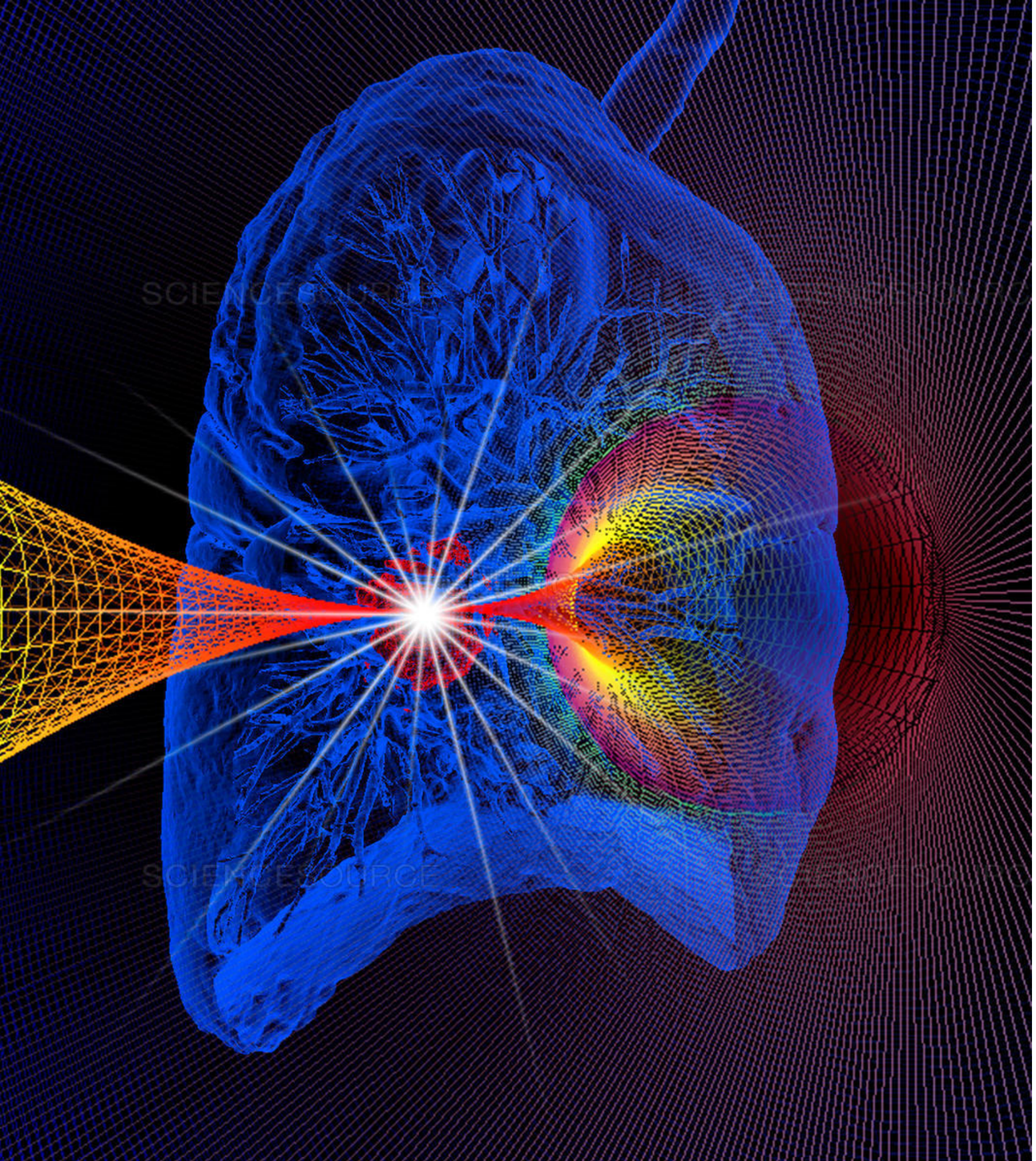
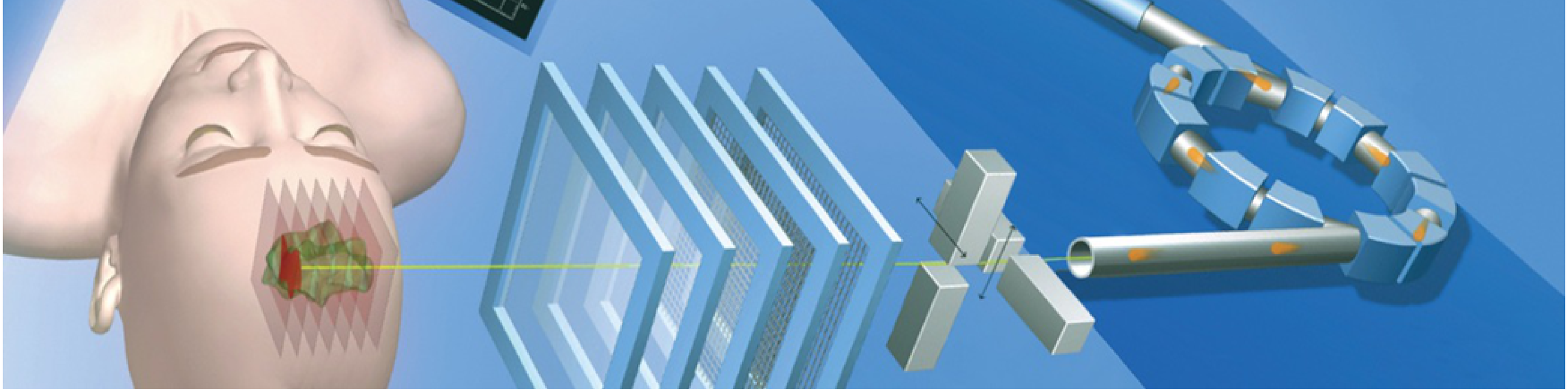


MATRAD

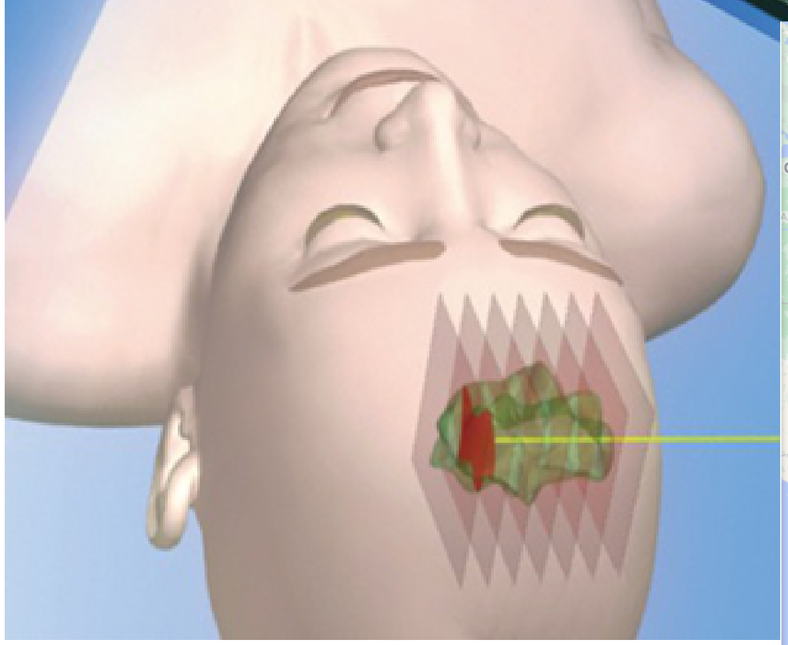
Riccardo.Ridolfi@bo.infn.it



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



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INFN BOLOGNA

Qualche definizione prima di iniziare...

GTV

VOLUME DELLA MASSA TUMORALE VISIBILE DALLA CT/MRI

PTV

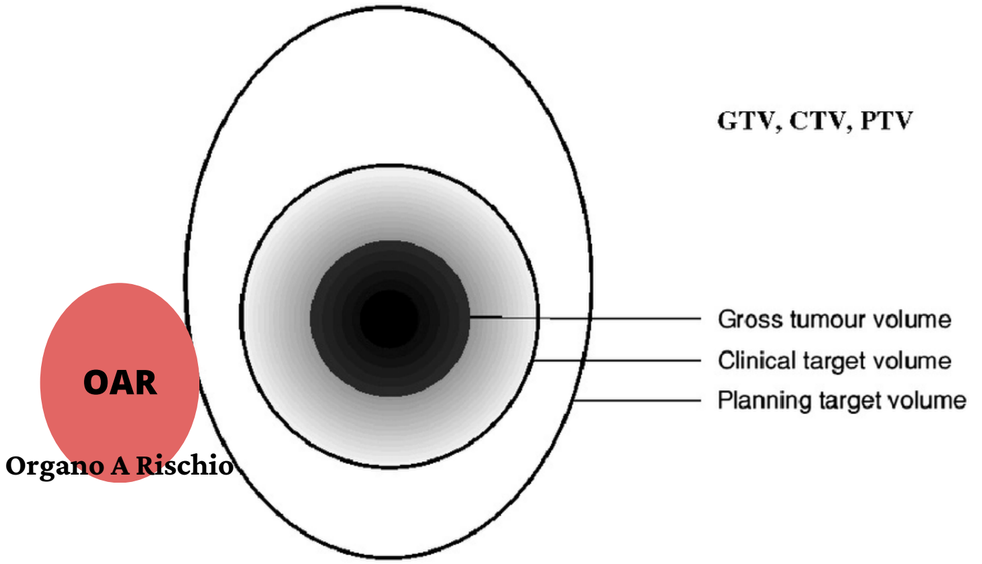
VOLUME DA IRRADIARE (CTV + INCERTEZZE)

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

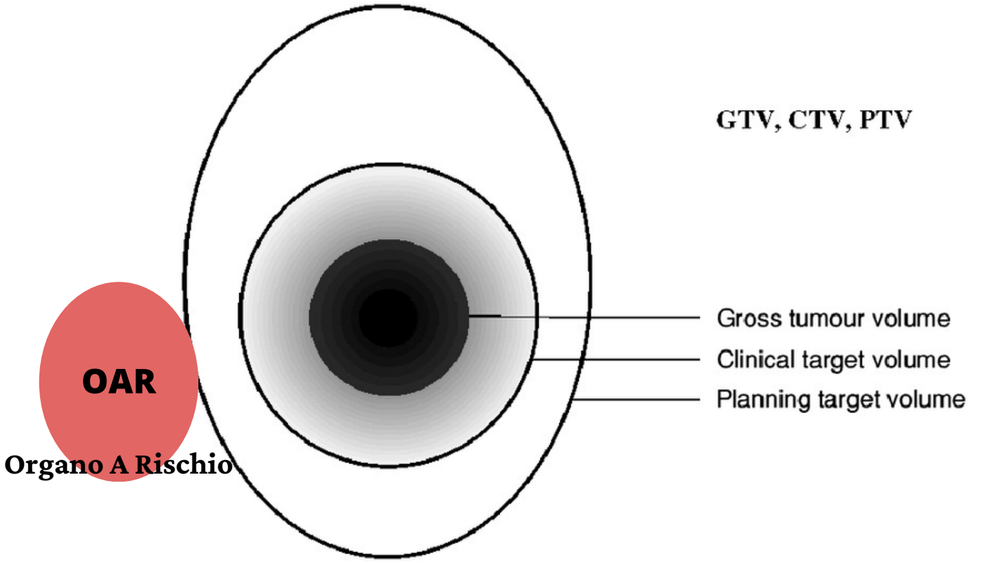
VOLUME DA IRRADIARE (CTV + INCERTEZZE)

