

User Guide for an `egs_brachy` Graphical User Interface (GUI)

A graphical user interface (GUI) to run `egs_brachy` with clinical data

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Abstract

This report provides an overview of `egs_brachy_GUI`, a code to read DICOM files, create a patient-specific model and launch **`egs_brachy`**. `egs_brachy_GUI` provides additional options to generate input files and run **`egs_brachy`**. It can convert files between the 3ddose and DICOM dose format. The GUI is programmed in c++ using the Qt5 framework.

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1 Installation and Set-up

1.1 Installing egs_brachy_GUI from Source Code

The egs_brachy_GUI package consists of a zip file in the following location:
`/home/sjarvis/egs_brachy_GUI.zip`.

The package requires that the user has;

- QT Software Development Kit installed. If you do not have QT installed, follow the installation instructions for UNIX at <https://doc.qt.io/qt-5/linux-building.html#> or windows at <https://doc.qt.io/qt-5/windows-deployment.html#>. It is recommended to use a UNIX/LINUX environment.
- egs_brachy installed. Installation instructions can be found in Section 3 of the egs_brachy user manual https://clrp-code.github.io/egs_brachy/pdf/egs_brachy_user_manual.pdf
- xmgrace to view DVH metrics
- For run time optimization of egs_brachy_GUI, it is recommended to use OpenGL libraries and a GPU (graphical processing unit)

To compile, begin by unzipping the egs_brachy_GUI package to the desired location (`path_of_desired_location` indicated below);

```
unzip /home/sjarvis/egs_brachy_GUI.zip -d path_of_desired_location
```

Then execute the following sequence of commands;

```
cd path_of_desired_location/egs_brachy_GUI/  
qmake  
make
```

The qmake command creates a MakeFile and meta-object compiler (moc) files. These are used to instruct the compiler on how to compile the program. The make command compiles the program. Compilation takes approximately one minute and warning messages will be displayed, these can be ignored.

1.2 Set-up and verification of default files

Before running egs_brachy_GUI it is recommended to verify the contents of the distributed default files. There are four files to be verified; `default_files.txt`, `default_CT_calib.hu2rho`, tissue assignment scheme (`.txt`) and air kerma (`.Sk`).

1.2.1 `default_files.txt`

The `default_files.txt` text file contains the paths of relevant files within the `egs_brachy` library. At the time of distribution, it contains existing paths. The user is encouraged to verify that the paths exist and correspond to the desired default files. Section 3.3 provides a description of the file and contents therein.

1.2.2 Default CT calibration and Tissue Assignment Scheme files

egs_brachy_GUI is distributed with a default CT calibration file (`default_CT_calib.hu2rho`) and default tissue assignment schemes (`egs_brachy_GUI/Tissue.Assignment.Schemes` folder). The user is encouraged to modify the contents of the files such that they are appropriate for the CT scanner and the patient contours, respectively.

The CT calibration file contains the conversion between CT number (HU) to mass density (g cm^{-3}). The calibration file depends on the CT scanner used. A description of the CT calibration file is provided in Table 1 of Section 3.1.

Each tissue assignment scheme file contains a mapping between each contour/organ in the patient to the tissues within the contour and their density threshold. The assignment scheme is used in conjunction with the voxel density and physician drawn contours (from the DICOM struct file) to assign the appropriate tissue to each voxel. A detailed description and example of the Tissue Assignment Scheme (TAS) file can be found in Section 3.2. If the user wishes to change the distributed tissue assignment scheme, they can do so by altering the text file within the `Tissue.Assignment.Schemes` folder. Each assignment scheme listed in the ‘Select an appropriate tissue assignment scheme’ panel of the GUI (shown in Figure 1) has a corresponding `.txt` file.

1.2.3 Air Kerma files

The user is encouraged to verify that each source model in `egs_brachy/lib/geometry/sources` folder has a corresponding air kerma file (located within the `Air_kerma` folder of the GUI). The Air kerma files are identified by a `.Sk` extension and contain the air kerma strength per history (S_K^{hist} , units: Gy cm³/history) of the source it is named after. The format of the file is further described in Section 3.4. The values were obtained from Section 9.1 of the `egs_brachy` user manual [3].

If a source model doesn't have a corresponding `.Sk` file in the `Air_kerma` directory, the GUI will ask for the file to be manually selected.

1.3 Running egs_brachy_GUI

Once the GUI has been compiled and set-up, the following commands are used to launch it;

```
cd path_of_GUI/egs_brachy_GUI/  
./egs_brachy_GUI
```

2 Using egs_brachy_GUI

`egs_brachy_GUI` extends the `egs_brachy` algorithm [1], created by the Carleton Laboratory for Radiotherapy Physics (CLRP), such that it can be implemented in clinical applications. It parses DICOM data to create a patient model and prepares `egs_brachy` input files. Additionally, it launches `egs_brachy`, calculates dose metrics and creates a DICOM dose file from the output. `egs_brachy_GUI` has further options such that the user can generate input files from pre-defined phantoms in the `egs_brachy` library.

This section provides an overview of the functions of `egs_brachy_GUI`. The GUI has three tabs: Using DICOM Data, Using the `egs_brachy` Library and Extra Options. Section 2.1 outlines the *Using DICOM Data* tab, Section 2.2 describes the function of the *Using the egs_brachy Library* tab and Section 2.3 describes the *Extra Options* tab.

2.1 Using DICOM Data

This tab is used to create a DICOM dose file from DICOM data. The DICOM data must contain CT, plan and structure files. From these data, a patient model is created, the input files are generated, **egs_brachy** is launched, metrics are calculated and a DICOM dose file is created. A detailed description of each button followed by a step-by-step guide is provided;

