

PARTICLE THERAPY MASTERCLASS

Hands-On Treatment Planning with matRad

Workflow step by step instructions

2nd Exercise

- Carbon ion treatment plan for a liver patient
- Defining treatment plan using photons and protons
- Analysing and comparing diferent treatment plans

1. Load the liver patient case via the Load *.mat button (LIVER.mat)

The screenshot displays the matRad software interface. The top toolbar contains several buttons: Refresh, Load *.mat data (highlighted with a red arrow), Calc. influence Mx, Optimize, Save to GUI, Load *.COM, Recalc, Export, Import Plan Bin..., and Import Dose. The status bar indicates 'plan is optimized'. The main window shows a 3D visualization of a patient case with the text 'axial plane z = 162.5 [mm]'. A 'Select File to Open' dialog box is open, showing a file list with 'LIVER' selected. The file list includes folders like standalone, tools, unitTest, vmc++ and files like BOXPHANTOM, carbon_Generic, HEAD_AND_NECK, LIVER, photons_Generic, PROSTATE, protons_Generic, and TG119. The file name field at the bottom of the dialog shows 'LIVER' and the file type is 'MAT-files (*.mat)'. The background interface also shows various settings for Plan, Objectives & constraints, and Visualization.

Workflow

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

Status: plan is optimized

Plan

bixel width in [mm] 20
Gantry Angle in ° 0 72 144 216 288
Couch Angle in ° 0 0 0 0
Radiation Mode protons
Machine Generic
IsoCenter in [mm] 251.3 236.4 162.6 Auto.
Fractions 30
Type of optimization const_RBExD Set Tissue

Objectives & constraints

	VOI name	VOI type	priority	obj. / const.	penalty	dose	EUD	volume
1	Core	OAR	2	max dose constraint	NaN	25	NaN	NaN
2	OuterTarget	TARGET	1	min dose constraint	NaN	50	NaN	NaN
3	BODY	OAR	3	square overdosing	100	30	NaN	NaN

Visualization

Slice Type of plot inten... GoTo lateral
Beam Plane axial Open 3D-View
Offset Displav option RBExDose

plot CT
plot contour
plot isolines
plot dose
plot isolines labels
plot iso center
visualize plan / be...

min n
max 61.45
Set IsoDose Levels
Viewer Options
Result (i.e. dose)
Window Dose
Custom
Window Center:
Window Width: 30.7
Range: 0 61.45
jet
Dose opacity: 1
Structure Visibility
 Core
 OuterTarget
 BODY
Info
v3.0.0
github.com/e0404/mat
About

2. Define your own photon treatment plan with approx. 4-5 beam directions.

Workflow

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

Status: ready for optimization

Plan

bixel width in [mm] 10 1

Gantry Angle in ° 0 180 225 270 315 2

Couch Angle in ° 0 0 0 0 2

Radiation Mode photons

Machine Generic

IsoCenter in [mm] 265.8 296.7 316.4 Auto.

Fractions 30

Type of optimization none Set Tissue

use MC (VMC++) dose calculations
 3D conformal
 Run Sequencing
 Stratification Levels 7
 Run Direct Aperture Optimizat...

Objectives & constraints

	VOI name	VOI type	priority	obj. / const.	penalty	dose	EUD	volume	ro
1	Skin	OAR	2	square overdosing	300	25	NaN	NaN	no
2	PTV	TARGET	1	square deviation	1000	45	NaN	NaN	no

Visualization

Slice Type of plot inten... GoTo lateral

Beam Plane axial Open 3D-View

Offset Dislay option physicalDose

Show DVH/QI

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

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axial plane z = 317.5 [mm]

min 0 max 3.706

Set IsoDose Levels

Viewer Options

Result (i.e. dose) Window Dose Custom Window Center: Window Width: 1.85 Range: 0 3.71 jet Dose opacity: 1

Structure Visibility

- GTV
- Kidney_R
- Kidney_L
- Stomach
- SmallBowel
- LargeBowel
- Celiac
- SMA_SMV
- Liver
- Heart
- SpinalCord
- DoseFalloff

