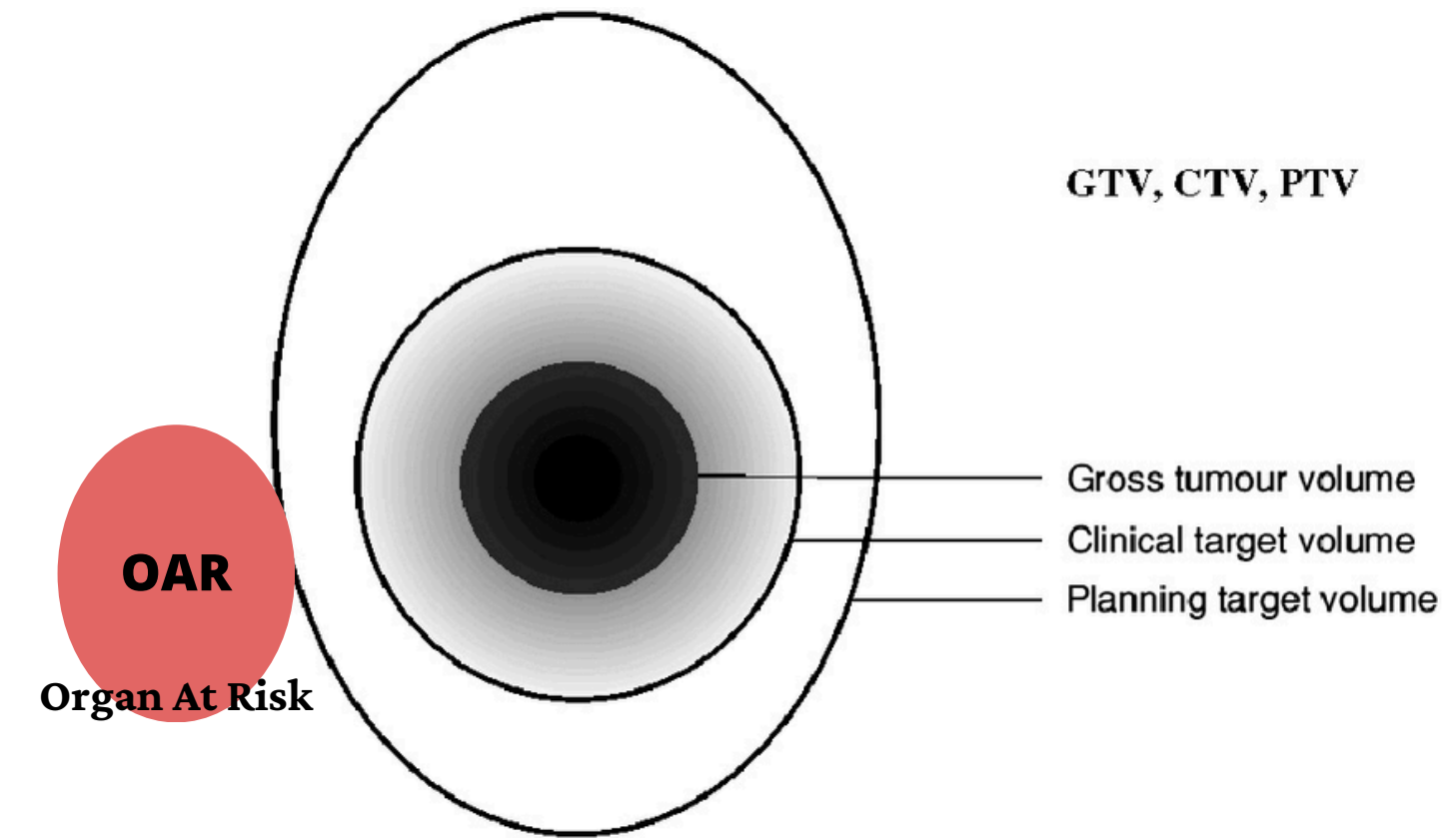
VOLUME TO BE IRRADIATED (CTV +
UNCERTAINTIES)

CTV

VOLUME WHERE THERE COULD BE
CANCER CELLS EVEN IF NOT VISIBLE

OAR

ORGAN SENSITIVE TO RADIATION THAT
MUST BE SPARED AS MUCH AS
POSSIBLE



A few keywords before starting...

GTV

TUMOUR VOLUME VISIBLE FROM CT/MRI

PTV

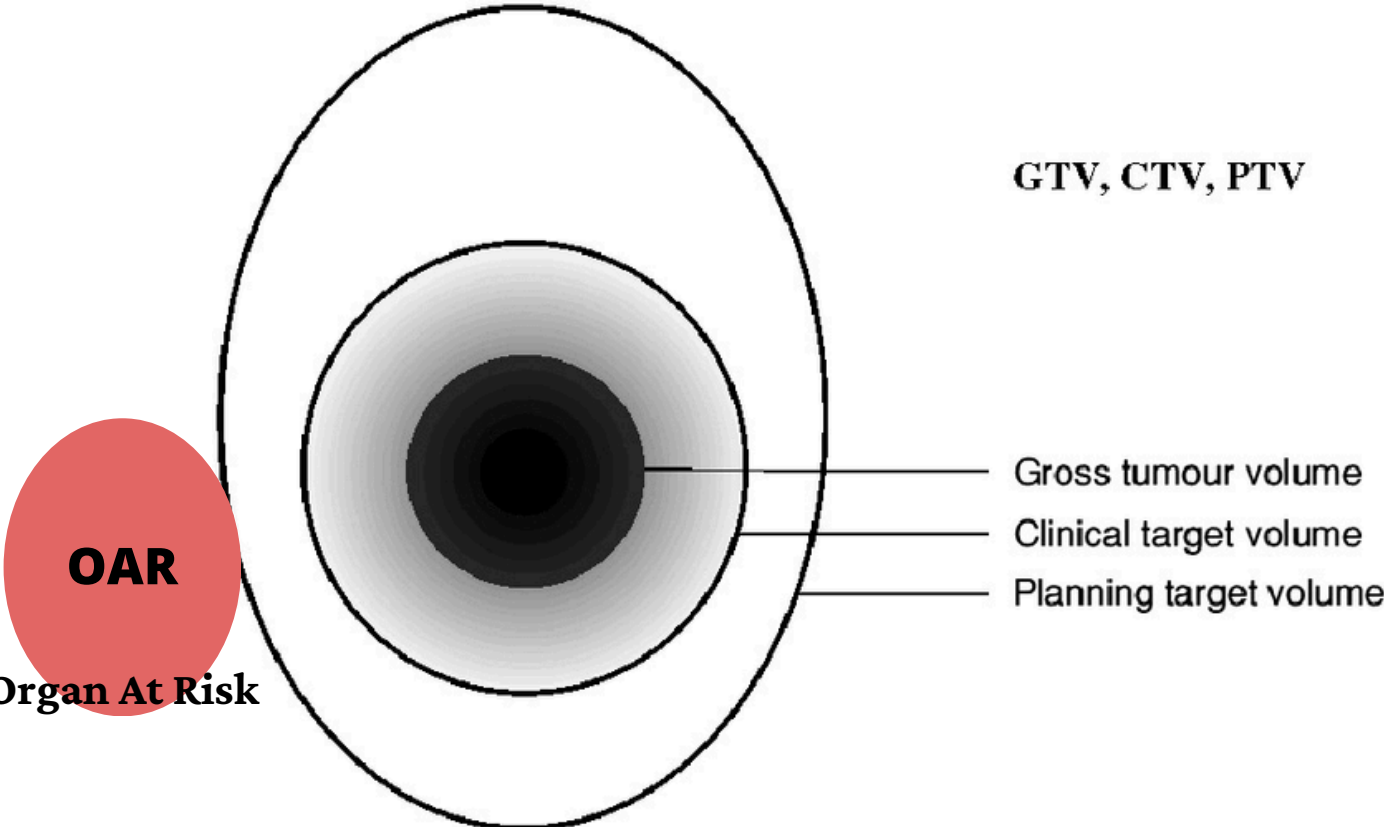
VOLUME TO BE IRRADIATED (CTV + UNCERTAINTIES)

CTV

VOLUME WHERE THERE COULD BE CANCER CELLS EVEN IF NOT VISIBLE

OAR

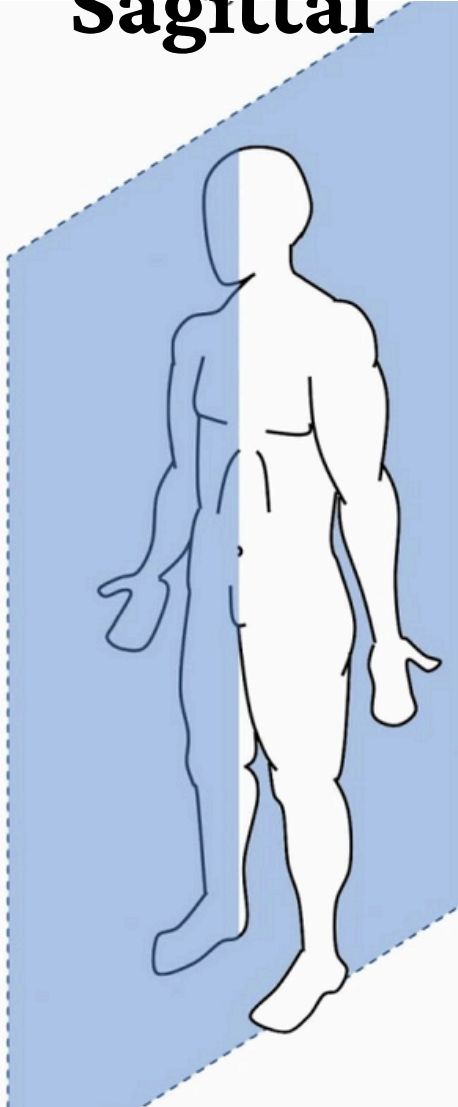
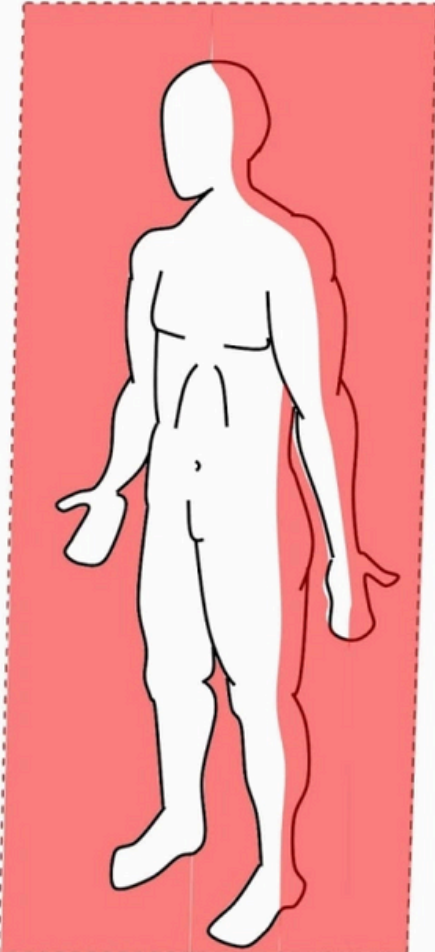
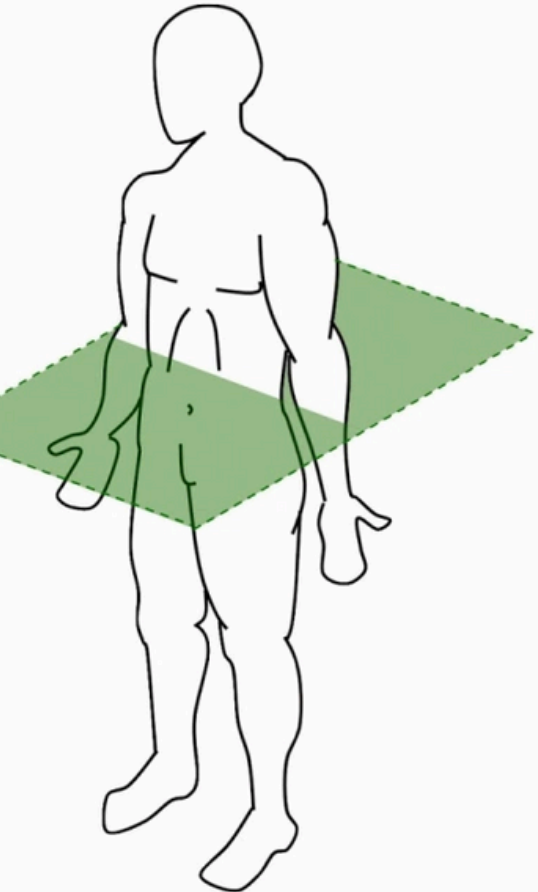
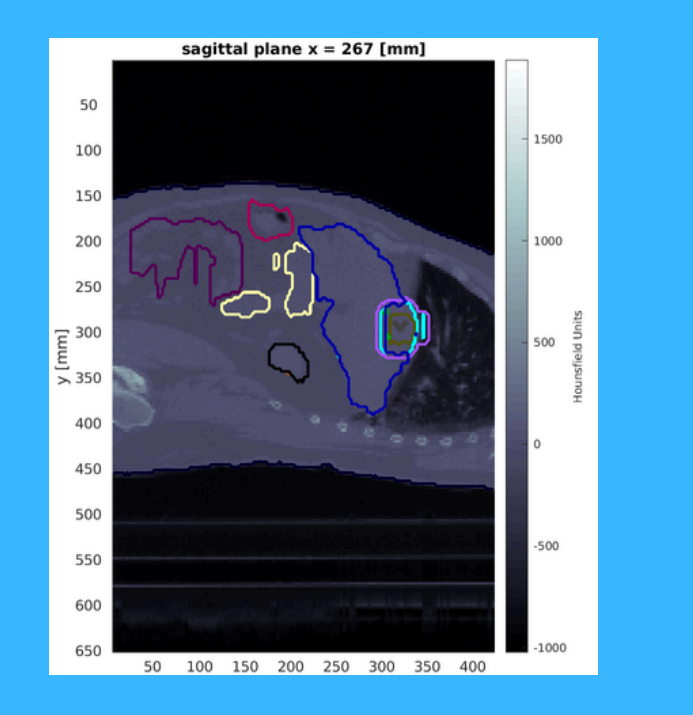
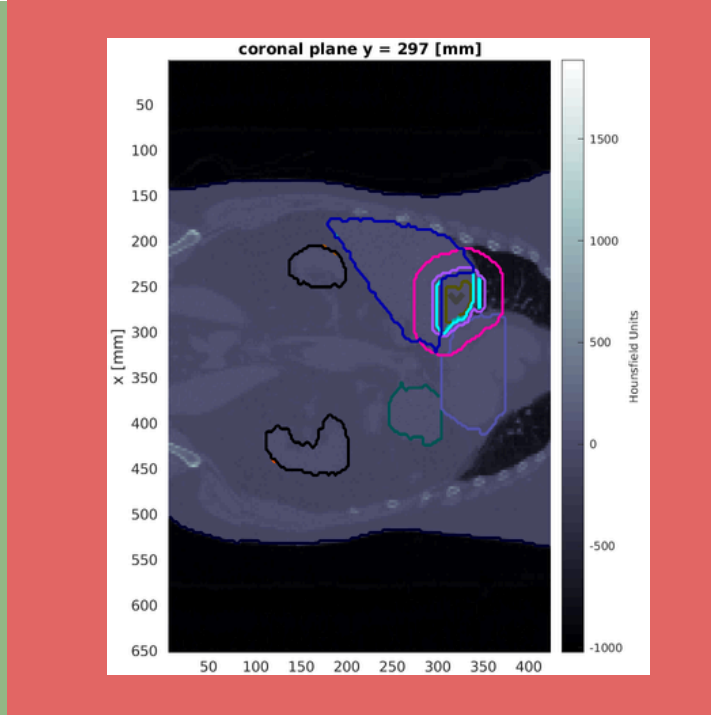
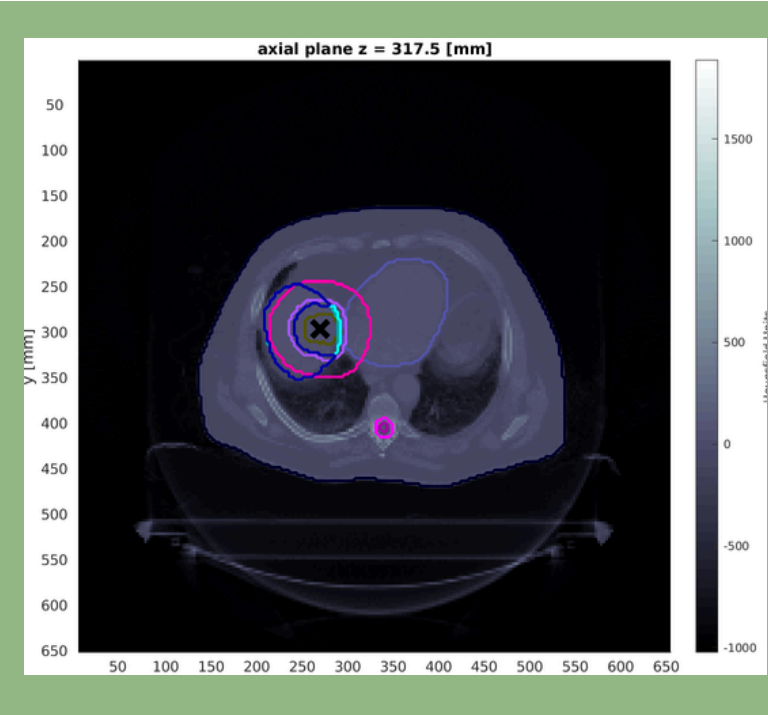
ORGAN SENSITIVE TO RADIATION THAT MUST BE SPARED AS MUCH AS POSSIBLE