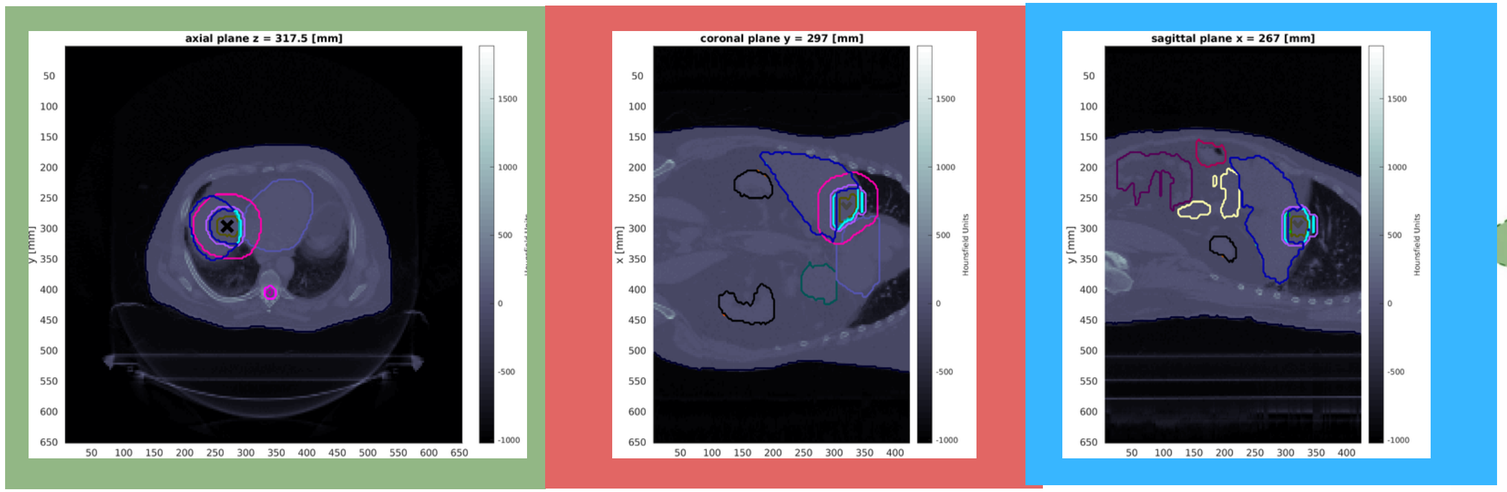
CTV

VOLUME DOVE SI TEME POSSANO ESSERCI CELLULE TUMORALI NON VISIBILI

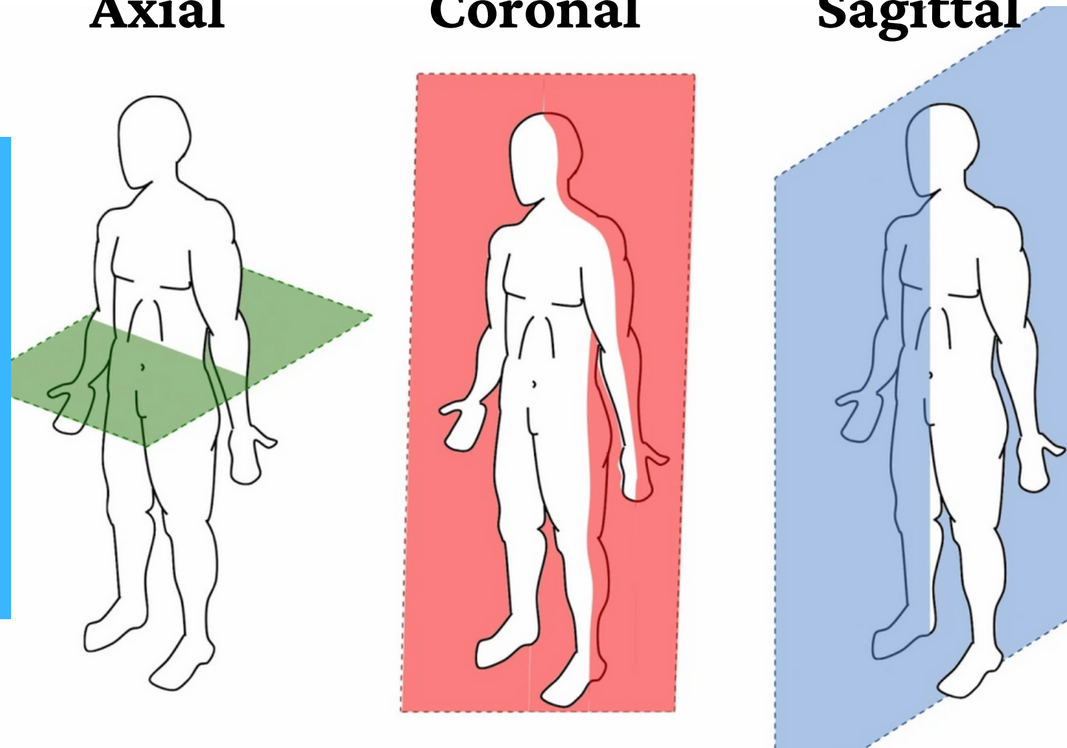
OAR

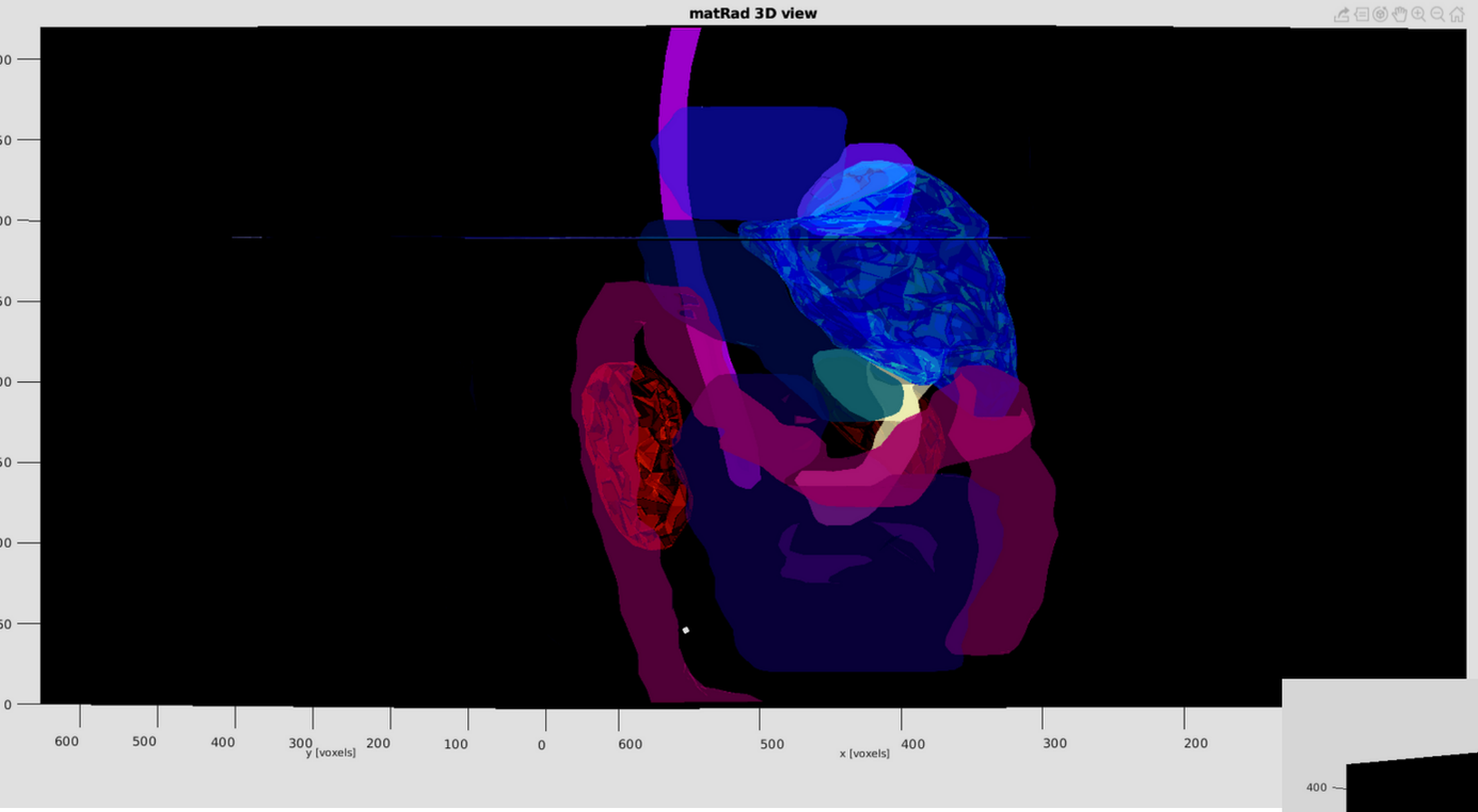
ORGANO SENSIBILE ALLA RADIAZIONE CHE VA RISPARMIATO IL PIÙ POSSIBILE



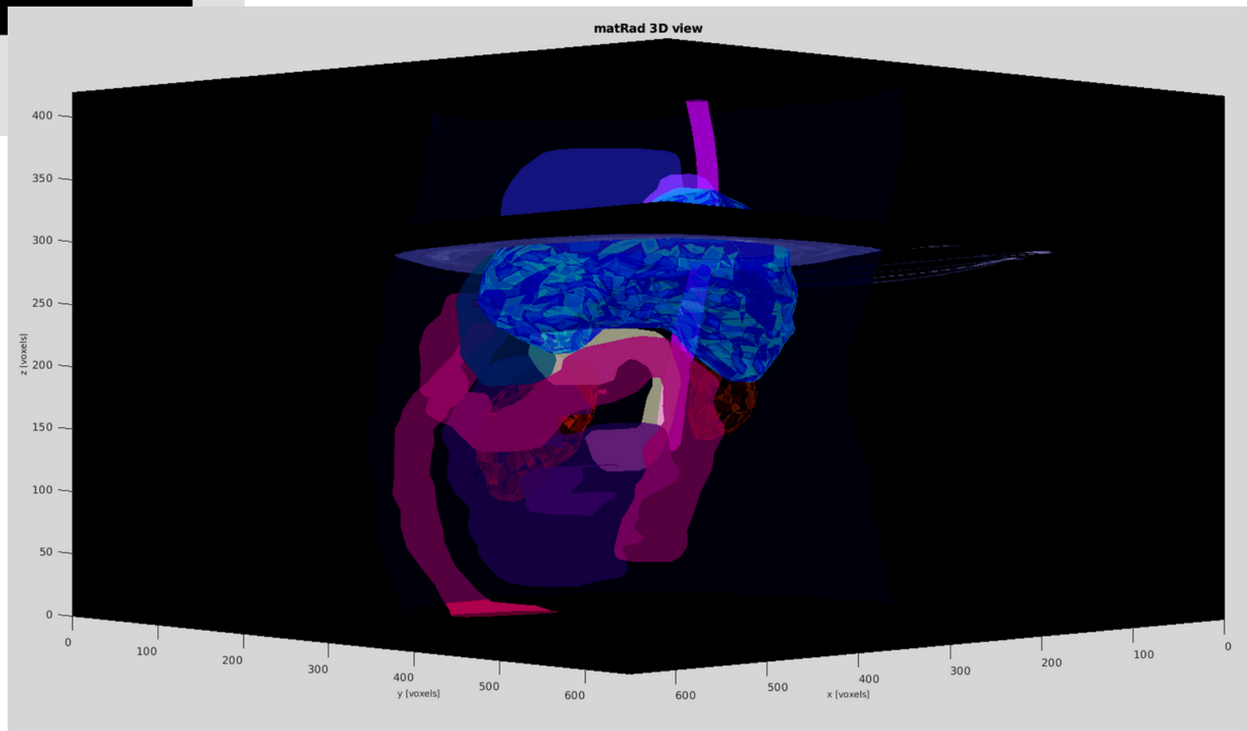


Axial **Coronal** **Sagittal**





Vista 3D



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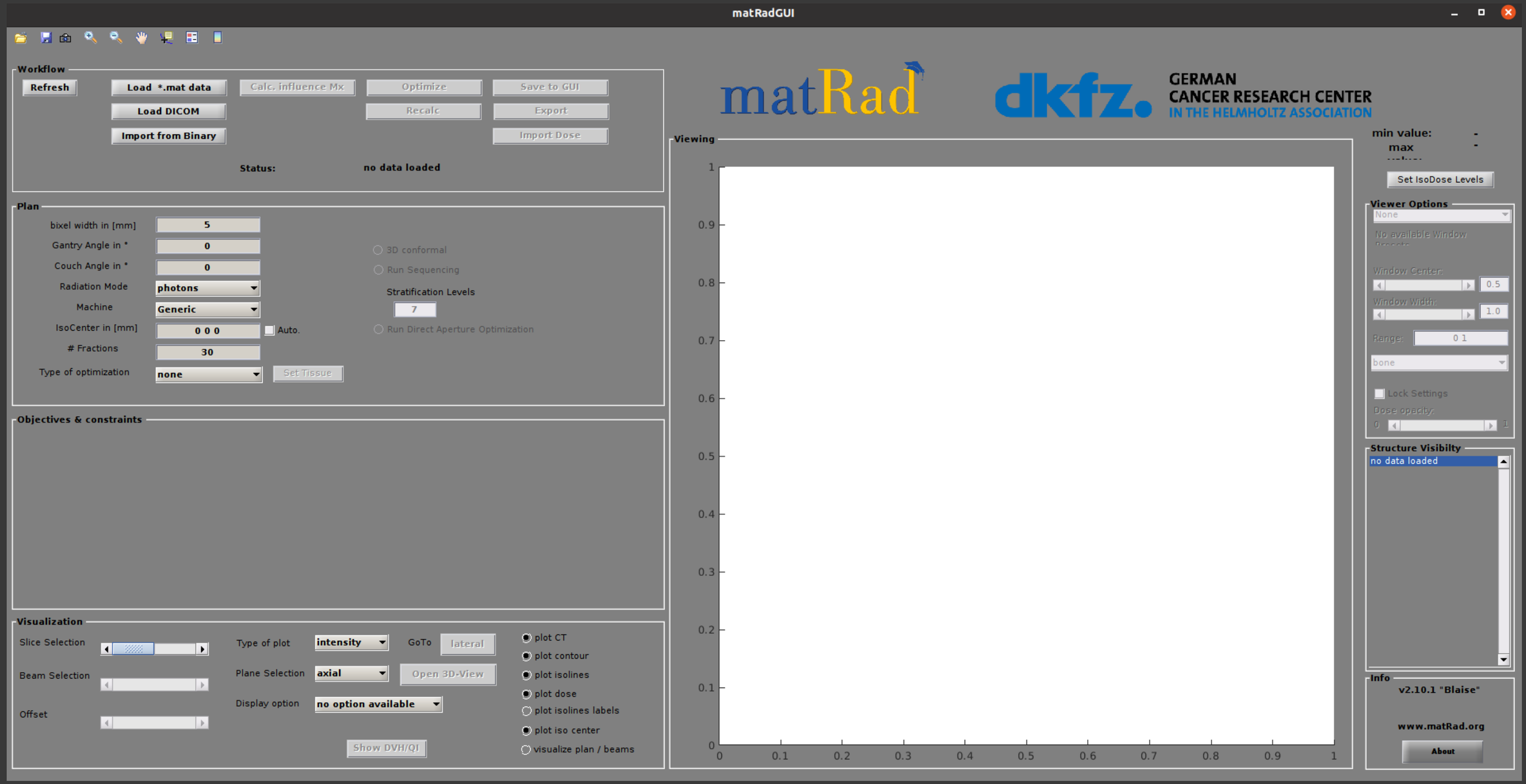
matRadGUI
Workflow
Refresh
Load *.mat data
Calc. influence Mx
Optimize
Save to GUI
Load DICOM
Recalc
Export
Import from Binary
Import Dose
Status:
no data loaded
matRad
dkfz.
GERMAN
CANCER RESEARCH CENTER
IN THE HELMHOLTZ ASSOCIATION
Plan
bixel width in [mm]
5
Gantry Angle in °
0
Couch Angle in °
0
Radiation 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
Beam Selection
Offset
Type of plot
intensity
GoTo
lateral
Plane Selection
axial
Open 3D-View
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
1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1