Info v3.0.0 github.com/e0404/mat About

3. Trigger dose calculation („Calc. Influence Mx“) and start inverse optimization („Optimize“).

The screenshot displays the matRad software interface, which is used for radiation therapy planning. The interface is divided into several sections:

- Workflow:** Contains buttons for 'Refresh', 'Load *.mat data', 'Load DICOM', 'Import from Bin...', 'Calc. influence Mx', 'Optimize', 'Save to GUI', 'Export', and 'Import Dose'. Red arrows point to 'Calc. influence Mx' (labeled '1') and 'Optimize' (labeled '2'). The status below indicates 'ready for optimization'.
- Plan:** Includes parameters for 'bixel width in [mm]' (10), 'Gantry Angle in °' (0 180 225 270 315), 'Couch Angle in °' (0 0 0 0), 'Radiation Mode' (photons), 'Machine' (Generic), 'IsoCenter in [mm]' (265.8 296.7 316.4), '# Fractions' (30), and 'Type of optimization' (none). It also has options for 'use MC (VMC++) dose calculations', '3D conformal', 'Run Sequencing', 'Stratification Levels' (7), and 'Run Direct Aperture Optimizat...'. A 'Set Tissue' button is also present.
- Objectives & constraints:** A table with columns for 'VOI name', 'VOI type', 'priority', 'obj. / const.', 'penalty', 'dose', 'EUD', 'volume', and 'ro'.

	VOI name	VOI type	priority	obj. / const.	penalty	dose	EUD	volume	ro
1	Skin	OAR	2	square overdosing	300	25	NaN	NaN	no
2	PTV	TARGET	1	square deviation	1000	45	NaN	NaN	no
- Visualization:** Includes 'Slice' and 'Beam' selection, 'Type of plot' (intensity), 'Plane' (axial), and 'Dislay option' (physicalDose). It also has 'GoTo' (lateral) and 'Open 3D-View' buttons. A 'Show DVH/QI' button is at the bottom.
- Viewing:** Shows an axial CT scan of a patient's head and neck at 'axial plane z = 317.5 [mm]'. The image displays dose contours in various colors (red, orange, yellow, green, blue) over the anatomical structures. A color scale on the right indicates 'physicalDose [Gy]' from 0 to 60.
- Viewer Options:** Includes 'Result (i.e. dose)', 'Window', 'Window Center', 'Window Width', 'Range', and 'Dose opacity'.
- Structure Visibility:** A list of anatomical structures with checkboxes: GTV, Kidney_R, Kidney_L, Stomach, SmallBowel, LargeBowel, Celiac, SMA_SMV, Liver, Heart, SpinalCord, and DoseFalloff.
- Info:** Shows version 'v3.0.0' and the GitHub repository 'github.com/e0404/mat'.

4. Save the optimization result via („Save to GUI“). Next, show the DVH by („Show DVH/QI“). Analyze dose distribution.

Workflow

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

Load DICOM Recalc

Import from Bin...

Status: plan is optimized

1

Plan

bixel width in [mm] 10 use MC (VMC++) dose calculations

Gantry Angle in ° 0 180 225 270 315 3D conformal

Couch Angle in ° 0 0 0 0 Run Sequencing

Radiation Mode photons Stratification Levels 7

Machine Generic Run Direct Aperture Optimizat...

IsoCenter in [mm] 265.8 296.7 316.4 Auto.

Fractions 30

Type of optimization none Set Tissue

Objectives & constraints

	VOI name	VOI type	priority	obj. / const.	penalty	dose	EUD	volume	ro
1	Skin	OAR	2	square overdosing	300	25	NaN	NaN	no
2	PTV	TARGET	1	square deviation	1000	45	NaN	NaN	no

save

Visualization

Slice Type of plot inten... GoTo lateral

Beam Plane axial Open 3D-View

Offset Dislay option physicalDose

2

Show DVH/QI

plot CT
 plot contour
 plot isolines
 plot dose
 plot isolines labels
 plot iso center
 visualize plan / be...

