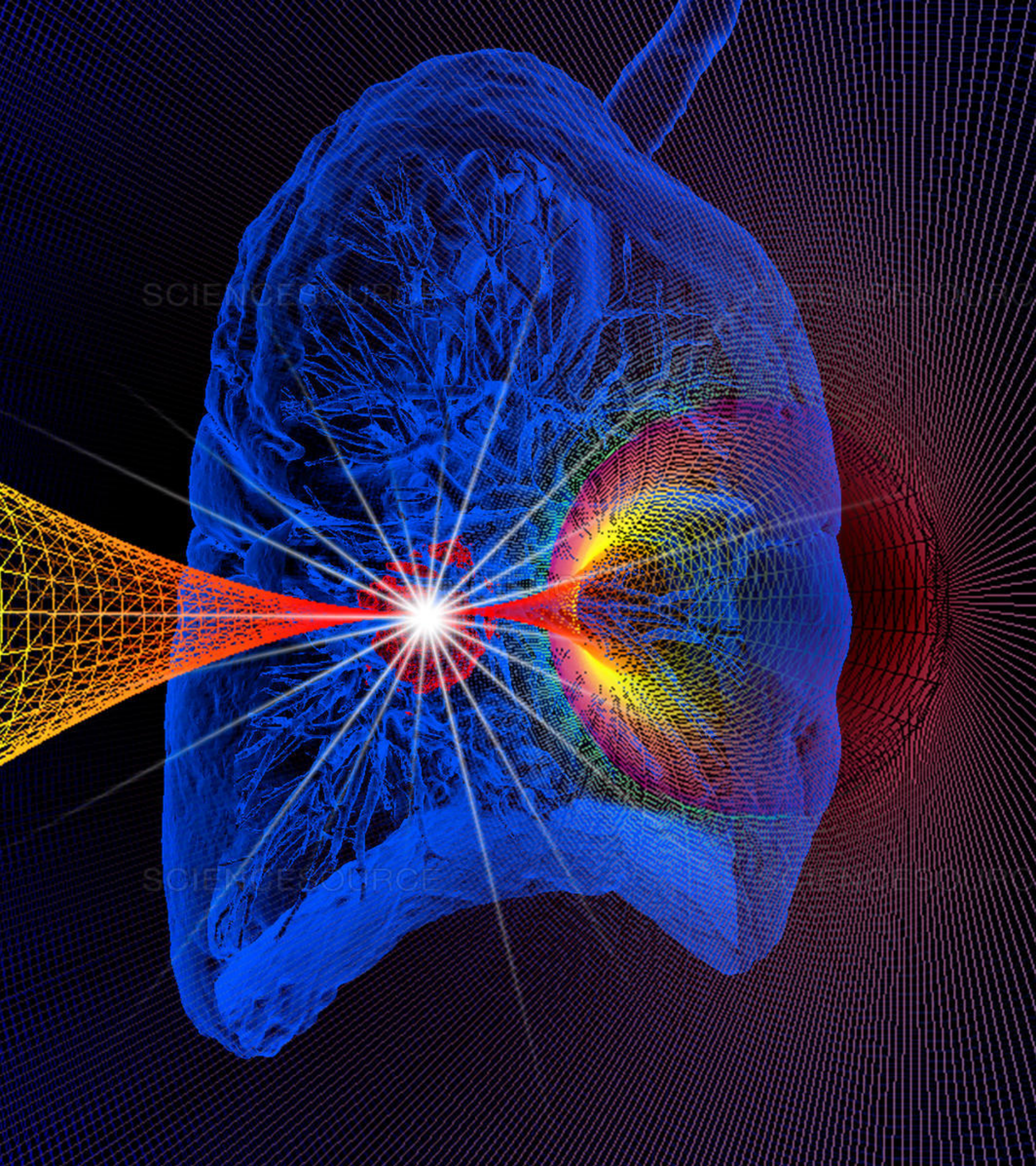
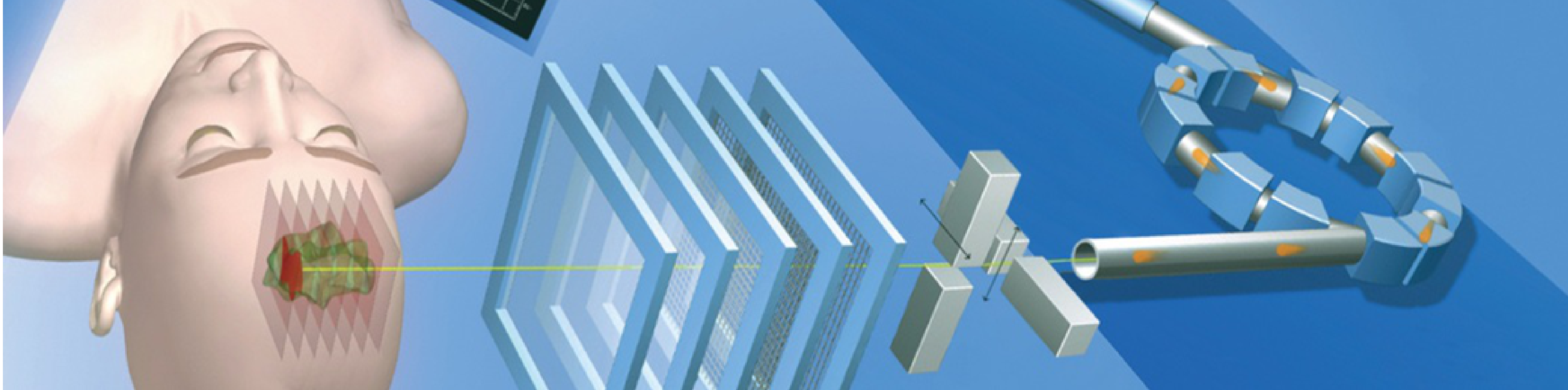




MATRAD

Riccardo.Ridolfi@bo.infn.it

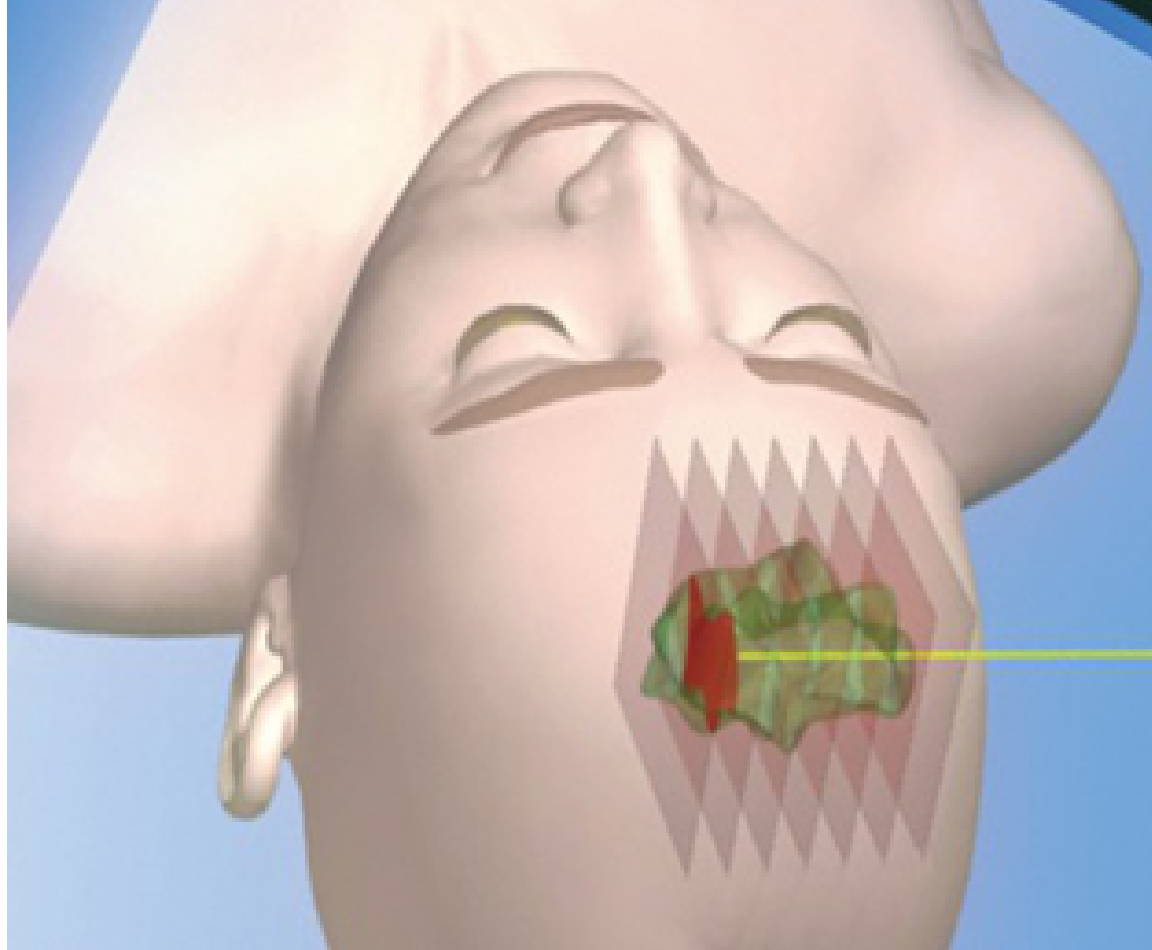




MATRAD è un software open source che simula un *treatment planning system* ed è basato su MATLAB

DKFZ è il principale sviluppatore

Non è usato nella pratica clinica ma è molto affidabile



MATRAD è un software open source che simula un *treatment planning system* ed è basato su MATLAB

DKFZ è il principale sviluppatore

Non è usato nella pratica clinica ma è molto affidabile

Qualche definizione prima di iniziare...

GTV

VOLUME DELLA MASSA TUMORALE
VISIBILE DALLA CT/MRI

PTV

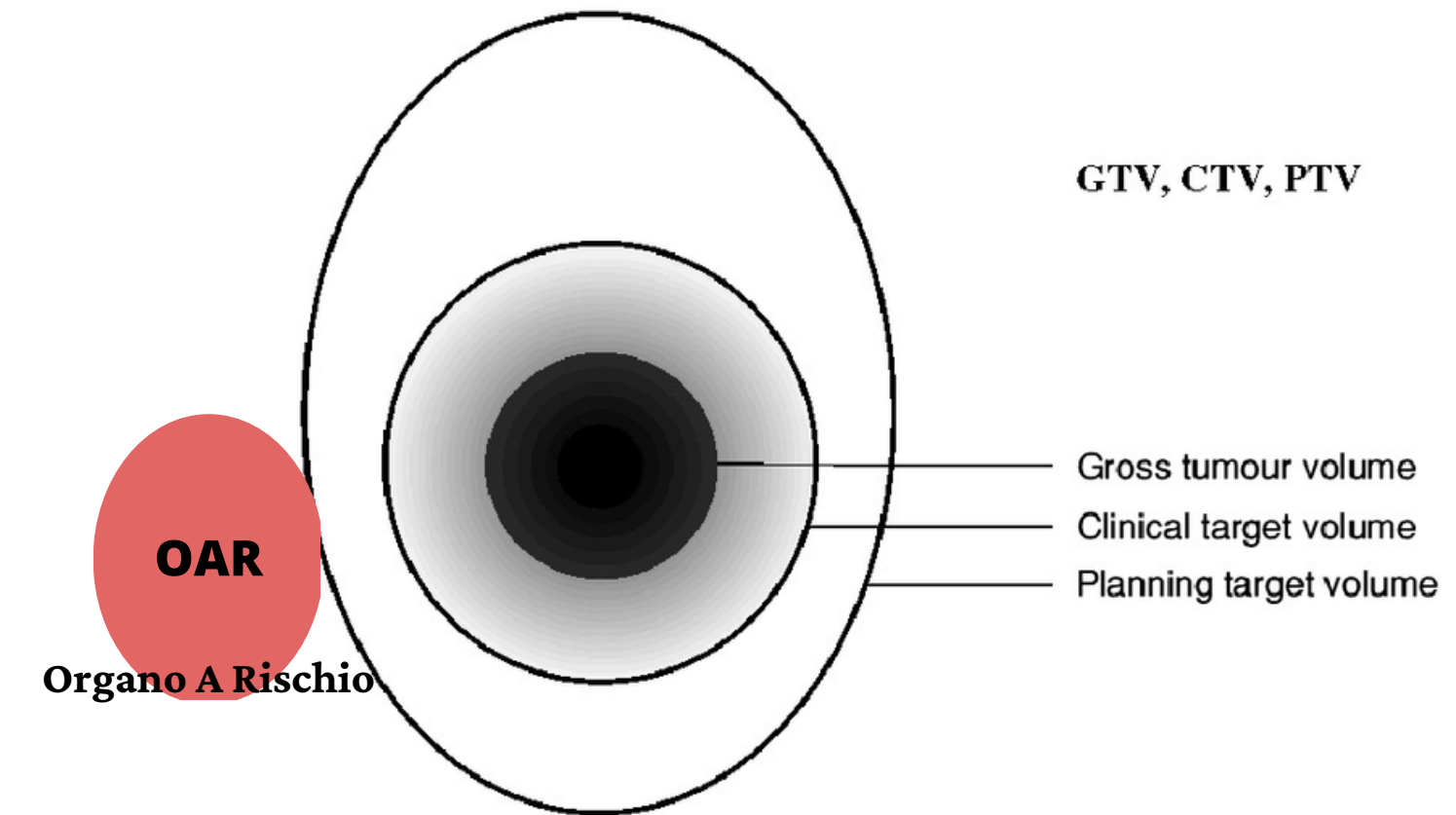
VOLUME DA IRRADIARE (CTV +
INCERTEZZE)

CTV

VOLUME DOVE SI TEME POSSANO
ESSERCI CELLULE TUMORALI NON
VISIBILI

OAR

ORGANO SENSIBILE ALLA RADIAZIONE
CHE VA RISPARMIATO IL PIÙ POSSIBILE



Qualche definizione prima di iniziare...

