VMAT TBI autoplanning script user guide

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Contents

1 Current script versions **2**

2 Updates from previous script versions **2**

3 Publications **3**

4 Introduction **3**

4.1 Treatment regiments, plan goals, and optimization constraints 3

5 Binary plug-in script **4**

5.1 Contouring/preparation 4

5.2 Tuning structure generation (TS Generation) 6

5.3 Beam Placement 9

5.4 Optimization Setup 10

5.4.1 Alternative path to set optimization objectives 12

5.5 Plan preparation 13

5.6 Some notes about the Scleroderma trial treatment regiment 15

5.7 Some notes on including FLASH in the optimization 18

5.8 Known issues and bugs 19

5.9 Planned features for future releases 20

6 Stand-alone executable **21**

6.1 Main program GUI 21

6.2 Optimization loop GUI 22

6.3 Program flow 25

6.4 Known issues and bugs 27

6.5 Planned features for future releases 27

7 Configuration file settings for the plug-in and executable scripts **27**

1 Current script versions

The below guide is valid and accurate for script versions:
Binary plug-in: 1.5
Executable: 1.0
Eclipse v15.6

2 Updates from previous script versions

Binary plug-in revisions from v1.4:

- fixed minor bugs
- fixed minor formatting errors in the GUI
- Added functionality to read-in a configuration file
  - A .ini file named 'VMAT_TBI_config.ini' (must be located in the same directory as the executing assembly, i.e., the .dll file location) is read by the plug-in when it is launched
  - This .ini file provides customization to the plug-in script so the user doesn't have to constantly adjust items in the code and recompile
  - E.g., things like if flash should be included by default, the available linacs, the calculation models, etc. all can be specified in this file
- See Section 7 below for more details on the functionality of the configuration settings
- A new tab has been added to the GUI to display the configuration parameters that were read by the plug-in script

Stand-alone executable revisions from v0.9:

- fixed minor bugs
- Added functionality to read-in a configuration file
  - Should be the same .ini file used to configure the plug-in script
  - The use can specify the default number of optimizations, plan objectives, plan normalization, etc. in this configuration file
- In this configuration file, the user can specify an arbitrary number of heater and cooler tuning structures that should be added during optimization
- The user can also specify appropriate conditions that must be met to add a particular heater/cooler structure (see Section 7 below for more details)

3 Publications

E. Simiele et al., ”A Step Toward Making VMAT TBI More Prevalent: Automating the Treatment Planning Process.” Practical radiation oncology, S1879-8500(21)00061-8 (2021), doi:10.1016/j.prro.2021.02.010

4 Introduction

The purpose of this document is to provide guidance for the VMAT TBI autoplanning scripts. Autoplanning for VMAT TBI is broken into two scripts: a binary plug-in that should be run from within Eclipse and a stand-alone executable that is designed to run outside of Eclipse (but access objects within). The reason for this design is because field placement in VMAT TBI is extremely important and needs to be reviewed and verified by the user before optimization as a single optimization loop can take up to 2 hours (at the time of writing). This document provides documentation for both the binary plug-in script and stand-alone executable application. The plug-in script focuses on generating tuning structures and target volumes, determining the appropriate number of isocenters and beams per isocenter, creating the VMAT and AP/PA plans (if AP/PA plan(s) is/are needed), setting the optimization and plan goals, and preparing the plan for treatment. The stand-alone executable is solely responsible for automating the optimization process where multiple optimizations are performed.

A video introducing VMAT TBI and the functionality of both scripts can be found at: `https://www.youtube.com/watch?v=q5xexSHzr0I&feature=share`

NOTE: THE ABOVE YOUTUBE VIDEO DEMONSTRATES OLDER SCRIPT VERSIONS. REFERENCE THIS DOCUMENT FOR THE MOST UP-TO-DATE SCRIPT VERSIONS!

4.1 Treatment regiments, plan goals, and optimization constraints

The binary plug-in script is designed to work with either template treatment regiments or free-form entry of the treatment setup. The template treatment regiments include: myeloablative (R_x = 1200 cGy), non-myeloablative (R_x = 200 cGy), and scleroderma trial (R_x = 800 cGy). The plan goals and optimization constraints for the non-myeloablative regime are shown in Tables I and II. Similarly, the plan goals and optimization constraints for the myeloablative and scleroderma trial regimens are shown in Tables III and IV and Tables V and VI, respectively.

The default structures spared for each treatment regiment are shown in Tables VII, VIII, and IX, respectively. When subtracting structures from the target PTV used for optimization, it is typical to include an additional margin, which is also indicated for the various structures in Tables VII, VIII, and IX. If the sparing type is set to ”Mean Dose < Rx Dose”, then this structure will be subtracted from the target. If the sparing type

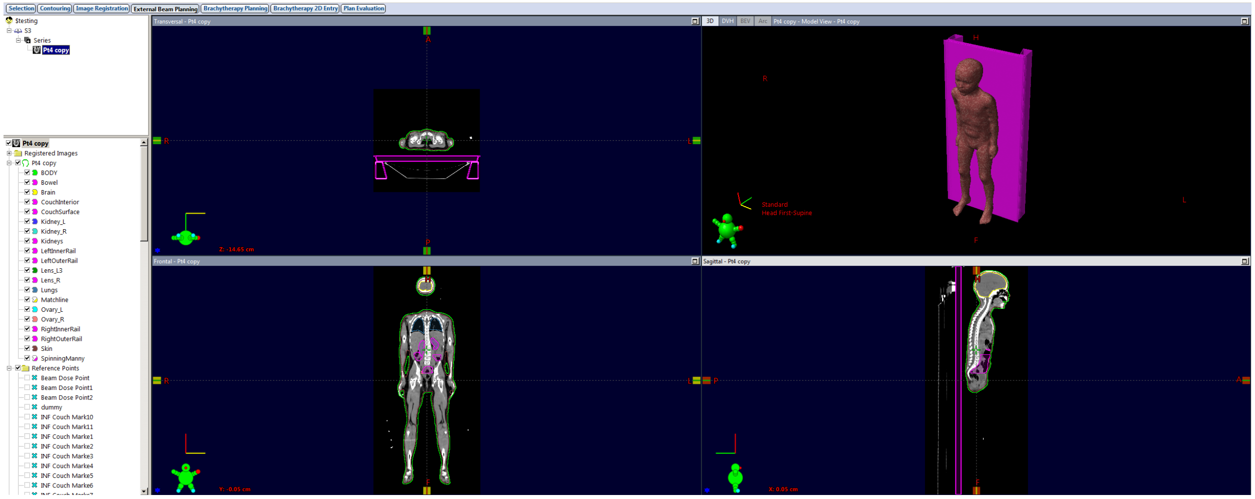


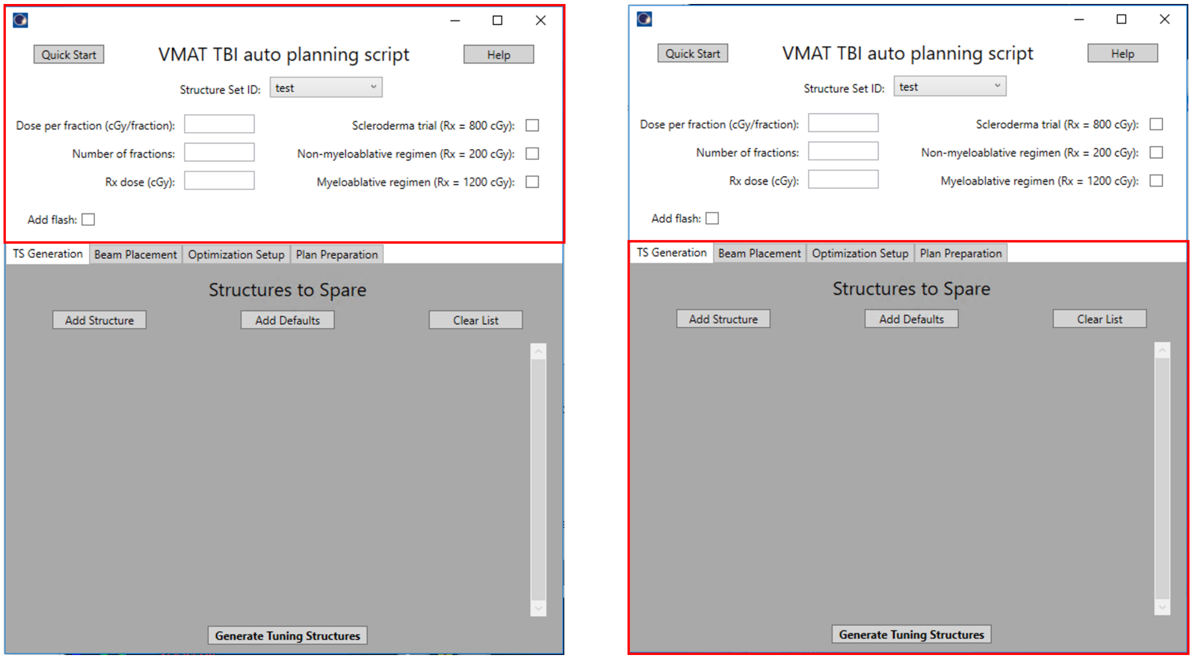
Figure 1: Initial setup for launching the VMAT TBI binary plug-in script.

is "Dmax ∼ Rx Dose", then this structure will NOT be subtracted from the target PTV, but optimization constraints will be applied to this structure to ensure the global hotspot is outside this structure. These template treatment regimens can be used as a base and modified/adjusted for each particular patient.