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:
0
1
Structure Visibilty
no data loaded
Info
v2.10.1 "Blaise"
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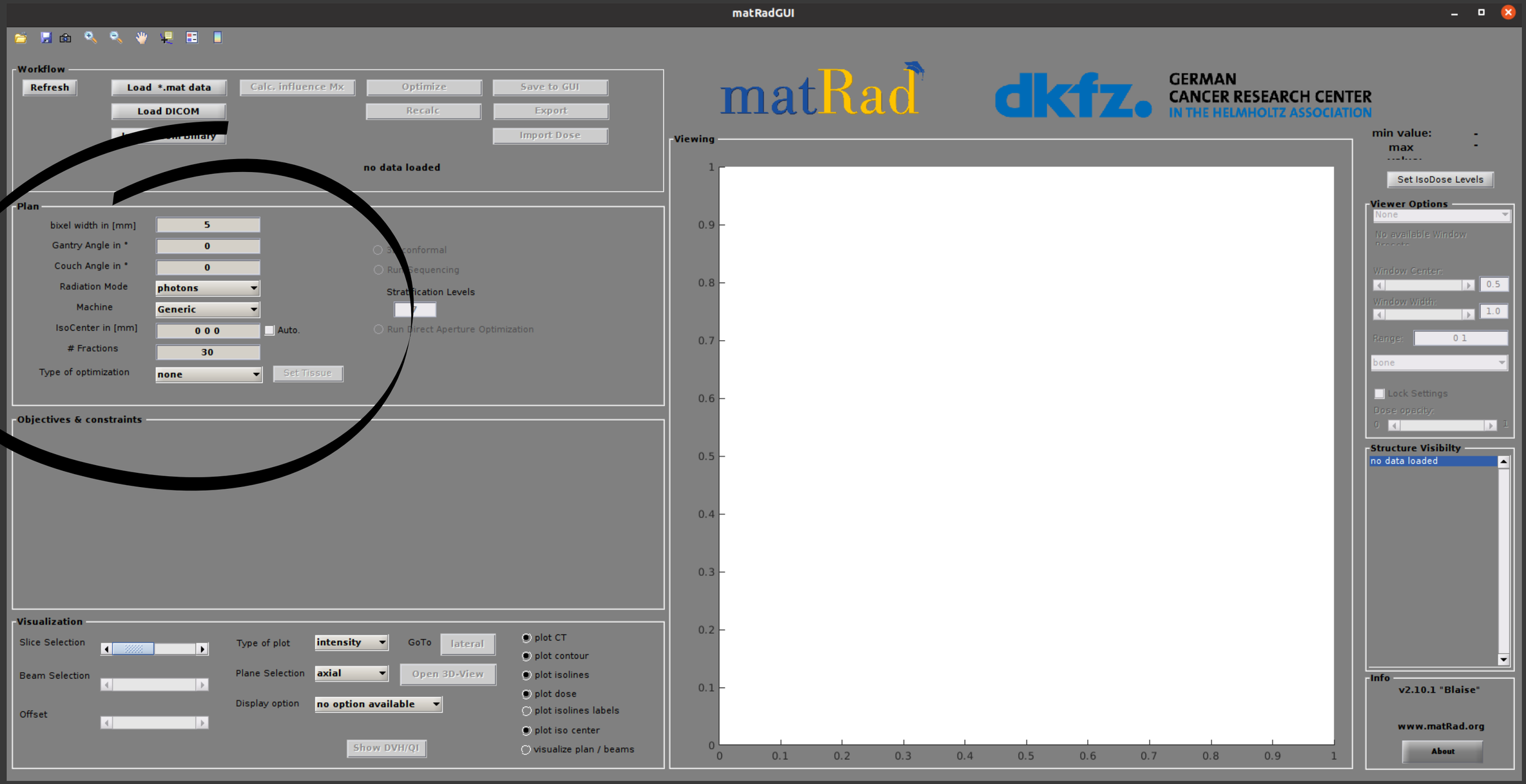
matRadGUI
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5
Gantry Angle in °
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Radiation Mode
photons
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0 0 0
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CANCER RESEARCH CENTER
IN THE 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:
Structure Visibilty
no data loaded
Info
v2.10.1 "Blaise"
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About

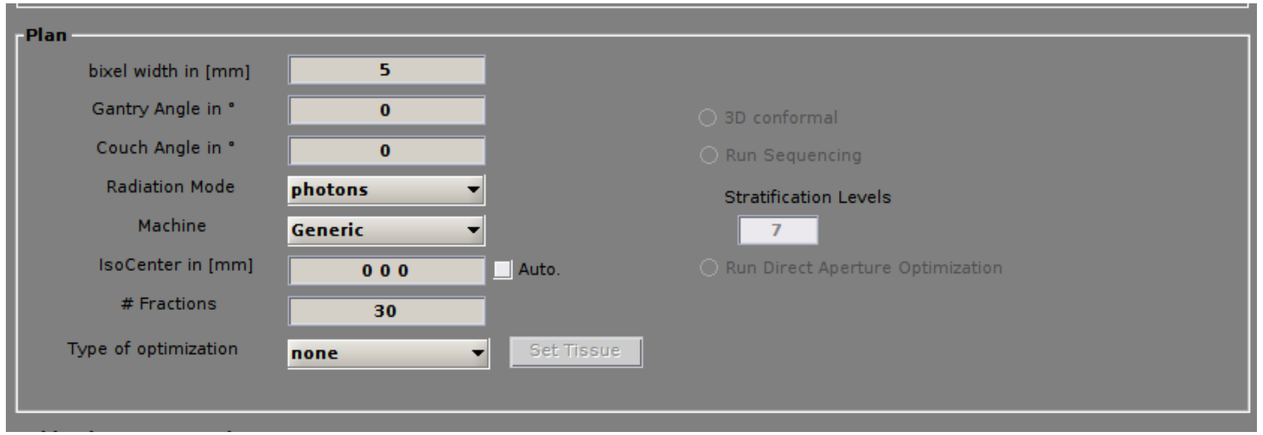
Iniziamo: plan

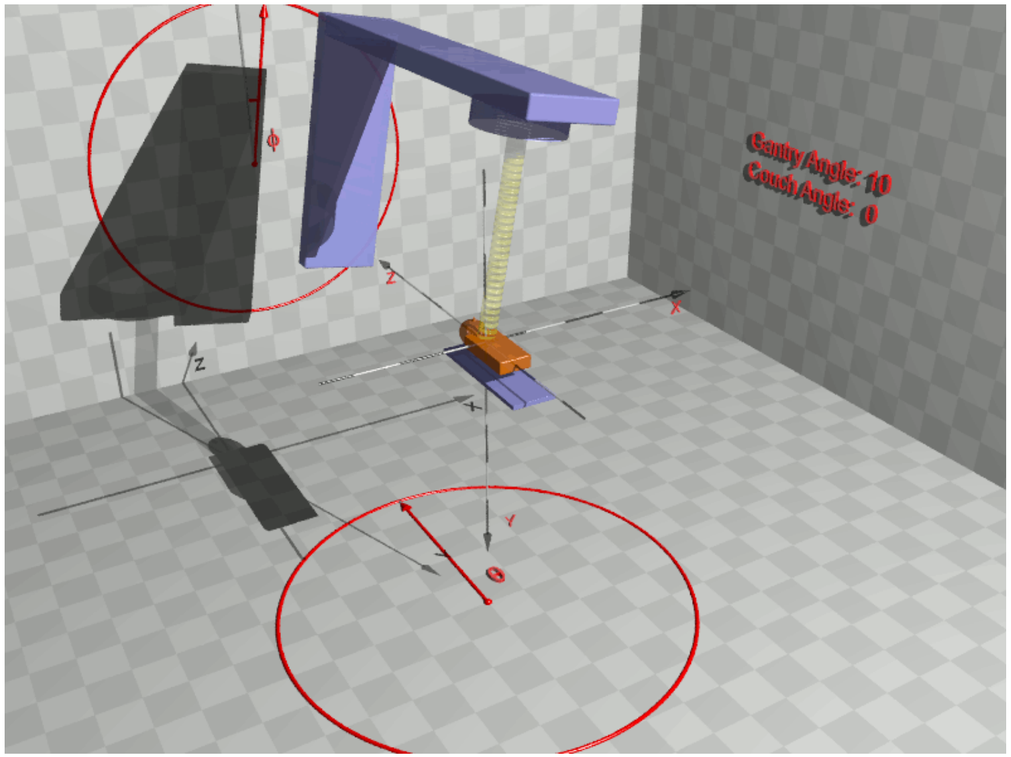
bixel width
dimensioni della griglia per il calcolo (non modificare)

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"





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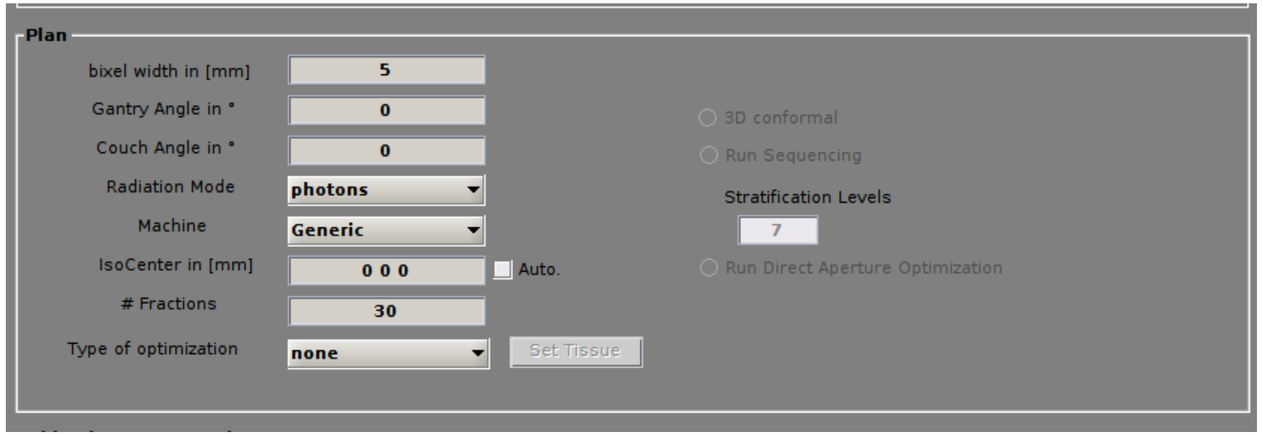

