**WiscPlankV Overview:**

WiscPlan is a treatment planning system that can perform dose calculation and optimization for both step and shoot and helical dose delivery.

I have created a folder for the 125 kVp x-ray source, and it is called: WiscPlanPhotonkV125

WiscPlankV dose calculation needs these inputs:

1. Geometry (DICOM file with contours)
2. Kernel file
   1. Needs EDK kernel outputs to generate Kernels.mat file
   2. Attenuation coefficients for the same energy as the kernel energy bin (unit: cm2/g)
   3. Normalized Source Spectrum (also explained as “fluence” here) in the same energy bin as the kernel energy bin

The folder “Kernels\_5keV-250keV” has both input and output for 5 keV to 250 keV kernels at 5 keV interval using the EGSnrc code: EDKnrc. Folder “KERNEL\_125\_keV” has output Folder: “keVoutput” which has consolidated output files“.keV”, text file for attenuation coefficient, and source spectrum txt file. The matlab file: “GenerateKernelFile125New.m” can be used to create the necessary Kernel.mat file, which is copied and saved in: … \WiscPlanPhotonkV125\matlab\_frontend\ryan

Attenuation coefficient of water at a given energy can also be extracted out from the EDKnrc output files with extension “.lst”. Use the MATLAB codes: “readEDKoutputMuNew.m” and “readEDKoutputPriFracNew.m”. Once they are extracted, they can be used to create the text file called “125keVmu\_mu-en.txt” in folder: \KERNEL\_125\_keV\keVoutput

The fluence spectrum of the x-ray tube is also required. One way to estimate it isby using the Excel chart called “TASMICS\_v1.0 .xlsx” in folder: KERNEL\_125\_keV. However, the best option is to actually measure the fluence spectrum and have that data. This information is used in the text file: “125keVfluence.txt” in folder: \KERNEL\_125\_keV\keVoutput

**Test run to use the WiscPlankV:**

NOTE: WiscPlan only take geometry input as DICOM data with necessary contour file. For my application, I downsampled (using script in folder; WiscPlanPhotonkV125\DownsampleScript) and sort the CT data, and then contour in the Pinnacle Treatment PlanningSoftware. Without target contour, geometry error will give error.

1. In MATLAB, first “set path”; Add with Subfolders: C:\WiscPhanPhotonkV
2. First run XTPS (note location is: WiscPlanPhotonkV125\matlab\_frontend\lab)
3. It returns a MATLAB GUI – a figure. It says; Figure 1. RDXTPS: No Patient.
4. Fig has 2 options. File and Tools.
5. File:
   1. 1. Import DicomRT Geometry 2. BeamletDose Calculation 3. Plan Optimization 4. Save Optimization Results. And then, also these options: Load geometry, Load OptResults, Save Geometry AS; Save OptResults As: Export Pinnacle Files.
   2. Tools: Plot DVH
6. (workspace returns ans = 1 x 1 XTPS)

**Import Geometry:**

1. When clicked File🡪 Import DicomRT Geometry, it asks for Step 1, and browser opens! – …\WiscPlanPhotonkV125\CT with Contours\DICOM\TomophantPlan01
2. Loading in progress:
3. Do you want to downsample the CT dataset? YES or NO.
4. Asks for target selection: options; couch, target, ROI\_1, ROI\_2. Select Target
5. Asks for : Please enter the BTV margin (cm): default is 0.6 cm, or 1 sigma, enter 0 to skip (I use 0.5 or 1.Note that unit is cm)
6. Asks for: Enter the ring margin (cm): Enter 1 or whatever is desired per application
7. Save geometry files: Save patient data to directory. …\WiscPlanPhotonkV\PatientData
8. It says, “Plan geometry created successfully in ….”
9. Say Ok, and you can adjust the Misc Settings on the lower corner of MATLAB GUI for better visualization. Can also select ROI display.