GTV

VOLUME DELLA MASSA TUMORALE
VISIBILE DALLA CT/MRI

PTV

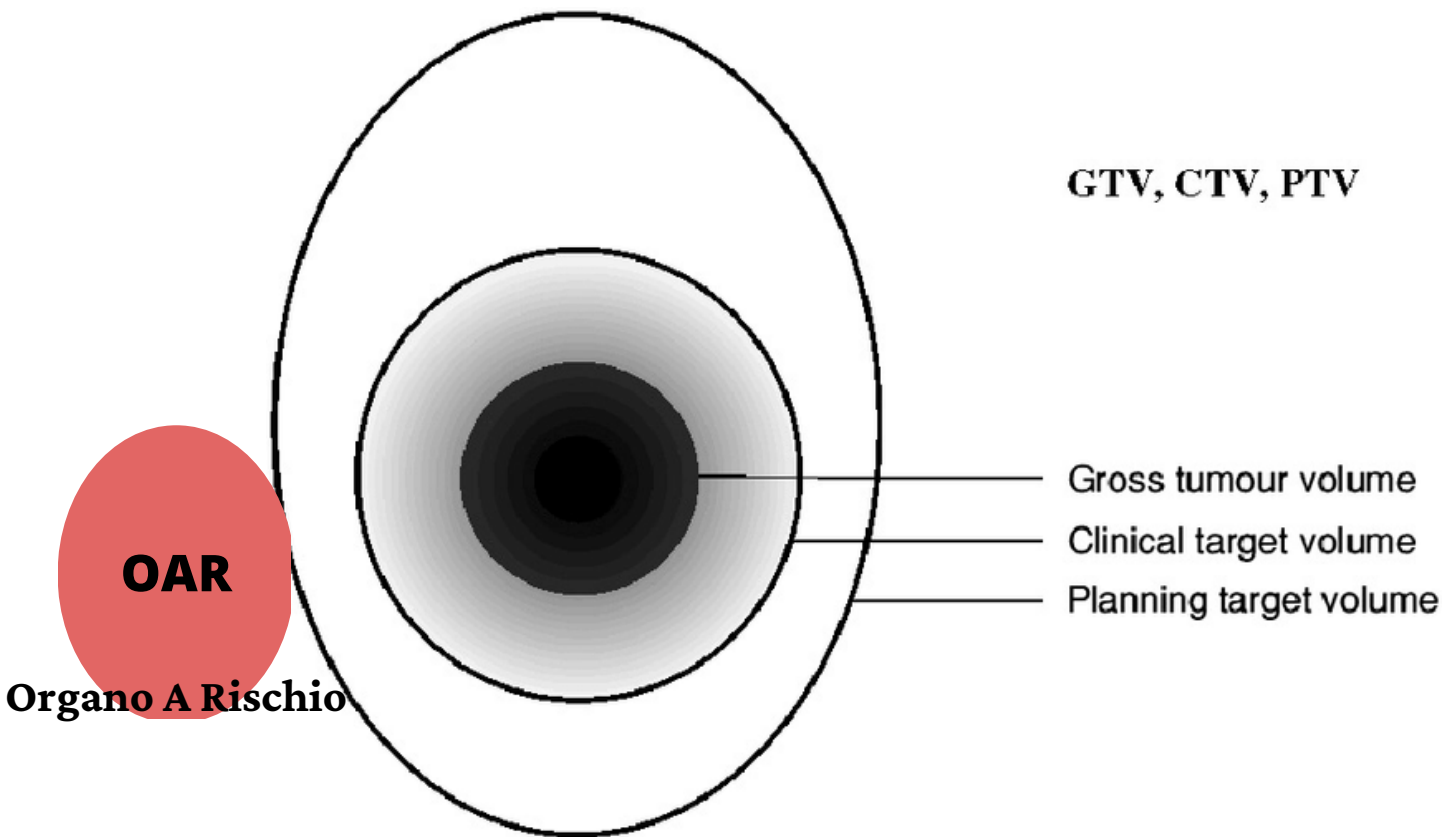
VOLUME DA IRRADIARE (CTV +
INCERTEZZE)

CTV

VOLUME DOVE SI TEME POSSANO
ESSERCI CELLULE TUMORALI NON
VISIBILI

OAR

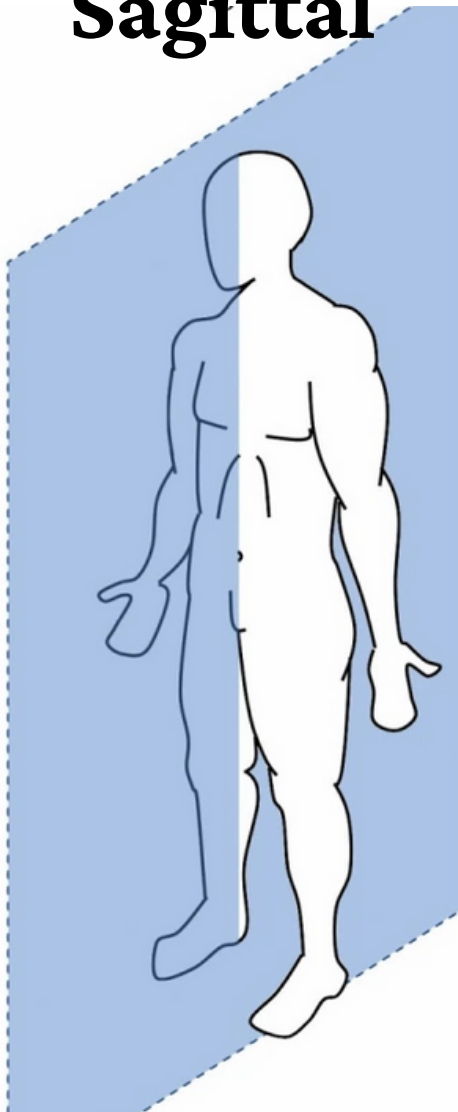
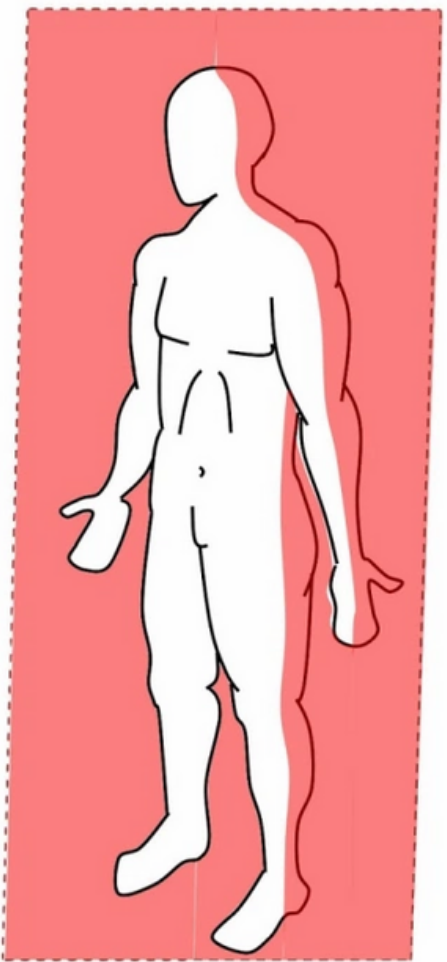
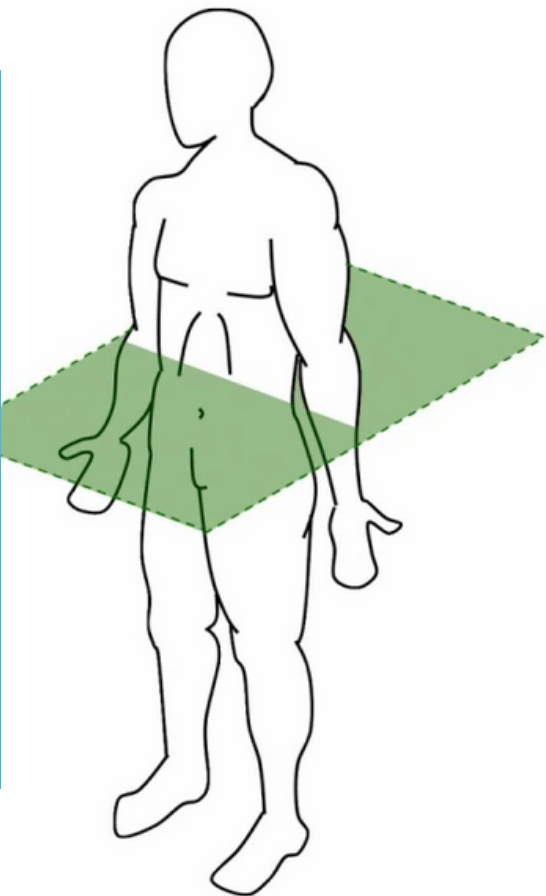
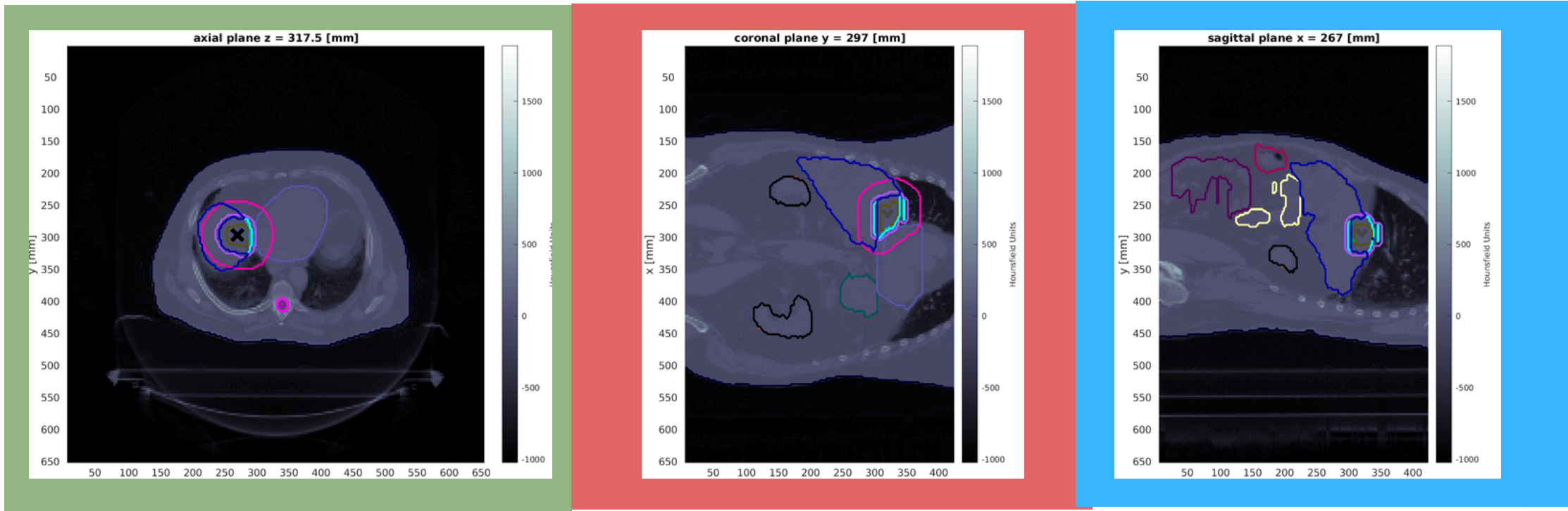
ORGANO SENSIBILE ALLA RADIAZIONE
CHE VA RISPARMIATO IL PIÙ POSSIBILE



Axial

Coronal

Sagittal





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]

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

Set Tissue

☐ 3D conformal☐ Run Sequencing

Stratification Levels

7

☐ Run Direct Aperture Optimization

Objectives & constraints

Visualization

Slice Selection



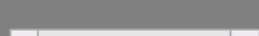
Type of plot

intensity

GoTo

lateral

Beam Selection



Plane Selection

axial

Open 3D-View

Offset



Display option

no option available

Show DVH/QI

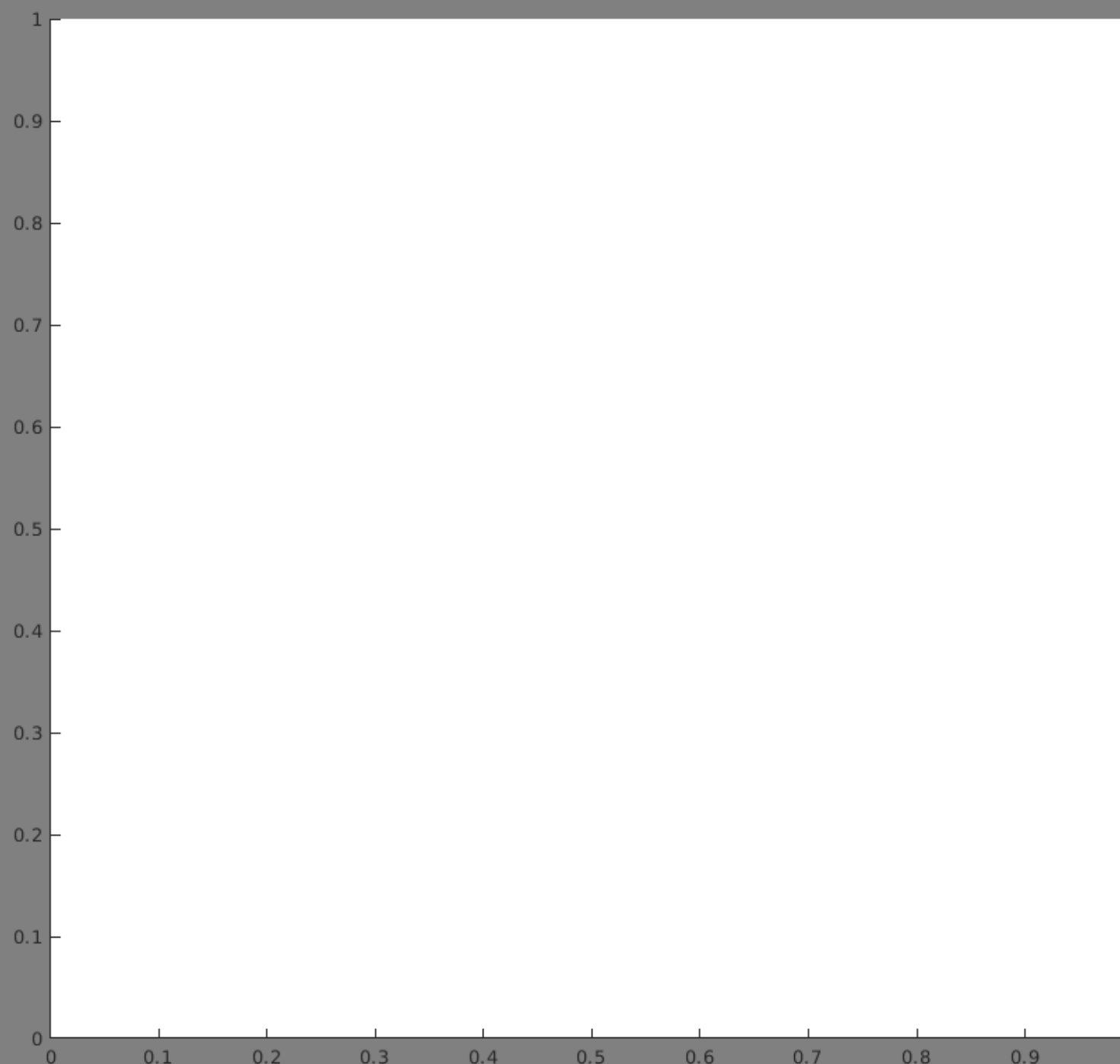
☒ plot CT☒ plot contour☒ plot isolines☒ plot dose☐ plot isolines labels☒ plot iso center☐ visualize plan / beams

matRad

dkfz.

