

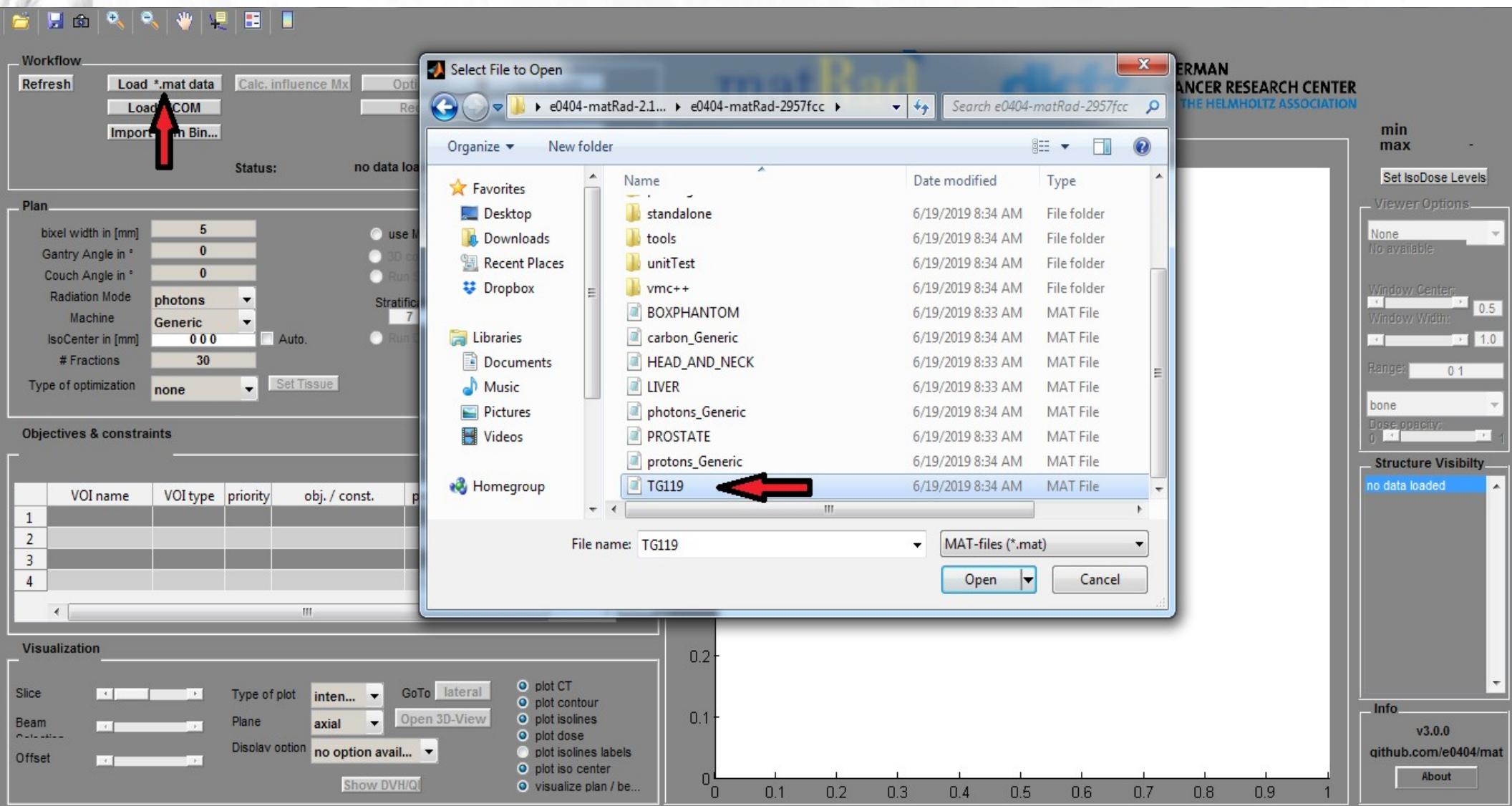
PARTICLE THERAPY MASTERCLASS

Hands-On Treatment Planning with matRad

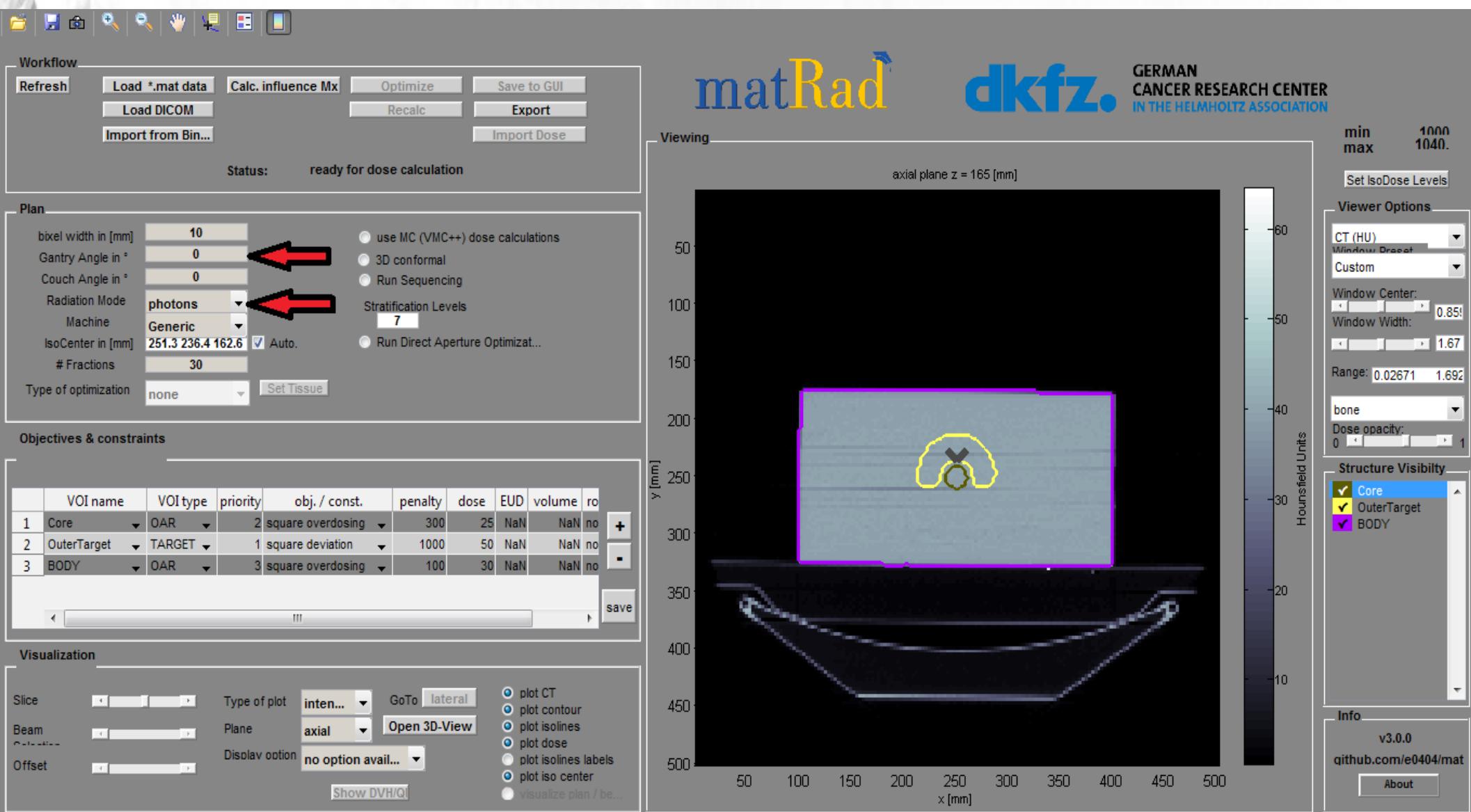
1st Exercise

- First steps on the TG119 phantom
- Radiotherapy treatment - photons vs. protons vs. carbon ions
- Analysing and comparing results

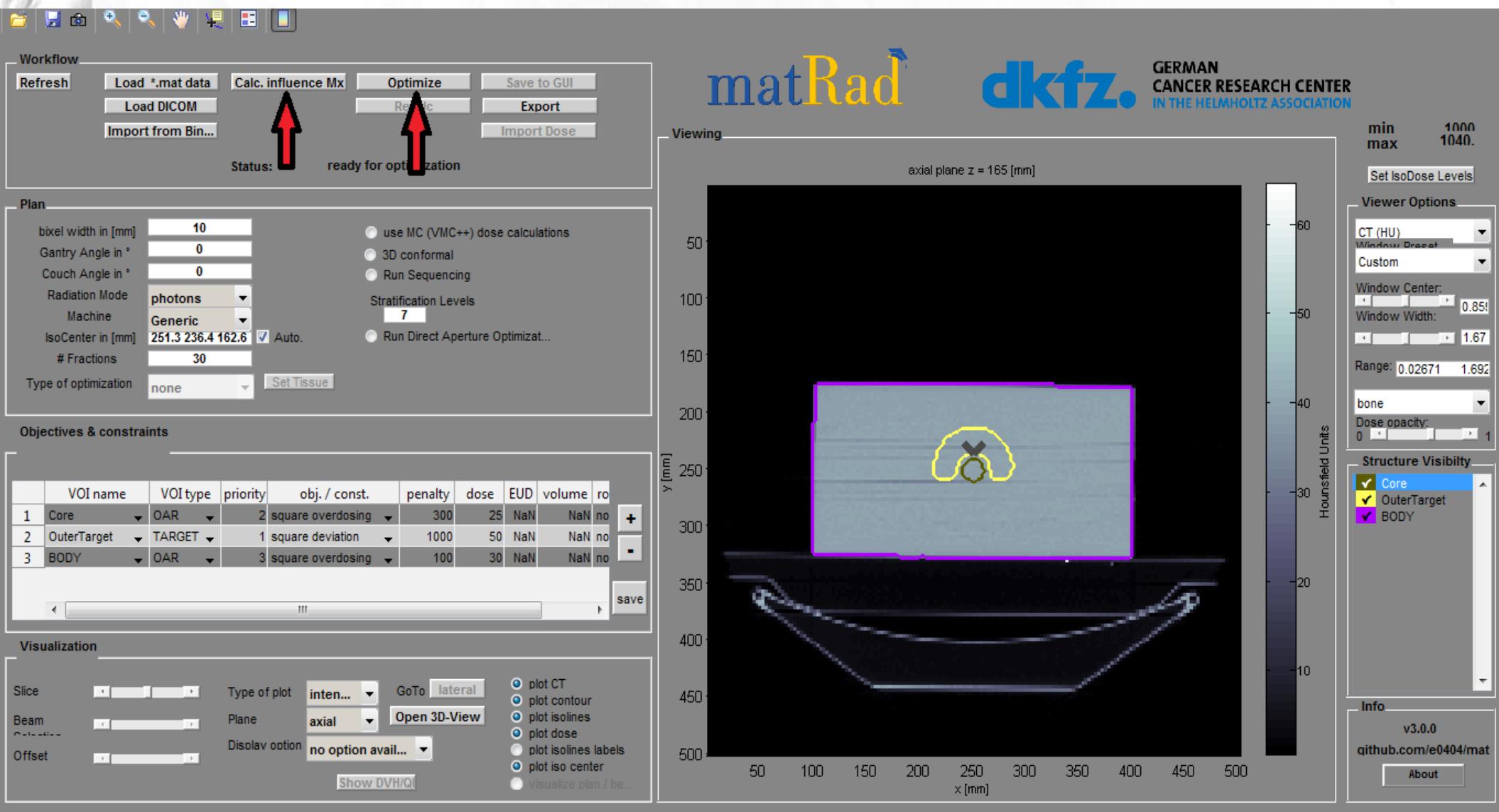
1. Load the TG119 phantom via the Load *.mat button (TG119.mat).



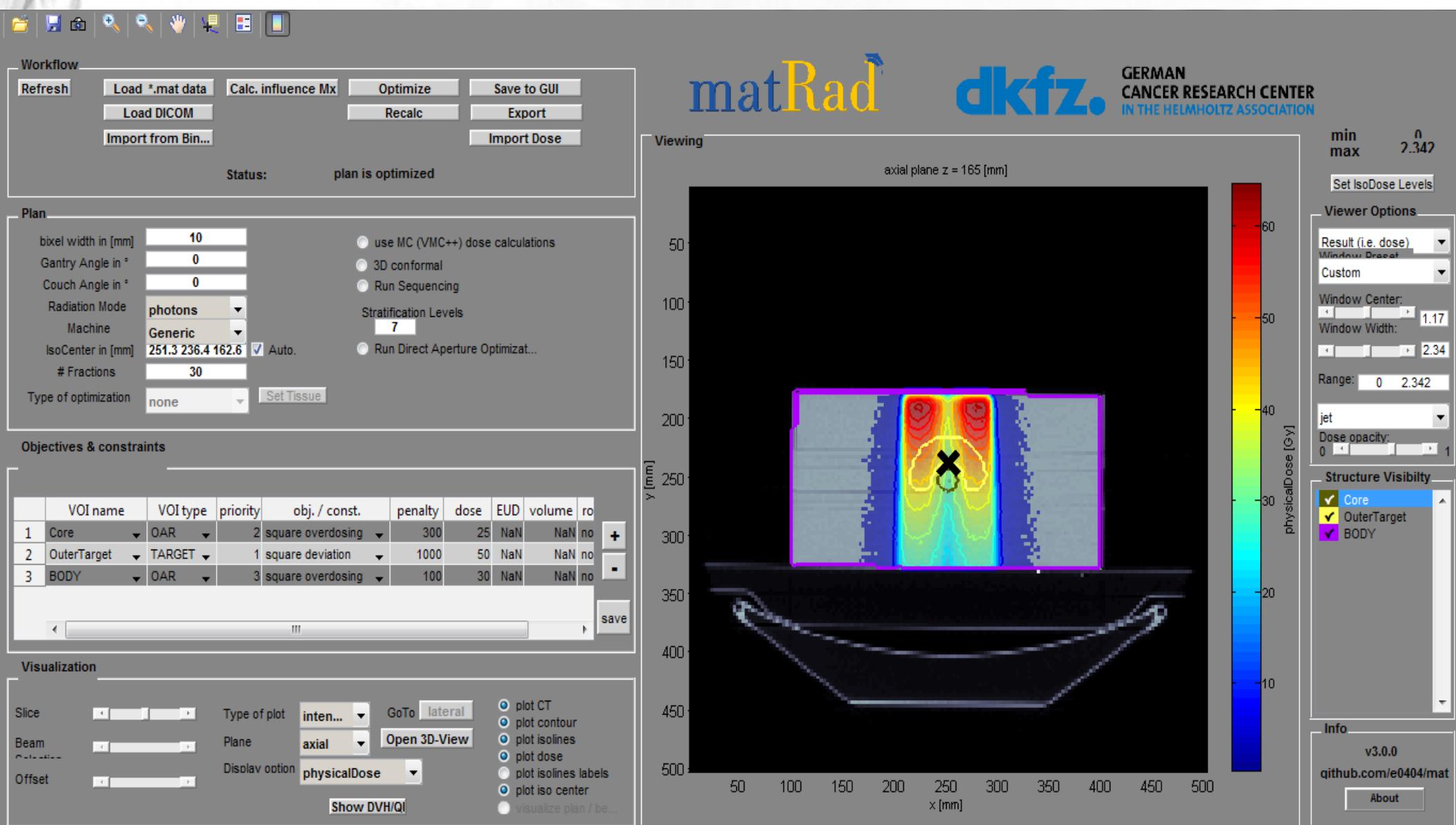
2. Set radiation modality to Photons and define one beam angle (gantry angle).



