PARTICLE THERAPY MASTERCLASS 2024

Session pratique avec le logiciel matRad

Instructions détaillés étape par étape

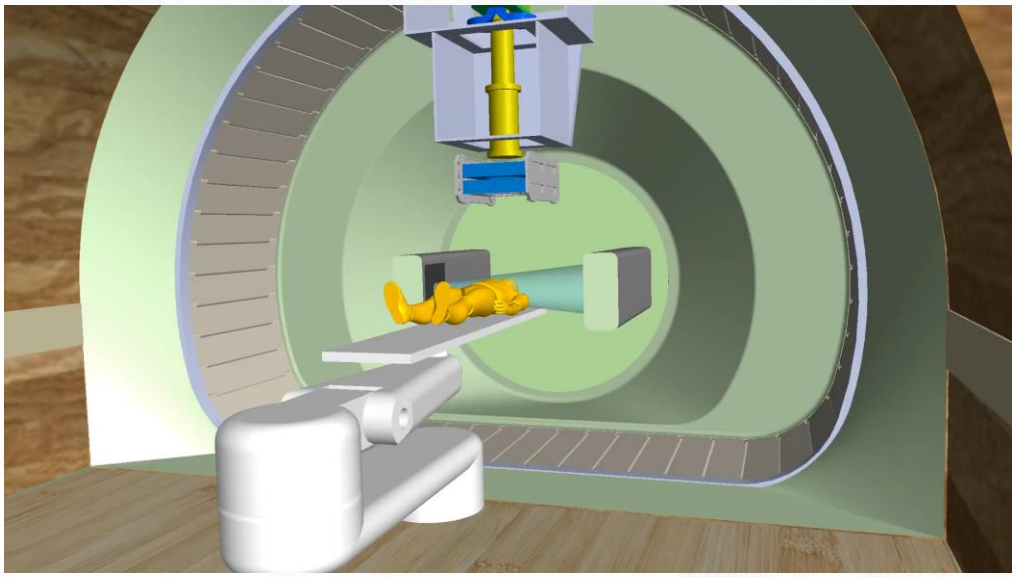
Luca Garolfi

Gantries

Développement d'un gantry Supra-conducteur rotatif pour les ions carbone :

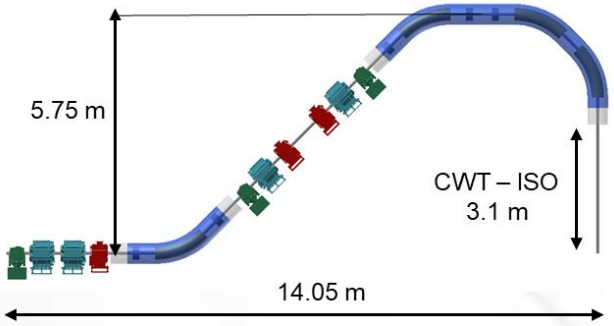
- CERN-INFN-CNAO-MedAustron: aimants, dose delivery, range verification, systeme de scanning
- HITRIplus projet EU (CNAO, RTU, SEEIIST, CERN: design de l'optique et de la mechanique

Salle de traitement



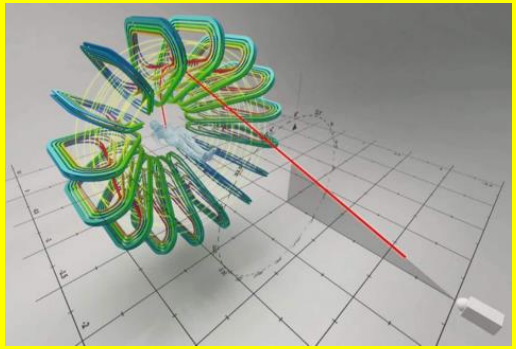
Courtesy L. Piacentini (CERN, RTU),
E. Felcini, M. Pullia (CNAO)

4 aimants, rotation a 45^0, 360^0



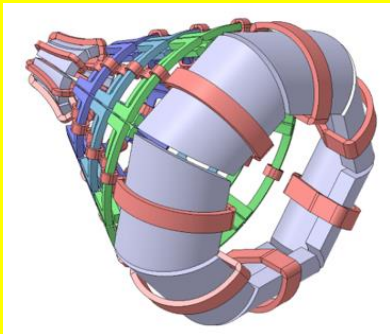
Développement d'un gantry toroidal (Gatoroid) au CERN.

- Etude des différentes versions pour proton and ion carbone.
- concentré sur une version non-supra pour électrons à tester avec des protons a faible énergie



Version VHEE du Gatoroid gantry, basée sur des aimants non-supra. Capabilité de la thérapie FLASH avec des traitements multidirectionnels. Design su CERN.

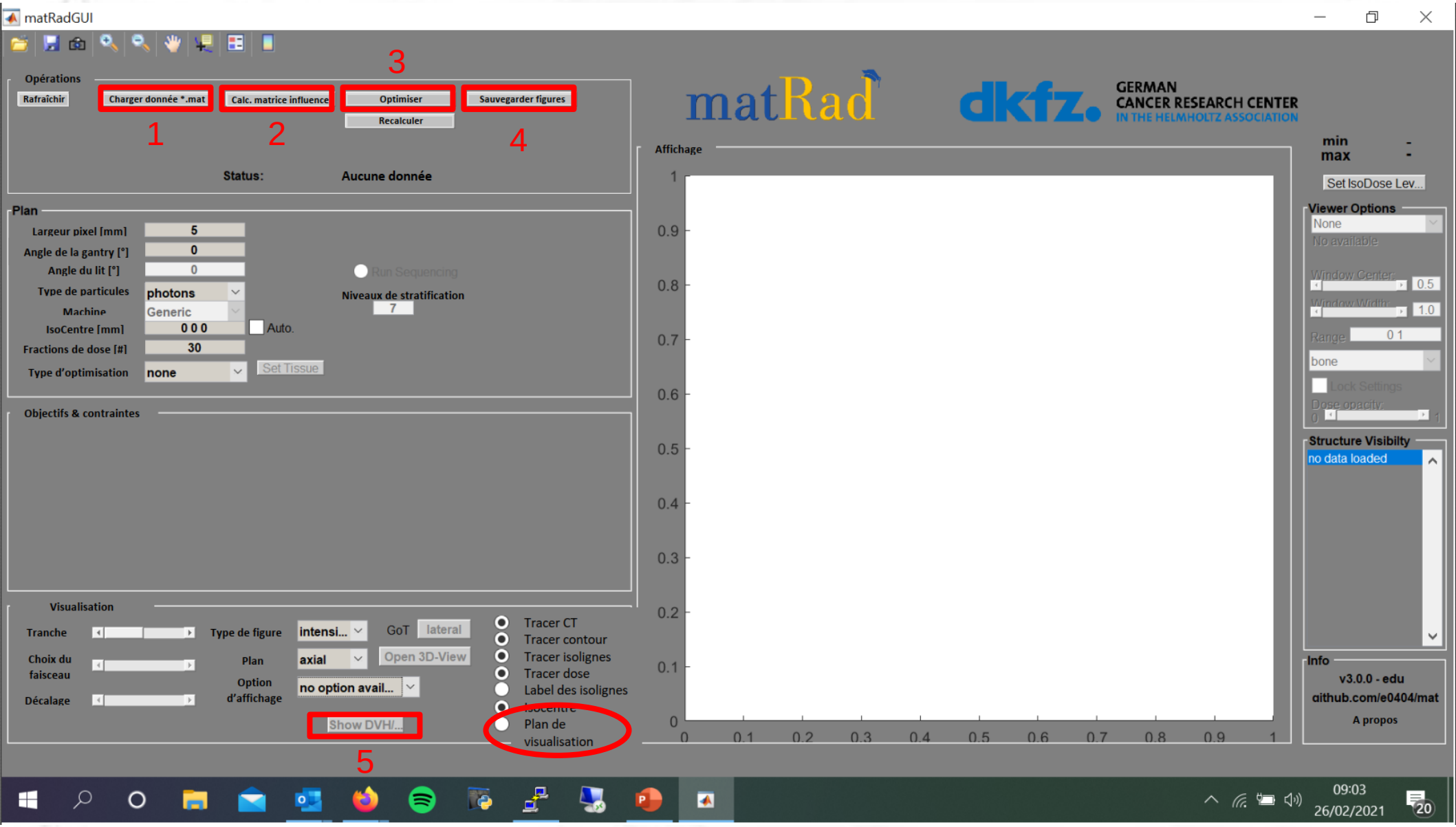
(image courtesy T. Lehtinen, L. Bottura)



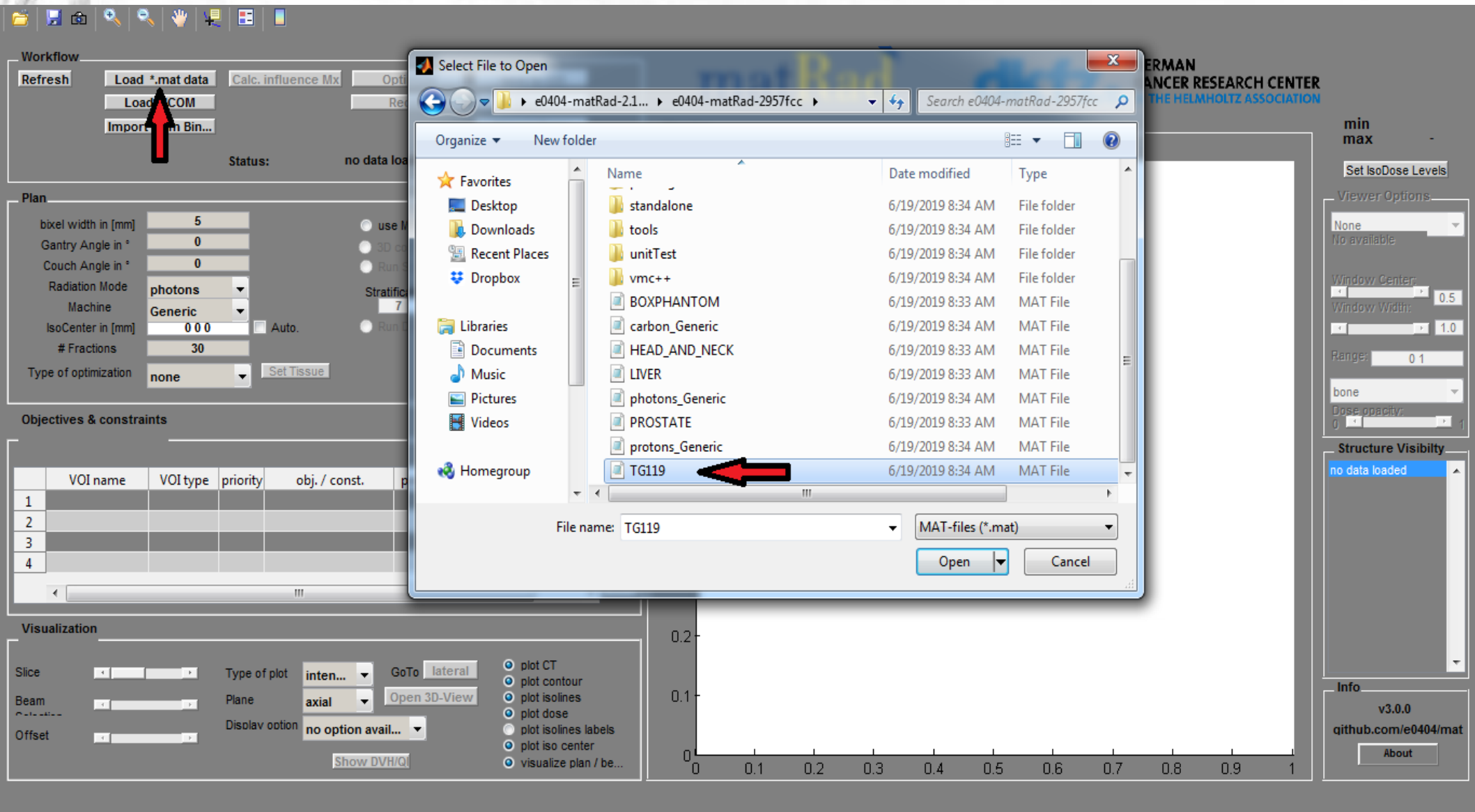
1er Exercise

- **Premiers pas sur le fantôme TG119**
- **Traitement par radiothérapie:**
  - **photons vs. protons vs. ions de carbone**
- **Analyser et comparer les résultats**

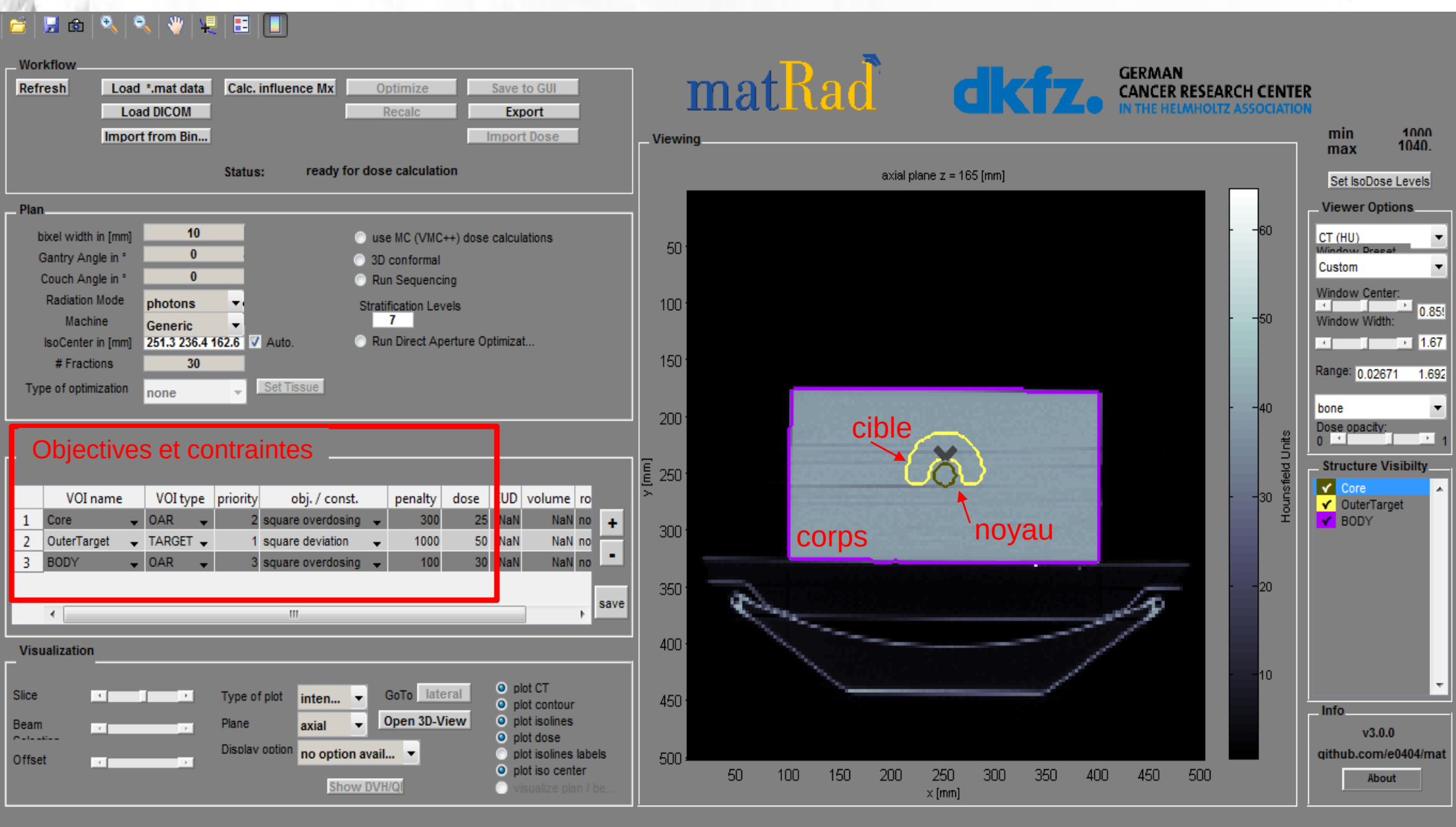
L'interface Graphique matRad



1. Charger le fantôme TG119 via le bouton Load *.mat data (TG119.mat)



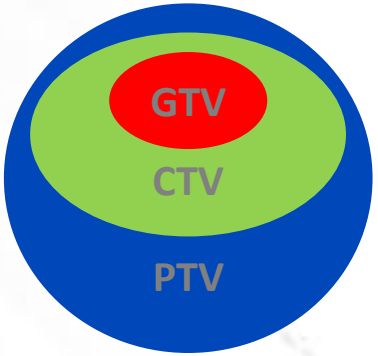
2. Analyse des contraintes et des objectives

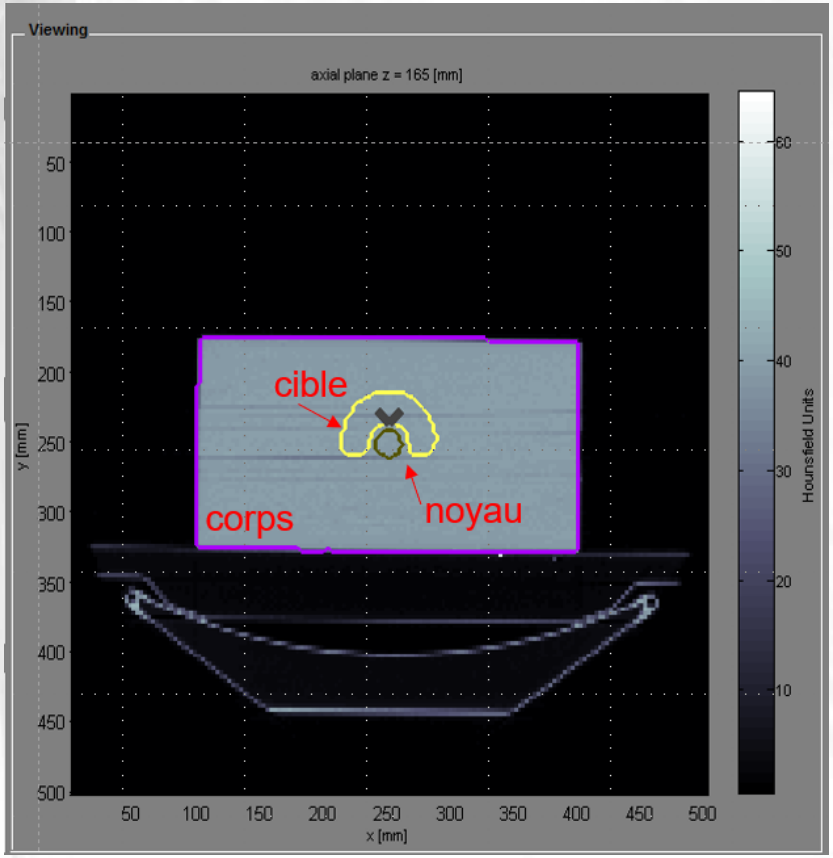


Concept à retenir

	VOI name	VOI type	priority	obj. / const.	penalty	dose
1	Core	OAR	2	square overdosing	300	25
2	OuterTarget	TARGET	1	square deviation	1000	50
3	BODY	OAR	3	square overdosing	100	30