GERMAN
CANCER RESEARCH CENTER
IN THE HELMHOLTZ ASSOCIATION

Viewing



min value:

max

no data

Set IsoDose Levels

Viewer Options

None

No available Window

Reset

Window Center:

0.5

Window Width:

1.0

Range:

0 1

bone

☐ Lock Settings

Dose opacity:

0 1

Structure Visibility

no data loaded

Info

v2.10.1 "Blaise"

www.matRad.org

About



Workflow

Refresh Load *.mat data Calc. influence Mx Optimize Save to GUI
Load DICOM Recalc Export
Load DICOM binary 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 Set Tissue

☐ Set conformal
☐ Run Sequencing
Stratification Levels 7
☐ Run Direct Aperture Optimization

Objectives & constraints

Visualization

Slice Selection Type of plot intensity GoTo lateral
Beam Selection Plane Selection axial Open 3D-View
Offset Display option no option available
Show DVH/QI

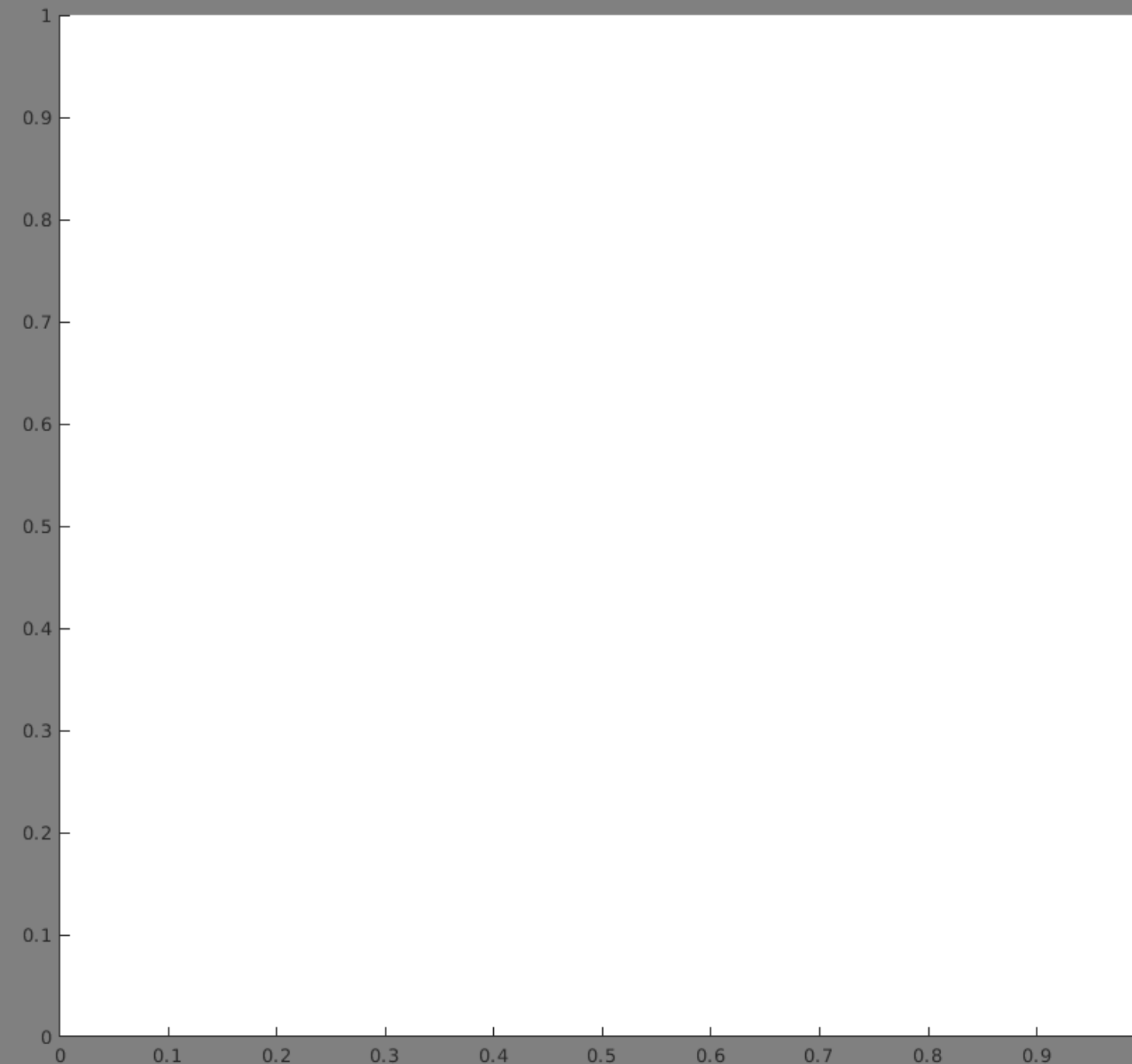
☒ plot CT
☒ plot contour
☒ plot isolines
☒ plot dose
☐ plot isolines labels
☒ plot iso center
☐ visualize plan / beams

matRad

dkfz.

GERMAN
CANCER RESEARCH CENTER
IN THE HELMHOLTZ ASSOCIATION

Viewing



min value: -
max -
Set IsoDose Levels

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
About

Iniziamo: plan

bixel width

dimensioni della
griglia per il calcolo
(non modificare)

gantry and couch angle

due liste ordinate di
angoli per la gantry e
per il lettino (da 0° a
360°)

radiation mode

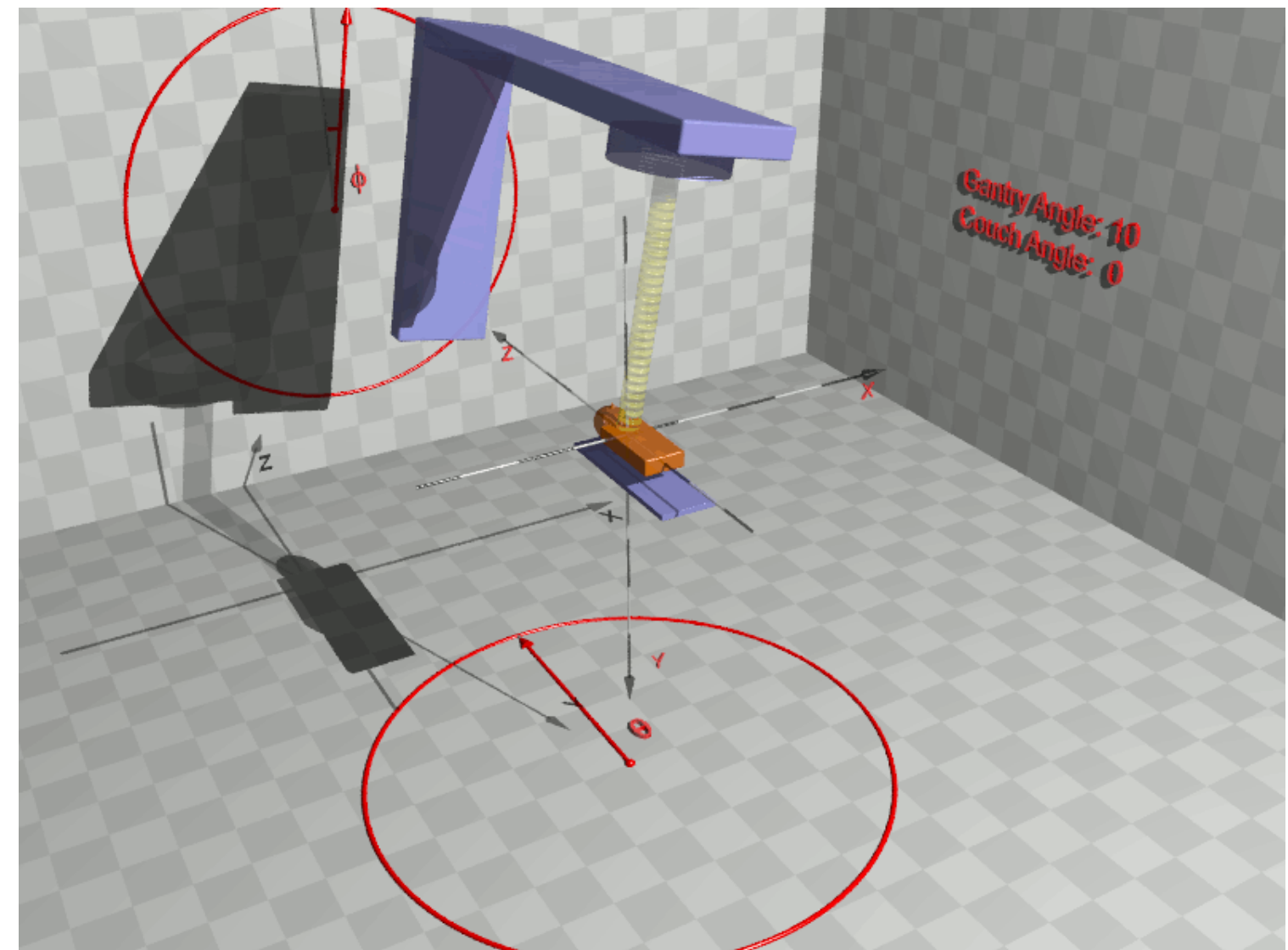
particella da
utilizzare nel
trattamento (fotoni,
protoni, ioni carbonio)

isocenter

punto centrale del
fascio di particelle,
spuntare "Auto"

Plan

bixel width in [mm]	5	
Gantry Angle in °	0	☐ 3D conformal
Couch Angle in °	0	☐ Run Sequencing
Radiation Mode	photons	Stratification Levels
Machine	Generic	7
IsoCenter in [mm]	0 0 0	☐ Run Direct Aperture Optimization
# Fractions	30	
Type of optimization	none	Set Tissue



Iniziamo: plan

bixel width

dimensioni della
griglia per il calcolo
(non modificare)

gantry and couch angle

due liste ordinate di
angoli per la gantry e
per il lettino (da 0° a
360°)

radiation mode

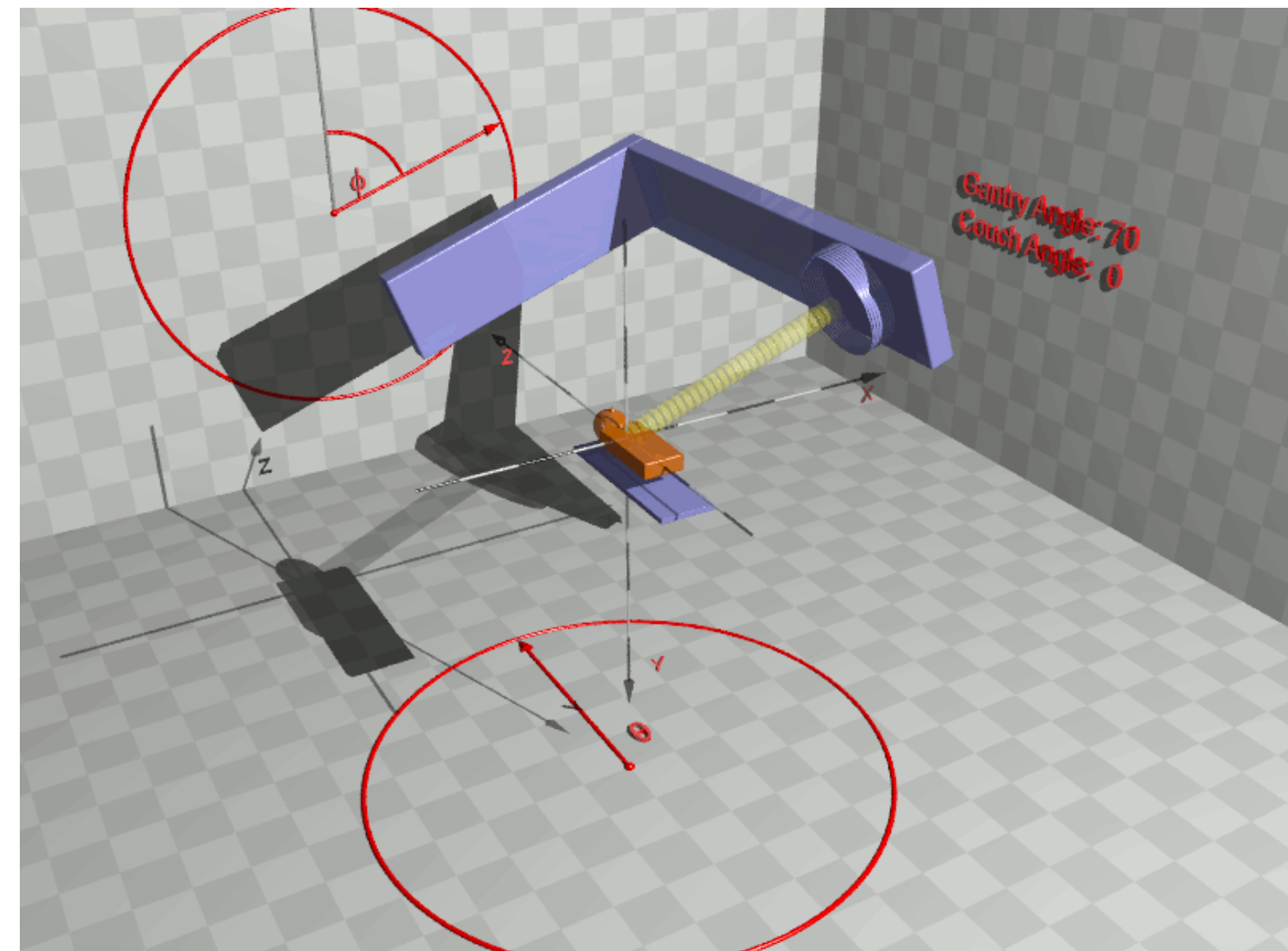
particella da
utilizzare nel
trattamento (fotoni,
protoni, ioni carbonio)

isocenter

punto centrale del
fascio di particelle,
spuntare "Auto"

Plan

bixel width in [mm]	5	
Gantry Angle in °	0	☐ 3D conformal
Couch Angle in °	0	☐ Run Sequencing
Radiation Mode	photons	Stratification Levels
Machine	Generic	7
IsoCenter in [mm]	0 0 0	☐ Run Direct Aperture Optimization
# Fractions	30	
Type of optimization	none	Set Tissue