5 Binary plug-in script

5.1 Contouring/preparation

- Bring the patient CT scan into Aria and contour the relevant structures for this particular case (e.g., lungs, kidneys, etc.)
  - **NOTE: THIS SCRIPT IS LOOKING FOR COMBINED LEFT AND RIGHT STRUCTURES FOR GENERATING TUNING STRUCTURES! For example, the script is looking for 'Kidneys' rather than the individual left and right kidney structures**
  - **Be sure to union all left/right structures that you are interested in using to create tuning structures**
  - **NOTE: you do NOT need to manually create substructures (e.g., Kidneys-1cm), as the script will determine if it is appropriate to create and add these structures to the structure set**
  - **NOTE: the script is not sensitive to the case of the structure ID's**
- Once contouring has been completed, open the STRUCTURE SET in the External Beam Planning workspace (Figure 1)

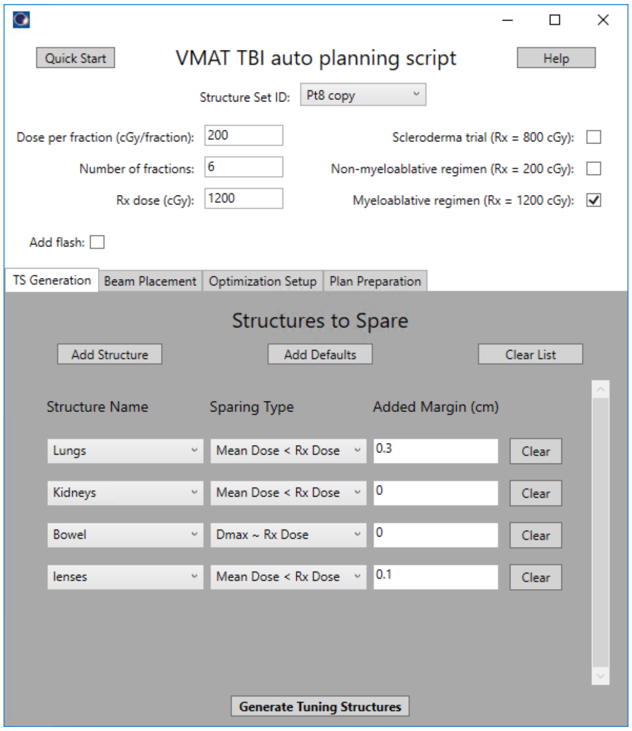

Quick Start
VMAT TBI auto planning script
Help
Structure Set ID: test
Dose per fraction (cGy/fraction):
Number of fractions:
Rx dose (cGy):
Scleroderma trial (Rx = 800 cGy): □
Non-myeloablative regimen (Rx = 200 cGy): □
Myeloablative regimen (Rx = 1200 cGy): □
Add flash: □
TS Generation
Beam Placement
Optimization Setup
Plan Preparation
Structures to Spare
Add Structure
Add Defaults
Clear List
Generate Tuning Structures
Quick Start
VMAT TBI auto planning script
Help
Structure Set ID: test
Dose per fraction (cGy/fraction):
Number of fractions:
Rx dose (cGy):
Scleroderma trial (Rx = 800 cGy): □
Non-myeloablative regimen (Rx = 200 cGy): □
Myeloablative regimen (Rx = 1200 cGy): □
Add flash: □
TS Generation
Beam Placement
Optimization Setup
Plan Preparation
Structures to Spare
Add Structure
Add Defaults
Clear List
Generate Tuning Structures

(a) (b)

Figure 2: a) The header and b) body of the GUI. In the header, the user can select the structure set of interest from all structure sets associated with the current patient and select the treatment regiment. The user can select one of the template treatment regiments or they can manually enter the prescription. The information contained in the header should remain constant throughout the use of the script. By default, the 'flash' option is selected to be included in the optimization (i.e., an additional user-defined margin added aroung the target solely used for optimization). See Section 5.7 for more details on including flash. If the user is confused or doesn't understand what certain warning messages mean, they can hit the help button, which will open this guide. In the body, the user can perform TS generation, beam placement, set optimization parameters, and perform plan preparation.

5.2 Tuning structure generation (TS Generation)

- Run the script 'VMATTBIautoPlan_vXX.dll'
- The two sections of the GUI, the header and body, are indicated in Figures 2a and 2b, respectively
- In the header of the GUI (Figure 2a), select a structure set from which to read and write structures
  - By default, the structure set in the current context will populate the Structure Set ID drop-down menu
- Select a treatment regiment if you want to use one of the templates. If not, you can manually enter the prescription
  - In this case, manually enter the dose per fraction (in cGy/fraction) and number of fractions
  - You can manually add the structures you want to spare one-by-one or you can hit the 'Add Defaults' button
- Hit the 'Add Defaults' button
  - If a template treatment regiment is selected, the script will scan the selected structure set for the default structures to spare (Tables VII, VIII, and IX)
  - If all the default structures are present and contoured in the selected structure set, the structures, sparing type, and added margin will populate in the 'TS Generation' tab (Figure 3)
  - If structures listed in the template are missing from the selected structure set, the script will inform you which structures are missing/the structures it can't find
  - Default structures can be specified in the .ini configuration file (Section 7) that will be added to the list, regardless of the selected options (including if a template treatment regiment is selected or not)
  - Currently, kidneys, Lungs, and Bowel are set as the default structures in the configuration list
- For finer control, select the 'Add Structure' button to add a blank structure to the list. The user can then select a structure contained within the selected structure set, select the sparing type for this structure, and enter an added margin
  - NOTE: the added margins are uniform margins
  - **NOTE: both positive and negative floating point values are accepted in the margin box. A positive margin means an outer margin and a negative margin means an inner margin**



Structure Set ID: Pt8 copy

Dose per fraction (cGy/fraction): 200

Number of fractions: 6

Rx dose (cGy): 1200

Scleroderma trial (Rx = 800 cGy): □

Non-myeloablative regimen (Rx = 200 cGy): □

Myeloablative regimen (Rx = 1200 cGy): ☑

Add flash: □

Structure Name	Sparing Type	Added Margin (cm)
Lungs	Mean Dose < Rx Dose	0.3
Kidneys	Mean Dose < Rx Dose	0
Bowel	Dmax ~ Rx Dose	0
lenses	Mean Dose < Rx Dose	0.1

Figure 3: Example list of the requested structures to spare including the structure name, sparing type, and added margin in cm. This is the default structures to spare for the myeloablative regiment (Table VIII) with the brain structure also added.

- NOTE: if the sparing type is set to ”Dmax $\sim$ Rx Dose” for a particular structure, the textbox for the ’Added Margin (cm)’ box will disappear as this value is not used for this sparing type

- If you don’t need to spare one of the structures in the current structure sparing list, you can remove it by simply hitting the ’Clear’ button

- If you are unhappy with the entire list of structures, you can hit the ’Clear List’ button to clear the entire list. You can then re-add structures one-by-one using the ’Add Structure’ button or use the ’Add Defaults’ button to pre-populate the list

- Once you are satisfied with the structure sparing parameter list, hit the ’Generate Tuning Structures’ button
  - **WARNING: IF THE SELECTED STRUCTURE SET IS REFERENCED IN OTHER PLANS THAT HAVE DOSE CALCULATED, THE SCRIPT WILL NOT BE ABLE TO MODIFY EXISTING CONTOURS!**
  - **YOU MUST RESET THE CALCULATION MATRIX IN THOSE PLANS FOR THE SCRIPT TO PROPERLY GENERATE TUNING STRUCTURES!**
  - This button will prompt the script to read-in the structure sparing parameter list and perform preliminary checks before generating the tuning structures. Such checks include if the user origin was set, if the height of the patient $>$ 116.0 cm was there a matchline contour, etc.
  - If one of the preliminary checks did not pass, a warning message will pop up and indicate there is a problem that should be fixed
  - Certain checks can be overridden by the user. If a warning message pops up and asks if you want to continue, you can override this interlock (e.g., if a patient height is 116.1 cm, we can choose to treat with VMAT only and override the interlock looking for the matchline contour)
  - Other checks cannot be overridden, such as not setting the user origin, because other properties of the planning process depend on these items being set
  - If all the preliminary checks passed (or are overridden), the tuning structures will be created and contoured
  - NOTE: If the patient has a matchline, the generation of the tuning structures may take some time. **Be patient!**

- If tuning structure generation was successful, a message will pop up indicating that structure generation was successful and the user can proceed to the Beam Placement tab

- **Don’t close the script yet!**

- See Section 5.7 for more details on including flash as there are some peculiarities with this feature

5.3 Beam Placement

- The Beam Placement tab when the script is first launched is shown in Figure 4a. After successful completion of generating the tuning structures, the Beam Placement tab will appear similar to Figure 4b
- During generation of the tuning structures, the script checks the height of the patient to determine if the spinning manny couch (or a matchline contour) should be present. From the determined height of the patient, the script calculates the required number of isocenters to cover the patient and if the plan should be VMAT-only or VMAT with AP/PA on the legs
  - The script automatically handles both types of TBI plans
  - The script automatically handles if the user wants to include flash in the optimization (or not)
  - From the calculated number of isocenters, the script also suggests names for each isocenter (contained between the '<>' in Figure 4b). These isocenter names will automatically be propagated to the generated plan(s) and beams
  - From the list of structures the user wants to spare, the script also proposes the number of beams that should be used for each isocenter. This number can be adjusted by the user if they want more or fewer beams at each isocenter (max number of fields per isocenter = 4)
  - NOTE: the number of beams per isocenter for the AP/PA isocenters <u>cannot</u> be adjusted
- Select the treatment machine and beam energy for all VMAT fields
  - The available treatment machines and beam energies that can be selected should be specified in the .ini configuration file
  - The beam energy for the AP/PA fields will always be set to 6X
- If you want to ensure coverage in the overlap region between fields in adjacent isocenters, you can select the 'Contour overlap between VMAT isocenters' option on the Beam Placement tab
  - When selected, another textbox will pop up asking for an additional margin. By default, an additional margin of 1.0 cm (can be adjusted in the configuration file) is applied to the overlap region to provide additional coverage
- If you are satisfied with the proposed number of isocenters and beams per isocenter, hit the 'Place Beams' button
  - This will prompt the script to read-in the number of beams per isocenter and store this information for use during plan generation

  - The script will determine if the patient has an existing course named 'VMAT TBI'. If so, it will load this course and check if a plan named '_VMAT TBI' exists in this course. If so, the script will throw an error message as ESAPI cannot remove external beam plans in the clinical system. If the course does not exist, the script will create it.
  - The script will add a plan named '_VMAT TBI' to the 'VMAT TBI' course. If this patient also requires AP/PA plans of the legs, an additional plan named '_AP/PA Legs' will also be added to the same course
    - From version 1.3, if there are two AP/PA isocenters, the script will ask if you want to put these isocenters into one plan or into separate plans
  - The isocenter separation will then be calculated based on the height of the TS_PTV_VMAT or TS_PTV_FLASH (if flash was included) structure. If the calculated isocenter separation is > 38.0 cm, the script will ask the user if they want to truncate the isocenter separation to 38.0 cm.
  - **A separation of 38.0 cm ensures there is at least 2.0 cm overlap between fields in adjacent isocenters**
  - If a patient requires an AP/PA plan(s) of the legs, the isocenter separation between the isocenters adjacent to the matchline will automatically be set to 38.0 cm

