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User guide for eb_gui

A Graphical User Interface for egs_brachy

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Latest version available at
https://github.com/clrp-code/eb_gui

Abstract

This report provides an overview of eb_gui, a graphical user interface for egs_brachy, a fast Monte Carlo code for simulating brachytherapy treatments. eb_gui facilitates use of clinical data with egs_brachy by reading patient DICOM files, creating a patient-specific model, and launching the egs_brachy code. It can convert 3ddose files to DICOM dose format. The GUI is programmed in C++ using the Qt5 framework.

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1. Introduction

egs_brachy is an efficient and versatile Monte Carlo simulation code specifically designed for brachytherapy applications. It was first introduced and benchmarked in 2016 [1], with an open-source release on GitHub in 2017 [2]. Built on the EGSnrc code system [3], egs_brachy uses an extended C++ class library from EGSnrc to model complex geometries necessary for clinical use. Extensive benchmarking has been conducted in previous studies [1, 4], and the ongoing development of a comprehensive library of sources and applicator models continues. For instance, photon-emitting sources and eye plaque models have been used to update the Carleton Laboratory for Radiotherapy (CLRP) TG43 and eye plaque databases [5-7]. Recent advancements include patient-specific simulations conducted using egs_brachy [8, 9], and the creation of a graphical user interface (GUI), eb_gui to simplify clinical implementations of egs_brachy.

eb_gui is a companion software designed to streamline the use of egs_brachy by providing a user-friendly interface for Monte Carlo dose evaluations in brachytherapy. The eb_gui technical note [10] describes its development and validation, offering a user-friendly platform for Monte Carlo dose evaluations in clinical settings. The software has been validated with WG-MBDCA IROC Houston test cases, with a primary focus on high-dose-rate (HDR) Ir-192 brachytherapy [11]. It supports commissioning across various HDR and low-dose-rate (LDR) scenarios, all aligned with TG-186 and AAPM WGDCAB Report 372 [12, 13] recommendations.

The eb_gui is a C++ code written in the Qt5 framework that allows users to convert the clinical DICOM format to EGSnrc friendly formats, and to run egs_brachy remotely. The eb_gui program allows users to import data from DICOM CT and associated structures found in DICOM RTSTRUCT files to build a phantom or virtual patient model. Additionally, the program allows the importation of relevant clinical brachytherapy plan data from DICOM RTPLAN files, which contain radioactive source information, for defining the source(s) for simulation. The amalgamated DICOM data can then be employed in simulating Monte Carlo code, ultimately enabling the calculation of a full patient dose distribution in the EGSnrc 3ddose format. Tools within eb_gui can then be used to generate phantom images, dose color maps, dose volume histogram (DVH), isodose contours, dose line profiles, and requested clinical dose metrics. Furthermore, eb_gui can also convert the egs_brachy output to a DICOM RTDOSE file, providing users with a versatile range of functionalities for comprehensive analysis and visualization. The CLRP eb_gui code is publicly available at https://github.com/clrp-code/eb_gui for installation and all computations here-in are performed with commit c14a205.

An overview of this user manual is as follows: Section 2 covers the eb_gui license and copyright information. Installation instructions for eb_gui are detailed in section 3, while section 4 explains how to run the application. An overview of eb_gui components can be found in section 5. Section 6 provides a step-by-step example of a test case simulation. Section 7 outlines the procedures for HDR simulation. Finally, section 8 discusses the limitations of eb_gui and outlines potential future developments.

2. License

3. Installation and Set-up

Before installing eb_gui, it is necessary to set up egs_brachy. The following steps outline the prerequisites for a successful installation.

3.1 Prerequisites

The installation and performance of egs_brachy depend on specific hardware components, as outlined below.

CPU - The CPU speed and core count are the primary factors affecting simulation duration. The CPU speed directly impacts the simulation speed, while the core count allows for parallelization of simulations.

RAM - For parallel simulations, allocate approximately 2GB of RAM per core that the user intends to use. Ensuring sufficient RAM is essential for optimal performance.

Drives - Operations can be conducted on a traditional Hard Disk Drive (HDD), though a Solid-State Drive (SSD) can significantly boost the speed of DICOM conversion tools, simulation startup, and output. An optimal setup involves a 256 GB SSD for installation and performing simulations, complemented by a 1+ TB HDD for storing the large data files during extended use.

Video Card - The DICOM conversion tools use OpenGL libraries for byte stream data transfer. While a GPU is not mandatory, it can provide substantial speed improvements. Additionally, a video card has the potential to accelerate auxiliary analysis tools.

3.2 Setting up a LINUX environment (Step 0)

It is recommended that the user performs this installation in a Linux system, either real or virtual. If the user has access to an up-to-date Windows 10 installation, **it is highly recommended** to install Windows Subsystem Linux (WSL). WSL provides the full functionality of a Linux installation (this guide will assume Ubuntu from here-on) within the active Windows environment. It allows access to all Windows files through Linux and all Linux files through Windows Explorer. The only requirement is enabling CPU Virtualization, a setting that can be confirmed in Task Manager, as shown in Figure 1.

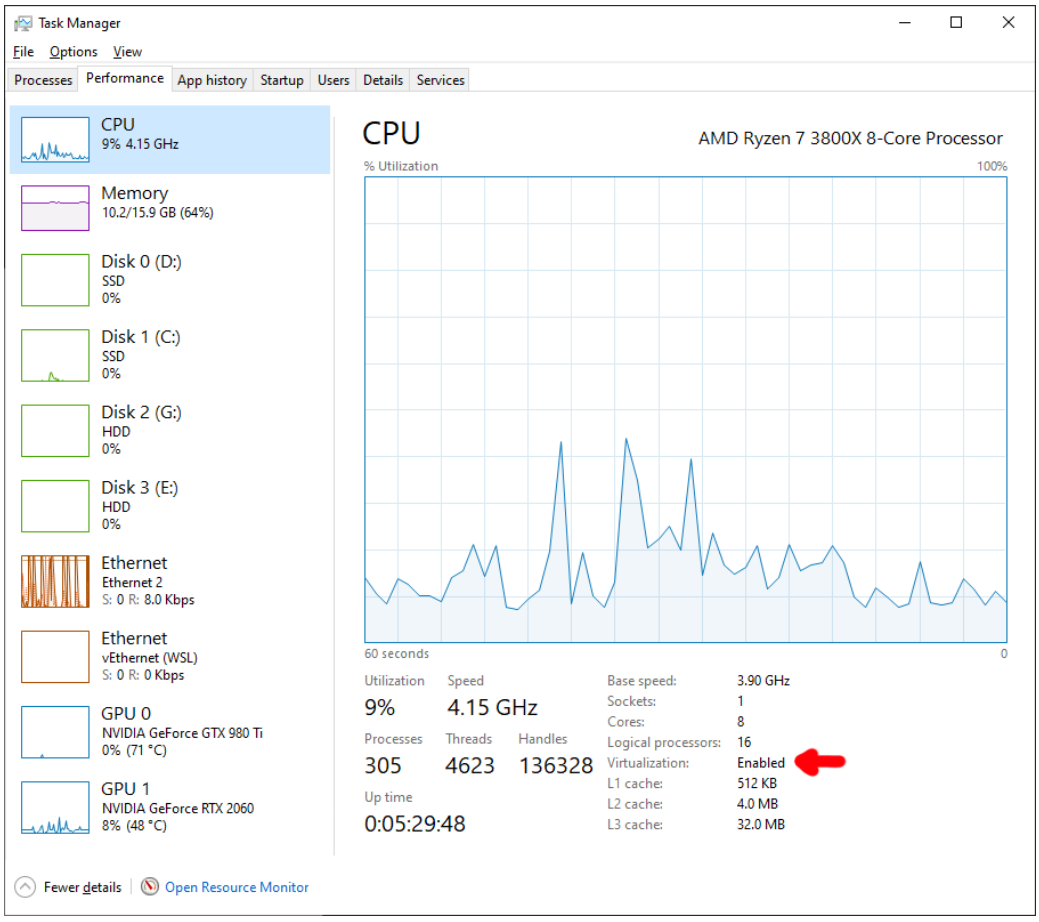


Figure 1. Enabled Virtualization option in Task Manager.

Most AMD and Intel CPUs support virtualization, referred to as Secure Virtual Machine (SVM) and Virtualization Technology for AMD and Intel, respectively. This feature can be activated in the BIOS if not enabled by default.

To install WSL, open the run window (Windows key + r) and enter the following command: optionalfeatures.exe

Scroll down to the "Windows Subsystem for Linux" option and make sure it is checked as shown in Figure 2. Afterward, restart Windows. Post-reboot, visit the Microsoft Store and install Ubuntu from https://ubuntu.com/download/desktop. Now, Windows will include an app called Ubuntu, allowing the user to launch the WSL kernel. Though the built-in console is sufficient, it is recommended to enhance the experience by downloading Mobaxterm, available at https://mobaxterm.mobatek.net/download.html, which includes a built-in X server for launching GUI windows. Alternatively, users not opting for Mobaxterm can install a third-party X server application, such as VcXsry, available at https://sourceforge.net/projects/vcxsrv/, to launch graphical user interfaces (GUIs).