Iniziamo: plan

bixel width

dimensioni della
griglia per il calcolo
(non modificare)

gantry and couch angle

due liste ordinate di
angoli per la gantry e
per il lettino (da 0° a
360°)

radiation mode

particella da
utilizzare nel
trattamento (fotoni,
protoni, ioni carbonio)

isocenter

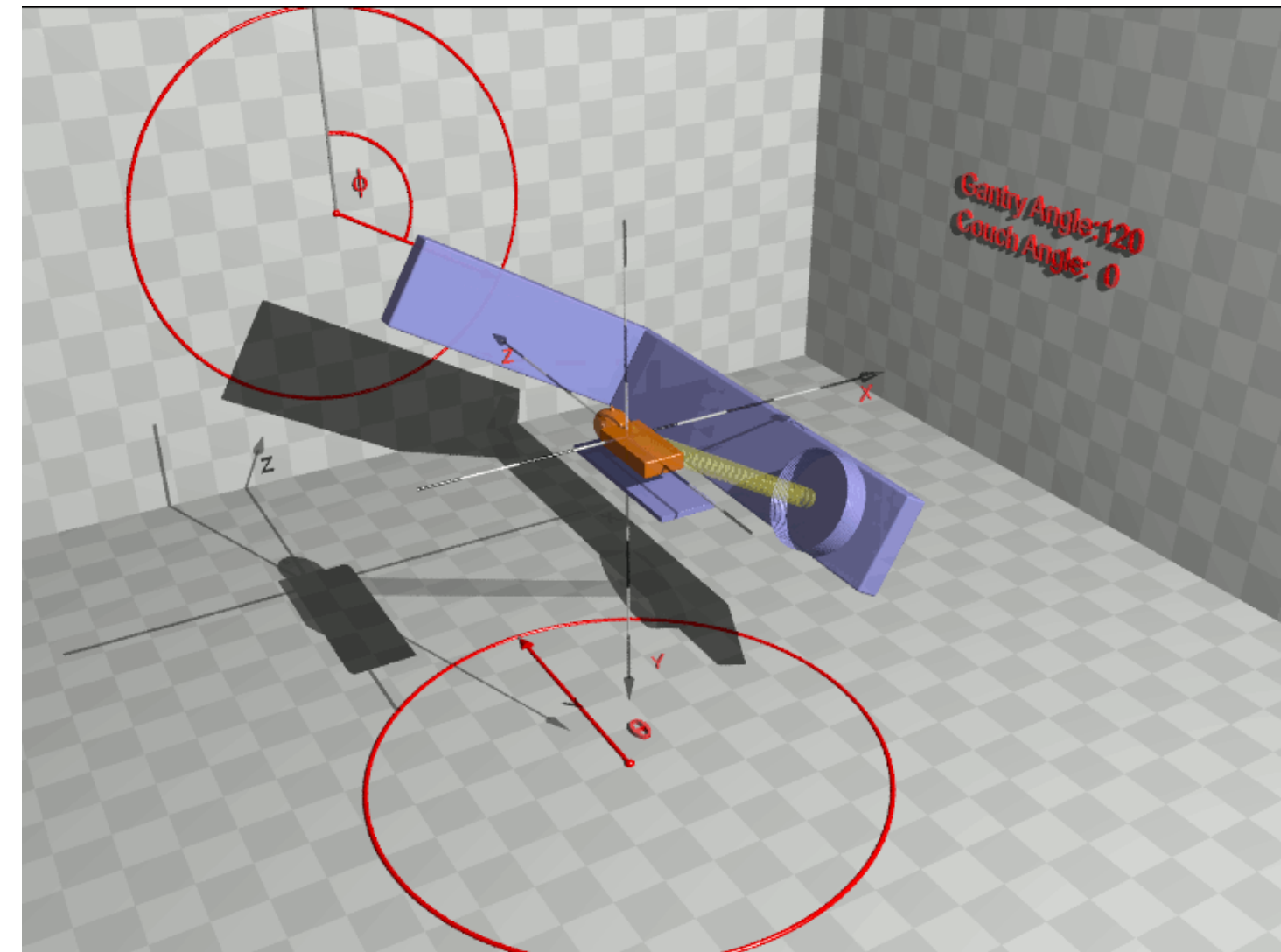
punto centrale del
fascio di particelle,
spuntare "Auto"

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 Set Tissue

☐ 3D conformal
☐ Run Sequencing
Stratification Levels

☐ Run Direct Aperture Optimization



Iniziamo: plan

bixel width

dimensioni della
griglia per il calcolo
(non modificare)

gantry and couch angle

due liste ordinate di
angoli per la gantry e
per il lettino (da 0° a
360°)

radiation mode

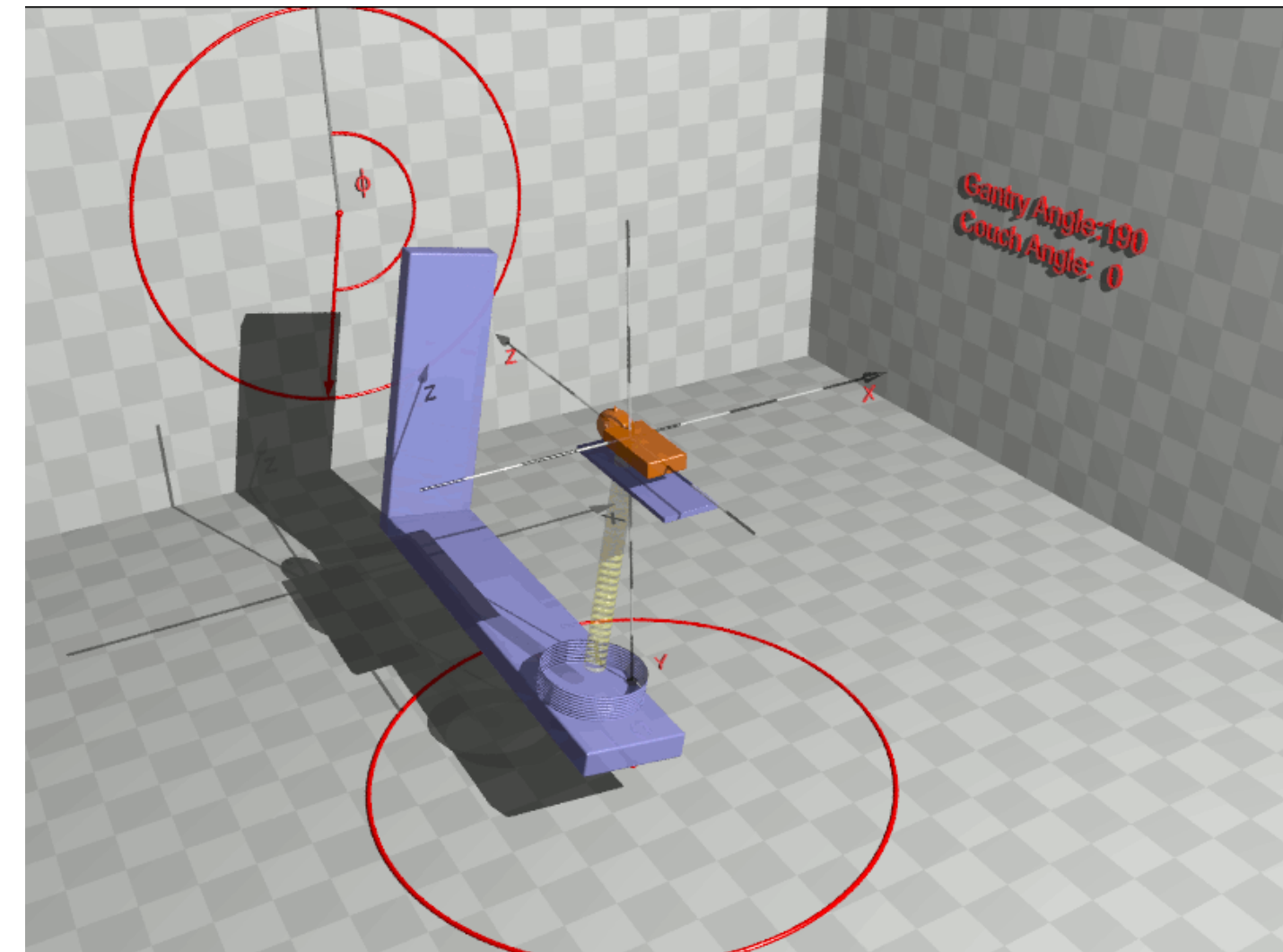
particella da
utilizzare nel
trattamento (fotoni,
protoni, ioni carbonio)

isocenter

punto centrale del
fascio di particelle,
spuntare "Auto"

Plan

bixel width in [mm]	5	
Gantry Angle in °	0	☐ 3D conformal
Couch Angle in °	0	☐ Run Sequencing
Radiation Mode	photons	Stratification Levels
Machine	Generic	7
IsoCenter in [mm]	0 0 0	☐ Run Direct Aperture Optimization
# Fractions	30	
Type of optimization	none	☐ Auto.
		Set Tissue



matRad

dkfz.

GERMAN
CANCER RESEARCH CENTER
IN THE HELMHOLTZ ASSOCIATION

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

Slice width in [mm]

Gantry Angle in °

Couch Angle in °

Radiation Mode

Machine

IsoCenter in [mm]

Fractions

Type of optimization

0

0

photons

Generic

0 0 0

Auto.

30

none

Set Tissue

☐ 3D conformal☐ Run Sequencing

Stratification Levels

7

☐ Run Direct Aperture Optimization

Objectives & constraints

Visualization

Slice Selection

Type of plot

intensity

GoTo

lateral

Beam Selection

Plane Selection

axial

Open 3D-View

Offset

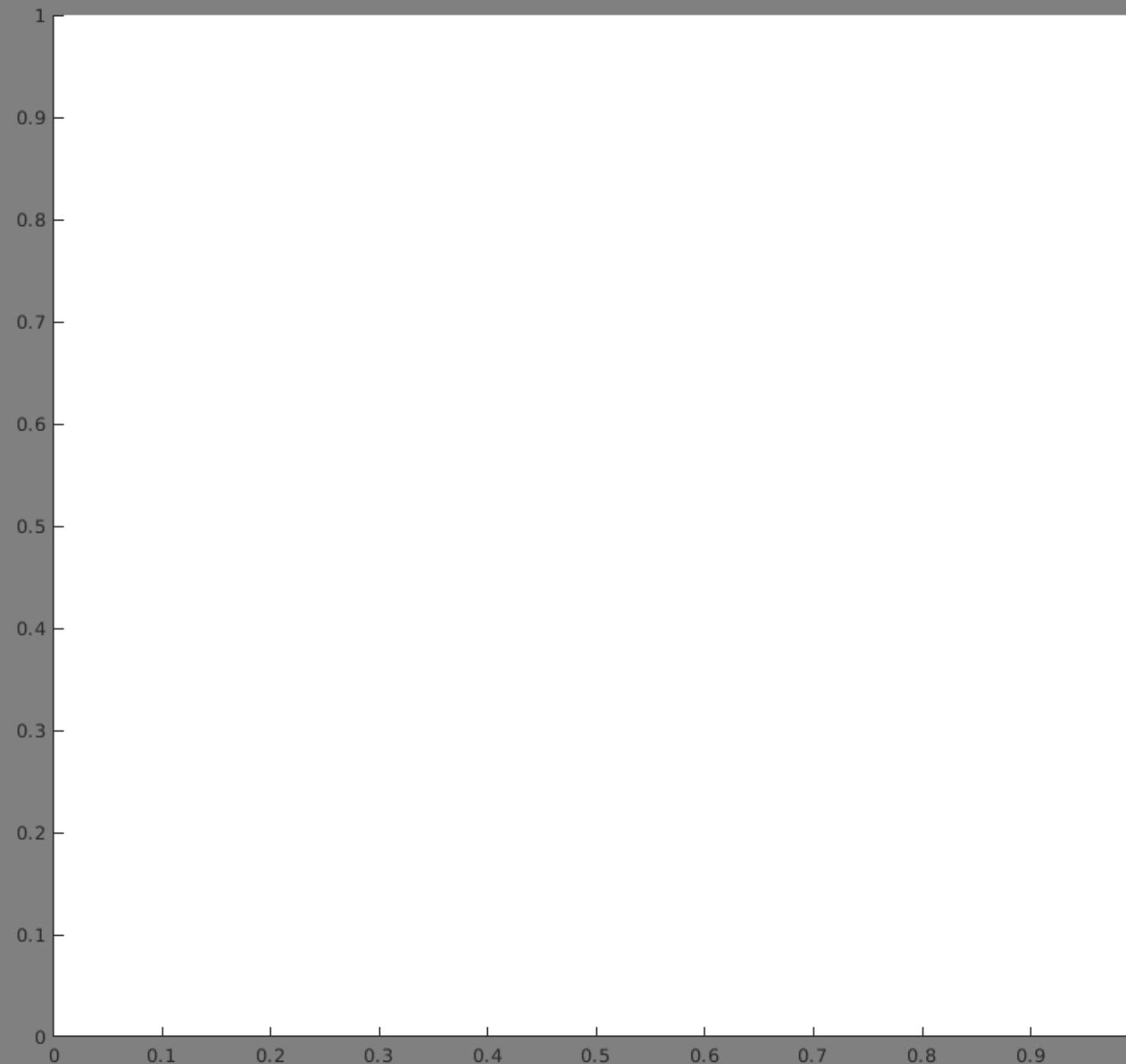
Display option

no option available

Show DVH/QI

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

Viewing

min value: -
max -
Set IsoDose Levels

Viewer Options

None

No available Window
Dose map

Window Center:

0.5

Window Width:

1.0

Range:

0 1

bone

☐ Lock Settings

Dose opacity:

0 1

Structure Visibility

no data loaded

Info

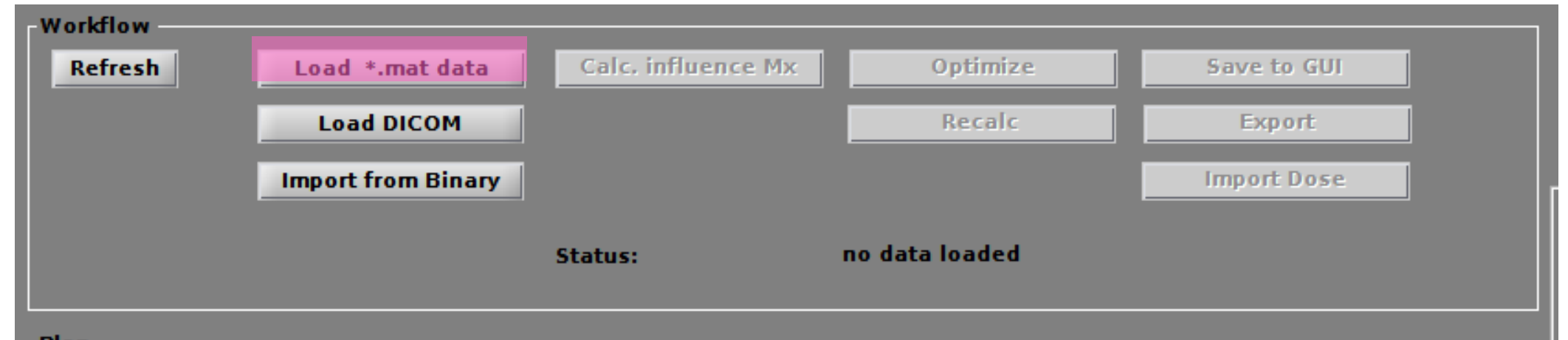
v2.10.1 "Blaise"

www.matRad.org

About

Iniziamo: workflow

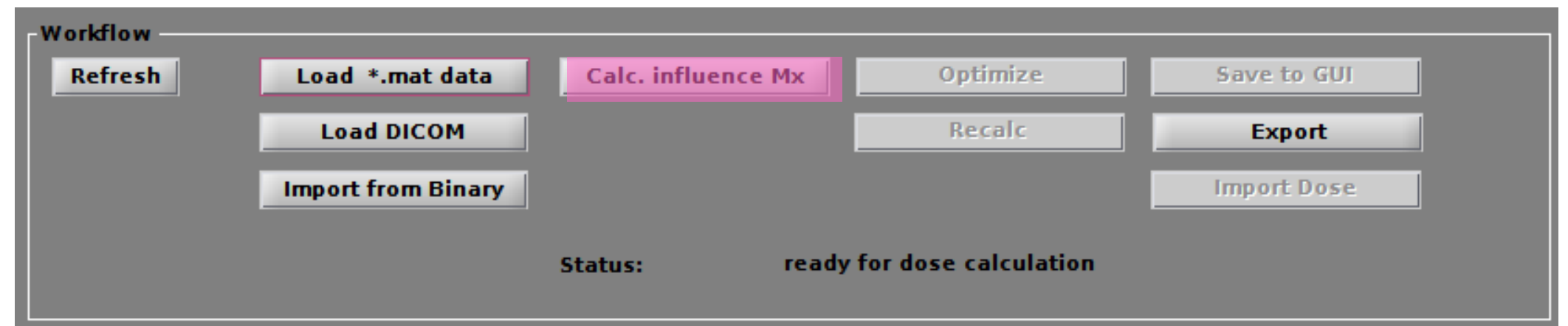
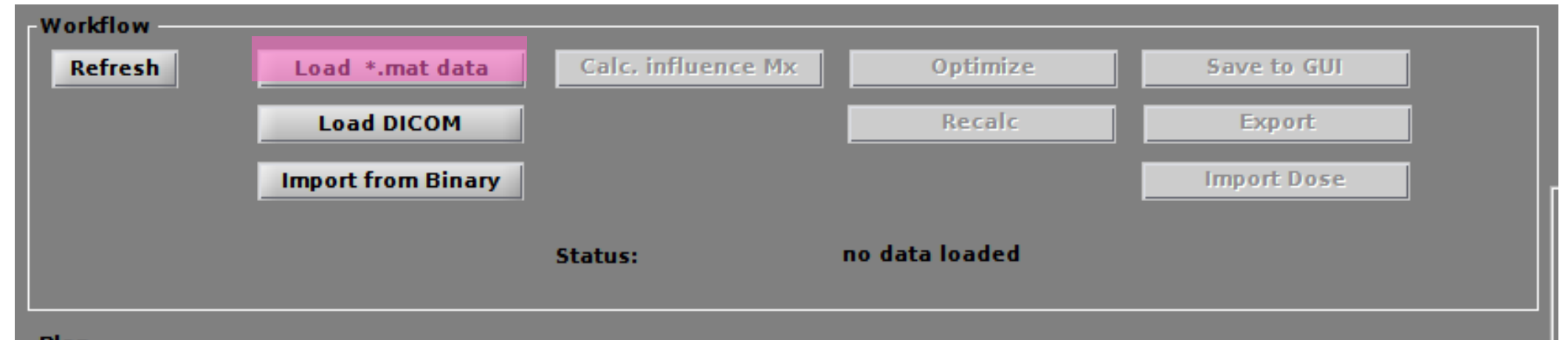
Premete "Load *.mat data"
e andate nella cartella MATRAD
applications/phantoms per
selezionare un caso studio