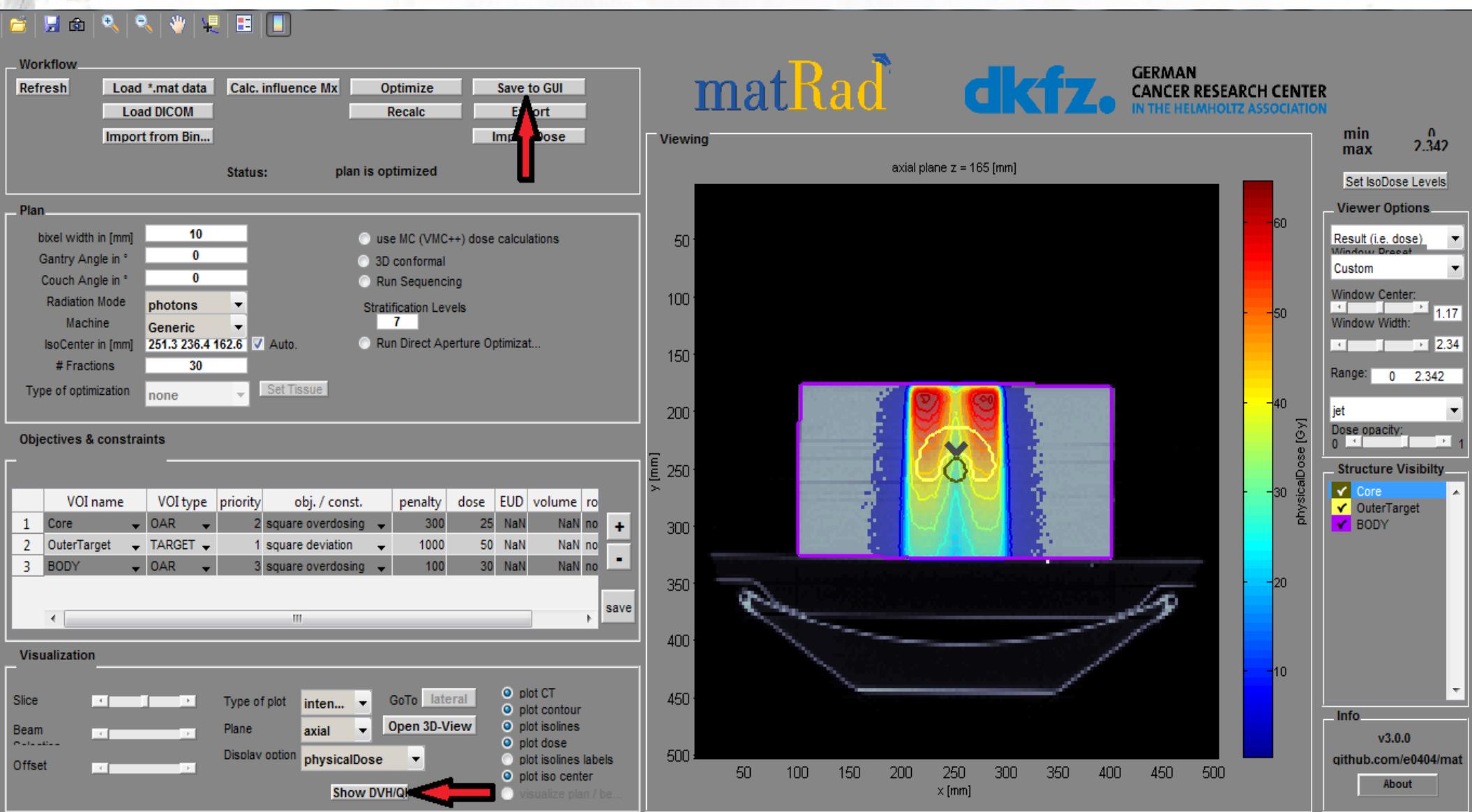
3. Trigger dose calculation via button („Calc. Influence Mx“) and start inverse optimization by clicking on („Optimize“).

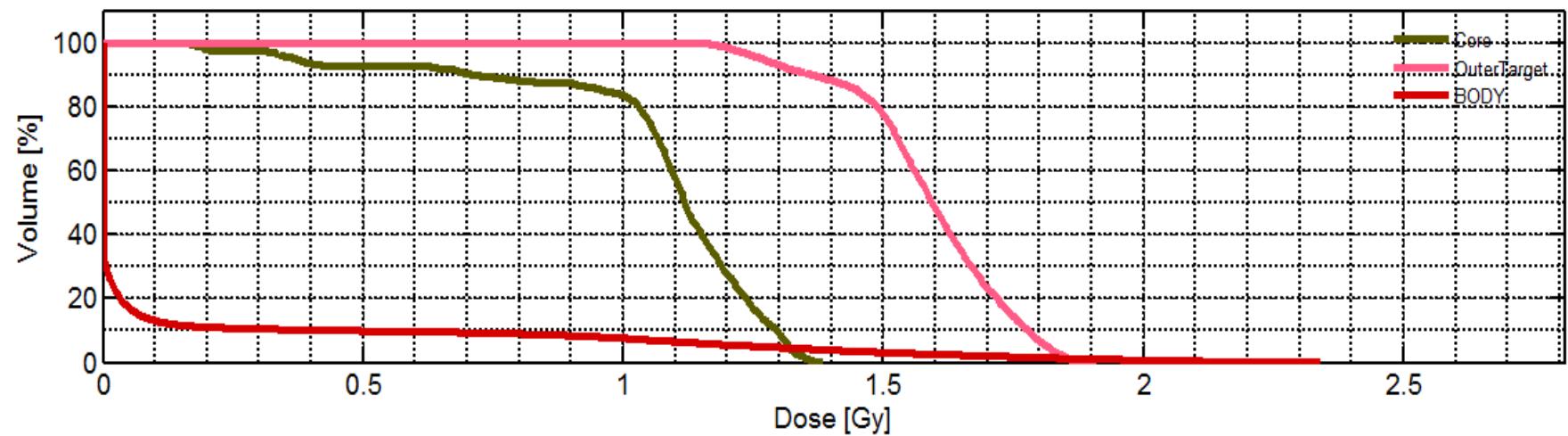


4. Analyze the resulting dose distribution.



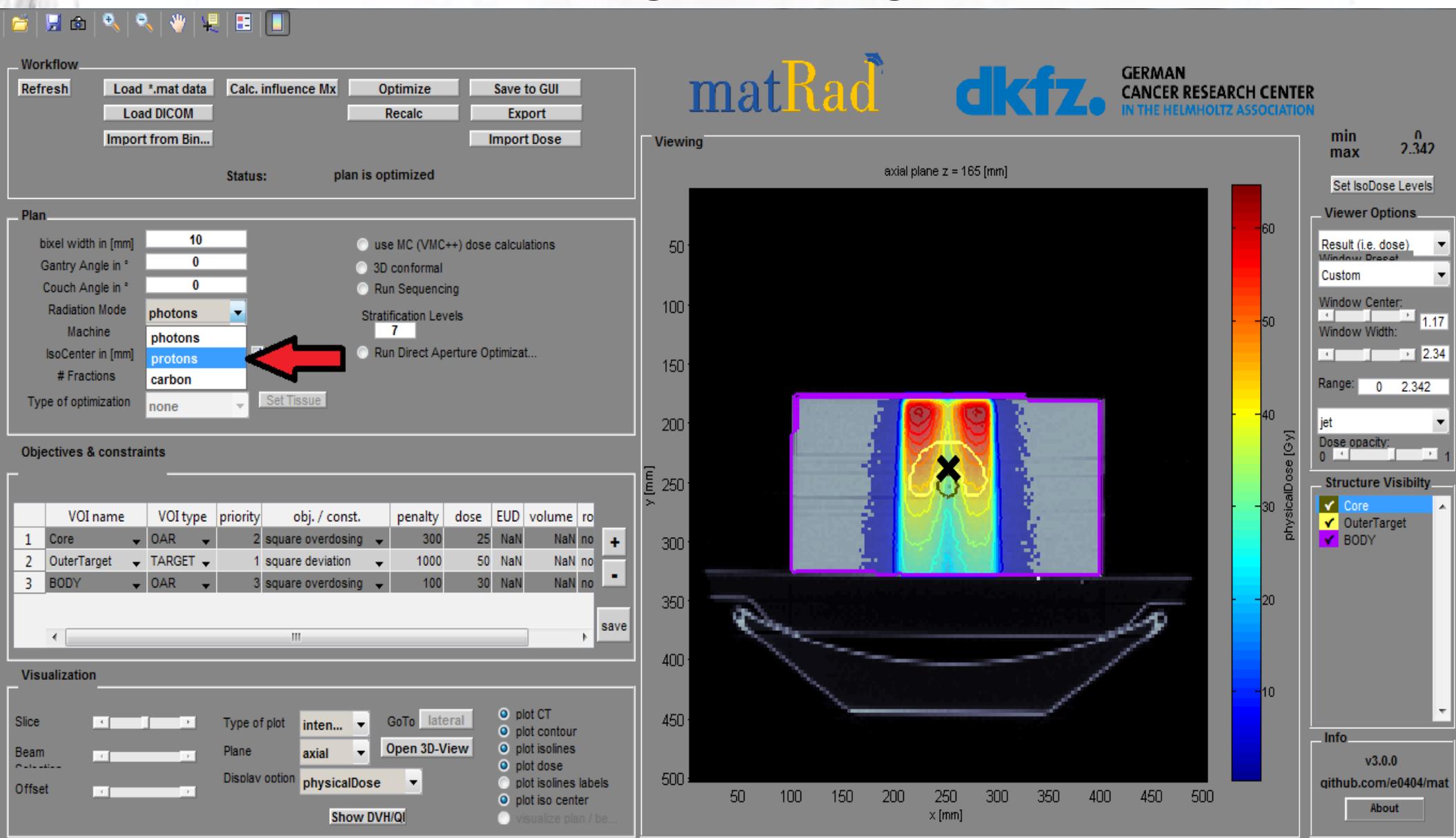
5. Save the optimization result via („Save to GUI“). Next, show the DVH by („Show DVH/QI“).



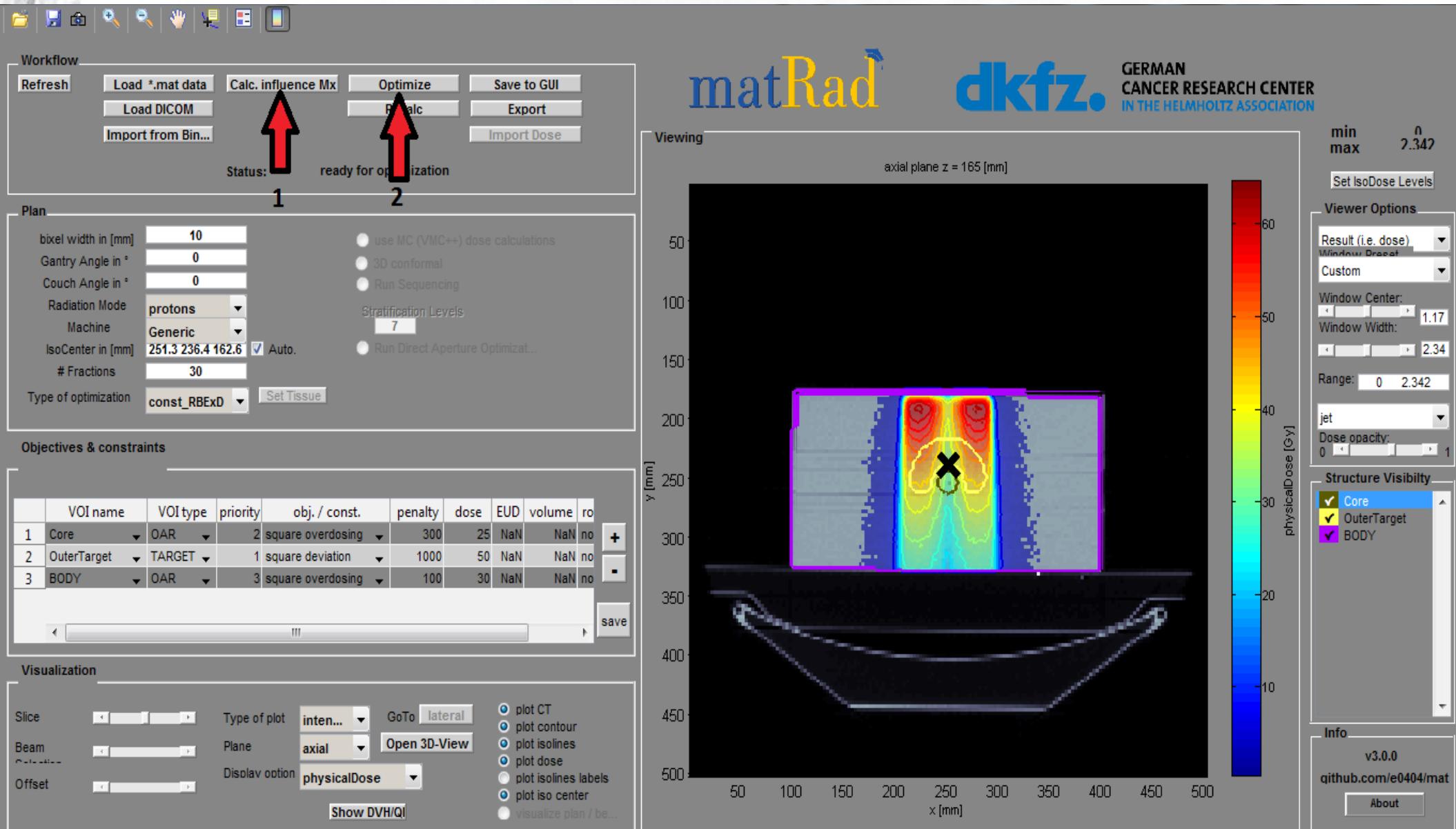


	mean	std	max	min	D ₂	D ₅	D ₅₀	D ₉₅	D ₉₈	V _{0Gy}	V _{0.4Gy}	V _{0.9Gy}	V _{1.4Gy}	V _{2.5Gy}
Core	1.0665	0.2554	1.3860	0.1329	1.3434	1.3187	1.1183	0.3706	0.1988	1	0.9341	0.8727	0	0
OuterTarget	1.5852	0.1536	1.9115	1.0935	1.8453	1.8153	1.5941	1.2663	1.2077	1	1	1	0.8824	0
BODY	0.1443	0.4168	2.3420	0	1.7203	1.2694	0	0	0	1	0.1019	0.0846	0.0393	0

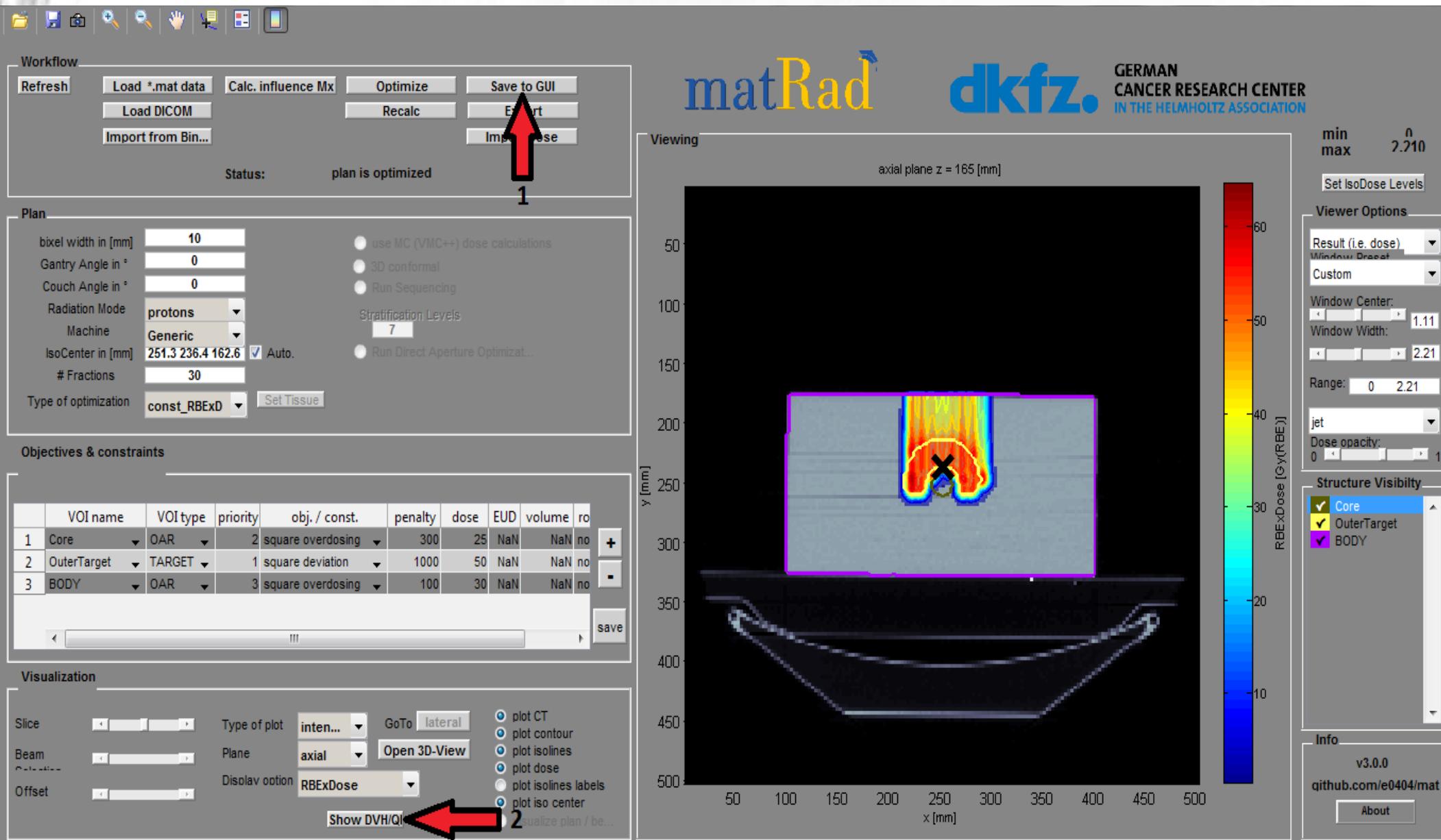
6. Change the radiation modality to: Protons and leave the beam angles unchanged.