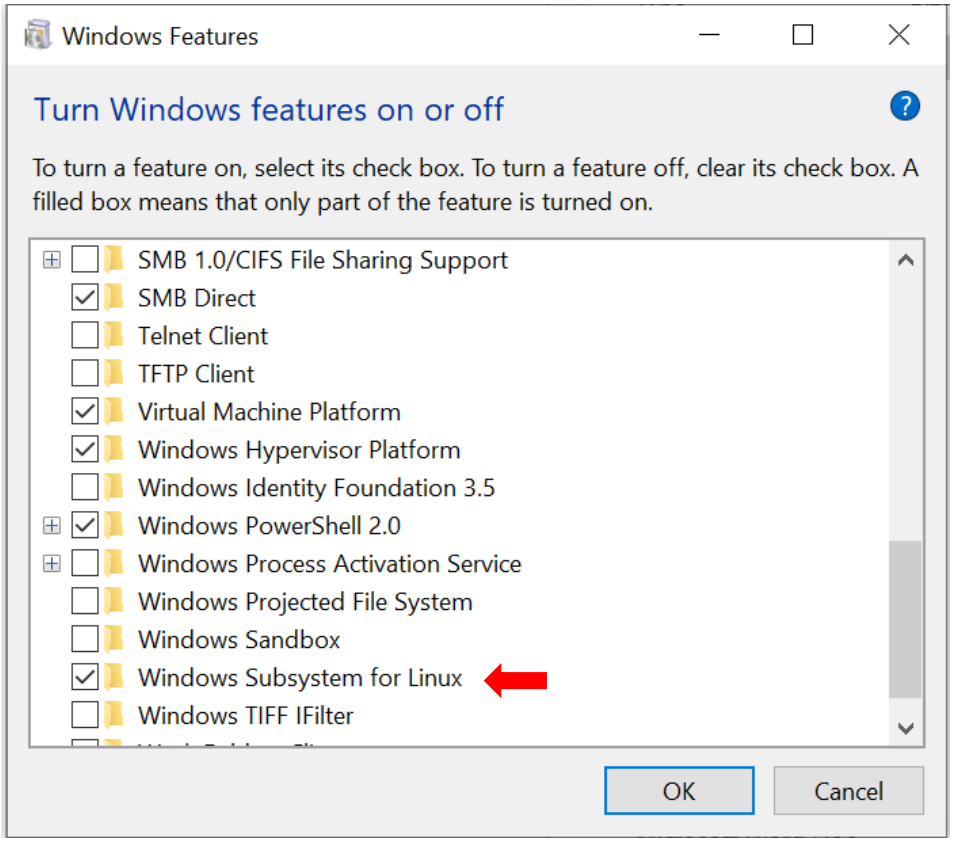


Figure 2. Set Windows subsystem for Linux

3.3 Installing Linux software essentials (for users new to Linux)

Upon entering the working Linux environment, typically located at /home/username, users can perform fundamental file operations using the following commands:
List all files in a directory: `ls`
Change to a directory named “Folder”: `cd Folder`
Change to a parent directory: `cd ..`
Copy a file X to a new one named Y: `cp X Y`
Delete a file named X: `rm X`
Move/Rename a file X to Y: `mv X Y`
Move a file X to a directory in the user’s home area called “Folder”:

```
mv X /home/username/Folder/
```

Files and folders in the Windows directory can be found at: \\wsl$\Ubuntu\home\username\ if using WSL. If one cannot open the Windows directory for the first time, open the WSL console and use the following command: `explorer.exe.`

It is recommended to familiarizes oneself with the above bash shell commands. For brand-new Linux environments (assuming Ubuntu), the following commands can install all the necessary essentials for egs_brachy:

```
sudo apt-get update -y
sudo apt-get install build-essential gfortran zlib1g-dev git qtdeclarative5-dev qttools5-dev libqt5charts5-dev python3
```

These commands utilize the package manager (apt for Ubuntu) and administrative privileges (sudo) to update the list of online packages, and install:

- build-essential: Essential compilers (C, C++)
- gfortran: Fortran compiler needed for EGSnrc
- zlib1g-dev: C++ library used in dose file compression
- git: Program for fetching the appropriate EGSnrc and egs_brachy repositories
- qtdeclarative5-dev: Necessary Qt libraries for egs_view and egs_brachy_GUI
- qttools5-dev: Includes the qmake tool used to compile egs_view and egs_brachy_GUI
- libqt5charts5-dev: Includes libraries for generating plots in Qt
- python3: Scripting language used in the egs_brachy testing scripts

3.4 Installing egs_brachy with the EGSnrc_CLRP GitHub repository

To install egs_brachy with the EGSnrc_CLRP GitHub repository, follow these steps:
Clone the online distribution of EGSnrc with built-in egs_brachy provided by CLRP. Navigate to the preferred installation location (assuming the home directory in this guide) and run the following command:
`git clone --recurse-submodules https://github.com/clrp-code/EGSnrc_CLRP.git`
This command creates the EGSnrc_CLRP folder '`/home/username/EGSnrc_CLRP`

In the EGSnrc_CLRP repository, the HEN_HOUSE folder contains all the source code and databases required for EGSnrc simulations, along with installation scripts for building user applications, such as egs_brachy.

To create a home area, the user first needs to navigate to the "scripts" directory: `cd EGSnrc_CLRP/HEN_HOUSE/scripts/` .Then, they need to invoke the configure script: `./configure`

This script will guide the user through all the installation options for EGSnrc. Below is a summary of the steps:

1. **Fortran Compiler**: The script will prompt for a Fortran compiler, listing options like gfortran, f77, and f95. Choose the default (gfortran) by pressing Enter.
2. **Standard Compilation Flags:** The default recommendation is -fPIC. Press Enter to accept unless you need a different setting.
3. **Optimization Flags**: The default is -O2 -mtune=native. Press Enter to proceed unless you require specific flags.
4. **Debugging Flags**: The default is -g. Press Enter unless you need something else.
5. **Additional Input Libraries**: Leave this blank and press Enter.
6. **C Compiler**: The script will list options like gcc, cc, and c89. Choose the default (gcc).
7. **Compiler Flags**: The default is -O2 -fPIC. Press Enter unless you need different flags.
8. **HEN_HOUSE Directory Path**: The default should be /home/username/EGSnrc_CLRP/HEN_HOUSE. Press Enter unless the path is incorrect.
9. **Configuration Name**: The default is likely linux.conf, but any name will work as long as it matches in step 15.
10. **C++ Compiler**: The only likely option is g++. Choose the default and proceed.
11. **Flag Changes**: The script will prompt for changing up to 8 different flag sets. Unless you have specific needs, proceed with the defaults.
12. **Finalization**: After compilation, the script will ask if you want to finalize for username. Choose Yes.
13. **User Code Installation Location**: You can select any location for user codes (like egs_brachy), but ensure it matches step 15.

14. **User Code Compilation**: When asked which user codes to compile, select "some" and enter egs_brachy. Compilation may take time.
15. **Environmental Variables**: After completion, the script will provide a list of environment variables to add to your .bashrc file. You need to update the following variables:
    - `EGS_HOME` should point to the directory chosen in step 13.
    - `EGS_CONFIG` should point to the configuration file chosen in step 9.
    - Ensure all paths reflect the location where EGSnrc_CLRP was cloned.

Additionally, set the EGS_BATCH_SYSTEM variable to “at”. If you used the default values, append the following lines to your .bashrc:

- export EGS_HOME=/home/username/EGSnrc_CLRP/egs_home/
- export EGS_CONFIG=/home/username/EGSnrc_CLRP/HEN_HOUSE/specs/linux.conf
- source /home/username/EGSnrc_CLRP/HEN_HOUSE/scripts/egsnrc_bashrc_additions
- export EGS_BATCH_SYSTEM=at

Alternatively, you can automatically append it to your bashrc file by running the following commands:

```
echo “export EGS_HOME=/home/username/EGSnrc_CLRP/egs_home/” > ~/.bashrc
echo “export EGS_CONFIG=/home/username/EGSnrc_CLRP/HEN_HOUSE/specs/linux.conf” > ~/.bashrc
echo “source /home/username/EGSnrc_CLRP/HEN_HOUSE/scripts/egsnrc_bashrc_additions” >
~/.bashrc
echo “export EGS_BATCH_SYSTEM=at” > ~/.bashrc
```

After all the above are set, the user can restart their console and be able to start their egs_brachy simulations. After resetting, the user can use the command `clrp_help` to list all the additional aliases in CLRP additions.

*egs_view installation

egs_view code can be used to visualize geometry. The user needs to navigate to:

```
cd $HEN_HOUSE/egs++/view/
```

And then invoke the two following commands:

```
make Makefile_linux
make
```

3.5 Installing eb_gui

The user should navigate to their preferred install location and clone the eb_gui code:
`git clone https://github.com/clrp-code/eb_GUI.git`
Once cloned, move to the source code directory: `cd eb_GUI/source/`
In the source code directory, run the following two commands to build the eb_gui executable in the parent directory: `qmake` and `make`
After the build process, navigate to the main eb_gui directory and launch the GUI: `./eb_gui`
This command will open the graphical user interface for eb_gui.