Iniziamo: workflow

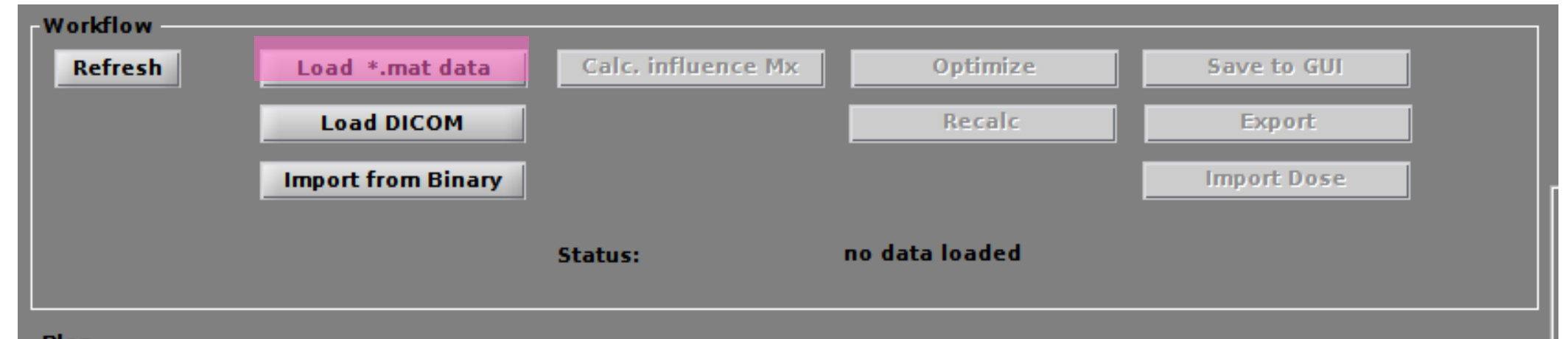
Premete "Load *.mat data"
e andate nella cartella MATRAD
applications/phantoms per
selezionare un caso studio

Premete "Calc. Influence MX"
per calcolare la matrice di influenza
relativa al caso in oggetto (apparirà
una barra di stato)

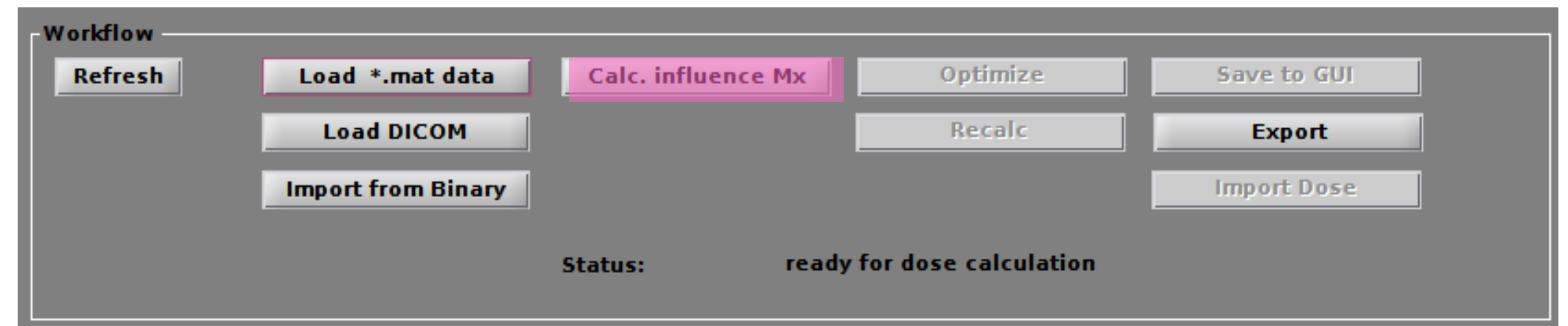


Iniziamo: workflow

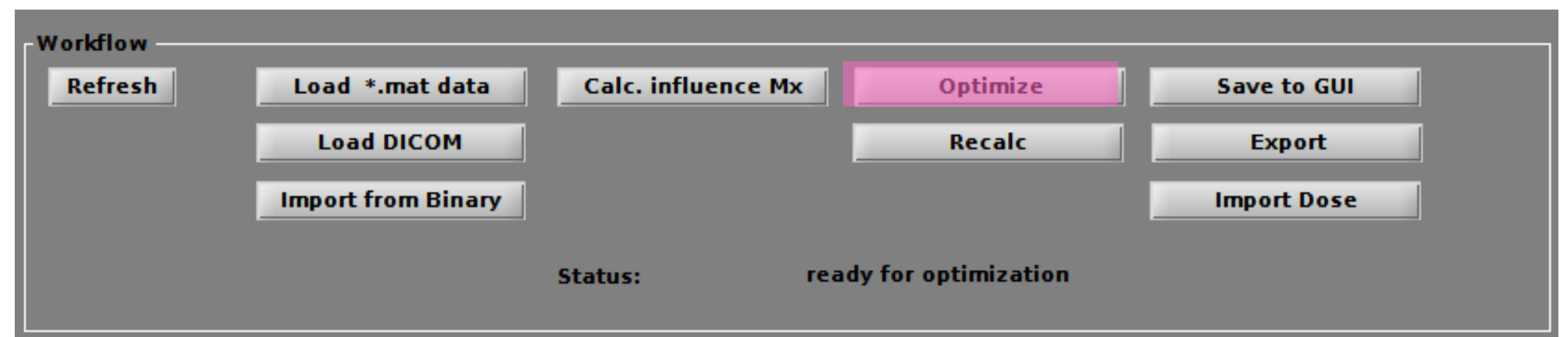
Premete "Load *.mat data"
e andate nella cartella MATRAD
applications/phantoms per
selezionare un caso studio



Premete "Calc. Influence MX"
per calcolare la matrice di influenza
relativa al caso in oggetto (apparirà
una barra di stato)



Ora il piano è pronto per
l'ottimizzazione quindi premete
"Optimize" (questa procedura può
durare un po')





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

Set Tissue

☐ 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

Open 3D-View

Offset

Display option physicalDose

Show DVH/QI

☒ plot CT

☒ plot contour

☒ plot isolines

☒ plot dose

☐ plot isolines labels

☒ plot iso center

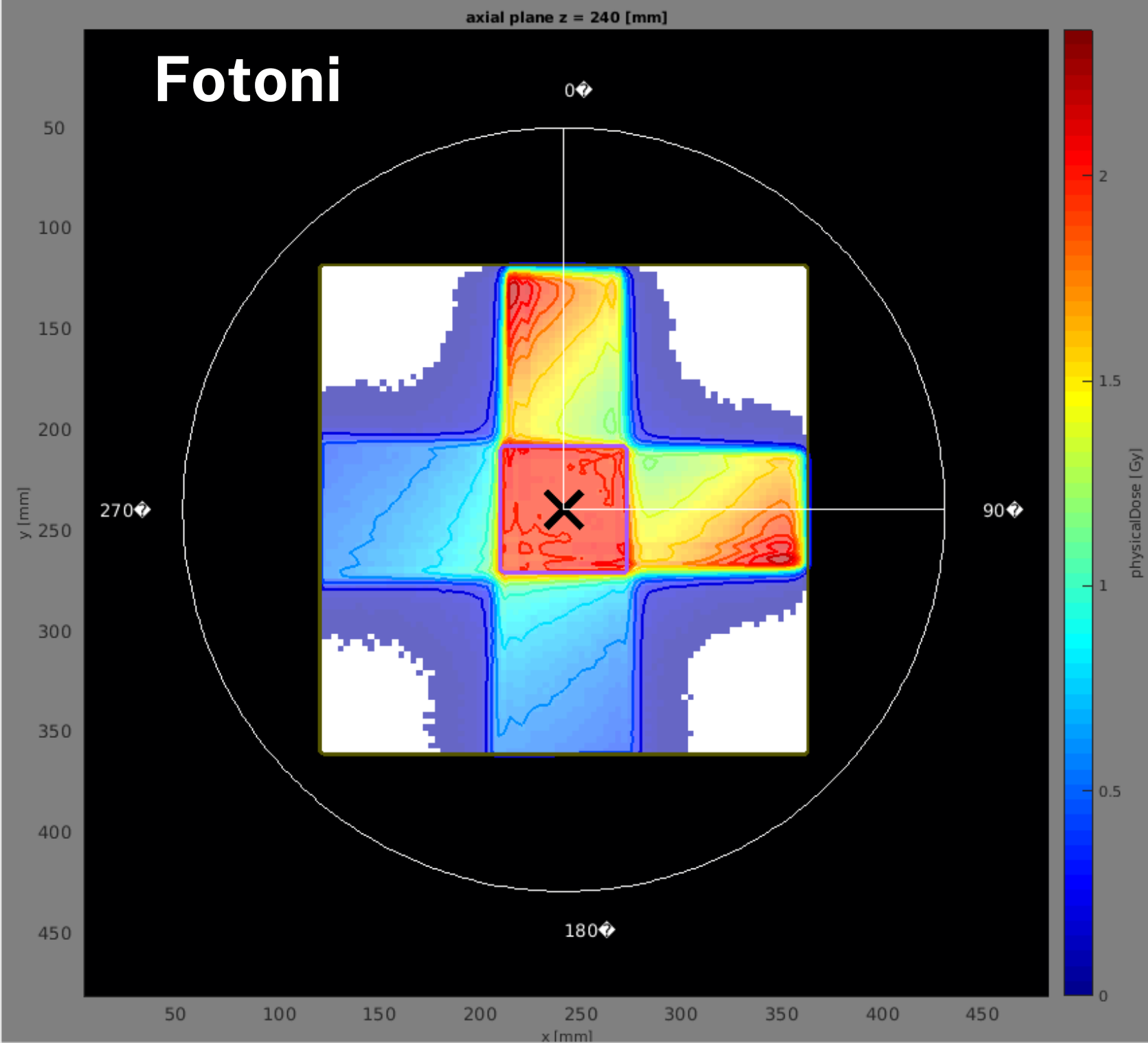
☒ visualize plan / beams

matRad

dkfz.

GERMAN
CANCER RESEARCH CENTER
IN THE HELMHOLTZ ASSOCIATION

Viewing





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

Couch Angle in °0

Radiation Modeprotons

MachineGeneric

IsoCenter in [mm]240 240 240

Fractions30

Type of optimizationconst_RBExD

3D conformal

Run Sequencing

Stratification Levels7

Run Direct Aperture Optimization

Auto.

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

Beam Selection

Offset

Type of plotintensity

Plane Selectionaxial

Display optionRBExDose

GoTo lateral

Open 3D-View

Show DVH/QI

plot CT

plot contour

plot isolines

plot dose

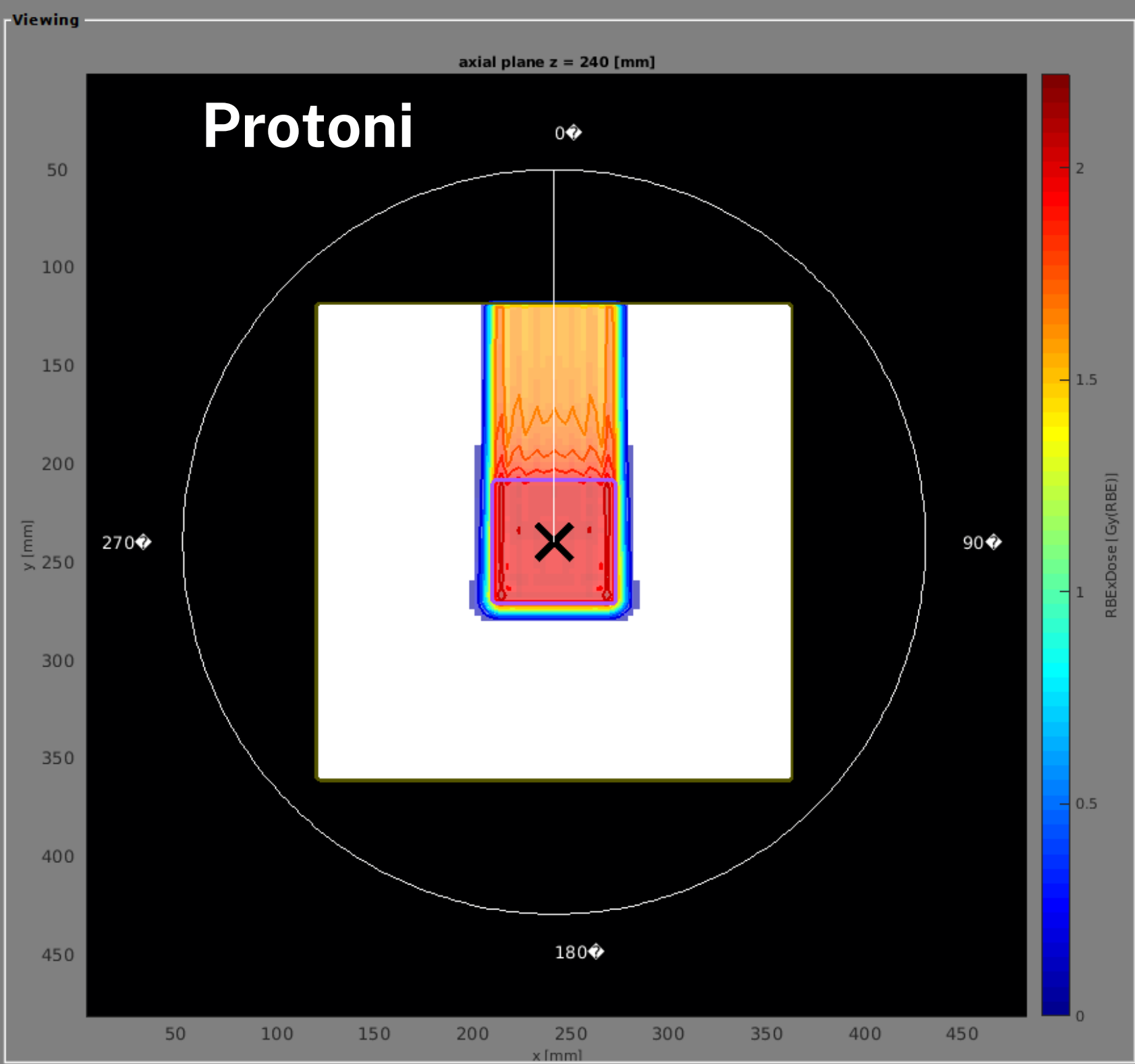
plot isolines labels

plot iso center

visualize plan / beams



GERMAN
CANCER RESEARCH CENTER
IN THE HELMHOLTZ ASSOCIATION





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

Couch Angle in °

0

Radiation Mode

carbon

Machine

Generic

IsoCenter in [mm]

240 240 240

☒ Auto.