- If beam placement is successful, a warning message will appear telling the user beam placement was successful and they can proceed to the Optimization Setup tab
  - If the patient is large, a warning message might pop up indicating that there is < 0.5 cm margin at the most-superior and inferior portions of the patient. In this case, review the beam placement carefully as it is possible that portions of the target might not be covered during optimization

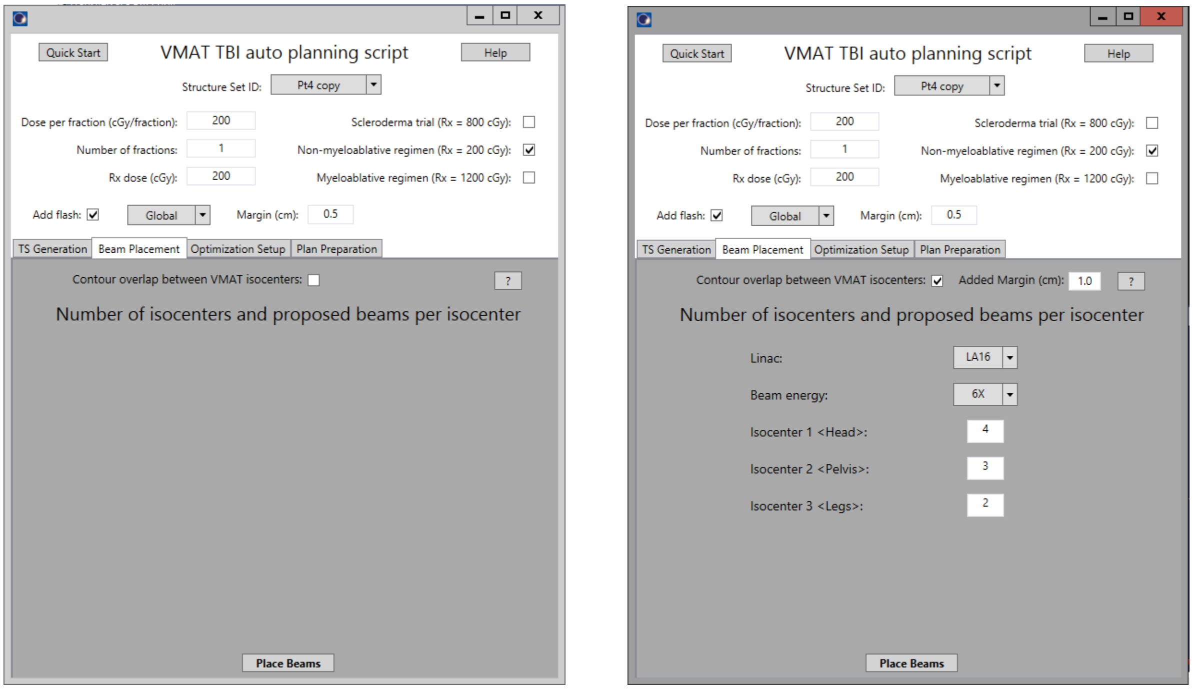
- At this point, you can exit this script or proceed to the Optimization Setup tab

5.4 Optimization Setup

- The Optimization Setup tab is shown in Figure 5a. After successfully generating the plans and placing the beams, the Optimization Setup tab will appear similar to Figure 5b

- During generation of the tuning structures, the script determines what structures the user wants to spare and what tuning structures need to be added to the structure set
  - This includes if the user wants to incorporate additional flash into the optimization

- From this information, the script assigns optimization objectives to each of these structures based on templates for each specific treatment regiment. If no treatment regiment is selected, a generic template will be applied



VMAT TBI auto planning script

Structure Set ID: Pt4 copy

Dose per fraction (cGy/fraction): 200

Number of fractions: 1

Rx dose (cGy): 200

Scleroderma trial (Rx = 800 cGy): □

Non-myeloablative regimen (Rx = 200 cGy): ☑

Myeloablative regimen (Rx = 1200 cGy): □

Add flash: ☑ Global Margin (cm): 0.5

Contour overlap between VMAT isocenters: □

Number of isocenters and proposed beams per isocenter

(a)

VMAT TBI auto planning script

Structure Set ID: Pt4 copy

Dose per fraction (cGy/fraction): 200

Number of fractions: 1

Rx dose (cGy): 200

Scleroderma trial (Rx = 800 cGy): □

Non-myeloablative regimen (Rx = 200 cGy): ☑

Myeloablative regimen (Rx = 1200 cGy): □

Add flash: ☑ Global Margin (cm): 0.5

Contour overlap between VMAT isocenters: ☑ Added Margin (cm): 1.0

Number of isocenters and proposed beams per isocenter

Linac: LA16

Beam energy: 6X

Isocenter 1 <Head>: 4

Isocenter 2 <Pelvis>: 3

Isocenter 3 <Legs>: 2

(b)

Figure 4: a) The Beam Placement tab when the script is initially launched and b) after successful completion of tuning structure generation. During tuning structure generation, the script calculates the required number of isocenters (based on the height of the patient) and the required number of beams per isocenter based on the structures the user wants to spare.

  - The optimization objectives for each treatment template and the generic template are fully customizable in the .ini configuration file (Section 7)

- The determined optimization objectives are displayed to the user in the Optimization Setup tab following the successful generation of the tuning structures. The intent here, is for the user to review all of the optimization objectives and adjust the constraints as they see fit

- Once the user is satisfied with the optimization objectives, they can hit the 'Set Optimization Constraints' button. This will assign the optimization objectives in the list to the '_VMAT TBI' plan.

- Upon successful assignment of the optimization objectives, a warning message (similar to Figure 6) will be displayed indicating the user needs to exit the script then review the generated tuning structures, placed isocenters and beams, and the assigned optimization objectives

- After reviewing the properties of the generated plans, hit the save button in Eclipse to save the changes to the patient. If you are unsatisfied with the produced plan, you can remove all changes by hitting the reload button in Eclipse

  - binary plug-in scripts cannot save changes to the database, the user must do this manually

- Example final output from the script for a VMAT-only patient (Figure 1) is shown in Figure 7

5.4.1 Alternative path to set optimization objectives

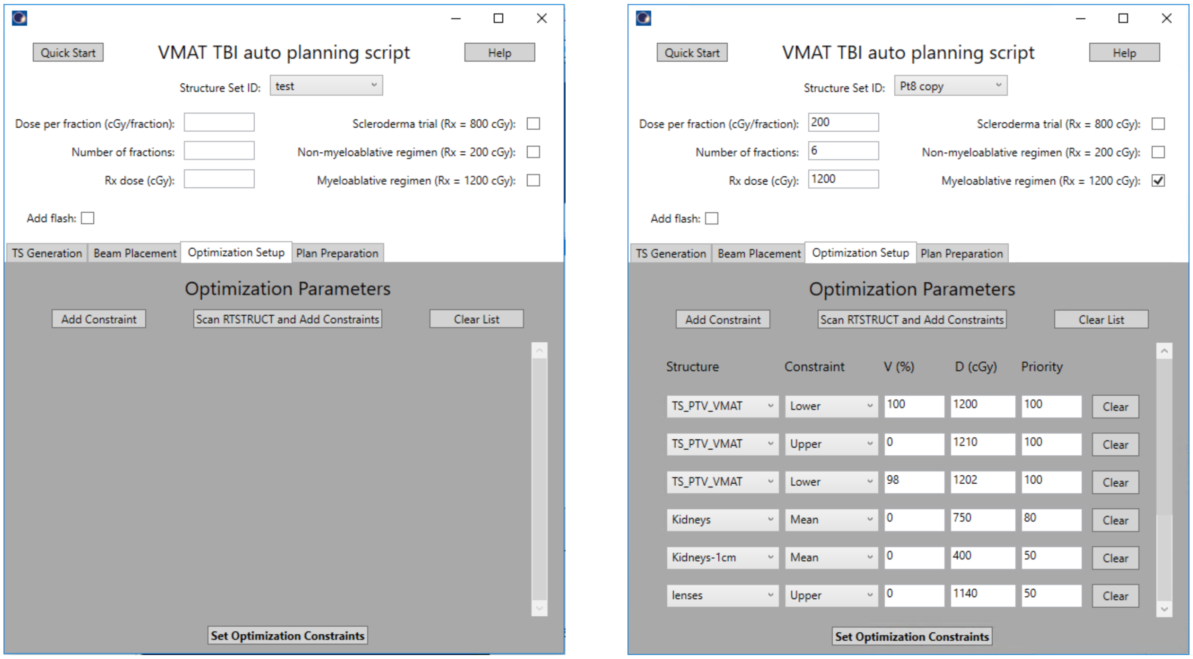
- If you previously generated the tuning structures, placed the isocenters and beams, then exited the script to review your work, you DON'T have to repeat the entire process to get to the Optimization Setup tab

- If you have previously generated the tuning structures using this script, you can proceed directly to the Optimization Setup tab. It will look like Figure 5a

- Select a treatment regiment or manually enter a prescription

- **NOTE: IF YOU INTEND TO INCLUDE FLASH IN THE OPTIMIZATION, YOU NEED TO ENSURE THE 'Add flash' CHECK BOX IS CHECKED! OTHERWISE, IT WILL ASSIGN THE WRONG STRUCTURE AS THE TARGET FOR OPTIMIZATION!**

- You can then hit the 'Scan RTSTRUCT and Add Constraints' button. The script will scan the selected structure set for structures of interest and, if it finds them, it will assign optimization objects based on the template constraints for the selected treatment regiment



Structure Set ID: test

Dose per fraction (cGy/fraction):

Number of fractions:

Rx dose (cGy):

Scleroderma trial (Rx = 800 cGy): □

Non-myeloablative regimen (Rx = 200 cGy): □

Myeloablative regimen (Rx = 1200 cGy): □

Add flash: □

(a)

Structure Set ID: Pt8 copy

Dose per fraction (cGy/fraction): 200

Number of fractions: 6

Rx dose (cGy): 1200

Scleroderma trial (Rx = 800 cGy): □

Non-myeloablative regimen (Rx = 200 cGy): □

Myeloablative regimen (Rx = 1200 cGy): ☑

Add flash: □

Structure	Constraint	V (%)	D (cGy)	Priority	
TS_PTV_VMAT	Lower	100	1200	100	Clear
TS_PTV_VMAT	Upper	0	1210	100	Clear
TS_PTV_VMAT	Lower	98	1202	100	Clear
Kidneys	Mean	0	750	80	Clear
Kidneys-1cm	Mean	0	400	50	Clear
lenses	Upper	0	1140	50	Clear