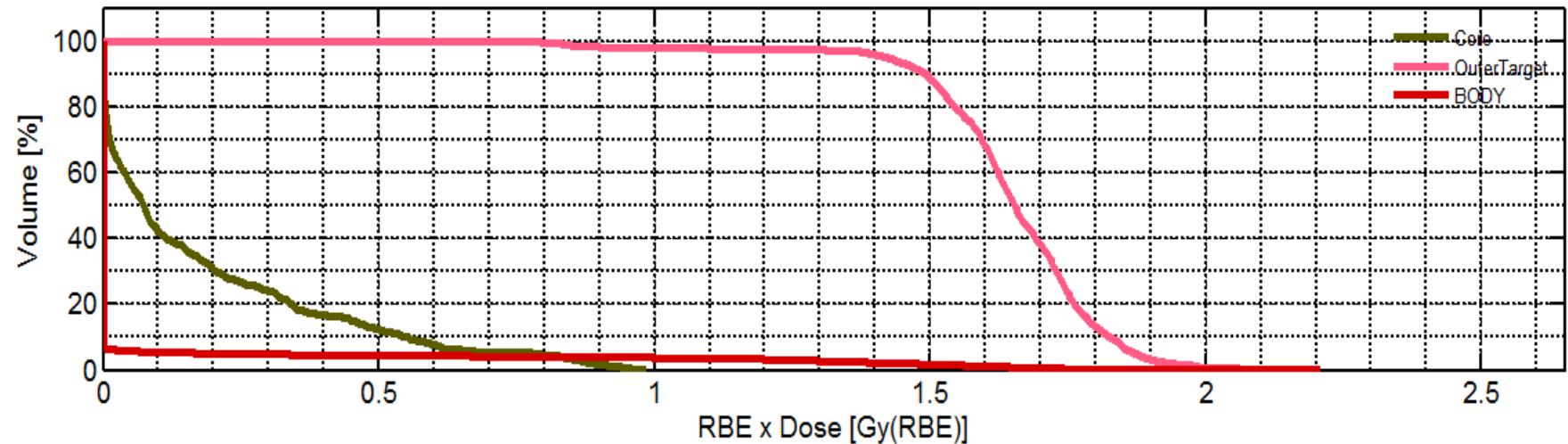


7. Trigger dose calculation via button („Calc. InfluenceMx“) and start inverse optimization by clicking on („Optimize“).



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





	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 _{1.5Gy}
Core	0.1815	0.2396	0.9866	2.0386e-09	0.8909	0.7849	0.0744	2.4933e-05	6.0723e-07	1	0.1682	0.0470	0	0
OuterTarget	1.6449	0.1770	2.1789	0.7475	1.9408	1.8726	1.6533	1.4205	0.9187	1	1	0.9949	0.9722	0
BODY	0.0640	0.2912	2.2101	0	1.4572	0.2364	0	0	0	1	0.0462	0.0405	0.0282	0

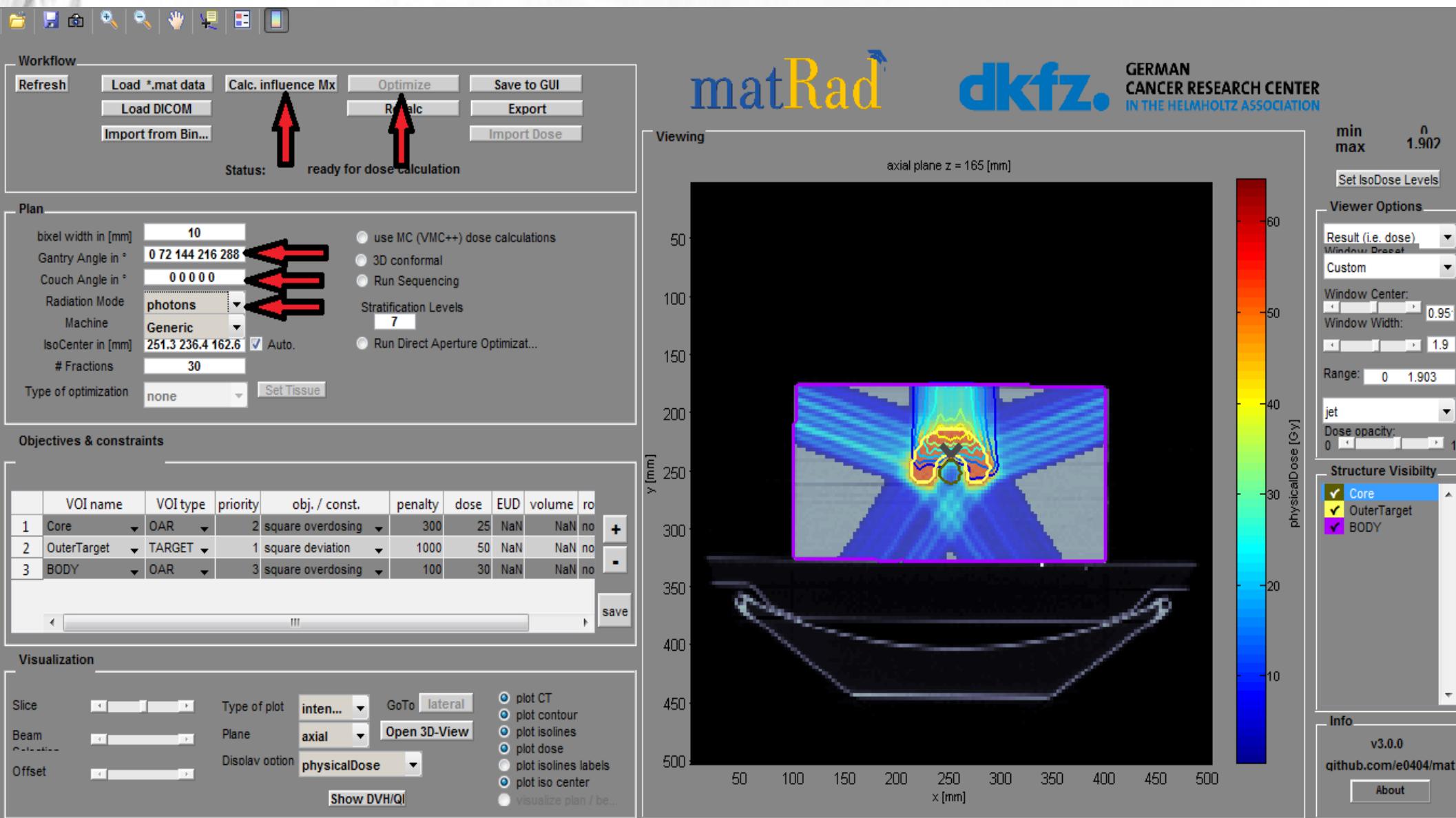
Results

- Mean doses for different regions (Gy):

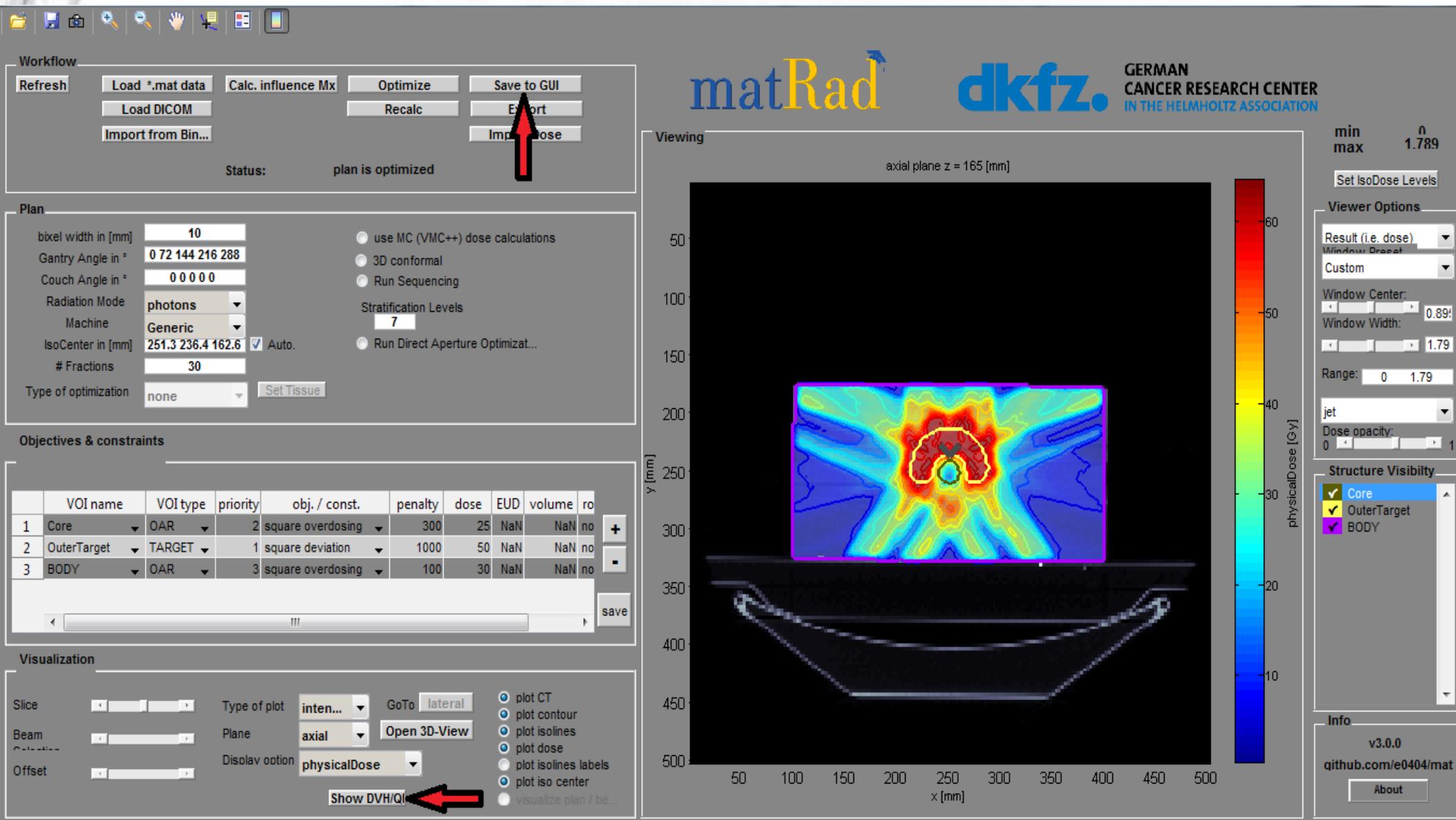
Region/Radiation	Photons	Protons
Core	1.0665	0.1815
Outer Target	1.5852	1.6449
Body	0.1443	0.0640

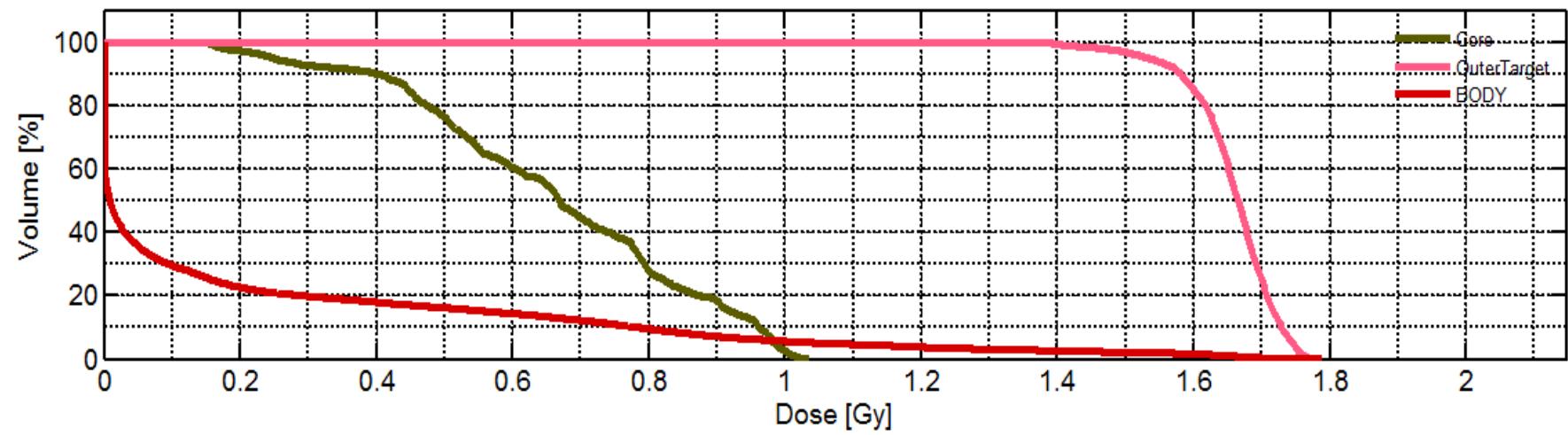
- Photons deliver highest dose at the surface
- Protons deliver highest dose at the target (tumor) and protect sensitive organs

9. Try to define a better photon treatment plan by defining more beam angles (e.g. [0, 72, 144, 216, 288]). Trigger dose calculation („Calc. Influence Mx“) and start inverse optimization („Optimize“).



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





	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
Core	0.6625	0.2176	1.0370	0.1450	1.0030	0.9853	0.6686	0.2460	0.1755	1	0.9265	0.4477	0.0250	
OuterTarget	1.6563	0.0659	1.7897	1.2866	1.7566	1.7450	1.6652	1.5323	1.4636	1	1	1	1	
BODY	0.1968	0.3777	1.7897	0	1.5510	1.0629	0.0091	0	0	1	0.1986	0.1230	0.0568	

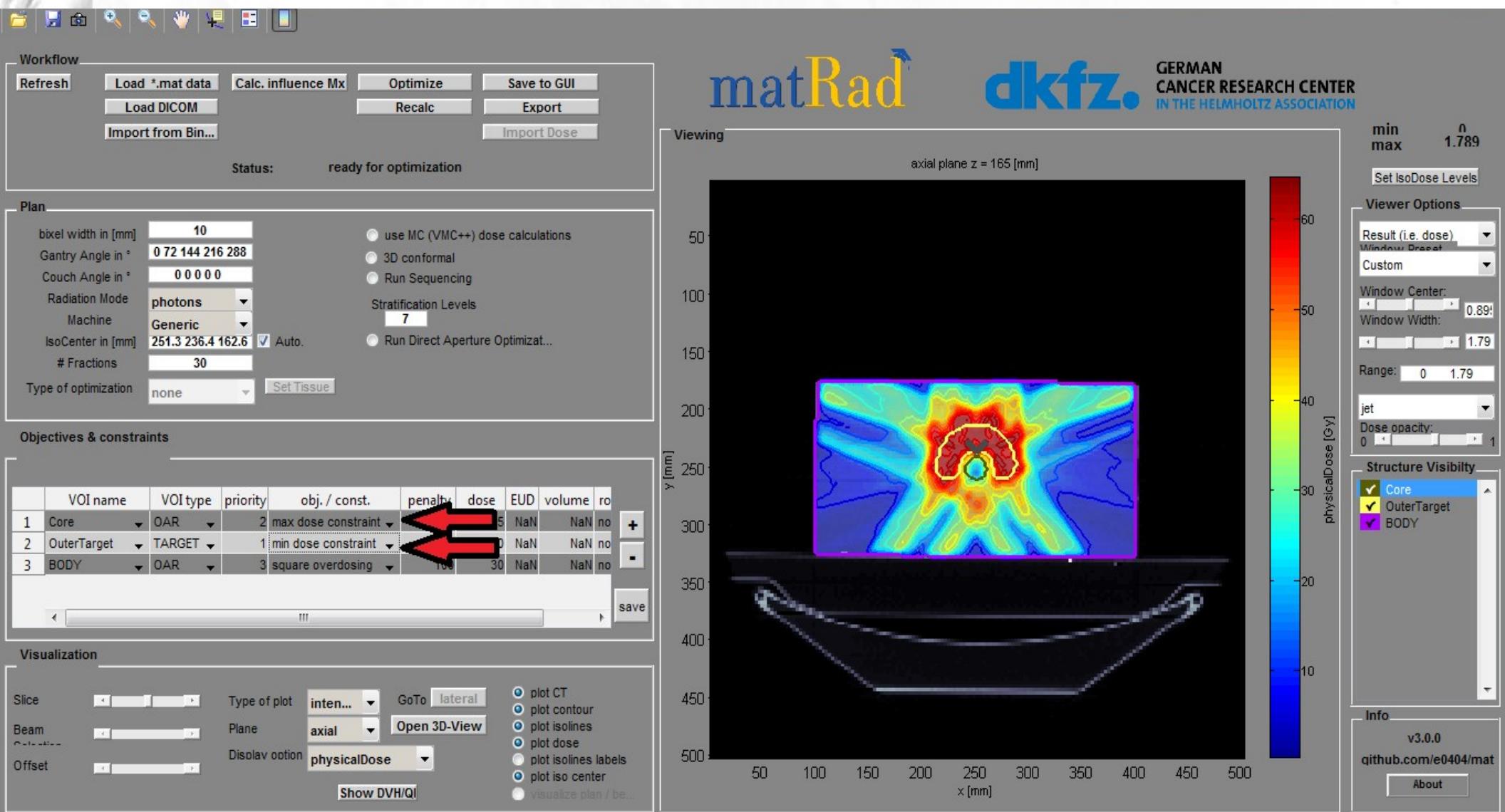
Results

- Mean doses for different regions (Gy):