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axial plane z = 317.5 [mm]

min max 0 1.572

Set IsoDose Levels

Viewer Options

Result (i.e. dose) Custom

Window Center: 0.781

Window Width: 1.57

Range: 0 1.572

jet

Dose opacity: 1

Structure Visibility

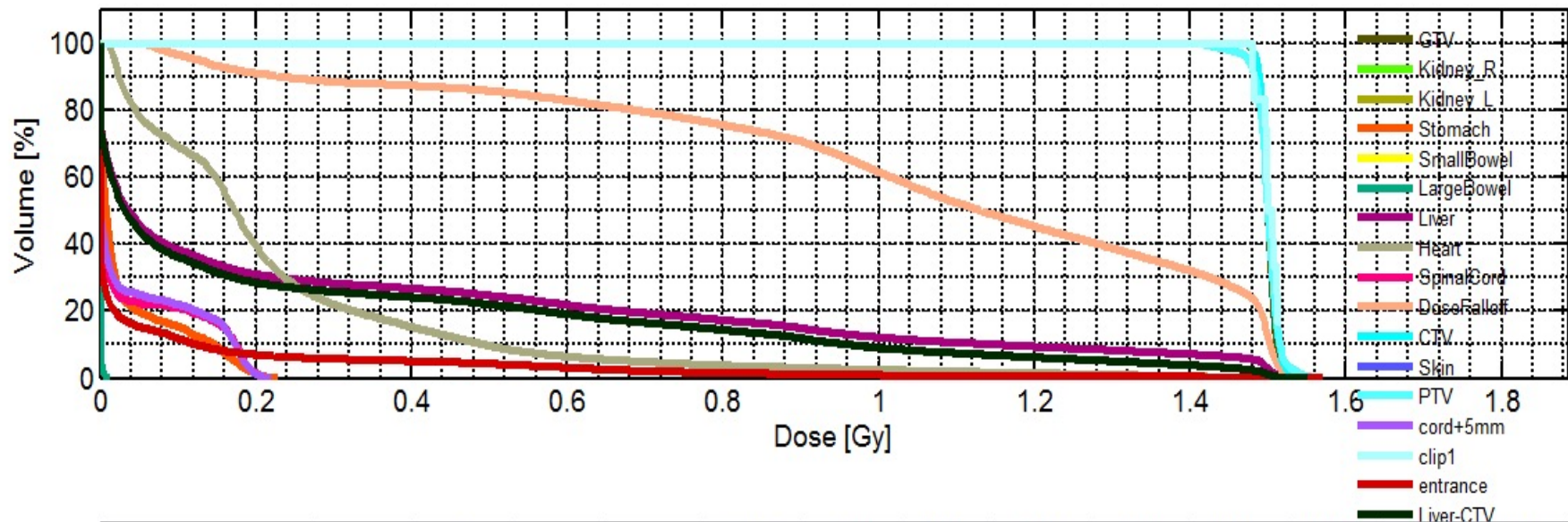
- GTV
- Kidney_R
- Kidney_L
- Stomach
- SmallBowel
- LargeBowel
- Celiac
- SMA_SMV
- Liver
- Heart
- SpinalCord
- DoseFalloff

Info

v3.0.0

github.com/e0404/mat

About



	mean	std	max	min	D_2	D_5	D_50	D_95	D_98	V_0Gy	V_0.3Gy	V_0.6Gy	V_0.9Gy
GTV	1.5000	0.0090	1.5281	1.4727	1.5188	1.5148	1.5002	1.4851	1.4796	1	1	1	
Kidney_R	0	0	0	0	0	0	0	0	0	1	0	0	
Kidney_L	0	0	0	0	0	0	0	0	0	1	0	0	
Stomach	0.0342	0.0566	0.2310	0	0.1940	0.1736	0.0082	0	0	1	0	0	
SmallBowel	0	0	0	0	0	0	0	0	0	1	0	0	
LargeBowel	2.6018e-04	0.0012	0.0147	0	0.0047	0.0019	0	0	0	1	0	0	
Celiac	0	0	0	0	0	0	0	0	0	1	0	0	
SMA_SMV	0	0	0	0	0	0	0	0	0	1	0	0	
Liver	0.3033	0.4713	1.5526	0	1.5042	1.4889	0.0367	0	0	1	0.2838	0.2190	0
Heart	0.2296	0.2426	1.5232	0.0066	1.1065	0.6913	0.1728	0.0182	0.0141	1	0.2202	0.0650	0
SpinalCord	0.0391	0.0686	0.2167	0	0.1969	0.1856	0	0	0	1	0	0	

5. Define your own proton treatment plan with one beam from e.g. 315°. Then trigger dose calculation („Calc. Influence Mx“) and start inverse optimization („Optimize“).