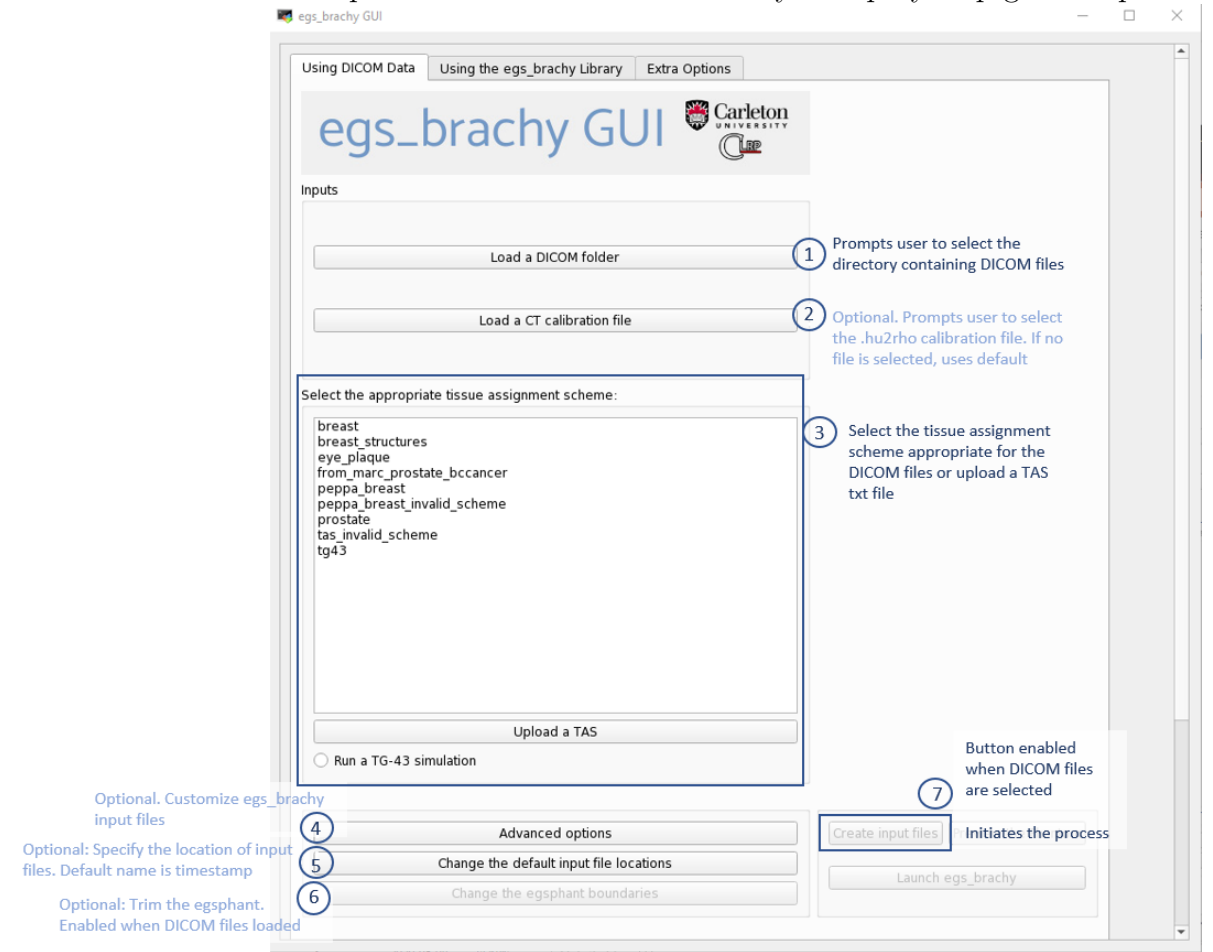


Figure 1: Snapshot of the 'Create Dose File From DICOM Data' tab with labels

1. **Load a DICOM folder:** This button prompts the user to select a DICOM directory. egs_brachy_GUI parses the files to extract all relevant information. When this button is pressed, the data for all previously loaded DICOM files is erased.
2. **Load a CT calibration file:** This button prompts the user to select a CT Calibration file. The file must be of the type .hu2rho and consist of a list of CT pixel numbers in Hounsfield Units and corresponding mass density (g cm^{-3}) measured from the CT scanner's calibration. If no file is uploaded, a default calibration file is used. The

default .hu2rho data is shown in Table 1 and the format of the file is described in Section 3.1.

3. **Select the appropriate tissue assignment scheme:** This pane requires the user to select the appropriate tissue assignment scheme for the DICOM data. Each selection has a corresponding text file containing the assignment scheme (located in `egs_brachy_GUI/Tissue.Assignment.Schemes`).

The tissue assignment scheme contains a mapping from each contour in the DICOM struct file to the tissues within the contour and their density threshold. The format of the file is outlined Section 3.2.

4. **Advanced options:** This button allows the user to change default parameters in the `egsinp` file. This includes allowing the user to specify the number of histories, select to score energy deposition, change the default `muen` file or select the transport parameter file. A short description of the role of each parameter follows;
 - **Number of histories:** The number of particles initialized, `ncase`. It is recommended to run at least $1e8$ histories (the default).
 - **Number of batches:** The number of checkpoints where the results are written, `nbatch`. To save time, the default is 1.
 - **Number of chunks:** The number of chunks the simulation is divided into, `nchunk`. The default is 10 for parallel runs.
 - **Score energy deposition:** By selecting yes, the energy deposited by dose is scored and outputted to `filename.phantom.edep.3ddose`. The default is no.
 - **Change the default muen:** The user can select and alternate `muen` file. This file contains μ_{en}/ρ data for each media. All tissues used in the tissue assignment scheme must be in the `muen` file. The default file is read from `default_files.txt`.
 - **Change the default transport parameter:** The transport parameter files are obtained from `egs_brachy/lib/transport`. If no file is selected, the default low or high energy file from `default_files.txt` is used.

For further information pertaining to the parameters, please refer to the `egs_brachy` user manual. [3]

5. **Change the default input file locations and settings:** This button is used to change the location and name of the `egs_brachy` input files. It also allows a header to be added to the `egsinp` file. The default file names used the date and timestamp. The default names are;
 - `egsinp_YYYYMMDDHHMMSS.egsinp`
 - `egsphamt_YYYYMMDDHHMMSS.egsphamt`
 - `transformation_YYYYMMDDHHMMSS` (the seed transformation file)
6. **Change the `egsphamt` boundaries:** This button is enabled after DICOM files have been loaded. It allows the user to change/trim the `egsphamt` boundaries.

2.1.1 Step-by-step guide

This subsection provides an overview of the recommended steps to generate a dose file from DICOM data. It assumed that Steps 1-6, depicted in Figure 1, have been completed successfully (i.e. DICOM data has been parsed and the user has made the appropriate selections). The terminal output should resemble;

```
Successfully parsed path_dicom_file_1.dcm.
      :
Successfully parsed path_dicom_file_nz.dcm.
Parsed the  $n_{input}$  DICOM files. Time elapsed is 4.51231 s.
Sorted the Z DICOM CT files along z. Time elapsed is 4.56216 s.
Extracted all HU data for the  $n_x$  x  $n_y$  slices. Time elapsed is 5.74517
Extracted data for all MANUAL brachytherapy seeds.
```

where n_{input} is the number of files parsed in the selected DICOM folder, Z is the number of CT files and n_x, n_y are the number of voxels in the x and y direction, respectively.

Once step 7, *Create input files*, has been selected the user will be guided through a series of windows. Throughout steps 8-13, the main window `egs_brachy_GUI` may be disabled unless the user clicks 'cancel'. The steps proceed as follows;

7. **Create input files:** To begin generating the `egs_brachy` input files, the user must click *Create input files*. This button is enabled after DICOM files have been loaded and parsed. It is highlighted in the following figure;

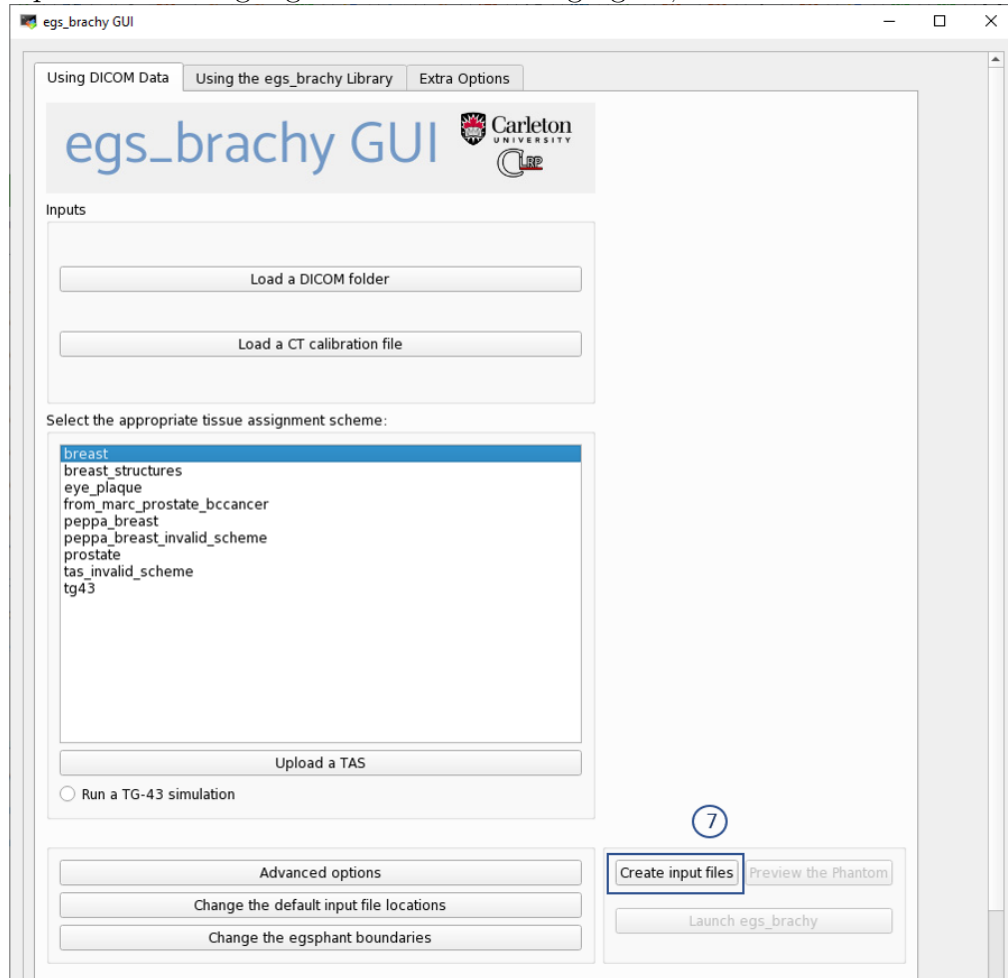


Figure 2: Snapshot of the GUI window with the *Create input files* button highlighted

If the user selects a TG-43 simulation via the *Run a TG-43 simulation* button, Steps 10-12 will be skipped.