- **VOI:** volume d'intérêt
- **OAR**: organ at risk = organe à risque
- **TARGET** = cible





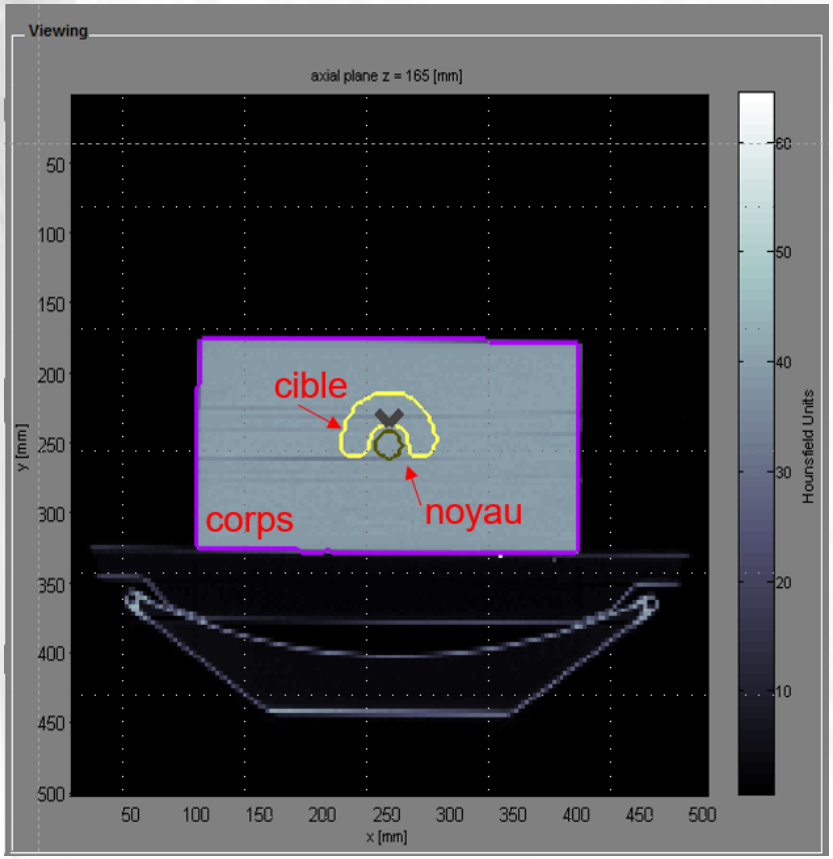
- **Gross Tumour Volume (GTV) =**
  Volume tumoral visible sur les images

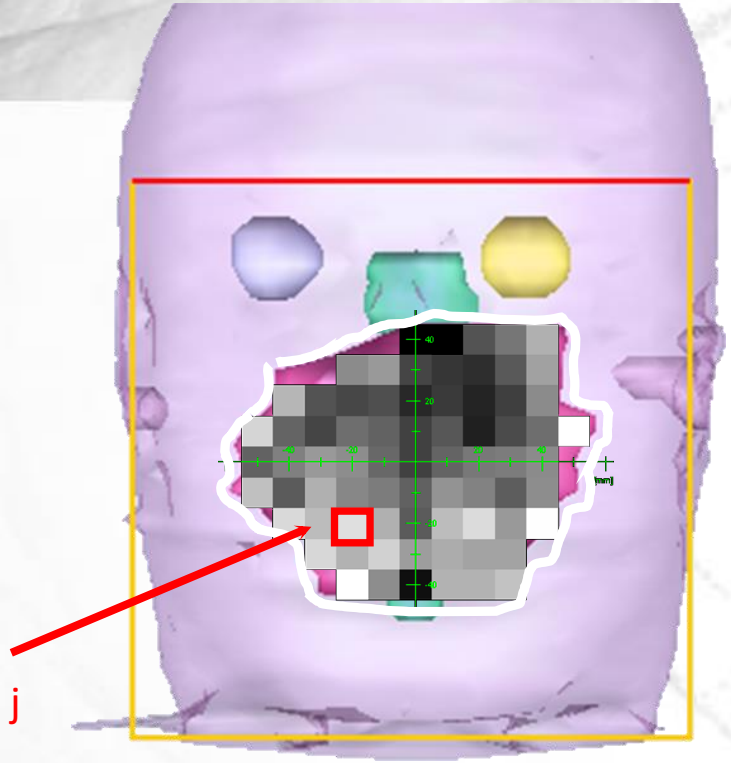
- **Clinical Target Volume (CTV) =**
  Le volume du tissu, y compris la GTV et les régions où le tissu tumoral invisible est attendu

- **Planning Target Volume (PTV) =**
  Comprend la GTV et la CTV ainsi qu'une marge de sécurité pour tenir compte des incertitudes.

Concept à retenir

	VOI name	VOI type	priority	obj. / const.	penalty	dose
1	Core	OAR	2	square overdosing	300	25
2	OuterTarget	TARGET	1	square deviation	1000	50
3	BODY	OAR	3	square overdosing	100	30



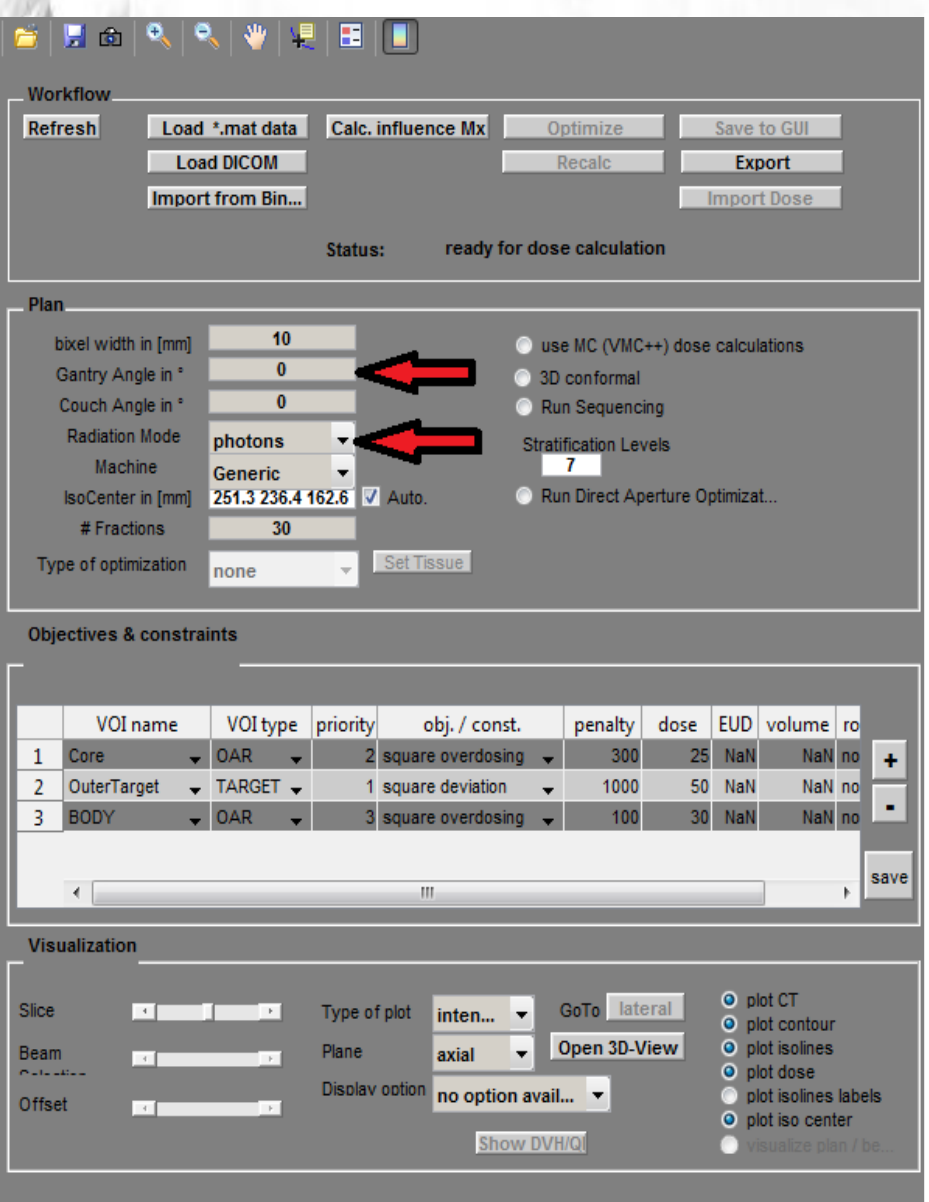


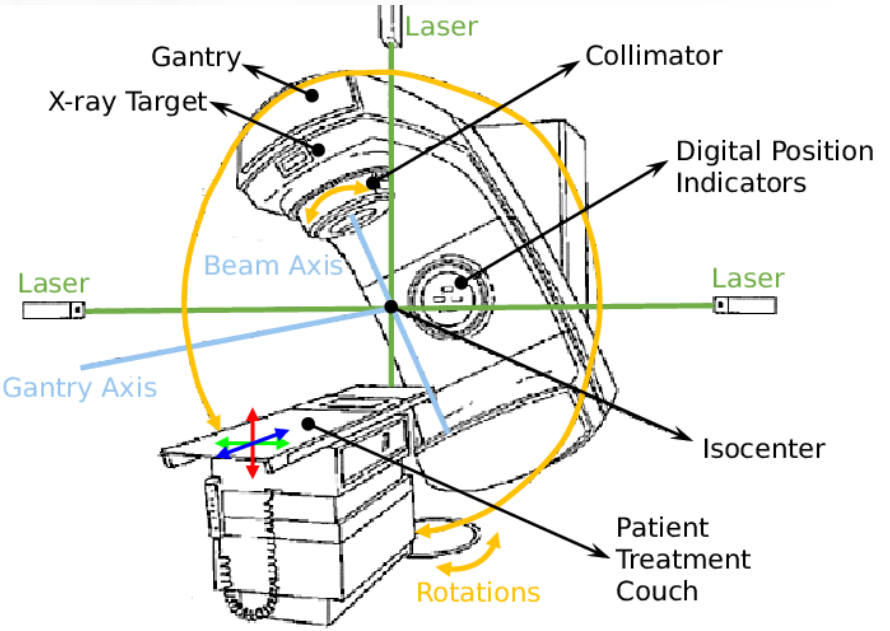
- **Dose absorbée** : énergie ionisante absorbée par unité de masse. Elle est mesurée en Gray (1 J/kg = 1 Gy)

- **Modulation d'intensité pour les photons avec pencil beams**
  "Pencil beams" forment un « pixel » dans la section transversale du faisceau (ou "fluence")
  = "bixel" (**B**eam + P**ixel**)
  Nous pondérons tous les pencil beams (plus/moins de photons) différemment

- **RBE : Efficacité biologique relative.** Facteur qui compare l'efficacité biologique (les dommages biologiques causés par) un type de rayonnement ionisant (p. ex., le rayonnement des particules) à l'efficacité biologique d'un rayonnement de référence (p. ex., le rayonnement de photons)

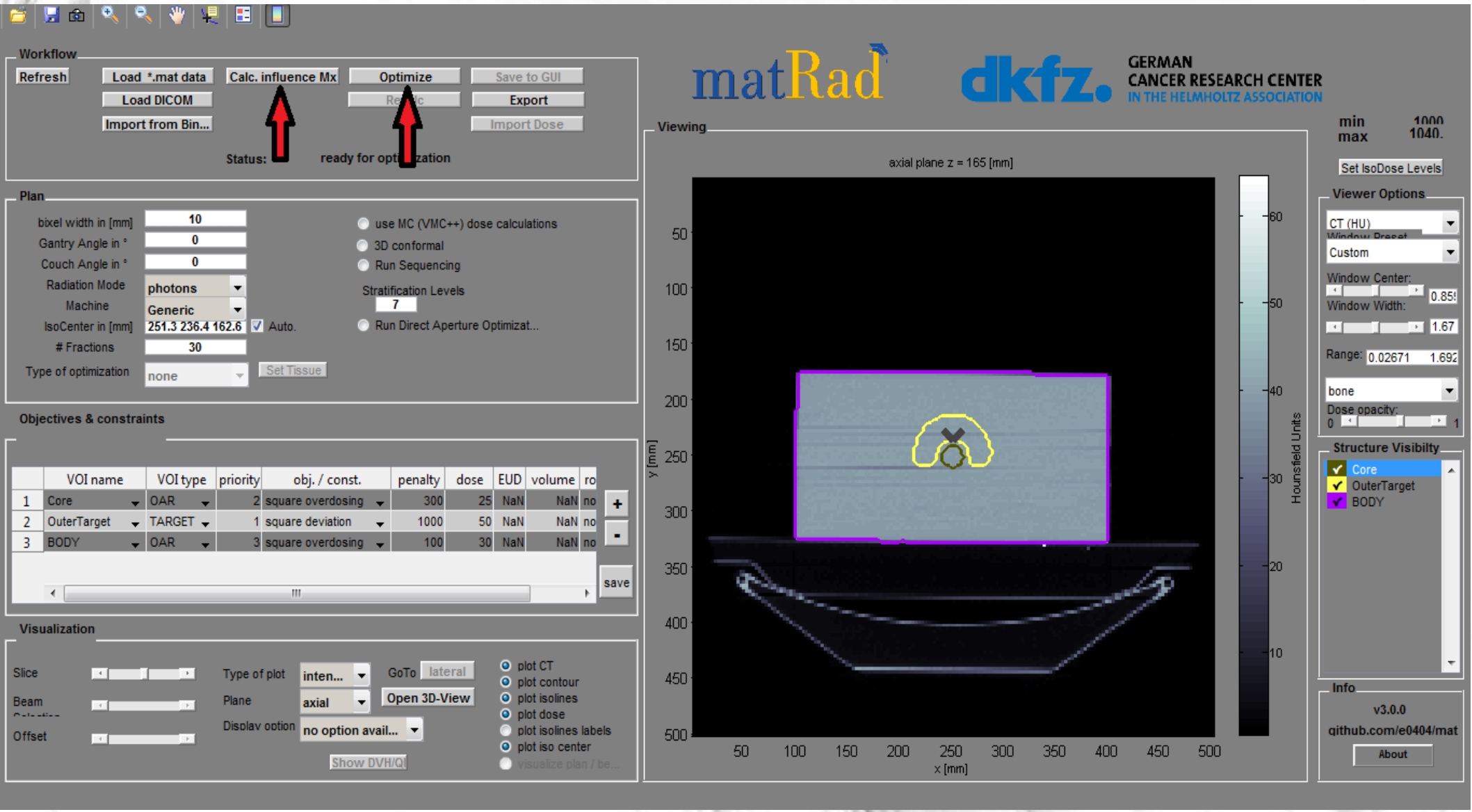
3. Régler la modalité de rayonnement sur Photons et définir un angle de faisceau (angle du gantry)



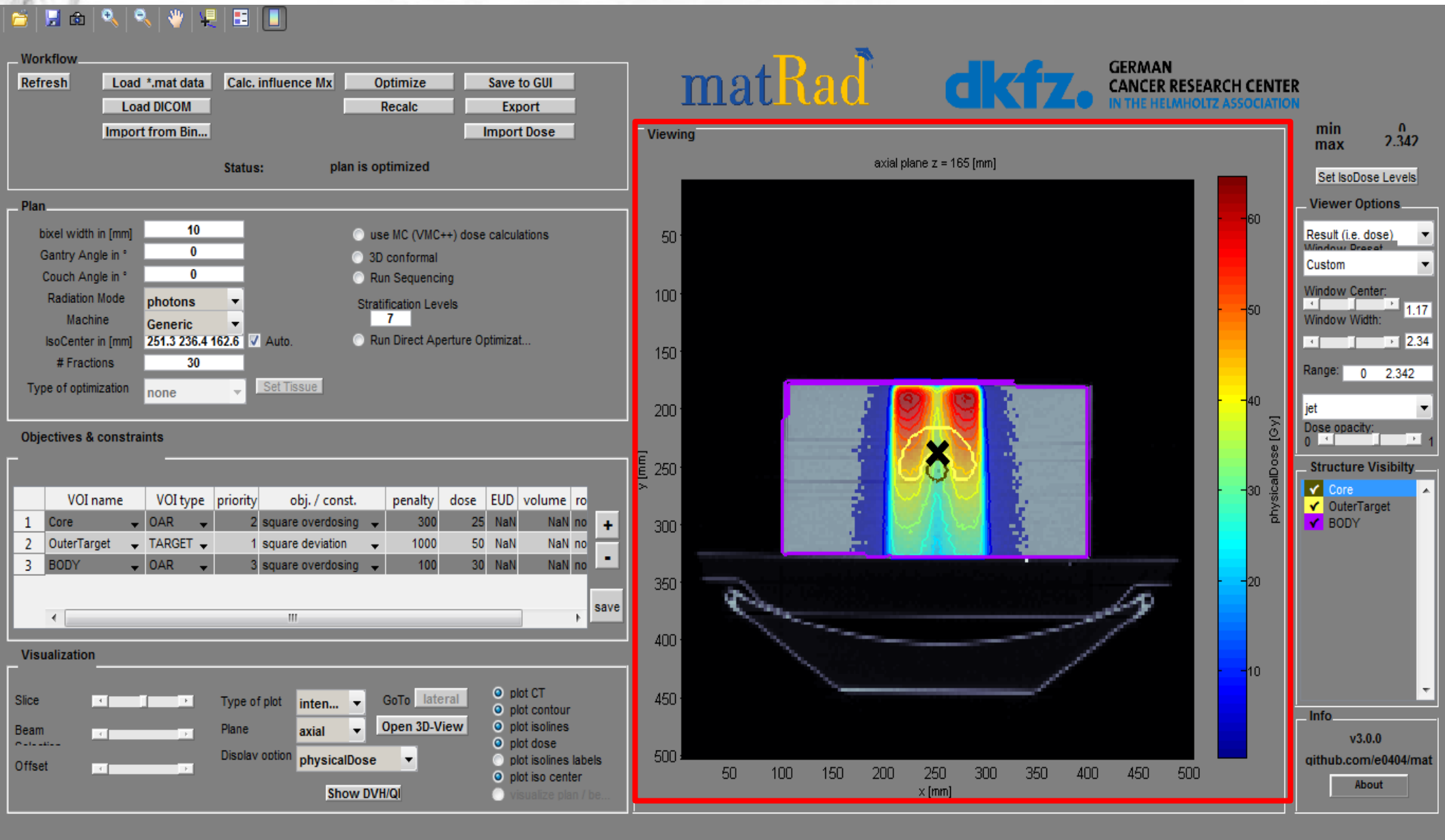


- **Photons** : sans masse, sans charge électrique et voyage toujours à la vitesse de la lumière
  - pas d'accélération, mais d'énergie dépendante de la fréquence
  - Comment générer? Nous pouvons accélérer les électrons!
  - les électrons accélérés touchent une cible
  - les électrons perdent de l'énergie en raison de « bremsstrahlung »
  - photons de haute énergie
- **gantry :** déplace la source de rayonnement autour du patient
- **lit :** fait pivoter le patient