Workflow

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

Status: ready for dose calculation

Plan

bixel width in [mm] 10
 Gantry Angle in ° 315
 Couch Angle in ° 0
 Radiation Mode protons
 Machine Generic
 IsoCenter in [mm] 265.8 296.7 316.4 Auto.
 # Fractions 30
 Type of optimization const_RBExD Set Tissue

use MC (VMC++) dose calculations
 3D conformal
 Run Sequencing
 Stratification Levels 7
 Run Direct Aperture Optimizat...

Objectives & constraints

	VOI name	VOI type	priority	obj. / const.	penalty	dose	EUD	volume	ro
1	Skin	OAR	2	square overdosing	300	25	NaN	NaN	no
2	PTV	TARGET	1	square deviation	1000	45	NaN	NaN	no

Visualization

Slice Type of plot inten... GoTo lateral
 Beam Plane axial Open 3D-View
 Offset Display option physicalDose

plot CT
 plot contour
 plot isolines
 plot dose
 plot isolines labels
 plot iso center
 visualize plan / be...

Show DVH/QI

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Viewing

axial plane z = 317.5 [mm]

min max n 1.572

Set IsoDose Levels

Viewer Options

Result (i.e. dose) Window Doseat Custom
 Window Center: 0.784
 Window Width: 1.57
 Range: 0 1.572
 jet
 Dose opacity: 1

Structure Visibility

- GTV
- Kidney_R
- Kidney_L
- Stomach
- SmallBowel
- LargeBowel
- Celiac
- SMA_SMV
- Liver
- Heart
- SpinalCord
- DoseFalloff

Info

v3.0.0
 github.com/e0404/mat
 About

6. Save the optimization result via („Save to GUI“). Next, show the DVH by („Show DVH/QI“). Analyze the resulting dose distribution.

The screenshot displays the matRad GUI interface. The top left contains a workflow panel with buttons for Refresh, Load *.mat data, Calc. influence Mx, Optimize, Save to GUI, Load DICOM, Recalc, Export, and Import from Bin... The status bar indicates 'plan is optimized' with a '1' and a red arrow pointing to the 'Save to GUI' button.

The 'Plan' section includes parameters for biixel width (10 mm), Gantry Angle (315°), Couch Angle (0°), Radiation Mode (protons), Machine (Generic), IsoCenter (265.8, 296.7, 316.4 mm), # Fractions (30), and Type of optimization (const_RBExD). It also features checkboxes for 'use MC (VMC++) dose calculations', '3D conformal', 'Run Sequencing', 'Stratification Levels' (7), and 'Run Direct Aperture Optimizat...'. A 'Set Tissue' button is also present.