8. **Select the source** The user will be asked to select the brachytherapy source model. The list of models is obtained from `egs_brachy/lib/geometry/sources/`.

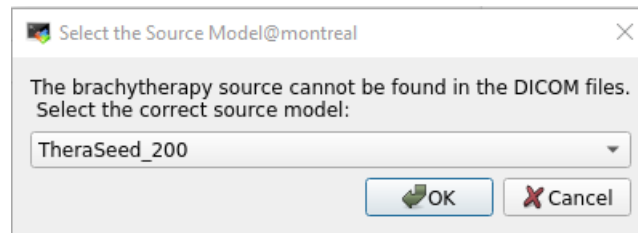


Figure 3: Snapshot of the 'Select the Source Model' window

If the corresponding air kerma (.Sk) file cannot be found, the user will be asked to manually select the appropriate file.

9. ***Simple threshold replacement (conditional)***: If the treatment type is high dose rate (HDR), a simple threshold replacement metallic artifact reduction is performed to mitigate the effect of seed artifacts in CT images. The user is prompted to specify the parameters and replacement values;

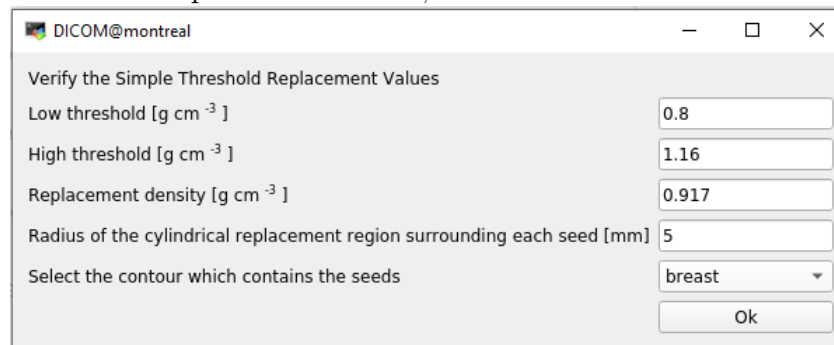


Figure 4: Snapshot of the Simple Threshold Replacement window

The density of voxels in a cylindrical region surrounding each seed is checked against the low and high threshold density values. If the voxel's density is outside of the threshold (above the high threshold or below the low threshold), it is replaced with the replacement density. Additionally, the user can select the contour which contains the seeds using the drop-down menu. If a contour is selected, all voxel's within the contour below the low threshold are replaced with the replacement value.

10. ***Select tissue assignment scheme (conditional)*** If the tissue assignment scheme file could not be read (i.e. it is in a location that cannot be read or the file contents don't comply to the requirements), the user will be prompted to select a new tissue assignment scheme file;

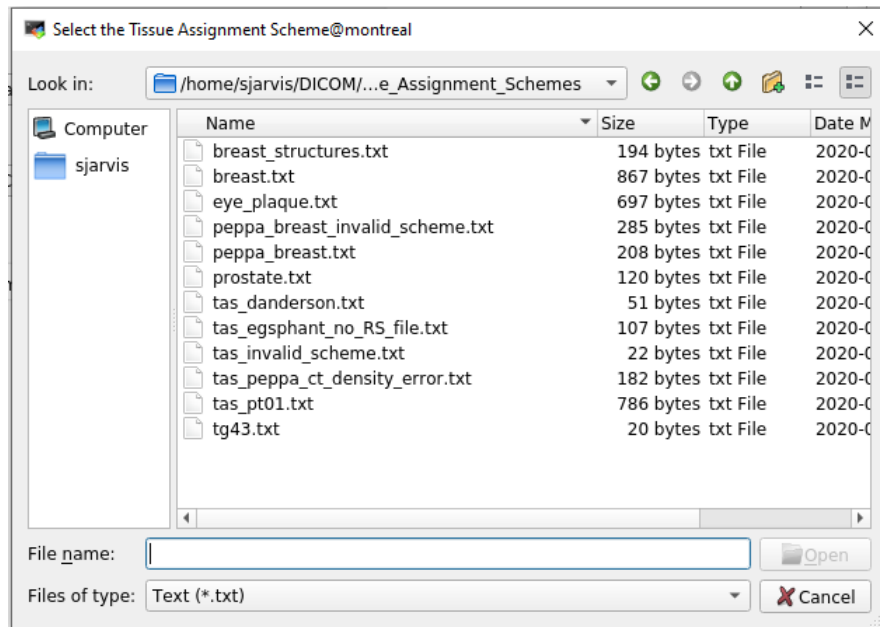


Figure 5: Snapshot of the 'Select the Tissue Assignment Scheme' window

11. **Verify the contour mapping** The user will be asked to verify the mapping between the DICOM structure contours to the organ name in the tissue assignment scheme file.

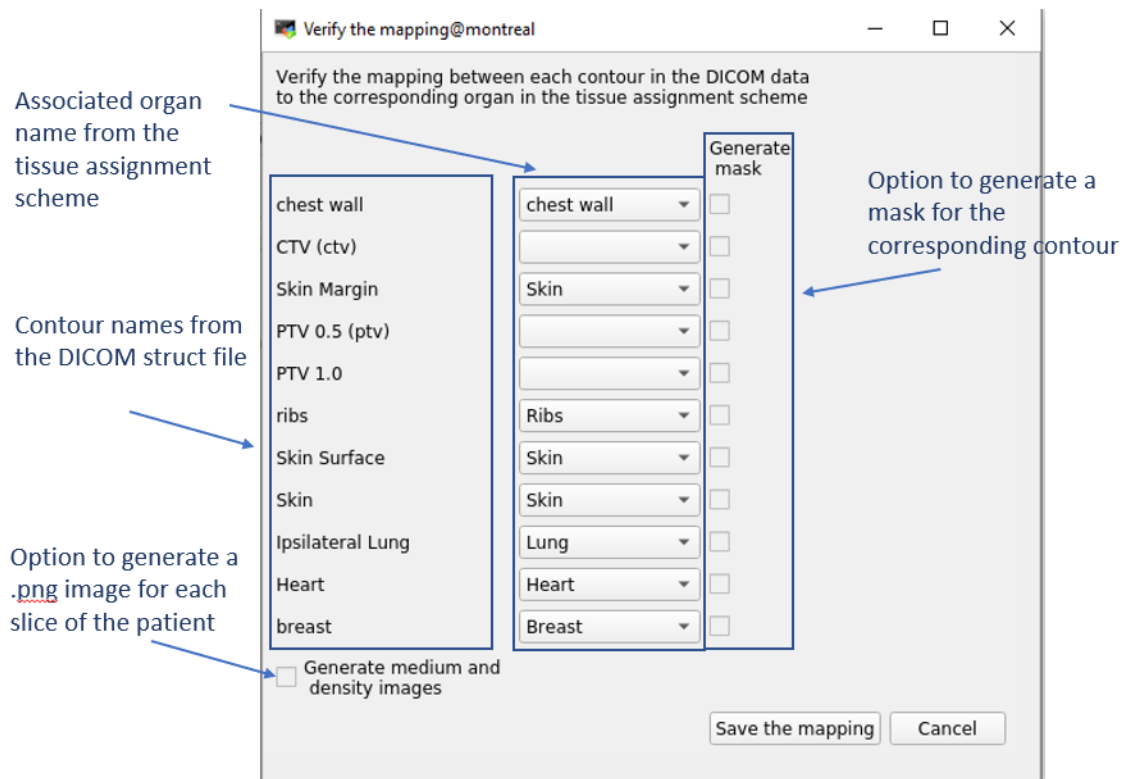


Figure 6: Snapshot of the 'Verify the mapping' window

The left-hand column displays the list of contour names from the DICOM file. Each contour has a corresponding drop-down box (the center column) from which the user can select the correct organ in the tissue assignment scheme. The default mapping is generated by the egs_brachy_GUI based on similarities between the DICOM contour and TAS organ names.