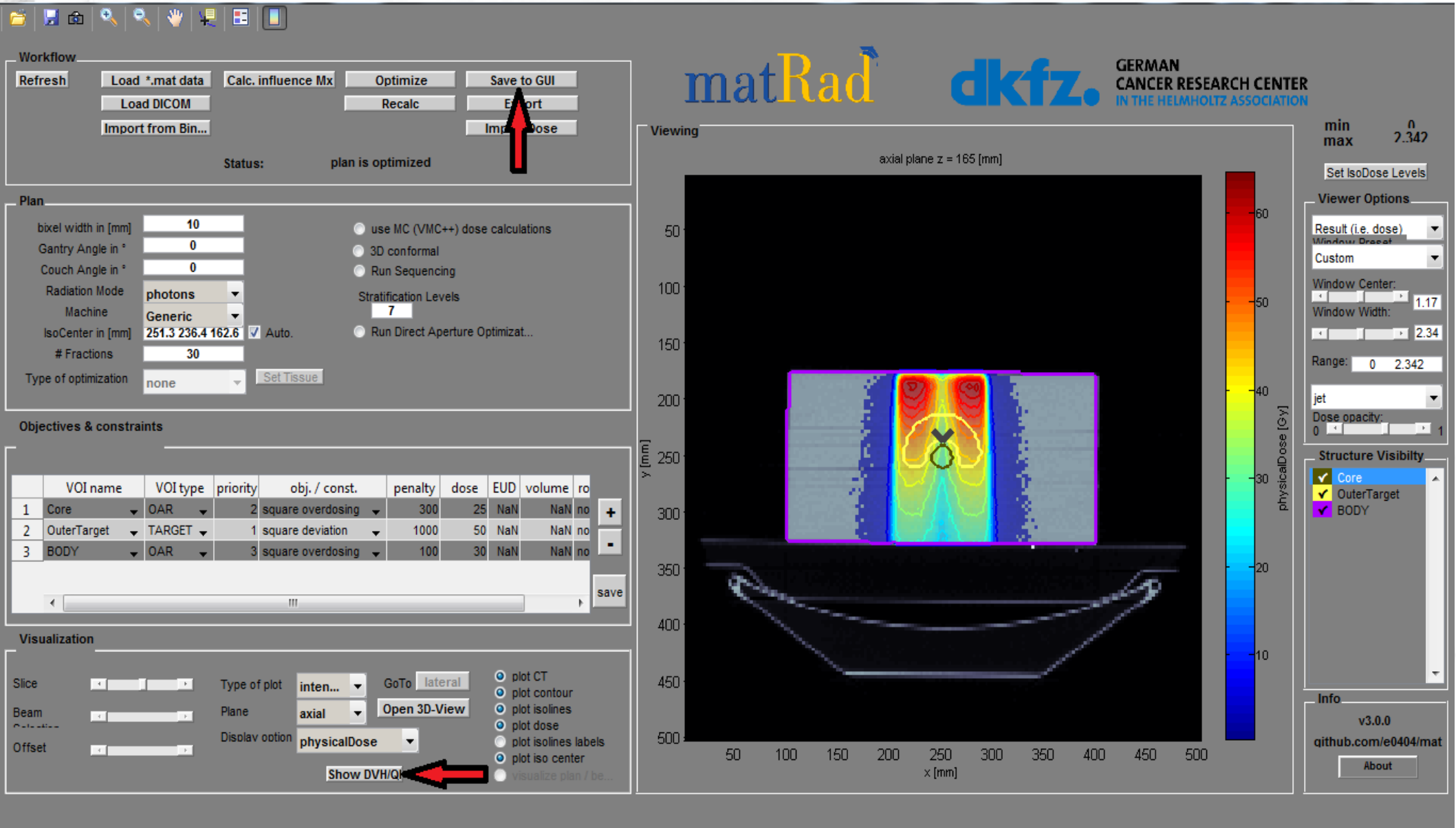
4. Déclencher le calcul de la dose via le bouton (« Calc. Influence Mx ») et lancer l'optimisation inverse en cliquant sur (« Optimize »)



5. Analyser la distribution de dose résultante

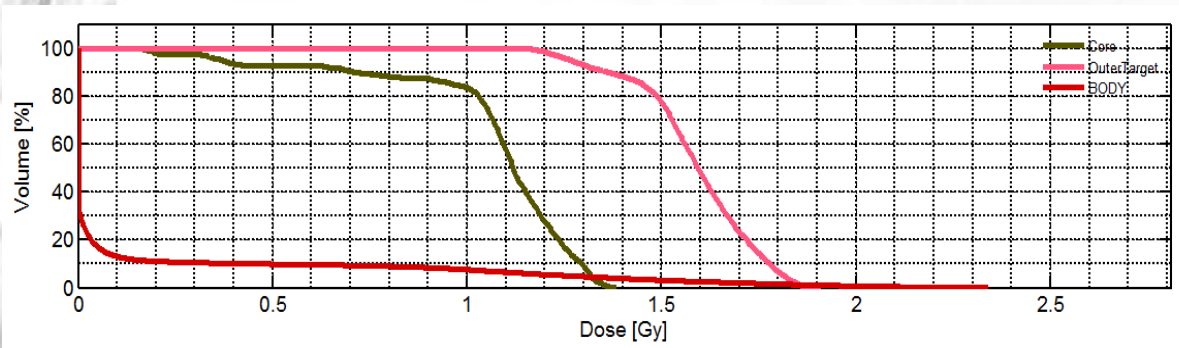


6. Enregistrer le résultat de l'optimisation via (« Save to GUI »)
Ensuite, afficher le DVH par (« Show DVH/QI »)

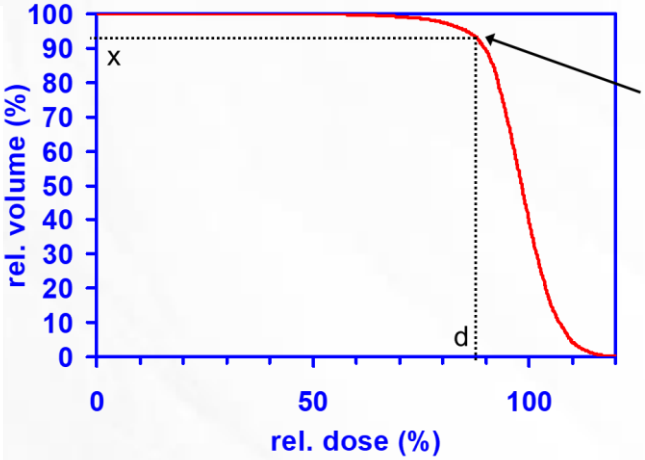


Concept à retenir

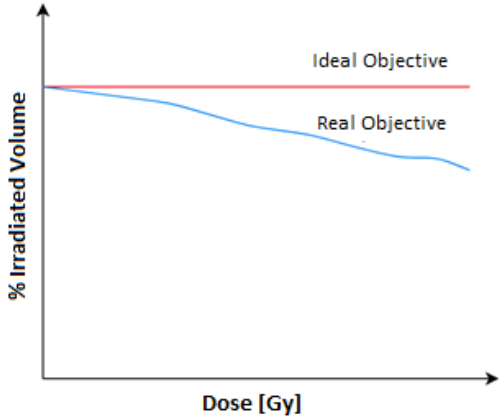
- **Show DVH/QI**: Histogram dose-volume

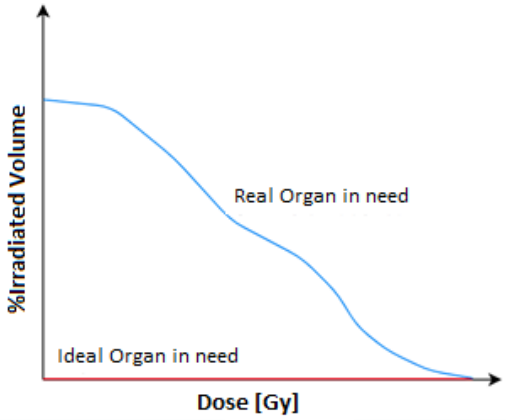


	mean	std	max	min	D_2	D_5	D_50	D_95	D_98	V_0Gy	V_0.4Gy	V_0.9Gy	V_1.4Gy	V_
Core	1.0665	0.2554	1.3860	0.1329	1.3434	1.3187	1.1183	0.3706	0.1988	1	0.9341	0.8727	0	
OuterTarget	1.5852	0.1536	1.9115	1.0935	1.8453	1.8153	1.5941	1.2663	1.2077	1	1	1	0.8824	
BODY	0.1443	0.4168	2.3420	0	1.7203	1.2694	0	0	0	1	0.1019	0.0846	0.0393	



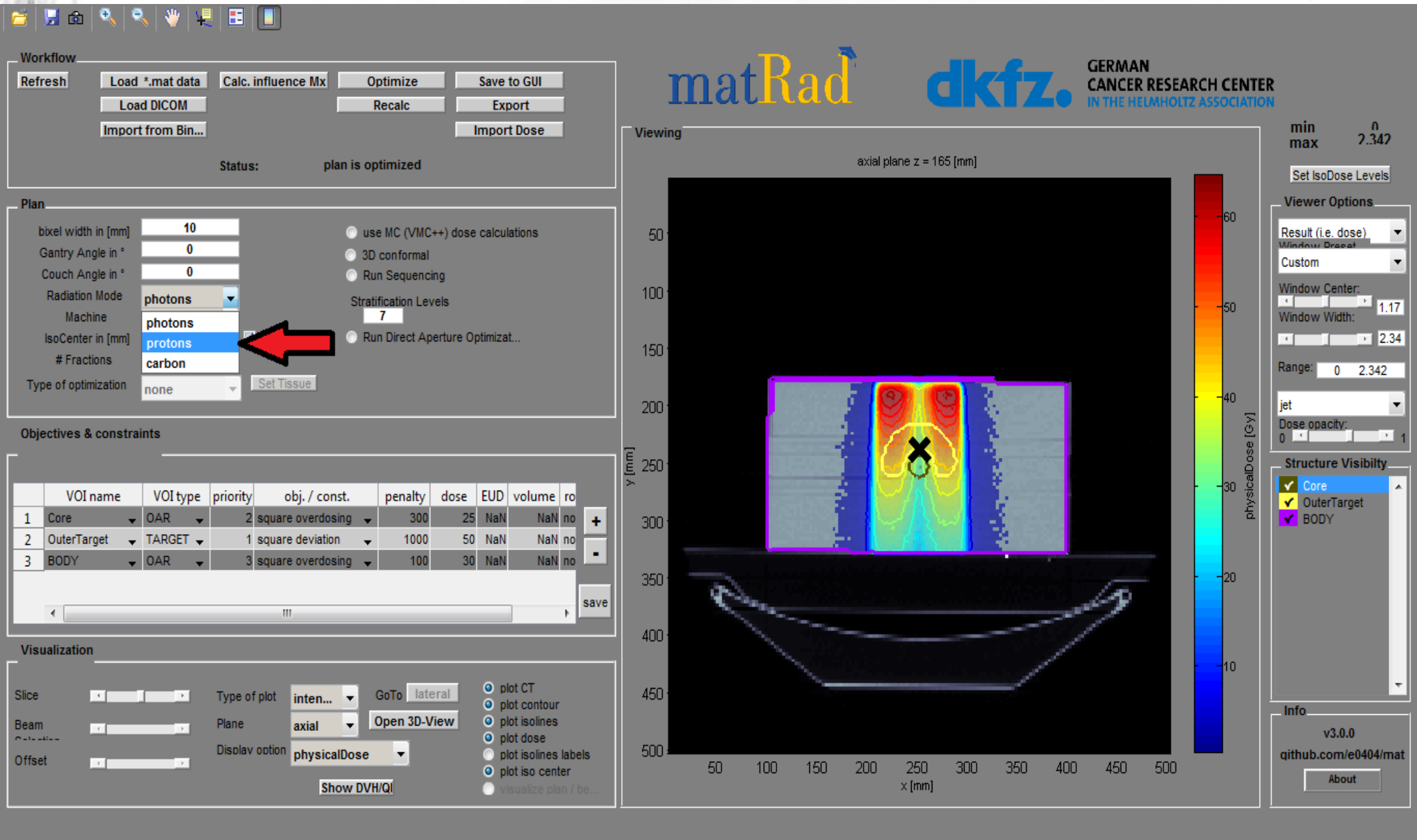
x% du volume atteint au moins d% de la dose prescrite



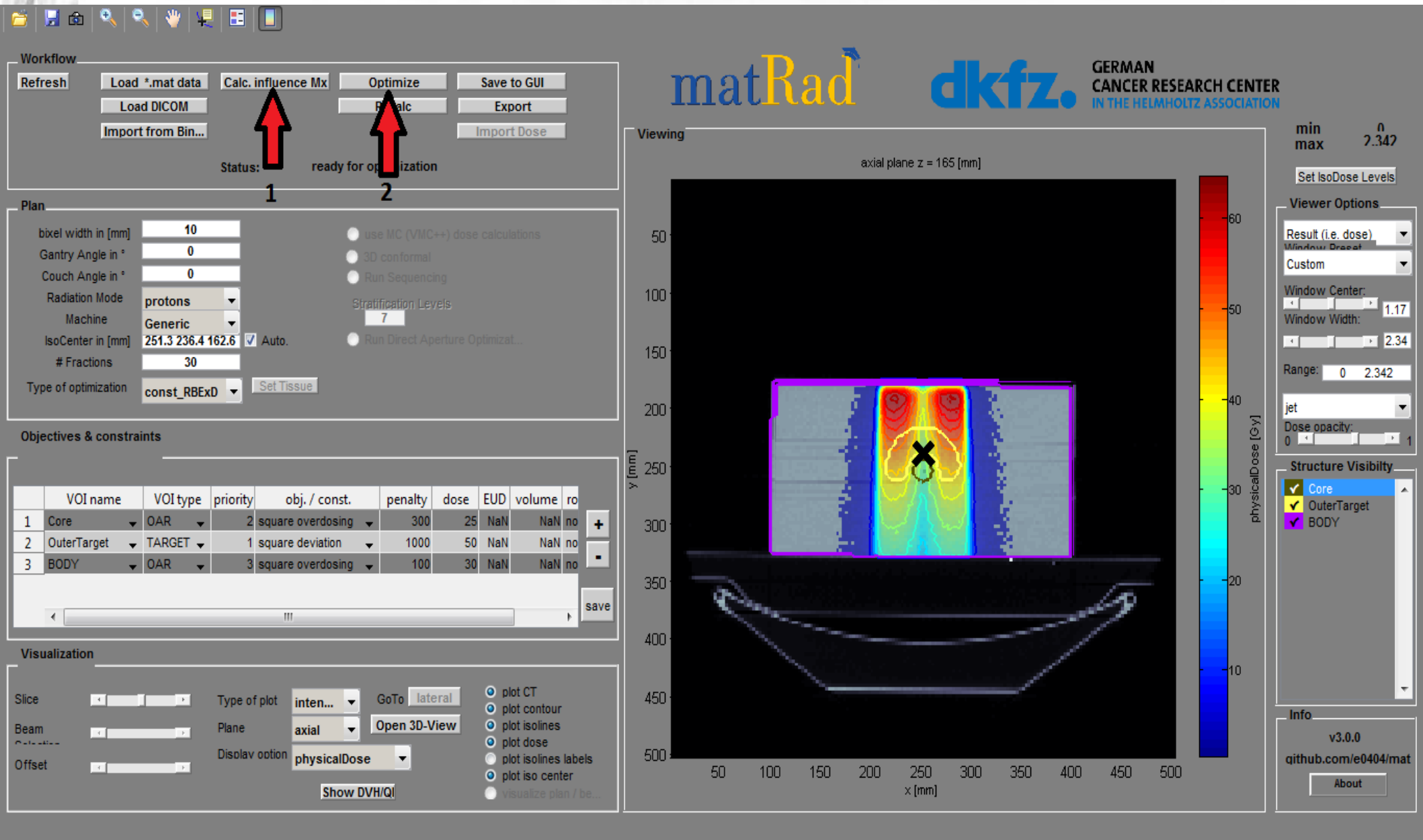


Dans le cas idéal, seule la tumeur est irradiée sans affecter les autres tissus (sains).

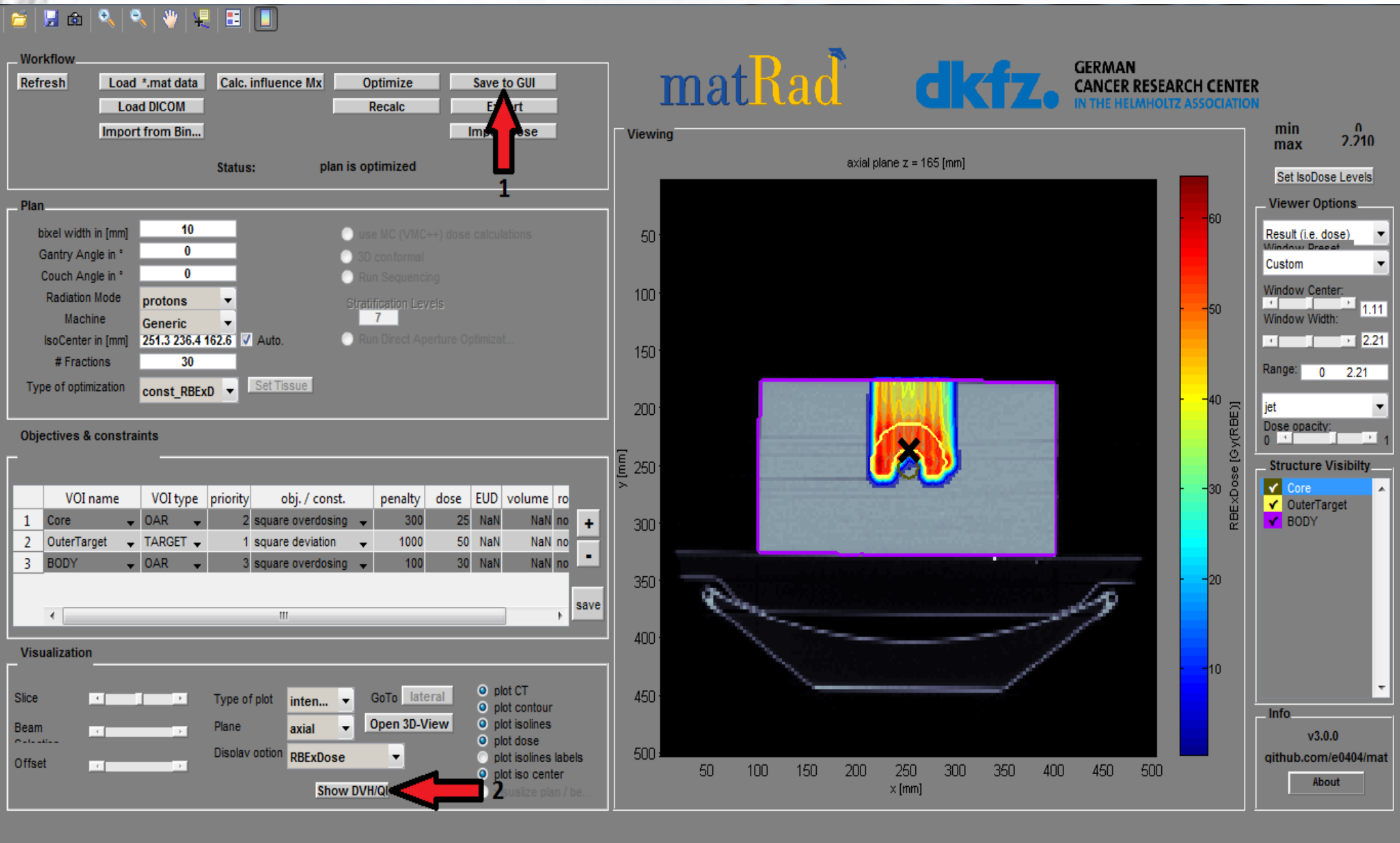
7. Remplacer la modalité de rayonnement par : Protons laisser les angles du faisceau inchangés.