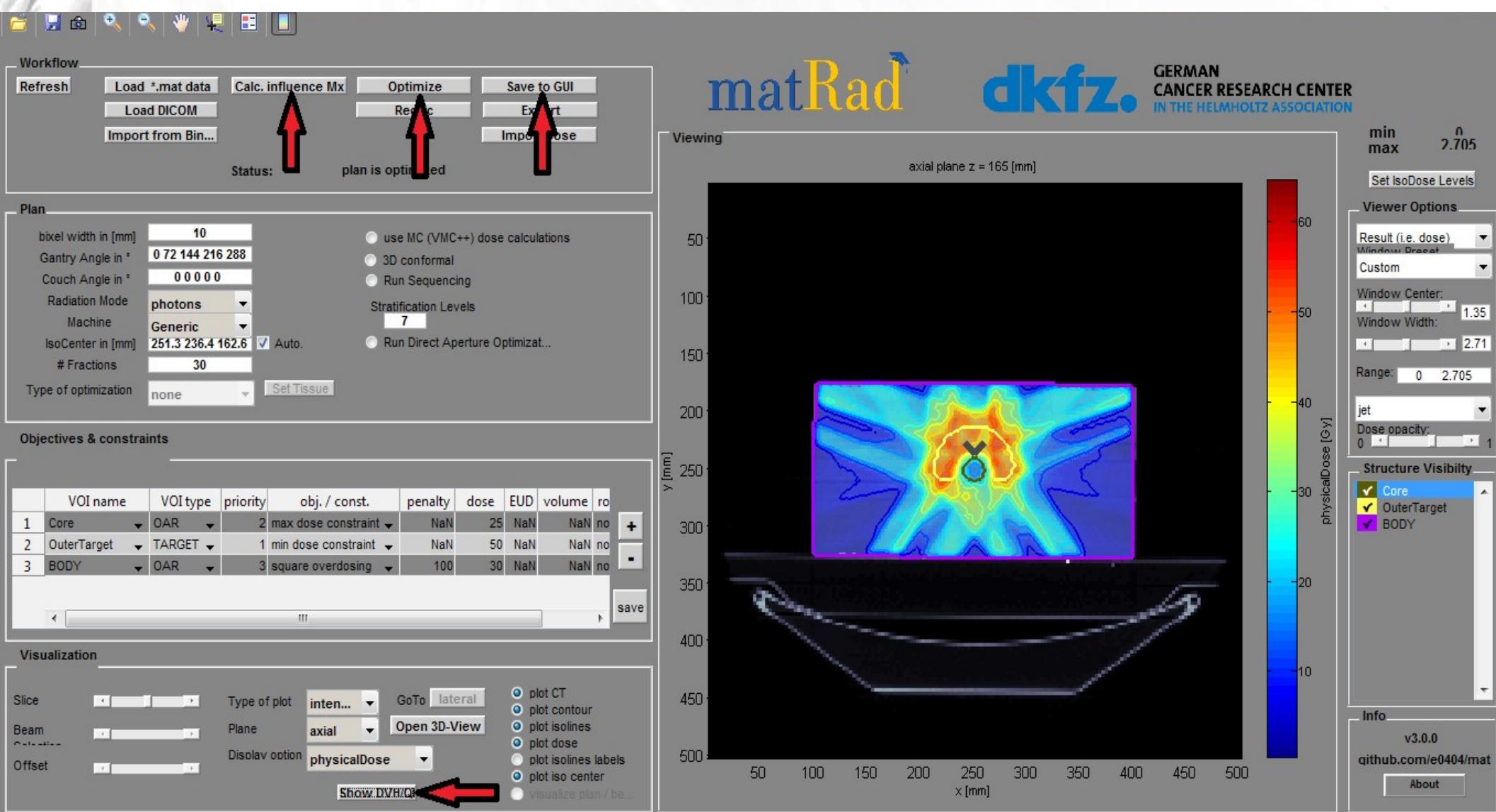
Region/Radiation(angles)	Photons(0)	Protons(0)	Photons (0,72,144,216,288)
Core	1.0665	0.1815	0.6625
Outer Target	1.5852	1.6449	1.6563
Body	0.1443	0.0640	0.1968

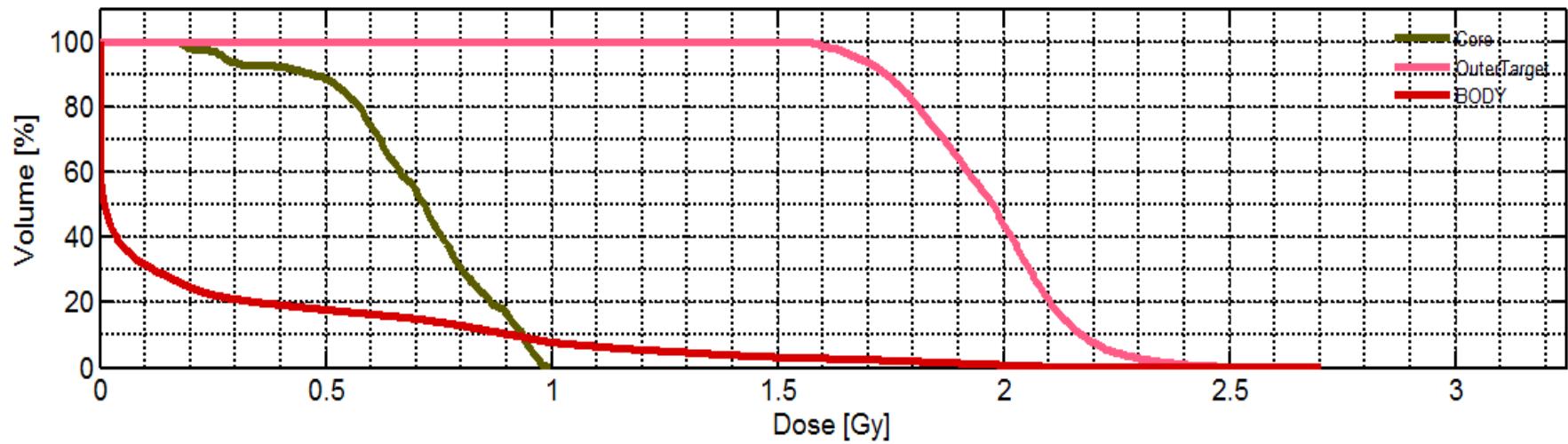
- Treatment plan using multiple photon beams gives better results than single photon beam.
- Best results are obtained using protons.

11. Change optimization objective to improve the photon treatment plan. Use Table („Objectives & constraints“) and add for e.g. maximal dose for the core or minimal dose for the outer target.



12. Trigger dose calculation („Calc. Influence Mx“) and start inverse optimization („Optimize“). Save the optimization result via („Save to GUI“). Next, show the DVH by („Show DVH/QI“).





	mean	std	max	min	D_2	D_5	D_50	D_95	D_98	V_0Gy	V_0.5Gy	V_1Gy	V_1.6Gy	V
Core	0.6974	0.1876	0.9986	0.1704	0.9743	0.9563	0.7189	0.2781	0.1981	1	0.8848	0	0	0
OuterTarget	1.9652	0.1732	2.7054	1.5511	2.3409	2.2397	1.9766	1.6761	1.6190	1	1	1	1	0.9857
BODY	0.2343	0.4481	2.7054	0	1.7993	1.2658	0.0110	0	0	1	0.1780	0.0784	0.0288	

Results

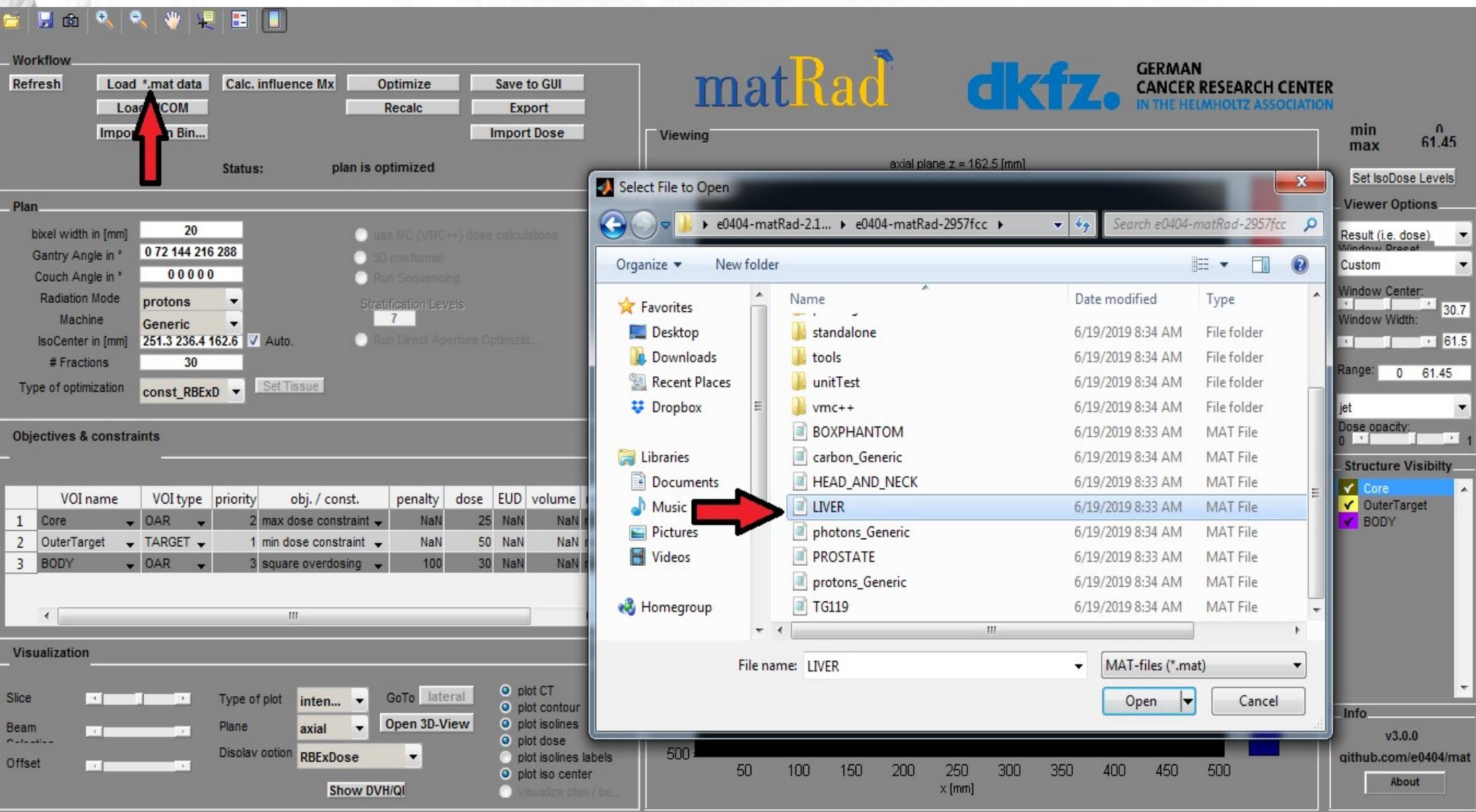
- Mean doses for different regions (Gy) using 5 beams with and without constraints:

Region/Radiation	With constraints	Without constraints
Core	0.6625	0.6974
Outer Target	1.6563	1.9652
Body	0.1968	0.2343

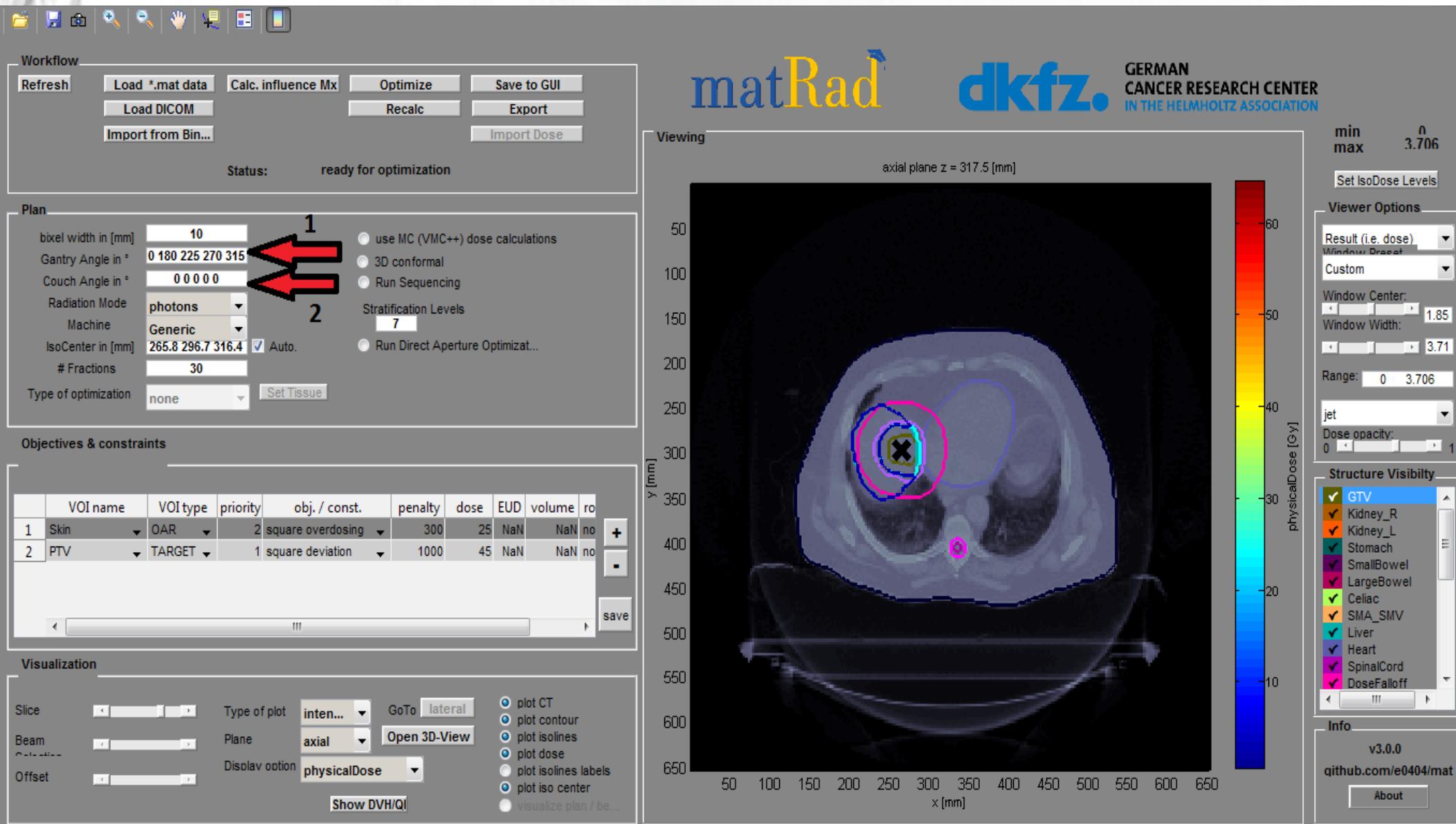
2nd Exercise

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

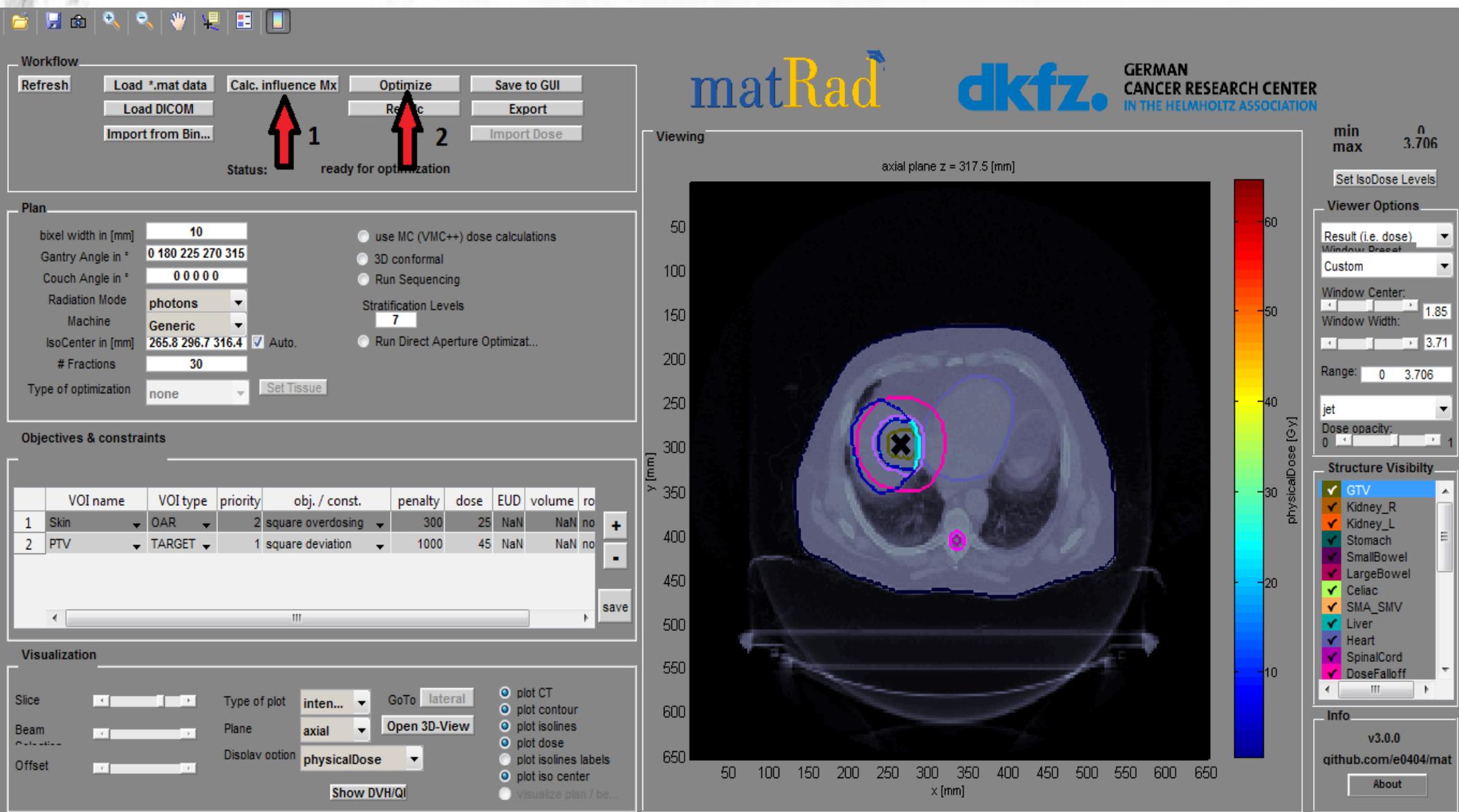
1. Load the liver patient case via the Load *.mat button (LIVER.mat)