3.6 Frequently encountered problems during installation

a. If you see the message "error while loading shared library: libQ5core.so.5", you'll need to remove the file to reset. This command should cover it:
`sudo strip --remove-section=.note.ABI-tag /usr/lib/x86_64-linux-gnu/libQt5Core.so.5`

b. If the above command doesn't work, and the x86_64-linux-gnu directory does not exist, check the compiler output above. It should list the location of libQ5core.so.5 it is checking.

c. If you see a lot of compiler error messages containing strings like "...was not declared in this scope", "no known conversion for argument 1 from 'std::_cxx11", or any general mention of "std", "cxx11", or "c++11", you will have to reinstall EGSnrc using configure as described in Step 2. The only difference is, during the install step 11 when the code requests flags, the user must add '-std=c++11' to the optimization options. Demonstrated here:

Using the following compiler/linker switches for creating/linking against dynamic shared objects (DSO, also known as shared library or DLL), where$(abs_dso) or $(ABS_DSO) below will be replaced with the absolute path to the EGSnrc DSO directory at compile/link time:
1) Optimization options: -O2 -mtune=native
2) Generation of position independent code: -fPIC
3) Preprocessor defines:
4) Flag for creating shared libraries: -shared
5) Output/dlopen library: -o $@ -ldl
6) DSO path encoded in the executable: -L$(abs_dso) -Wl,-rpath,$(abs_dso)
7) Linking against library some_lib: -lsome_lib
8) Fortran libraries needed by C++ linker: -lgfortran –lquadmath
Input option to change, or enter to proceed: 1

Input Optimization options: -std=c++11

The user should then proceed as normal, i.e., hit enter to proceed and go back to installation step 12.

4. Running eb_gui

The eb_gui application extends the capabilities of the egs_brachy application [1] developed by the Carleton Laboratory for Radiotherapy Physics (CLRP). This extension facilitates its integration into clinical applications, enabling efficient parsing of DICOM data to construct a patient model and prepare the requisite input files for subsequent execution by egs_brachy. The process further involves launching egs_brachy, calculating dose metrics, and generating a DICOM dose file based on the obtained results. Noteworthy is the additional feature of eb_gui, providing users with the flexibility to create input files from pre-defined phantoms within the egs_brachy library. A visual representation of these steps is presented in the accompanying flowchart (Figure 3).

This section provides an overview of eb_gui, organized into five tabs: Run egs_brachy; Import DICOM plan; Import DICOM Virtual Patient Model; Analyze Results; and Export Results. The following sections present theses tabs in more detail, starting with the import DICOM files. Furthermore, a detailed test case simulation, presented step by step is available in the next section of this document.

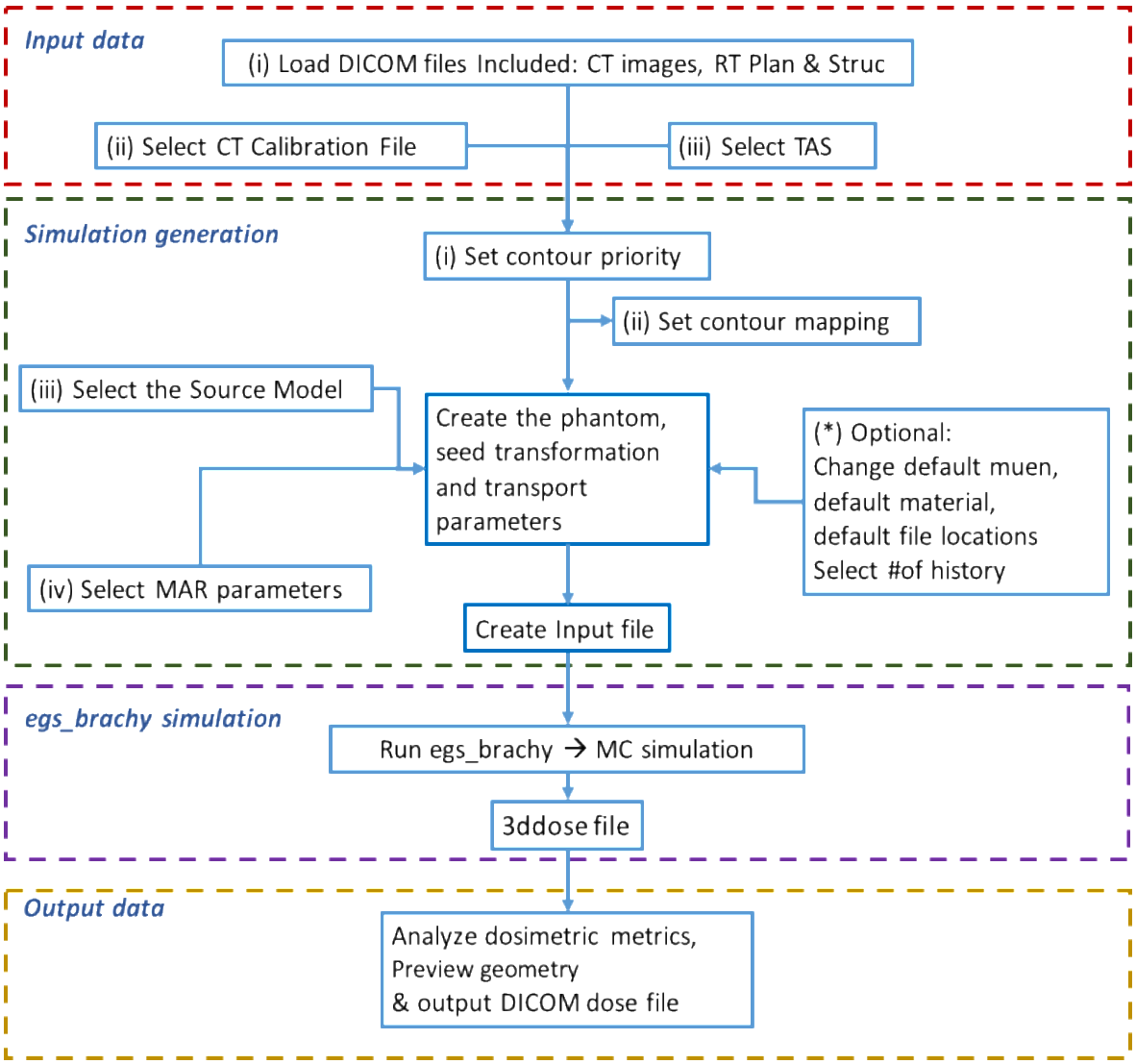


Figure 3. Flowchart of step-by-step process to use eb_gui

4.1 Import DICOM Plan tab

Import DICOM RT PLAN Data: As shown in Figure 4, click on Load to select RT plan file, input a name in the "Plan name" box, and then click on Import. Upon importing the RT plan, a text file will appear, containing detailed information about the treatment and source such as treatment type, technique, time, isotope, air kerma rate, air kerma strength, half-life, the date when the air kerma strength was measured, and the location of seeds. After closing this text file, all related source fields under the "RT PLAN Data" section will be automatically filled. Also, the given plan name will appear in the "Source Locations" panel. The RT PLAN log file and source location transformations will be saved in the 'home/username/eb_gui/database/transformation' directory.

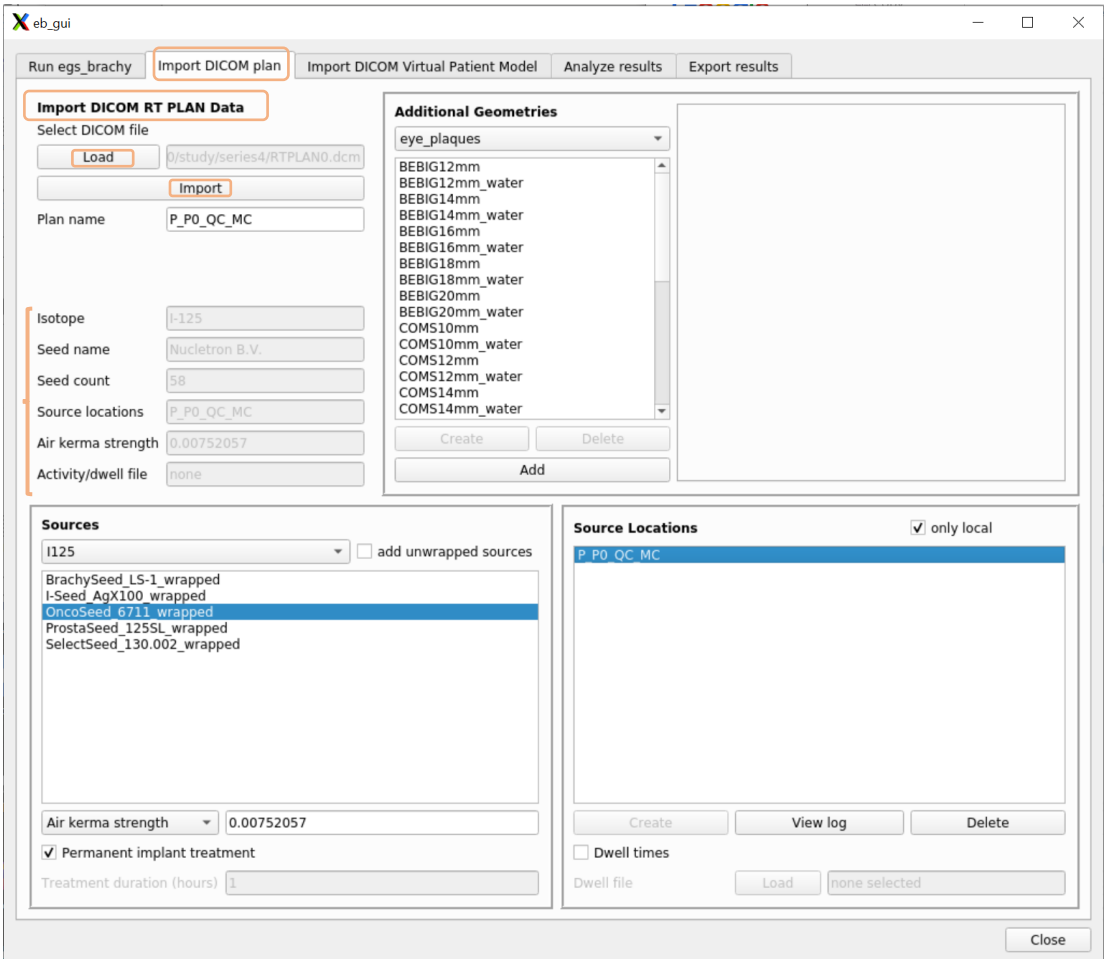


Figure 4. Snapshot of the 'Import DICOM plan' tab

Additional Geometries: Pre-defined geometries including eye_plaques and TG186_applicator can be selected from this tab to add to the simulation.