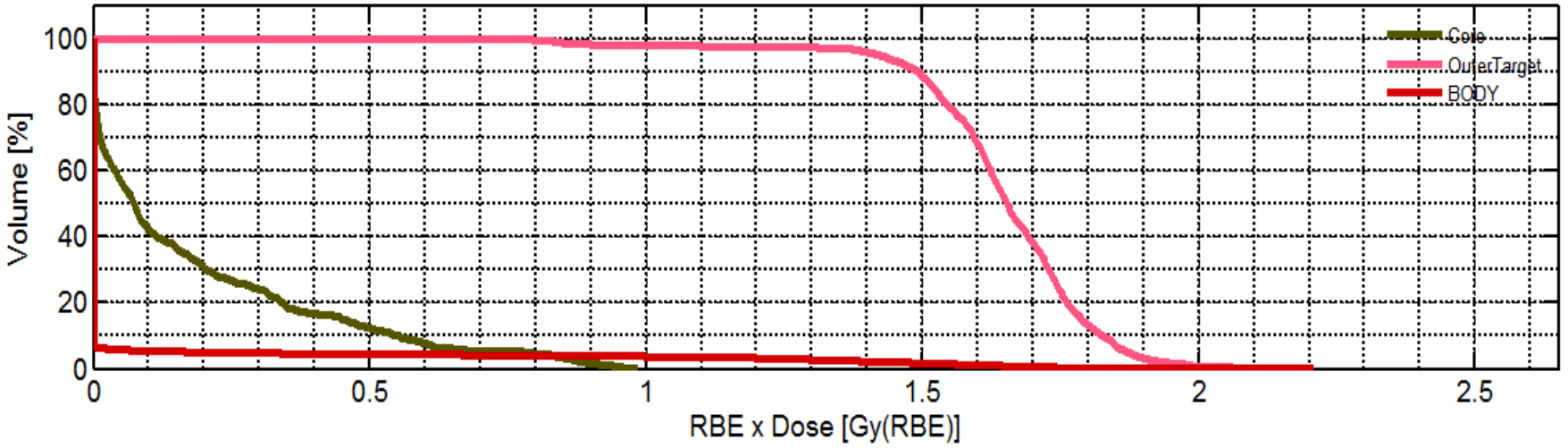
8. Déclencher le calcul de la dose via le bouton (« Calc. Influence Mx ») et lancer l'optimisation inverse en cliquant sur (« Optimize »)



9. Enregistrer le résultat de l'optimisation via (« Save to GUI »)
Ensuite, afficher le DVH par (« Show DVH/QI »)



Show DVH/QI



	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_
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	
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	
BODY	0.0640	0.2912	2.2101	0	1.4572	0.2364	0	0	0	1	0.0462	0.0405	0.0282	

Comparaison des résultats

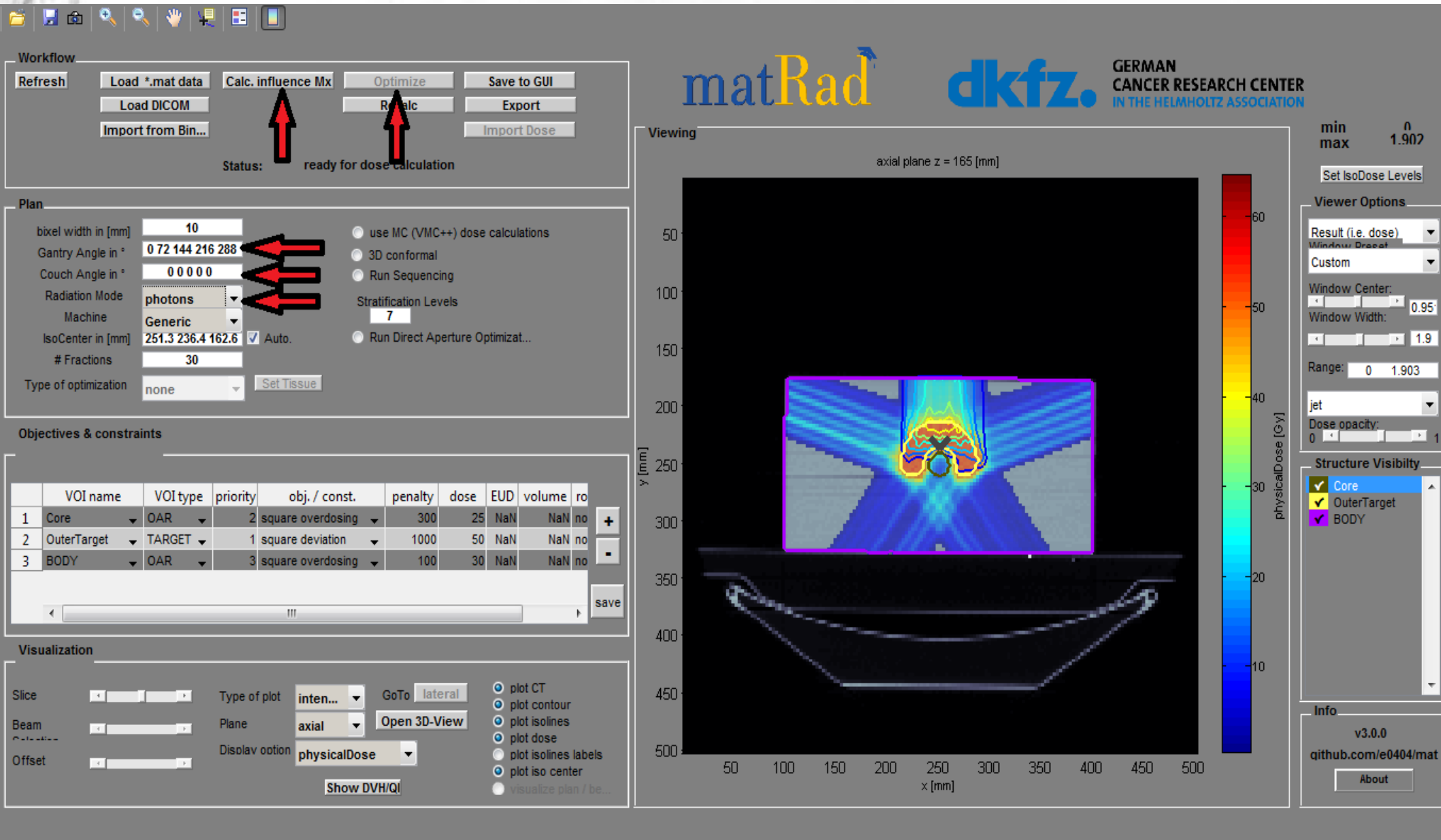
- doses moyennes pour différent régions (Gy):

Region/Radiation	Photons	Protons
Base	1.0665	0.1815
Cible	1.5852	1.6449
Corps	0.1443	0.0640

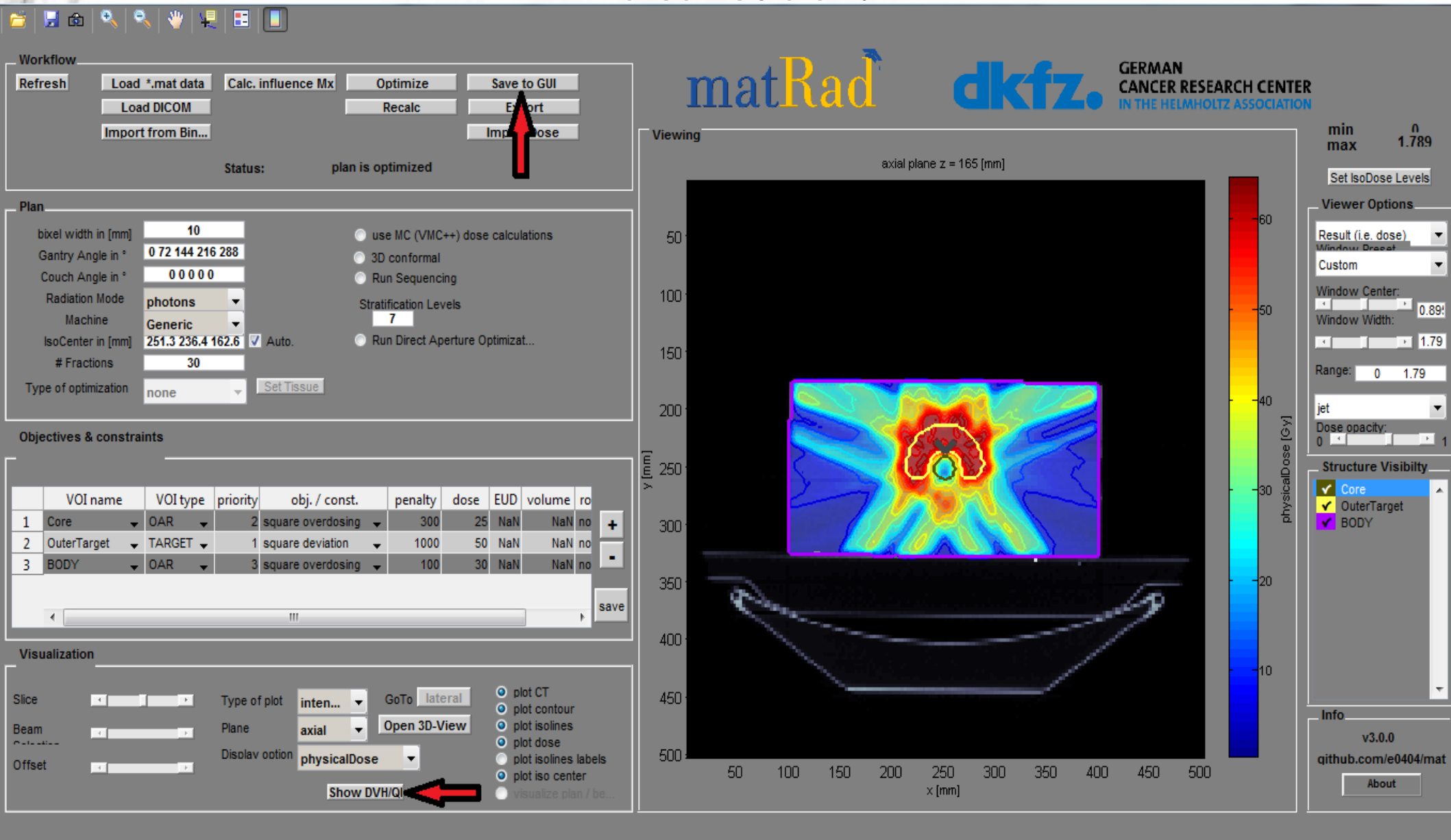
- Le treatment par **Photons** délivre la dose la plus élevée à la surface
- Les **Protons** délivrent la dose la plus élevée à la cible (tumeur) et protègent les organes sensibles

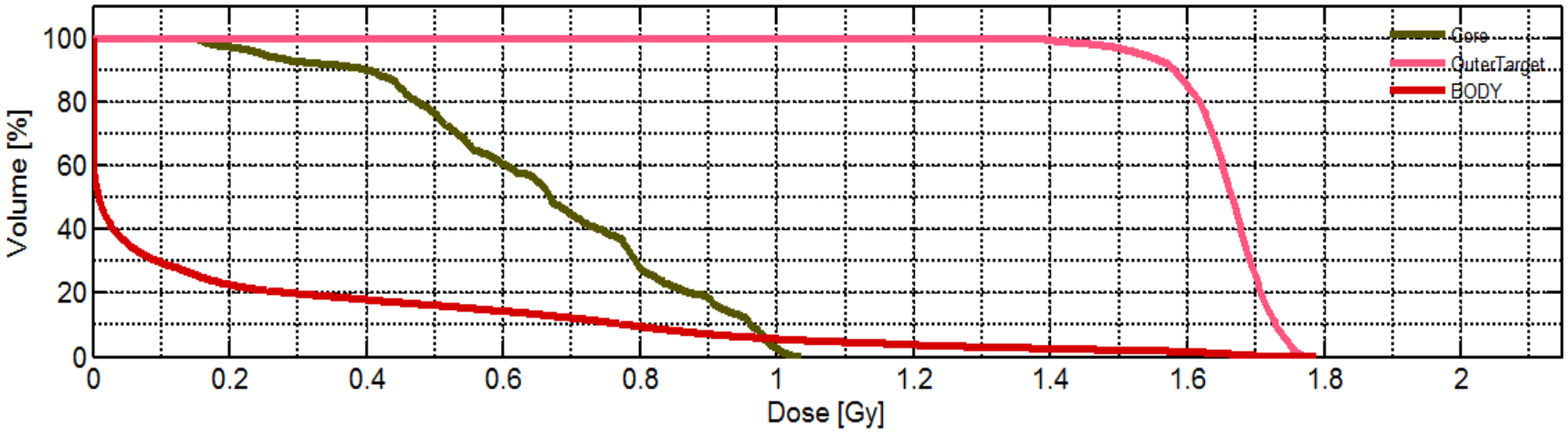
C’est tout pour ce matin !

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	

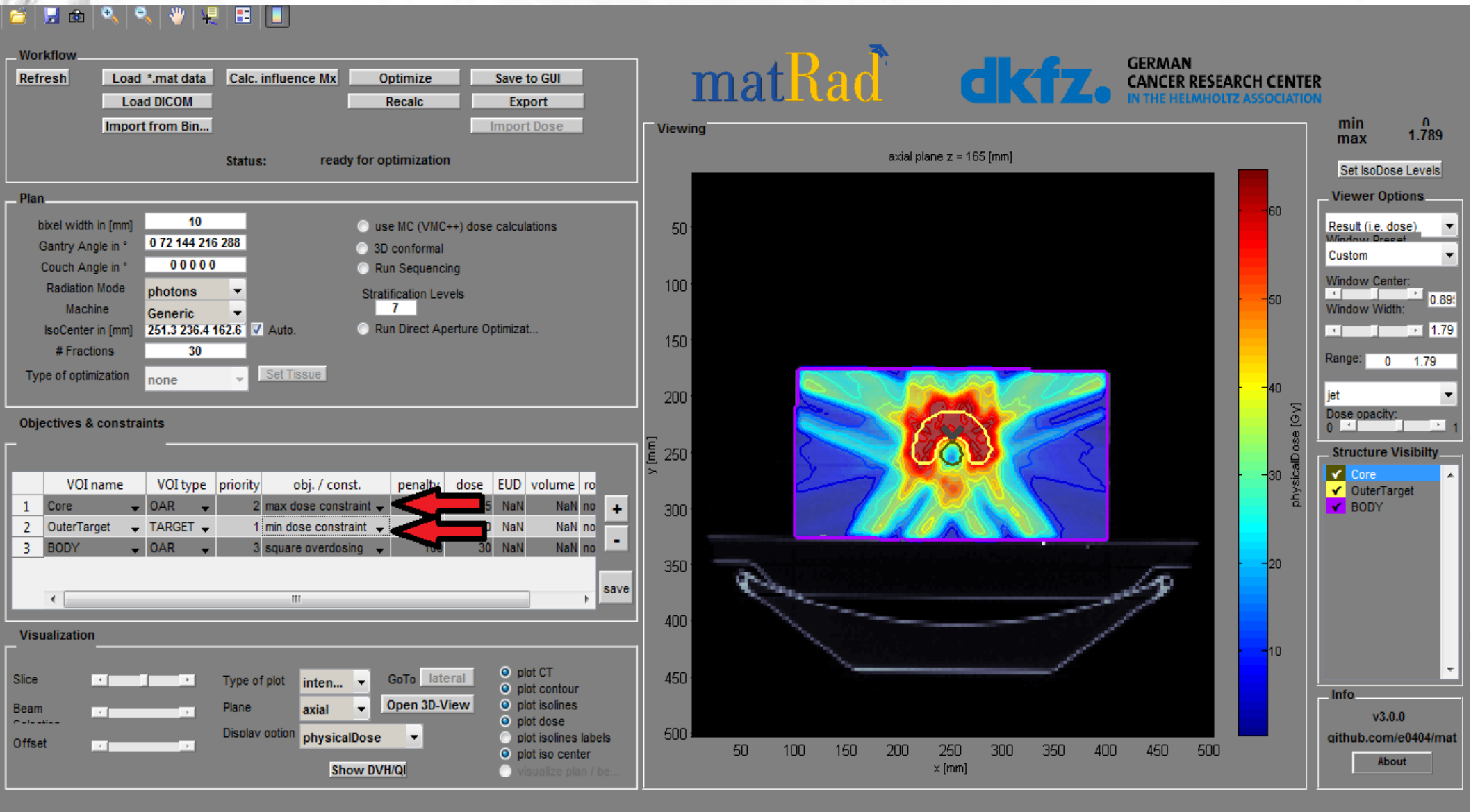
Results

- Mean doses for different regions (Gy):