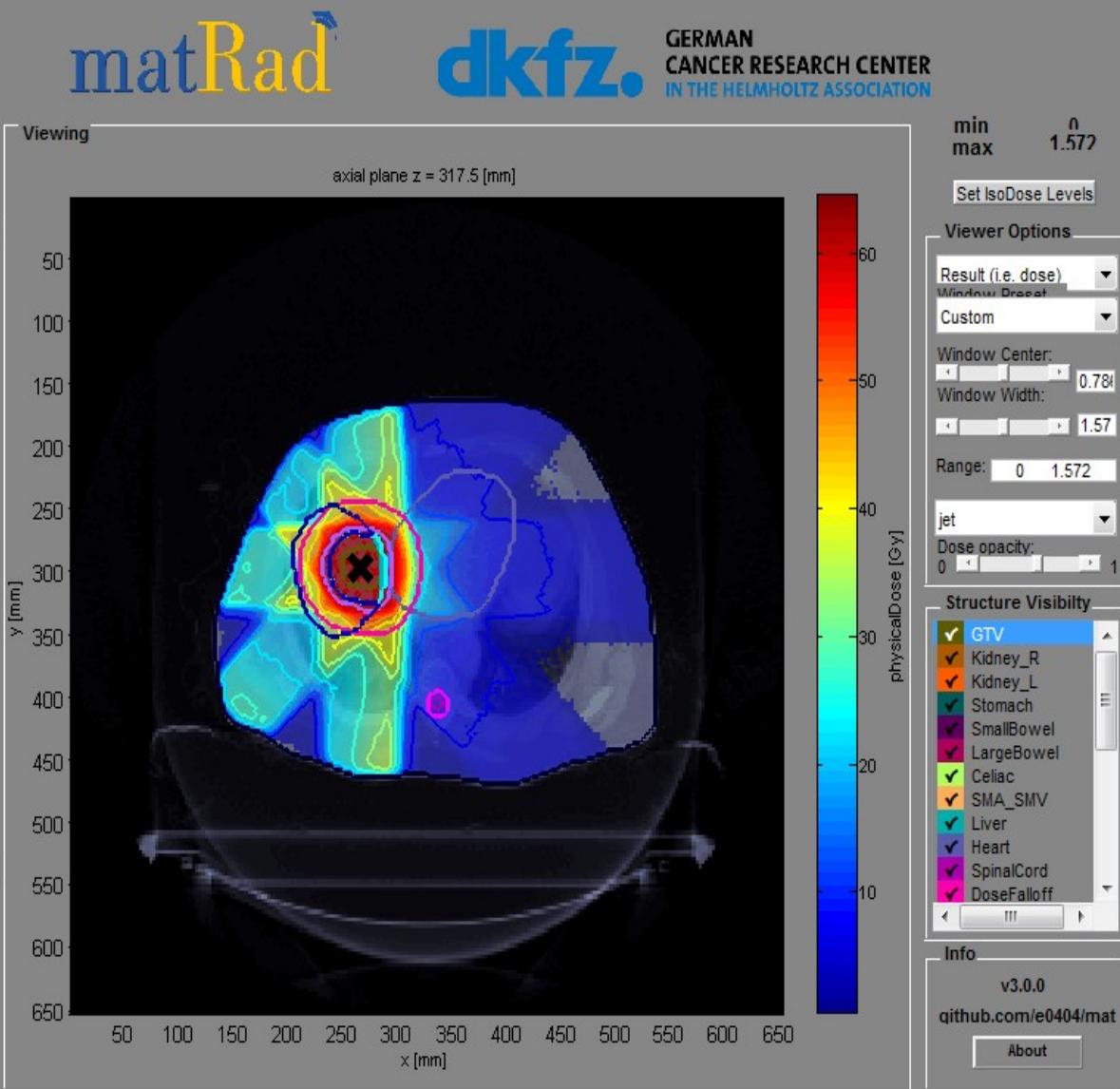
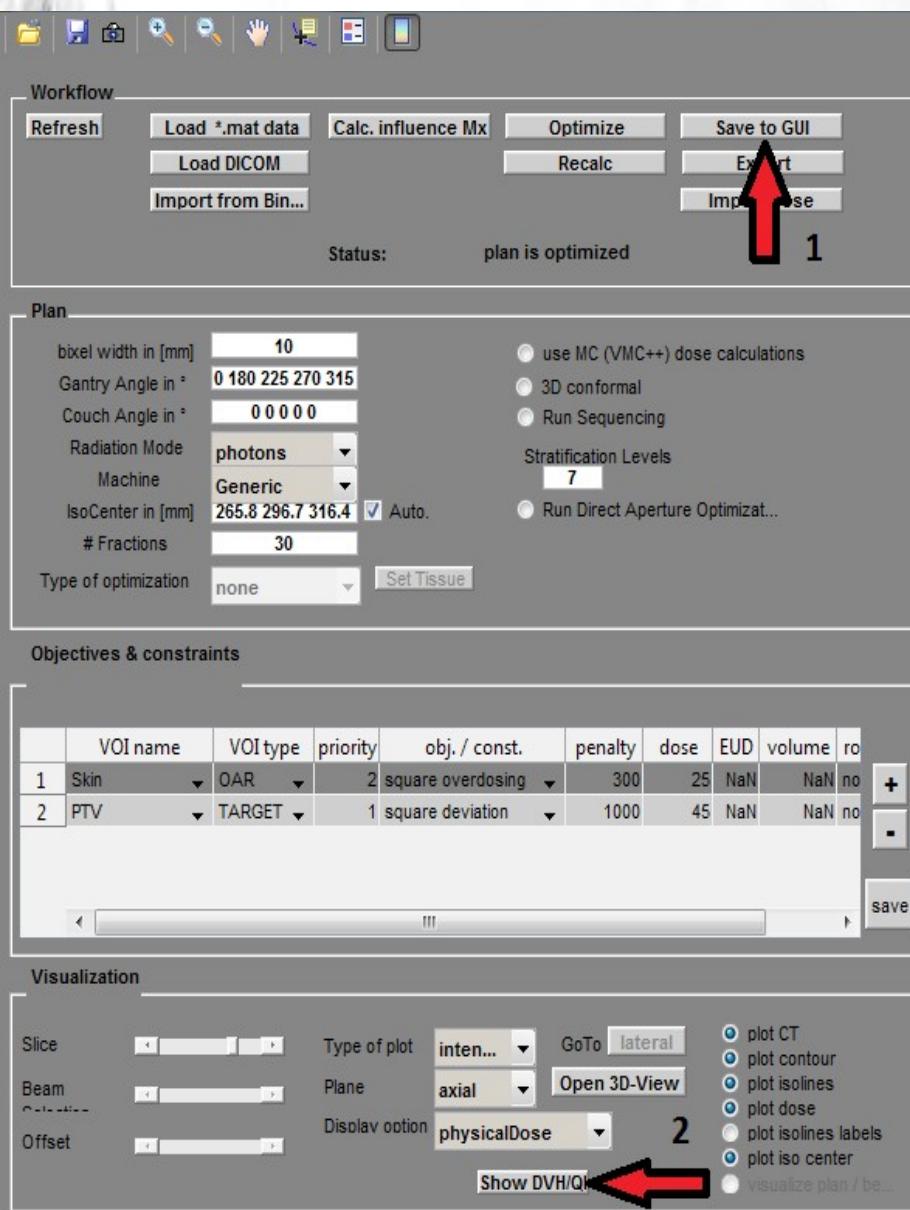
2. Define your own photon treatment plan with approx. 4-5 beam directions.

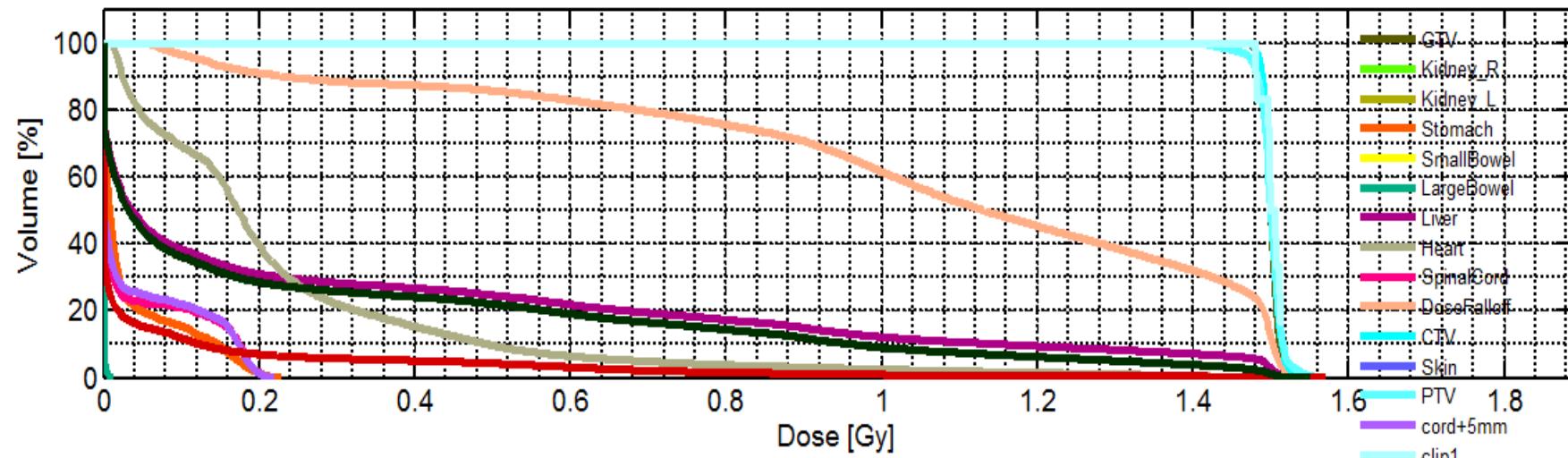


3. Trigger dose calculation („Calc. Influence Mx“) and start inverse optimization („Optimize“).



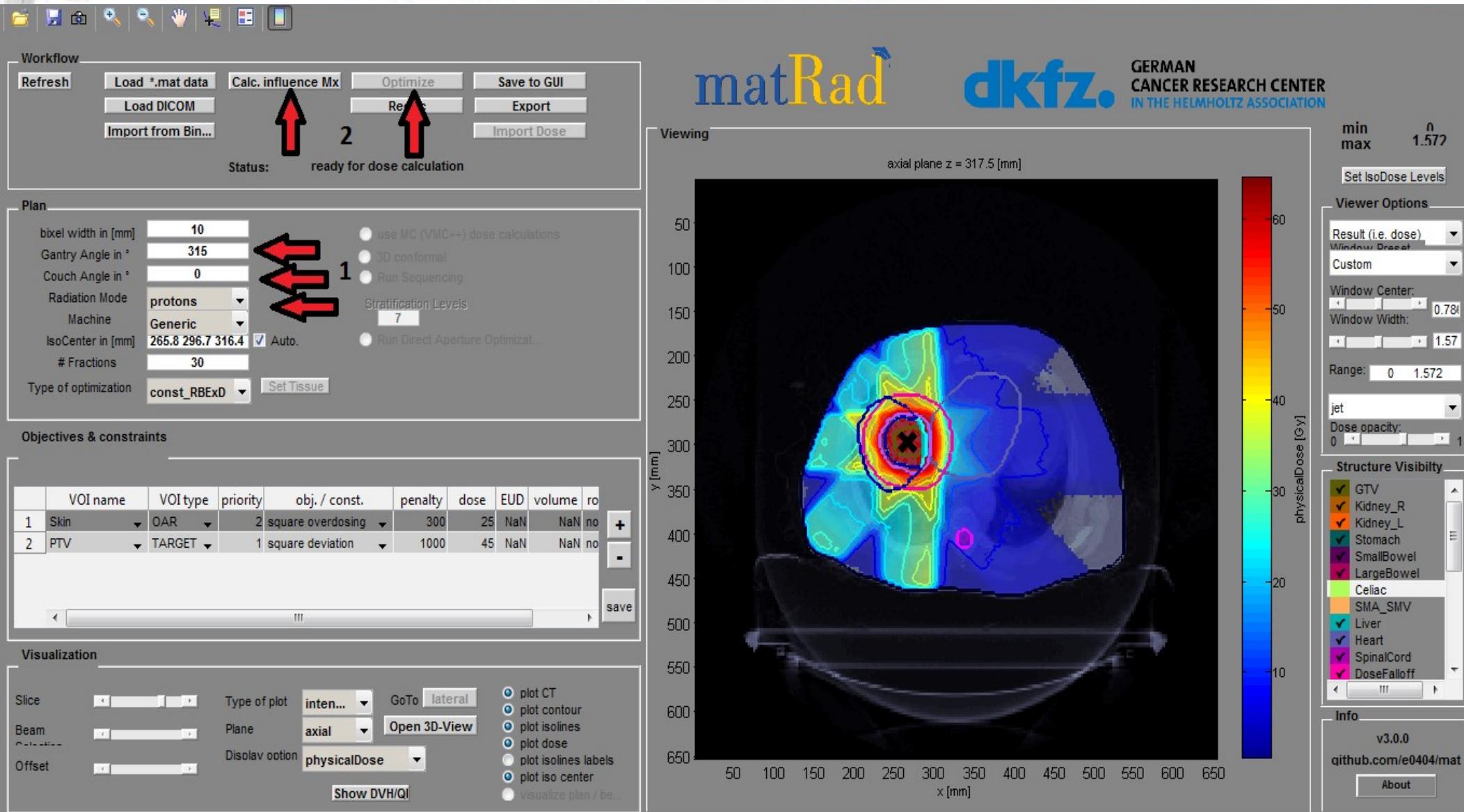
4. Save the optimization result via („Save to GUI“). Next, show the DVH by („Show DVH/QI“). Analyze dose distribution.