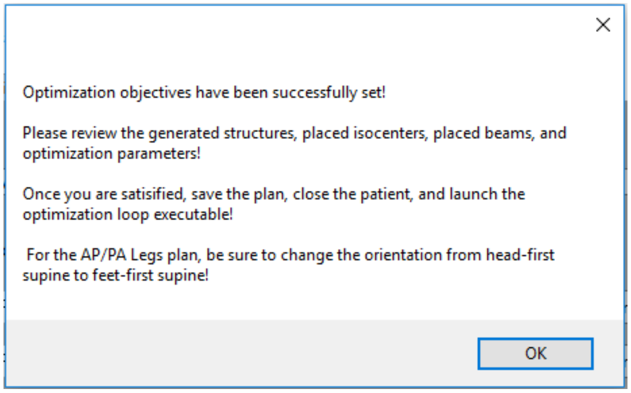
(b)

Figure 5: a) The Optimization Setup tab when the script is initially launched and b) after successful generation of the tuning structures. From generating the tuning structures, the script determines which structures the user wants to spare/target, creates a lists of optimization constraints for these structures from a template, and displays them to the user so they can review the various constraints. Each constraint can be adjusted individually and additional constraints can be added if necessary.

- The script will then display the generated optimization objectives for the user to review
- When you hit the Set Optimization Constraints button, the script will look for the '_VMAT TBI' plan in the 'VMAT TBI' course. If either of these items are missing, the script will throw an error message

5.5 Plan preparation

- The Plan Preparation tab of the GUI was added to assist the user with preparation of the plan for treatment including separation of the combined VMAT plan into separate plans, generating setup fields, creating a plan sum, etc.
- Currently, the functionality is limited due to limitations in ESAPI v15.6. The available functions include generating the shift note for the plan (this automatically handles if there is a/are separate AP/PA plan(s) for the legs), separating the isocenters into separate plans, and recalculating the dose for each separated plan



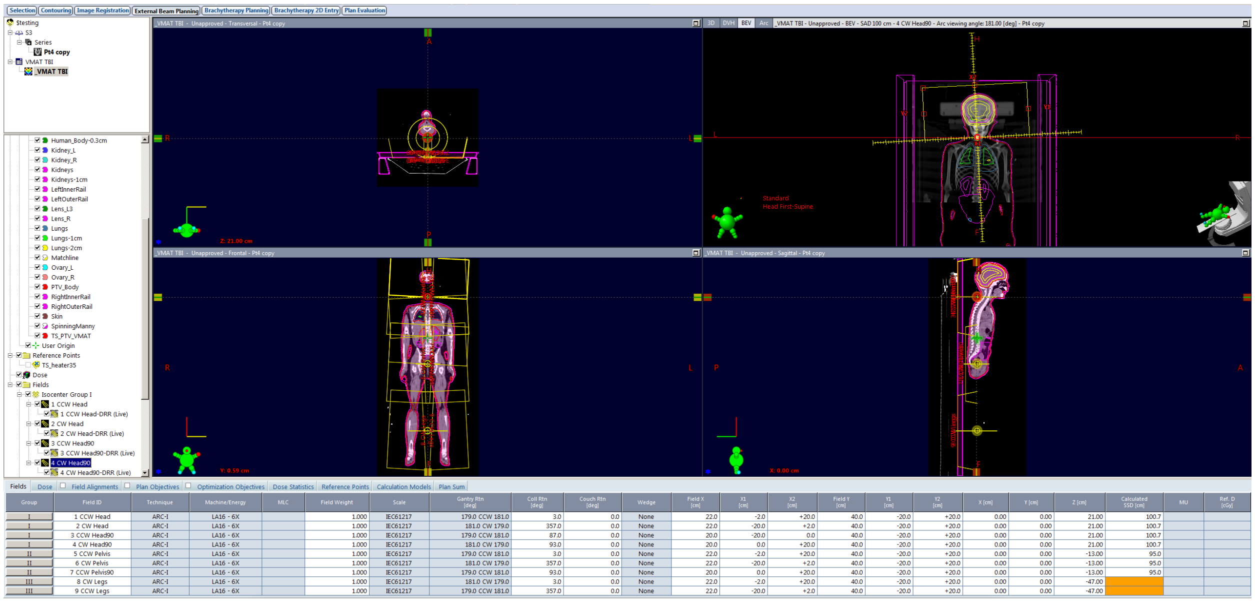
Optimization objectives have been successfully set!

Please review the generated structures, placed isocenters, placed beams, and optimization parameters!

Once you are satisified, save the plan, close the patient, and launch the optimization loop executable!

For the AP/PA Legs plan, be sure to change the orientation from head-first supine to feet-first supine!

Figure 6: Success message following the successful completion of tuning structure generation, plan creation, beam placement, and optimization constraints assignment.



Group	Field ID	Technique	Machine/Energy	MLC	Field Weight	Scale	Gantry Rtn [deg]	Coll Rtn [deg]	Couch Rtn [deg]	Wedge	Field X [cm]	X1 [cm]	X2 [cm]	Field Y [cm]	Y1 [cm]	Y2 [cm]	X [cm]	Y [cm]	Z [cm]	Calculated SSD [cm]	MU	Ref. D [cGy]
I	1 CCW Head	ARC-I	LA16 - 6X		1.000	IEC61217	179.0 CCW 181.0	3.0	0.0	None	22.0	-2.0	+20.0	40.0	-20.0	+20.0	0.00	0.00	21.00	100.7		
I	2 CW Head	ARC-I	LA16 - 6X		1.000	IEC61217	181.0 CW 179.0	357.0	0.0	None	22.0	-20.0	+2.0	40.0	-20.0	+20.0	0.00	0.00	21.00	100.7		
I	3 CCW Head90	ARC-I	LA16 - 6X		1.000	IEC61217	179.0 CCW 181.0	87.0	0.0	None	20.0	-20.0	0.0	40.0	-20.0	+20.0	0.00	0.00	21.00	100.7		
I	4 CW Head90	ARC-I	LA16 - 6X		1.000	IEC61217	181.0 CW 179.0	93.0	0.0	None	20.0	0.0	+20.0	40.0	-20.0	+20.0	0.00	0.00	21.00	100.7		
II	5 CCW Pelvis	ARC-I	LA16 - 6X		1.000	IEC61217	179.0 CCW 181.0	3.0	0.0	None	22.0	-2.0	+20.0	40.0	-20.0	+20.0	0.00	0.00	-13.00	95.0		
II	6 CW Pelvis	ARC-I	LA16 - 6X		1.000	IEC61217	181.0 CW 179.0	357.0	0.0	None	22.0	-20.0	+2.0	40.0	-20.0	+20.0	0.00	0.00	-13.00	95.0		
II	7 CCW Pelvis90	ARC-I	LA16 - 6X		1.000	IEC61217	179.0 CCW 181.0	93.0	0.0	None	20.0	0.0	+20.0	40.0	-20.0	+20.0	0.00	0.00	-13.00	95.0		
III	8 CW Legs	ARC-I	LA16 - 6X		1.000	IEC61217	181.0 CW 179.0	3.0	0.0	None	22.0	-2.0	+20.0	40.0	-20.0	+20.0	0.00	0.00	-47.00			
III	9 CCW Legs	ARC-I	LA16 - 6X		1.000	IEC61217	179.0 CCW 181.0	357.0	0.0	None	22.0	-20.0	+2.0	40.0	-20.0	+20.0	0.00	0.00	-47.00			

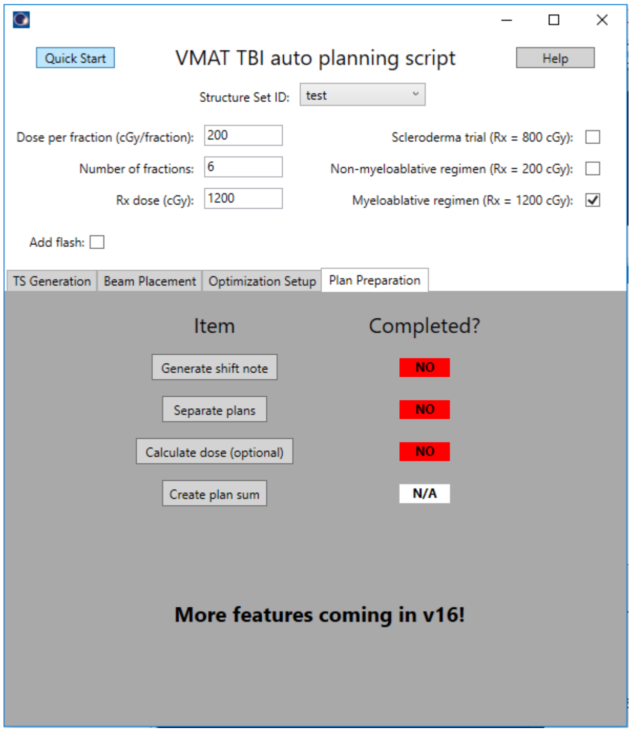
Figure 7: Output from the VMAT TBI autoplanning binary plug-in script.