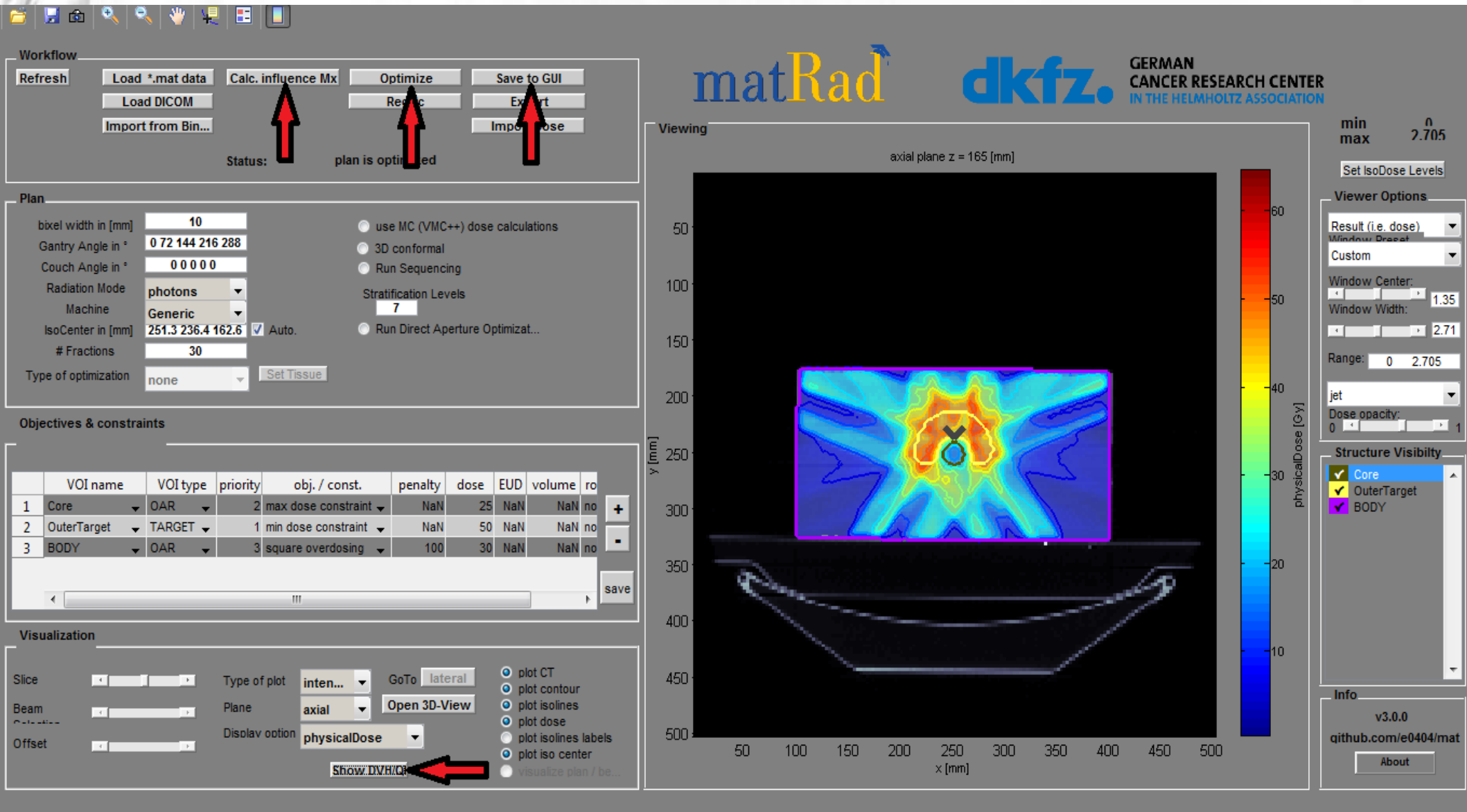
Region/Radiation(angles)	Photons(0)	Protons(0)	Photons (0,72,144,216,288)
Core	1.0665	0.1815	0.6625
Outer Target	1.5852	1.6449	1.6563
Body	0.1443	0.0640	0.1968

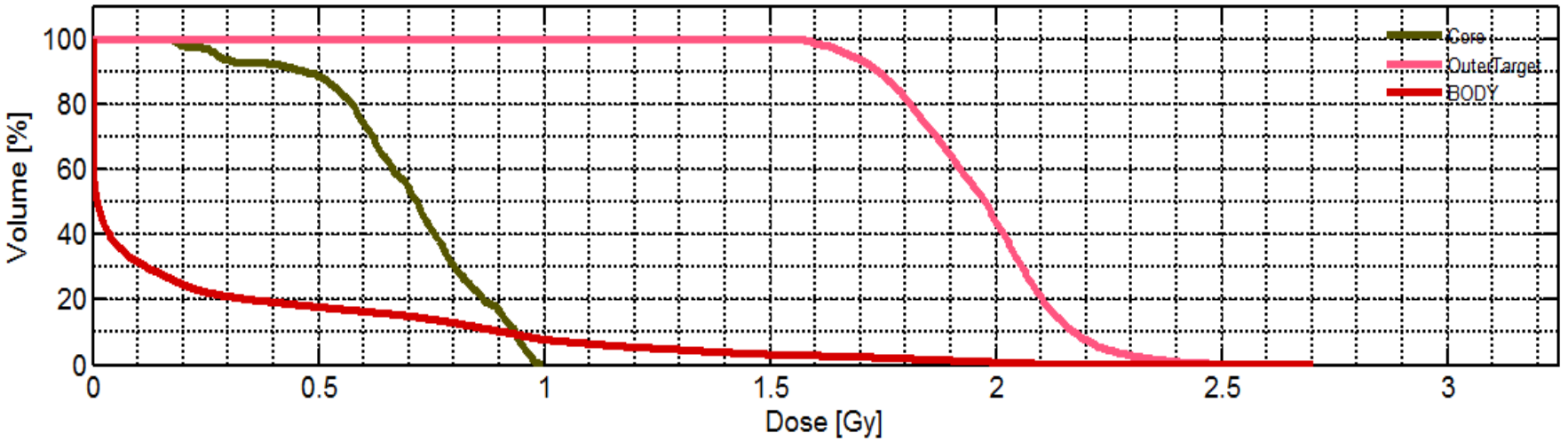
- Treatment plan using multiple photon beams gives better results than single photon beam.
- Best results are obtained using protons.

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	
OuterTarget	1.9652	0.1732	2.7054	1.5511	2.3409	2.2397	1.9766	1.6761	1.6190	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

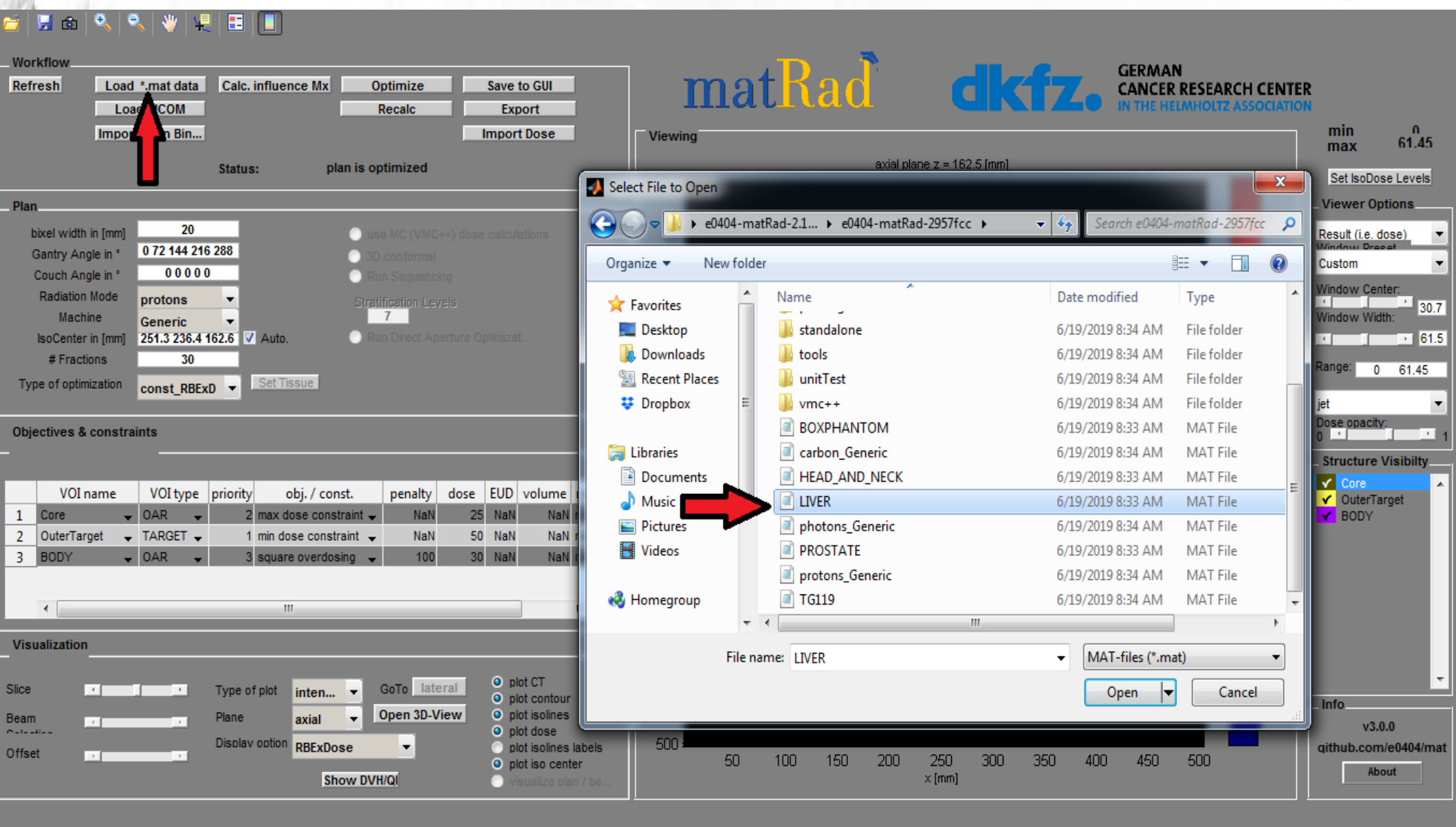
- Mean doses for different regions (Gy) using 5 beams with and without constraints:

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

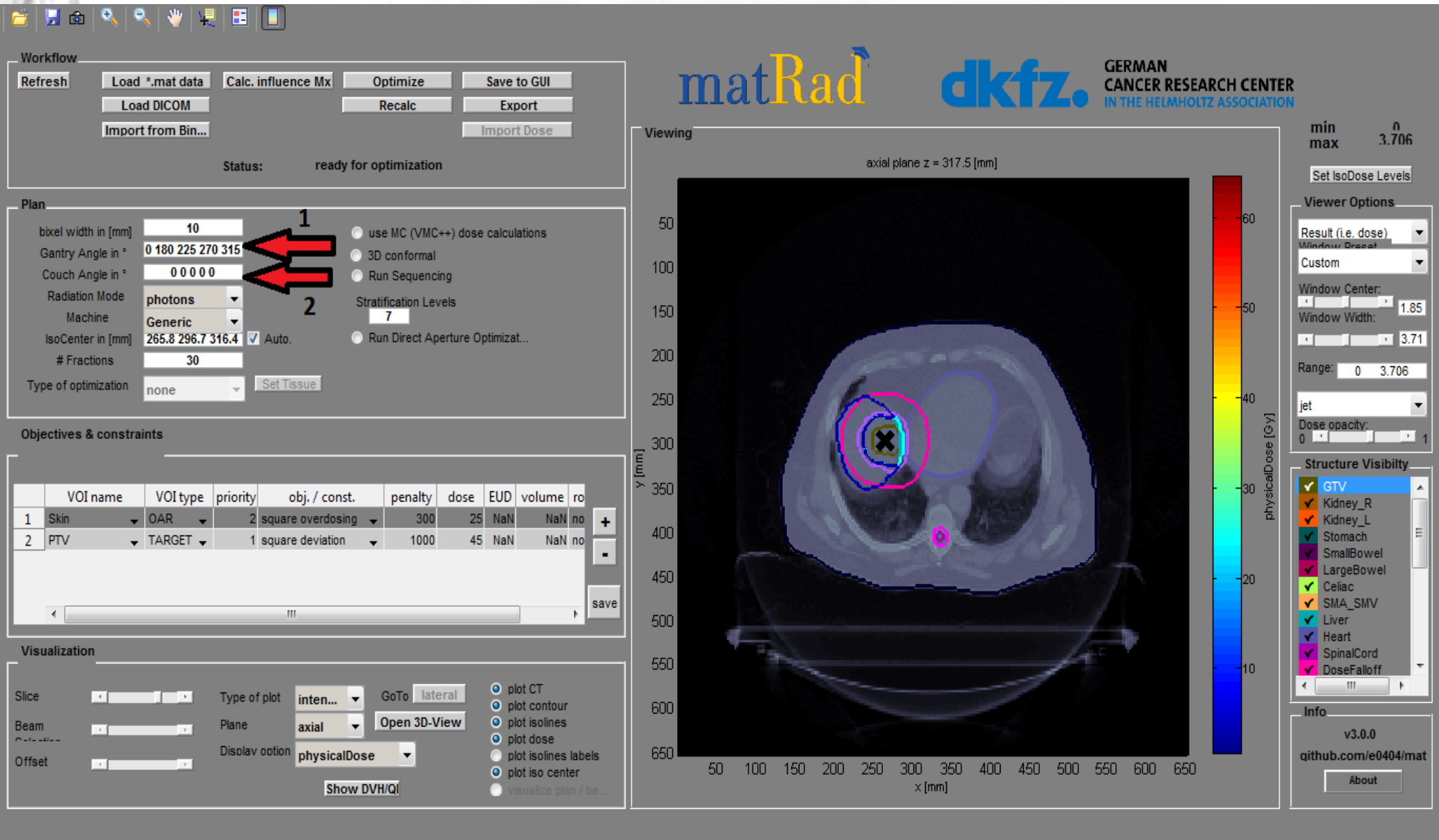
2nd Exercise

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

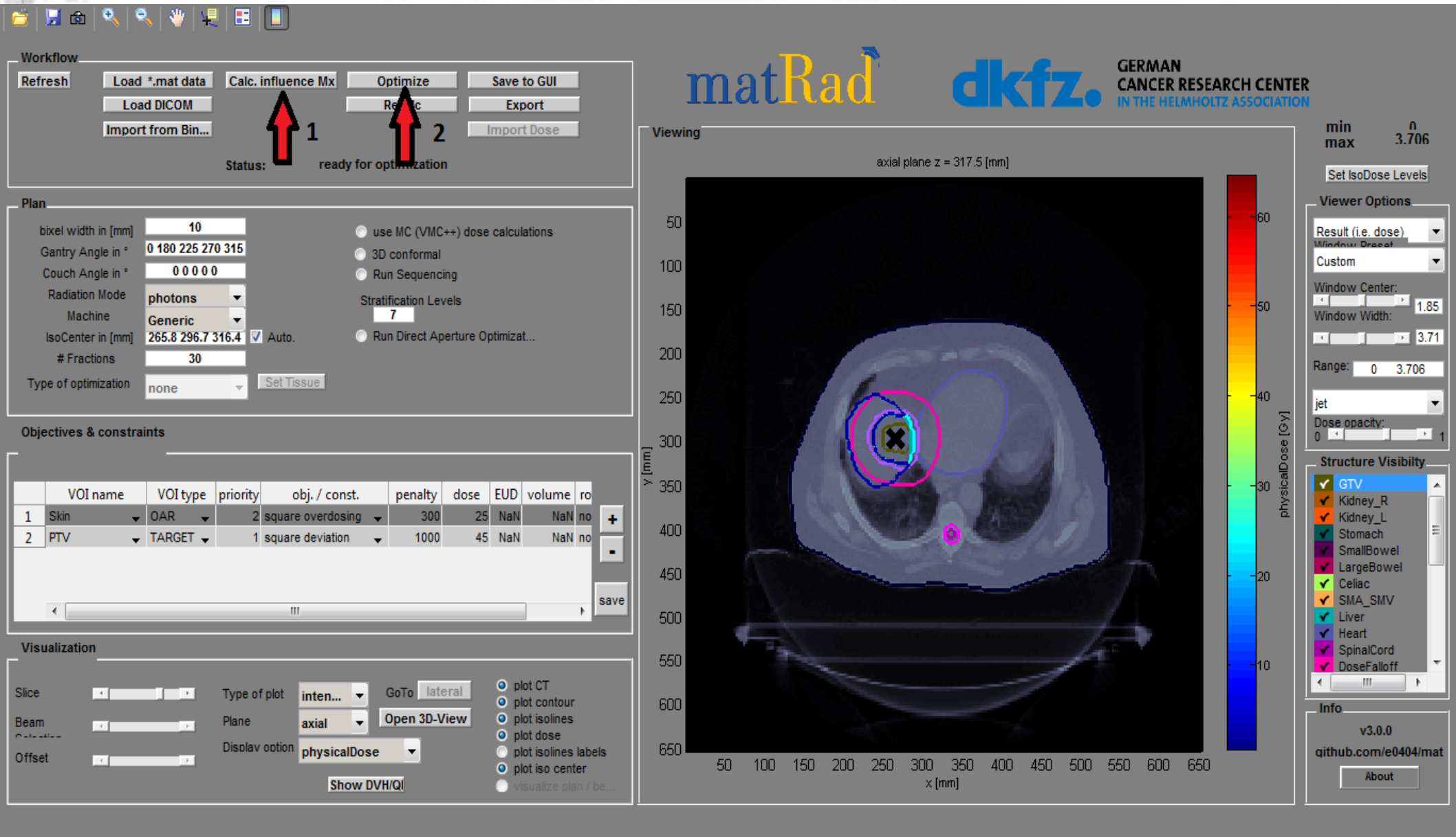
1. Load the liver patient case via the Load *.mat button (LIVER.mat)



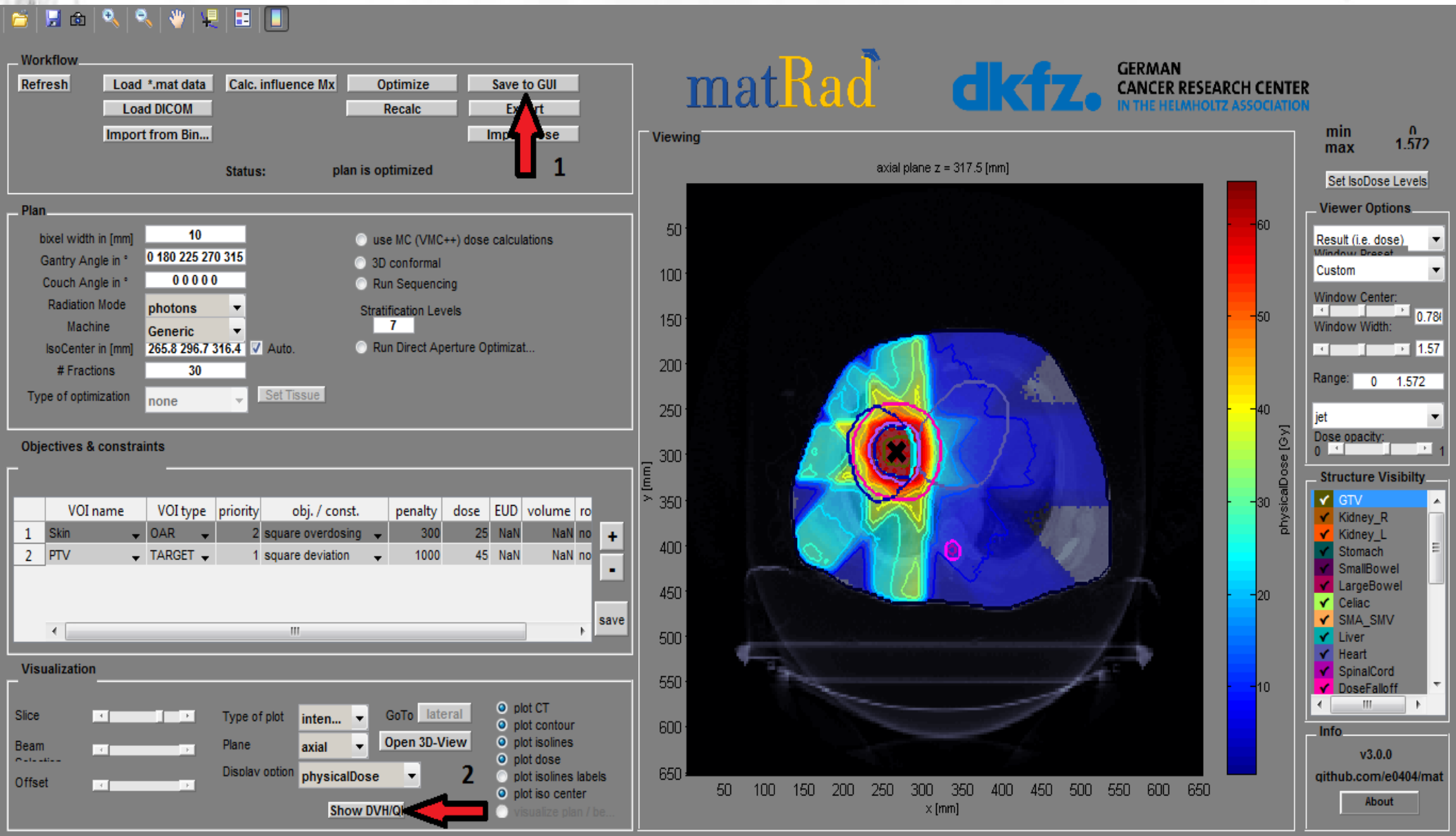
2. Define your own photon treatment plan with approx. 4-5 beam directions.