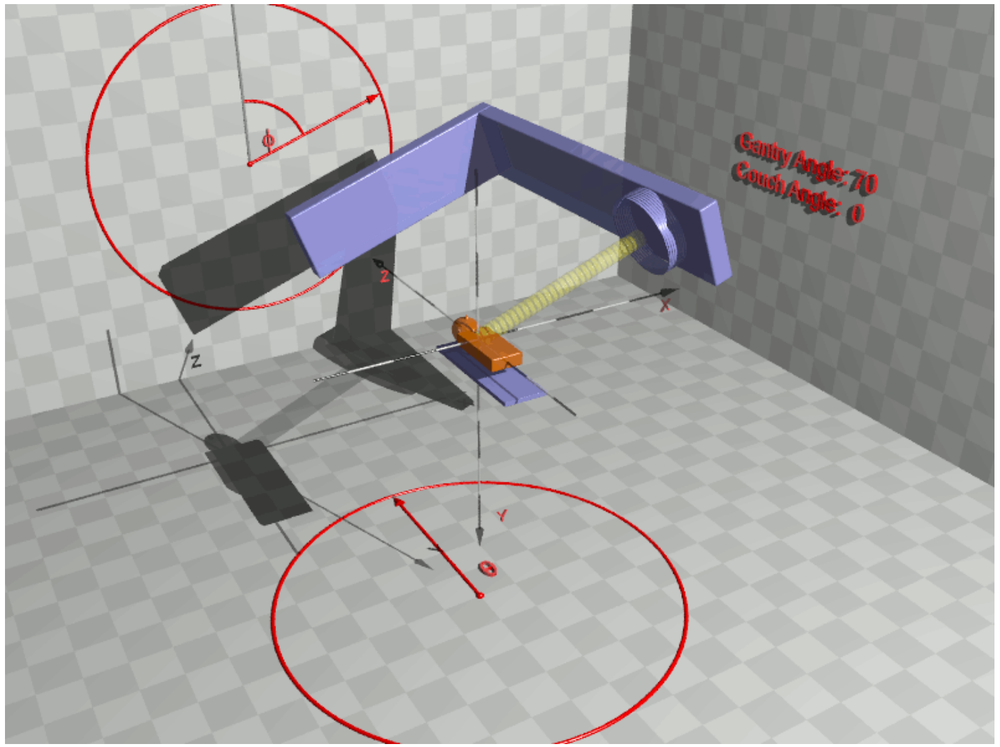

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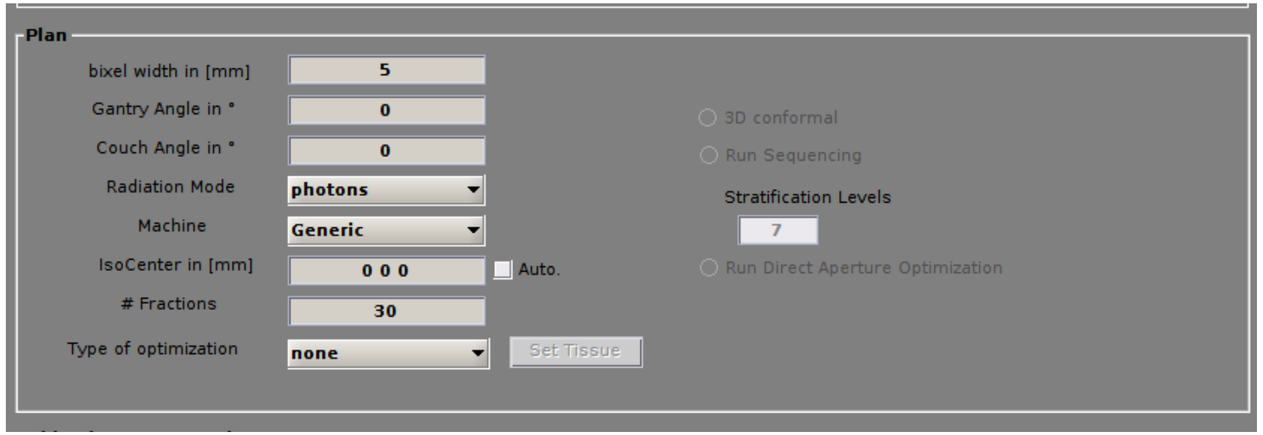

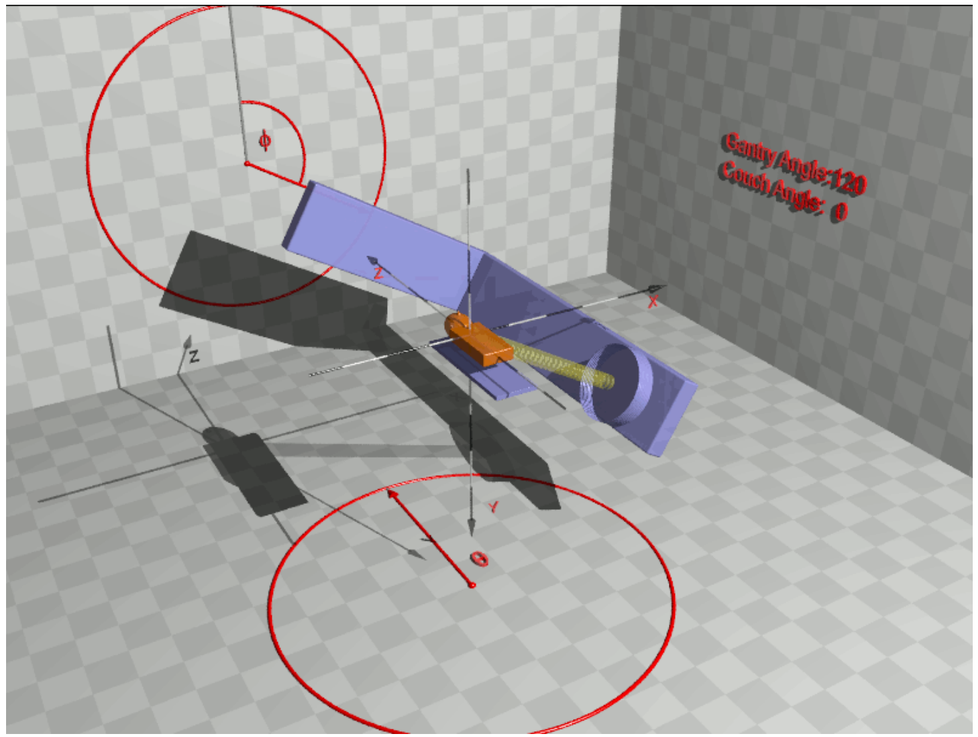

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bixel width
dimensioni della griglia per il calcolo (non modificare)

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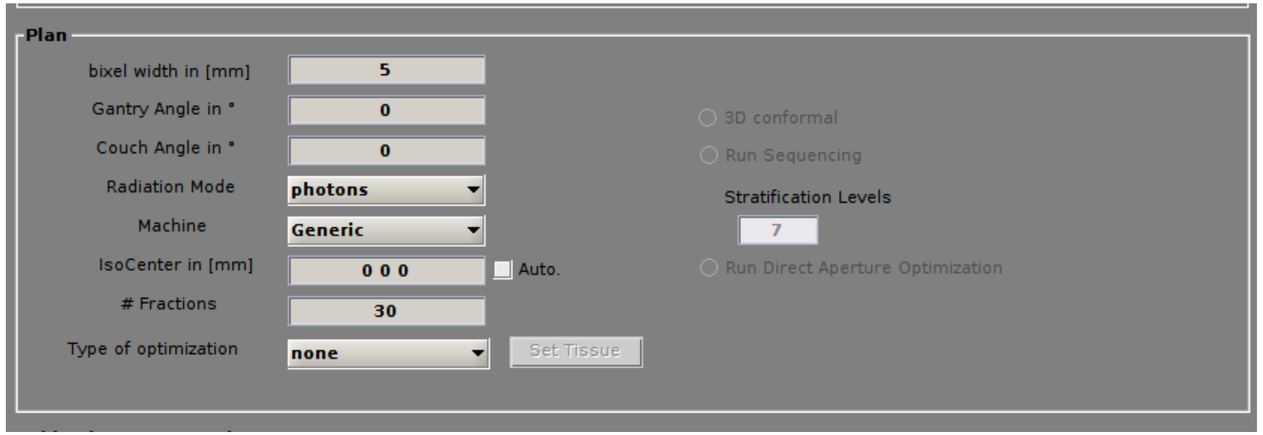