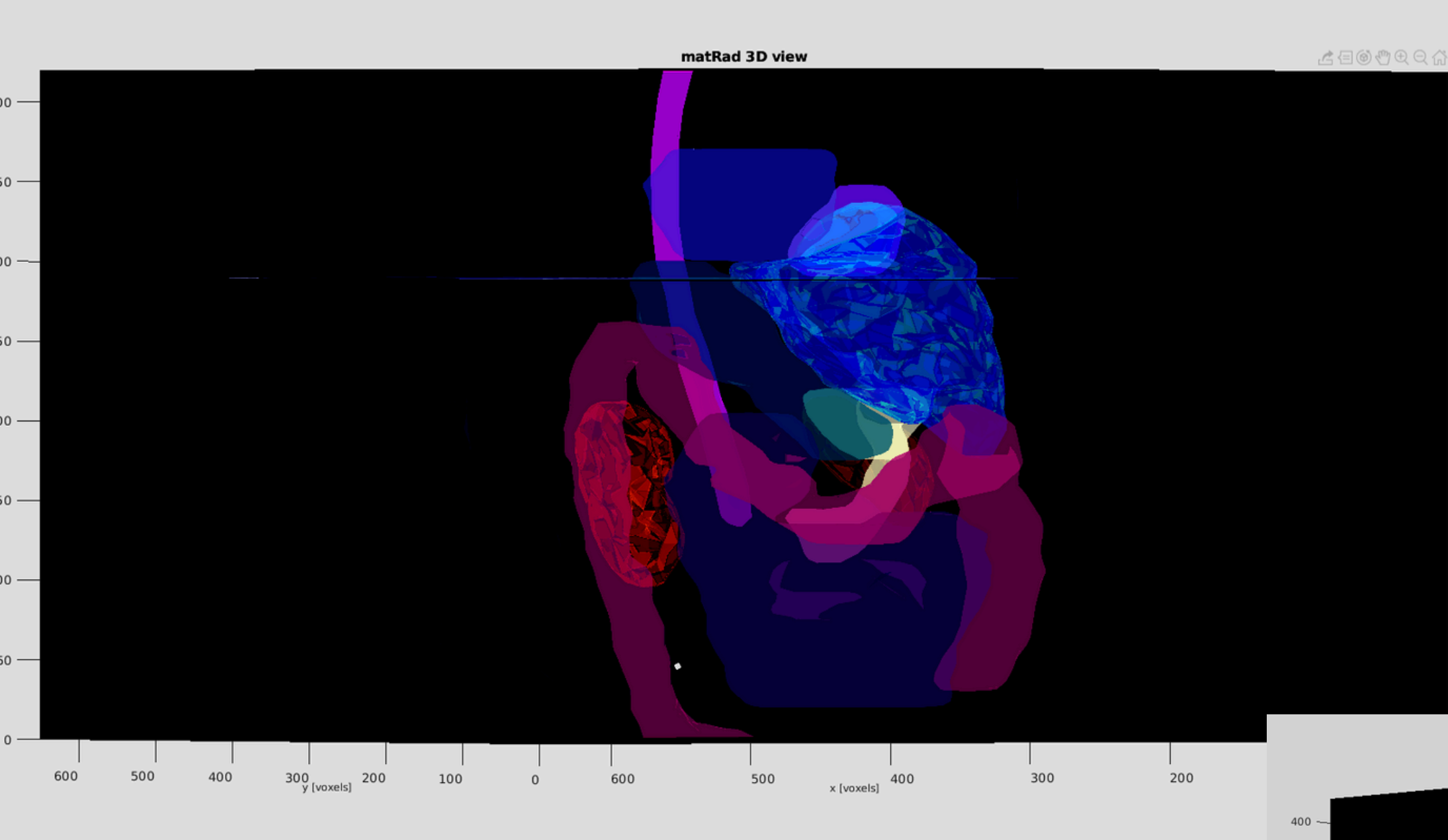


Axial

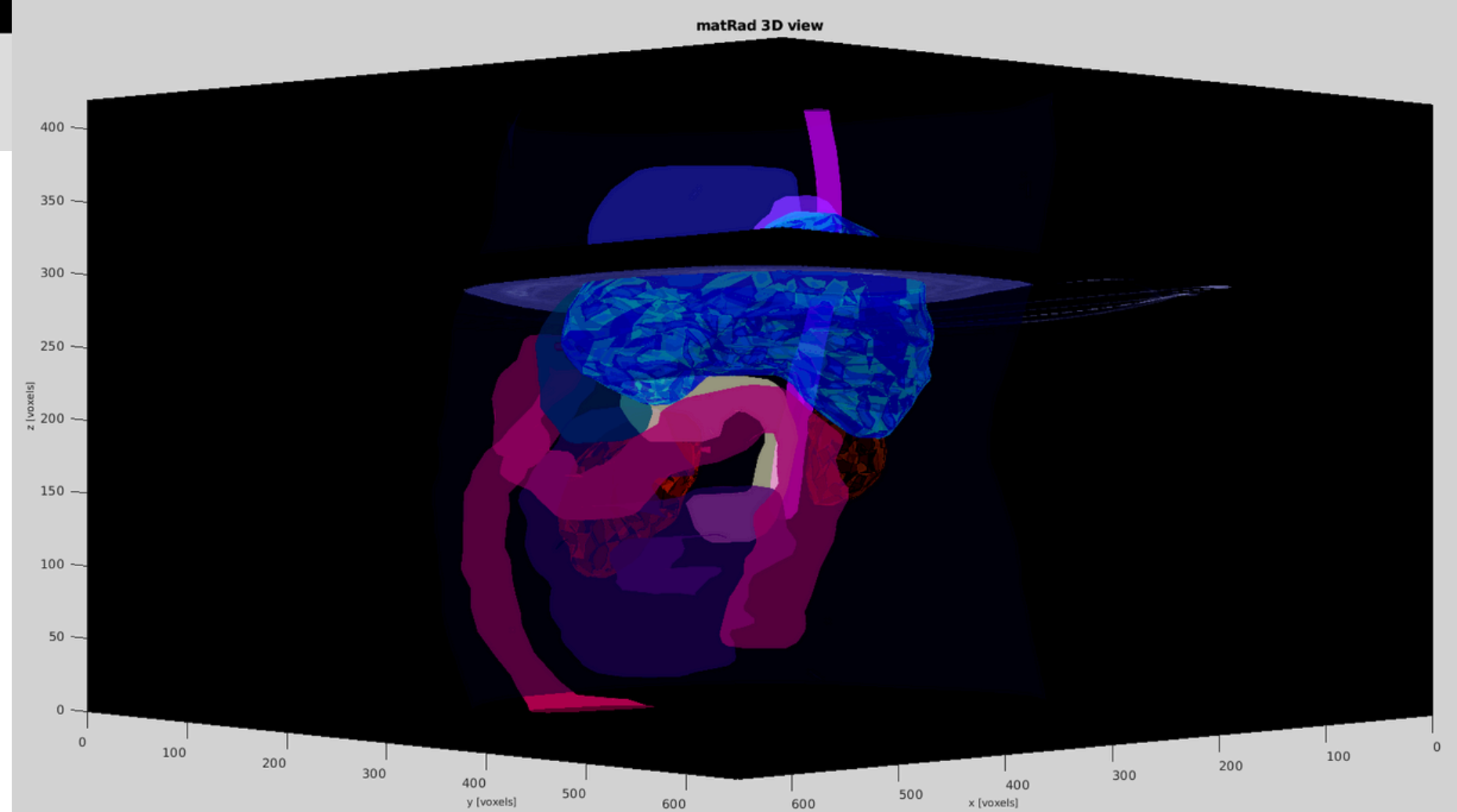
Coronal

Sagittal





3D view





Workflow

Refresh Load *.mat data Calc. influence Mx Optimize Save to GUI

Load DICOM Recalc Export

Import from Binary Import Dose

Status: no data loaded

Plan

bixel width in [mm]

Gantry Angle in ° 3D conformal

Couch Angle in ° Run Sequencing

Radiation Mode Stratification Levels

Machine Run Direct Aperture Optimization

IsoCenter in [mm] Auto.

Fractions

Type of optimization

Objectives & constraints

Visualization

Slice Selection Type of plot GoTo plot CT

Beam Selection Plane Selection plot contour

Offset Display option plot isolines

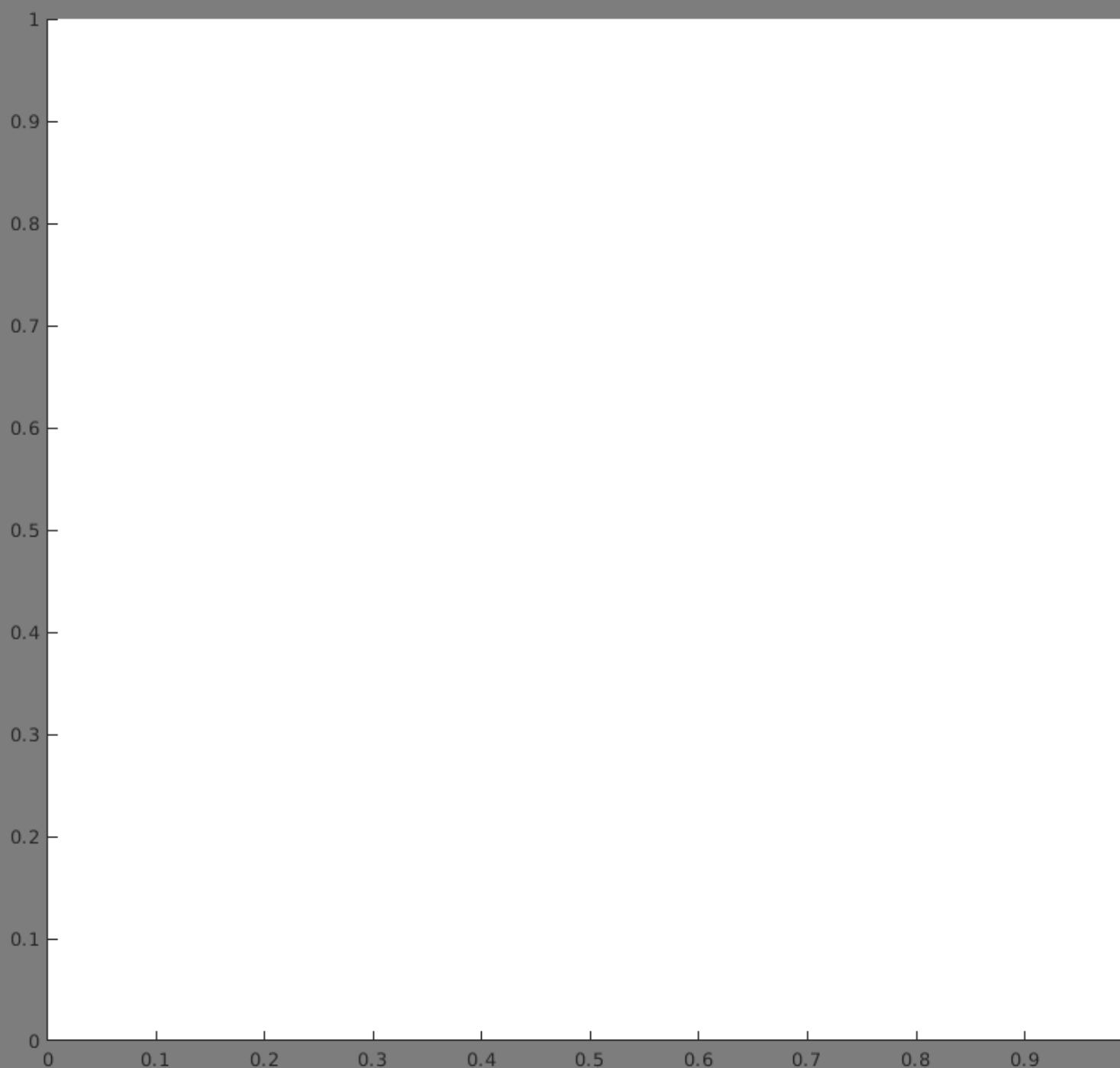
 plot dose

plot isolines labels

plot iso center

visualize plan / beams

Viewing



min value: -

max -

Viewer Options

No available Window

Window Center:

Window Width:

Range:

Lock Settings

Dose opacity:

Structure Visibility

Info

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Workflow

Refresh Load *.mat data Calc. influence Mx Optimize Save to GUI
 Load DICOM Recalc Export
 Import Dose

no data loaded

Plan

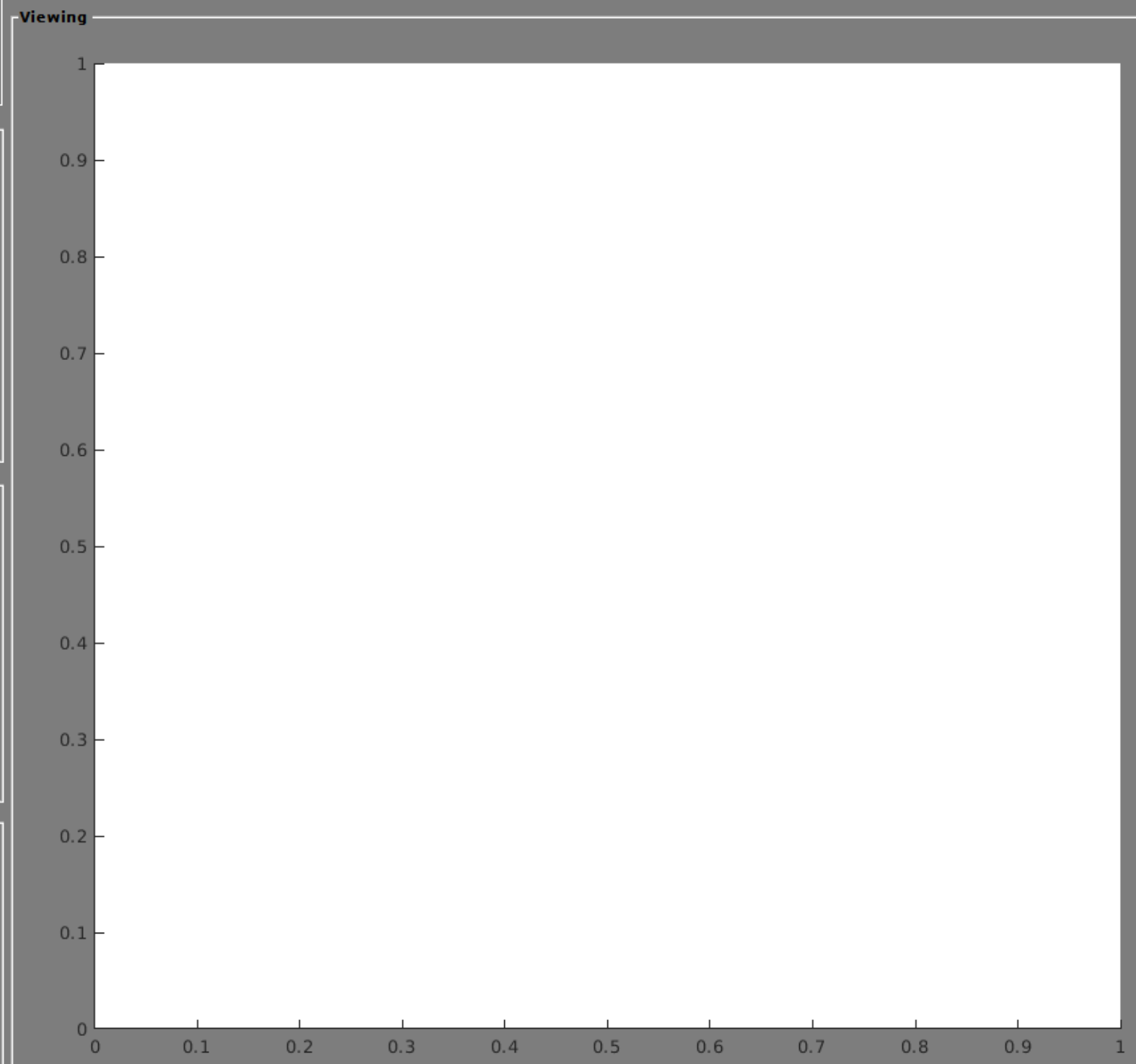
bixel width in [mm] 5
 Gantry Angle in ° 0
 Couch Angle in ° 0
 Radiation Mode photons
 Machine Generic
 IsoCenter in [mm] 0 0 0 Auto.
 # Fractions 30
 Type of optimization none

Run conformal
 Run Sequencing
 Stratification Levels 7
 Run Direct Aperture Optimization

Objectives & constraints

Visualization

Slice Selection Type of plot intensity GoTo lateral plot CT
 Beam Selection Plane Selection axial plot contour
 Offset Display option no option available plot isolines
 plot dose
 plot isolines labels
 plot iso center
 visualize plan / beams



min value: -
 max: -

Viewer Options

None
 No available Window
 Window Center: 0.5
 Window Width: 1.0
 Range: 0 1
 bone
 Lock Settings
 Dose opacity: 1

Structure Visibility

no data loaded

Info

v2.10.1 "Blaise"
 www.matRad.org

Let's start: plan

bixel width

mesh size for the
dose calculation
(do not change)

gantry and couch angle

two sorted lists of
angles for the gantry
and for the couch
(from 0° to 360°)

radiation mode

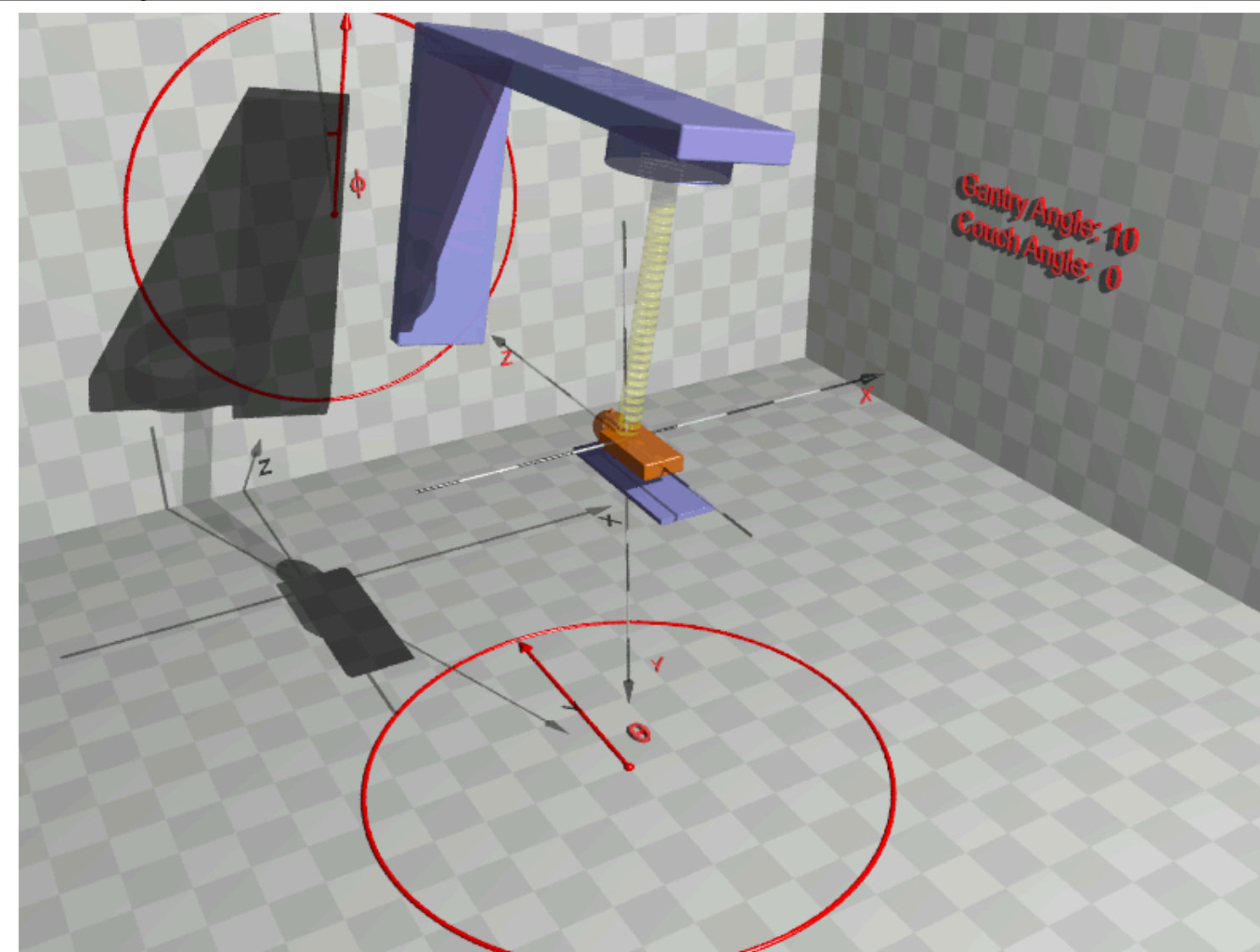
particle to be used in
the treatment
(photons, protons,
carbon ions)

isocenter

focus of particle
beam, tick "Auto"

Plan

bixel width in [mm]	<input type="text" value="5"/>	
Gantry Angle in °	<input type="text" value="0"/>	<input type="radio"/> 3D conformal
Couch Angle in °	<input type="text" value="0"/>	<input type="radio"/> Run Sequencing
Radiation Mode	<input type="text" value="photons"/>	Stratification Levels
Machine	<input type="text" value="Generic"/>	<input type="text" value="7"/>
IsoCenter in [mm]	<input type="text" value="0 0 0"/> <input type="checkbox"/> Auto.	<input type="radio"/> Run Direct Aperture Optimization
# Fractions	<input type="text" value="30"/>	
Type of optimization	<input type="text" value="none"/>	<input type="button" value="Set Tissue"/>



Let's start: plan

bixel width

mesh size for the
dose calculation
(do not change)

gantry and couch angle

two sorted lists of
angles for the gantry
and for the couch
(from 0° to 360°)

radiation mode

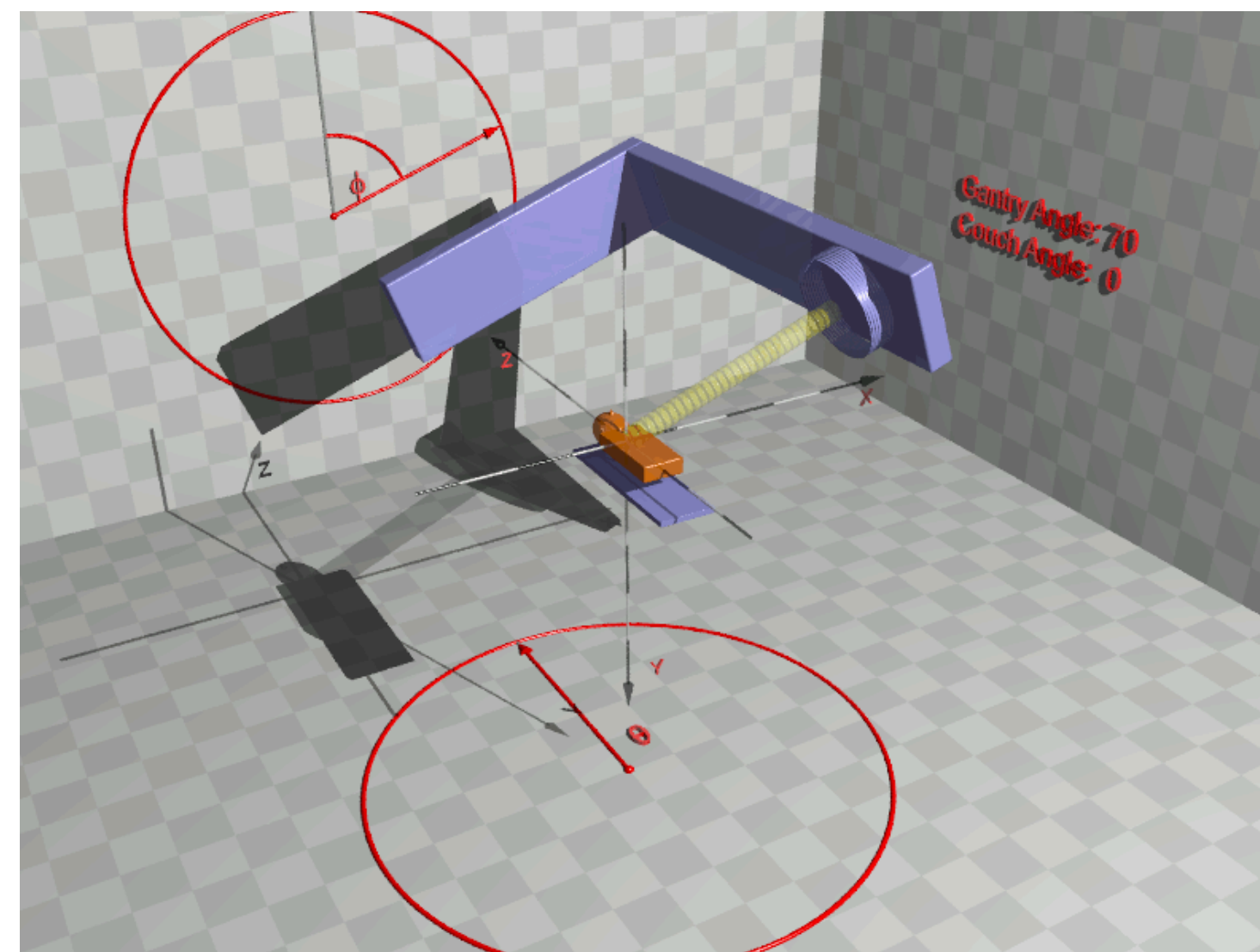
particle to be used in
the treatment
(photons, protons,
carbon ions)

isocenter

focus of particle
beam, tick "Auto"