Fractions

30

Type of optimization

LEMIV_RBExD

Set Tissue

☐ 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

Beam Selection

Offset

Type of plot

intensity

Plane Selection

axial

Open 3D-View

Display option

RBExDose

Show DVH/QI

☒ plot CT

☒ plot contour

☒ plot isolines

☒ plot dose

☐ plot isolines labels

☒ plot iso center

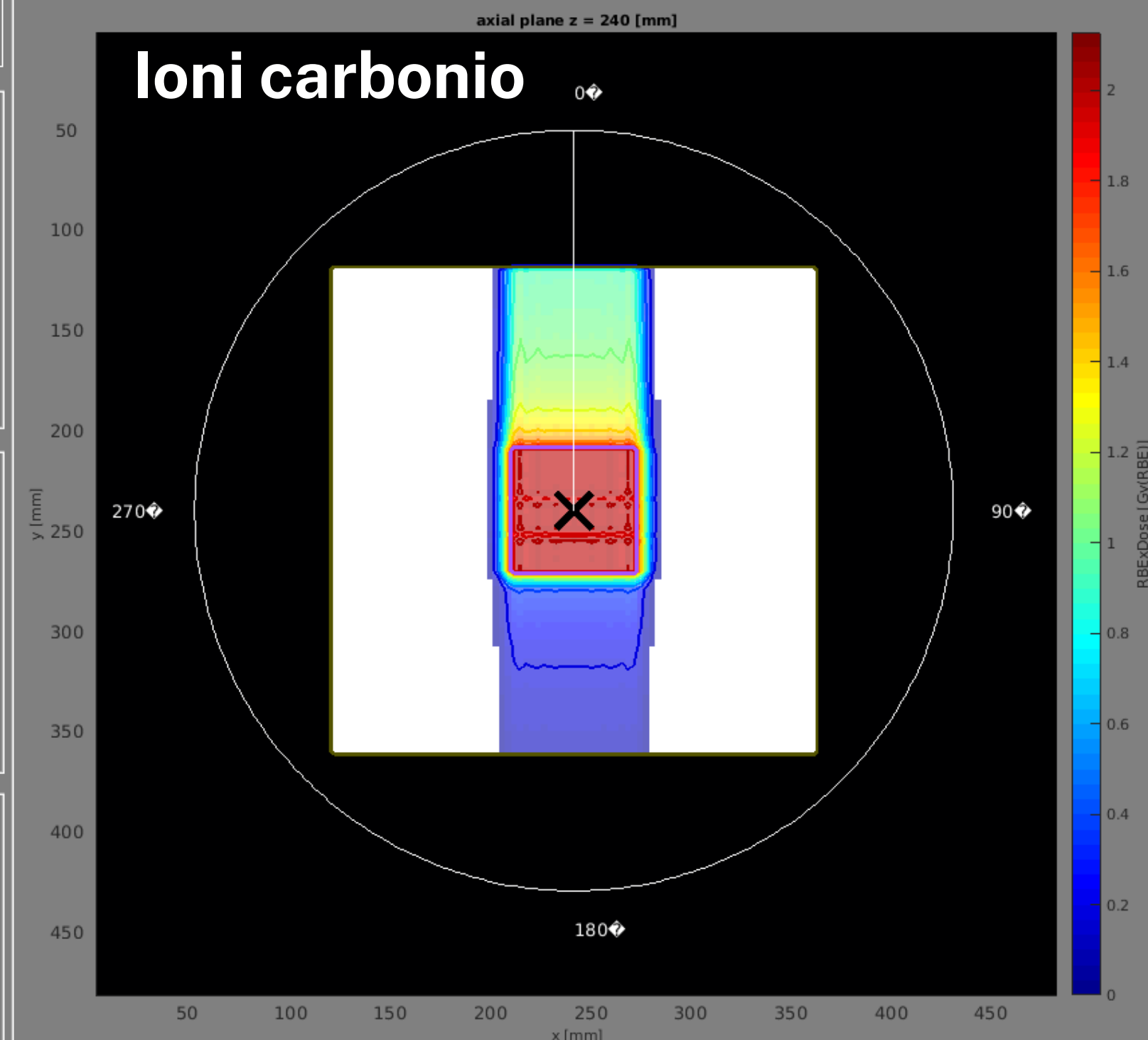
☒ visualize plan / beams

matRad

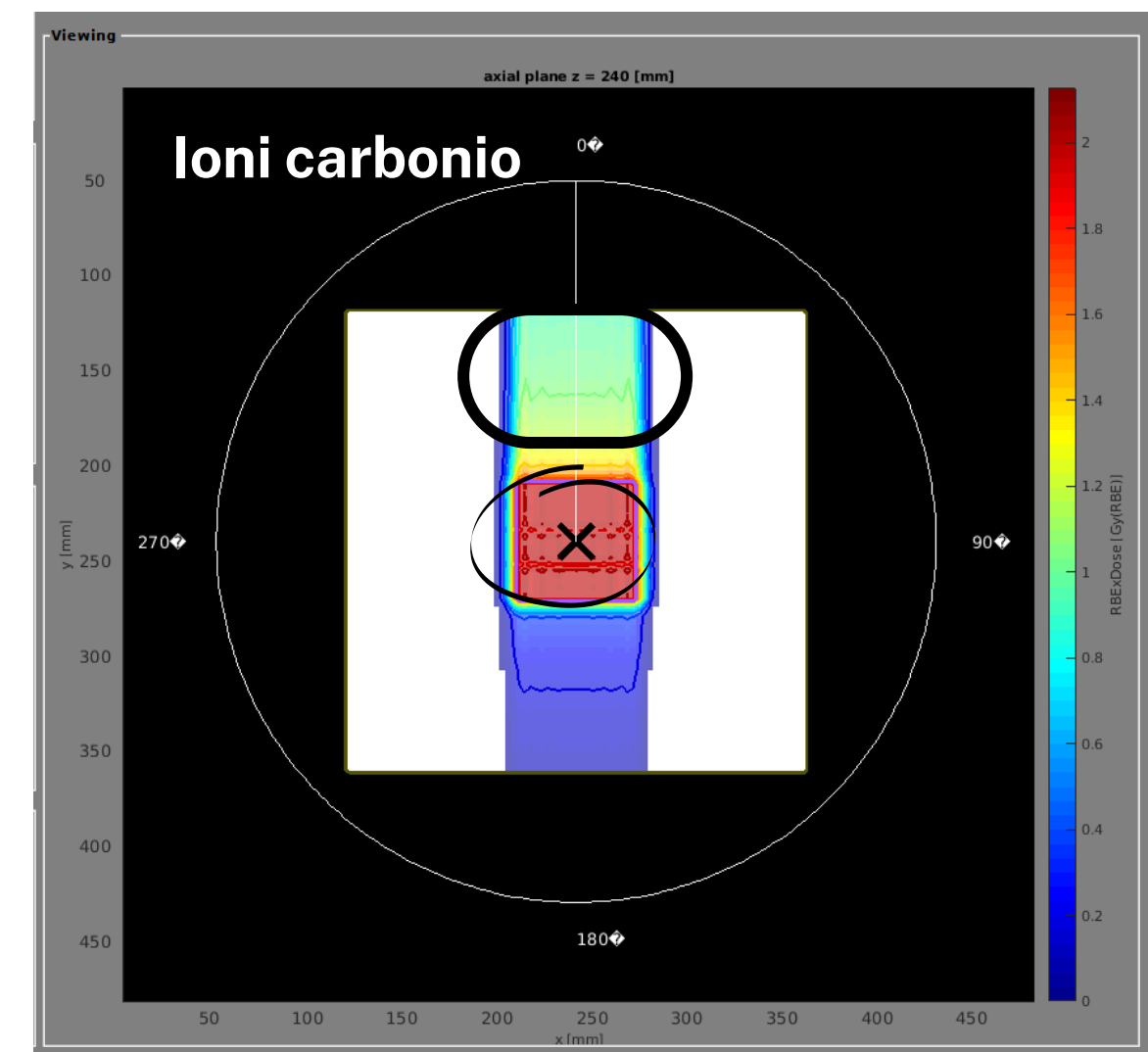
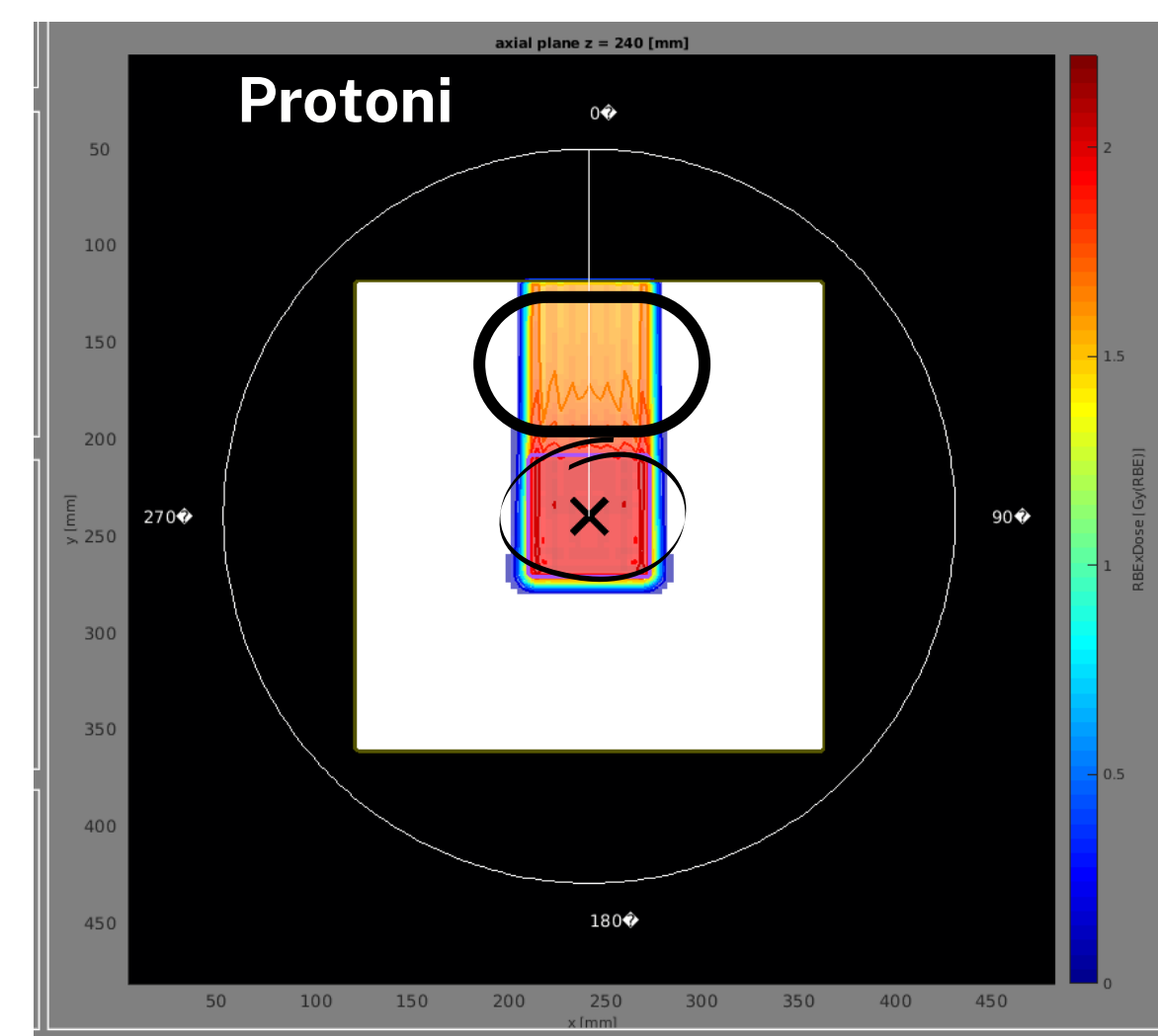
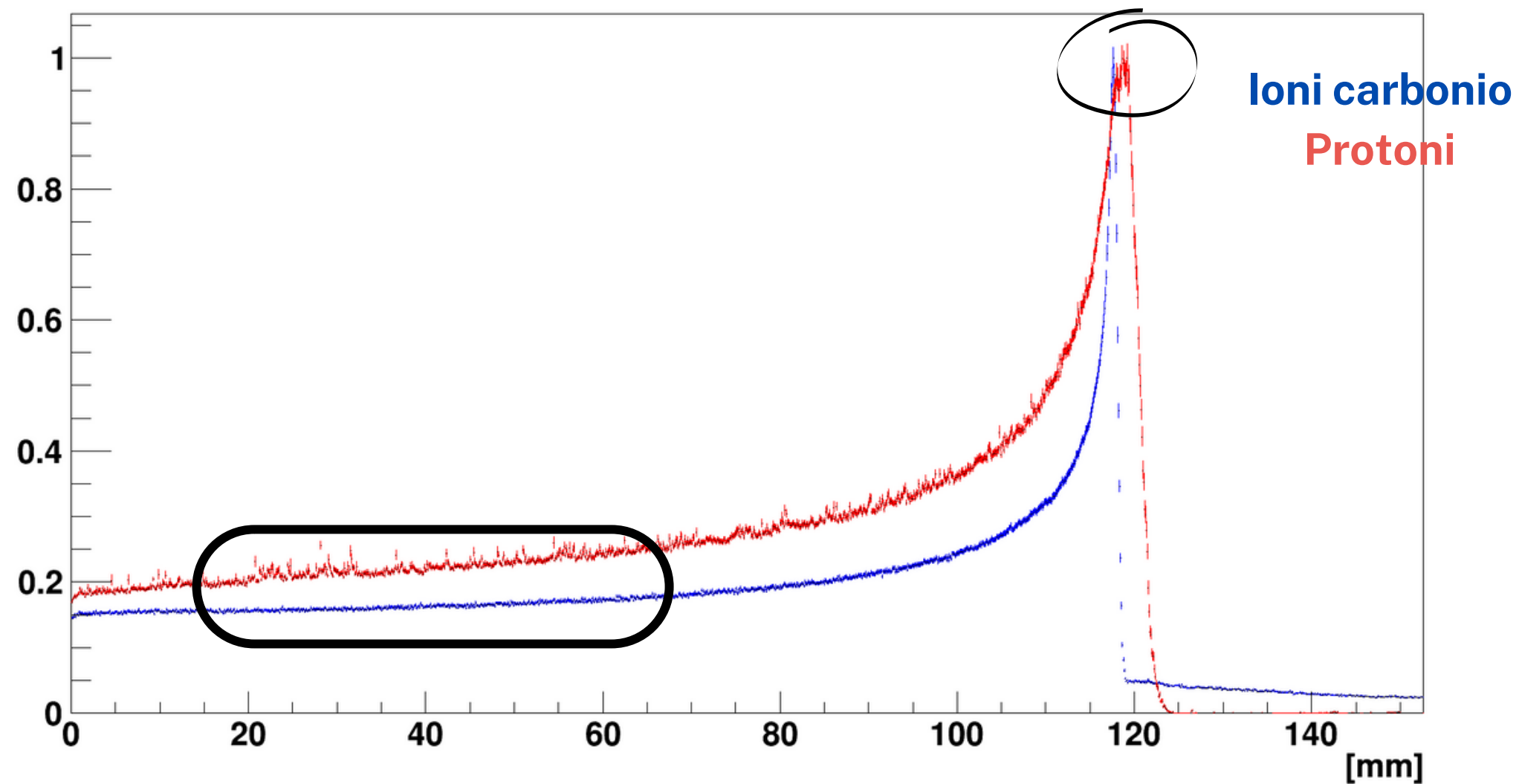
dkfz.