- Hitting the 'Generate shift note' button does what it says on the box. Once the shift note has been copied to the clipboard, paste it into the excel spreadsheet containing the shift information for the plan and into a journal note
- Hitting the separate plans button will separate the '_VMAT TBI' and '_Legs' plans (if applicable) into separate plans for each isocenter.
  - If there are multiple plans in the VMAT TBI course with IDs not equal to '_Legs', the script will prompt you to select the final VMAT plan that should be prepared for treatment
  - The script can handle the case where the Legs plan was previously separated into two plans (to make dose calculation easier)
  - **NOTE: YOU WILL NEED TO MANUALLY SET THE PRIMARY REFERENCE POINT AND TARGET STRUCTURE IN EACH OF THE SEPARATED PLANS AS ESAPI V15.6 DOES NOT ALLOW YOU TO SET THESE PLAN PROPERTIES**
  - Hitting this button will also check if you opted to include flash in the optimization (specifically, it looks for the keyword "flash" in the structure IDs). If it finds any structures with this keyword, it will ask if you want to remove these structures (it will automatically reset the body contour to what it was before flash was added)
    - ∗ If you chose to remove the flash structures, the existing calculated dose in this plan and any other plans that reference this structure set will need to be cleared. A calculate dose button will appear in this case
    - ∗ Hitting this button is optional, but it recalculates dose for each plan that it had to clear the dose from IN THE CURRENT COURSE ONLY! If you hit this button, the dose recalculation will take some time as each plan is calculated sequentially. However, it is a nice excuse to take a coffee break while it is calculating :)
- The rest of the desired functionality (e.g., create a plan sum) is not currently present in Eclipse v15.5, but was introduced in v16.0.
- These features will be added once the upgrade to v16.0 or greater has been completed

---

5.6 Some notes about the Scleroderma trial treatment regiment

- There are some unique items about Scleroderma trial patients that require special attention
- For this treatment regiment, block volumes are needed for both the lungs and kidneys where these volumes are generated using asymmetric margins. Furthermore, it is these block volumes that are subtracted from the body contour rather than the actual lung or kidney contours themselves



Structure Set ID: test

Dose per fraction (cGy/fraction): 200

Number of fractions: 6

Rx dose (cGy): 1200

Scleroderma trial (Rx = 800 cGy): □

Non-myeloablative regimen (Rx = 200 cGy): □

Myeloablative regimen (Rx = 1200 cGy): ☑

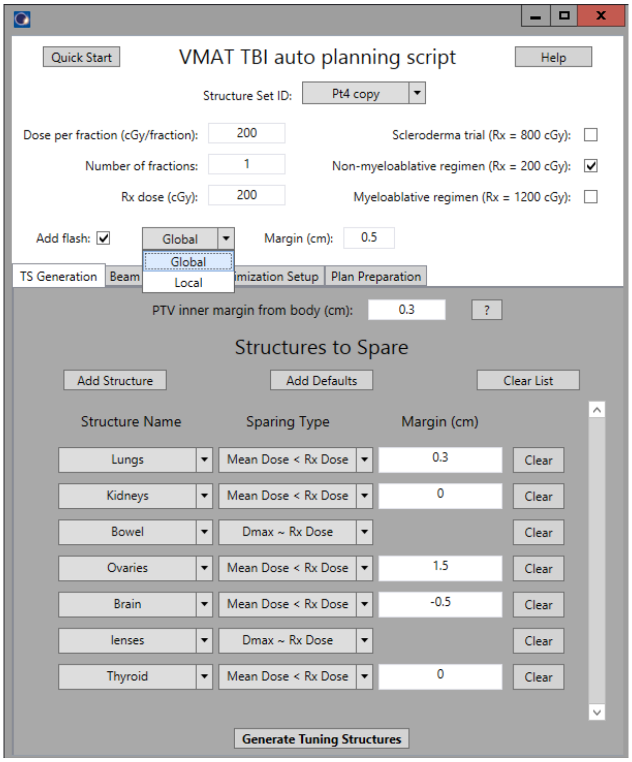
Add flash: □

Item	Completed?
Generate shift note	NO
Separate plans	NO
Calculate dose (optional)	NO
Create plan sum	N/A

More features coming in v16!

Figure 8: The Plan Preparation tab of the GUI. The rest of this functionality will be added when Eclipse is upgraded to v16 or later.

- **NOTE: THE USER DOES NOT NEED TO MANUALLY CONTOUR THESE STRUCTURES! THE SCRIPT WAS DESIGNED TO CREATE THESE STRUCTURES IF THE SCLERODERMA TRIAL TREATMENT REGIMENT WAS SELECTED AND THE LUNGS AND KIDNEYS WERE ADDED TO THE STRUCTURE SPARING LIST**
  - To generate these structures using the script, you need to contour the combined lungs and combined kidneys volumes (same as above)
  - On the TS Generation tab, add the combined lungs and kidneys volumes as structures to spare with the sparing type set to ”Mean Dose < Rx Dose”. The script will then automatically generate the block volumes for these structures
  - If the Scleroderma trial checkbox is selected, the script will ignore the values entered into the ’Added Margin (cm)’ box for the lungs and kidneys volumes
  - Do to the unique nature of this treatment regiment, it is strongly recommended for all Scleroderma trial patients that the Scleroderma trial checkbox be selected to ensure the script properly generates the required tuning structures and optimization constraints



VMAT TBI auto planning script

Structure Set ID: Pt4 copy

Dose per fraction (cGy/fraction): 200

Number of fractions: 1

Rx dose (cGy): 200

Scleroderma trial (Rx = 800 cGy): □

Non-myeloablative regimen (Rx = 200 cGy): ☑

Myeloablative regimen (Rx = 1200 cGy): □

Add flash: ☑ Global

Margin (cm): 0.5

PTV inner margin from body (cm): 0.3

Structures to Spare

Structure Name	Sparing Type	Margin (cm)
Lungs	Mean Dose < Rx Dose	0.3
Kidneys	Mean Dose < Rx Dose	0
Bowel	Dmax ~ Rx Dose	
Ovaries	Mean Dose < Rx Dose	1.5
Brain	Mean Dose < Rx Dose	-0.5
lenses	Dmax ~ Rx Dose	
Thyroid	Mean Dose < Rx Dose	0

Figure 9: Available options for including flash in the optimization. This option is selected by default with a 0.5 cm margin with the flash type set to Global.

5.7 Some notes on including FLASH in the optimization

- The user can elect to include ”flash” in the optimization by checking the ’Add flash’ checkbox. Once this box is checked, a drop-down menu and an added margin textbox will appear in the GUI as shown in Figure 9.
  - As of v1.1, the margins are UNIFORM! This might be adjusted in the future. Note: only positive floating point values between 0.0 and 5.0 (units of cm) are accepted
- By default, the ”flash type” is set to GLOBAL. This means the original body structure will be used to create flash
- The flash type can alternatively be set to LOCAL. For this case, another drop-down menu will apear on the GUI prompting the user to select which structure they want to use to create flash
  - This is useful for the case where you want to create flash in only one region of the body (e.g., arms)
  - NOTE: If the resulting bolus structure has null volume, the script will thrown an warning and exit (it won’t crash). At this point, you should reload the patient data and try again with a larger margin or increase the size of the contour used to create flash
- Once the flash parameters have been set and the ’Generate Tuning Structures’ button is hit, the script will go through the normal process of generating the tuning structures (which is why you will still end up with PTV_BODY, TS_PTV_VMAT, an TS_PTV_LEGS volumes)
- The add flash feature resides as a separate subroutine within the TS generation class that is executed AFTER the original tuning structures are generated
  - **WARNING! EACH OF THE STRUCTURES CREATED FROM THIS SUBROUTINE HAVE THE KEYWORD ’FLASH’ IN THEIR ID! THIS IS IMPORTANT FOR PROPER FUNCTIONING OF THIS SCRIPT AND OF THE OPTIMIZATION LOOP EXECUTABLE! DO NOT CHANGE THE IDs OF THE CREATED FLASH STRUCURES!**
  - The first structure the script will create is ’bolus_flash’ (pretty self-explanatory). The HU value for this structure is automatically set to 0.0
  - Next, the body structure is union-ed with bolus_flash
  - Once the new body structure has been created, the script will go through the process of generating the target structures for the new body structure
  - The new target structures are called: TS_FLASH_TARGET (analogous to PTV_BODY), TS_PTV_FLASH (analogous to TS_PTV_VMAT), and (if applicable) TS_LEGS_FLASH (analogous to TS_PTV_LEGS).

- **NOTE: FOLLOWING FLASH GENERATION, THE 'Human_Body' STRUCTURE IS A COPY OF THE ORIGINAL BODY STRUCTURE (PRE-FLASH). DO NOT DELETE THIS STRUCTURE AS IT WILL BE USED LATER DURING PLAN PREPARATION!**

- **IF SOMETHING GOT MESSED UP WITH THE SCRIPT, BE SURE TO PASTE THIS STRUCTURE OVER THE BODY STRUCTURE BEFORE RUNNING THE SCRIPT AGAIN! OTHERWISE, YOU RISK ADDING FLASH TWICE!**

- When the executable is run, it checks for the keyword 'flash' in the structure IDs. If it finds that keyword in ANY of the structures, it assumes you want to use flash and will make adjustments accordingly (the executable will provide an FYI in the progress window that it assumes you want to include flash)

- See the below documentation for the executable (Program flow section) to see the specific adjustments that are made to the program flow

- Once the you have an optimized plan, physician verbal approval for the plan, and intend to prepare the plan for final physician review and approval, open the _VMAT TBI plan in Eclipse and launch the plug-in script

- Proceed to the Plan preparation tab and follow the buttons from top to bottom to prepare the plan. The 'Separate plans' button will automatically look for structures used to generate flash in the plan

  - **YOU DO NOT NEED TO DO ANY MANUAL CLEANUP OF THESE STRUCTURES BEFORE PREPARING THE PLAN! THE SCRIPT CAN AUTOMATICALLY REMOVE THESE STRUCTURES AND RESET THE BODY STRUCTURE TO WHAT IT WAS BEFORE GENERATING FLASH!**

5.8 Known issues and bugs

The following are known issues with the script:

- If a structure has a DICOM type of 'NONE' (see structure –> properties), the script will NOT be able to remove this structure from the structure set, which impacts the tuning structure generation

- As mentioned in Section 2.2, if the selected structure set is referenced by a plan that has calculated dose, no modifications can be made to the structure set

- The script is setup to place a maximum of five isocenters (three VMAT isocenters and two AP/PA isocenters)

  - However, both the executable and the plan preparation functions of the plug-in script can accommodate a 6th isocenter (e.g., if the user needed to add a 6th isocenter to ensure coverage after using the plug-in script)

Known limitations in ESAPI v15.5 (limits the functionality of the script):

- It is not possible to set the target volume ID in a newly created plan in ESAPI v15.5 (fixed in v16.0)
- It is not possible to assign a primary reference point in a newly created plan in ESAPI v15.5. A primary reference point is automatically created and can't be changed (fixed in v16.0)
- It is not possible to assign a base dose plan for optimization in the script in ESAPI v15.5 (fixed in v16.0)
- It is not possible to create setup fields for plans in ESAPI v15.5 (fixed in v16.0)
- It is not possible to create or remove plan sums from the script in ESAPI v15.5 (fixed in v16.0)
- It is not possible to assign plan goals for plans in ESAPI v15.5
- It is not possible to remove the automatic normal tissue objective (NTO) in optimization in ESAPI v15.5. However, the script does not remove the NTO, but assigns the priority to 0
- It is not possible to set a MU objective for optimization in ESAPI v15.5
- It is not possible to set the patient orientation for a plan in ESAPI v15.5. This impacts the generation of the '_AP/PA Legs' plan as the patient will always be oriented head-first supine. To fix, the user will have to set the patient orientation manually
  - **DO NOT ADJUST THE JAW/FIELDS AS THEY ALREADY TAKE THIS ISSUE INTO ACCOUNT!**

5.9 Planned features for future releases

- Option to change the number of isocenters
- Option to skip TS Generation and proceed directly to Beam Placement (for the case where the tuning structures have already been created)

6 Stand-alone executable

This is the second half of the auto planning script that focuses on performing multiple optimizations to obtain a clinically acceptable plan.