Sources: The source model will be selected from drop-down box in this tab. The list of available models is obtained from the directory egs_brachy/lib/geometry/sources/. The Air_kerma strength will be automatically filled from RT Plan file. For HDR cases, the option "Permanent implant treatment" should be unchecked. In such cases, the "Treatment duration (hours)" field will be displayed.

Source Locations: All imported plans are shown in this panel. One can review the log file again by clicking on View log. A source can also be removed from the source location by clicking on the Delete bottom. The transformation folder located in the 'EGSnrc_CLRP/egs_home/eb_gui/database/transformation' directory contains the location of the source(s). Note that eb_gui is unable to determine the source rotation as the source rotation information is not available in DICOM file.
For HDR cases, ensure the "Dwell times" option is checked, and the dwell file can be selected from the transformation folder in the same directory.

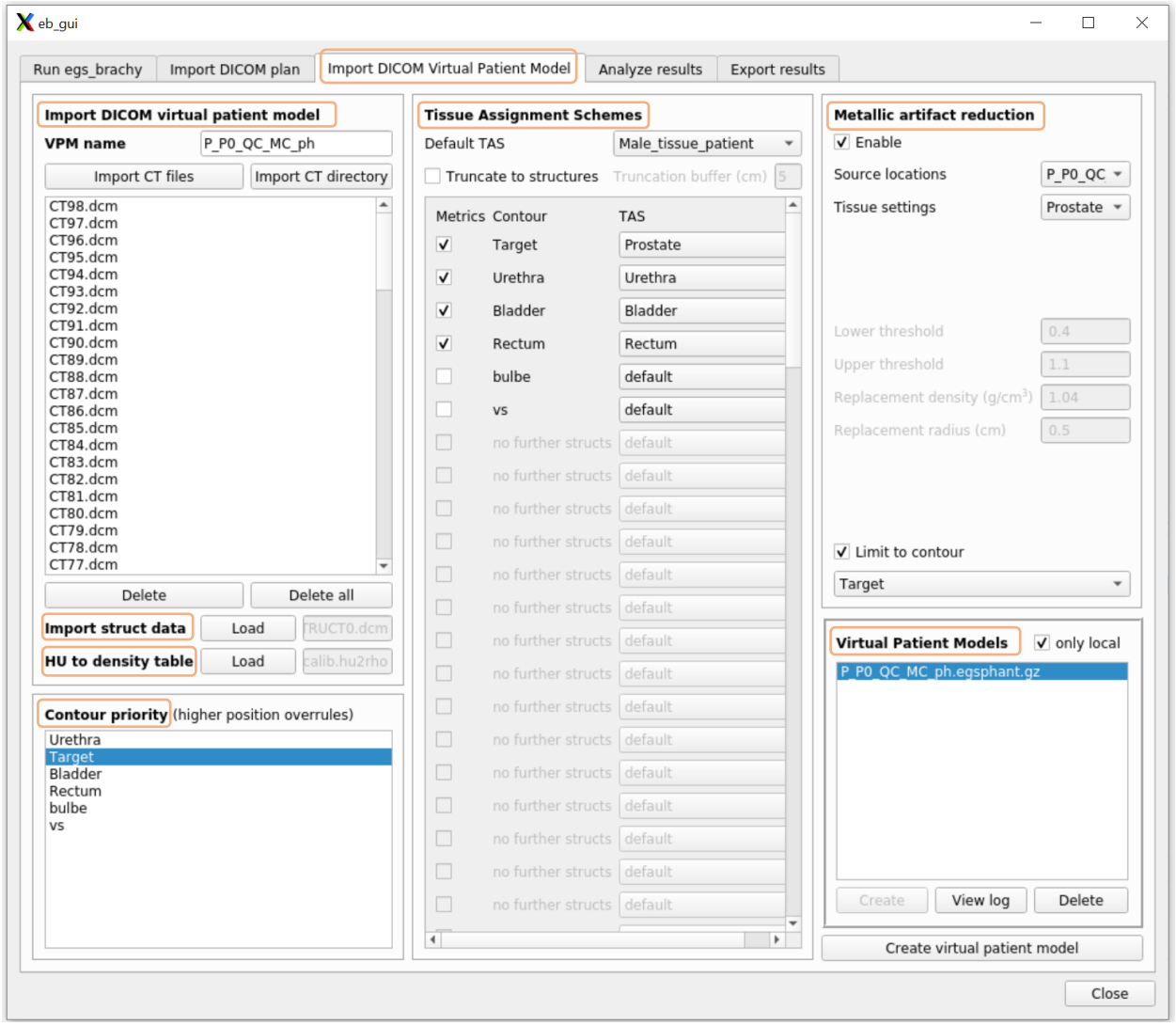


Figure 5. Snapshot of the ‘Import DICOM Virtual Patient Model’ tab

4.2 Import DICOM Virtual Patient Model tab

Import DICOM virtual patient model: In this panel as depicted in Figure 5, the CT image, structure file (struct data) and HU to density table can be imported. The initial step involves importing CT DICOM files by choosing either Import CT files or Import CT directory. Subsequently, the user is required to assign a name to the Virtual Patient Model (VPM). A confirmation window will appear, verifying the successful import of the CT files.

Using Load button, next to **Import struct data**, users can upload the RTstruct file associated with clinical tests. In the eb_gui, a default table is used to convert HU value to mass density. However, users are required to load a specific conversion lookup table corresponding to their CT machine by using the Load button next to the **HU to density table**. The file should be generated as a text file, with a mandatory *.hu2rho extension. It should consist of a list associating CT pixel number in Hounsfield Units with their respective mass density (g/cm^3), as measured through the calibration of the CT scanner. If no file is loaded, a default calibration file is used. Table 1 displays the default data within default CT calib.hu2rho distributed with eb_gui.

Table 1. Default HU to density table

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

Contour priority: This panel displays a list of contours, and users should organize them based on their specific cases. The priority is used if a voxel falls within two or more contours. In such cases, the higher priority will be assigned to the top contour. The priority of a contour is modified by selecting and dragging it to the desired position in the list. The contours with the highest priority are located at the top of the list.

Tissue Assignment Schemes: Within this panel, users are prompted to establish a mapping between DICOM structure contours and organ names specified in the tissue assignment scheme file. Various selections are available, each corresponding to a text file that encompasses the assignment scheme. These text files can be found in the 'eb_gui/database/ tissue_assignment_scheme' directory. The tissue assignment scheme (TAS) contains a mapping from each contour in the DICOM RTstruct file to the tissues within the contour and their density threshold. TAS is a space delimited .txt file where each line has tissue name and maximum density threshold. The tissues for each contour are listed in order of increasing density. Figure 6 shows tissue assignment schemes and Contour priority for breast cases.

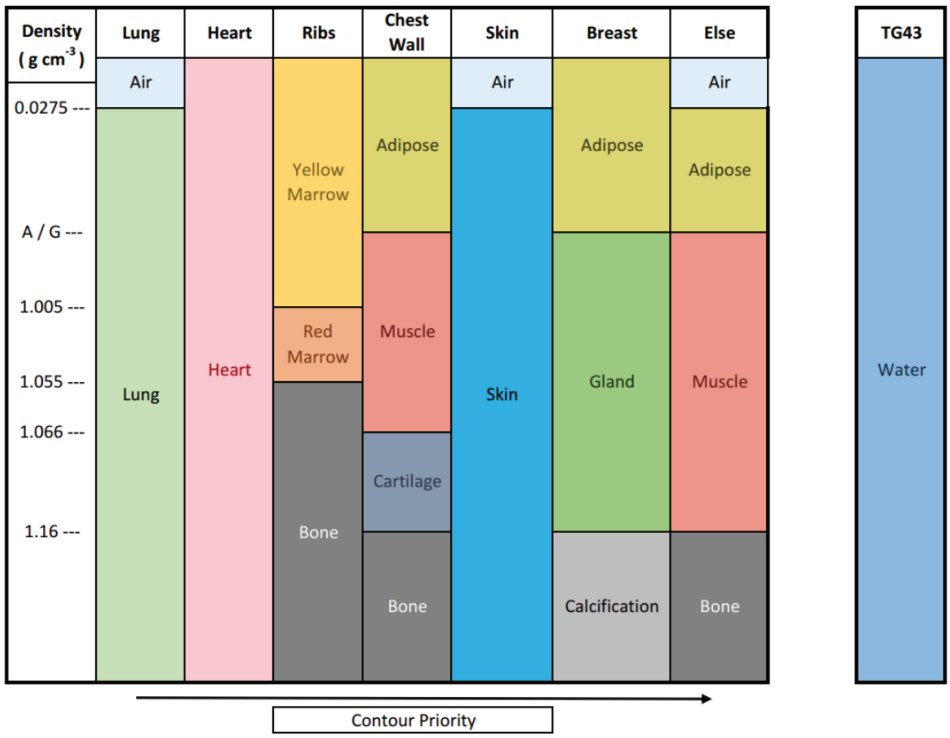


Figure 6. Overview of tissue assignment schemes and contour priority for breast cases. Vertical axis density values are not to scale [14]

The left-hand column in Tissue Assignment Schemes panel displays the list of **contour** names from the DICOM file (Figure 5). Each contour is accompanied by a corresponding drop-down box, enabling users to designate the relevant organ from the tissue assignment scheme. By default, eb_gui generates a mapping based on the similarities between DICOM contour and TAS organ names. If the drop-down selection is left blank (e.g. in Figure 5 the contour "vs" has no associated organ), the contour will be automatically assigned to the default tissue. The **Metric** option allows the users to generate a mask for the selected contour. This mask, formatted as an egsphant file, consists of 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. The **Truncate to structures** option allows the users to limit the simulation to a specific volume by selecting the buffer size. For example, in LDR cases, a minimum 5 cm buffer (from last seed) can be selected to simulate full scattering. This feature diminishes the VPM size and significantly accelerates simulation times. Workflow for eb_gui tissue assignment is presented in Figure 7.