Plan

bixel width in [mm]	<input type="text" value="5"/>	
Gantry Angle in °	<input type="text" value="0"/>	<input type="radio"/> 3D conformal
Couch Angle in °	<input type="text" value="0"/>	<input type="radio"/> Run Sequencing
Radiation Mode	<input type="text" value="photons"/>	Stratification Levels
Machine	<input type="text" value="Generic"/>	<input type="text" value="7"/>
IsoCenter in [mm]	<input type="text" value="0 0 0"/> <input type="checkbox"/> Auto.	<input type="radio"/> Run Direct Aperture Optimization
# Fractions	<input type="text" value="30"/>	
Type of optimization	<input type="text" value="none"/>	<input type="button" value="Set Tissue"/>



Let's start: plan

bixel width

mesh size for the
dose calculation
(do not change)

gantry and couch angle

two sorted lists of
angles for the gantry
and for the couch
(from 0° to 360°)

radiation mode

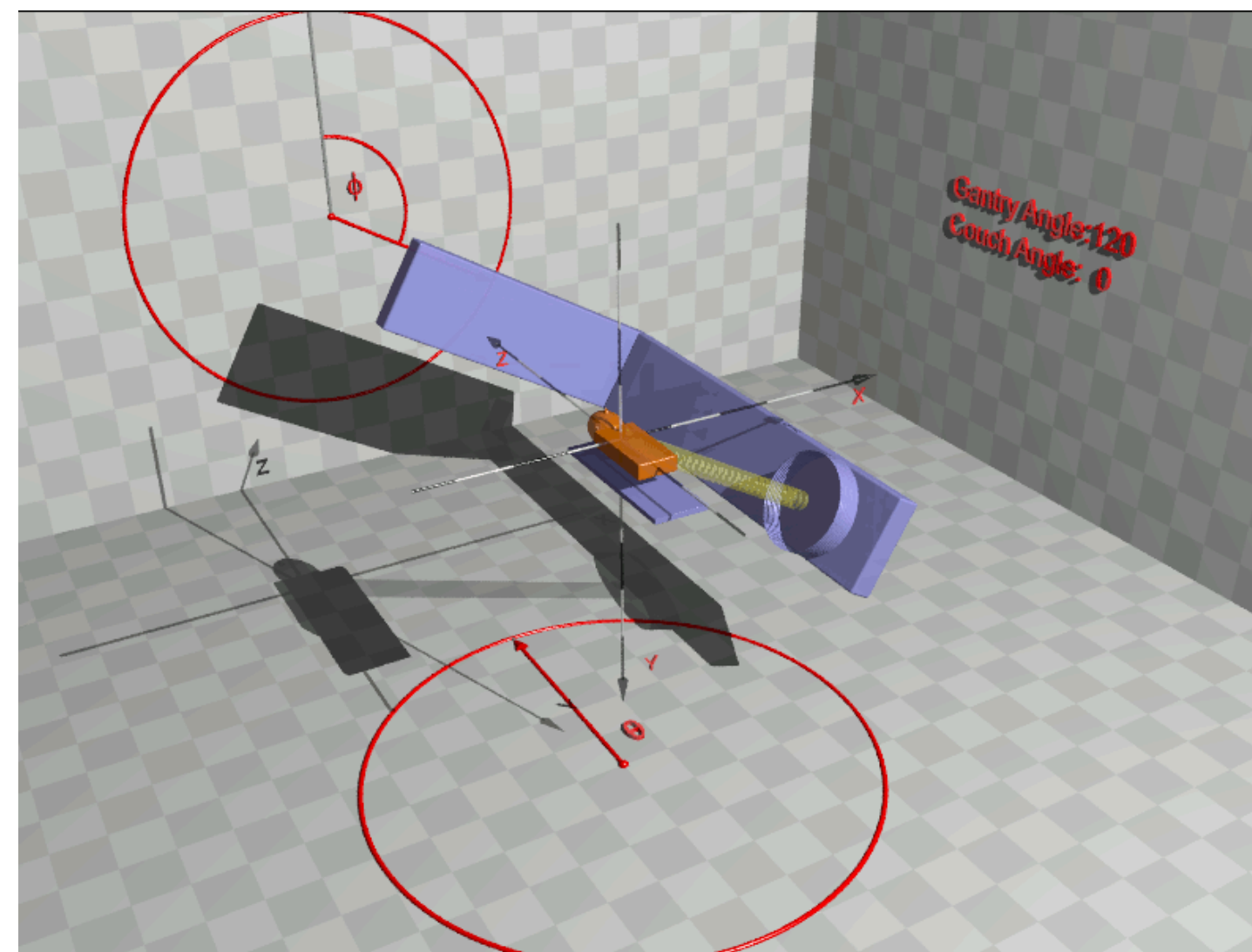
particle to be used in
the treatment
(photons, protons,
carbon ions)

isocenter

focus of particle
beam, tick "Auto"

Plan

bixel width in [mm]	<input type="text" value="5"/>	
Gantry Angle in °	<input type="text" value="0"/>	<input type="radio"/> 3D conformal
Couch Angle in °	<input type="text" value="0"/>	<input type="radio"/> Run Sequencing
Radiation Mode	<input type="text" value="photons"/>	Stratification Levels
Machine	<input type="text" value="Generic"/>	<input type="text" value="7"/>
IsoCenter in [mm]	<input type="text" value="0 0 0"/> <input type="checkbox"/> Auto.	<input type="radio"/> Run Direct Aperture Optimization
# Fractions	<input type="text" value="30"/>	
Type of optimization	<input type="text" value="none"/>	<input type="button" value="Set Tissue"/>



Let's start: plan

bixel width

mesh size for the
dose calculation
(do not change)

gantry and couch angle

two sorted lists of
angles for the gantry
and for the couch
(from 0° to 360°)

radiation mode

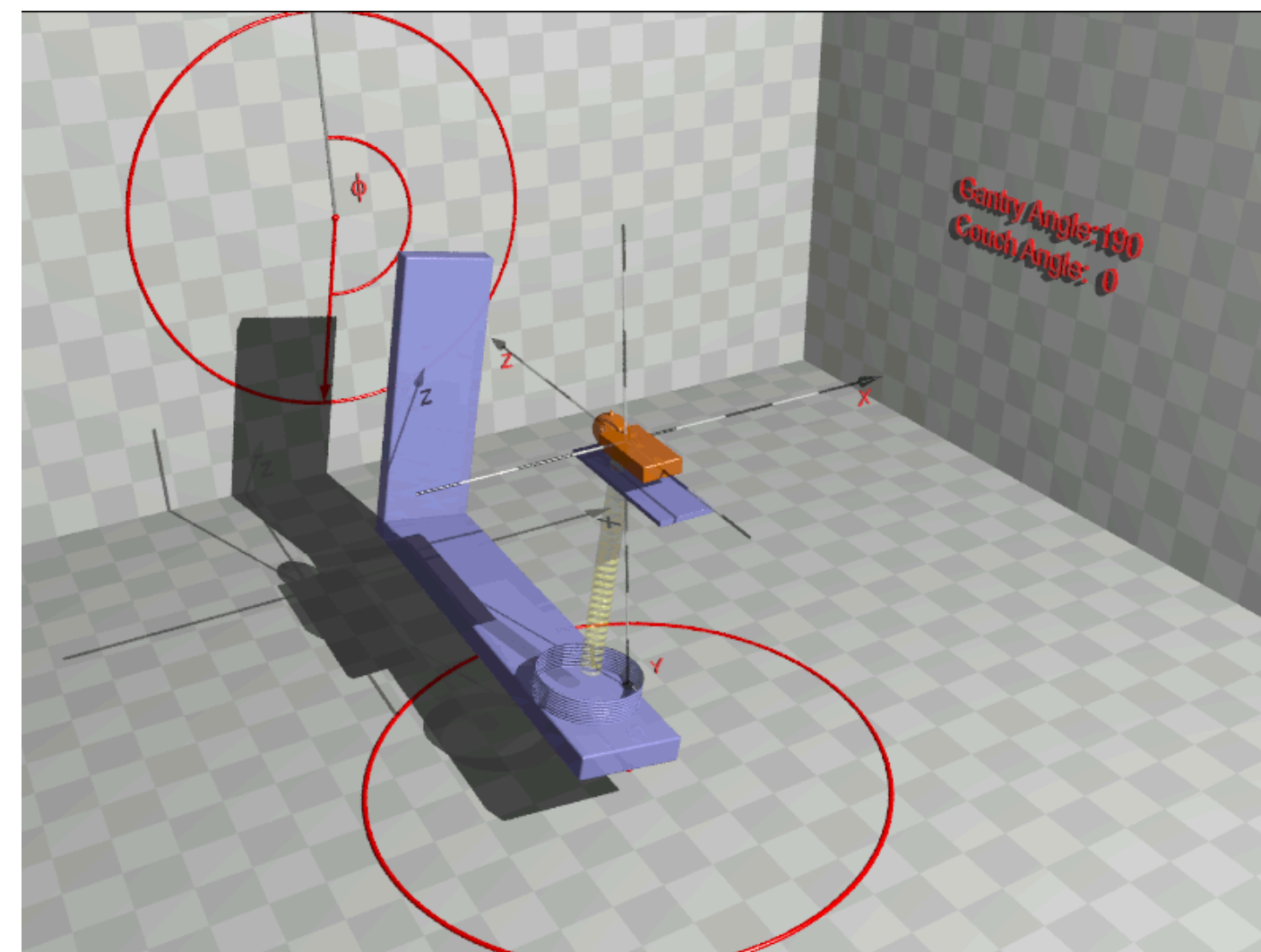
particle to be used in
the treatment
(photons, protons,
carbon ions)

isocenter

focus of particle
beam, tick "Auto"

Plan

bixel width in [mm]	<input type="text" value="5"/>	
Gantry Angle in °	<input type="text" value="0"/>	<input type="radio"/> 3D conformal
Couch Angle in °	<input type="text" value="0"/>	<input type="radio"/> Run Sequencing
Radiation Mode	<input type="text" value="photons"/>	Stratification Levels
Machine	<input type="text" value="Generic"/>	<input type="text" value="7"/>
IsoCenter in [mm]	<input type="text" value="0 0 0"/> <input type="checkbox"/> Auto.	<input type="radio"/> Run Direct Aperture Optimization
# Fractions	<input type="text" value="30"/>	
Type of optimization	<input type="text" value="none"/>	<input type="button" value="Set Tissue"/>



Workflow

Refresh Load *.mat data Calc. influence Mx Optimize Save to GUI

Load DICOM Recalc Export

Import from Binary Import Dose

Status: no data loaded

Plan

Level width in [mm]

Gantry Angle in 3D conformal

Couch Angle in Run Sequencing

Radiation Mode: photons Stratification Levels: 7

Machine: Generic Run Direct Aperture Optimization

IsoCenter in [mm]: 0 0 0 Auto.

Fractions: 30

Type of optimization: none

Objectives & constraints

Visualization

Slice Selection:

Beam Selection:

Offset:

Type of plot: intensity GoTo: lateral plot CT

Plane Selection: axial plot contour

Display option: no option available plot isolines

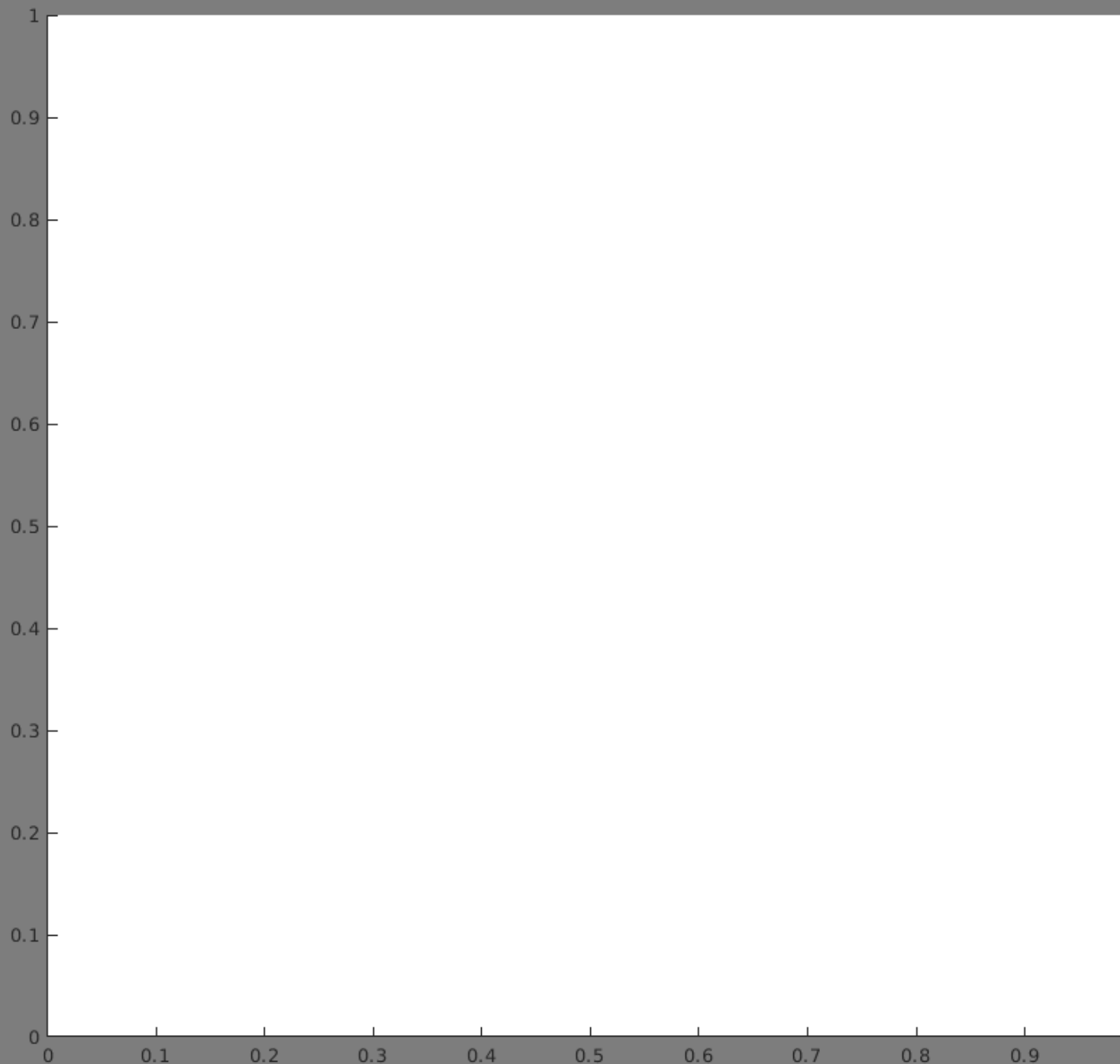
 plot dose

plot isolines labels

plot iso center

visualize plan / beams

Viewing



min value: -

max: -

Viewer Options

None

No available Window

Window Center: 0.5

Window Width: 1.0

Range: 0.1

bone

Lock Settings

Dose opacity: 1

Structure Visibility

no data loaded

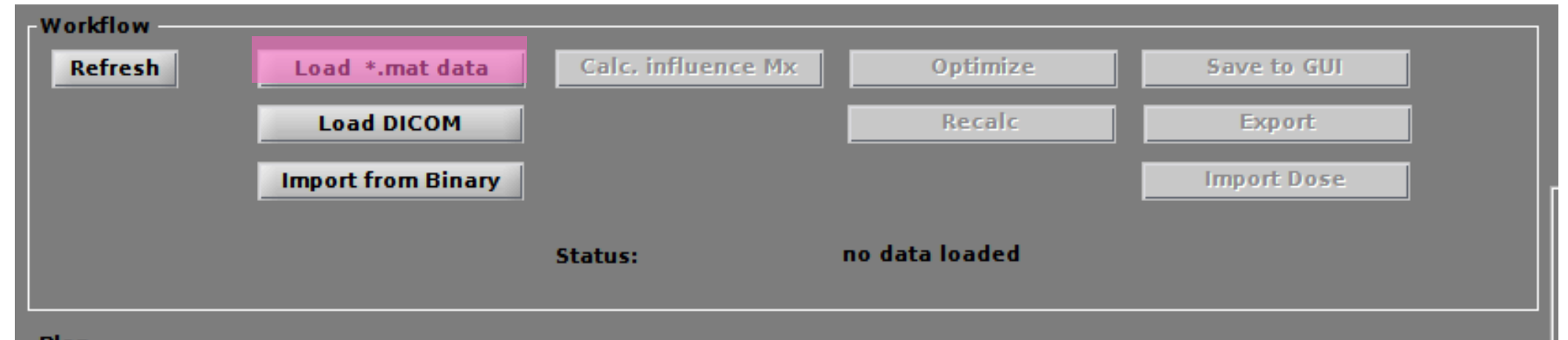
Info

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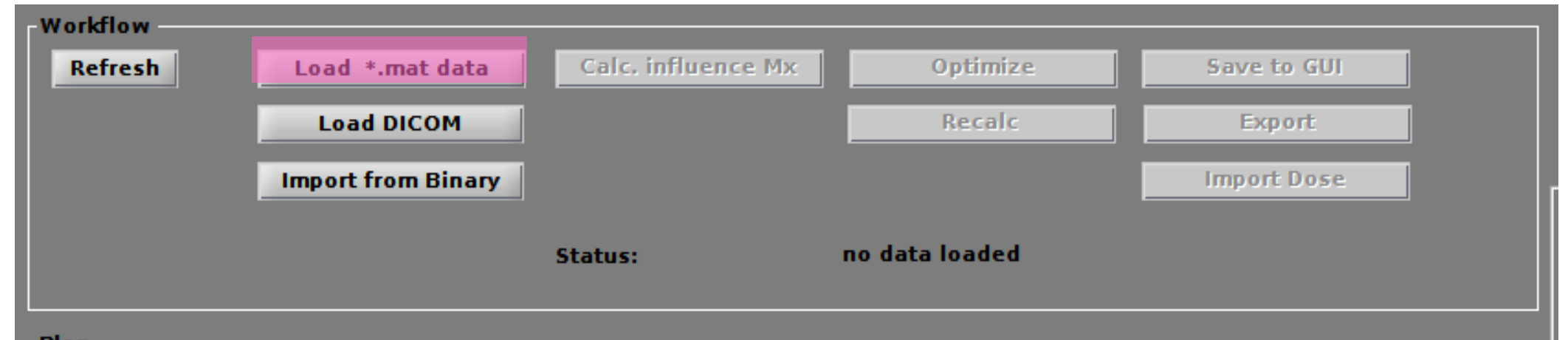
Next step: workflow

Press "Load *.mat data"
and get to MATRAD folder
applications/phantoms
to choose a case study

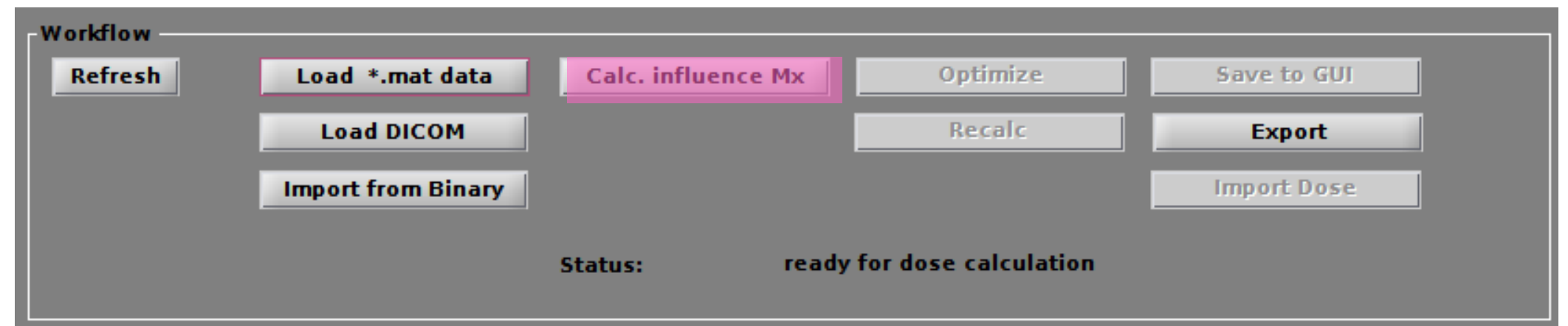


Next step: workflow

Press "Load *.mat data"
and get to MATRAD folder
applications/phantoms
to choose a case study

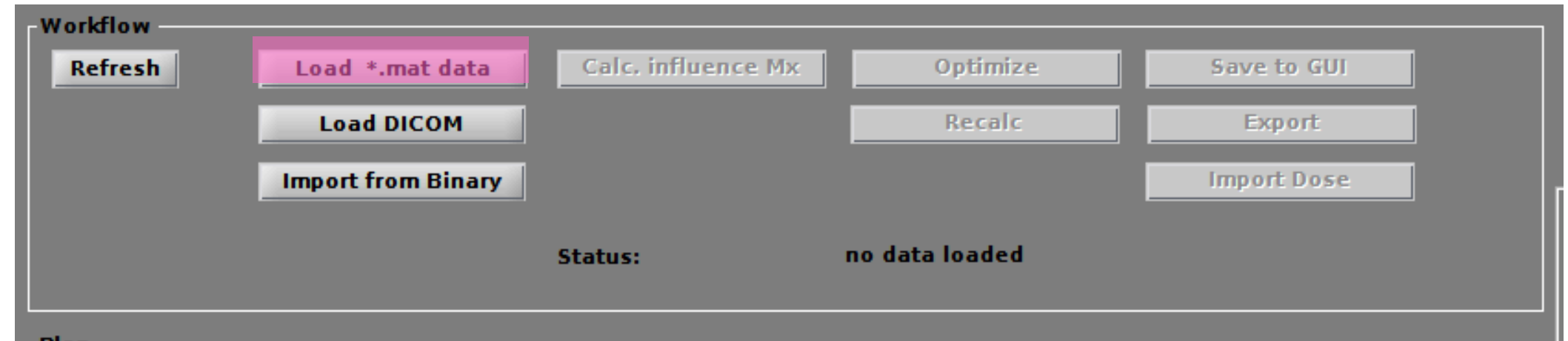


Press "Calc. Influence MX"
to calculate the influence matrix for
the selected case study (there will
be a status bar)

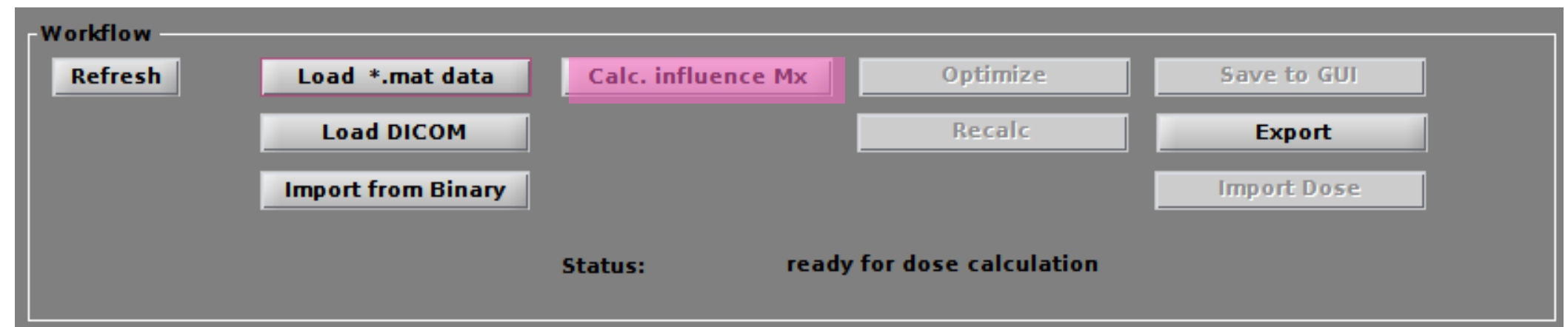


Next step: workflow

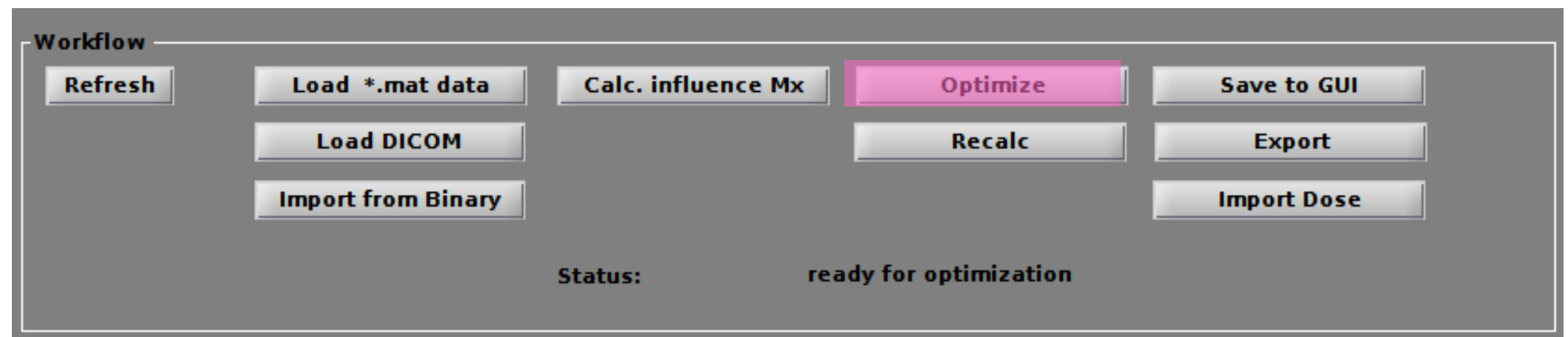
Press "Load *.mat data"
and get to MATRAD folder
applications/phantoms
to choose a case study



Press "Calc. Influence MX"
to calculate the influence matrix for
the selected case study (there will
be a status bar)



Now the plan is ready to be
optimized thus press "Optimize"
(this will take a while)





Workflow

Refresh Load *.mat data Calc. influence Mx Optimize Save to GUI
 Load DICOM Recalc Export
 Import from Binary Import Dose

Status: plan is optimized

Plan

bixel width in [mm]: 5
 Gantry Angle in °: 0 90
 Couch Angle in °: 0 0
 Radiation Mode: photons
 Machine: Generic
 IsoCenter in [mm]: 240 240 240 Auto.
 # Fractions: 30
 Type of optimization: none

3D conformal
 Run Sequencing
 Stratification Levels: 7
 Run Direct Aperture Optimization

Objectives & constraints

+/-	VOI name	VOI type	OP	Function	p	Parameters
-	BODY	OAR	2	Squared Overdo...	100	d^{max} : 5
-	OuterTarget	TARGET	1	Squared Deviation	800	d^{ref} : 60
+	BODY					

Visualization

Slice Selection: Type of plot: intensity GoTo: lateral
 Beam Selection: Plane Selection: axial
 Offset: Display option: physicalDose