6.1 Main program GUI

- Launch the program 'VMATTBI_optLoopMT_vXX.exe', which should be on your desktop
- The UI when the stand-alone executable is first launched is shown in Figure 10a. It should look familiar to the UI of the binary plug-in script (Figure 2a)
- The UI in this script was designed to be relatively rigid where the user can review and make adjustments to the plan optimization parameters
- **You cannot modify the plan prescription in this program!**
- To begin, open a patient by entering the MRN in the 'Patient MRN:' box and hitting the 'Open Patient' button
  - **NOTE: THE SCRIPT IS LOOKING FOR A PLAN NAMED '_VMAT TBI' CONTAINED IN A COURSE NAMED 'VMAT TBI'!**
  - **IF THE PATIENT DOES NOT HAVE EITHER OF THESE, THE PROGRAM <u>WILL NOT</u> FIND THE PLAN!**
  - If the script can't find the entered MRN, the script will throw a warning
  - If the script finds the patient associated with the entered MRN (with a VMAT TBI plan), the GUI will look similar to Figure 10b
- From Figure 10b, you can:
  - choose to run a coverage check before the optimization loop
    - This is an optimization with no intermediate dose where all optimization objective priorities are set to zero except for the target objective (i.e., if we are jsut trying to cover the target, how well can we do it?). If the global hotspot is $>$ 140%, that indicates we are missing part of the target
  - adjust any of the optimization constraints, which were read from the '_VMAT TBI' plan in the 'VMAT TBI' course
  - adjust the maximum number of optimizations that will be performed
  - choose to perform an additional optimization to reduce the plan hotspots
    - **This optimization is performed <u>AFTER</u> the main optimization loop**

  - select whether the script should save each optimized plan. This option copies the resulting plan from each optimization iteration and saves it to the VMAT TBI course with the name ”opt itr <count>” where <count> is the current optimization iteration
    - * This is useful if you want to see how the optimization is progressing with each iteration. In addition, it also gives you multiple plans to choose from to do final adjustments (I've noticed cases where the plan from the second optimization had some better qualities than the plan from the third optimization)

- If you elected to include additional flash in the optimization (from the binary plug-in script), you <u>DON'T</u> need to do anything. The script automatically detects if you want to include flash will make adjustments accordingly

- If there were no optimization constraints stored in the '_VMAT TBI' plan, you can add them manually, however, it is recommended that you close this script and use the binary plug-in script described above to set the optimization constraints

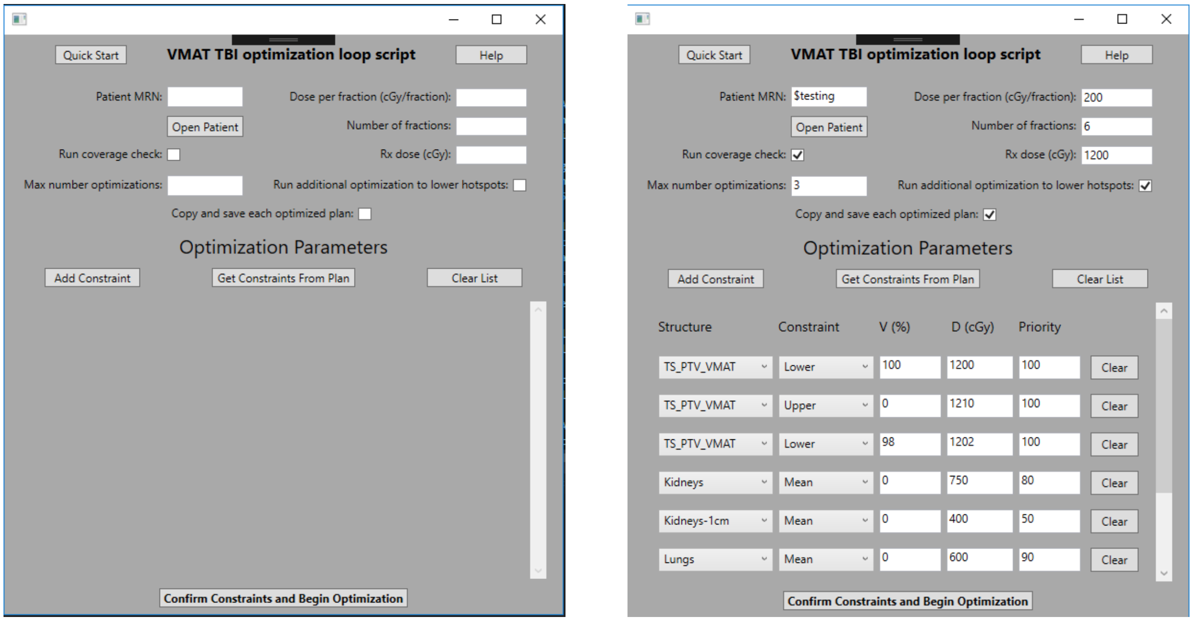
- Once you are satisfied with the constraints, hit the 'Confirm Constraints and Begin Optimization' button to start the optimization loop

6.2 Optimization loop GUI

- The UI when the optimization loop is started is shown in Figure 11a. The UI was designed to inform the user of the progress of the optimization loop and how the program is adjusting the optimization constraints after each iteration (Figure 11b)

- The status of the program is represented as 'Running', 'Canceling', 'Aborted', 'Failed', or 'Finished' as shown in the text box in the bottom left of Figure 11.

- The user has the option the abort the optimization loop using the 'Abort' button in the bottom left of Figure 11. This will tell the program the user wants to stop the optimization loop
  - **NOTE: THE PROGRAM WILL (LIKELY) NOT STOP IMMEDIATELY WHEN YOU HIT THE 'ABORT' BUTTON! THIS IS BECAUSE THE PROGRAM IS TIED UP IN PERFORMING A COMPUTATIONALLY EXPENSIVE TASK IN ECLIPSE (e.g., DOSE CALCULATION) AND THERE IS NO SAFE WAY OF TERMINATING THAT PROCESS IN THE API**
  - **<u>BE PATIENT!</u> THE PROGRAM IS ROUTINELY CHECKING IF THE USER WANTS TO STOP THE OPTIMIZATION LOOP AND WILL TERMINATE WHEN AN ACCEPTABLE STOPPING POINT HAS BEEN REACHED**


Quick Start
VMAT TBI optimization loop script
Help
Open Patient
Optimization Parameters
Add Constraint
Get Constraints From Plan
Clear List
Confirm Constraints and Begin Optimization

(a)

Patient MRN:

Dose per fraction (cGy/fraction):

Number of fractions:

Rx dose (cGy):

Run coverage check: □

Max number optimizations:

Run additional optimization to lower hotspots: □

Copy and save each optimized plan: □

(b)

Patient MRN: $testing

Dose per fraction (cGy/fraction): 200

Number of fractions: 6

Rx dose (cGy): 1200

Run coverage check: ☑

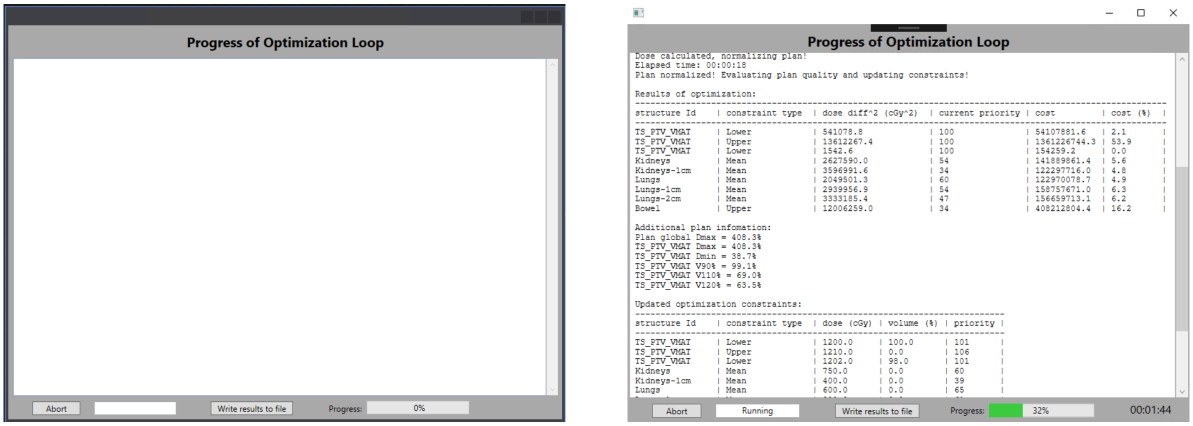
Max number optimizations: 3

Run additional optimization to lower hotspots: ☑

Copy and save each optimized plan: ☑

Structure	Constraint	V (%)	D (cGy)	Priority	
TS_PTV_VMAT	Lower	100	1200	100	Clear
TS_PTV_VMAT	Upper	0	1210	100	Clear
TS_PTV_VMAT	Lower	98	1202	100	Clear
Kidneys	Mean	0	750	80	Clear
Kidneys-1cm	Mean	0	400	50	Clear
Lungs	Mean	0	600	90	Clear