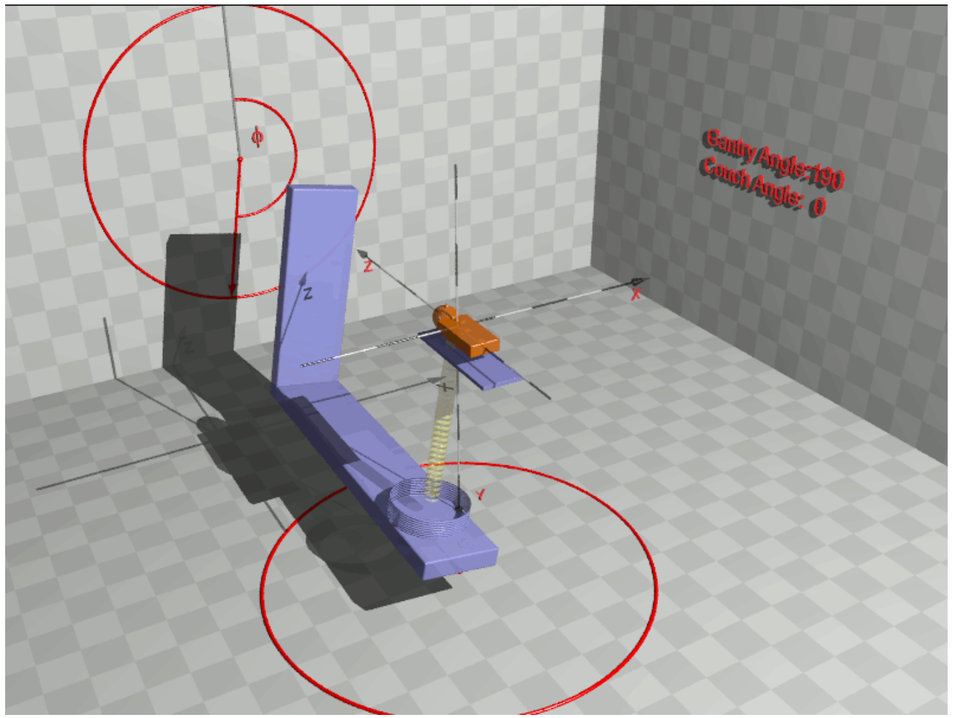

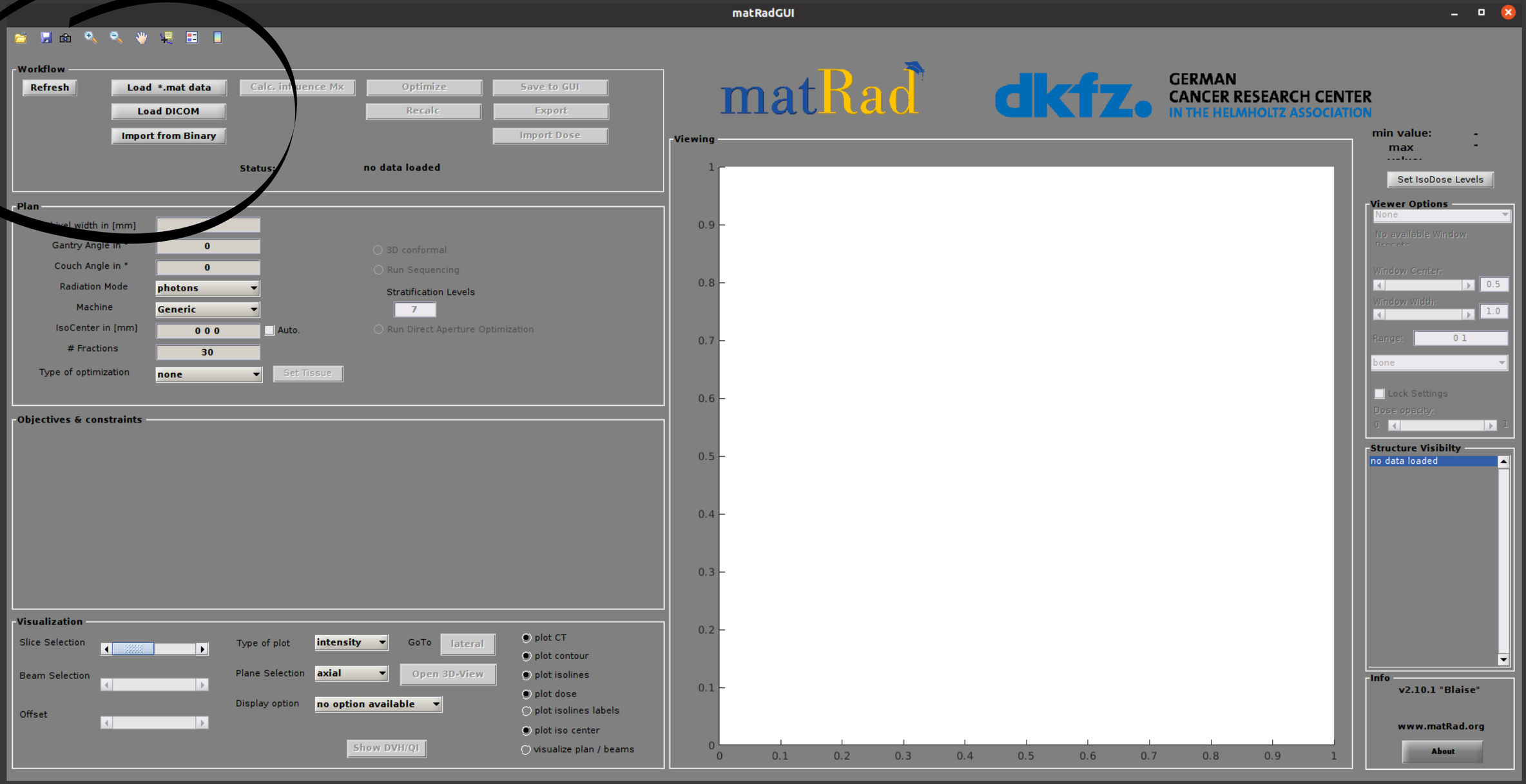
matRadGUI
Workflow
Refresh
Load *.mat data
Calc. influence Mx
Optimize
Save to GUI
Load DICOM
Recalc
Export
Import from Binary
Import Dose
Status:
no data loaded
matRad
dkfz.
GERMAN
CANCER RESEARCH CENTER
IN THE HELMHOLTZ ASSOCIATION
Plan
Gantry Angle in °
0
Couch Angle in °
0
Radiation Mode
photons
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
Beam Selection
Offset
Type of plot
intensity
Plane Selection
axial
Display option
no option available
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
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:
Structure Visibilty
no data loaded
Info
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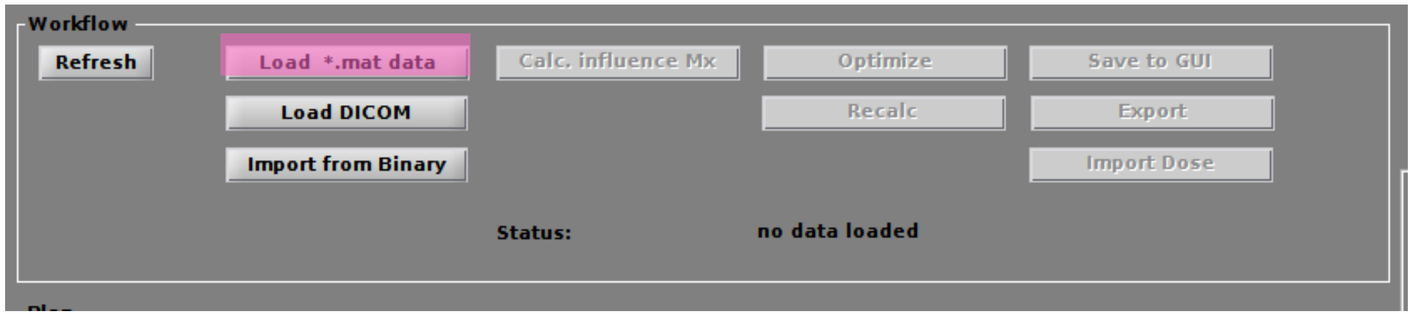
About

Iniziamo: workflow

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



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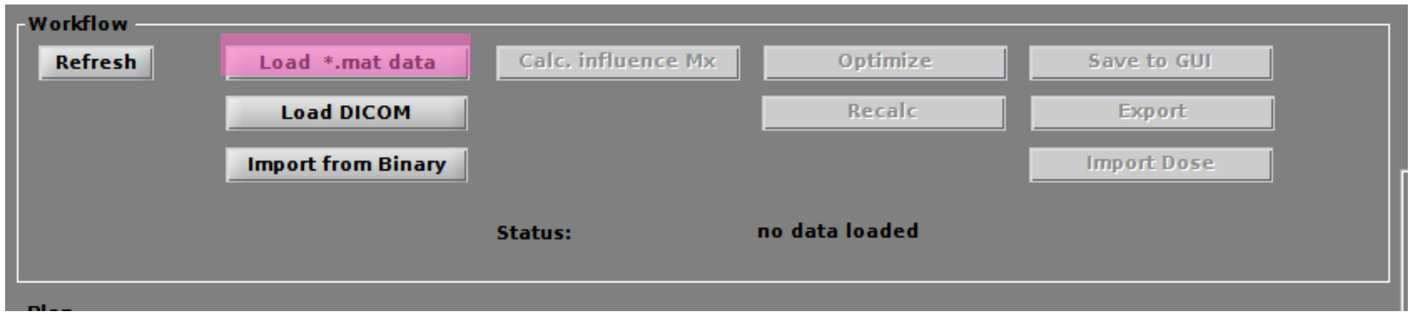
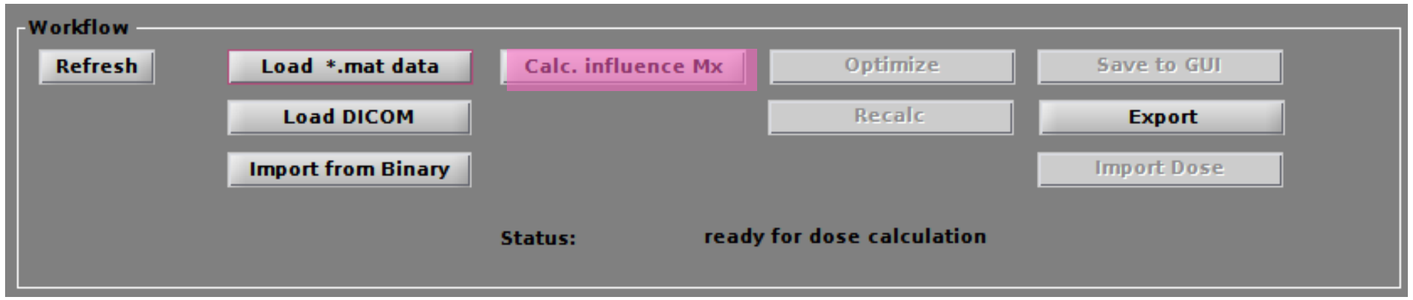


Premete "Calc. Influence MX"
per calcolare la matrice di influenza
relativa al caso in oggetto (apparirà
una barra di stato)



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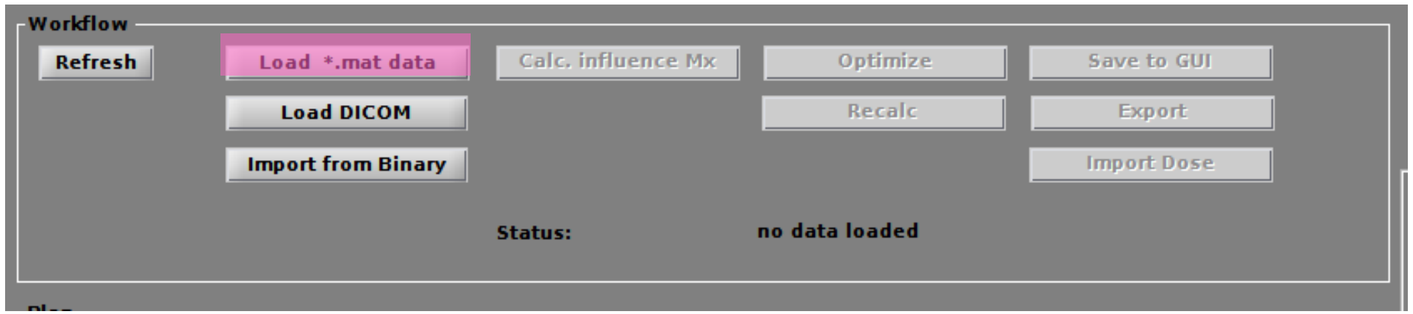

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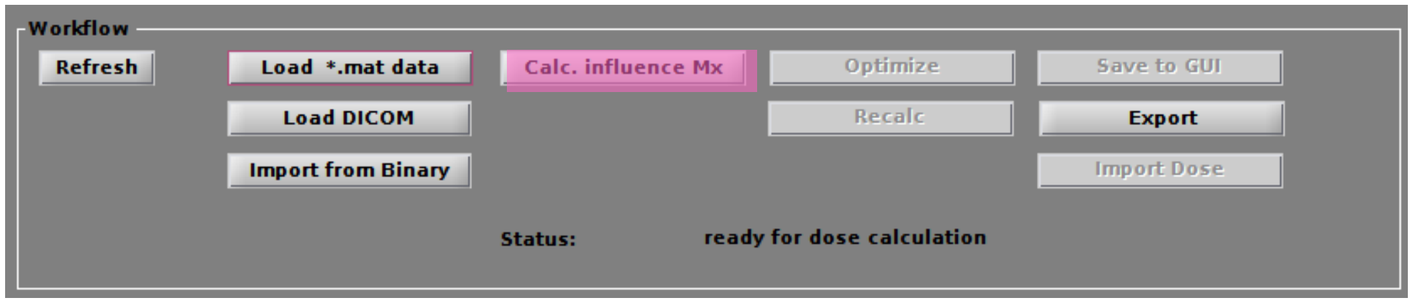
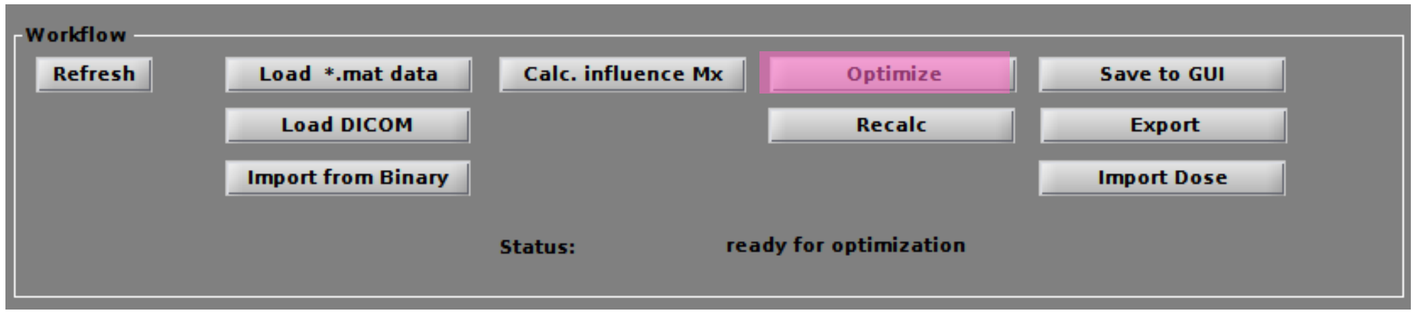
una barra di stato)



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



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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]	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