**Dose Calculation:**

1. **In MATLAB command window, run “helicalDosecalcSetup5.m”. (location:** **WiscPlanPhotonkV125\matlab\_frontend)**
2. It will ask you to select target: so, select “Target”
3. **Now you have two options: type ‘y’ to run beamlets locally in the computer**

**Or type ‘n’ to wait and prepare running the beamlets in the Linux server**

1. If ‘y’ is typed, it will bring up two command window (2 cores for example) and starts beamlet calculation
2. **After beamlet calculation is done in the command windows, go back to MATLAB command window, and run: “merge\_beamlets.m”**

**If running in Linux server**

1. Use Putty.exe to log in to your Linux server:

Host:

Port:

Log in and password;

1. To transfer files, I used a program called, WinSCP. For example: create a new folder called “testCase” and transfer the following files/folders from local computer:

… \WiscPlanPhotonkV\PatientData

Folders: beamspecbatches, geometryfiles, kernelfiles

Text files: ConvolutionSubmit.txt, geometryFilenamesCHTC.txt, geometryFilernamesCondot.txt

1. The source folder also needs to be in the server, and needs to be compiled to get the linux executable. This executable file needs to be transferred to the current testCase folder. In the test folder, once you have these 3 folders, 3 files and the executable, it is ready to run dose calculation.

In Putty: condor\_submit convolutionSubmit.txt (use the text fiel to submit)

1. Once the dose calculation is done, you will see 2 files named like: batch\_dose0.bin, batch\_dose1.bin, etc.
2. When dose calculation is done in CHTC server, use WinSCP to copy these bin files back to the local computer: … \WiscPlanPhotonkV125\PatientData
3. Rest of the step is same, regardless of if you did dose calculation locally or in the server.
4. In MATLAB command window, run MATLAB code: merge\_beamlets.m. Edit the code before running if necessary depending upon number of cores used to breakdown the dose calculation to batches (change: num\_batches). Once this is done, it will create a new bin file: batch\_dose.bin
5. If you want to read individual beamlets, use the script: “read\_ryan\_beamlets.m”

**Optimization**

1. Go back to MATLAB GUI: File 🡪 3. Plan Optimization
2. Select the patient directory- C:\WiscPlanPhotonkV125\PatientData
3. It brings up the Optimization window: It asks for:
   1. Max number of iterations: 20000
   2. Save result every? Iterations: 200
   3. Modulation factor: (typically 5 for SS, 2 for DET)
4. Brings up Target selection window: select “target”
5. Now, it will bring up a windows command window; and also a MATLAB interface notice: “Start optimization. Run this if not started automatically: .\RDXoptimizer.exe “ … \WiscPlanPhotonkV125\PatientData\optInput.txt”
6. On the Windows Command window:
   1. cd /d C:\WiscPlanPhotonkV125\WiscPlanEXE\RDXoptimizer.exe “C:\WiscPlanPhotonkV\PatientData\optInput.txt”
   2. Enter
   3. It will bring up RDXoptimizer GUI with a DVH. You can also adjust parameters as needed like “importance”. It will also bring up a Windows Command window which will display the number of iterations- which constantly updates and states objective function value for the iteration.
   4. Select all ROIs expect couch
   5. Click Pause/Resume button in the lower left corner to start
   6. (optional) Pause>adjust parameters. Resume
   7. Pause when satisfied, and close the optimizer applications (window)

**Save Optimization**

1. Back to the MATLAB GUI, (restart if needed), go to File 🡪 4. Save optimization results
   1. Choose patient folder as: C:\WiscPlanPhotonkV125\PatientData
   2. In MATLAB command prompt, Use code: “get\_full\_dose.m” to get dose outside of used POIs
   3. In the dose display panel, chose colorwash or play with other options defining different isodose curves
2. Previously saved data can also be used to reviswed.
   1. (optional) If no geometry loaded, go to File 🡪 Load Geometry, and select : C:\WiscPlanPhotonkV125\PatientData \matlab\_files\Geometry.mat
   2. Plan optimization: Load OptResults, and select

C:\WiscPlanPhotonkV125\PatientData \matlab\_files\optResults.mat

NOTE: If you want to run another dose calculation using another data, you might want to save this data by copying the whole “PateintData” folder into a different folder because it will override.