Figure 10: The GUI for the stand-alone executable when a) the program is first launched and b) when a patient is opened. Once a patient is opened, the user can adjust the maximum number of optimizations performed and add/subtract/modify constraints. In addition, the user can check whether they want to perform an additional optimization AFTER the optimization loop to try and reduce plan hotspots. The user can also choose to perform a coverage check before the optimization loop and to save each optimized plan. The user cannot adjust the plan prescription, this information is just provided as an FYI. The 'Get Constraints From Plan' button just reads the optimization constraints contained in the '_VMAT TBI' plan, it does not populate the list using constraints from a template.



```
Dose calculated, normalizing plan!
Elapsed time: 00:00:18
Plan normalized! Evaluating plan quality and updating constraints!

Results of optimization:
-----------------------------------------------------------------------------------------------------------
structure Id    | constraint type  | dose diff^2 (cGy^2)  | current priority | cost          | cost (%)  |
-----------------------------------------------------------------------------------------------------------
TS_PTV_VMAT     | Lower            | 541078.8             | 100              | 54107881.6    | 2.1       |
TS_PTV_VMAT     | Upper            | 13612267.4           | 100              | 1361226744.3  | 53.9      |
TS_PTV_VMAT     | Lower            | 1542.6               | 100              | 154259.2      | 0.0       |
Kidneys         | Mean             | 2627590.0            | 54               | 141889861.4   | 5.6       |
Kidneys-1cm     | Mean             | 3596991.6            | 34               | 122297716.0   | 4.8       |
Lungs           | Mean             | 2049501.3            | 60               | 122970078.7   | 4.9       |
Lungs-1cm       | Mean             | 2939956.9            | 54               | 158757671.0   | 6.3       |
Lungs-2cm       | Mean             | 3333185.4            | 47               | 156659713.1   | 6.2       |
Bowel           | Upper            | 12006259.0           | 34               | 408212804.4   | 16.2      |

Additional plan infomation:
Plan global Dmax = 408.3%
TS_PTV_VMAT Dmax = 408.3%
TS_PTV_VMAT Dmin = 38.7%
TS_PTV_VMAT V90% = 99.1%
TS_PTV_VMAT V110% = 69.0%
TS_PTV_VMAT V120% = 63.5%

Updated optimization constraints:
-------------------------------------------------------------------------------
structure Id    | constraint type  | dose (cGy) | volume (%) | priority |
-------------------------------------------------------------------------------
TS_PTV_VMAT     | Lower            | 1200.0     | 100.0      | 101      |
TS_PTV_VMAT     | Upper            | 1210.0     | 0.0        | 106      |
TS_PTV_VMAT     | Lower            | 1202.0     | 98.0       | 101      |
Kidneys         | Mean             | 750.0      | 0.0        | 60       |
Kidneys-1cm     | Mean             | 400.0      | 0.0        | 39       |
Lungs           | Mean             | 600.0      | 0.0        | 65       |
```

(a)

(b)

Figure 11: The optimization loop progress window a) without an optimization running and b) with an optimization running. While the optimization loop is running, the user can abort the optimization loop by hitting the 'Abort' button. NOTE: THE PROGRAM MAY NOT TERMINATE IMMEDIATELY WHEN THIS BUTTON IS HIT. The window reports the progress and percent completion of the optimization loop and prints useful information to the user. The user can write the text output to a text file using the 'Write results to file' button.

- NOTE: DO NOT try to close the window while the optimization loop is running! This will not terminate the optimization loop immediately. A safeguard (basically, a bunch of annoying pop up windows) has been implemented to prevent the user from closing the window before the optimization loop has finished or been safely aborted
- The GUI window can be closed only when the program status is 'Aborted', 'Failed', or 'Finished'
- The percent completion of the optimization loop routine is shown in the progress bar in the bottom right of Figure 11
- At any time, the user can write the displayed text output to a text file at a location of their choosing by hitting the 'Write results to file'. Note, this will overwrite an existing file
  - This function can be useful for your own records or for research
  - NOTE: Code was added to the executable program to write all text output in the window to a text log file in a user-specified location (see Section 7 for more details). The name of the text file will be the patient MRN. This log file will be updated EVERY time text is added to the progress window

6.3 Program flow

- Once the 'Confirm Constraints and Begin Optimization' button is hit, the program reads in the optimization constraint list and stores these parameters

- Preliminary checks are then performed where various plan items are checked including if the user origin was set, are the isocenter positions set correctly (i.e., all z-positions are rounded-off, x/y positions = 0.0, etc.), etc.

- The program also checks if a couch structure is present. If it is not, it will ask if you want to continue anyway or stop and insert the couch. If the couch and spinning manny couches are inserted, the script checks to see if these structures have contours in the first and last slices of the CT image. If so, the script will ask if you want to remove the contours on those image planes

  - We've found through testing that if these structures are present on the first and last slices of the CT image, Eclipse will give a pop-up message box after each dose calculation saying that beams are transported through a structure where CT image ends.
  - This is just a warning message from Eclipse, but it halts the progression of the program until that warning message is closed (which could be disappointing if you start running the program at night and don't check back until morning)

- If all the preliminary checks pass, a message will appear in the progress window informing the user that the plan is ready for optimization

- If you elected to run a coverage check, the script will then perform the coverage check by zero-ing the optimization constraints for all OARs and running an optimization with no intermediate dose. Following the optimization, dose is calculated and the plan is normalized to deliver 100% of the Rx dose to 90% of the TS_PTV_VMAT or TS_PTV_FLASH (if appropriate) volume

- If the hotspot in the resulting plan is > 140%, a warning message will be printed to the progress window saying the beam arrangement is likely under-covering the target volume (at this point, you should consider stopping the optimization and adjusting the beam orientations)

  - The plan global hotspot is used as a surrogate measure of the quality of target coverage
  - NOTE: even if this warning message appears, the optimization loop will not stop

- Following the coverage check (if run), the OAR objective priorities are changed from zero to a fraction of the priority specified by the user for each OAR (specifically, 2/3 of the specified priority)

- The optimization loop is then executed. Each optimization loop iteration consists of:

  - A VMAT optimization with intermediate dose switched on
  - A dose calculation following the optimization. The calculation algorithm is used-specified (Section 7) and the dose grid resolution is the default for your Eclipse configuration (if you didn't modify the resolution after running the plug-in script)
  - Normalization of the plan dose to deliver 100% of the Rx dose to 90% of either the TS_PTV_VMAT volume or the TS_PTV_FLASH volume (if flash was included in the optimization)
  - Plan evaluation to determine if the user-specified plan goals were met (Section 7)
  - If the plan goals were met, the optimization loop is broken. If the goals were not met, the script reviews the relative cost associated with each optimization object and determines how to adjust each optimization parameter
  - Cooler and heater tuning structures can also generated after each loop iteration to try and reduce hotspots and improve target coverage, respectively
    - The user can specify what heater and cooler structures and under what conditions should be added after each optimization (see Section 7)
    - Although there is no limit on the number of heater and cooler structures that can be added, it should be cautioned to not add too many as this will slow down the optimization loop and will increase the memory requirements of the program
  - The optimization parameters for the cooler and heater tuning structures (if added) and the updated optimization parameters for the original target and OAR structures are assigned to the plan
  - If the user elected to save the resulting plan from each optimization, the resulting normalized plan from this iteration is copied and saved to the VMAT TBI course
    - NOTE: If the user did <u>NOT</u> elect to run one additional optimization, the number of "opt itr" plans will be one less than the number of requested optimization iterations. This avoids having two copies of the same plan from the final iteration of the optimization loop
  - The next iteration of the optimization loop is started

- The number of loop iterations requested by the user (Figure 10b) are performed

- If the user requested an additional optimization to reduce the plan hotspots (Figure 10b), the cooler tuning structures (if added) segmenting the high dose regions from the final optimization iteration is/are obtained and:
  - The priority for these objectives is/are increased to the maximum of the current cooler structure priority or 90% of the maximum priority in the optimization constraints list, whichever is greater
  - The objective dose for these constraints is lowered to 98% of its current dose objective

- The additional optimization is then performed by continuing the previous optimzation using the previously calculated dose as the intermediate dose. The optimization should start from the default

- If the user included flash in the optimization, following the optimization loop and one additional optimization to reduce hotspots (if selected), the program will grab the BOLUS_FLASH structure and un-assign its HU, recalculate the dose, and normalize the plan to the TS_PTV_VMAT structure (i.e., the 'true' target volume)

- Once the script finishes, the user is informed the optimization loop is complete and the results are written to the '_VMAT TBI' plan

- You can now open the '_VMAT TBI' plan for the patient and evaluate the quality of the resulting plan(s). If you are completely unhappy, you can reset the dose calculation matrix, delete the MLCs for each field, and try again with different parameters

6.4 Known issues and bugs

- Occasionally, Eclipse will throw a warning message that says something like 'Dose in isocenter is too small to use for normalization', particularly when the executable needs to recalculate dose to the AP/PA plan. The progression of the executable halts until this message box closes. Thankfully, these messages generally appear at the very end of the program execution (after all relevant tasks have finished) and do not impact the final script result. It just looks like the script got stuck. Working on a fix (12-28-2020).

6.5 Planned features for future releases

- Further refine the algorithm used to update the optimization constraints

7 Configuration file settings for the plug-in and executable scripts

- Both scripts were modified to read-in a .ini configuration file upon execution

- This modification was made to reduce the number of times an end-user would have to make changes to the underlying code then recompile (especially for trivial items such as default margins)

- This configuration file **MUST** be named 'VMAT_TBI_config.ini' and it **MUST** be placed in the same location as the .dll and .exe files
  - This is because the both scripts look for this file in the executing assembly location (i.e., the script looks in the same directory that it was called from)

- **NOTE: THERE CAN BE NO EMPTY LINES IN THIS FILE! THIS WILL CAUSE PARSING TO FAIL!**
- Should parsing fail, the scripts will ignore all parameters in the .ini file and use the hard-coded defaults.
  - It is recommended during commissioning of these scripts to change the hard-coded defaults to your clinics needs
- Comments can be added to the configuration file using the ’%’ character (similar to MATLAB)
- Different sections of the configuration file are specified using similar syntax to the EGSnrc Monte Carlo code:

```
:begin XX configuration:
parameter XX 1=value
parameter XX 2=value
:end XX configuration:
%
%
:begin YY configuration:
parameter YY 1=value
add YY array parameter{value 1,value 2,value 3,value 5,...}
:end YY configuration:
```

- Because the configuration file can be broken into different sections, the configuration settings for the binary plug-in and executable can be specified in the same .ini file (it’s easier to maintain one configuration file for both programs rather than maintaining multiple configuration files)
- The configuration file provided with the code already lists the available options that can be modified in the plug-in script
- As illustrated above, configuration settings in the .ini file are of two types: single parameters and array parameters
  - single parameter type: parameter=value
  - array parameter type: add array parameter{value 1,value 2,value 3,...}
- Array parameters will always contain the assigned values between the ’{}’ braces
- **IMPORTANT:**
  - For single parameter types, there can be no spaces between the parameter, ’=’ character, and assigned value!