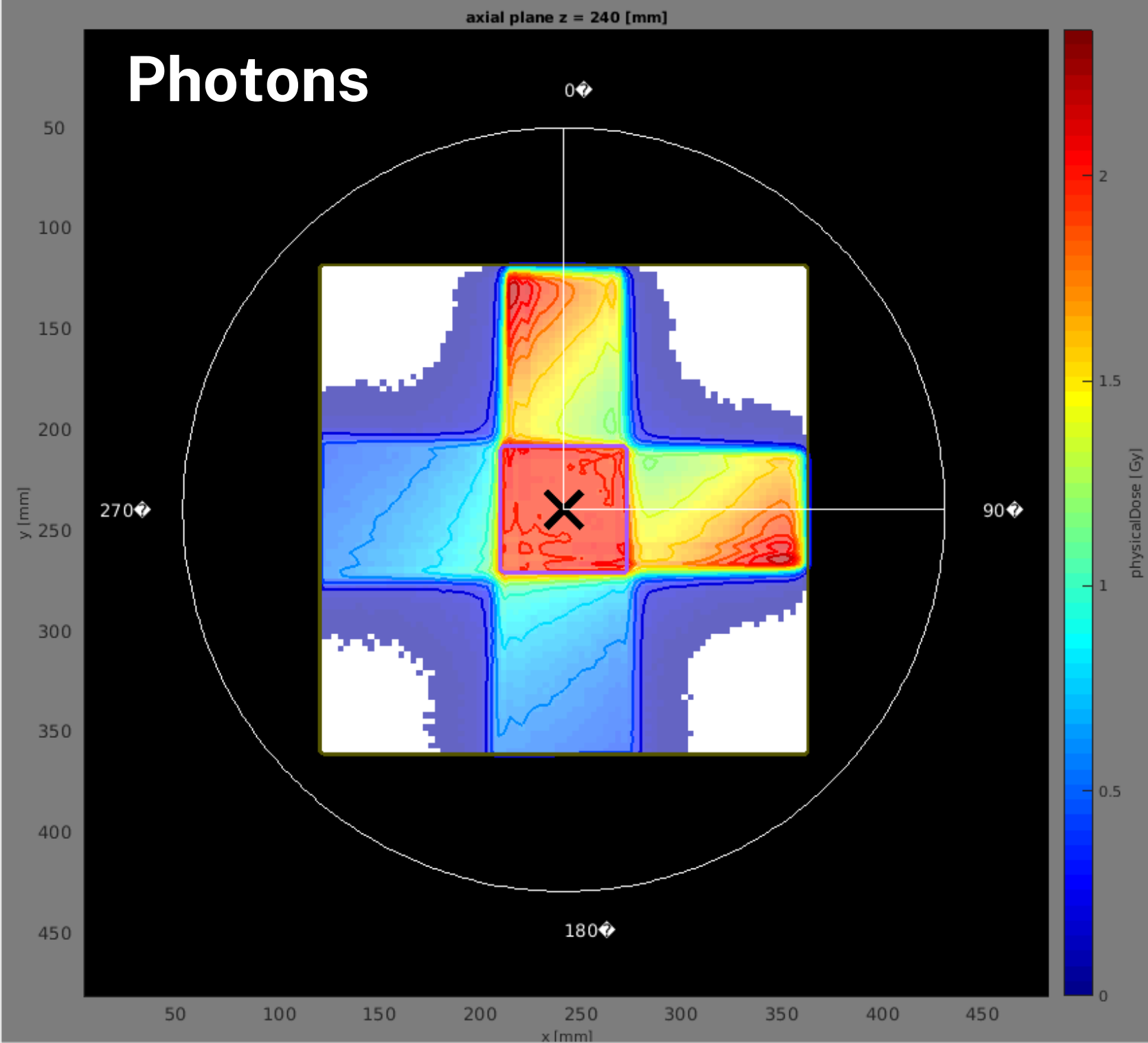
plot CT
 plot contour
 plot isolines
 plot dose
 plot isolines labels
 plot iso center
 visualize plan / beams

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Viewing



min value: 0
max: 2.357

Viewer Options

Result (i.e. dose)
 Window Preset: Custom
 Window Center: 1.18
 Window Width: 2.36
 Range: 0 2.358
 jet
 Lock Settings
 Dose opacity: 1

Structure Visibility

BODY
 OuterTarget

Info

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Workflow

Status: plan is optimized

Plan

bixel width in [mm]:

Gantry Angle in °:

Couch Angle in °:

Radiation Mode:

Machine:

IsoCenter in [mm]: Auto.

Fractions:

Type of optimization:

3D conformal
 Run Sequencing
 Stratification Levels:
 Run Direct Aperture Optimization

Objectives & constraints

+/-	VOI name	VOI type	OP	Function	p	Parameters
-	BODY	OAR	2	Squared Overdo...	100	d^{max} : 5
-	OuterTarget	TARGET	1	Squared Deviation	800	d^{ref} : 60
+	BODY					

Visualization

Slice Selection:

Beam Selection:

Offset:

Type of plot:

Plane Selection:

Display option:

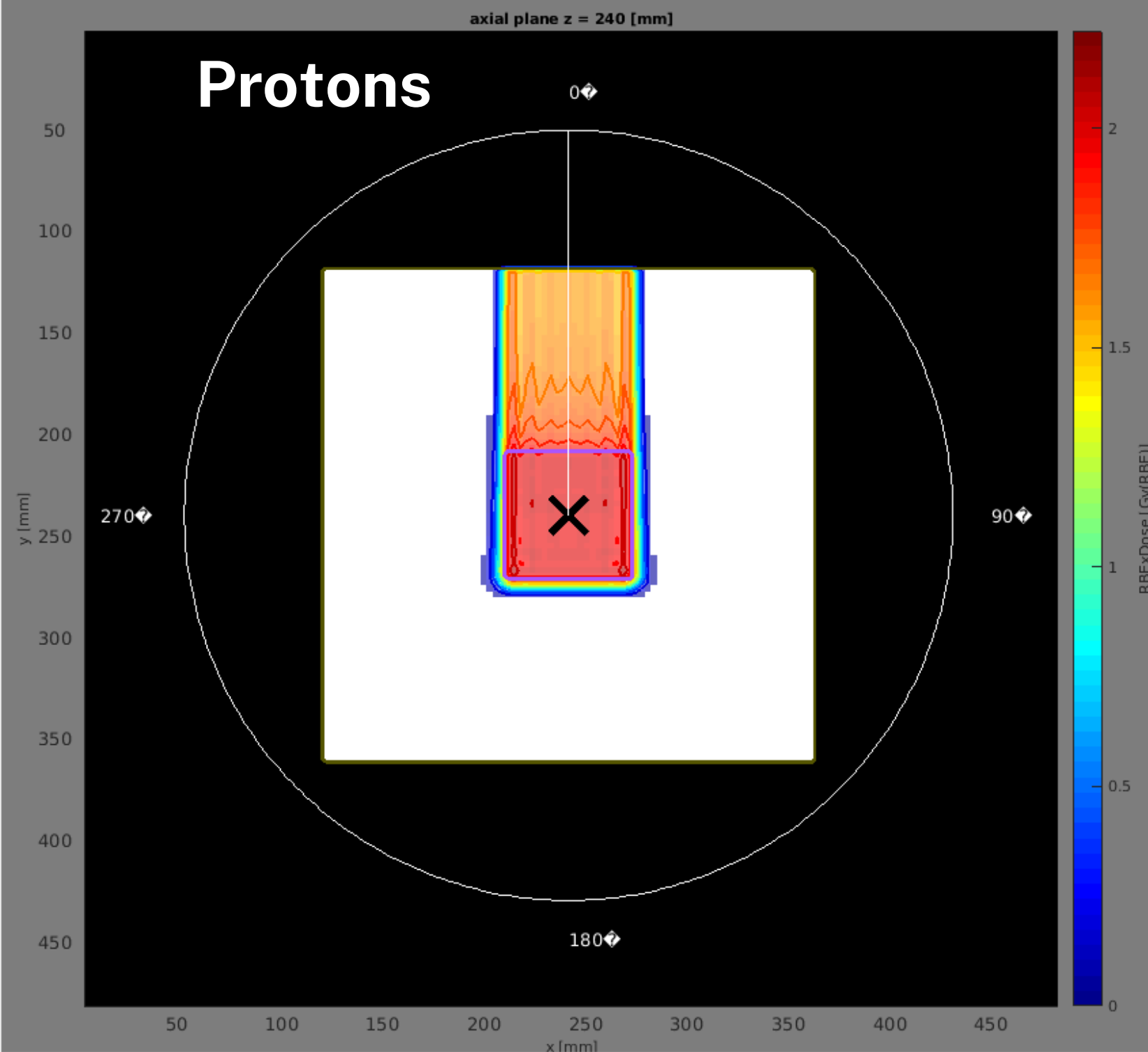
- plot CT
- plot contour
- plot isolines
- plot dose
- plot isolines labels
- plot iso center
- visualize plan / beams

matRad

dkfz.

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IN THE HELMHOLTZ ASSOCIATION

Viewing



min value: 0
max: 2.222

Viewer Options

Result (i.e. dose):

Window Preset:

Window Center:

Window Width:

Range:

jet:

Lock Settings

Dose opacity:

Structure Visibility

- BODY
- OuterTarget

Info

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Workflow

Refresh Load *.mat data Calc. influence Mx Optimize Save to GUI

Load DICOM Recalc Export

Import from Binary Import Dose

Status: plan is optimized

Plan

bixel width in [mm]

Gantry Angle in ° 3D conformal

Couch Angle in ° Run Sequencing

Radiation Mode **carbon** Stratification Levels

Machine **Generic** Run Direct Aperture Optimization

IsoCenter in [mm] Auto.

Fractions

Type of optimization **LEMIV_RBExD** Set Tissue

Objectives & constraints

+/-	VOI name	VOI type	OP	Function	p	Parameters
-	BODY	OAR	2	Squared Overdo...	100	d ^{max} : 5
-	OuterTarget	TARGET	1	Squared Deviation	800	d ^{ref} : 60
+	BODY					

Visualization

Slice Selection Type of plot **intensity** GoTo **lateral** plot CT

Beam Selection Plane Selection **axial** **Open 3D-View** plot contour

Offset Display option **RBExDose** plot isolines

plot dose

plot isolines labels

plot iso center

visualize plan / beams

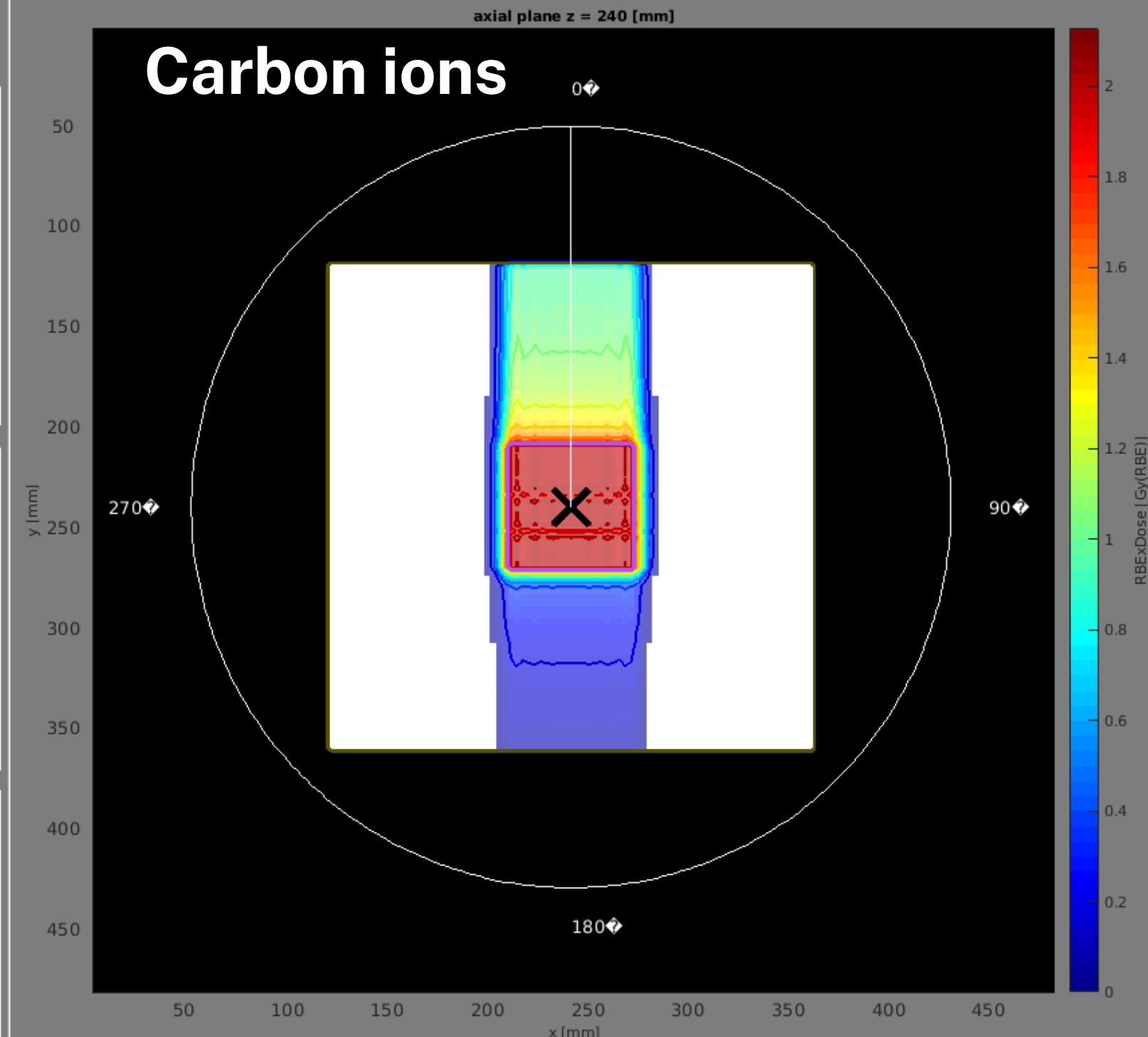
Show DVH/QI

matRad

dkfz.