If the drop-down selection is left blank (e.g. in Figure 6 the contour CTV has no associated organ), the contour will be assigned to the default tissue(s).

The right-hand column allows the user to generate a mask for the selected contour. A mask is an egspant format file consisting of a phantom with 0's and 1's, where a 1 indicates that the voxel is within the contour and a 0 indicates the contour is outside the voxel.

At the bottom of the window, the user can select to generate medium and density images. This options creates two .png images for each slice of the phantom. They are saved in the **Images** folder within the working directory of egs_brachy_GUI. One should note that the generation of the images is a timely process.

Once the contour to organ mapping has been verified, 'Save the mapping' is clicked to proceed.

12. **Verify the contour priority** The user will be prompted to assign the contour priority. The priority is used if a given voxel is within two or more contours, where, it will be assigned to the higher priority contour. If in Step 11, the drop-down organ selection for all contours was blank, the user will not have to assign contour priority and this window will not be displayed.

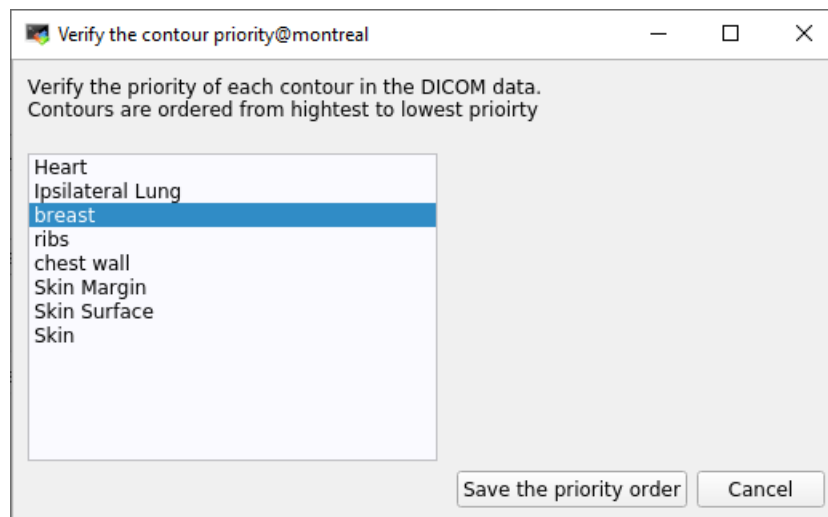


Figure 7: Snapshot of the 'Verify the mapping' window

The priority of a given contour is modified by selecting and dragging it to the desired location. The contours with the highest priority are located at the top of the list. Once the order has been verified, click 'Save the priority order' to proceed.

13. **Generating the egs_brachy files** A loading bar will appear to notify the user that egs_brachy_GUI is generating the **egs.brachy** input files. Once this is completed, the GUI window will become enabled and the console will output a message notifying the

user that all files have been generated. An example of the console output is shown;

```
Successfully generated egssphant (dimensions x: [x1,x2], y:[y1,y2], z:[z1,z2]).  
Time elapsed is 263.719 s.  
Egssphant file compressed. Location:file_path. Time elapsed is 301.598 s.  
Successfully created the source transformation file. Location:file_path  
Successfully created egssinp. Location:file_path
```

A description of each `egs_brachy` input file follows;

- **egssinp:** The `egssinp` file instructs `egs_brachy` to setup and run the simulation. It defines the media, geometry, sources and scoring options. Further information on the `egssinp` parameters are outlined in the `egs_brachy` user manual [3].
- **egssphant:** This file contains the media in the phantom, voxel boundaries in the x,y and z directions, array of medium numbers for each z-slice and the density of each voxel. Further information on the `egssphant` file can be obtained from Section 16.6 of the DOSXYZnrc user manual [4].
- **Source transformation:** contains the location of the source(s) in the patient. `egs_brachy_GUI` is unable to determine the source rotation.

Once the input files have been generated, the GUI window and two additional buttons (*Preview the phantom* and *Launch egs-brachy*) become enabled.

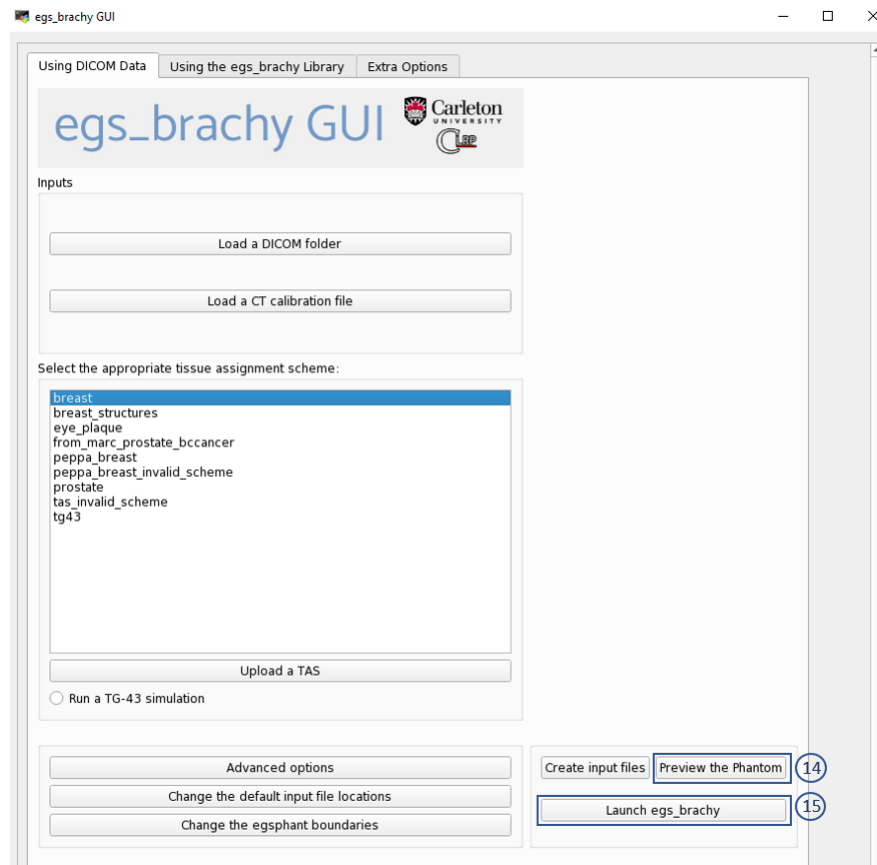


Figure 8: Snapshot of the egs_brachy_GUI window with all buttons enabled

14. **Preview the phantom** When this button is clicked, a new window is created and displays the phantom data such that the user can view and step through each z-slice of the phantom. The axis, depth and resolution of the image can be adjusted. When hovering over the image, the coordinates of the position in the patient are shown below the image.
15. **Launch egs_brachy** This button creates a console window and automatically launches egs_brachy.