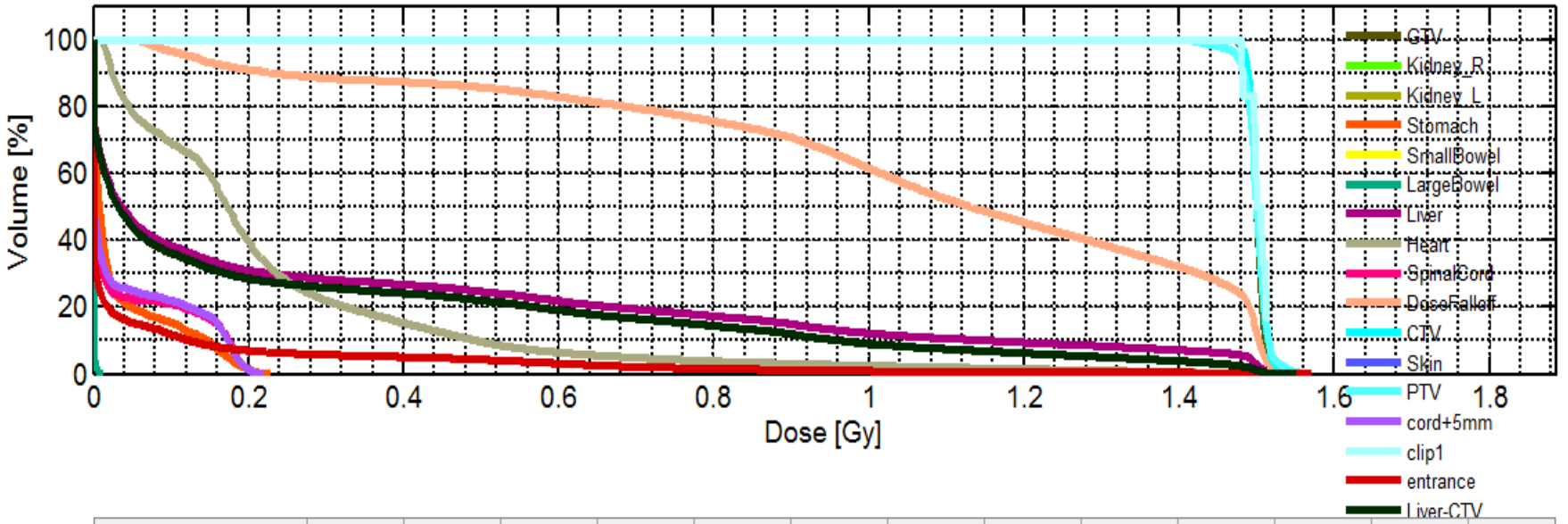


3. Trigger dose calculation („Calc. Influence Mx“) and start inverse optimization („Optimize“).



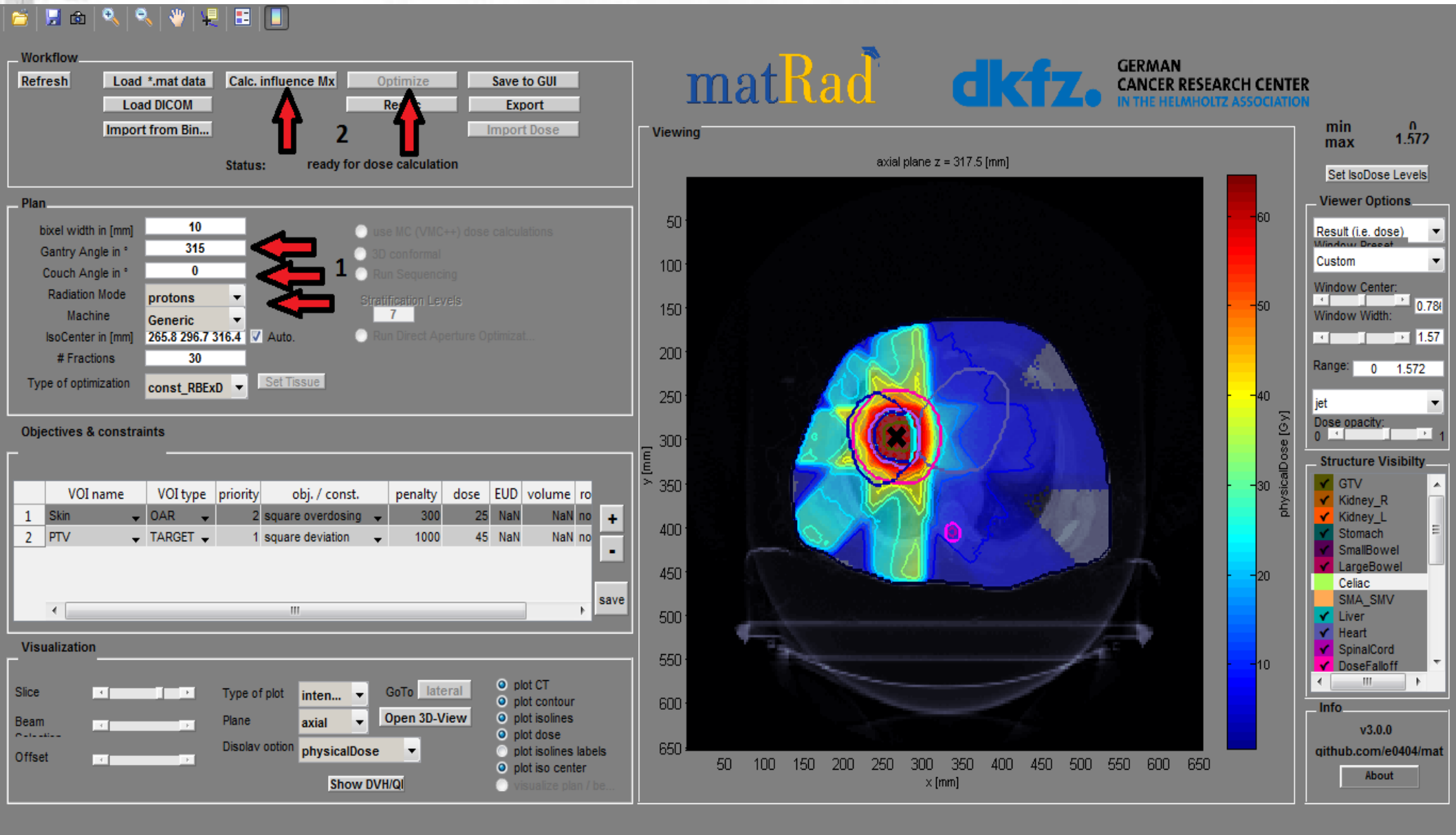
4. Save the optimization result via („Save to GUI“). Next, show the DVH by („Show DVH/QI”). Analyze dose distribution.



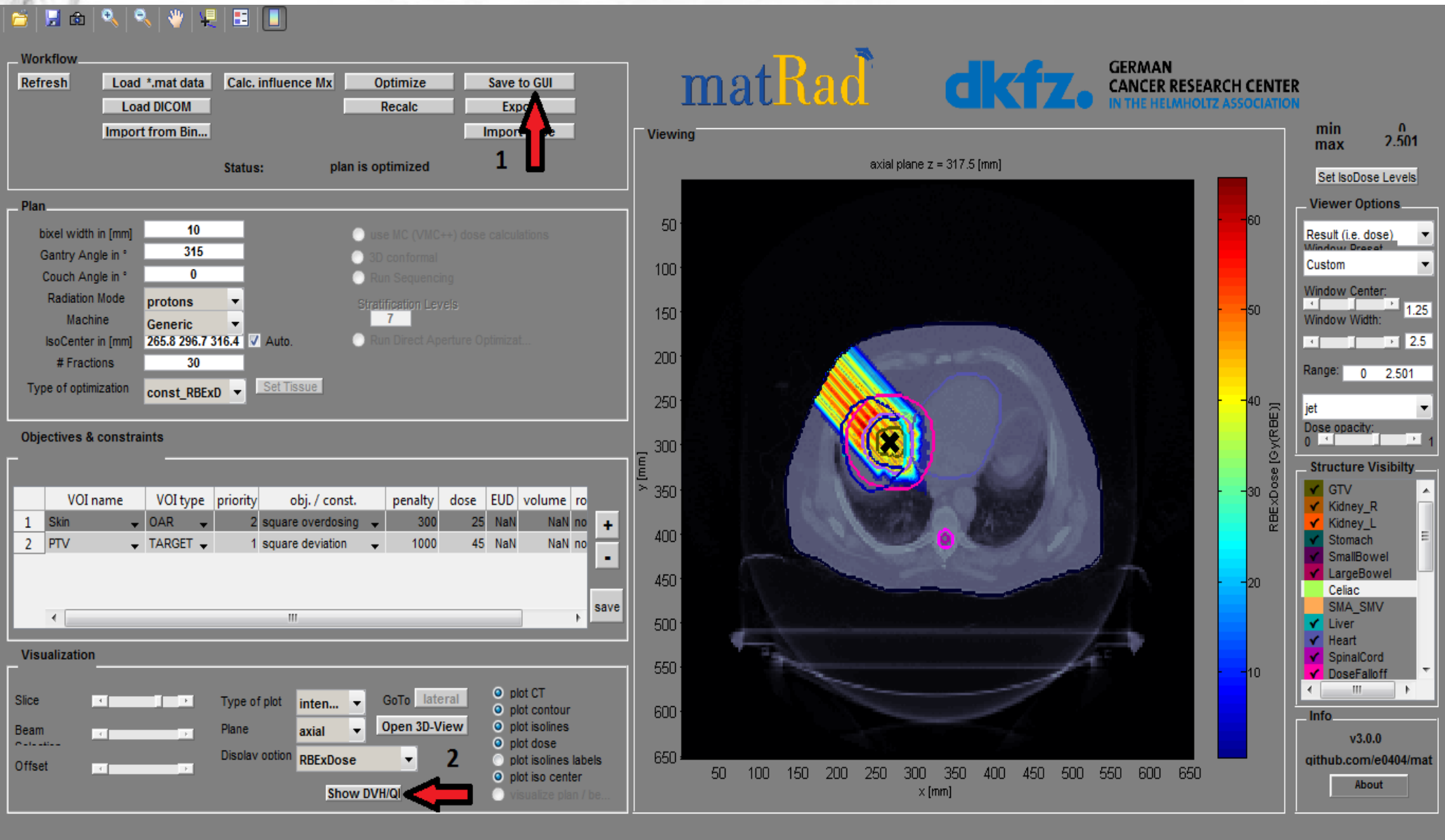


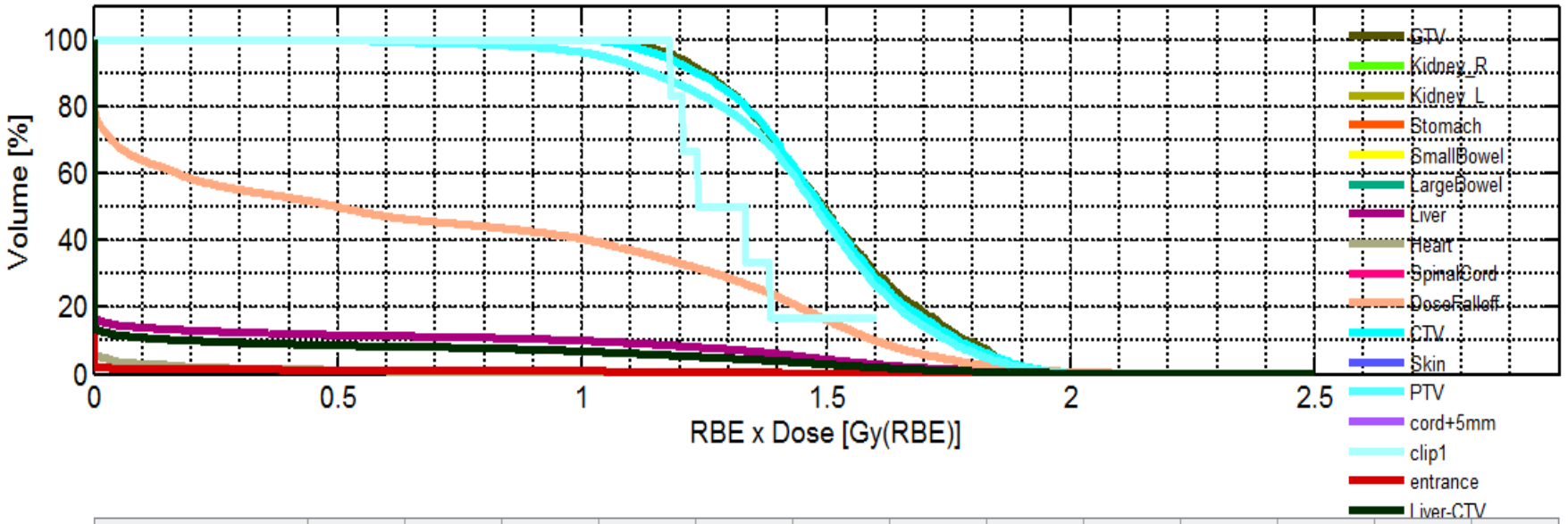
	mean	std	max	min	D_2	D_5	D_50	D_95	D_98	V_0Gy	V_0.3Gy	V_0.6Gy	V_0.9(
GTV	1.5000	0.0090	1.5281	1.4727	1.5188	1.5148	1.5002	1.4851	1.4796	1	1	1	
Kidney_R	0	0	0	0	0	0	0	0	0	1	0	0	
Kidney_L	0	0	0	0	0	0	0	0	0	1	0	0	
Stomach	0.0342	0.0566	0.2310	0	0.1940	0.1736	0.0082	0	0	1	0	0	
SmallBowel	0	0	0	0	0	0	0	0	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“).



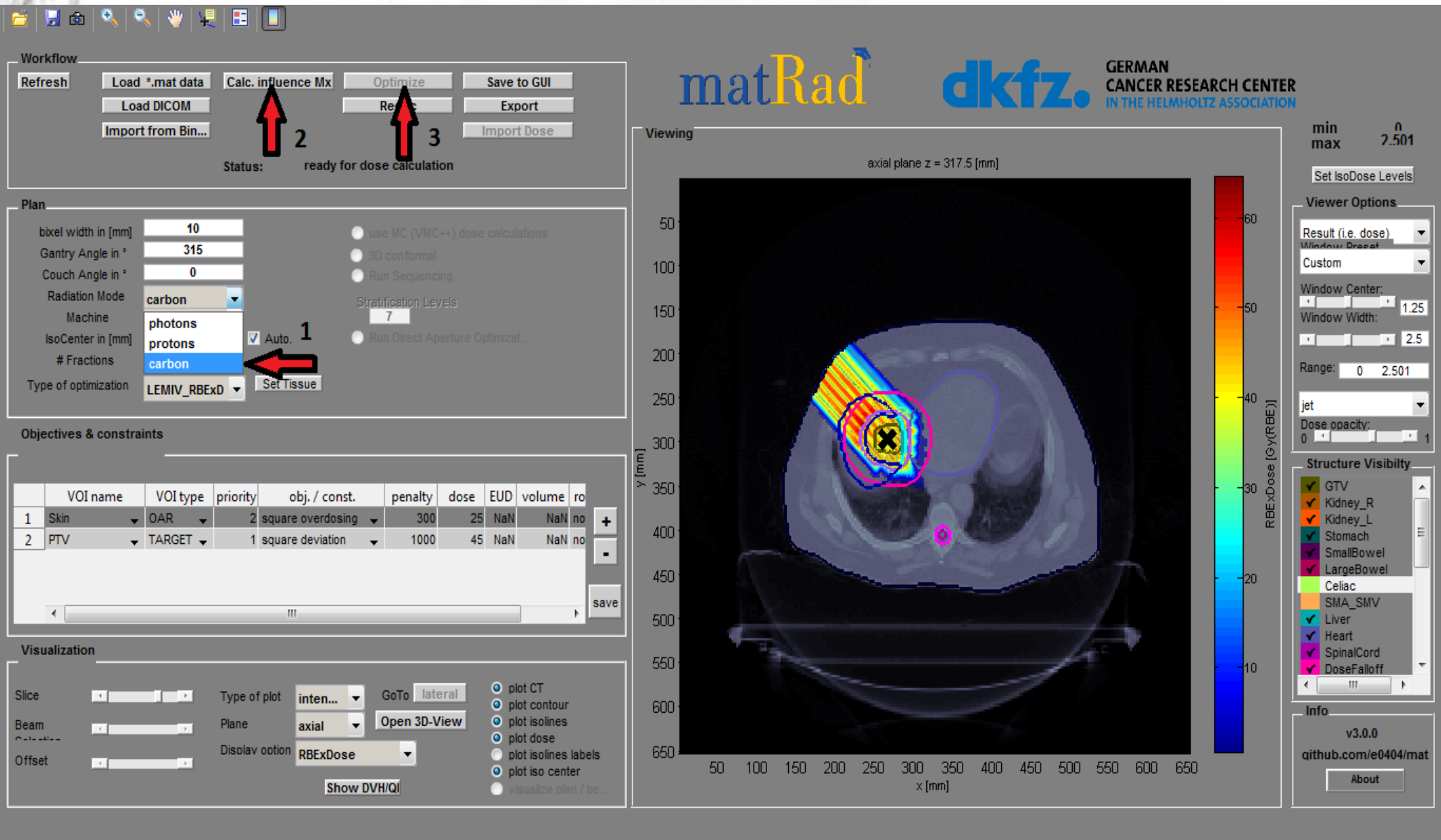
6. Save the optimization result via („Save to GUI“). Next, show the DVH by („Show DVH/QI”). Analyze the resulting dose distribution.