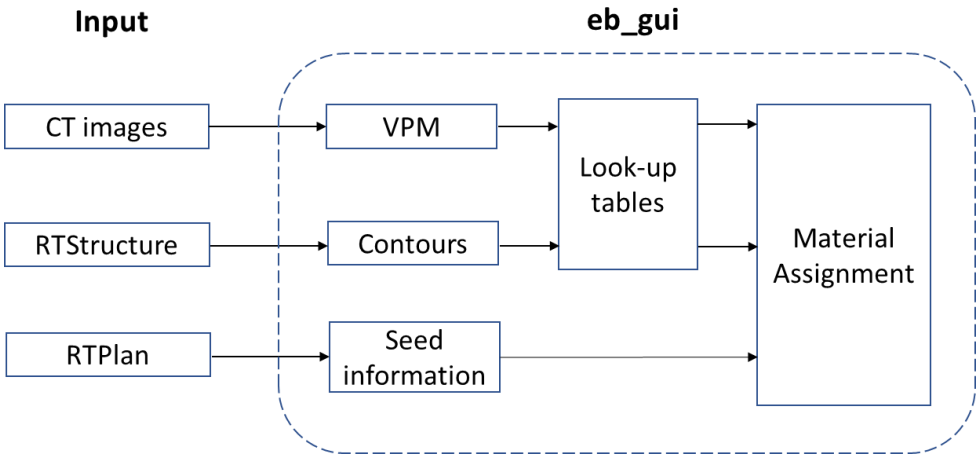


Figure 7. Workflow for eb_gui material assignment

Metallic artifact reduction (MAR): In LDR cases, a simple threshold replacement metallic artifact reduction can be performed to mitigate the effect of seed artifacts in CT images by checking Enable. Users should select the corresponding source location file created in the previous tab and choose an eb_gui default replacement values by selecting ***Prostate*** or ***Breast*** from "Tissue settings" drop-down. Alternatively, users can opt for the ***Generic*** or ***Custom*** option, allowing them to manually enter the replacement values.

The MAR process involves checking the density of voxels within a cylindrical region (0.5 cm radius and extending two slices above and below) surrounding each seed against defined low and high threshold density values. If a voxel's density falls outside of the specific threshold range (above the high threshold or below the low threshold), it is substituted with the replacement density. Additionally, users have the option to refine this process by selecting a contour that contains the seeds. By checking the ***limit to contour*** option, all voxels within the contour outside of the threshold are replaced with the replacement value. In the Figure 5, for example, the Target contour was selected for this purpose.

Virtual Patient Models: Upon clicking Create virtual patient model, a VPM in the egsphant.gz format will be added to the list in Virtual Patient Models panel. The VPM is saved in the '/home/username/EGSnrc_CLRP/egs_home/eb_gui/database/egsphant' directory. This panel provides an overview of all previously generated phantoms, allowing users to highlight a specific VPM for actions such as viewing the log file or deleting the file. An example of VPM log file is presented in Figure 8.

The egsphant file contains details including the media in the phantom, voxel boundaries in the x, y and z directions, an array of medium numbers for each z-slice, and the density of each voxel. Further information on the egsphant file can be obtained from Section 16.6 of the DOSXYZnrc user manual [15].

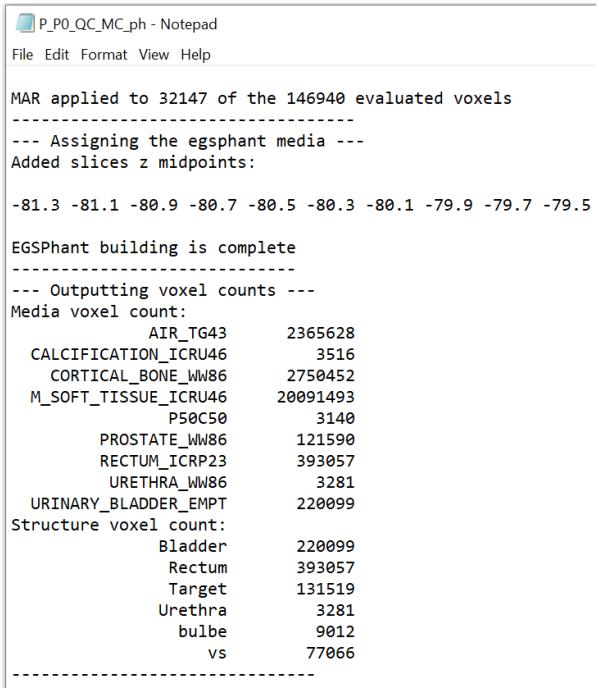


Figure 8. Snapshot of an example of VPM log file

4.3 Run egs_brachy tab

Illustrated in Figure 9, this tab serves two primary purposes: i) executing pre-prepared egs_brachy input files; and ii) running egs_brachy at the final step after importing DICOM files and creating VPM and input file. Different sections within this tab will be briefly explained as follows.

Virtual Patient Models: Within this panel, users can choose the desired VPM from a list of all the predefined or user defined VPM (by checking “only local” box) created by eb_gui. Users are provided with the options to View log file or Delete a selected VPM.

Sources: In this section, users have two options. The recommended approach is to select a source model from wrapped models. Alternatively, users can click the checkbox for “add unwrapped sources” to view all source models without a wrapper. The list of models is retrieved from /home/username/EGSnrc_CLRP/egs_home/egs_brachy/lib/geometry/sources/. The eb_gui automatically imports Air_kerma strength from DICOM file.

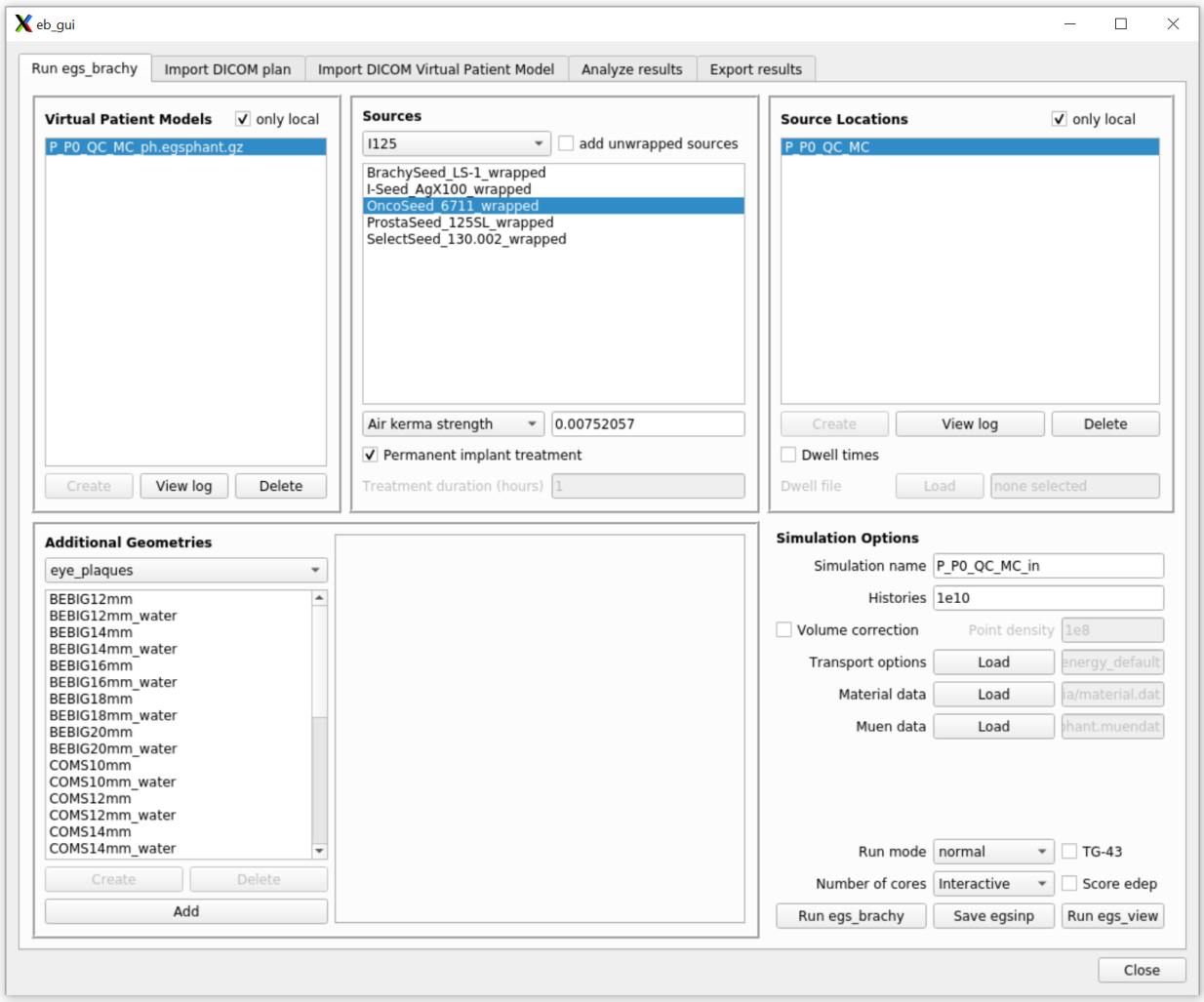


Figure 9. Snapshot of the eb_gui window with the Run egs_brachy tab highlighted

****Note**: If you are using a source file defined previously in eb_gui, the Air kerma strength will be displayed here as 1. To rectify this, select the plan file in **Source Locations**, click on View log to open the file, and copy the Air kerma strength from there. Then, paste it into the text box in front of Air kerma strength in this panel.
The "Permanent implant treatment" check will be selected unless an HDR case is uploaded. In this case, the "Treatment duration (hours)" field will be automatically imported.