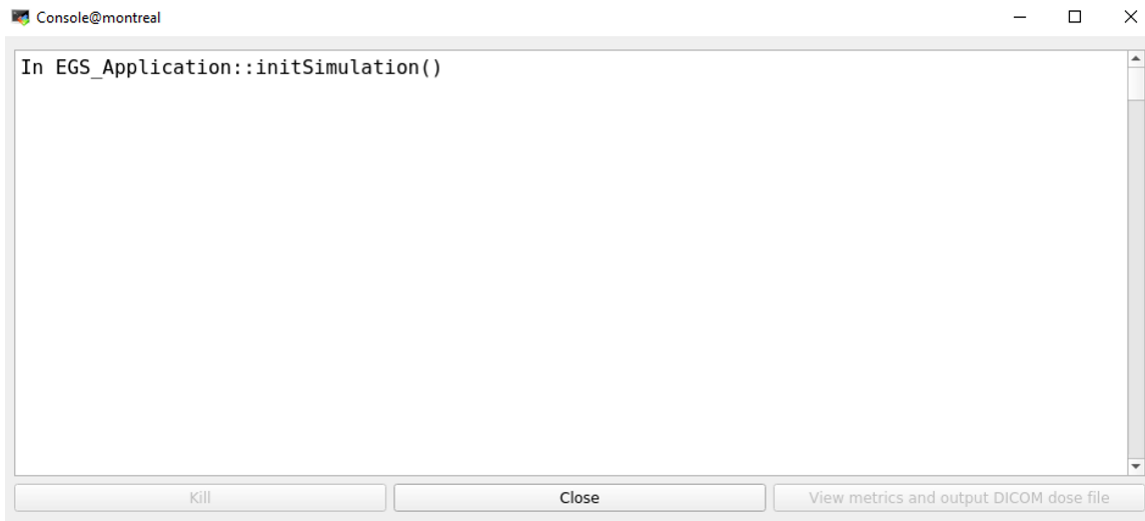


Figure 9: Launch `egs_brachy` window

The console displays the `egs_brachy` output and has 3 buttons;

- **Kill:** This button kills the running `egs_brachy` process
- **Close:** This button is used to close the console window and if `egs_brachy` hasn't completed running, it will continue in the background.
- **View Metrics and Create DICOM Dose File:** After `egs_brachy` has successfully run, the 'View Metrics and Create DICOM Dose File' button on the console is enabled. The `egs_brachy` output, `.3ddose` file, is read and converted to a DICOM dose file. The user is prompted to save the file. Then, dose and volume metrics are calculated and displayed in a new metrics window.
 - **Metrics:** The user can change the contour selected to view the metrics for each DICOM contour. A dose volume histogram (DVH) plot is created and is displayed in `xmgrace` when the 'View DVH Plot' button is clicked. The mean, peak and minimum dose is calculated along with the homogeneity index and conformity index. Dose metrics (D_{50} , D_{60} , D_{70} , D_{80} and D_{90}) and volume metrics (V_{90} , V_{100} , V_{150} , V_{200}) are displayed. The user can output the metrics to a text file.

When `egs_brachy` has successfully run, the output will resemble the following console;

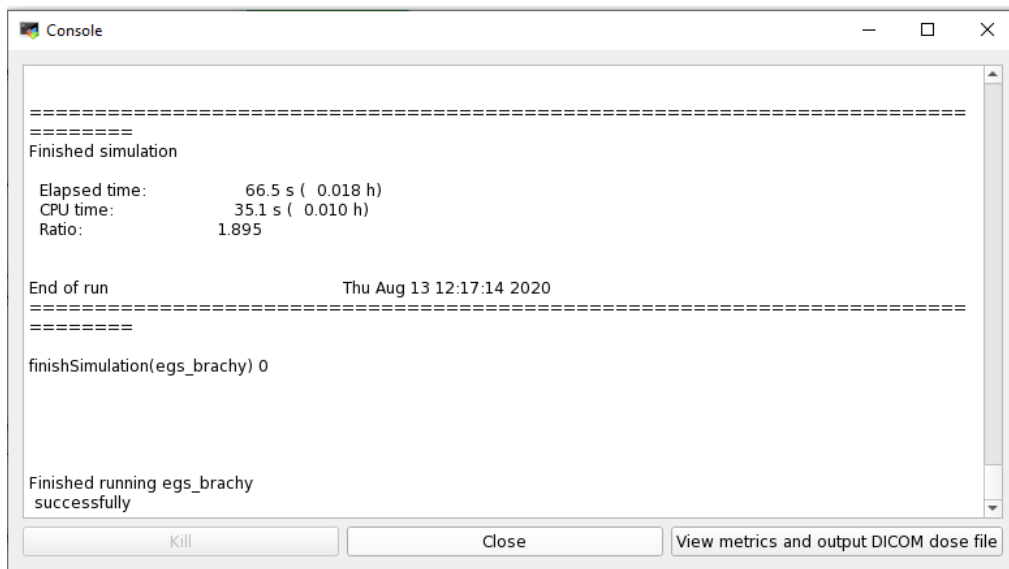


Figure 10: Snapshot of a successful `egs_brachy` simulation

2.2 Using the `egs_brachy` Library

This tab is used to create `egs_brachy` input files from an existing phantom and seed transformation file. A labelled snapshot of the tab followed by a detailed description of each button is provided;

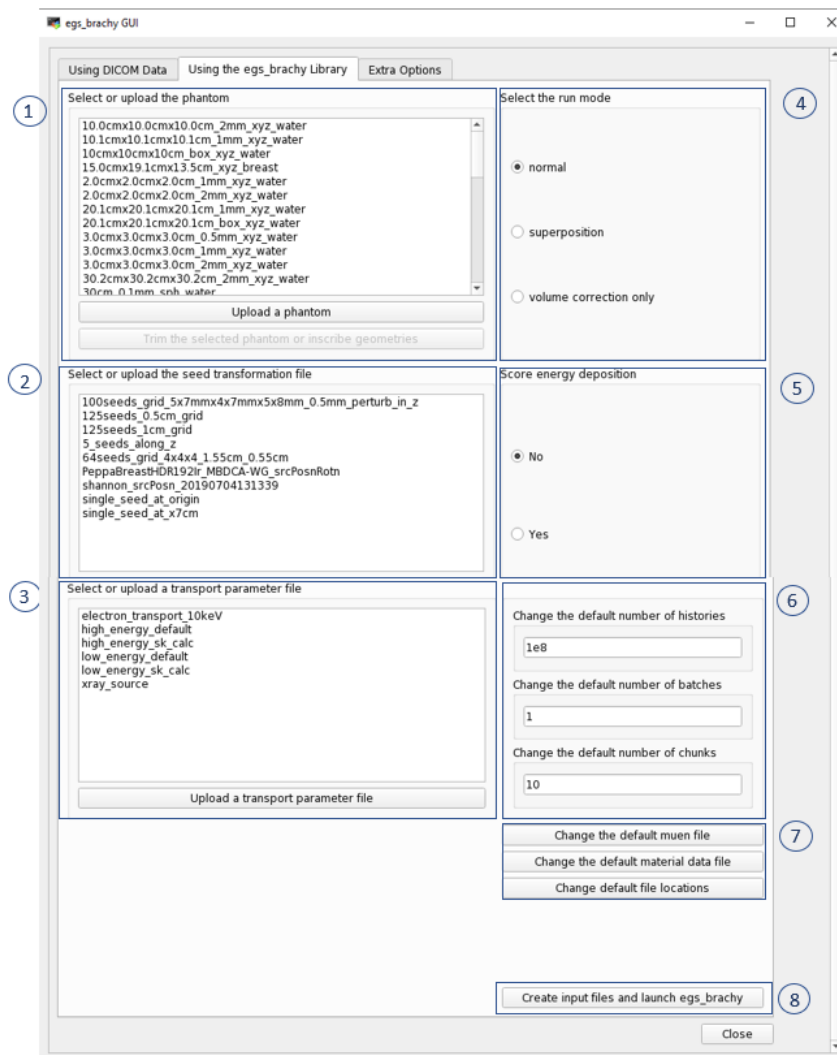
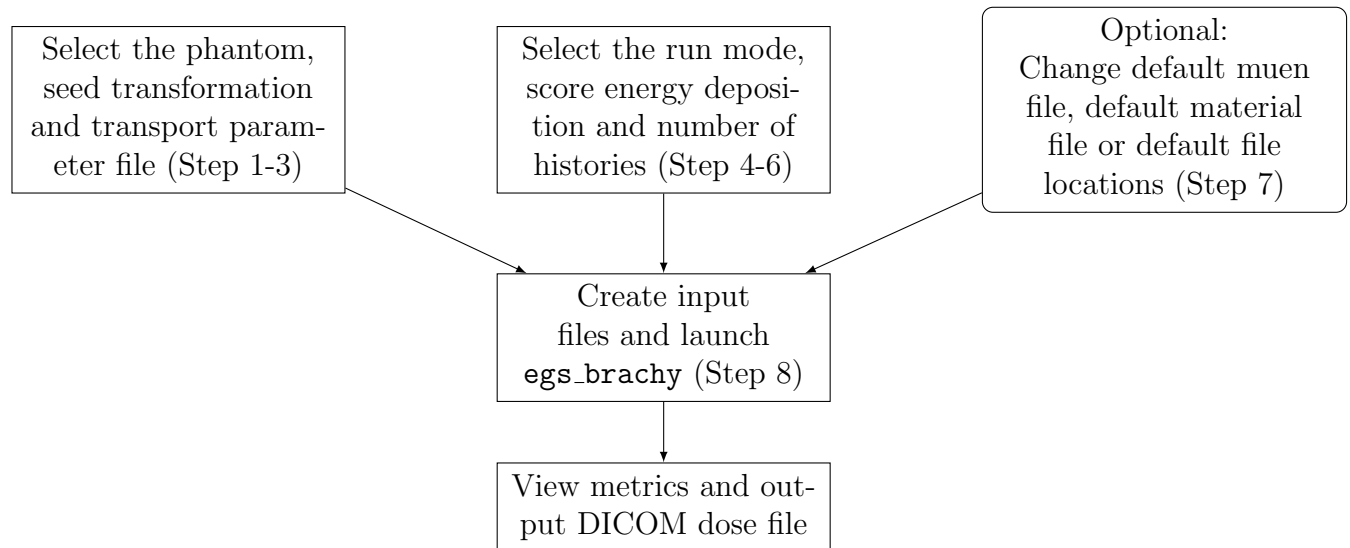