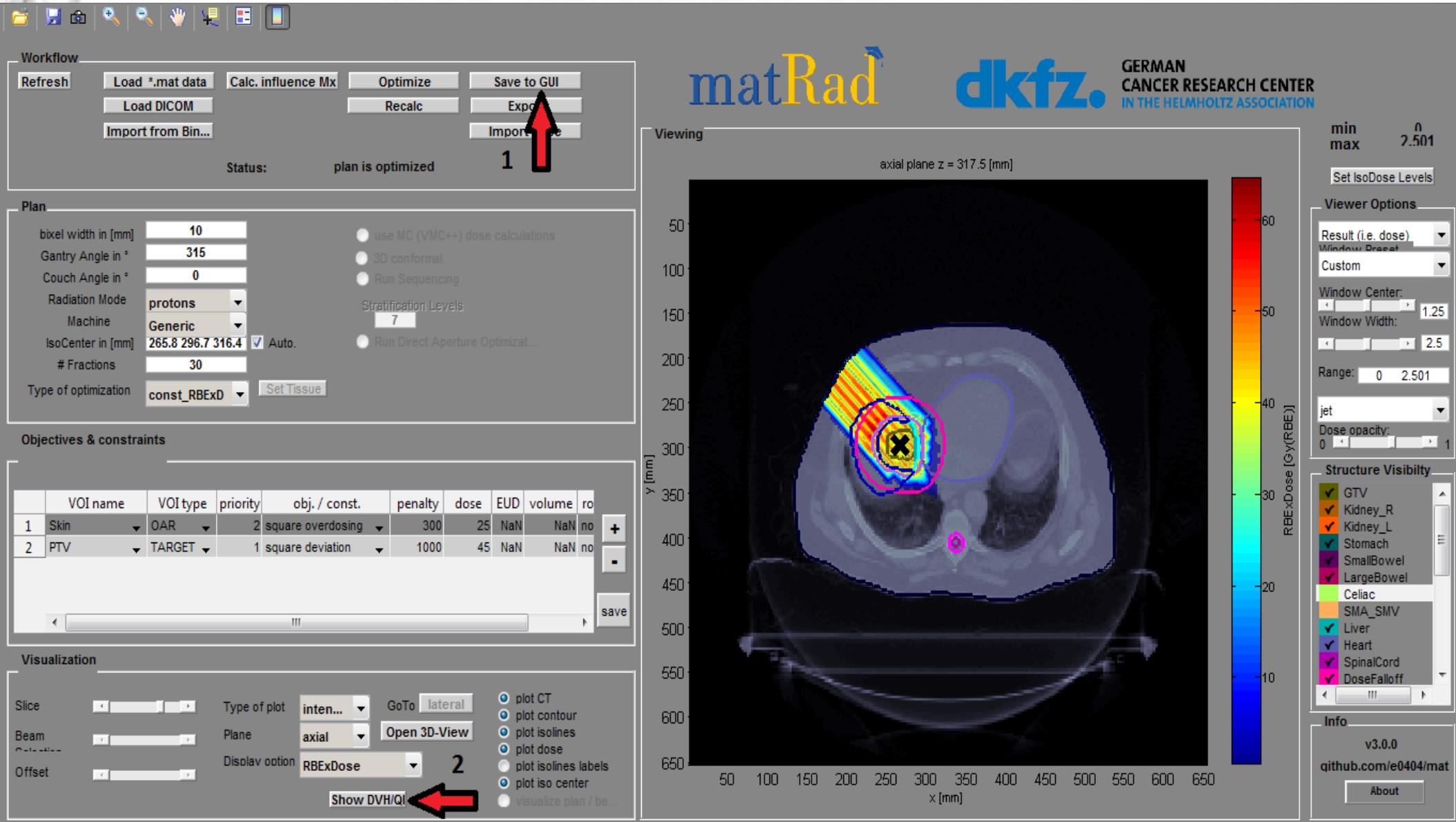


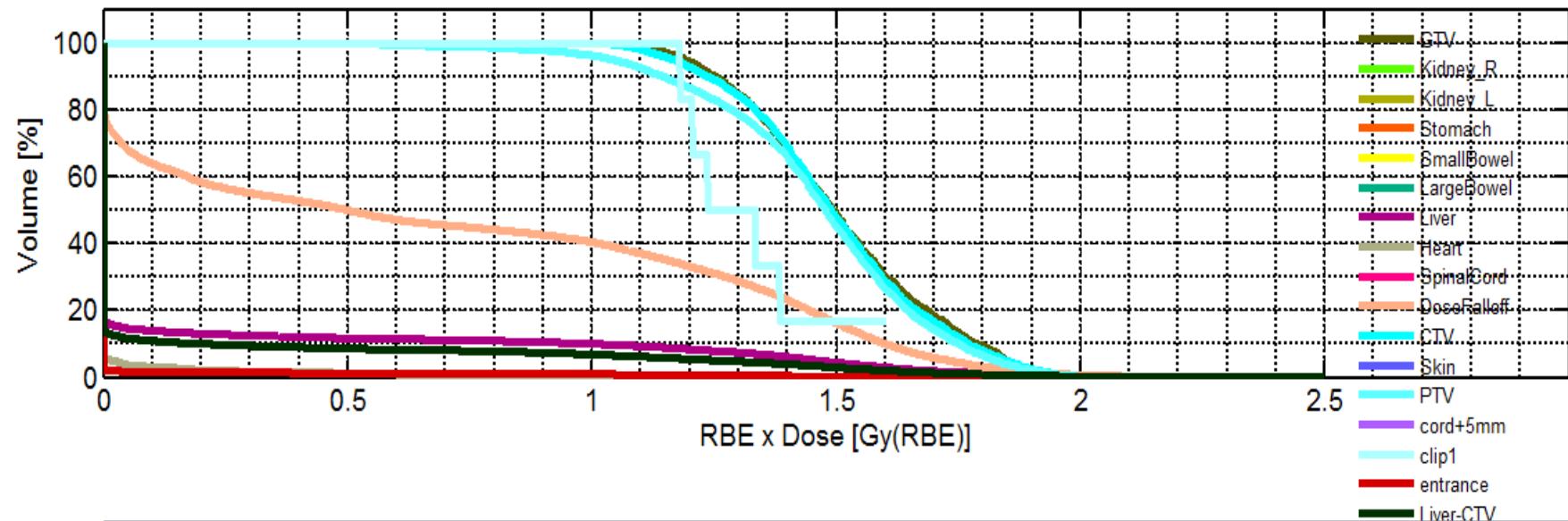
	mean	std	max	min	D_2	D_5	D_50	D_95	D_98	V_0Gy	V_0.3Gy	V_0.6Gy	V_0.9G
GTV	1.5000	0.0090	1.5281	1.4727	1.5188	1.5148	1.5002	1.4851	1.4796	1	1	1	1
Kidney_R	0	0	0	0	0	0	0	0	0	1	0	0	0
Kidney_L	0	0	0	0	0	0	0	0	0	1	0	0	0
Stomach	0.0342	0.0566	0.2310	0	0.1940	0.1736	0.0082	0	0	1	0	0	0
SmallBowel	0	0	0	0	0	0	0	0	0	1	0	0	0
LargeBowel	2.6018e-04	0.0012	0.0147	0	0.0047	0.0019	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	0.3033	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	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“).



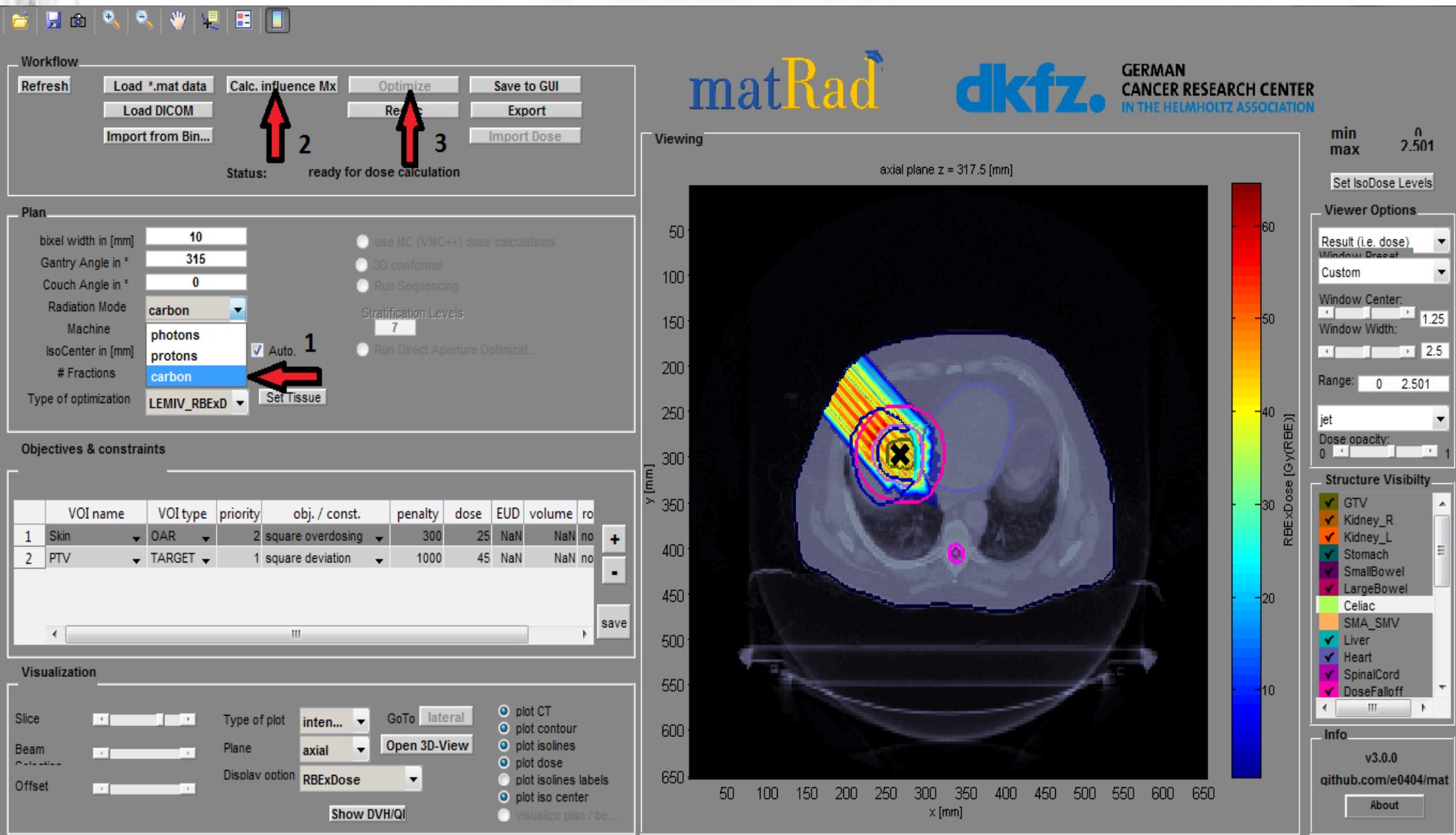
6. Save the optimization result via („Save to GUI“). Next, show the DVH by („Show DVH/QI“). Analyze the resulting dose distribution.



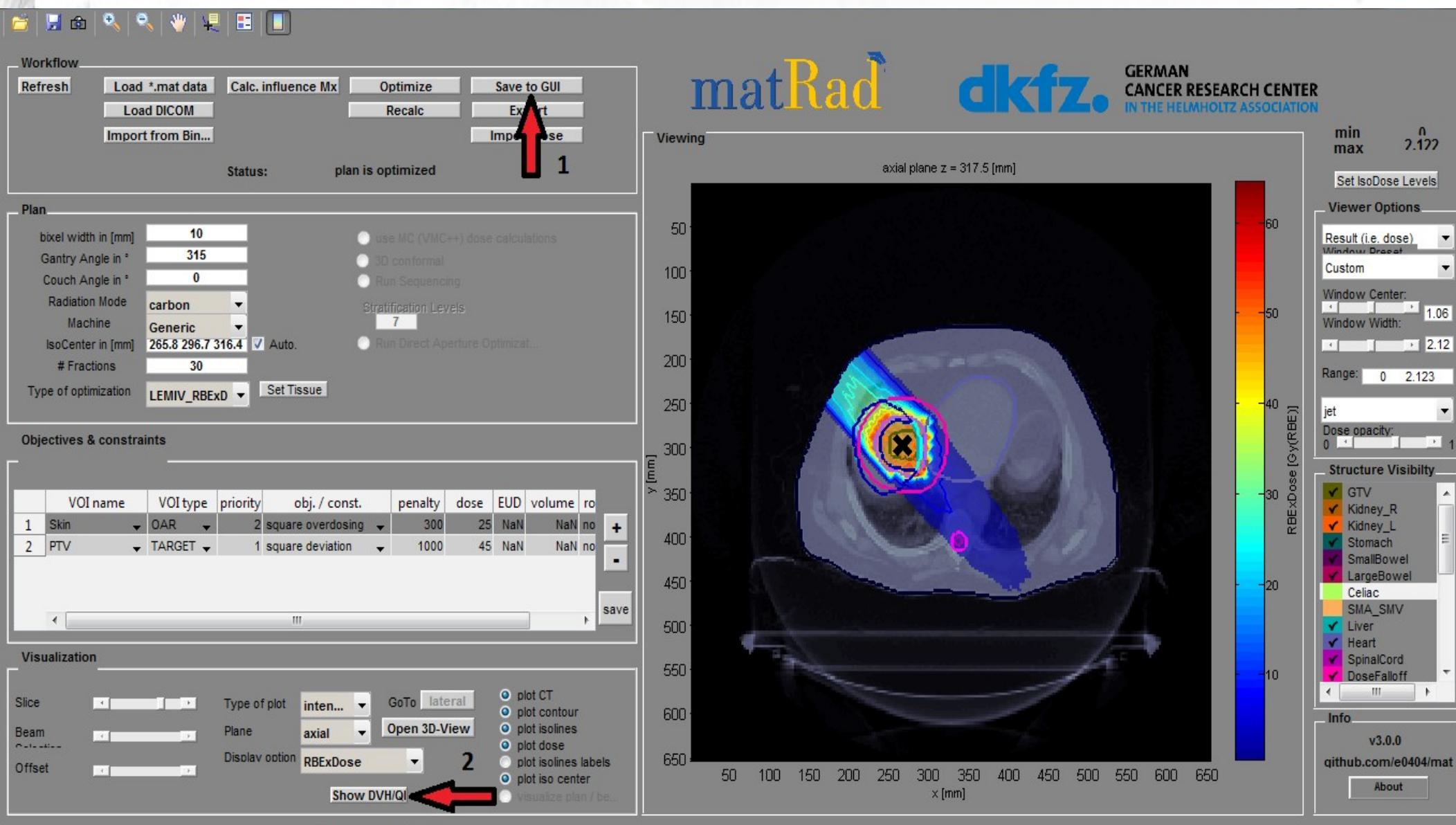


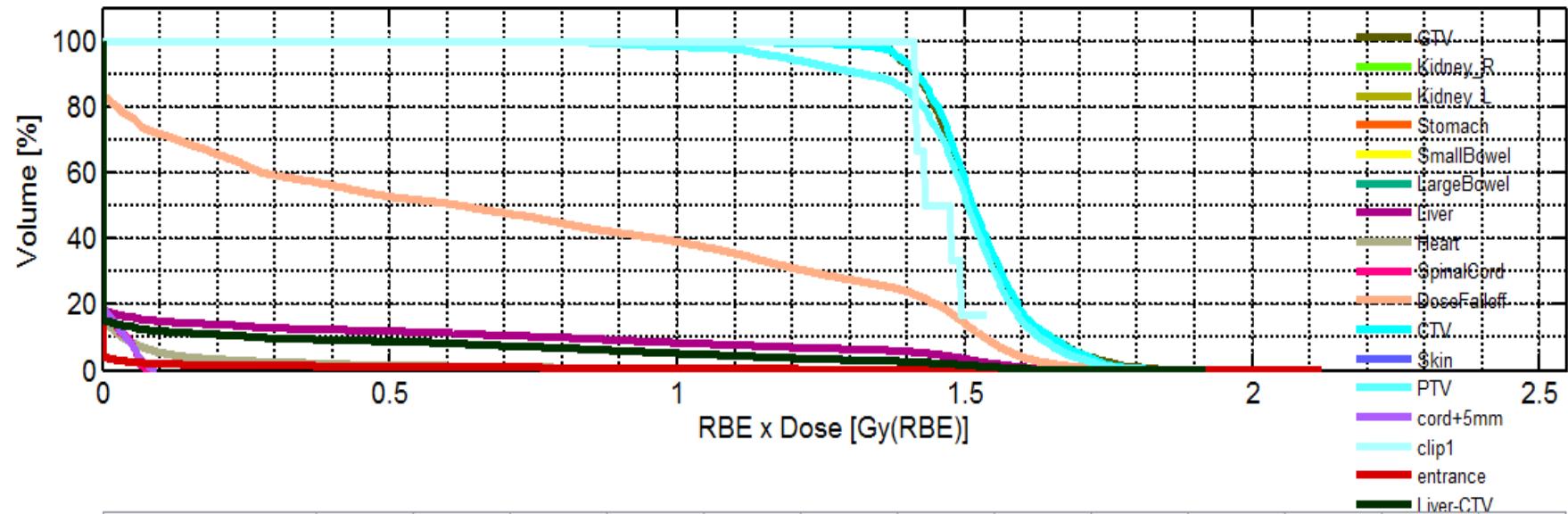
	mean	std	max	min	D_2	D_5	D_50	D_95	D_98	V_0Gy	V_0.5Gy	V_1Gy	V_1.5Gy
GTV	1.5053	0.1981	2.0110	1.0341	1.8973	1.8506	1.4947	1.1921	1.1231	1	1	1	0
Kidney_R	0	0	0	0	0	0	0	0	0	1	0	0	0
Kidney_L	0	0	0	0	0	0	0	0	0	1	0	0	0
Stomach	0	0	0	0	0	0	0	0	0	1	0	0	0
SmallBowel	0	0	0	0	0	0	0	0	0	1	0	0	0
LargeBowel	0	0	0	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?