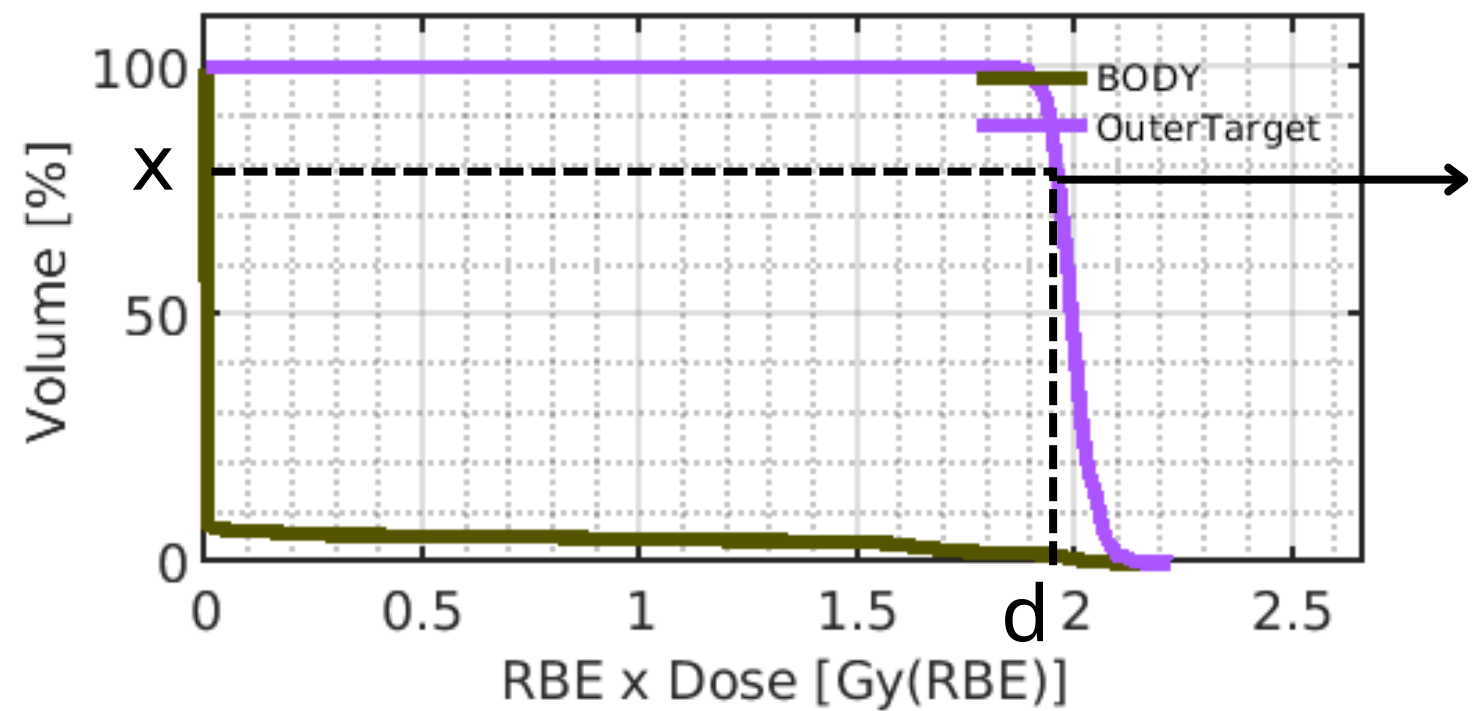
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Viewing



Useful tools: DVH

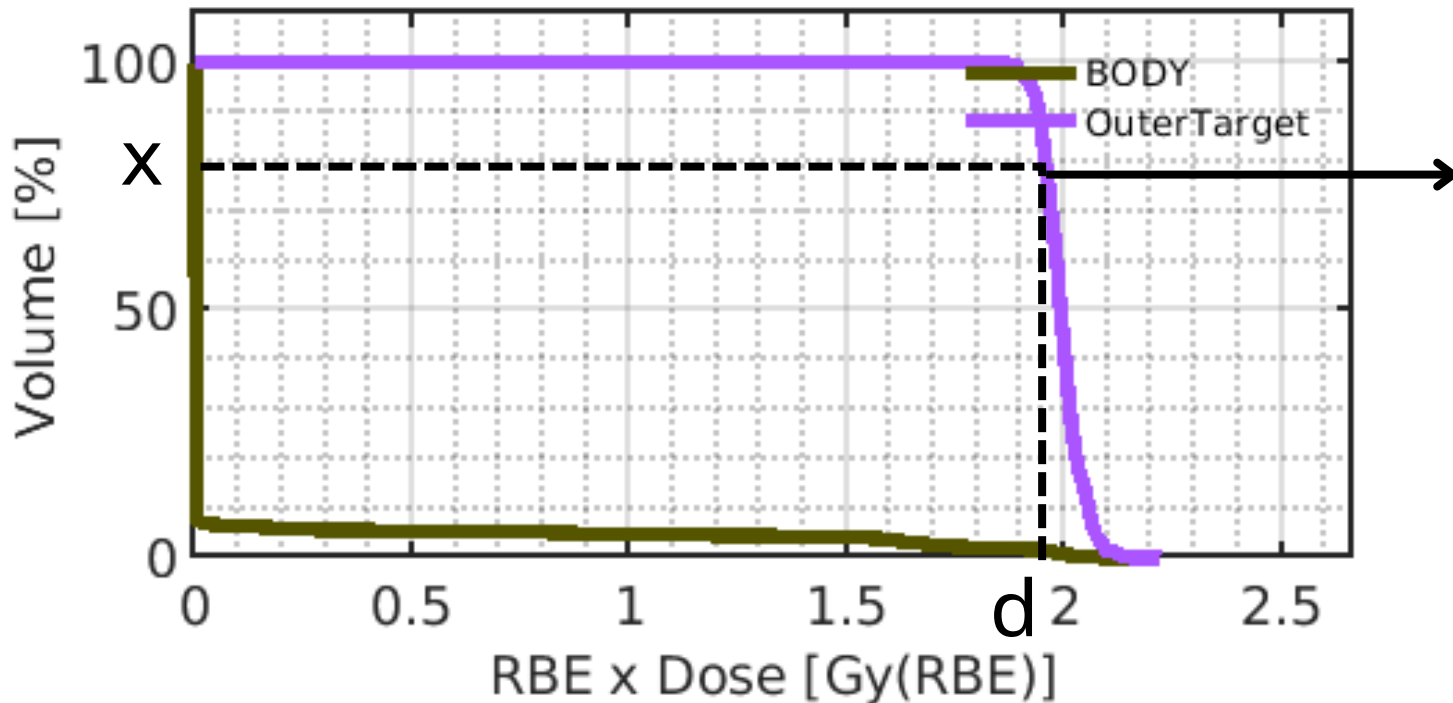
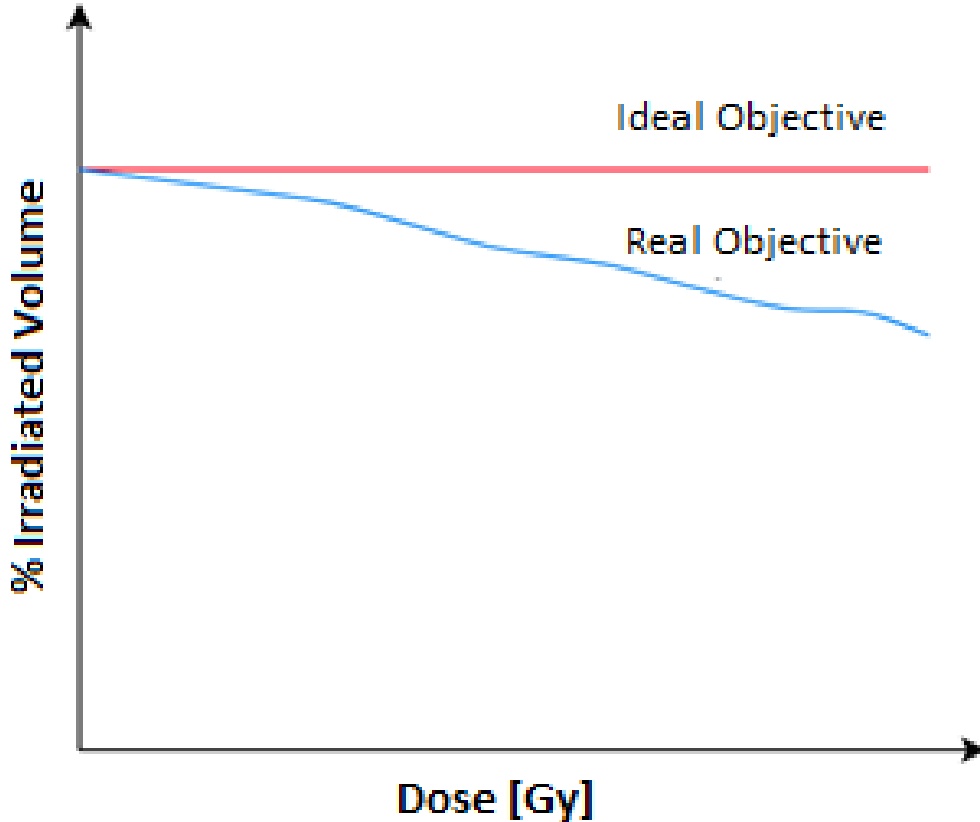
DVH (Dose Volume Histogram) is a very useful tool to evaluate the quality of the treatment plan



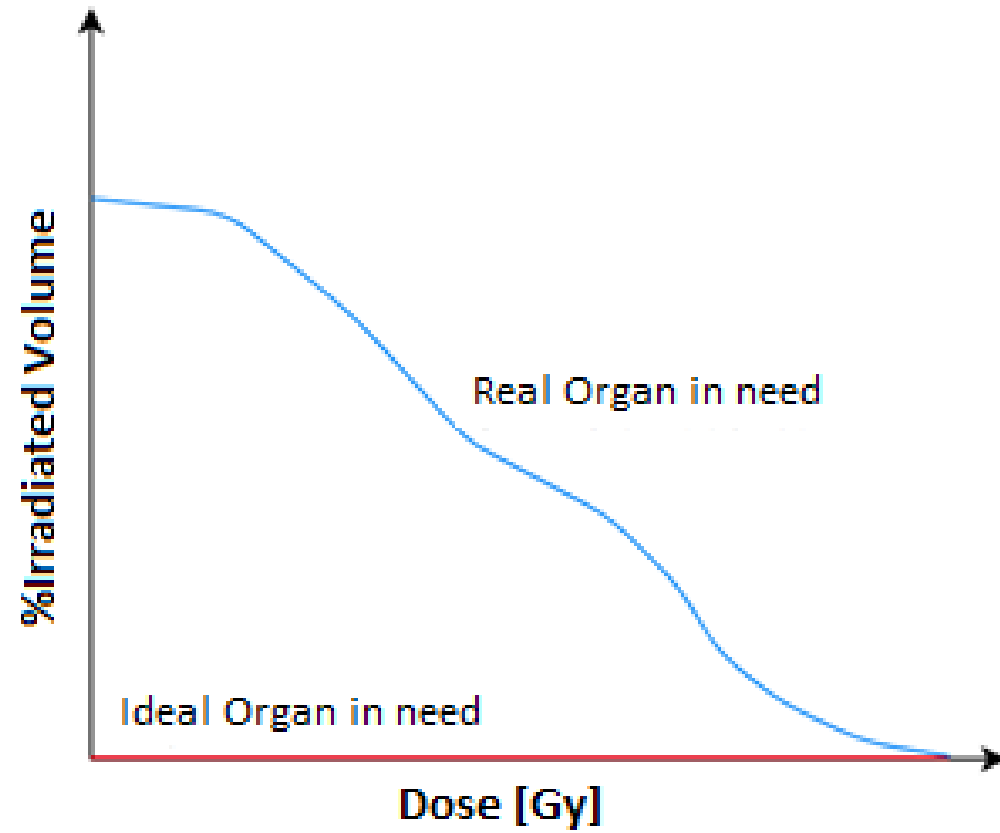
x% of the volume that received at least a dose d

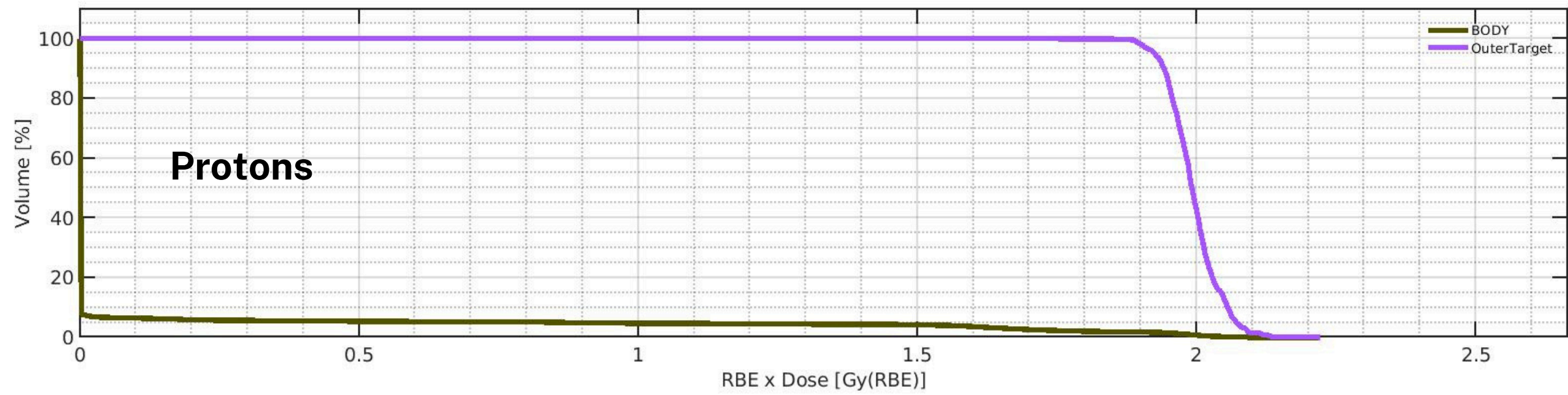
Useful tools: DVH

DVH (Dose Volume Histogram) is a very useful tool to evaluate the quality of the treatment plan

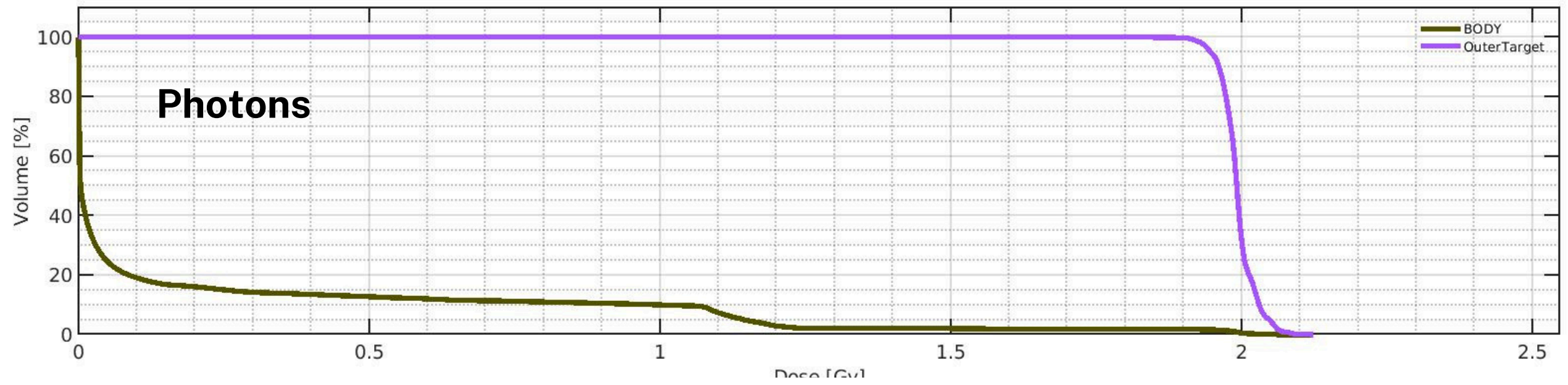


x% of the volume that received at least a dose d





	mean	std	max	min	D_2	D_5	D_50	D_95	D_98	V_0Gy	V_0.4Gy	V_0.8Gy	V_1.3Gy	V_1.7Gy	V_2.2Gy	CI_2Gy	H_2Gy	
BODY	0.0904	0.3789	2.2224	0	1.8071	0.8541	0	0	0	1	0.0551	0.0513	0.0442	0.0263	7.5267e...	-	-	
OuterTarget	1.9940	0.0455	2.2224	1.7502	2.0924	2.0710	1.9916	1.9252	1.9010	1	1	1	1	1	1	4.3192e...	0.9510	7.0001