- **Source Locations**: This panel enables users to select the relevant source plan from the list of files generated by eb_gui. The option to delete or view log file of RT plan file is also available.

"Dwell times": This option will be used if there is an HDR case. The dwell time files will be automatically created during the process of generating the source file and can be found in '/home/username/EGSnrc_CLRP/egs_home/eb_gui/database/transformation'.

- **Additional Geometries**: As explained before, users have the flexibility to incorporate predefined geometries from the provided list here. For example, one can add an applicator for HDR cases or utilize eye_plaque geometry as needed.

- **Simulation Options:** In this panel, users can change default parameters in the input 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:

Users have the option to provide a specific name for the simulation in front of ***Simulation name*** to save the input file with that name or leave it as is with automatically generated name. The input file, denoted with egsinp extension, will be saved at '/home/username/eb_gui/database/dose' directory.

Users can set the number of histories by entering the desired value in front of ***Histories***. This represents the number of particles initialized (ncase). It is recommended to run simulations with at least 10^8 histories. To achieve an acceptable level of uncertainty in the breast and prostate regions, our targets, 10^9 and 10^{10} histories are recommended for LDR breast and LDR prostate simulations, respectively.

The ***Volume correction*** option takes into consideration the volume of the seed in a voxel and subtracts it from that voxel. Essentially, the seed volume is removed from the Virtual Patient Model. For both breast and prostate cases, the optimal point density is 10^8.

In addition, users have the option to load ***Transport options***, ***Material data*** and ***Muen data***. By default, eb_gui has already selected files with default values for each data, and it is generally recommended to run simulations using these default options. The Transport parameter files are obtained from '/home/username/EGSnrc_CLRP/egs_home/egs_brachy/lib/transport'. The muen file contains μ_{en}/ρ data for each media. Default material data file defines material properties for each media in the patient model. The default file is listed in the '/home/username/EGSnrc_CLRP/egs_home/egs_brachy/lib' directory. For more detailed information regarding the parameters, please refer to the egs_brachy user manual [2].

Users can choose the ***Run mode*** based on their simulation requirements. The recommended mode is '**normal'** for a full tissue composite simulation following TG186 recommendations. In normal mode, sources are present at all locations, as is realistic for most LDR brachytherapy seed treatments. Alternatively, users can opt for the '**superposition'** mode where only the source in which a particle is generated is present for that particle's history. The superposition mode is appropriate for HDR simulations. It is also useful for TG43 based simulations and is automatically

selected by checking the **TG-43** checkbox. It is important to note that this is a Monte Carlo simulation under TG-43 conditions (tissues assigned as water; no interseed attenuation), not a TG43 calculation.

Number of cores, by default, is set to '**interactive'**, indicating that one core will be utilized for the simulation. To run a parallel simulation, users can select the desired number of cores based on their system.

By selecting **Score edep** option, the energy deposited by dose is scored and outputted to the file named filename.phantom.edep.3ddose, providing additional 3D dose file. The default setting is unchecked.

The created input file can be saved using Save egsinp. The egsinp file instructs egs_brachy to set up and execute the simulation, including definitions for media, geometry, sources, and scoring options. More detailed information on the egsinp parameters are outlined in the egs_brachy user manual [2].

Before running the simulation, users can select Run egs_view to visualize any geometries based on the same photon transport used by egs_brachy. This ensures that the geometry will be displayed as true to the simulation as possible. An example of using egs_view is illustrated in Figure 10.

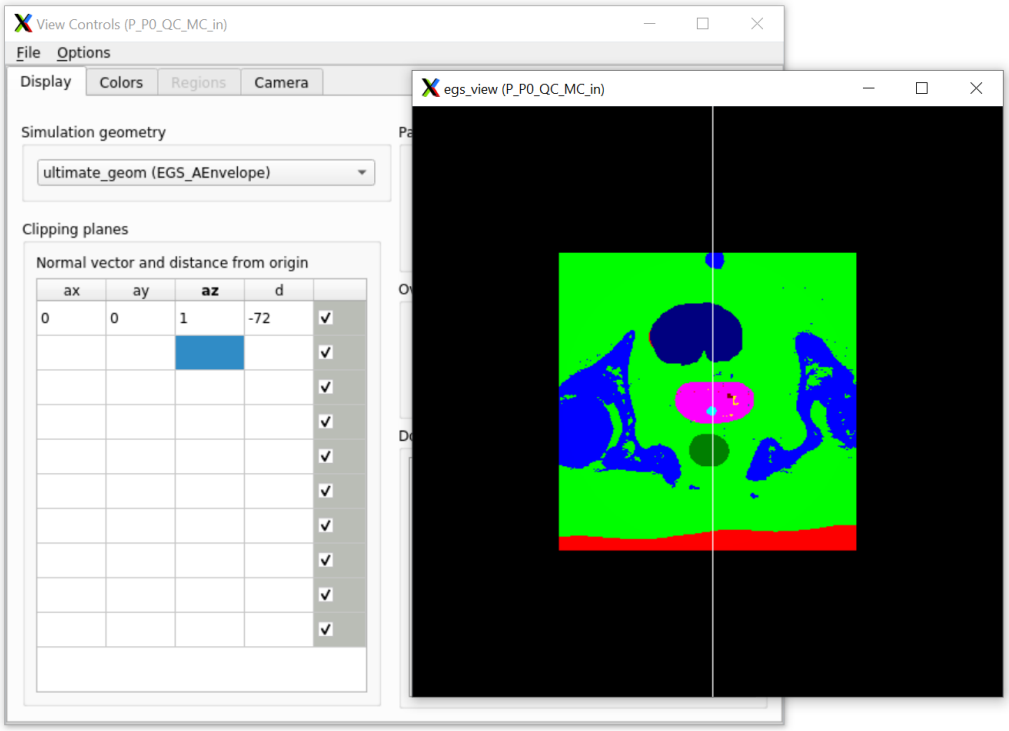


Figure 10. Displaying VPM using egs_view. A specific slice was selected here.

Using the Run egs_brachy button, egs_brachy will be launched to simulate the test case or clinical case. The console will open, and users will initially see a brief line before any additional data is displayed. This will be followed by simulation information, including ECUT, Muen, run mode, geometry specifics, seed locations, and eventually, the start of the simulation in the console. The console will display the egs brachy output and provide three options, as shown in Figure 11:

- Save: Saves the console output after the simulation run is complete.
- Kill: Terminates the running egs_brachy process.
- Close: Closes the console window. If egs_brachy has not yet finished running, it will continue executing in the background.