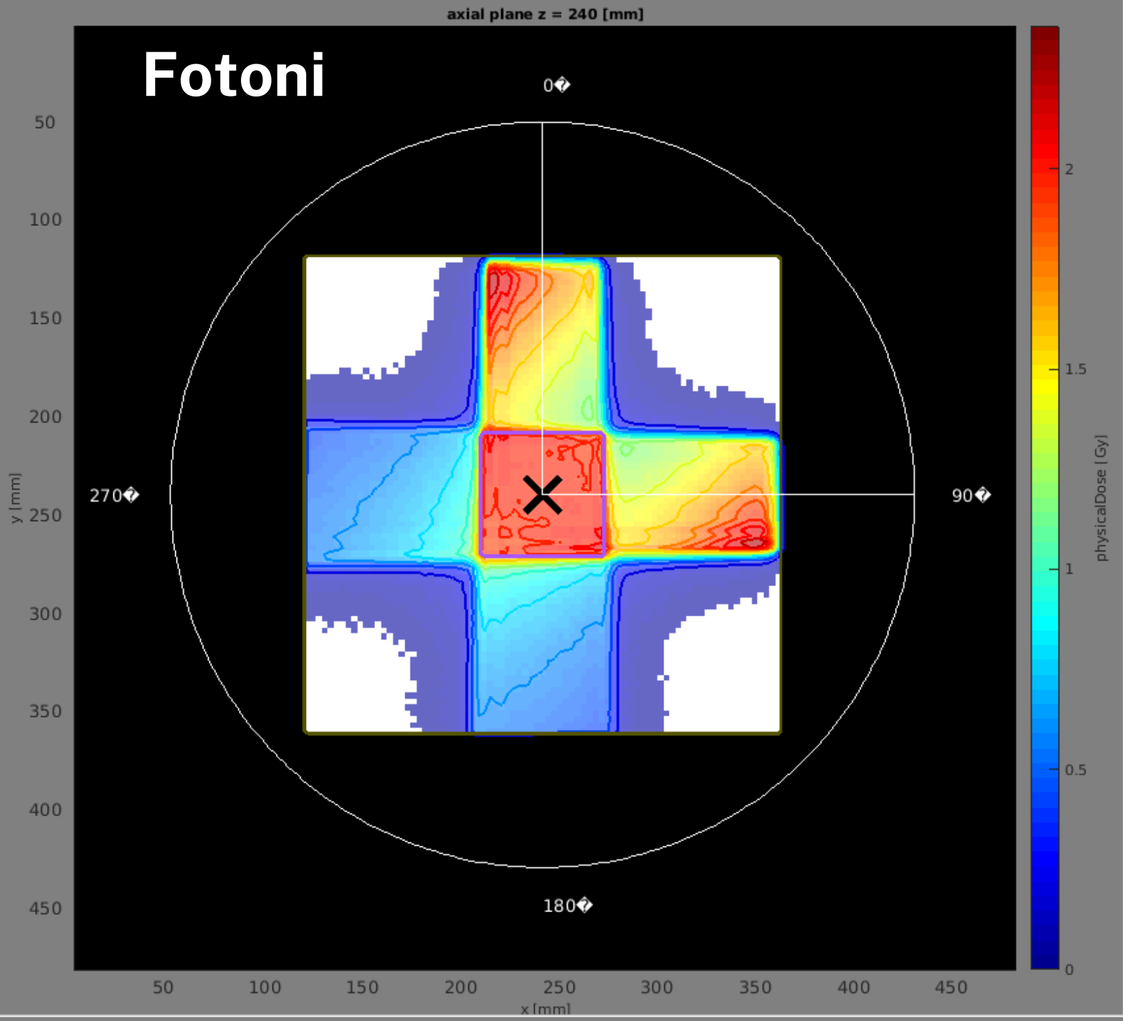
+/-	VOI name	VOI type	OP	Function	p	Parameters
-	BODY	OAR	2	Squared Overdo...	100	d^{max}: 5
-	OuterTarget	TARGET	1	Squared Deviation	800	d^{ref}: 60
+	BODY					

Visualization

Slice Selection
Beam Selection
Offset
Type of plot: intensity | GoTo: lateral
Plane Selection: axial | Open 3D-View
Display option: physicalDose
Show DVH/QI

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

Viewing



min value: 0
max value: 2.357

Set IsoDose Levels

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: 0 1

Structure Visibilty

BODY
OuterTarget

Info

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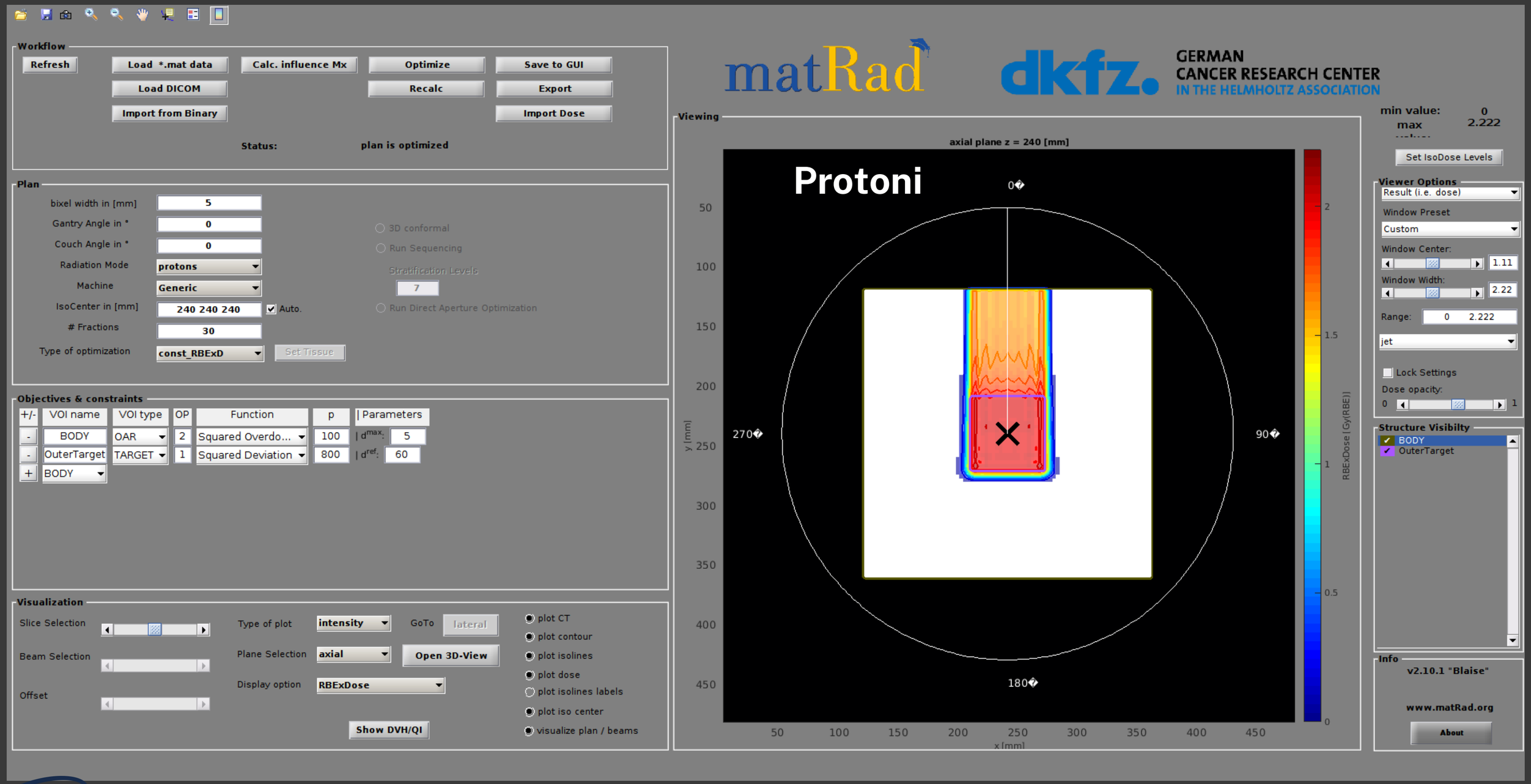
Workflow
Refresh
Load *.mat data
Calc. influence Mx
Optimize
Save to GUI
Load DICOM
Recalc
Export
Import from Binary
Import Dose
Status:
plan is optimized
matRad
dkfz.
GERMAN CANCER RESEARCH CENTER
IN THE HELMHOLTZ ASSOCIATION
Plan
bixel width in [mm]
5
Gantry Angle in °
0
Couch Angle in °
0
Radiation Mode
protons
Machine
Generic
IsoCenter in [mm]
240 240 240
Auto.
Fractions
30
Type of optimization
const_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
GoTo
lateral
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
Viewing
axial plane z = 240 [mm]
Protoni
0°
90°
180°
270°
y [mm]
x [mm]
RBExDose [Gy(RBE)]
min value: 0
max 2.222
Set IsoDose Levels
Viewer Options
Result (i.e. dose)
Window Preset
Custom
Window Center:
1.11
Window Width:
2.22
Range:
0 2.222
jet
Lock Settings
Dose opacity:
Structure Visibilty
BODY
OuterTarget
Info
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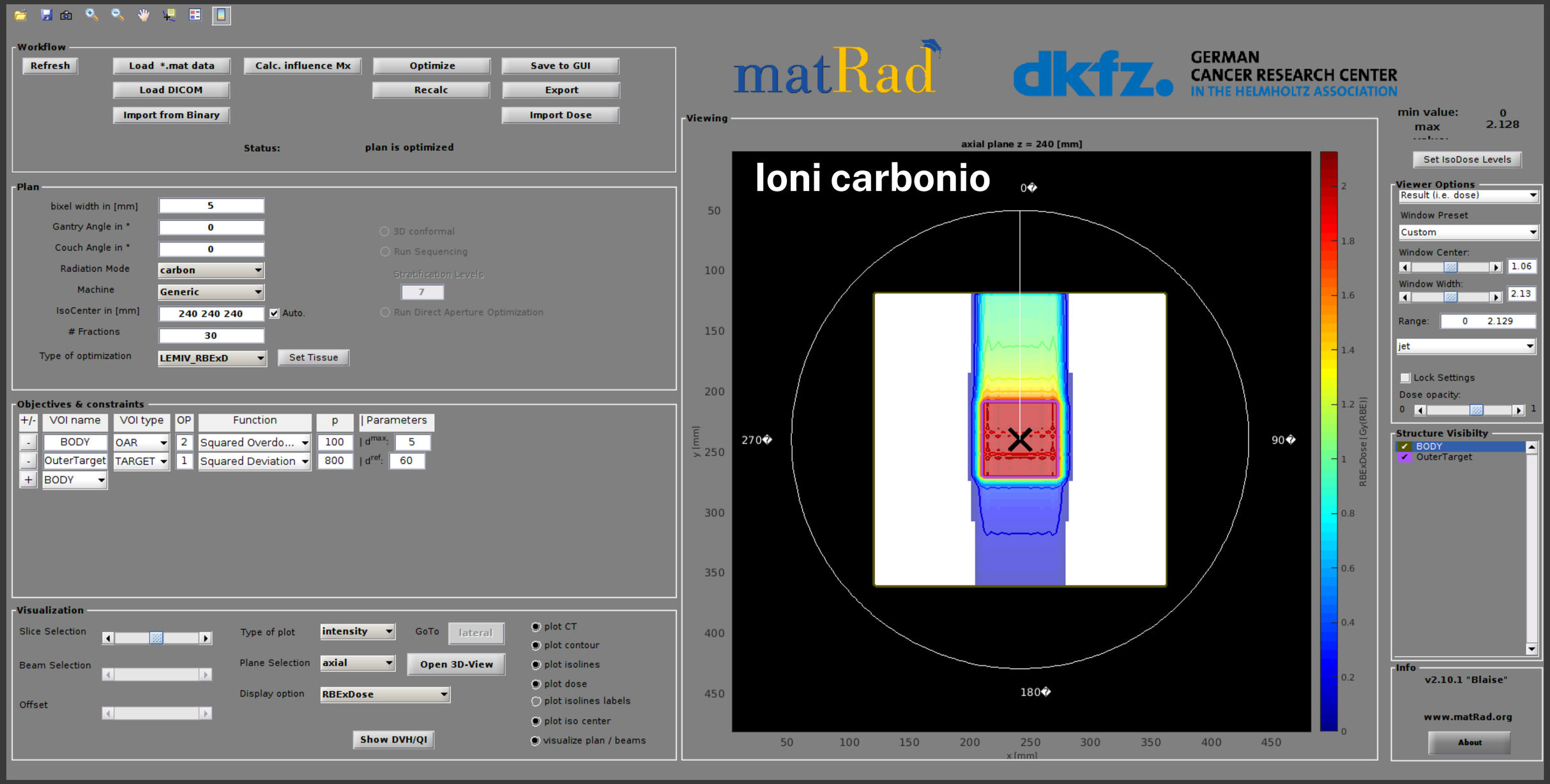
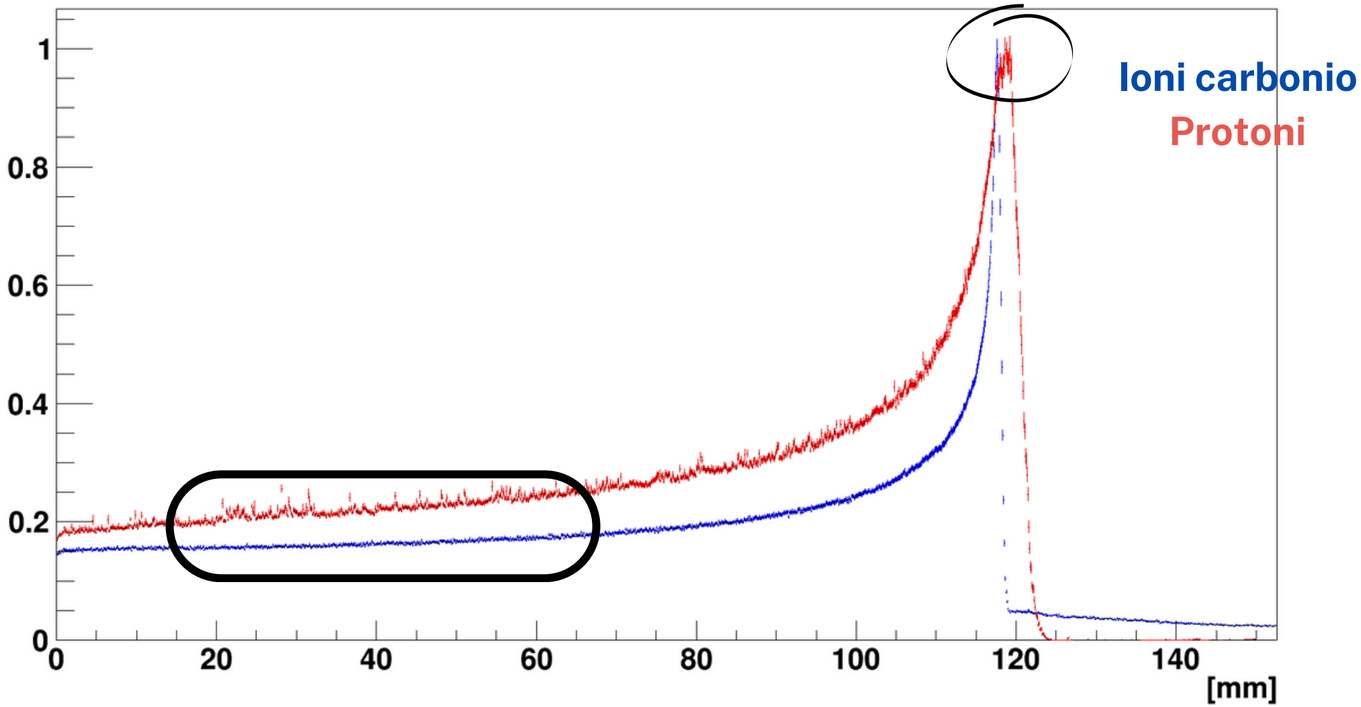
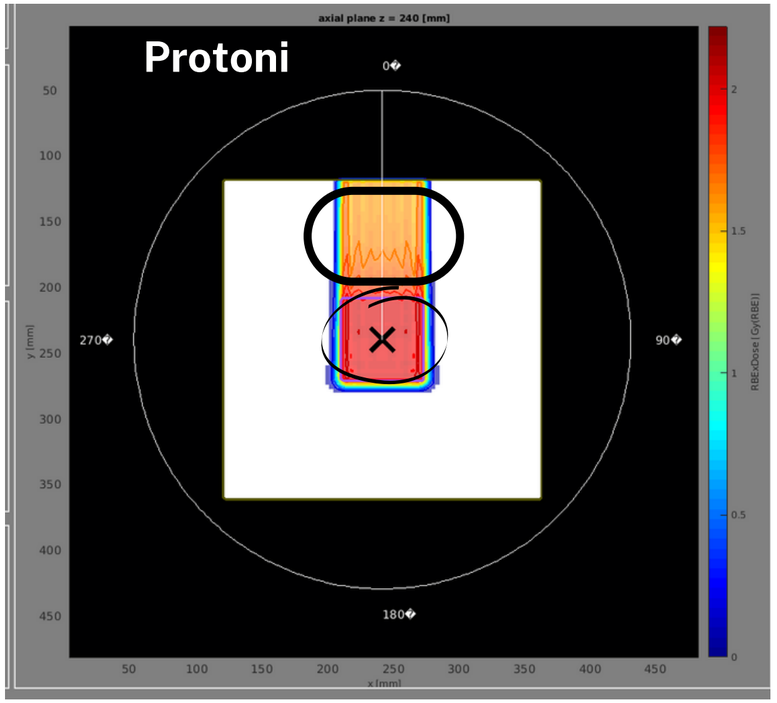
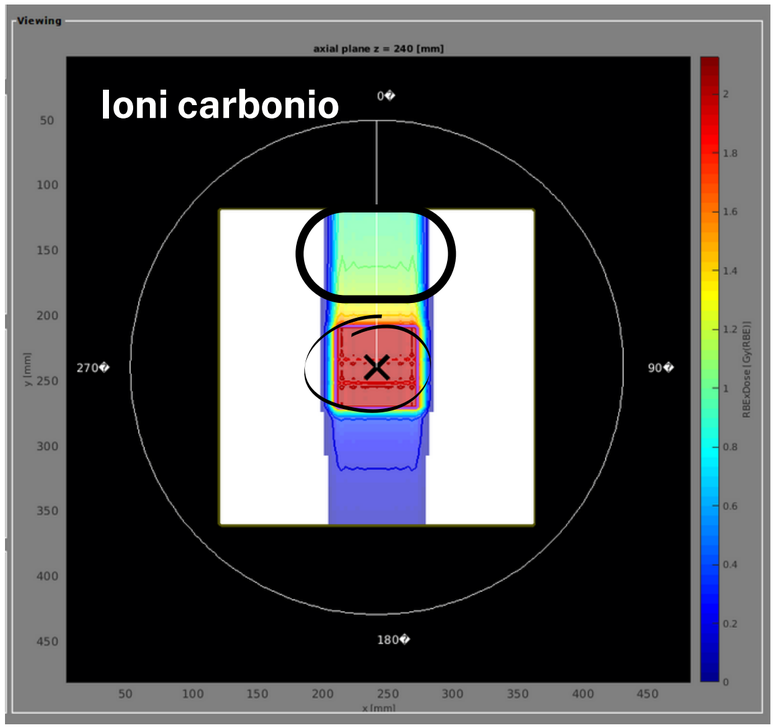