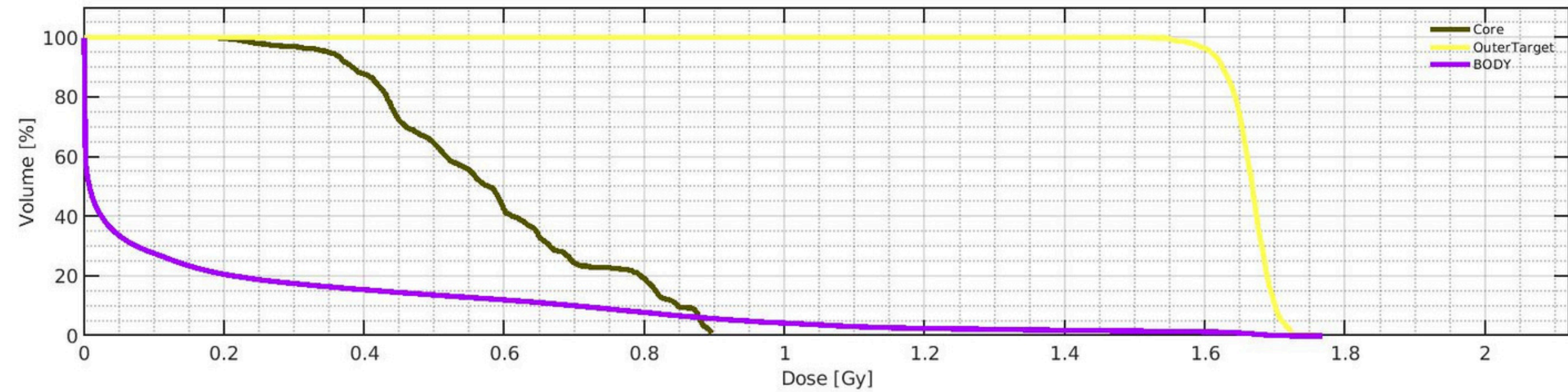
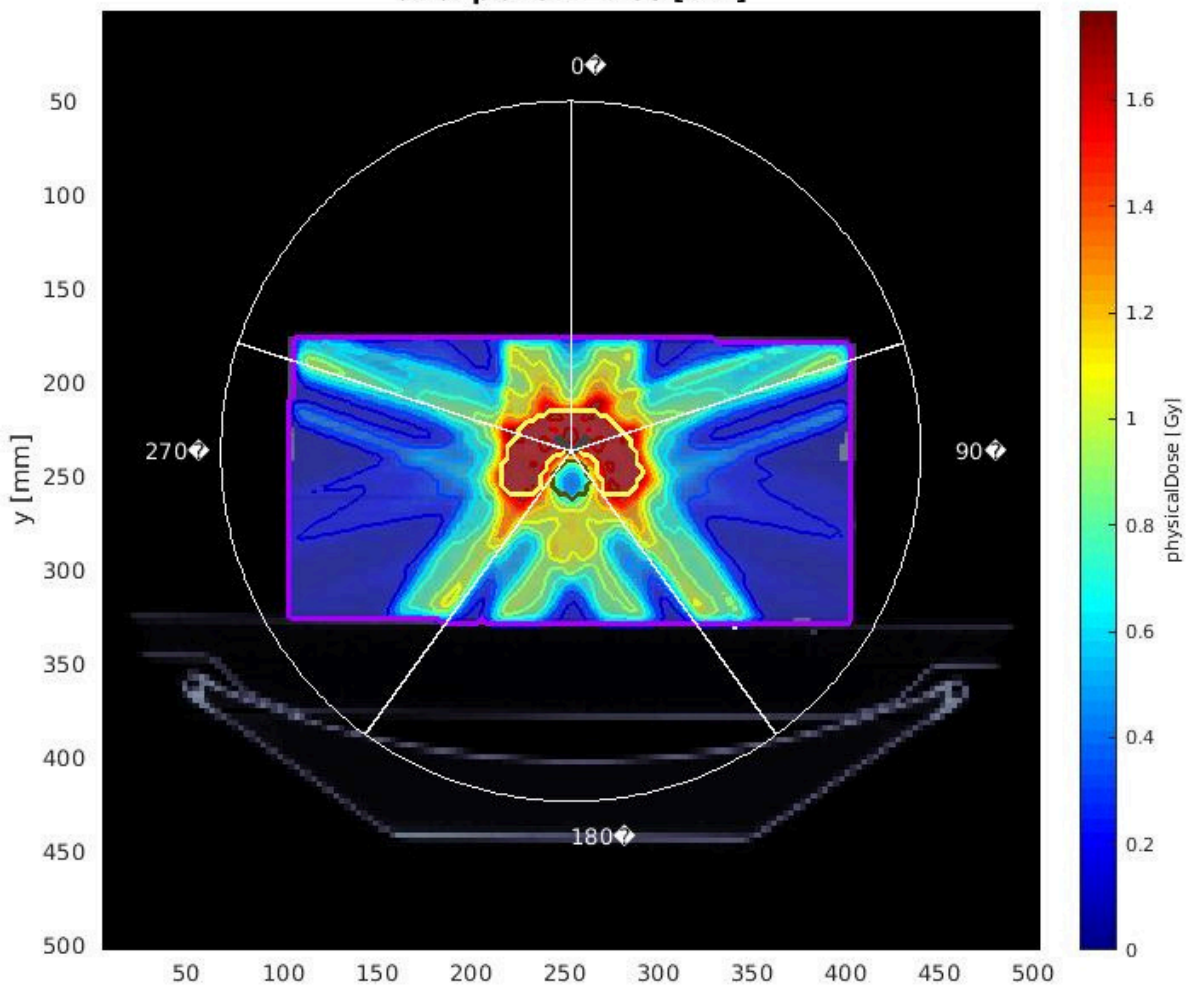
	mean	std	max	min	D_2	D_5	D_50	D_95	D_98	V_0Gy	V_0.4Gy	V_0.8Gy	V_1.2Gy	V_1.6Gy	V_2.1Gy	CI_2Gy	H_2Gy
BODY	0.1731	0.4109	2.1239	0	1.5308	1.1449	0.0036	0	0	1	0.1353	0.1101	0.0292	0.0176	1.8317e...	-	-
OuterTarget	1.9900	0.0290	2.1239	1.6441	2.0906	2.0479	1.9916	1.9464	1.9312	1	1	1	1	1	0.0011	0.9975	5.0750



<https://pandora.infn.it/public/oph2024--it>

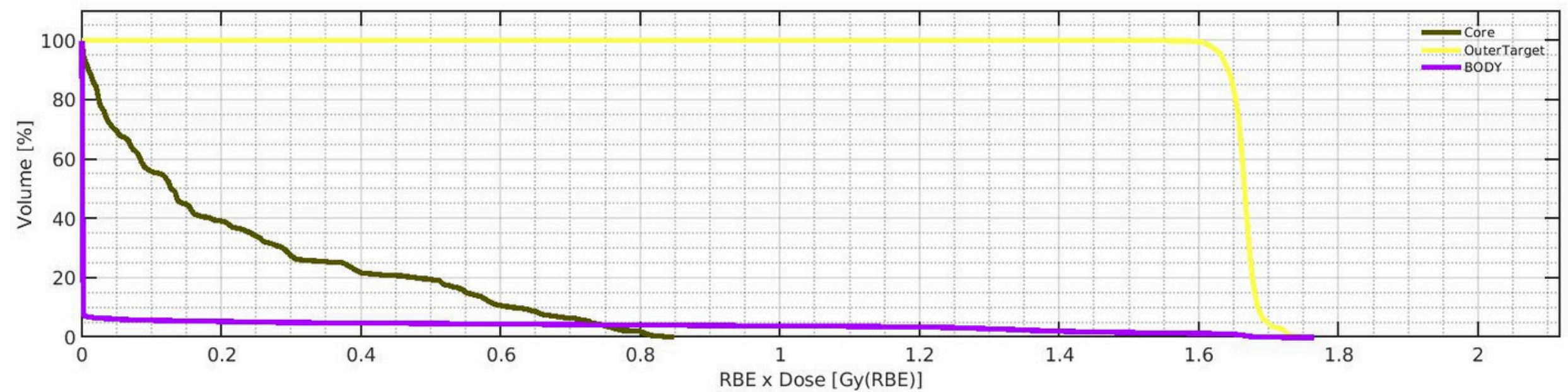
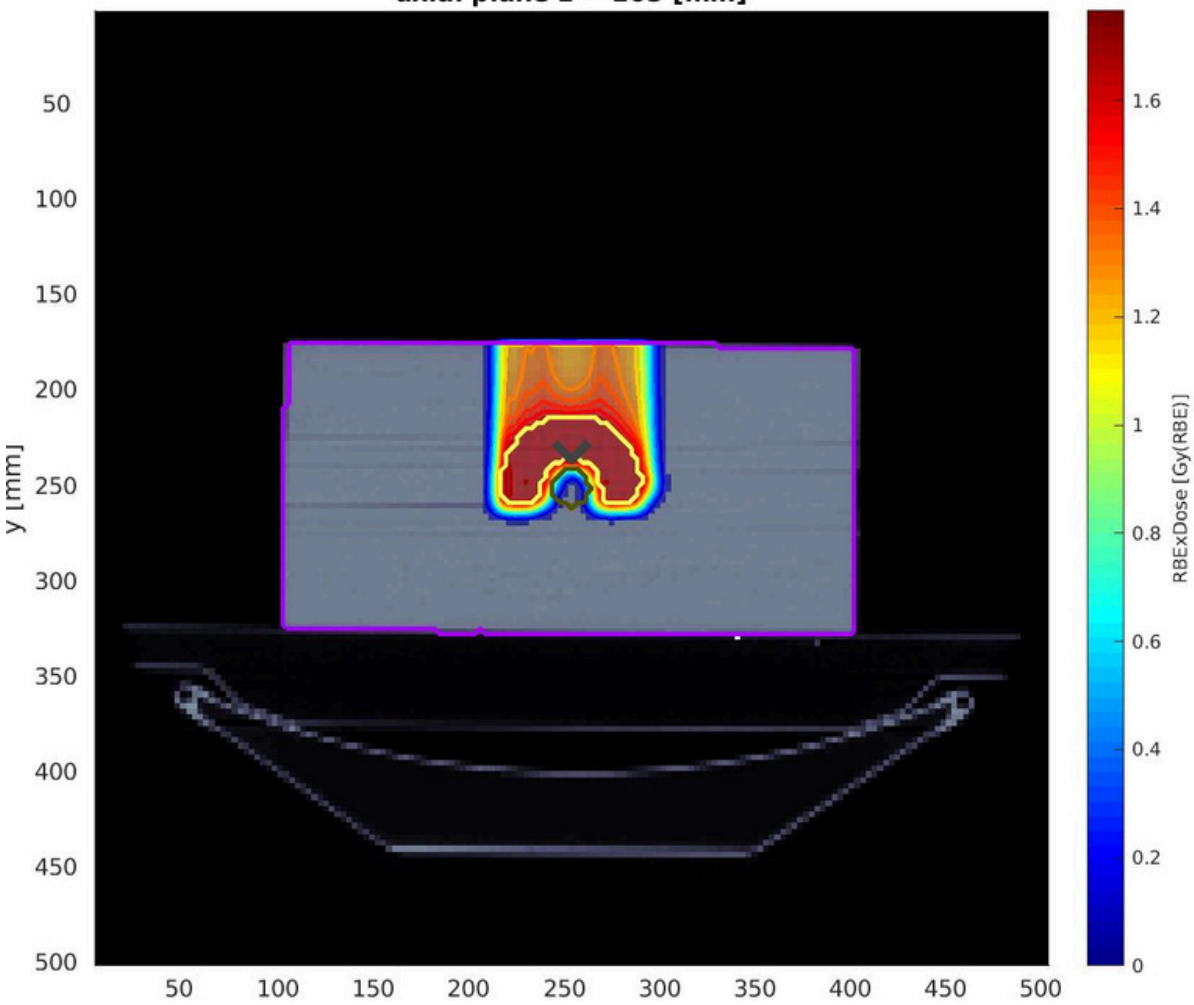
Let's move to TG119

axial plane z = 165 [mm]



	mean	std	max	min	D_2	D_5	D_50	D_95	D_98	V_0Gy	V_0.3Gy	V_0.7Gy	V_1Gy	V_1.4Gy	V_1.7Gy	Cl_1.67Gy	HI_1.67Gy
Core	0.5875	0.1726	0.8975	0.1930	0.8924	0.8797	0.5789	0.3516	0.2542	1	0.9697	0.2447	0	0	0	-	-
OuterTarget	1.6643	0.0314	1.7681	1.5184	1.7209	1.7102	1.6674	1.6086	1.5818	1	1	1	1	1	0.1004	0.8414	6.0946
BODY	0.1696	0.3412	1.7681	0	1.3545	0.9468	0.0077	0	0	1	0.1756	0.1011	0.0429	0.0189	0.0015	-	-

axial plane z = 165 [mm]



	mean	std	max	min	D_2	D_5	D_50	D_95	D_98	V_0Gy	V_0.3Gy	V_0.7Gy	V_1Gy	V_1.4Gy	V_1.7Gy	Cl_1.67Gy	HI_1.67Gy
Core	0.2258	0.2368	0.8483	0	0.7995	0.7284	0.1284	0.0028	1.6025e...	1	0.2742	0.0652	0	0	0	-	-
OuterTarget	1.6649	0.0206	1.7653	1.5506	1.7231	1.6976	1.6651	1.6319	1.6175	1	1	1	1	1	0.0444	0.8998	3.9420
BODY	0.0652	0.2890	1.7653	0	1.4134	0.3066	0	0	0	1	0.0501	0.0431	0.0386	0.0208	5.5008e...	-	-

Except for the “tail” carbon ions release less dose in healthy tissues wrt to protons given the same dose release in the tumour!