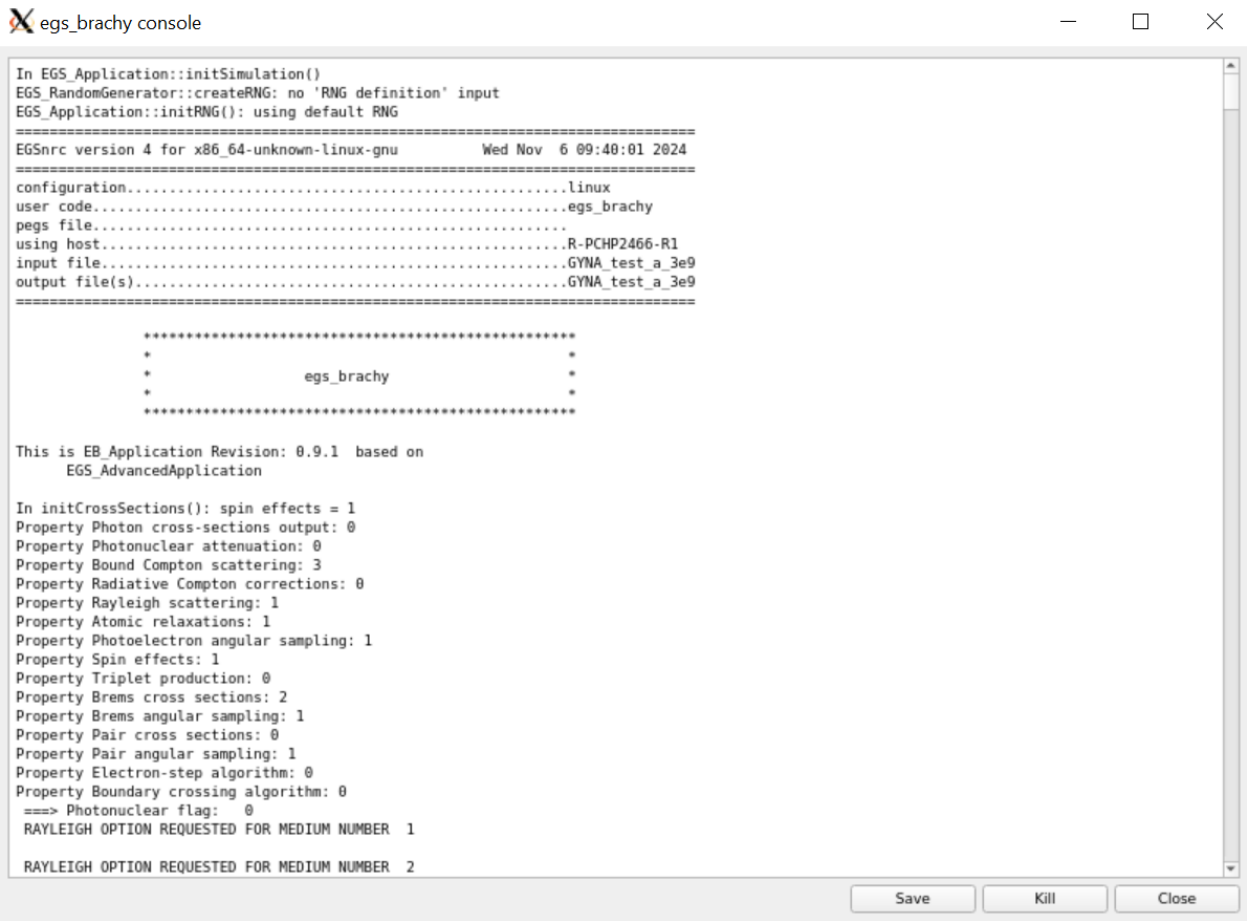


Figure 11. Snapshot of the egs_brachy console

After successfully completing the simulation run, the last lines of the console will display information about the simulation time and CPU usage. The output files are saved in the local eb_gui directory. Users can start by running a simulation with, for example, 10^5 histories. Then, based on the "Histories per hour" information, they can estimate the duration of a simulation with a higher ncase.

4.4 Analyze Results

This tab consists of three different sub-tabs: Preview, DVH, and Profile.

Preview: This sub-tab allows users to display phantom data, enabling them to view and step through each x-, y-, and z-slice of the phantom (see Figure 12). The axis, depth, and resolution of the image can be adjusted. By clicking on the image, the coordinates of the selected position in the patient are displayed below the image. Scrolling the mouse wheel allows users to navigate between slices. Users can select the VPM from drop down menu and click on Render to preview the selected VPM. If the *Live render* option is checked (recommended), the image will be shown instantly. When selecting the VPM, the image may initially appear black; in this case, clicking the reset button will adjust the image axis to the center of the VPM or within the boundaries of the CT images.

At the bottom of the VPM selection, users can choose to view either *media* or *density* images. One should expect that loading a phantom file may take a short time, typically less than 1 min. Users can also select the *legend* option to add a legend (e.g., isodose lines in Gy) to the VPM image or color map.

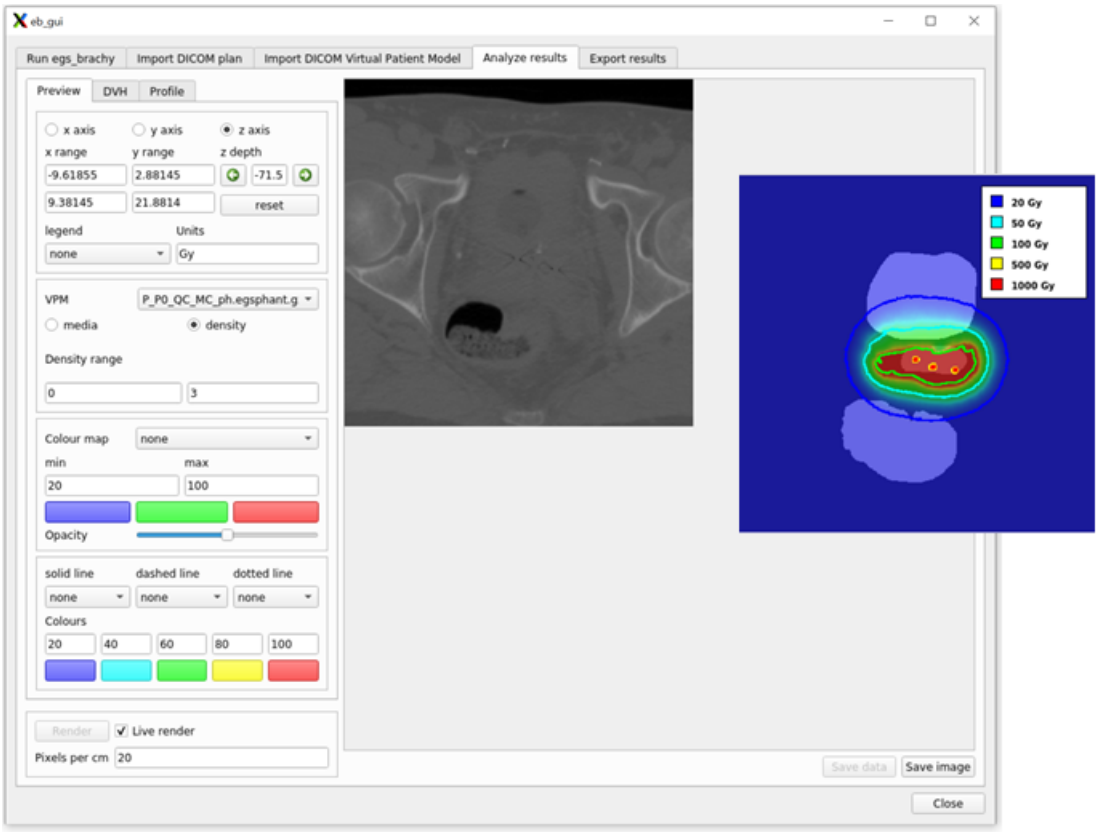


Figure 12. Snapshot of the eb_gui window, with the Analyze results tab highlighted

Users have the option to visualize the dose as a *colour map* over the VPM images. The *min* and *max* options, which determine the dose range in Gy, can be adjusted to enhance dose visualization. Additionally, users can compare three different dose calculations by selecting the corresponding 3ddose files from the drop-down boxes under *solid/ dashed/ dotted* setting. The isodose lines will be rendered accordingly. Users can further customize dose values and colors based on their preferences. Upon clicking on the image, position, material and its density, and point dose information will be displayed at the bottom of the page. To adjust the image size in the preview, users can modify the *Pixels per cm* value. Lastly, the image can be saved by clicking the Save image button.

DVH: The dose and volume metrics are calculated in this tab. Users can also plot the dose volume histogram (DVH) as depicted in Figure 13. The first step in this tab is to load the Virtual patient model, which may take about 1 minute, with a progress bar indicating the loading status. If users have defined masks by checking *Metrics Contour* in the Import DICOM Virtual Patient Model tab during the pervious step, the file containing data for those masks will appear in the drop-

down list in front of *Structure*. Users can then select the specific mask for a body region or choose a medium from the *Media* panel to plot the DVH for that particular mask.

In the *Doses* section, the user needs to select and load the appropriate 3ddose file. Once loaded, by clicking the Render button, eb_gui will plot the cumulative DVH in the right panel. The legend will display the 3ddose file name if Legend box is checked. Multiple 3ddose files can be loaded for DVH comparison. Users can also choose the *Differential* option to plot a non-cumulative histogram of doses.

Using Save data, DVH data are saved in .csv format. To calculate dosimetric matrices, users can select a value from the *Metrics* drop-down list or choose the Custom option and enter values in the Dx (%) box for dose matrices and the Vx box for volume matrices. For example, to see D90 and D99, enter 90 and 99 (separated by commas) in the Dx box.

eb_gui provides three options for outputting results: (i) Click the Calculate button to view dosimetric data, (ii) Use the Output metrics button to save the data in a text file, or (iii) Use the Output raw data button to save the raw data.