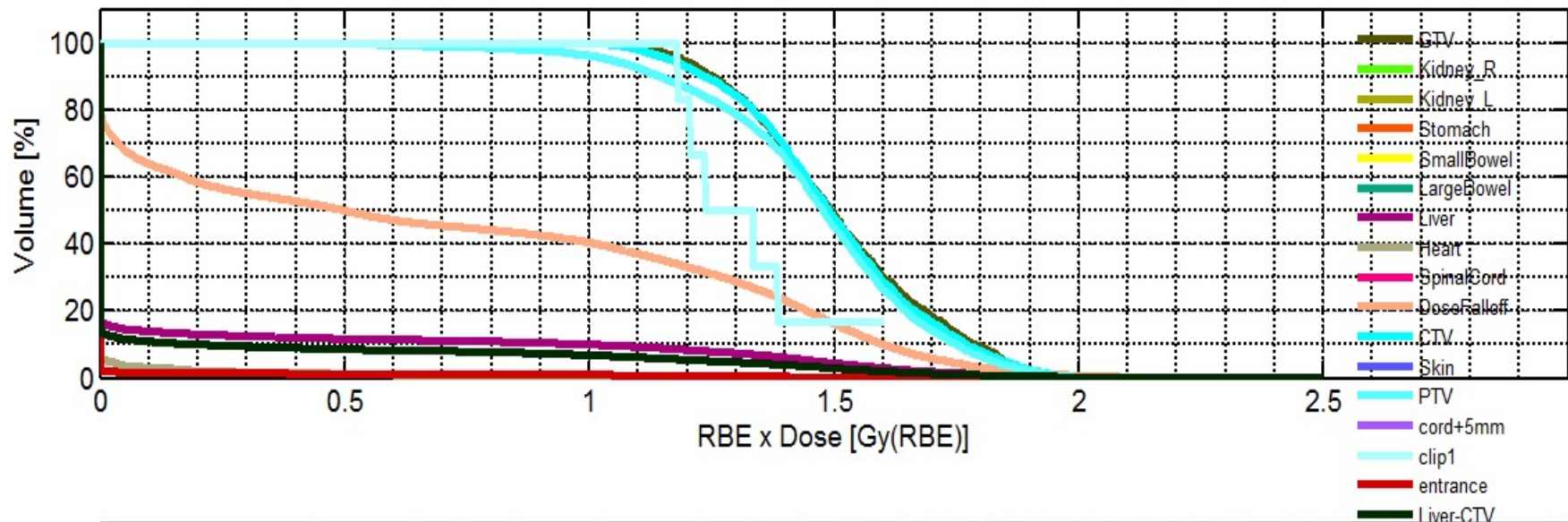
The 'Objectives & constraints' table is as follows:

	VOI name	VOI type	priority	obj. / const.	penalty	dose	EUD	volume	ro
1	Skin	OAR	2	square overdosing	300	25	NaN	NaN	no
2	PTV	TARGET	1	square deviation	1000	45	NaN	NaN	no

The 'Visualization' section includes controls for Slice, Beam, and Offset, along with 'Type of plot' (inten...), 'GoTo' (lateral), 'Plane' (axial), 'Open 3D-View', and 'Dislay option' (RBExDose). A '2' and a red arrow point to the 'Show DVH/QI' button.

The 'Viewing' window shows an axial plane at z = 317.5 [mm]. The dose distribution is visualized as a color map on a CT scan, with a color scale for RBExDose [Gy(RBE)] ranging from 0 to 60. The 'min' is 0 and the 'max' is 2.501. The 'Viewer Options' panel includes 'Result (i.e. dose)', 'Window: Doseat', 'Custom', 'Window Center: 1.25', 'Window Width: 2.5', 'Range: 0 2.501', 'jet' color map, and 'Dose opacity: 1'. The 'Structure Visibility' panel lists GTV, Kidney_R, Kidney_L, Stomach, SmallBowel, LargeBowel, Celiac, SMA_SMV, Liver, Heart, SpinalCord, and DoseFalloff, all of which are checked.

The 'Info' panel at the bottom right shows 'v3.0.0' and 'github.com/e0404/mat' with an 'About' button.



	mean	std	max	min	D_2	D_5	D_50	D_95	D_98	V_0Gy	V_0.5Gy	V_1Gy	V_1.5Gy
GTV	1.5053	0.1981	2.0110	1.0341	1.8973	1.8506	1.4947	1.1921	1.1231	1	1	1	0
Kidney_R	0	0	0	0	0	0	0	0	0	1	0	0	0
Kidney_L	0	0	0	0	0	0	0	0	0	1	0	0	0
Stomach	0	0	0	0	0	0	0	0	0	1	0	0	0
SmallBowel	0	0	0	0	0	0	0	0	0	1	0	0	0
LargeBowel	0	0	0	0	0	0	0	0	0	1	0	0	0
Celiac	0	0	0	0	0	0	0	0	0	1	0	0	0
SMA_SMV	0	0	0	0	0	0	0	0	0	1	0	0	0
Liver	0.1694	0.4605	2.5011	0	1.6940	1.4688	0	0	0	1	0.1177	0.1008	0
Heart	0.0172	0.1143	1.8597	0	0.2483	0.0195	0	0	0	1	0.0127	0.0050	0
SpinalCord	0	0	0	0	0	0	0	0	0	1	0	0	0

7. Create a carbon ion treatment with the exact same settings as used for the proton treatment plan – What difference can now be observed?