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





	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	1
Kidney_R	0	0	0	0	0	0	0	0	0	0	1	0	0
Kidney_L	0	0	0	0	0	0	0	0	0	0	1	0	0
Stomach	0	0	0	0	0	0	0	0	0	0	1	0	0
SmallBowel	0	0	0	0	0	0	0	0	0	0	1	0	0
LargeBowel	0	0	0	0	0	0	0	0	0	0	1	0	0
Celiac	0	0	0	0	0	0	0	0	0	0	1	0	0
SMA_SMV	0	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.
Heart	0.0277	0.1314	1.8137	0	0.4139	0.1145	0	0	0	1	0.0212	0.0088	0.
SpinalCord	0.0077	0.0187	0.0855	0	0.0659	0.0582	0	0	0	1	0	0	0

Results

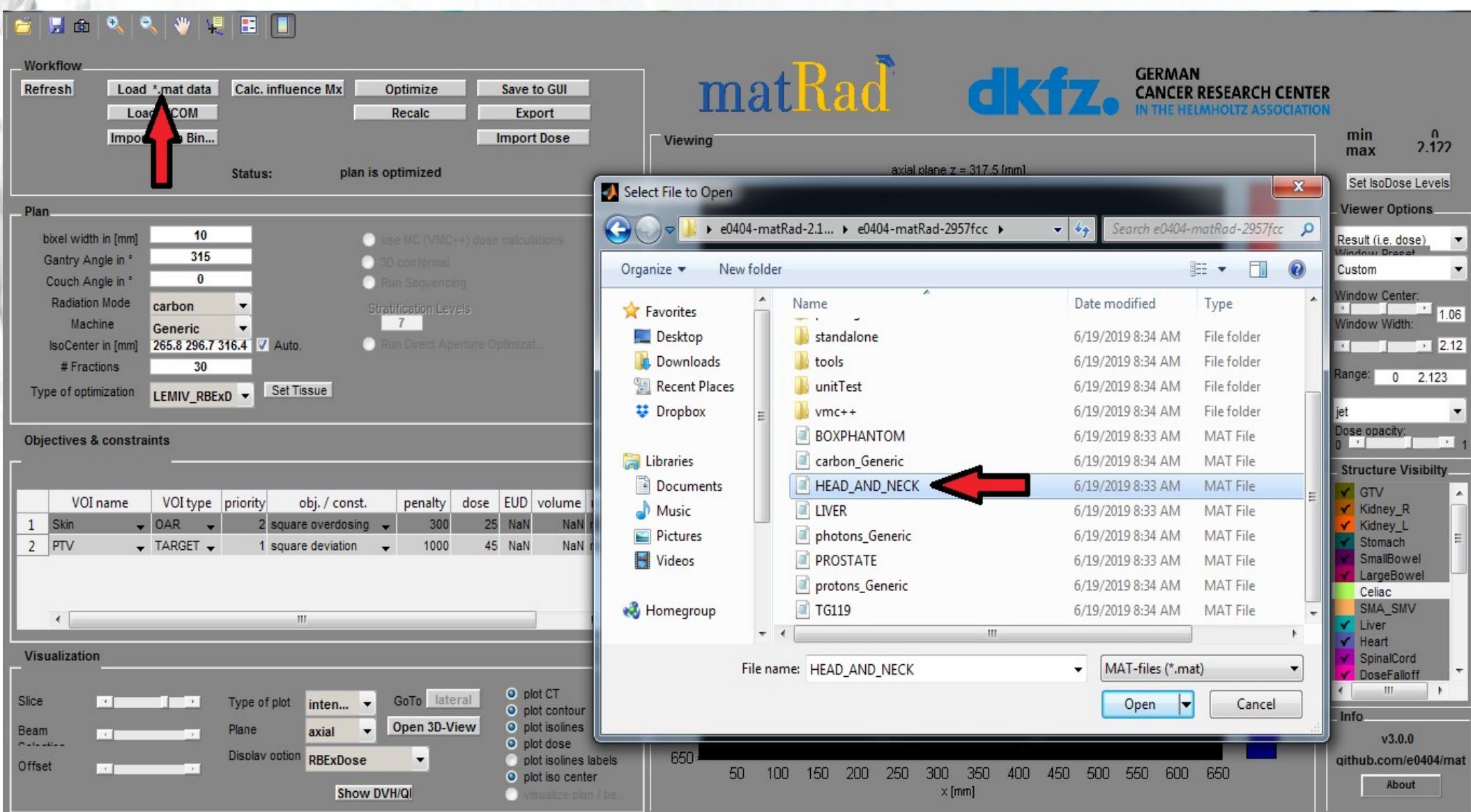
- Mean doses for different regions (Gy) using 5 photon beams, single proton beam and carbon ion beam:

Region/ Radiation(angles)	Photons(0,180,22 5,270,315)	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

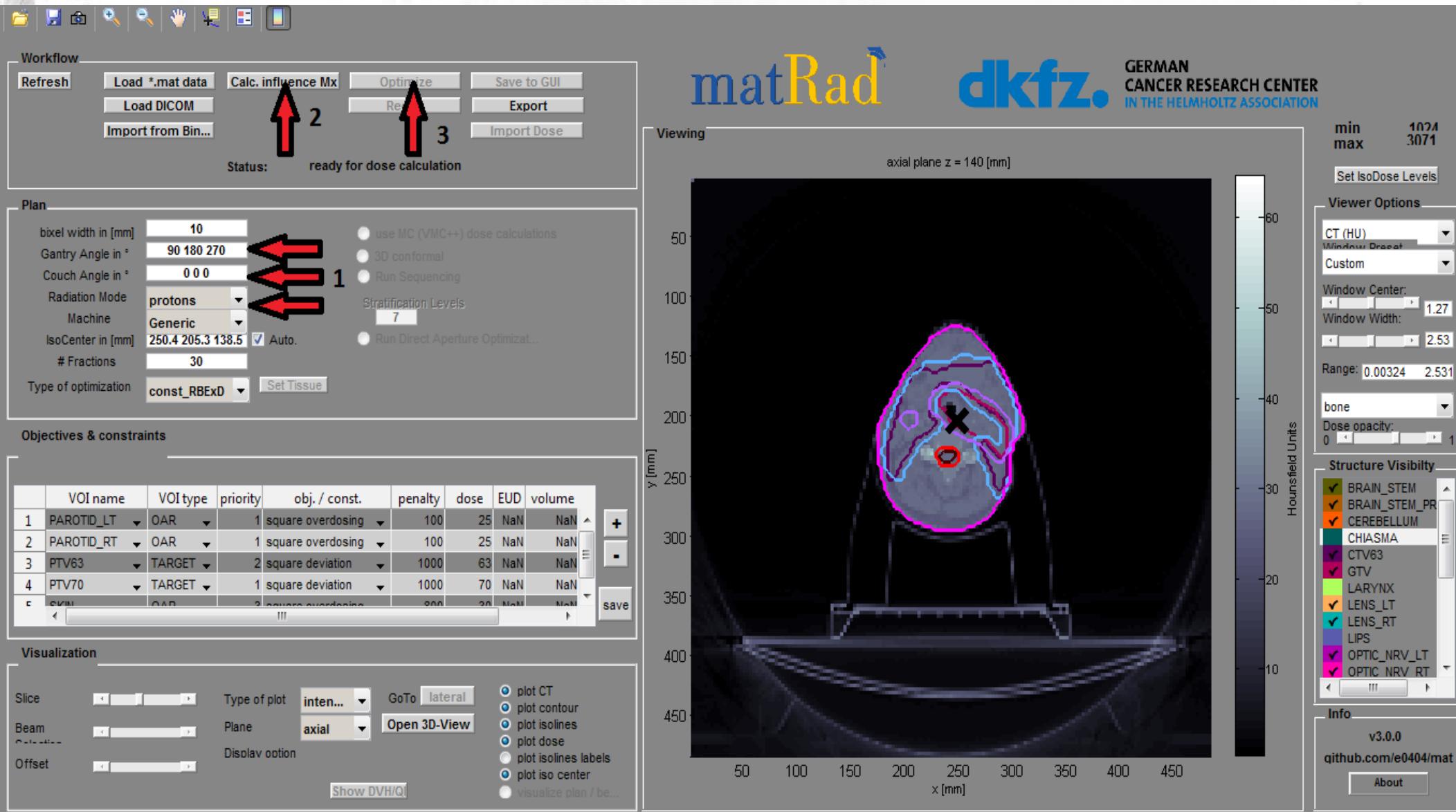
3rd Exercise

- Treatment planning uncertainties
- Proton radiotherapy plan for patients head
- Simulating a patient positioning error
- Analysing and comparing resulting dose distributions

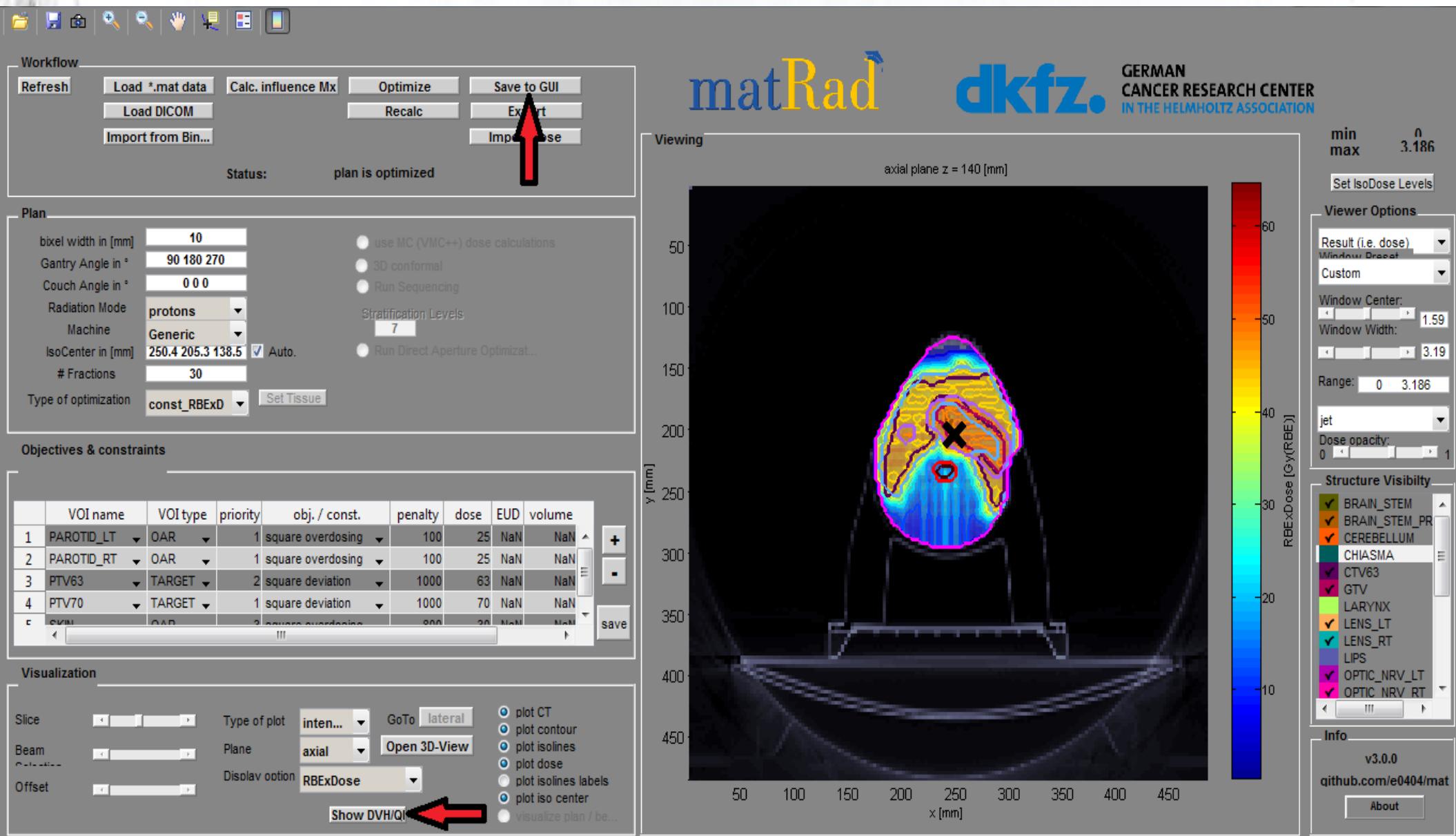
1. Load a head patient case (HEAD_AND_NECK or ALDERSON.mat)