Figure 11: Snapshot of the Create Dose File From Phantom tab with labels

2.2.1 Flowchart

The following flowchart indicates the processes of the 'Create a DICOM Dose File from Phantom' tab.



2.2.2 Step-by-step Guide

This section provides a guide on generating an `egsinp` file and running `egs_brachy` using a phantom and seed transformation file. The number of each steps corresponds to the number in Figure 11. The selections for the phantom, seed transformation and transport parameter file (Steps 1-3) are obtained from the `egs_brachy` library.

1. **Select or upload the phantom:** The user can either select a phantom from the provided list or upload their own. The list of phantoms includes all files with the `.geom` or `.egsphant` extension in the `egs_brachy` phantom library (`/lib/geometry/phantoms/`). If the user uploads a phantom, it will appear and be selected in the list of phantoms.
2. **Select or upload the seed transformation file:** The user can either select a seed transformation file from the provided list or upload their own. The list includes all files in the `/lib/geometry/transformations/` directory. If the user uploads a file, it will appear and be selected in the list.
3. **Select or upload a transport parameter file:** The user can either select a transport parameter from the provided list or upload their own. The list includes all files in the `/lib/transport/` directory of `egs_brachy` (excluding the `README` file). If the user uploads a transport parameter file, it will appear and be selected in the list.
4. **Select the run mode:** The default run mode of `egs_brachy` simulations is normal.

The user can select the run mode to be normal, superposition or volume correction only.

5. **Score energy deposition:** By selecting yes, the energy deposited by dose is scored and outputted to filename.phantom.edep.3ddose. The default is no.
6.
 - **Change the default number of histories:** Changes the number of particles
 - **Change the default number of batches:** Changes the number of checkpoints within each chunk where data is saved
 - **Change the default number of chunks:** Changes the number of chunks to break the simulation into
7.
 - **Change the default muen:** The muen file contains μ_{en}/ρ data for each media. If no file is selected, the muen file listed in default_files.txt of the egs_brachy_GUI directory is used. A description of this file and contents therein is provided in Section 3.3.
 - **Change the default material data file:** This file defines the materials properties for each media in the patient model. If no file is selected, the default file listed in default_files.txt of the egs_brachy_GUI directory is used.
 - **Change the default file locations:** Used to change the location and name of egsinp file. The default egsinp name is generated using the time stamp; egsinp_YYYYMMDDHHMMSS.egsinp. Additionally, the user can add a header to the egsinp file.
8. **Create input files and launch egs_brachy:** When this button is clicked, egs_brachy_GUI verifies that a selection has been made in Steps 1 to 3 (selected a phantom, seed transformation file and transport parameter file). If the user has not made all the selections, an error message will be displayed asking the user to select the required file(s). If all required selections are made, egs_brachy_GUI prompts the user to select the source which corresponds to the selected source transformation file;

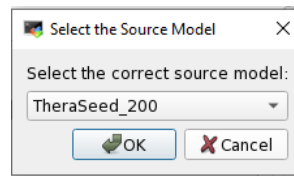


Figure 12: Snapshot of the source selection

Then, `egs_brachy` is launched in a console;

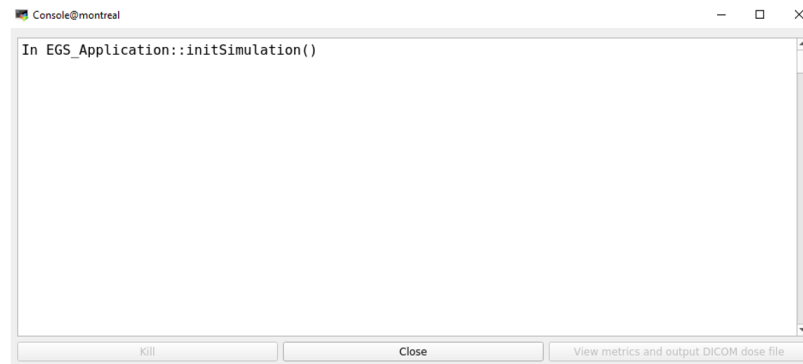


Figure 13: Snapshot of the `egs_brachy` console

After the simulation has run, the user can view metrics and generate a DICOM dose file.

2.3 Extra Options

This tab implements additional tools to manipulate DICOM and 3ddose files.