Workflow

Refresh Load *.mat data **Calc. influence Mx** **Optimize** Save to GUI
 Load DICOM Re Import Dose
 Import from Bin...

Status: ready for dose calculation

Plan

bixel width in [mm] 10
 Gantry Angle in ° 315
 Couch Angle in ° 0
 Radiation Mode **carbon**
 Machine photons
 IsoCenter in [mm] # Fractions
 Type of optimization LEMIV_RBExD

use MC (VMC++) dose calculations
 3D conformal
 Run Sequencing
 Stratification Levels 7
 Run Direct Aperture Optimizat...

Objectives & constraints

	VOI name	VOI type	priority	obj. / const.	penalty	dose	EUD	volume	ro
1	Skin	OAR	2	square overdosing	300	25	NaN	NaN	no
2	PTV	TARGET	1	square deviation	1000	45	NaN	NaN	no

Visualization

Slice Type of plot inten... GoTo lateral
 Beam Plane axial Open 3D-View
 Offset Dislay option RBExDose

plot CT
 plot contour
 plot isolines
 plot dose
 plot isolines labels
 plot iso center
 visualize plan / be...

matRad **dkfz.** GERMAN CANCER RESEARCH CENTER IN THE HELMHOLTZ ASSOCIATION

axial plane z = 317.5 [mm]

min max 2.501
 Set IsoDose Levels

Viewer Options
 Result (i.e. dose)
 Window: Default Custom
 Window Center: 1.25
 Window Width: 2.5
 Range: 0 2.501
 jet
 Dose opacity: 1

Structure Visibility
 GTV
 Kidney_R
 Kidney_L
 Stomach
 SmallBowel
 LargeBowel
 Cellac
 SMA_SMV
 Liver
 Heart
 SpinalCord
 DoseFalloff

Info
 v3.0.0
 github.com/e0404/mat
 About

8. Save the optimization result via („Save to GUI“). Next, show the DVH by („Show DVH/QI“). Analyze the resulting dose distribution.

Workflow

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

Load DICOM Recalc

Import from Bin...

Status: plan is optimized

1

Plan

bixel width in [mm]: 10 use MC (VMC++) dose calculations

Gantry Angle in °: 315 3D conformal

Couch Angle in °: 0 Run Sequencing

Radiation Mode: carbon Stratification Levels: 7

Machine: Generic Run Direct Aperture Optimizat...

IsoCenter in [mm]: 265.8 296.7 316.4 Auto.

Fractions: 30

Type of optimization: LEMIV_RBExD Set Tissue

Objectives & constraints

	VOI name	VOI type	priority	obj. / const.	penalty	dose	EUD	volume	ro
1	Skin	OAR	2	square overdosing	300	25	NaN	NaN	no
2	PTV	TARGET	1	square deviation	1000	45	NaN	NaN	no

save

Visualization

Slice: Type of plot: inten... GoTo: lateral plot CT

Beam: Plane: axial Open 3D-View plot contour

Offset: Dislay option: RBExDose **2** plot isolines

Show DVH/QI plot dose

plot isolines labels

plot iso center

visualize plan / be...

3

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axial plane z = 317.5 [mm]