GERMAN
CANCER RESEARCH CENTER
IN THE HELMHOLTZ ASSOCIATION

Viewing

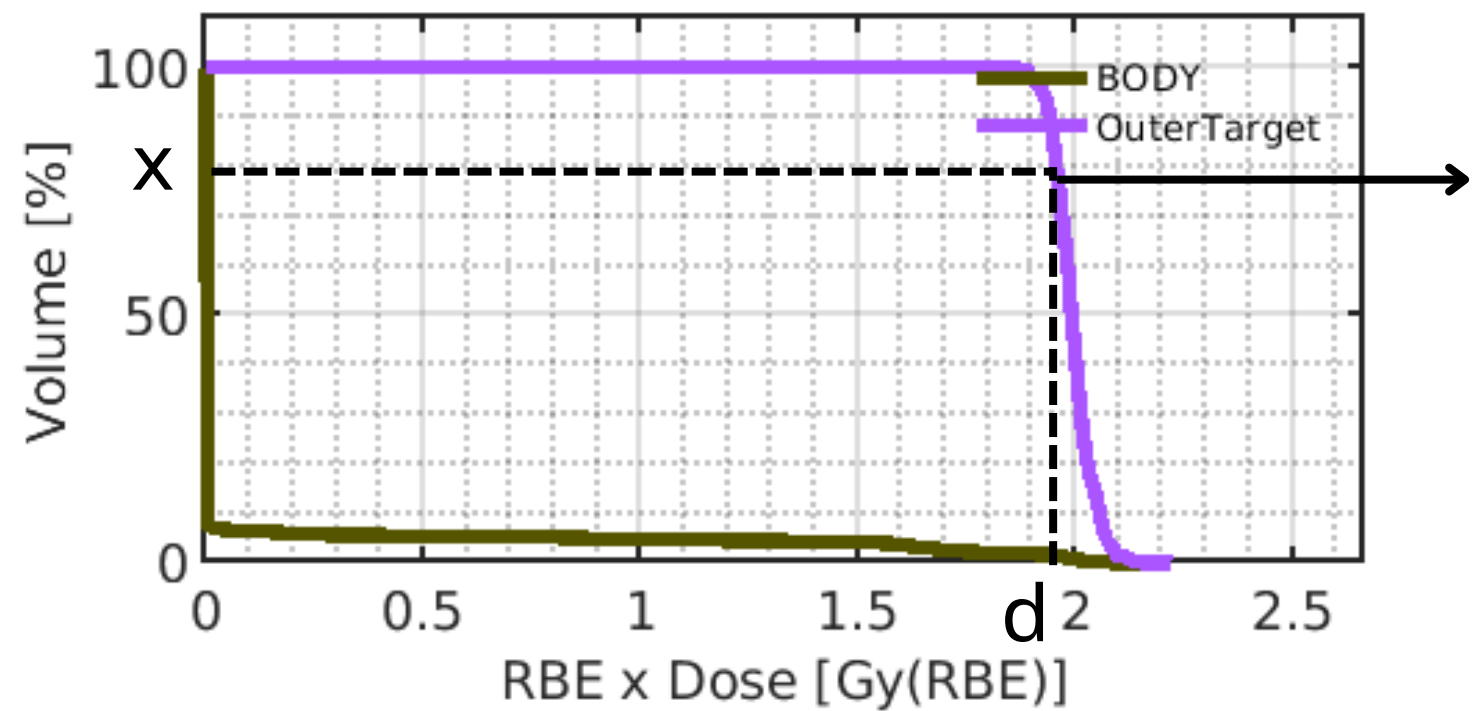


Al netto della "coda", gli ioni carbonio rilasciano meno dose nei tessuti sani a parità di dose rilasciata nel tumore!



Strumenti utili: DVH

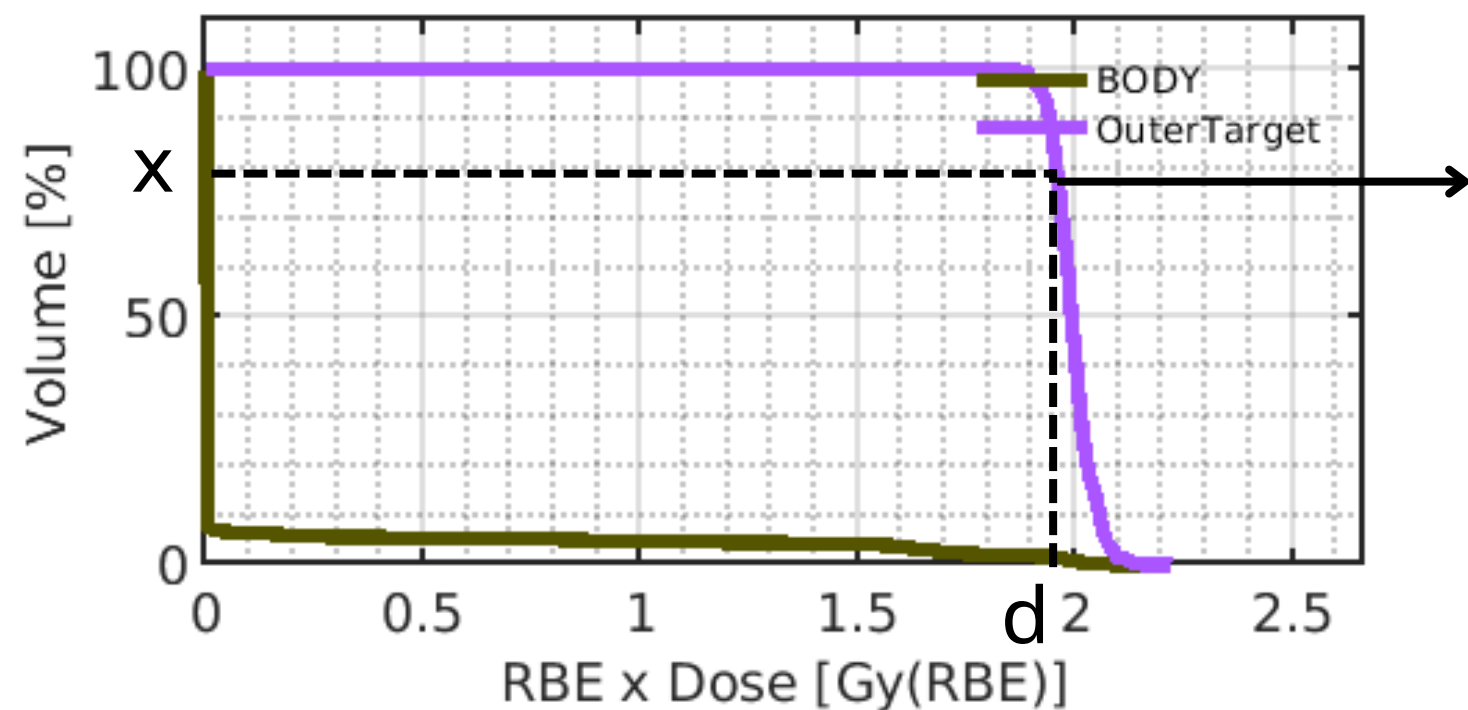
DVH (Dose Volume Histogram) è uno strumento molto utile per valutare la bontà di un piano di trattamento



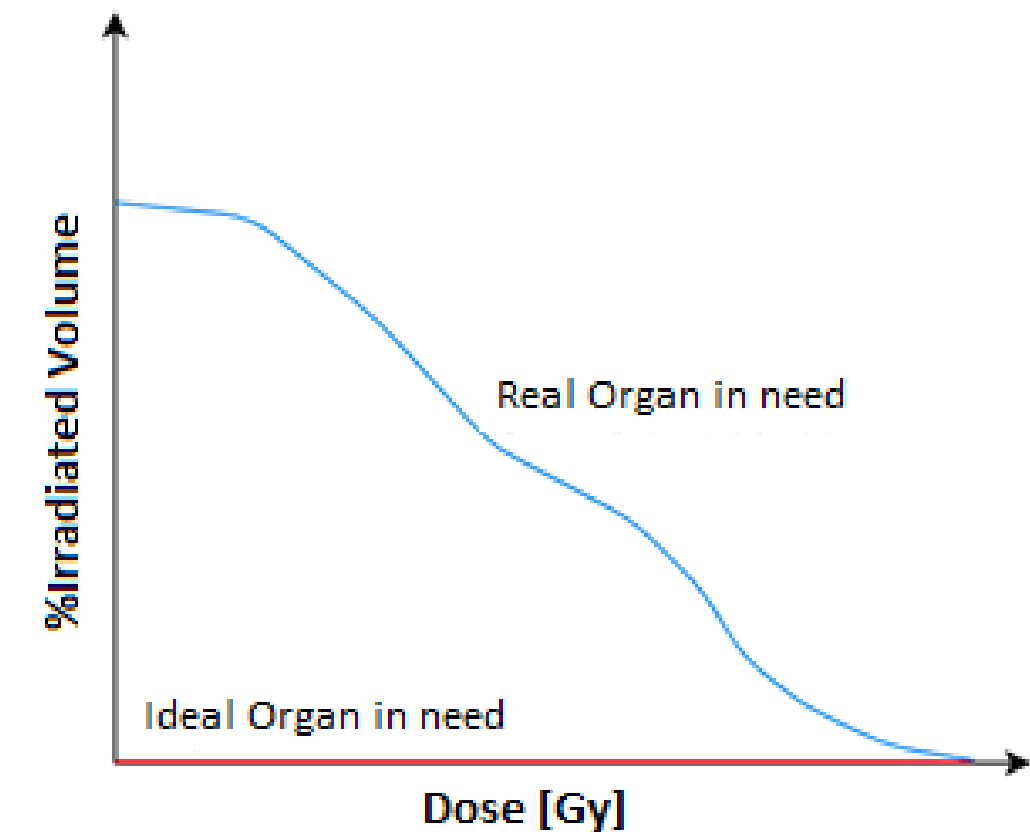
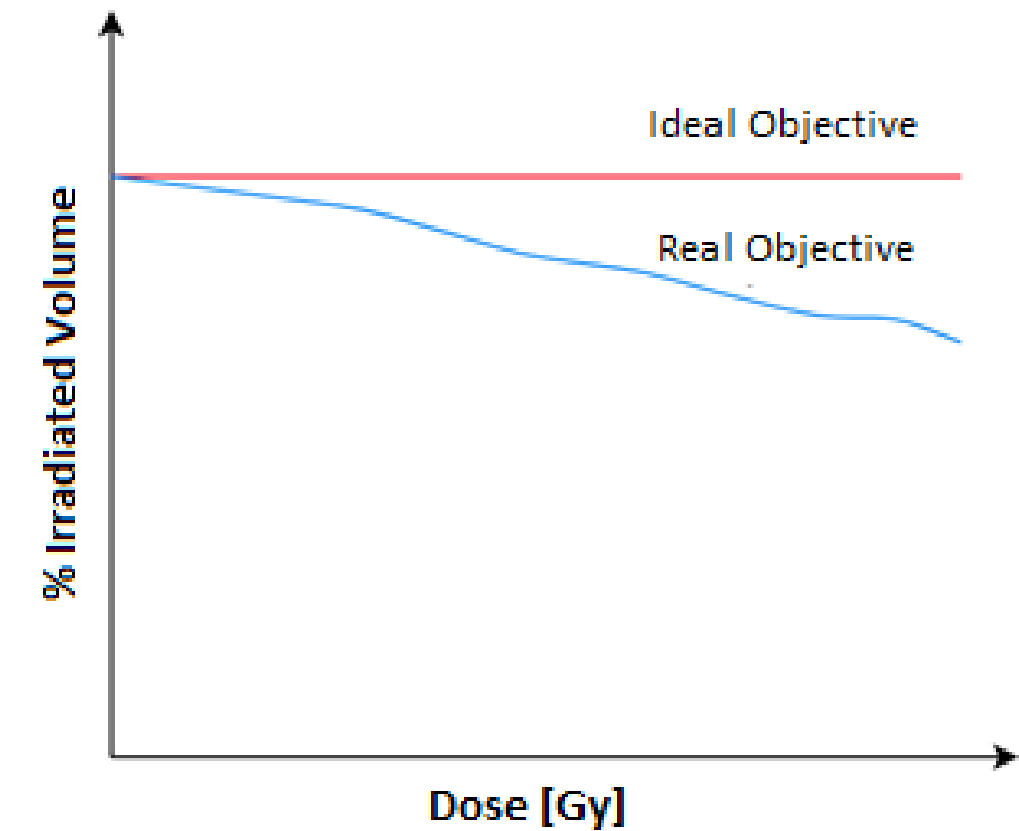
x% del volume ha ricevuto almeno una dose d

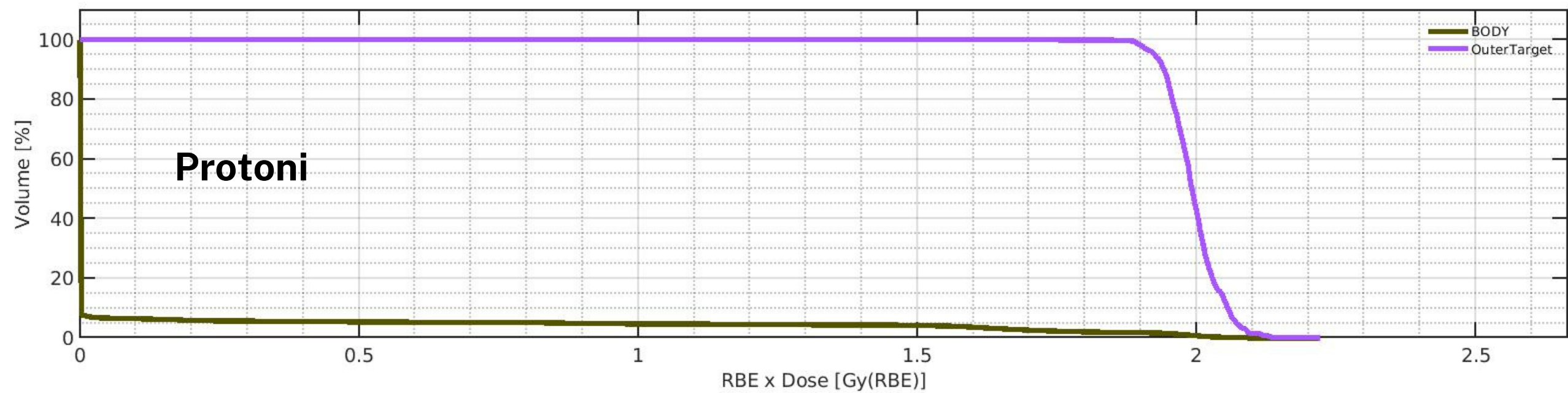
Strumenti utili: DVH

DVH (Dose Volume Histogram) è uno strumento molto utile per valutare la bontà di un piano di trattamento