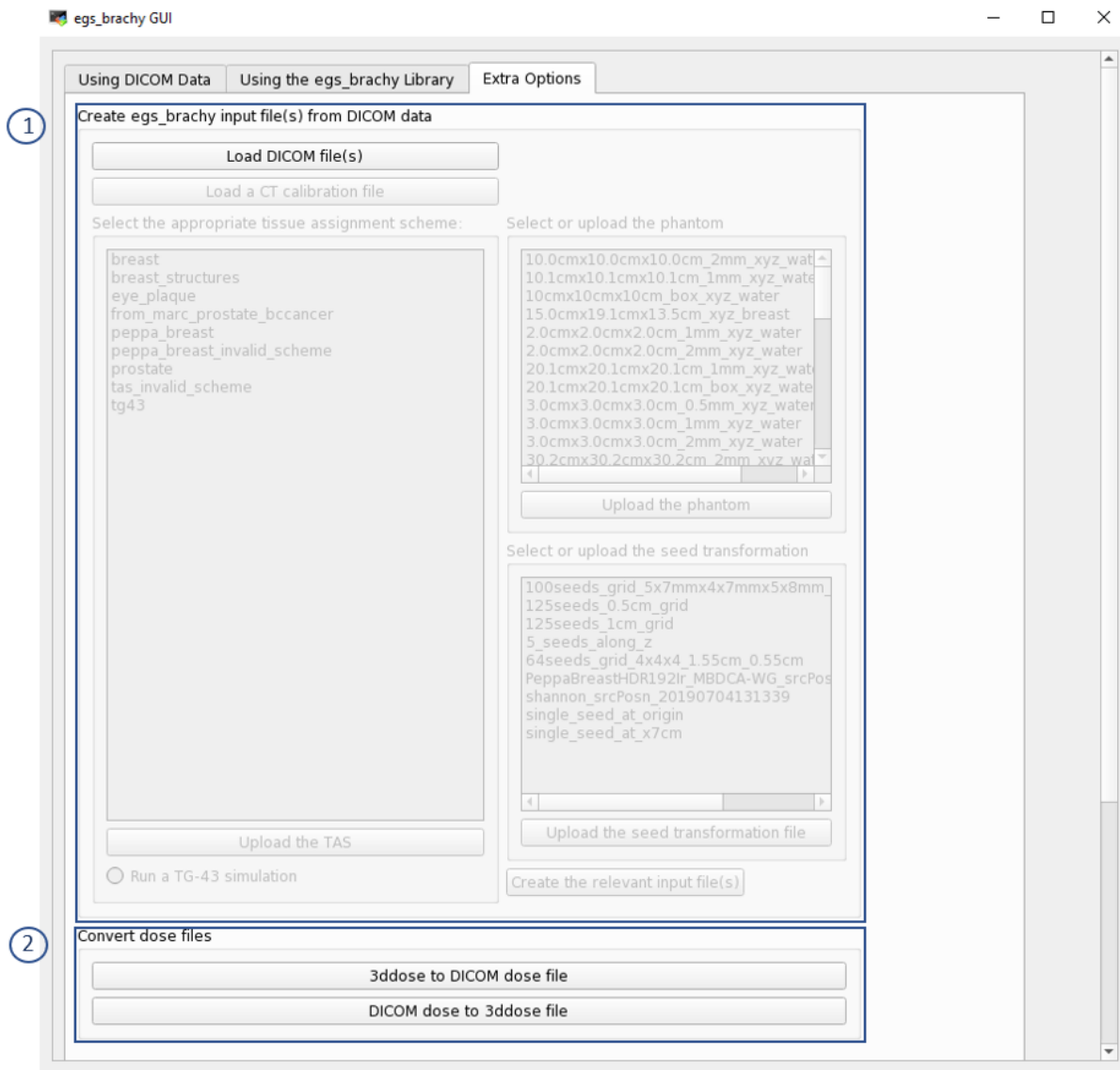


Figure 14: Snapshot of the 'Additional Functionality' window

In region 1, the user begins by loading DICOM files (structure, plan and/or CT). Based on the type of DCIOM file(s), different portions of the window will become enabled. Once the selections are made, clicking on *Create the relevant input file(s)* will commence the generation of the relevant **egs_brachy** input files.

In region 2, selecting *3ddose to DICOM dose file* will convert a **egs_brachy** 3ddose file into a DICOM dose file. Conversely, *DICOM dose to 3ddose file* converts a DICOM dose file to a 3ddose file format.

2.3.1 Create egs_brachy input file(s) from DICOM data

Description of Components

This pane allows the user to create the relevant **egs_brachy** file(s) corresponding to the selected DICOM file(s). Based on the modality of the DICOM file(s) (RTSTRUCT, RTDOSE or RTIMAGE), the appropriate elements in the pane are enabled.

- **Load DICOM file(s):** This button prompts the user to load the DICOM files. When this button is clicked, all previously loaded DICOM data is deleted from memory.
- **Load a CT calibration file:** If CT DICOM file(s) are loaded, this button becomes enabled. The button prompts the user to select a CT Calibration file. The file must be of the type .hu2rho and consist of a list of CT pixel numbers in Hounsfield Units and corresponding mass density measured from the CT scanner's calibration. If no file is uploaded, a default calibration is used. The default .hu2rho data is shown in Table 1 and Section 3.1 describes the format of the file.
- **Select the appropriate tissue assignment scheme:** If CT DICOM file(s) and a Structure file is loaded, this pane is enabled and the user must select the corresponding tissue assignment scheme for the CT data. This scheme contains a mapping from organ names to the tissues within the organ and the density threshold of each tissue. The format of the tissue assignment scheme is outlined in Section 3.2.
- **Select or upload a phantom:** If a DICOM Plan file is loaded and no DICOM CT files are loaded, the phantom pane will become enabled. This selection is used to create the egsinp file. When selecting the phantom, the user can either select one from the provided list or upload their own phantom. The list of phantoms includes all files with the .geom or .egsphant extension in the **egs_brachy** phantom library (/lib/geometry/phantoms/). If the user uploads a phantom, it will appear and be selected in the list of phantoms.
- **Select or upload the seed transformation:** If a DICOM Plan file is not loaded, the seed transformation pane will become enabled. This selection is used to create the egsinp file. When selecting the seed transformation file, the user can either select one from the provided list or upload their own. The list includes all files with in the

egs_brachy library (/lib/geometry/transformations/). If the user uploads a file, it will appear and be selected in the list.

- **Create the relevant input file(s):** This button creates the relevant input files;
 - **egsinp:** This file is created if the user uploads all the required DICOM files (CT and struct) or if the user has made the phantom and seed transformation file selections, if enabled. If the egsinp file will not be generated, a message will appear to the user asking if they would like to return to the tab such that the appropriate selections can be made and an egsinp can be generated. An example of the message window when loaded DICOM CT files and a structure file is shown below;

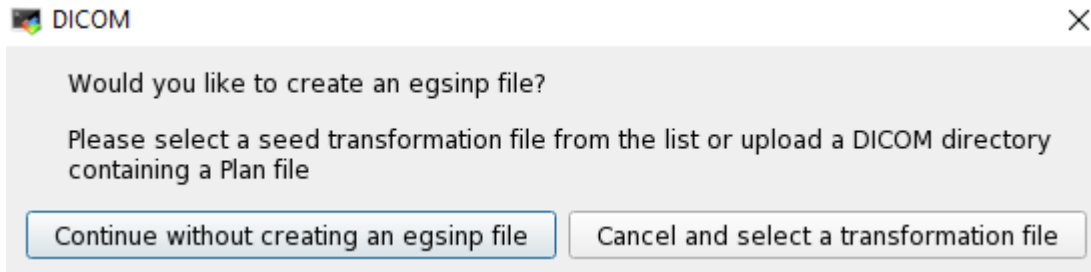


Figure 15: Snapshot of a warning message when loaded DICOM CT and structure files and no seed transformation file is selected

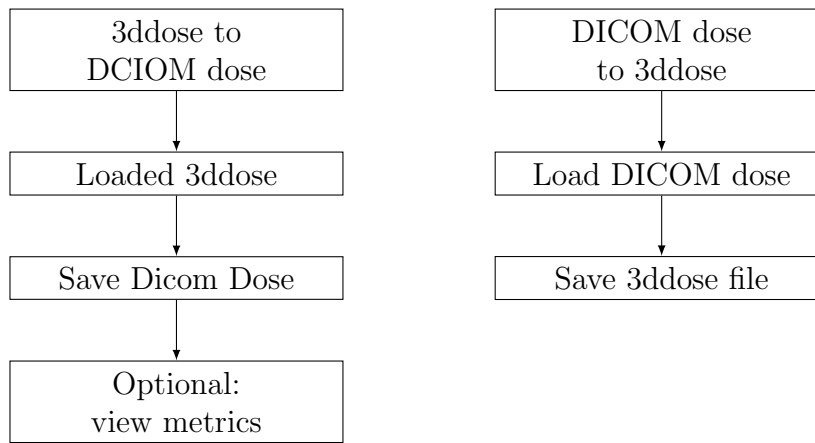
The user will be asked to select the source model.

- **egsphamt:** This file is created if CT file(s) are loaded. If a DICOM structure file is loaded, the user will have the option to select a tissue assignment scheme. If not, a TG-43 simulation is preformed.
- **seed transformation:** The seed transformation file is created if a plan file is loaded. Note that the dose scaling factor and source weights are required by the egsinp. If the DICOM plan file is not loaded and an egsinp is generated, a warning message is output to the terminal.

Based on the type of files loaded, the user will be asked to verify the location(s) of the input file(s). A message window will appear when the input file(s) have been successfully created.

2.3.2 Convert dose files

Flowchart



Description of Components

This pane is used to convert between the .3ddose and DICOM dose format.

- **3ddose to DICOM dose file:** This button reads a .3ddose file and formats the data to be outputted as a DICOM dose file. After the DICOM dose file has been created, the user will be asked if they would like to view the metrics for the entire phantom. The dose error from the .3ddose file isn't included in the DICOM dose file.
- **DICOM dose to 3ddose file:** This button reads a DICOM dose file and converts it to a 3ddose file. The .3ddose file won't contain the error value array (information pertaining to the error on the dose).