  - For array parameter types, there can be no spaces between values (i.e., no space between value n, ',' character, and value n+1)!

- Having extra spaces in the parameter-value arguments will result in failed parsing
- It was assumed that the parameters contained within the configuration file would not be modified very often. Therefore, minimal error checking code was added to the scripts, which is why the formatting is very strict in the configuration file
- The order of parameters in the configuration file does not matter
- Plug-in specific comments:
  - There are general and case-specific parameters that can be set in the configuration file
  - Examples of general parameters are the calculation model, documentation path, etc.
  - Examples of case-specific parameters include the dose per fraction, number of fractions, optimization constraints, etc.
  - The case-specific parameters need to be specified inside the appropriate begin-end configuration statements (e.g., :begin myeloablative case configuration: ... :end myeloablative case configuration:)
  - default sparing structure array syntax:
    add default sparing structure{<Structure ID>,<Sparing type>,<add margin>}
  - optimization constraint array syntax:
    add opt constraint{<Structure ID>,<Constraint type>,<dose (cGy)>,<Volume at dose (%)>,<priority>}
  - NOTE: ALL VALUE ENTRIES ARE CASE SENSITIVE!
  - In general, the comments in the provided configuration file should give you an idea of what each command does and how it should be formatted
- Executable-specific comments:
  - The 'demo' parameter is a useful feature that allows the user to run the executable without performing intensive optimization or dose calculations. Instead the program is instructed to sleep for three seconds. This is useful for things like troubleshooting the executable ensure it runs in your clinical environment
  - There are Scleroderma trial plan objectives and general plan objectives that can be added to the configuration file
  - NOTE: the Scleroderma trial plan objectives are IN ADDITION to the general plan objectives!

- The syntax for adding plan objectives is:
  add plan objective{<Structure ID>,<objective type>,<dose (cGy)>,<volume (%)>,<dose value presentation>}
- NOTE: The structure IDs for the target need to be set to '<targetId>' in the plan objective! The reason is because it allows flexibility in overriding the structure Id depending on if flash was included or not (easier than hard coding it in)
- Multiple tuning structures (i.e., heater and cooler structures) can be specified in the configuration file to be added following each optimization
- The user can also specify a list of conditions that must ALL be met to add a particular tuning structure
- The syntax for adding tuning structures is:
  add TS structure{<Structure ID>,<lower dose level (%)>,<upper dose level (%)>,<volume (%)>,<priority>,{<condition 1>,<condition 2>,...}}
- The structure ID should contain either 'TS_cooler' or 'TS_heater'
- NOTE: The upper dose level value is only considered for heater structures! Leave it as 0.0 for cooler structures
- If you always want a particular tuning structure added at the end of each optimization, leave the list of conditions blank (i.e., place nothing in between the inner {} brackets)
- Available conditions include: 'Dmax>dose (%)', 'Vdose (%)<volume (%)', 'Vdose (%)>volume (%)', 'finalOpt'
- For example, the following command adds a cooler structure named 'TS_cooler120, segments V120%, N/A, 0.0% volume should receive this dose, priority of 80, and should only be added if Dmax > 130% AND V110%>10% AND it is the final optimization:
  add TS structure{TS_cooler120,110.0,0.0,0.0,80,{Dmax>130.0,V110>10.0,finalOpt}}
- NOTE: Final optimization means that it is the optimization that is performed AFTER the optimization loop to lower hotspots
- The conditions to add tuning structures can be specified in any order

Appendix

Table I: Plan goals for the non-myeloablative regime (R_x=200 cGy).

Structure	**Dosimetric parameter**	**Limit**
PTV_Body	D90% >=	200 cGy (100%)
	D_{max} <=	240 cGy (120%)
	V110% <=	5%
Lungs_Eval (Lungs-1cm)	D_{mean} <=	200 cGy (50%)
Lungs	D_{mean} <=	120 cGy (60%)
Kidneys	D_{mean} <=	210 cGy (105%)
	D_{max}% <=	210cGy (105%)
Testes/Ovaries	D_{mean} <=	ALARA (< 100 cGy required)
	D_{max}% <=	ALARA (< 100 cGy required)
Brain_Eval (Brain-1cm)	D_{mean} <=	100 cGy (50%)
Thyroid	D_{mean} <=	150 cGy (75%)

Table II: Optimization constraints for the non-myeloablative regime ($\mathrm{R_x}$=200 cGy).

Structure	Optimization constraints	Priority
TS_PTV_VMAT	$D_{\mathrm{min}} = 200$ cGy	100
	$D_{\mathrm{max}} = 203$ cGy	100
	D98% = 201 cGy	100
Kidneys	$D_{\mathrm{mean}} < 120$ cGy	80
Kidneys-1cm	$D_{\mathrm{mean}} < 120$ cGy	50
Lungs	$D_{\mathrm{mean}} < 75$ cGy	90
Lungs_Eval (Lungs-1cm)	$D_{\mathrm{mean}} < 50$ cGy	80
Lungs-2cm	$D_{\mathrm{mean}} < 25$ cGy	70
Testes/Ovaries	$D_{\mathrm{mean}} < 50$ cGy	50
Testes/Ovaries	$D_{\mathrm{max}} < 75$ cGy	50
Lenses	$D_{\mathrm{max}} < 190$ cGy	50
Brain	$D_{\mathrm{mean}} < 150$ cGy	60
Brain_Eval (Brain-1cm)	$D_{\mathrm{mean}} < 100$ cGy	50
Brain-2cm	$D_{\mathrm{mean}} < 75$ cGy	50
Brain-3cm	$D_{\mathrm{mean}} < 50$ cGy	50
Bowel	$D_{\mathrm{max}} < 201$ cGy	50

Table III: Plan goals for the myeloablative regime ($\mathrm{R_x}$=1200 cGy).

Structure	Dosimetric parameter	Limit
PTV_Body	D90% >=	1200 cGy (100%)
	D_{max} <=	1440 cGy (120%)
	V110% <=	5%
Lungs_Eval (Lungs-1cm)	D_{mean} <=	600 cGy (50%)
Lungs	D_{mean} <=	720 cGy (60%)
Kidneys	D_{mean} <=	1260 cGy (105%)
	D_{max}% <=	1260cGy (105%)
Testes/Ovaries	D_{mean} <=	ALARA (< 100 cGy required)
	D_{max}% <=	ALARA (< 100 cGy required)
Brain_Eval (Brain-1cm)	D_{mean} <=	600 cGy (50%)

Table IV: Optimization constraints for the myeloablative regime (R_x=1200 cGy).

Structure	**Optimization constraints**	**Priority**
TS_PTV_VMAT	D_{min} = 1200 cGy	100
	D_{max} = 1210 cGy	100
	D98% = 1202 cGy	100
Kidneys	D_{mean} <750 cGy	80
Kidneys-1cm	D_{mean} < 400 cGy	50
Lungs	D_{mean} < 600 cGy	90
Lungs_Eval (Lungs-1cm)	D_{mean} < 300 cGy	80
Lungs-2cm	D_{mean} < 200 cGy	70
Bowel	D_{max} < 1205 cGy	50

Table V: Plan goals for the scleroderma trial regime (R_x=800 cGy).

Structure	**Dosimetric parameter**	**Limit**
PTV_Body	D90% >=	800 cGy (100%)
	D_{max} <=	1040 cGy (130%)
Lungs_Eval (Lungs-1cm)	D_{mean} <=	200 cGy
Kidneys	D_{mean} <=	200 cGy

Table VI: Optimization constraints for the scleroderma trial regime (R_x=800 cGy).

Structure	**Optimization constraints**	**Priority**
TS_PTV_VMAT	D_{min} = 800 cGy	100
	D_{max} = 812 cGy	100
	D98% = 802 cGy	100
Kidneys	D_{mean} <100 cGy	80
Kidneys-1cm	D_{mean} < 25 cGy	80
Lungs	D_{mean} < 150 cGy	80
Lungs_Eval (Lungs-1cm)	D_{mean} < 100 cGy	80
Lungs-2cm	D_{mean} < 50 cGy	80
Bowel	D_{max} < 850 cGy	50

Table VII: Default sparing structures for the non-myeloablative regime (R_x=200 cGy).

Structure	**Sparing type**	**added margin (cm)**
Lungs	Mean Dose < Rx Dose	0.3
Lungs_Eval (Lungs-1cm)	Mean Dose	0
Lungs-2cm	Mean Dose < Rx Dose	0
Kidneys	Mean Dose < Rx Dose	0
Kidneys-1cm	Mean Dose < Rx Dose	0
Bowel	Dmax ∼ Rx Dose	0
Testes/Ovaries	Mean Dose < Rx Dose	1.0 (ovaries)/2.0 (testes)
Lenses	Dmax ∼ Rx Dose	0
Brain	Mean Dose < Rx Dose	0
Brain_Eval (Brain-1cm)	Mean Dose < Rx Dose	0
Brain-2cm	Mean Dose < Rx Dose	0
Brain-3cm	Mean Dose < Rx Dose	0

Table VIII: Default sparing structures for the myeloablative regime (R_x=1200 cGy).

Structure	**Sparing type**	**added margin (cm)**
Lungs	Mean Dose < Rx Dose	0.3
Lungs_Eval (Lungs-1cm)	Mean Dose < Rx Dose	0
Lungs-2cm	Mean Dose < Rx Dose	0
Kidneys	Mean Dose < Rx Dose	0
Kidneys-1cm	Mean Dose < Rx Dose	0
Bowel	Dmax ∼ Rx Dose	0

Table IX: Default sparing structures for the scleroderma trial regime (R_x=800 cGy).

Structure	**Sparing type**	**added margin (cm)**
Lungs	Mean Dose < Rx Dose	0.5
Lungs-1cm	Mean Dose < Rx Dose	0
Lungs-2cm	Mean Dose < Rx Dose	0
Kidneys	Mean Dose < Rx Dose	0.5 cm medial, else 2.0 cm
Kidneys-1cm	Mean Dose < Rx Dose	0
Bowel	Dmax ∼ Rx Dose	0