

Hello everyone, this is a tutorial for the particle therapy masterclass and the material can be found on the respective link. For the PTMC we use a simplified version of a professional open access treatment-planning tool called matRad. In the next few minutes we are going to see an overview of the matRad software, explain the use of each button and perform some simulations with data of a testing sample and a liver case of cancer.

To begin with, matRad is an open source software for radiation treatment planning of intensity-modulated photon, proton, and carbon ion therapy. MatRad is developed for educational and research purposes and it is entirely written in MATLAB.

For a Windows device, matRad software can be found in the file of "application", in the storage directory that you have selected, after the installation. Double click on the app icon and wait for the initial matRad screen to appear. Opening the software one can observe four different fields in the visualization panel (name them and show).

Starting from **the plan selection**, there is the bixel width, which is an element, used for constructing the target. Following up we have the gantry and the couch angles, where we set their parameters as pairs i.e. five couch angles for 5 gantry angles. In any case, the values of the couch angles are blocked intentionally in this simplified version of the software by the developers. Then we have the radiation mode button with which we choose the particle beam for the therapy treatment. Matrad offers the variety of three choices. The isocenter is the point from which the central rays of the irradiated beam passes and it is automatically verified. Next one is the number of fractions of the total dose prescribed in the objective and constraints panel and in the end we have the running sequence button, which is used to shape the target area with the help of collimator. In our case, it will be set to false.

In **the visualization panel**, we have the button of the slices illustrated in the 3D image and by clicking on the right or left choice of the slice selection, one can slide and obtain a specific slice (the isocenter sign, complete X sign). In addition, there is the plain selection button with the choices of axial, sagittal and coronal. Important is the visualize plan/beam lines button, which you can enable for a deeper understanding of the different angles of the irradiation.

In the center, we have **the viewing panel** where the 3D image of the irradiated region will appear and on the right hand side, the structure visibility will provide the names of the illustrated organs.

Regarding the **workflow panel**, there is the Load mat data button (click), which loads the data of each case (describe data cases, C-phantom-> a specified acrylic shaped testing sample used from profs for testing the equipment) and information about the target tissue and the surrounding healthy organs.

The objectives and constraints panel is enabled after inserting the data for each case, showing the organs of interest (e.g target), as well as the organs at risk (e.g body, core etc.) that are about to be irradiated and we want to avoid obtaining more dose.

Next button in the **workflow panel** is the calculating the matrix of influence (of radiation) button (click), with which the algorithm of the software analyzes the dose distribution in the shaped tissue formed by bixels in cubic size (more details in the continuation of the procedure). Afterwards, we have the optimize button (click) that finds the minimum radiation flux per bixel and illustrates an exponential graph.

Our calculations must be saved in the Graphical User Interface, by clicking the Save to GUI button (click and describe the save form). Last one is the Dose Volume Histogram button that depicts the dose deposited in the target volume per percentage. Together we receive the corresponding table. Explain how to save the files.

Procedure:

C-phantom

- I) Photons mode-> 1 angle 0 degrees. Repeat for 5 angles of 72 degrees step. Spot the differences from DVH.
- II) Protons mode-> 1 angle at 0 degrees. Spot differences with the 5 angles of photons.

Liver case

- I) Photons with 5 angles same as the previous step. Subtract visualization of extra organs. Set new photon angles-> 0, 180, 270, 315 degrees. Spot the differences. The beams are focused only on the liver side we want to radiate.
- II) Protons for 1 angle of 315 degrees. Differences with the irradiation of the new 5 angles DVH. The dose distributed with the proton beam in the nearby healthy organs is significantly less.
- III) Carbons for 1 angle of 315 degrees. Spot the differences with the previous objectives.

Things to say during optimization:

- matRad's dose influence matrix calculation algorithms are split into two parts: First we determine the irradiation geometry by generating the steering information for the desired beam setup. In a second step, we generate dosimetric information by pre-computing dose influence matrices for inverse planning. The dose deposition of each beamlet for unit intensity is being calculated.
- Optimizer optimizes a nonlinear optimization problem, using an algorithm. The objective function and constraint functions are built from the specific objectives one can set in the table. The goal of the optimization is to find a set of bixel/spot weights that yield the best possible dose distribution according to the clinical objectives and constraints underlying the radiation treatment. The objective function converges while the number of iterations is increased showing a better approximation to our calculation.
- Radiation zones, red zone highly irradiated, blue not much irradiated and grey zone not irradiated at all.
- RAM memory for different PCs. Until 15 angles have been tested with 16 GB RAM from our associates from Mexico.
- Since matRad is always optimizing the fraction-dose, you now have to check if the maximum dose constraint to the core structure is not violated. Check in the DVH and in the quality indicators if the dose to the core structure does not exceed 25 Gy / 30 fractions = 0.833 Gy per fraction.