Al netto della "coda", gli ioni carbonio rilasciano meno dose nei tessuti sani a parità di dose rilasciata nel tumore!

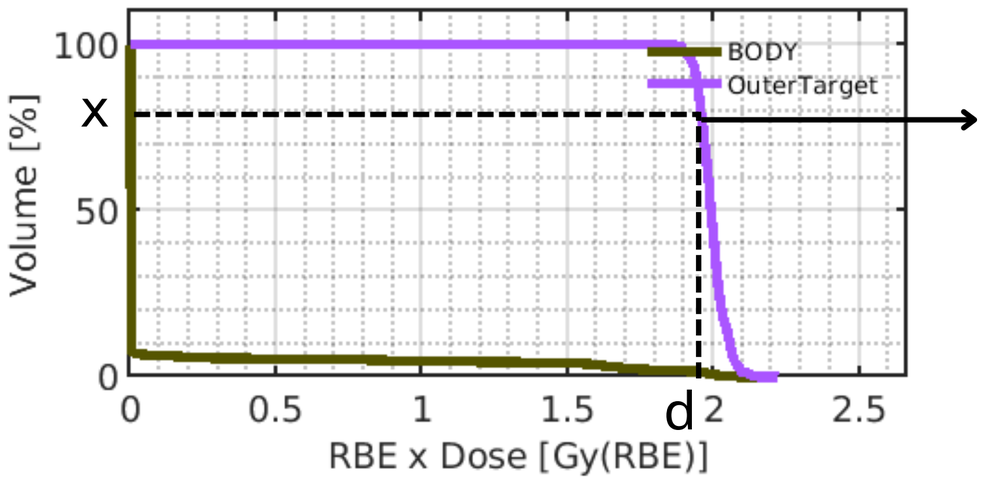






Strumenti utili: DVH

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

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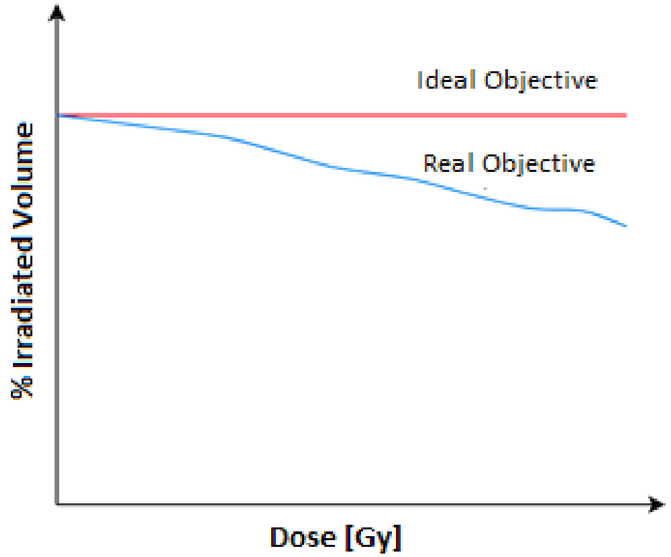
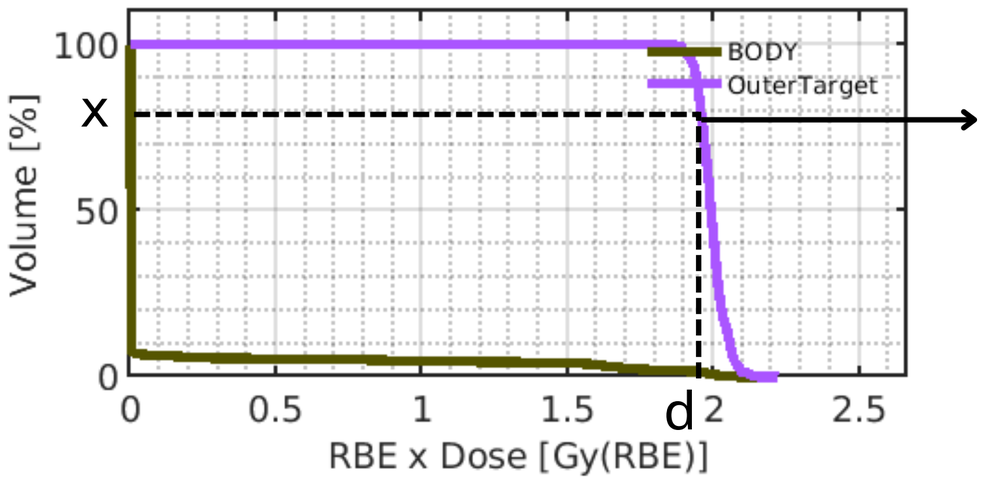
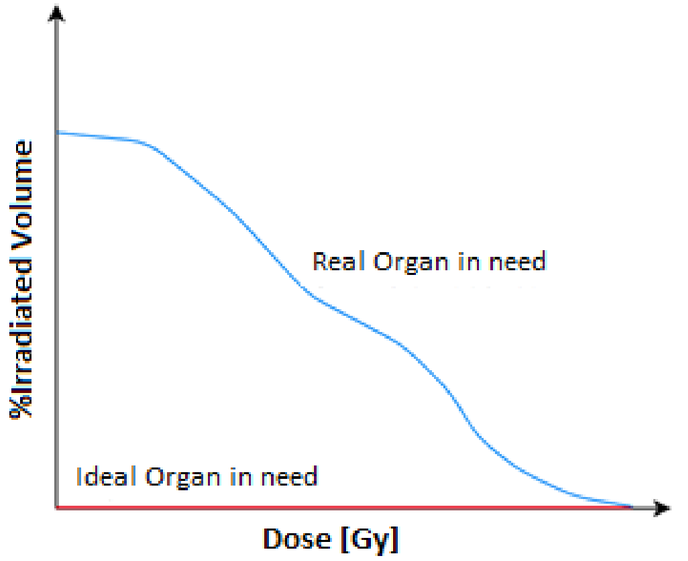
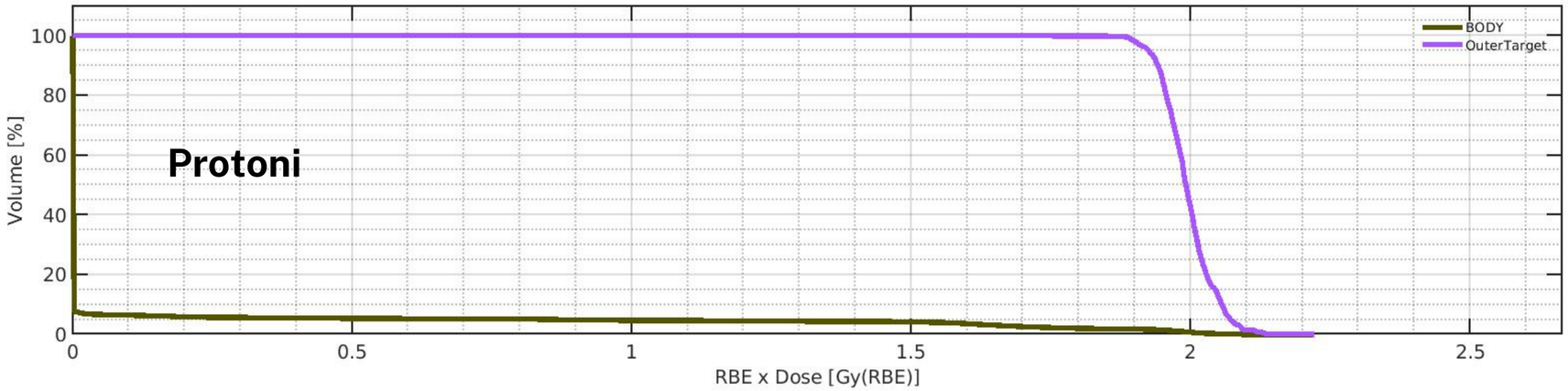
DVH (Dose Volume Histogram) è uno strumento molto utile per valutare la bontà di un piano di trattamento