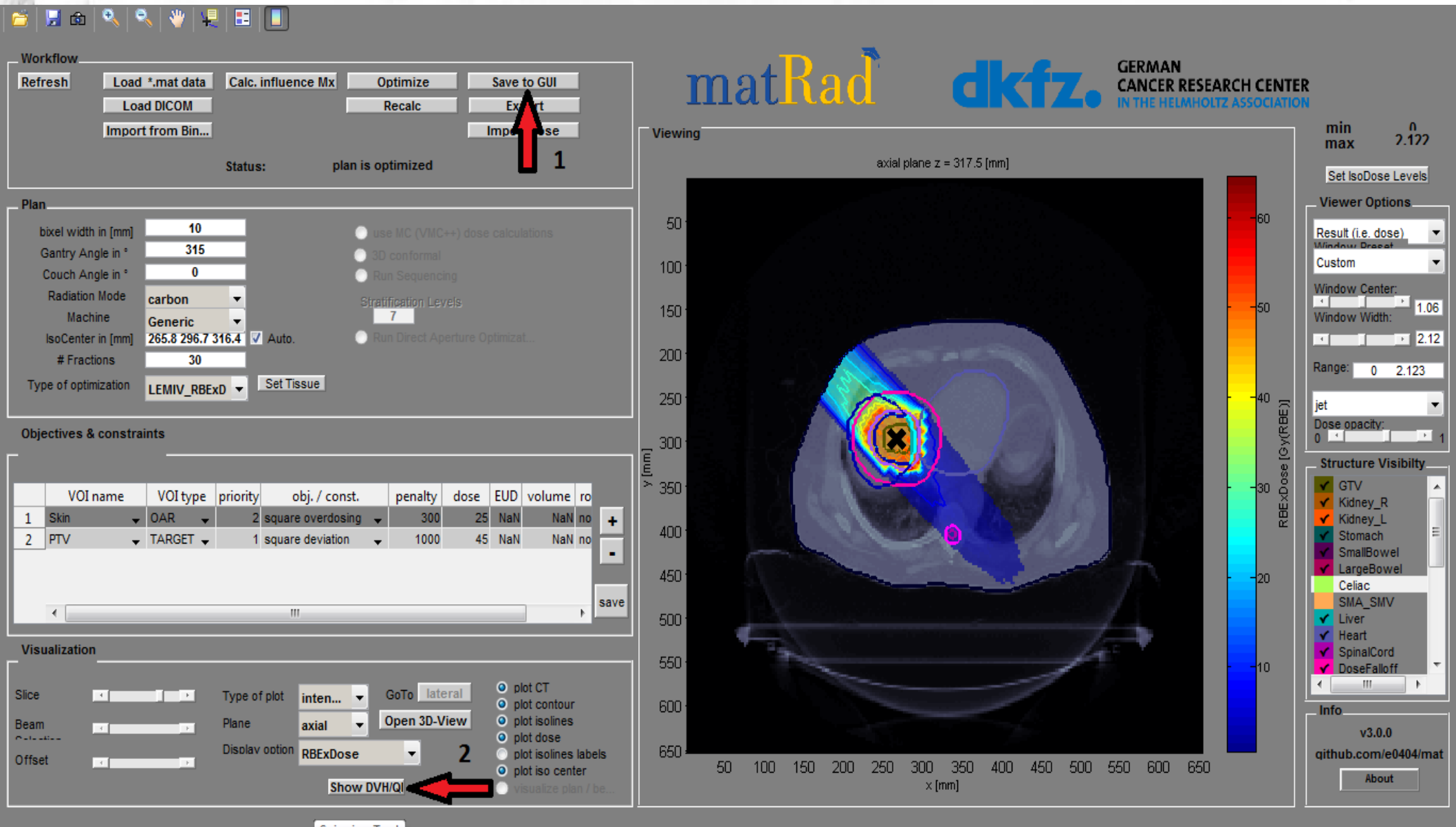


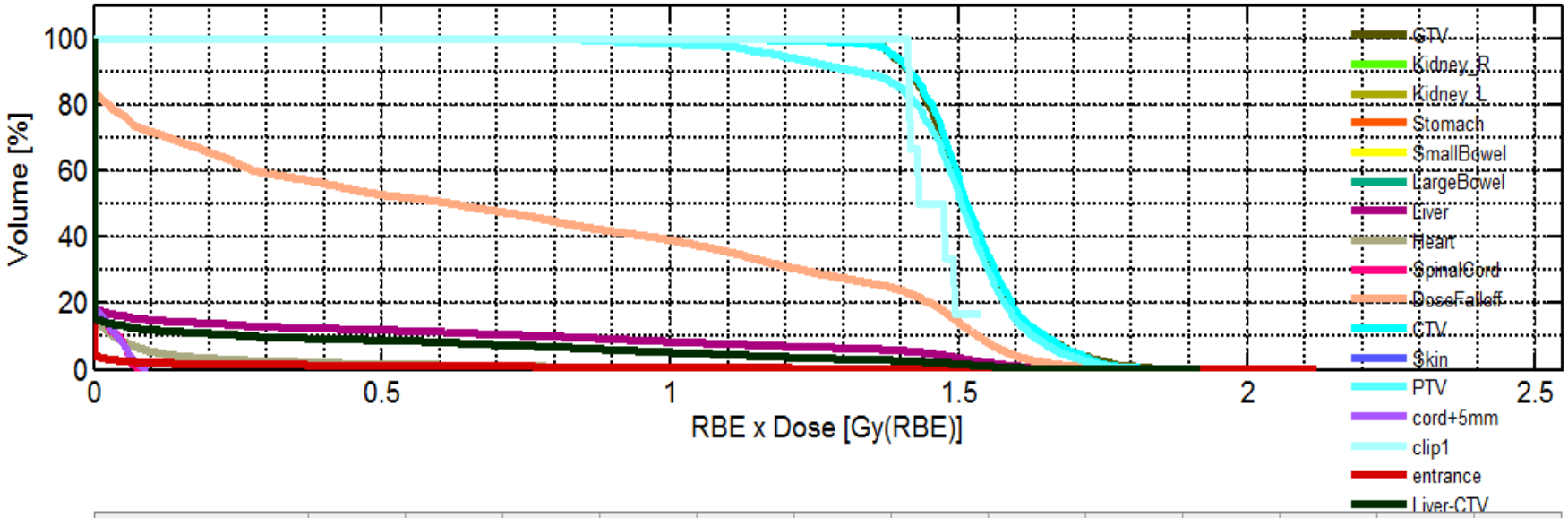
	mean	std	max	min	D_2	D_5	D_50	D_95	D_98	V_0Gy	V_0.5Gy	V_1Gy	V_1.5(
GTV	1.5053	0.1981	2.0110	1.0341	1.8973	1.8506	1.4947	1.1921	1.1231	1	1	1	0.
Kidney_R	0	0	0	0	0	0	0	0	0	1	0	0	
Kidney_L	0	0	0	0	0	0	0	0	0	1	0	0	
Stomach	0	0	0	0	0	0	0	0	0	1	0	0	
SmallBowel	0	0	0	0	0	0	0	0	0	1	0	0	
LargeBowel	0	0	0	0	0	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	0.1694	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	

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_1.2(
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.
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	

Results

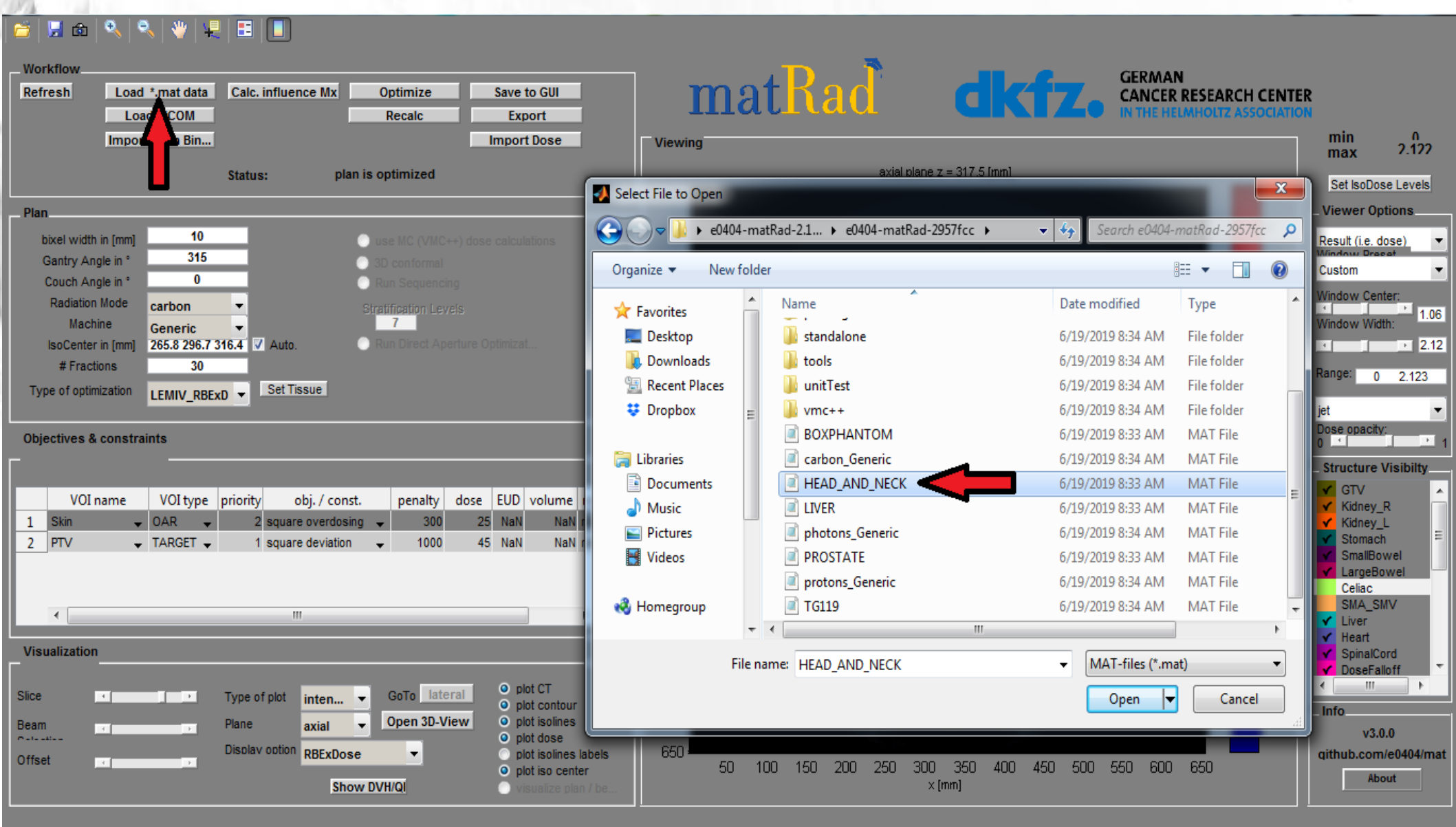
- Mean doses for different regions (Gy) using 5 photon beams, sigle proton beam and carbon ion beam:

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

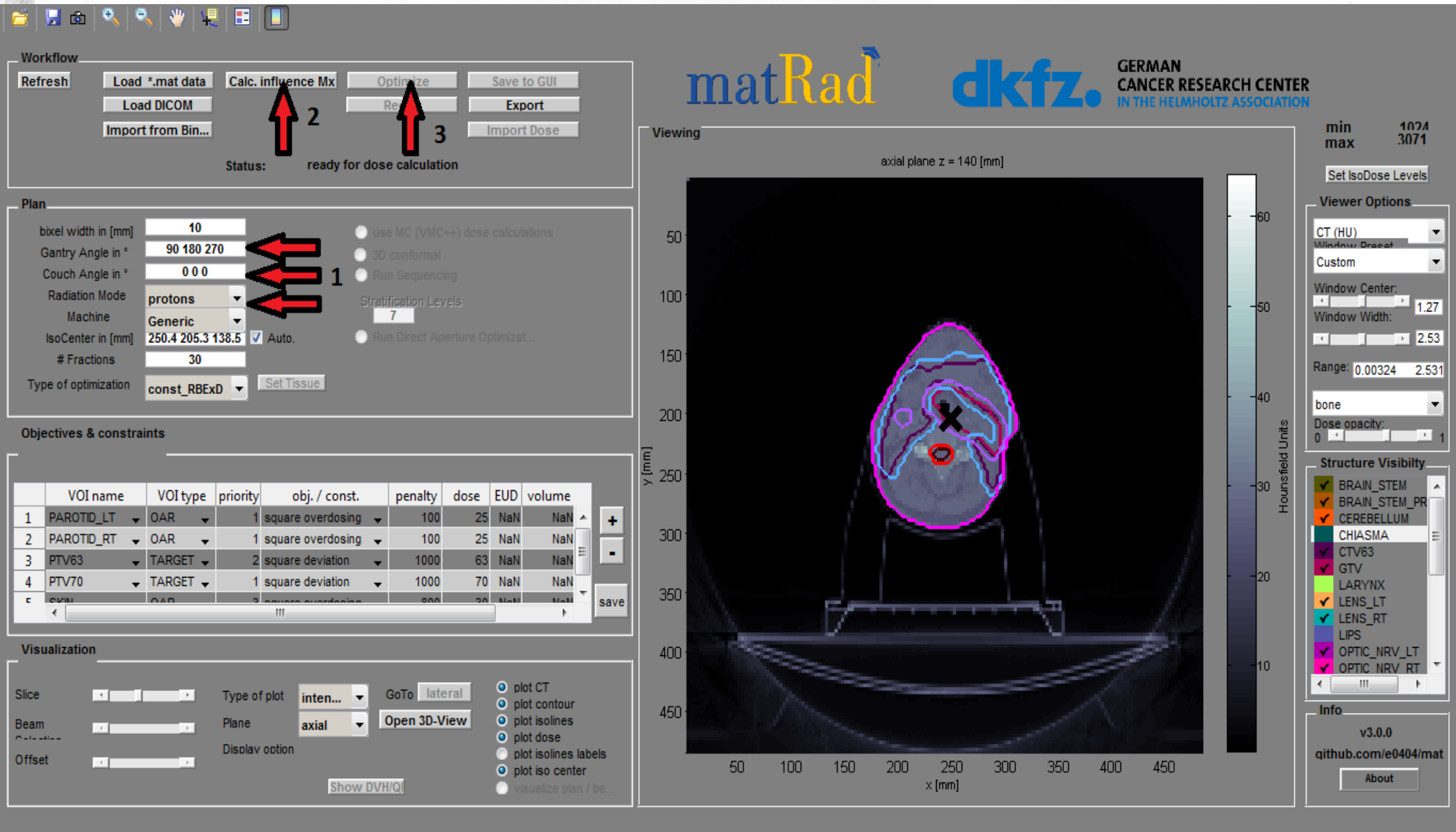
3rd Exercise

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

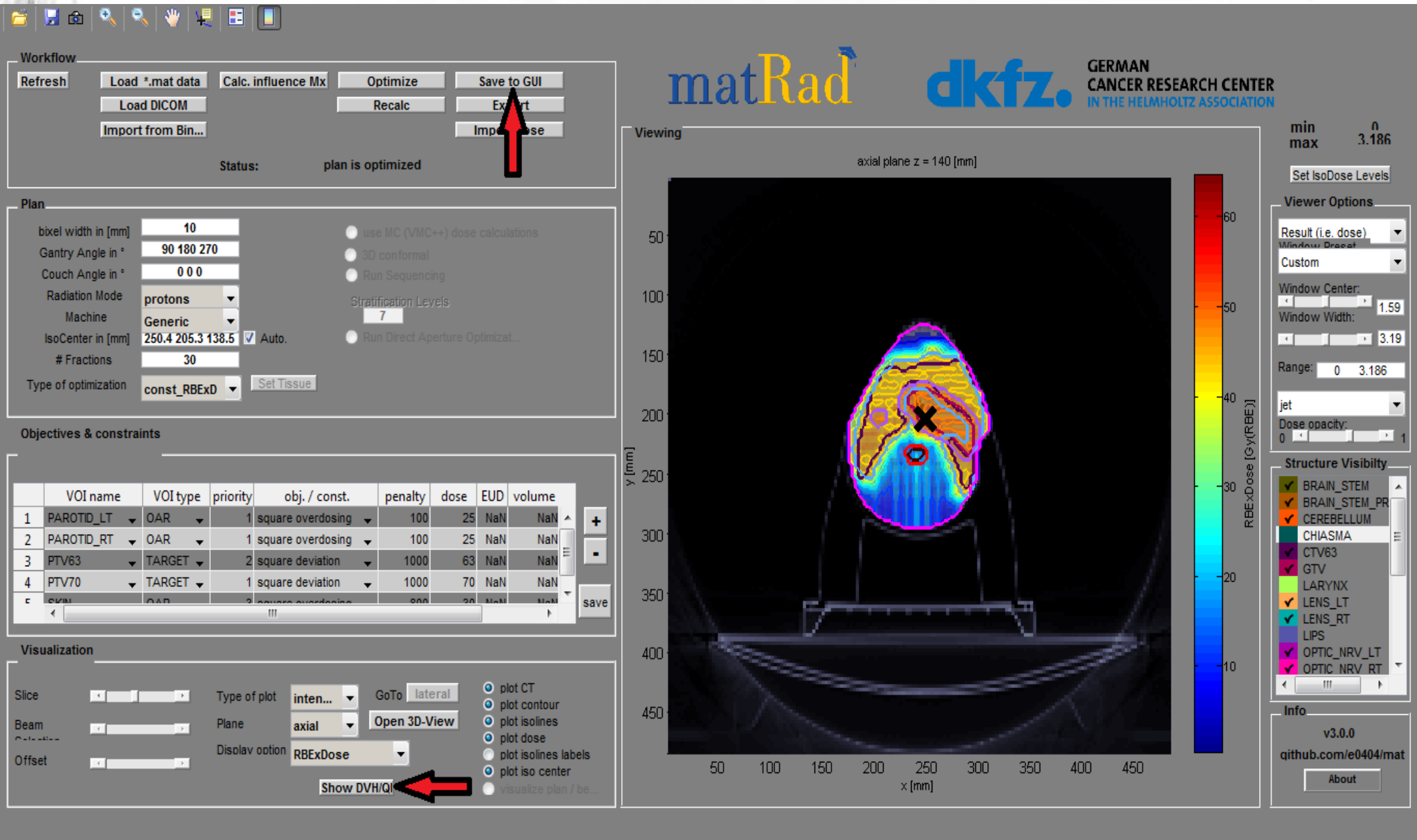
1. Load a head patient case (HEAD_AND_NECK orALDERSON.mat)