A description of the 3ddose file format can be identified in Section 12.1 of the DOSXYZnrc user manual [4].

3 Format of files used in egs_brachy_GUI

3.1 .hu2rho

The .hu2rho file contains the calibration data to convert the CT pixel values in Hounsfield units to a mass density (g cm^{-3}). It is a space delimited file. The first value corresponds to the CT number and the second value is the mass density.

Table 1 displays the default data within `default_CT_calib.hu2rho` distributed with egs_brachy_GUI.

Table 1: Default CT Calibration Curve Data

CT Number / HU	Mass Density / g cm^{-3}
-3025	0.001
-1000	0.001
0	1.008
61.9	1.073
1000	1.667
2000	2.300
3000	2.933
3100	2.999
5000	2.999
10000	7.365
20000	10.000
25000	10.000

When using the GUI, if a user loads DICOM CT files, they have the option to select a CT calibration file (Step 2 in Figure 1 and Step 1 in Figure 14). If no file is selected, the default file (`default_CT_calib.hu2rho`) is used.

3.2 Tissue Assignment Scheme

Each voxel in the patient phantom is assigned a tissue based on its density and the organ/contour it is within. The name of each contour and optionally the type (organ, PTV, CTV, external, applicator...) is identified in the DICOM struct file. The tissue assignment scheme (TAS) is used to identify the tissues and density threshold for each contour. It is a space delimited `.txt` file where each line has the following structure; Organ name, tissue name and maximum density threshold. The tissues for each contour are listed in order of increasing density. The minimum density of the first listed tissue of a contour is 0. The minimum density for each tissue within the same contour thereafter is the maximum threshold of the tissue above it.

Each tissue assignment scheme must have contour(s) named either;

- **default_internal and default_external** if the DICOM struct file has identified an external patient contour (i.e. there is a contour where the DICOM RT ROI Interpreted Type Attribute, tag 3006 00A4, is EXTERNAL). The default_external tissues are used

for all un-assigned voxels outside of the external patient contour and default_internal tissues are used for all un-assigned voxels within the external patient contour.

- **default** is used if the DICOM struct file does not contain an external patient contour. All voxels outside of a contour will be assigned to the default tissue(s).
 - Note: If there is a DICOM contour named 'Body' and default_internal has been included in the tissue assignment scheme, it is recommended to assign the contour to the default_internal tissue(s).

If the required contour name(s) are missing in the TAS, a message will be output to the console and the user will be asked to select a valid file. It is recommended to include all default schemes; default_internal, default_external and default. Additionally, all spaces in the contour name must be replaced by an underscore (i.e. chest wall must be written as chest_wall).

An example of a breast tissue assignment scheme generated from Stephen Deering's thesis [2] is shown below;

```

Lung AIR_TG43 0.0275
Lung LUNG_BLOODFILLED_WW86 3
Heart HEART_BLOODFILLED_WW86 3
Ribs YELLOW_MARROW_WW86 1.005
Ribs RED_MARROW_WW86 1.055
Ribs CORTICAL_BONE_WW86 3
chest_wall ADIPOSE2_WW86 0.9476
chest_wall MUSCLE2_WW86 1.066
chest_wall CARTILAGE_WW86 1.16
chest_wall CORTICAL_BONE_WW86 3
Skin AIR_TG43 0.0275
Skin SKIN2_WW86 3
Breast ADIPOSE2_WW86 0.9476
Breast GLAND2_WW86 1.16
Breast CALCIFICATION_ICRU46 3
default_external AIR_TG43 0.0275
default_external ADIPOSE2_WW86 0.9476
default_external MUSCLE2_WW86 1.16
default_external CORTICAL_BONE_WW86 3
default_internal AIR_TG43 0.0275
default_internal ADIPOSE2_WW86 0.9476
default_internal MUSCLE2_WW86 1.16
default_internal CORTICAL_BONE_WW86 3
default AIR_TG43 0.0275
default ADIPOSE2_WW86 0.9476
default MUSCLE2_WW86 1.16
default CORTICAL_BONE_WW86 3

```

3.3 default_files.txt

This file is used to set the location of default files in `egs_brachy`. The information for each line in `default_files.txt` corresponds to the file path in `egs_brachy` as follows;

1. Material data file
2. Muen file
3. Default low energy transport parameter file
4. Default high energy transport parameter file

5. Remaining lines contain the default locations of all spectrum files. The spectrum files must be named such that all characters before the first underscore correspond to a brachytherapy radionuclide (for example, Pd103_NNDC_2.6_line.spectrum).

The contents of the `default_files.txt` distributed with egs_brachy_GUI is shown below;

Table 2: Contents of the distributed `default_files.txt` file

```
/lib/media/material.dat
/lib/muen/brachy_xcom_1.5MeV.muendat
/lib/transport/low_energy_default
/lib/transport/high_energy_default
/lib/spectra/bareco60_line.spectrum
/lib/spectra/Cs131_NNDC_2.6_line.spectrum
/lib/spectra/Cs137_NNDC_2.6_line.spectrum
/lib/spectra/I125_NCRP_line.spectrum
/lib/spectra/Ir192_NNDC_2.6_line.spectrum
/lib/spectra/Pd103_NNDC_2.6_line.spectrum
/lib/spectra/Rh106_ICRU72_line.spectrum
/lib/spectra/Yb169_NNDC_2.6_line.spectrum
```

3.4 Air Kerma (.Sk)

The air kerma value for each source model is saved as a `.Sk` file within the **Air kerma** directory of egs_brachy_GUI. Each file is named based on the `egs_brachy` source model and contains the corresponding air kerma per history value (S_K^{hist} , units: Gy cm³/history), without the margin of error. The data is obtained from Section 9.1 of the `egs_brachy` user manual [3].

4 Limitations of egs_brachy_GUI

This section describes some limitations and user warnings for egs_brachy_GUI.

4.1 Using a Subset of DICOM Data CT Images

If using a subset of CT images to create the `egs_brachy` input files, caution must be taken. It is required that all contour data (from the DICOM structure file) is within the bounds of the patient model. In other words, each contour point must correspond to a CT image.

4.2 Size of DICOM Dose Data

When converting the 3ddose file to a DICOM dose file, there is a limit on the size of dose data that can be outputted to a DICOM file. Since each DICOM data element has a corresponding length value, the maximum length of any data is the maximum value of a 32 bit unsigned integer (4,294,967,295 bits). This corresponds to a maximum phantom size of 1,073,741,823 voxels as each voxel dose number requires 4 bits to write.

4.3 Size of egsphant

When running `egs_brachy` simulations, one needs to be conscious of the size of egsphant. If the egsphant is very large, `egs_brachy` may be killed when attempting to output the 3ddose file, due to its size. If the egsphant is greater than 300 slices, it is recommended to use the trim functionality to reduce the number of voxels.

4.4 Computer Architecture

To obtain an accurate egsphant, the GUI must be ran on a computer using a discreet GPU with a vendor implementation of OpenGL. Computers using software implementations of OpenGL will result in inaccuracies.

5 References

- ¹ M. J. P. Chamberland, R. E. P. Taylor, D. W. O. Rogers, and R. M. Thomson, egs_brachy: a versatile and fast Monte Carlo code for brachytherapy, Phys. Med. Biol. 61, 82148231 (2016)
- ² Deering, S. (2017). Monte Carlo Dose Calculations for Permanent Breast Seed Implant Brachytherapy (Master's thesis). Retrieved from <https://curve.carleton.ca/450b147b-d385-47a3-8f12-c0a479f2ece7> (p 21, 83).
- ³ Rowan M. Thomson, Randle E. P. Taylor, Marc J. P. Chamberland, and D. W. O. Rogers, Report CLRP-17-02, Carleton Laboratory for Radiotherapy

Physics, Department of Physics, Carleton University, Ottawa, Canada. https://clrp-code.github.io/egs_brachy/pdf/egs_brachy_user_manual.pdf, 2017.

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