min 0 max 2.122

Set IsoDose Levels

Viewer Options

Result (i.e. dose): Window Doseat

Custom

Window Center: 1.06

Window Width: 2.12

Range: 0 2.123

jet

Dose opacity: 1

Structure Visibility

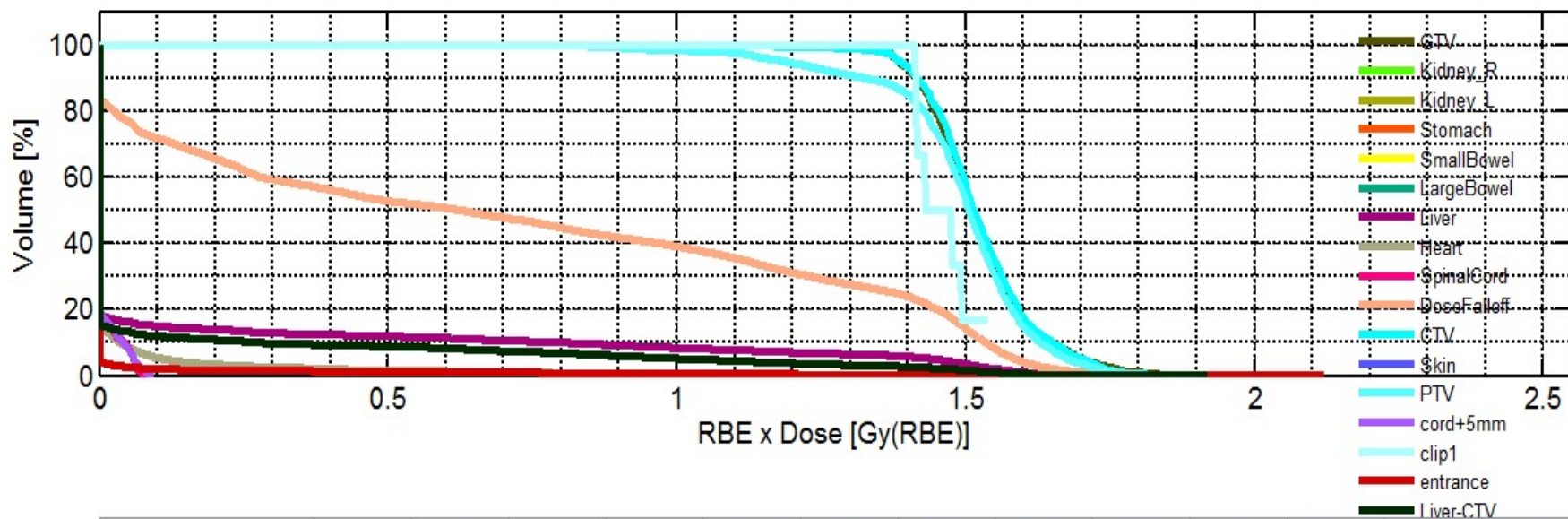
- GTV
- Kidney_R
- Kidney_L
- Stomach
- SmallBowel
- LargeBowel
- Celac
- SMA_SMV
- Liver
- Heart
- SpinalCord
- DoseFalloff

Info

v3.0.0

github.com/e0404/mat

About



	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
GTV	1.5212	0.0930	1.8920	1.2809	1.7595	1.7032	1.5090	1.3845	1.3641	1	1	1	
Kidney_R	0	0	0	0	0	0	0	0	0	1	0	0	
Kidney_L	0	0	0	0	0	0	0	0	0	1	0	0	
Stomach	0	0	0	0	0	0	0	0	0	1	0	0	
SmallBowel	0	0	0	0	0	0	0	0	0	1	0	0	
LargeBowel	0	0	0	0	0	0	0	0	0	1	0	0	
Celiac	0	0	0	0	0	0	0	0	0	1	0	0	
SMA_SMV	0	0	0	0	0	0	0	0	0	1	0	0	
Liver	0.1570	0.4178	1.9880	0	1.5533	1.4456	0	0	0	1	0.1243	0.1004	0.0000
Heart	0.0277	0.1314	1.8137	0	0.4139	0.1145	0	0	0	1	0.0212	0.0088	0.0000
SpinalCord	0.0077	0.0187	0.0855	0	0.0659	0.0582	0	0	0	1	0	0	

Results

- Mean doses for different regions (Gy) using 5 photon beams, single proton beam and carbon ion beam:

Region/Radiation(angles)	Photons(0,180,225,270,315)	Protons(315)	Carbon(315)
GTV	1.5	1.5053	1.5212
Kidneys	0	0	0
Stomach	0.0342	0	0
Liver	0.3033	0.1694	0.1570
Heart	0.2296	0.0172	0.0277
Spinal Cord	0.0391	0	0.0077
CTV	1.5015	1.4981	1.5236
PTV	1.4991	1.4595	1.4868
Skin	0.0568	0.0179	0.0162