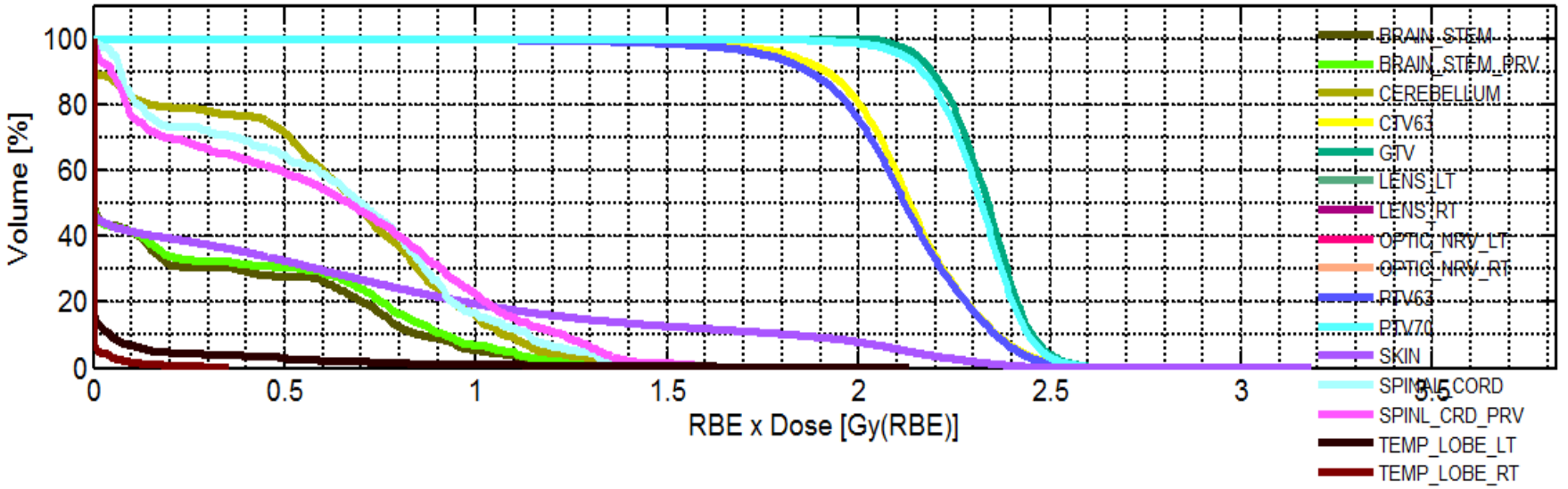


2. Add three proton beam angles on your own. Calculate and optimize the dose („Calc. Influence Mx“ & „Optimize“).



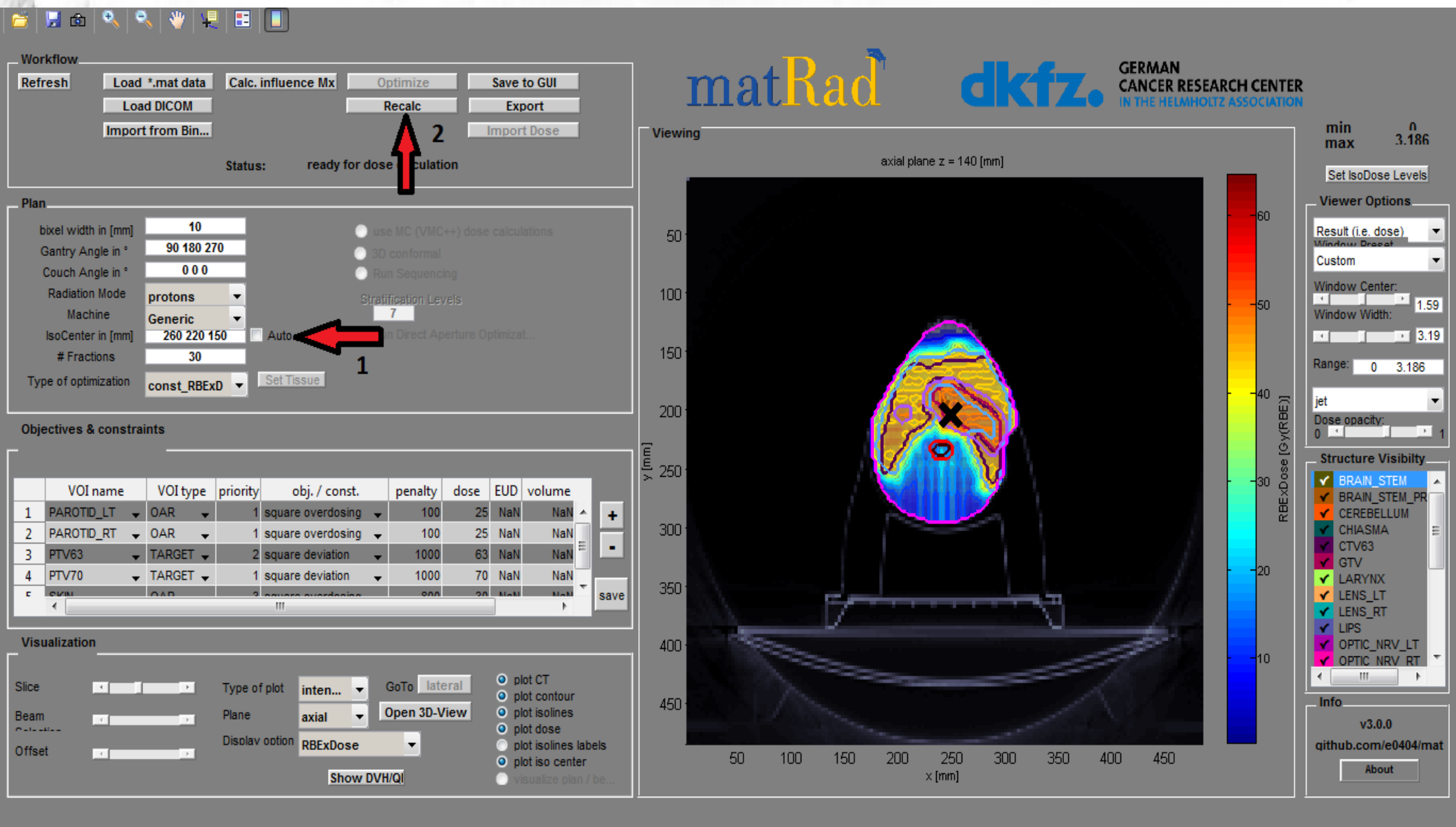
3. Analyze the result (dose& DVH) and save it („Save to GUI“).

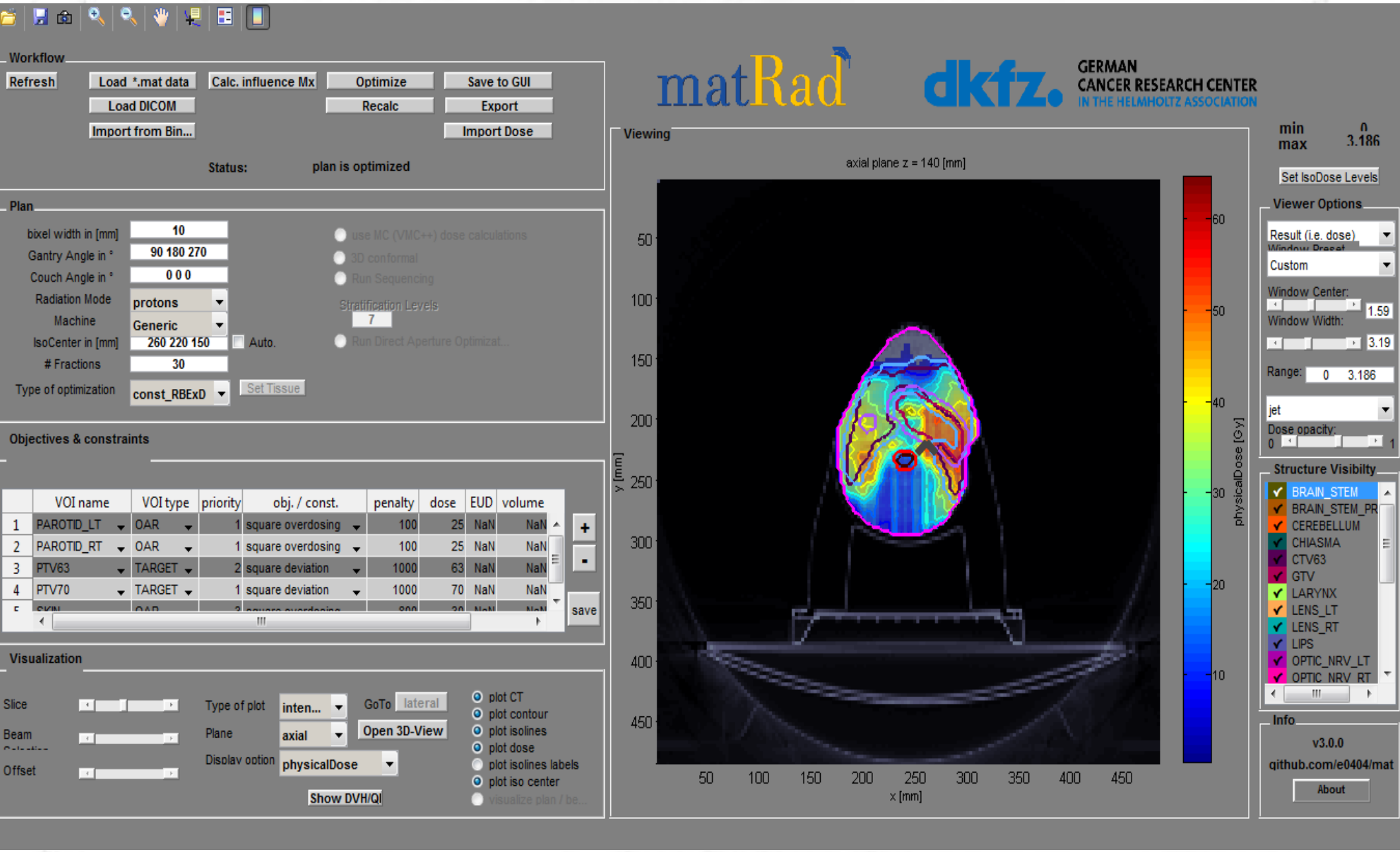




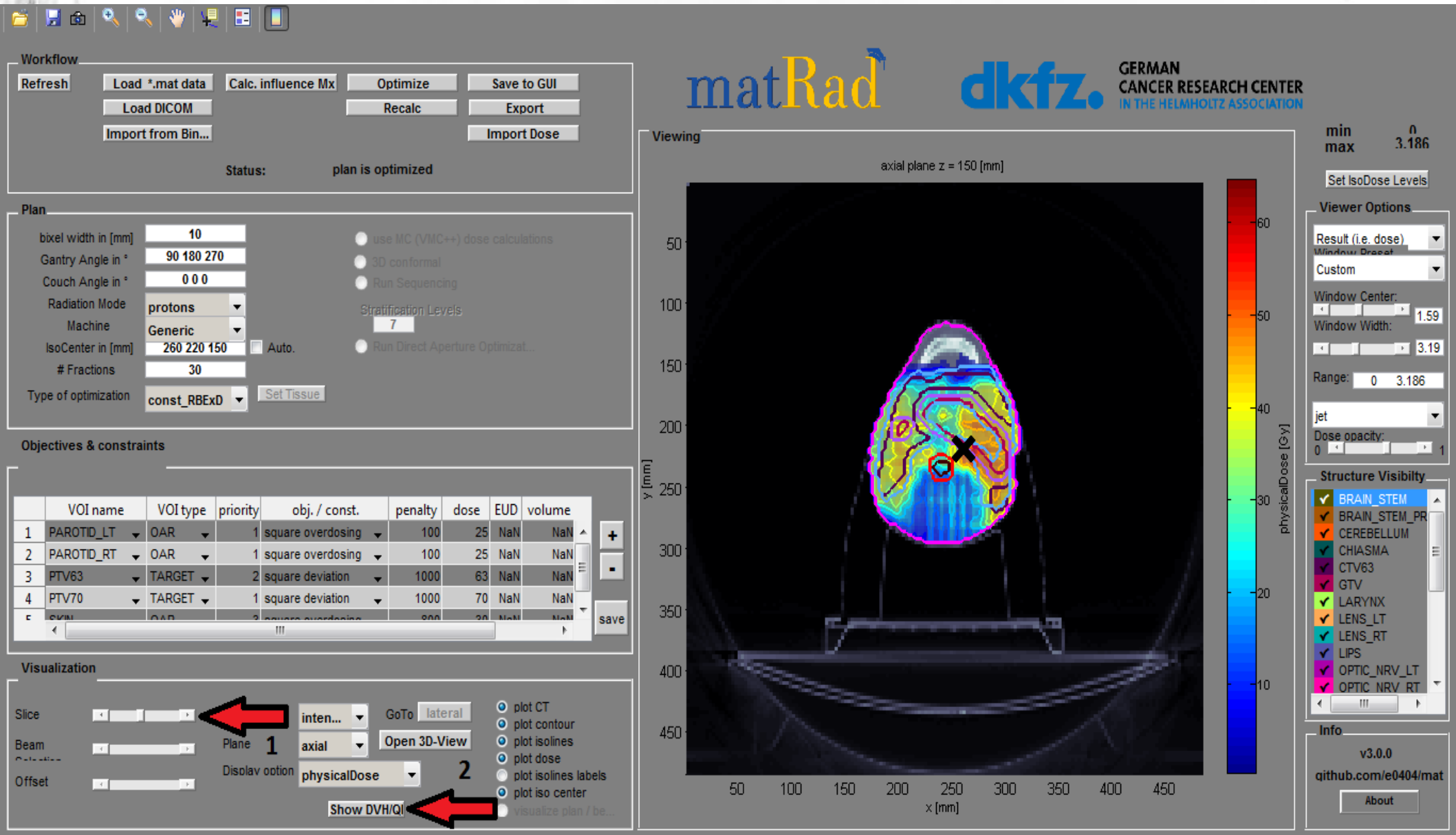
	mean	std	max	min	D_2	D_5	D_50	D_95	D_98	V_0Gy	V_0.6Gy	V_1.2Gy	V_1.9(
BRAIN_STEM	0.2645	0.3831	1.5408	0	1.1597	1.0153	0.0030	0	0	1	0.2649	0.0167	
BRAIN_STEM_PRV	0.2906	0.4099	1.5754	0	1.2980	1.0952	0.0016	0	0	1	0.2896	0.0251	
CEREBELLUM	0.6355	0.3774	2.0785	0	1.3512	1.1661	0.6933	0	0	1	0.5998	0.0469	7.3233
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.
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.
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	

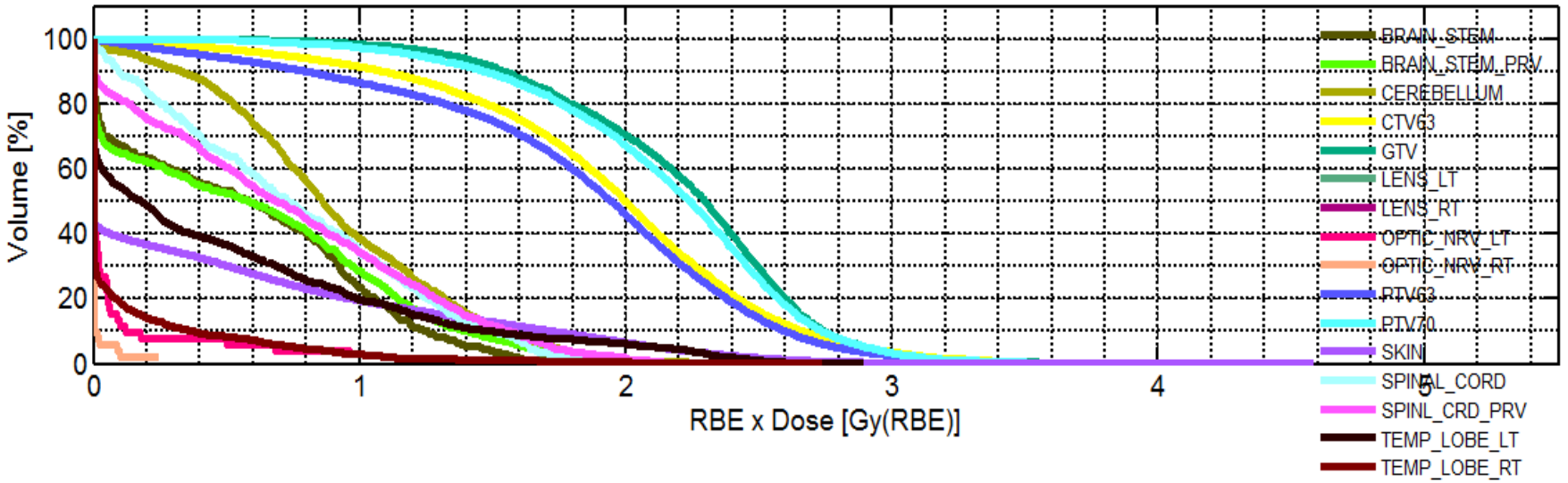
4. Simulate a patient positioning error: Remove the hook at the auto iso-center checkbox and define a new iso-center. Recalculate the dose by clicking on the „Recalc“.




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 Bin...
Import Dose
Status: plan is optimized
Plan
bixel width in [mm] 10
Gantry Angle in ° 90 180 270
Couch Angle in ° 0 0 0
Radiation Mode protons
Machine Generic
IsoCenter in [mm] 260 220 150
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
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
save
Visualization
Slice
Beam
Offset
Type of plot inten...
Plane axial
Display option physicalDose
GoTo lateral
Open 3D-View
Show DVH/QI
plot CT
plot contour
plot isolines
plot dose
plot isolines labels
plot iso center
visualize plan / be...
Viewing
axial plane z = 140 [mm]
y [mm]
x [mm]
physicalDose [Gy]
min 0
max 3.186
Set IsoDose Levels
Viewer Options
Result (i.e. dose)
Custom
Window Center: 1.59
Window Width: 3.19
Range: 0 3.186
jet
Dose opacity: 0 1
Structure Visibilty
BRAIN_STEM
BRAIN_STEM_PR
CEREBELLUM
CHIASMA
CTV63
GTV
LARYNX
LENS_LT
LENS_RT
LIPS
OPTIC_NRV_LT
OPTIC_NRV_RT
Info
v3.0.0
github.com/e0404/mat
About

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_2.7(
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.
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.
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 diferent 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 :)