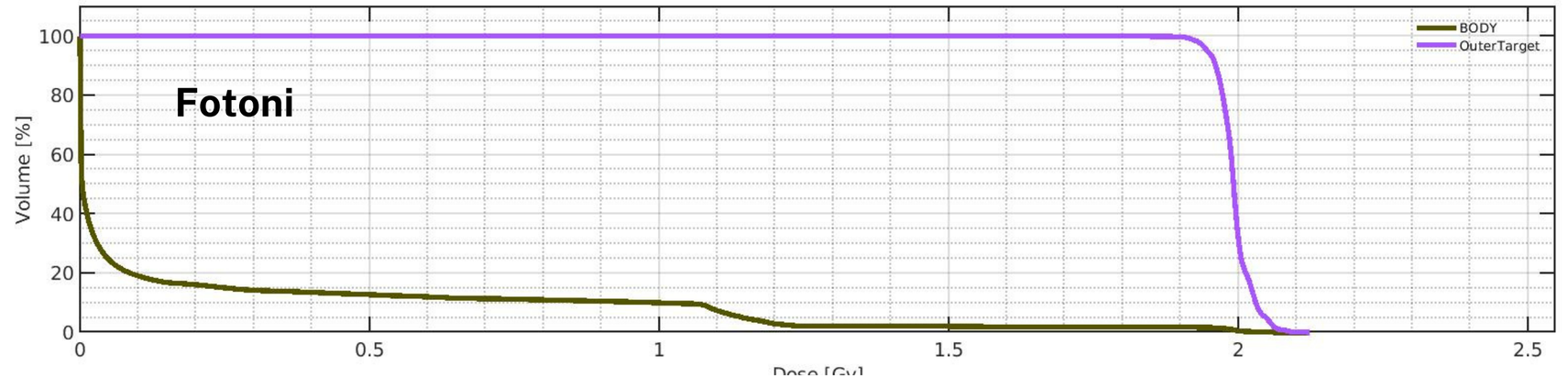


x% del volume ha ricevuto almeno una dose d



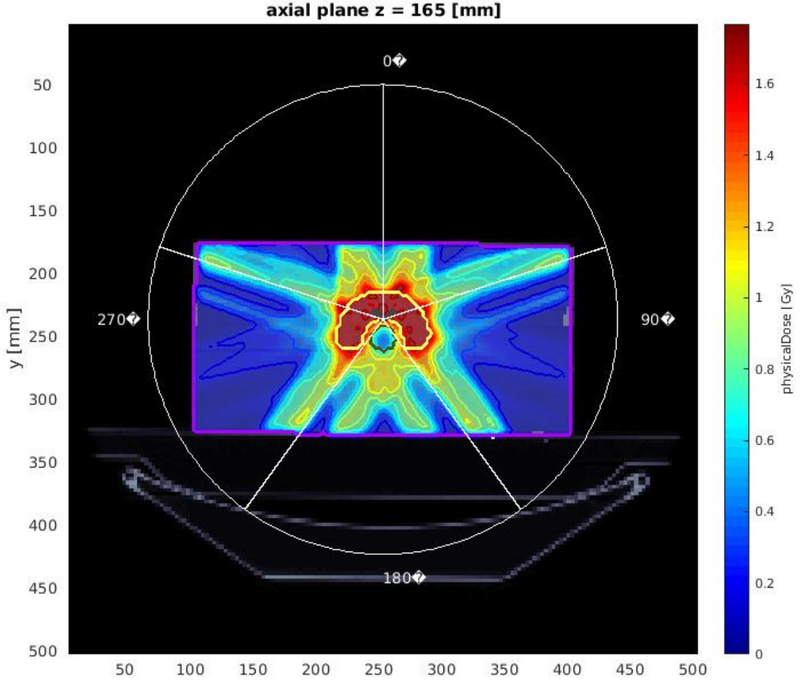


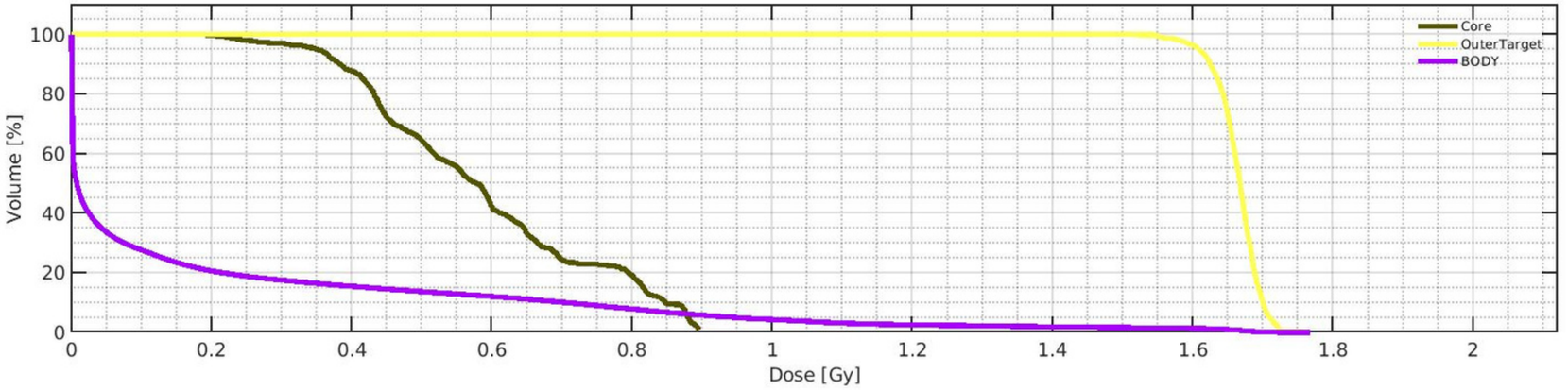
	mean	std	max	min	D_2	D_5	D_50	D_95	D_98	V_0Gy	V_0.4Gy	V_0.8Gy	V_1.3Gy	V_1.7Gy	V_2.2Gy	CI_2Gy	H_2Gy
BODY	0.0904	0.3789	2.2224	0	1.8071	0.8541	0	0	0	1	0.0351	0.0513	0.0442	0.0263	7.5267e...	-	-
OuterTarget	1.9943	0.0455	2.2224	1.7532	2.0924	2.0713	1.9916	1.9252	1.9013	1	1	1	1	1	4.3192e...	0.9513	7.3031



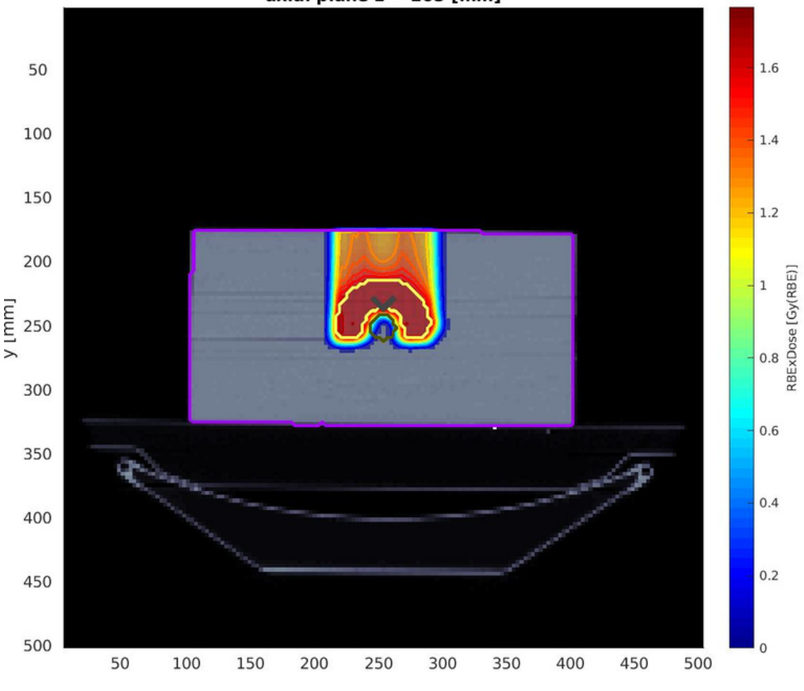
	mean	std	max	min	D_2	D_5	D_50	D_95	D_98	V_0Gy	V_0.4Gy	V_0.8Gy	V_1.2Gy	V_1.6Gy	V_2.1Gy	CI_2Gy	H_2Gy
BODY	0.1731	0.4109	2.1239	0	1.5368	1.1449	0.0036	0	0	1	0.1353	0.1101	0.0292	0.0176	1.8817e...	-	-
OuterTarget	1.9930	0.0290	2.1239	1.8441	2.0806	2.0479	1.9916	1.9464	1.9312	1	1	1	1	1	0.0011	0.9975	5.0750

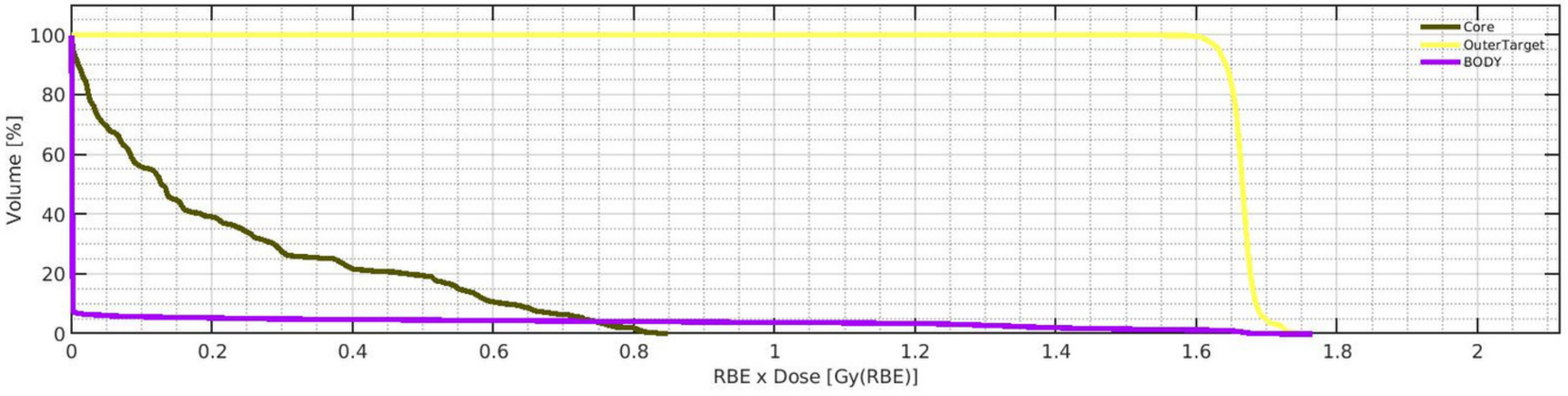
Procediamo con il caso TG119





	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...	-	-