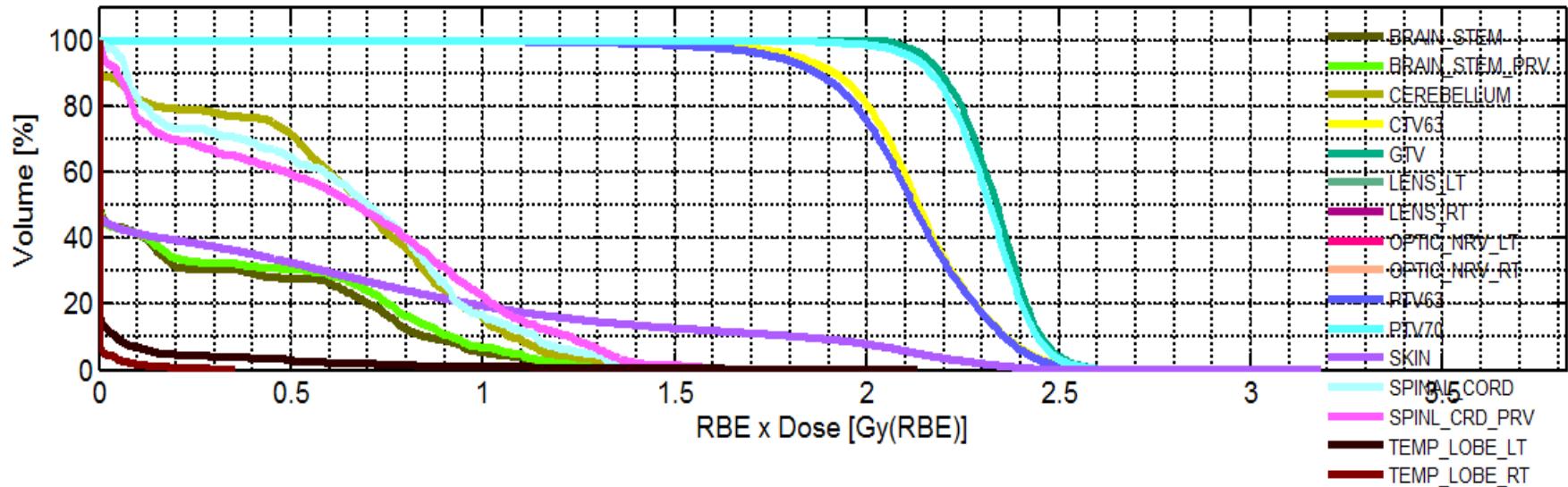


2. Add three proton beam angles on your own. Calculate and optimize the dose („Calc. Influence Mx“ & „Optimize“).



3. Analyze the result (dose& DVH) and save it („Save to GUI“).

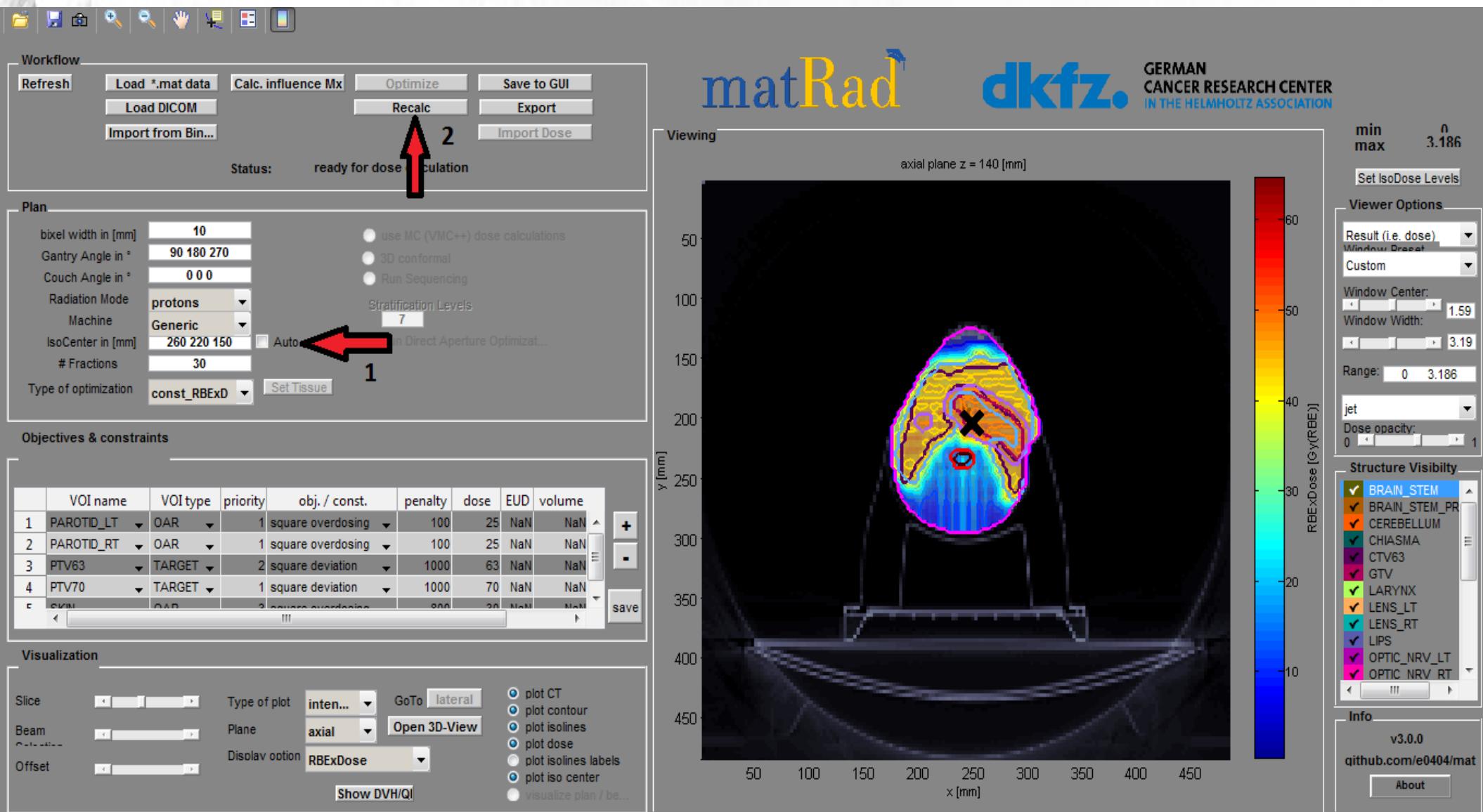




	mean	std	max	min	D_2	D_5	D_50	D_95	D_98	V_0Gy	V_0.6Gy	V_1.2Gy	V_1.9Gy
BRAIN_STEM	0.2645	0.3831	1.5408	0	1.1597	1.0153	0.0030	0	0	1	0.2649	0.0167	
BRAIN_STEM_PRV	0.2906	0.4099	1.5754	0	1.2980	1.0952	0.0016	0	0	1	0.2896	0.0251	
CEREBELLUM	0.6355	0.3774	2.0785	0	1.3512	1.1661	0.6933	0	0	1	0.5998	0.0469	7.3233
CHIASMA	0	0	0	0	0	0	0	0	0	1	0	0	
CTV63	2.1304	0.1945	3.1861	0.9407	2.4868	2.4230	2.1346	1.8175	1.6587	1	1	0.9973	0.0027
GTV	2.3305	0.1036	2.7047	1.9940	2.5353	2.4898	2.3381	2.1496	2.0935	1	1	1	
LARYNX	0.9230	0.4283	1.9861	0.2391	1.8607	1.7473	0.8058	0.3375	0.2819	1	0.7891	0.2585	0.0000
LENS_LT	0	0	0	0	0	0	0	0	0	1	0	0	
LENS_RT	0	0	0	0	0	0	0	0	0	1	0	0	
LIPS	0.0157	0.0412	0.2352	1.1603e-35	0.1705	0.1231	5.8836e-06	4.7064e-25	6.6316e-30	1	0	0	
OPTIC_NRV_LT	0	0	0	0	0	0	0	0	0	1	0	0	

4. Simulate a patient positioning error:

Remove the hook at the auto iso-center checkbox and define a new iso-center. Recalculate the dose by clicking on the „Recalc“.



Workflow

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

Status: plan is optimized

Plan

bixel width in [mm]	10	<input type="radio"/> use MC (VMC++) dose calculations
Gantry Angle in °	90 180 270	<input type="radio"/> 3D conformal
Couch Angle in °	0 0 0	<input type="radio"/> Run Sequencing
Radiation Mode	protons	Stratification Levels
Machine	Generic	<input type="radio"/> 7
IsoCenter in [mm]	260 220 150	<input type="radio"/> Run Direct Aperture Optimiz...
# Fractions	30	
Type of optimization	const_RBExD	<input type="checkbox"/> Auto.
<input type="button" value="Set Tissue"/>		

Objectives & constraints

VOI name	VOI type	priority	obj. / const.	penalty	dose	EUD	volume
1 PAROTID_LT	OAR	1	square overdosing	100	25	NaN	NaN
2 PAROTID_RT	OAR	1	square overdosing	100	25	NaN	NaN
3 PTV63	TARGET	2	square deviation	1000	63	NaN	NaN
4 PTV70	TARGET	1	square deviation	1000	70	NaN	NaN
5 SKIN	OAR	3	square overdosing	000	30	NaN	NaN

Visualization

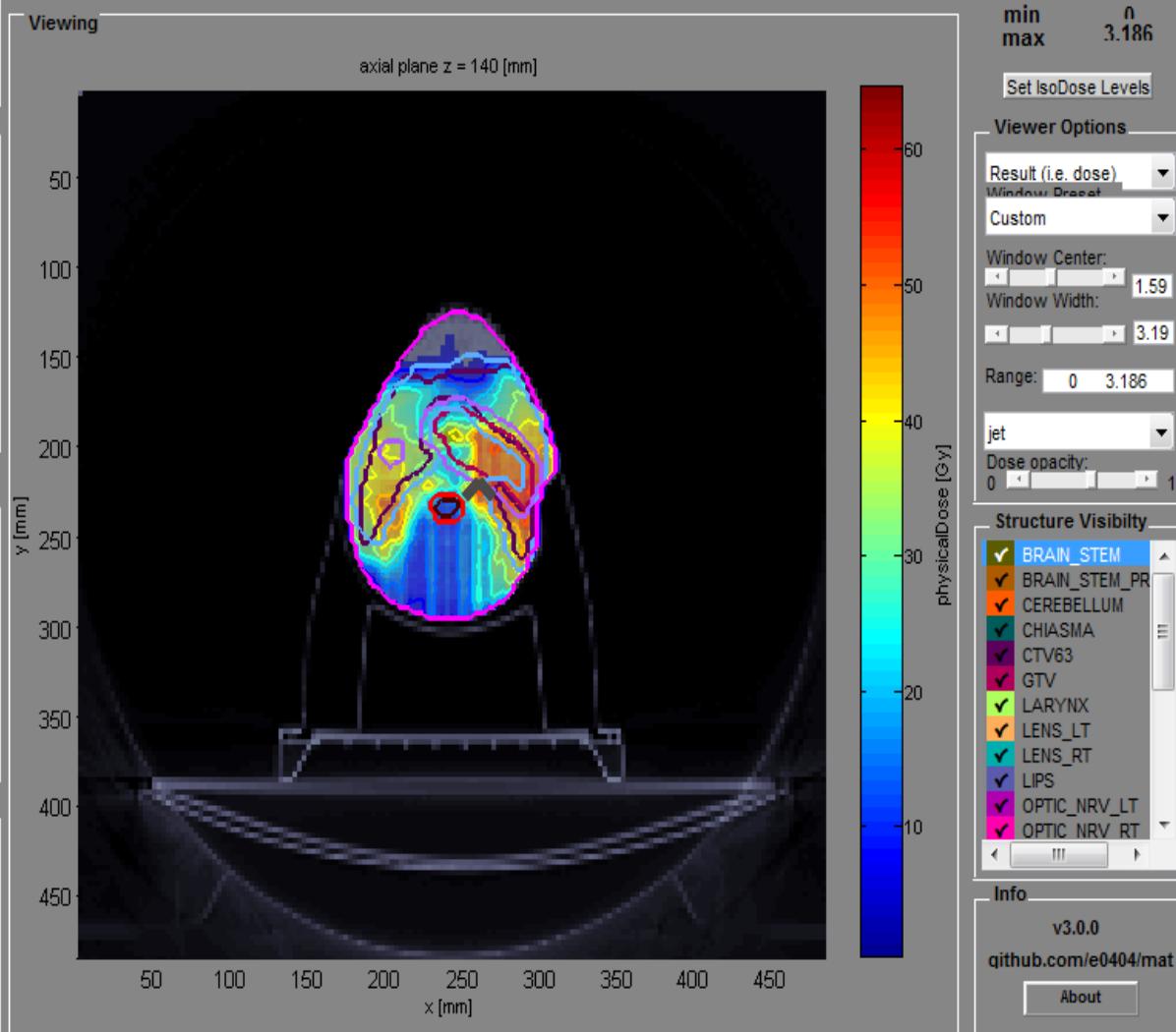
Slice Type of plot: inten... GoTo lateral
 Beam Plane: axial Open 3D-View
 Offset Display option: physicalDose

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

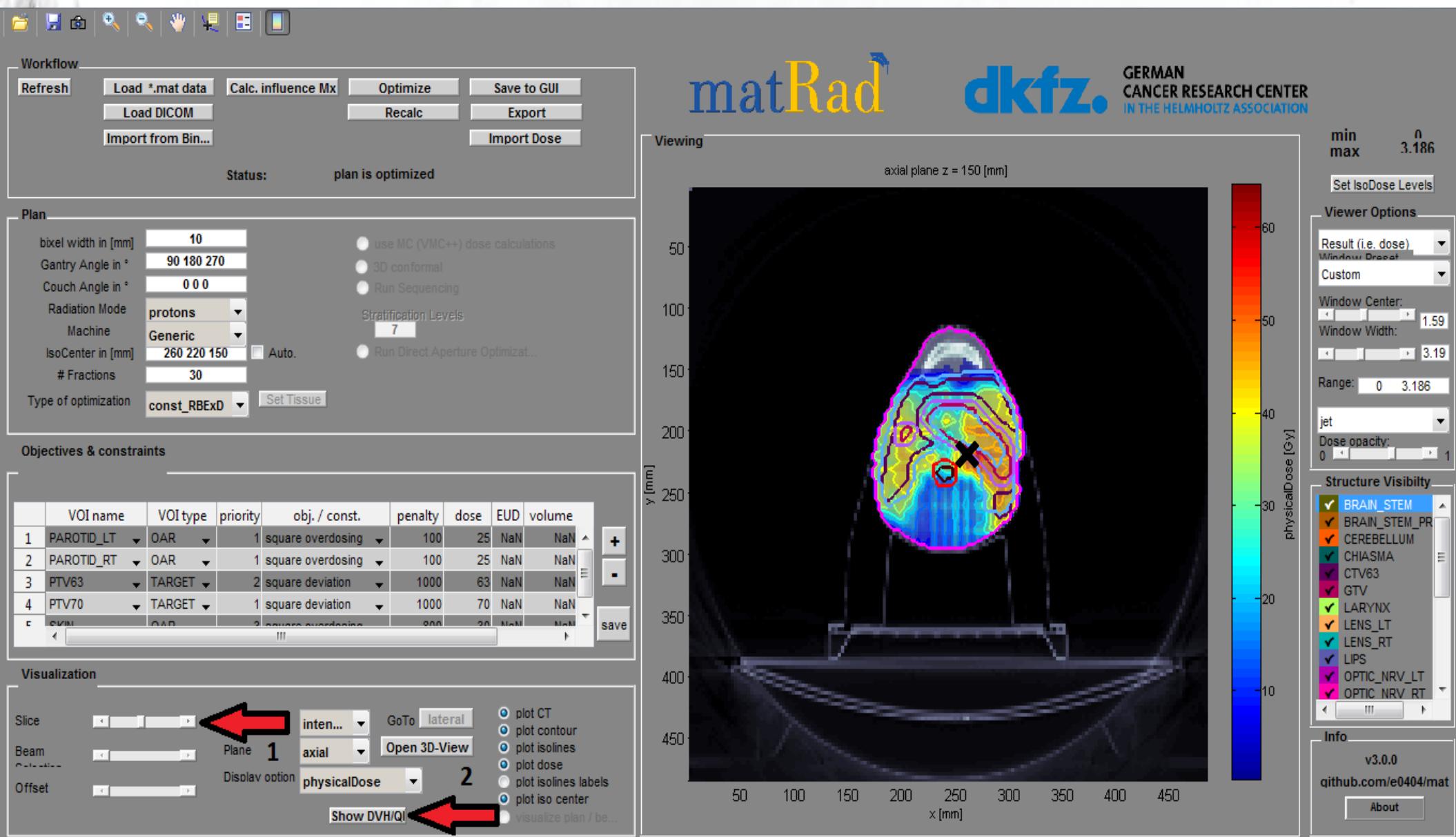
matRad

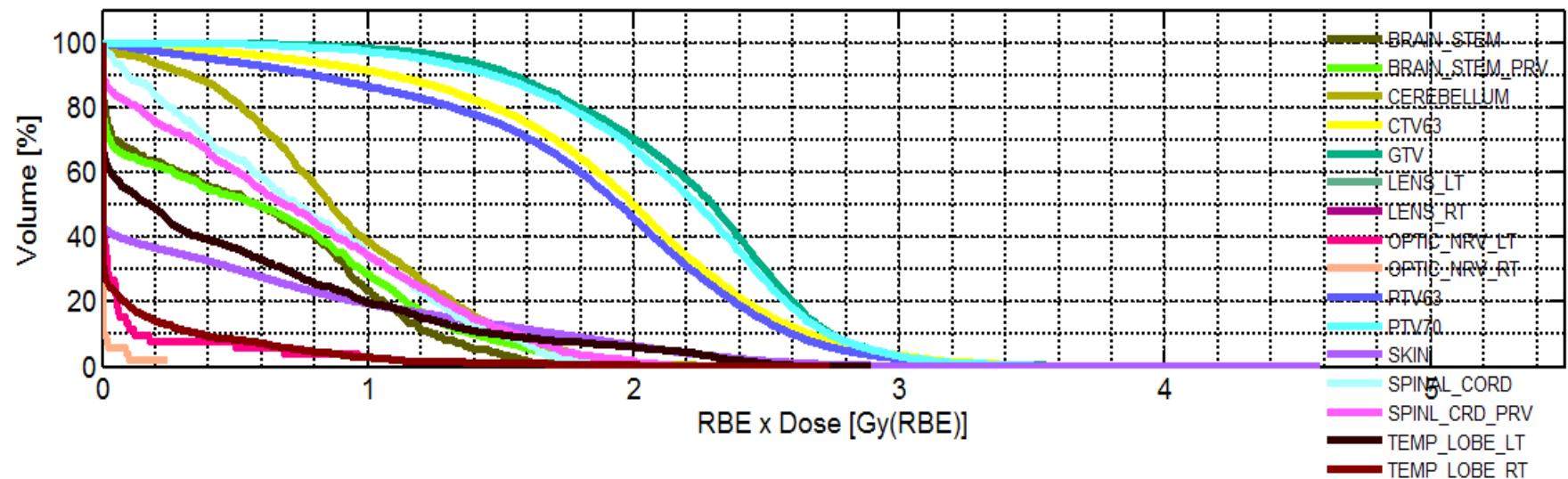


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5. Moving “Slice” option find iso-center and analyze and compare the resulting dose distribution.





	mean	std	max	min	D_2	D_5	D_50	D_95	D_98	V_0Gy	V_0.9Gy	V_1.8Gy	V_2.7Gy
BRAIN_STEM	0.5784	0.5092	1.8823	0	1.5814	1.4499	0.5847	0	0	1	0.3294	0.0048	
BRAIN_STEM_PRV	0.6153	0.5759	2.3528	0	1.8157	1.6326	0.5786	0	0	1	0.3519	0.0240	
CEREBELLUM	0.9112	0.4681	2.5823	0	1.9049	1.7408	0.8620	0.1636	0.0032	1	0.4588	0.0373	
CHIASMA	0.2487	0.2353	0.8091	0.0071	0.7505	0.6536	0.2672	0.0169	0.0118	1	0	0	
CTV63	1.9376	0.6348	4.0525	0.0093	3.1482	2.8966	1.9997	0.7051	0.3469	1	0.9282	0.6441	0.1000
GTV	2.2150	0.4918	3.9825	0.4100	3.1008	2.8992	2.2980	1.3330	1.0648	1	0.9886	0.7991	0.0000
LARYNX	0.5702	0.3493	1.7209	0.0422	1.5158	1.2552	0.4717	0.1262	0.1006	1	0.1769	0	
LENS_LT	0	0	0	0	0	0	0	0	0	1	0	0	
LENS_RT	0	0	0	0	0	0	0	0	0	1	0	0	
LIPS	0.0064	0.0261	0.2268	0	0.0963	0.0371	8.7893e-18	0	0	1	0	0	
OPTIC_NRV_LT	0.0775	0.2143	0.9674	0	0.9571	0.5805	7.5343e-04	0	0	1	0.0385	0	

Results

- Mean doses for different regions (Gy) using three proton beams, with and without patients movement:

Region/Iso-center	Without movement	With movement
Brain Stem	0.2645	0.5784
Cerebellum	0.6355	0.9112
CTV63	2.1304	1.9376
GTV	2.3305	2.2150
Lenses (L,D)	0,0	0,0
Skin	0.4682	0.4555
Optic Nerv (L,D)	0,0	0.0775, 0.0092
Spinal Cord	0.6268	0.7466
PTV63	2.1092	1.8369
PTV70	2.3102	2.1671

Thank you :)