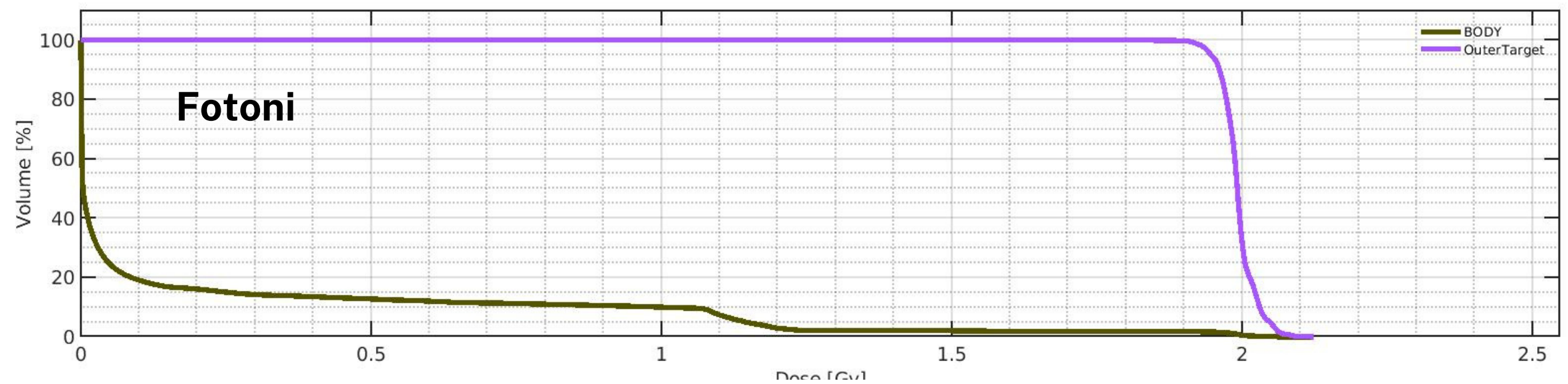


x% del volume ha ricevuto almeno una dose d



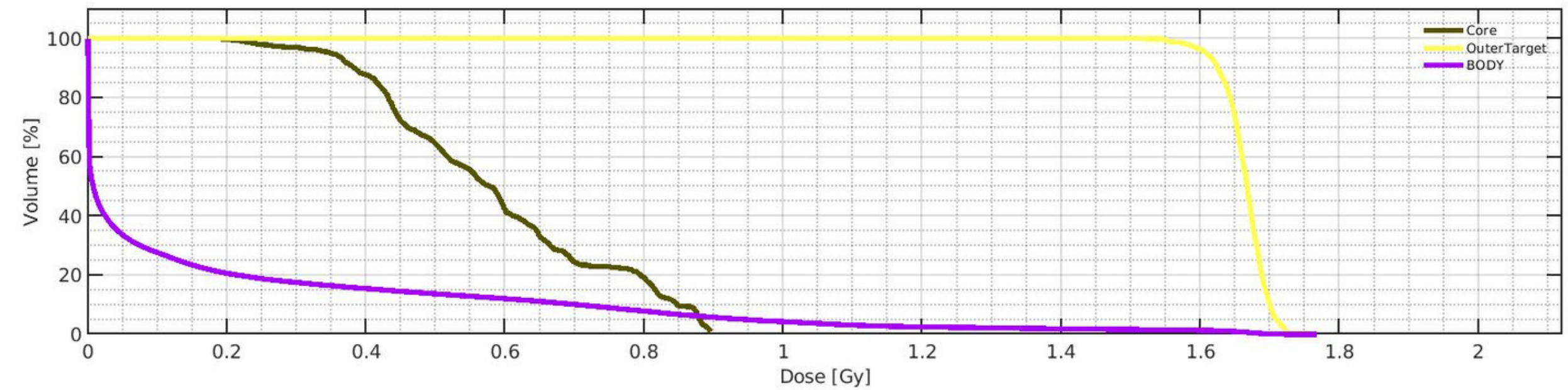
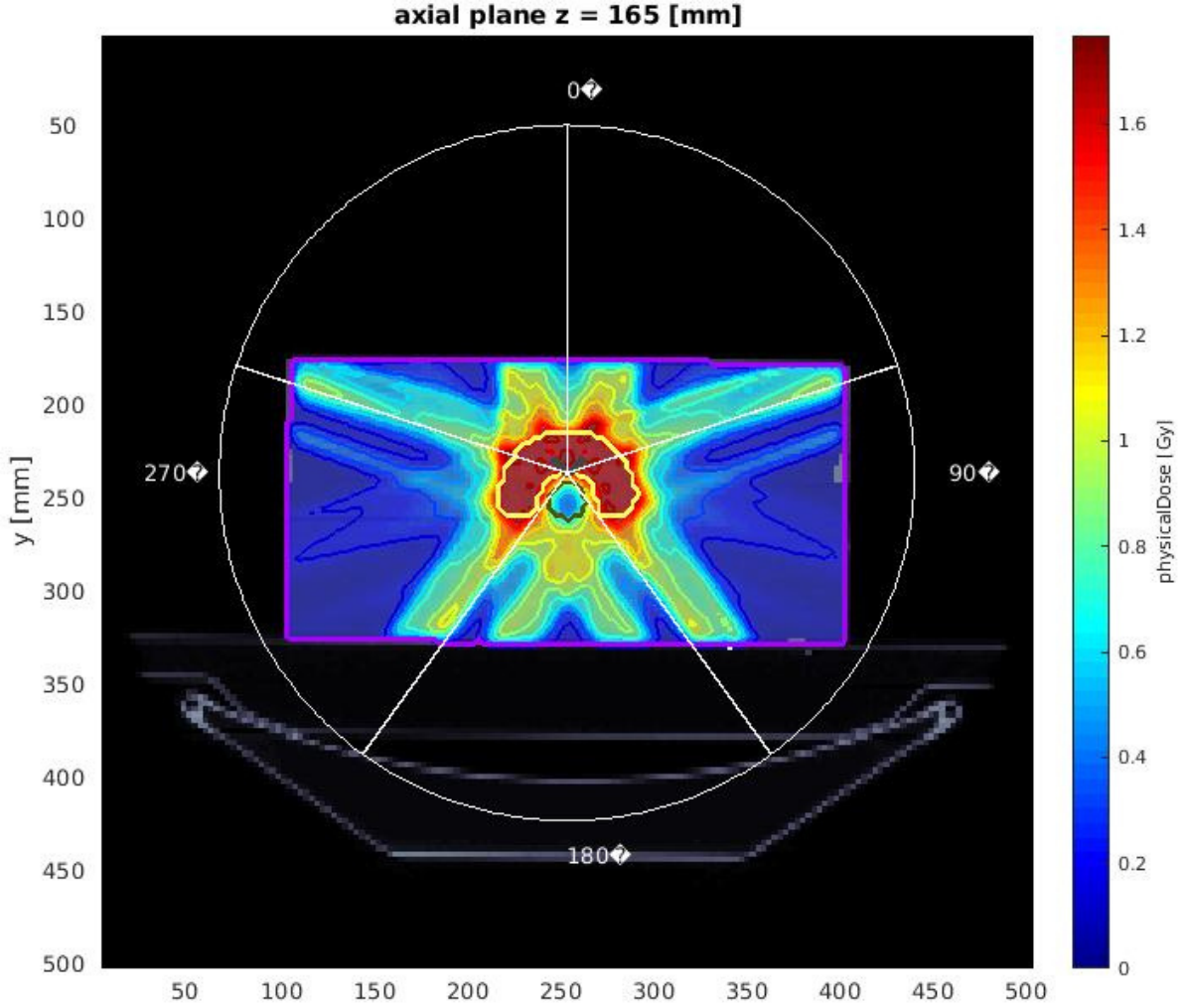


	mean	std	max	min	D_2	D_5	D_50	D_95	D_98	V_0Gy	V_0.4Gy	V_0.8Gy	V_1.3Gy	V_1.7Gy	V_2.2Gy	CI_2Gy	H_2Gy
BODY	0.0904	0.3789	2.2224	0	1.8071	0.8541	0	0	0	1	0.0551	0.0513	0.0442	0.0263	7.5267e...	-	-
OuterTarget	1.9940	0.0455	2.2224	1.7502	2.0924	2.0710	1.9916	1.9252	1.9010	1	1	1	1	1	4.3192e...	0.9510	7.3001

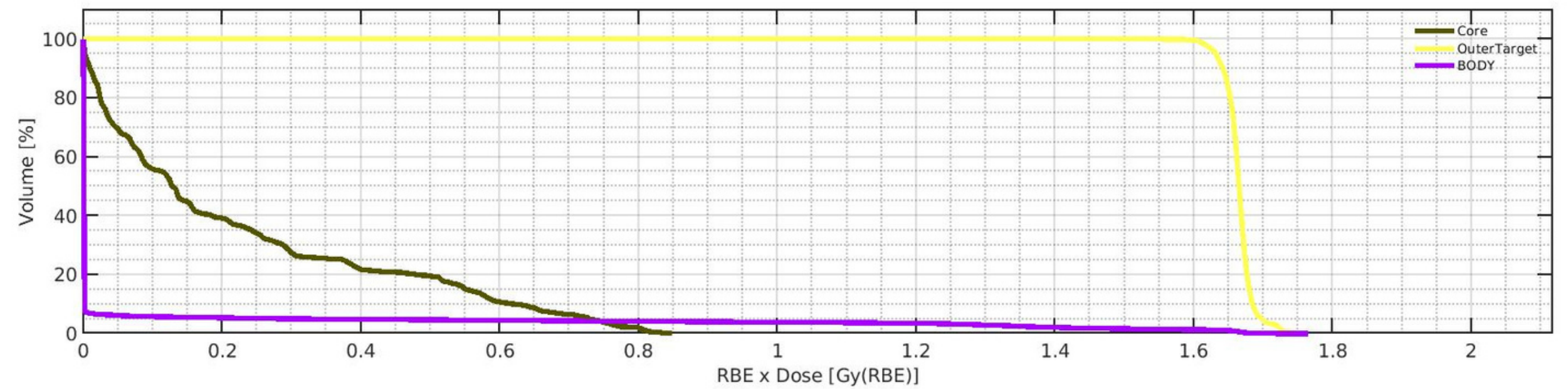
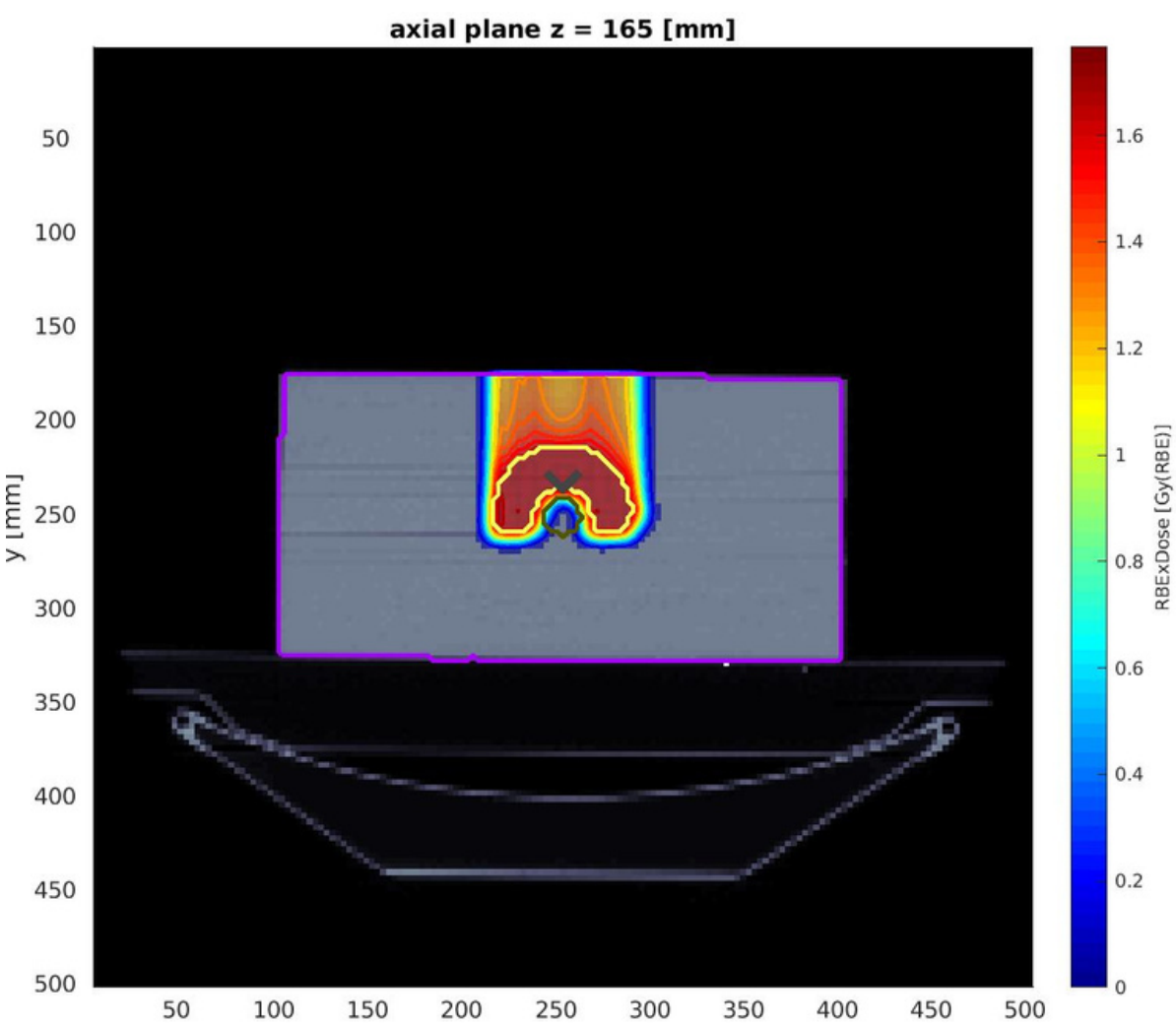


	mean	std	max	min	D_2	D_5	D_50	D_95	D_98	V_0Gy	V_0.4Gy	V_0.8Gy	V_1.2Gy	V_1.6Gy	V_2.1Gy	CI_2Gy	H_2Gy
BODY	0.1731	0.4109	2.1239	0	1.5308	1.1449	0.0036	0	0	1	0.1353	0.1101	0.0292	0.0176	1.8817e...	-	-
OuterTarget	1.9900	0.0290	2.1239	1.8441	2.0906	2.0479	1.9916	1.9464	1.9312	1	1	1	1	1	0.0011	0.9975	5.0750

Procediamo con il caso TG119



	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	CI_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	-	-



	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	CI_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...	-	-