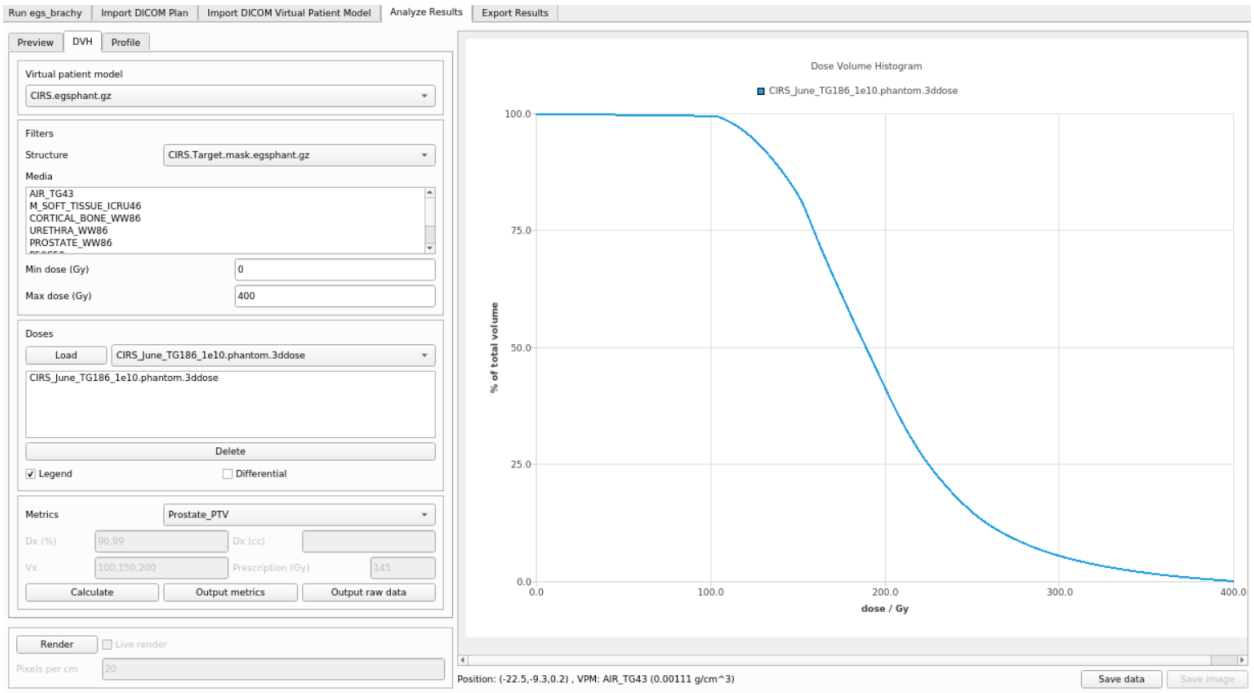


Figure 13. Snapshot of the eb_gui window with the DVH sub tab in the Analyze results tab highlighted

Profile: In this sub-tab, users can load the dose data to plot a specific line profile for the simulation case. To create the profile, users will select the coordinates for the start (x, y, z) and stop (x, y, z) points. After selecting the coordinates, clicking the Render button will plot the profile

by sampling doses along the line from the start point to the stop point. An example of a line profile is shown in Figure 14.

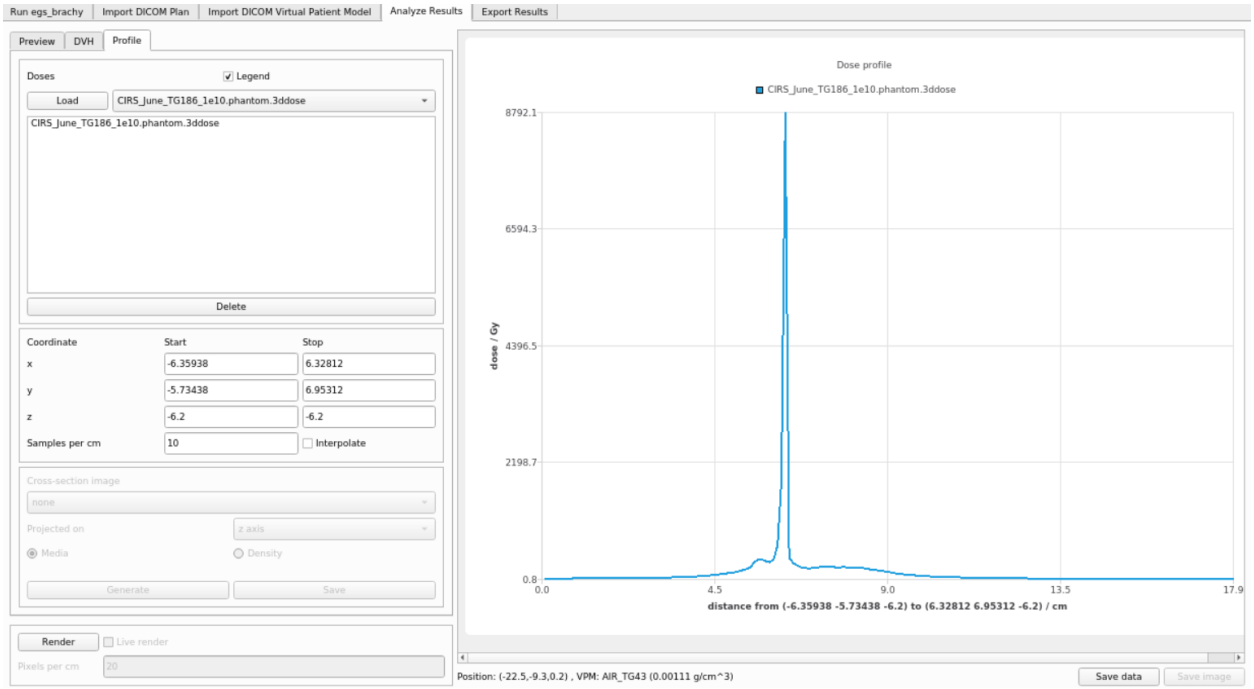


Figure 14. Snapshot of the eb_gui window with the Profile sub tab in the Analyze results tab highlighted

4.5 Export Results

The last tab is designed to output all simulation files and results, with a key function being the ability to save the dose distributions in a DICOM file (see Figure 15). After finishing the simulation run, the list in the **Dose Distributions** panel will be populated. Users can select the desired 3ddose file and click on Output RT Dose to save the RT dose file, which includes both the RT dose file and an error file.

Within the right panel, users should select the appropriate **Patient Geometry**, **Source Positions** and **Dose** files. A list of contours will appear under *Contour*, and users should define the *Metrics* related to each contour from the drop-down list. If desired, users can check the boxes for *Output DVH* and *Output Differential* to save this data for the selected contour. Finally, by clicking Output all data (csv metrics), users will generate a series of csv files and folders containing egsphant, transformation, dose, input files, associated logs, and selected metric in the patient folder.

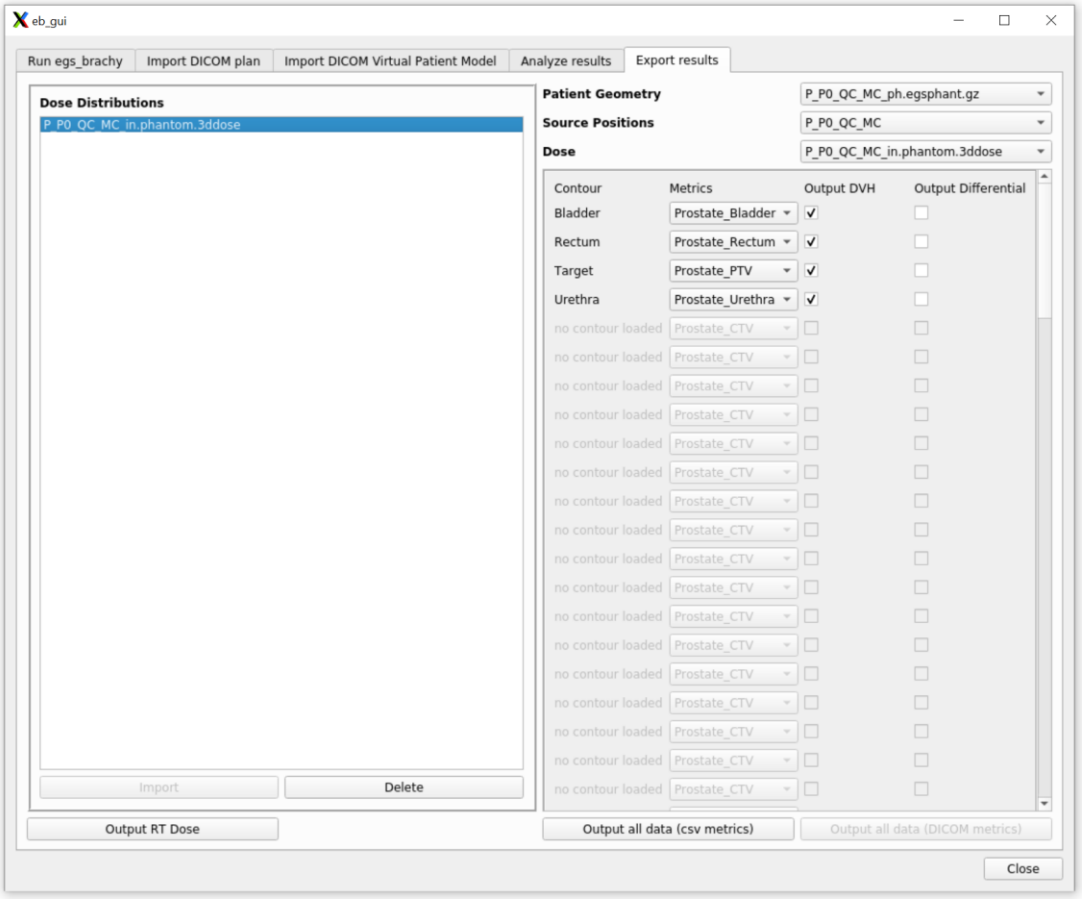


Figure 15. Snapshot of the eb_gui window with the Export Results tab highlighted, showing the metrics selection for a specific patient.

5. Brief description of default files

5.1 CT calibration file

A CT calibration file contains the mass density (gcm^{-3}) of each voxel, which is obtained by converting the Hounsfield units (HU) from the CT machine. Specific CT calibration curves have been pre-determined for various test cases, including LDR breast [14], LDR prostate [16], and HDR breast cases [17]. The details are summarized in Table 2, with further details provided below:

i. LDR Breast Test Cases: For these test cases, the CT calibration curve [14] is integrated directly into eb_gui as the default HU-to-density conversion file. This eliminates the need for users to upload a calibration file for LDR breast cases. The default file path is: home/user/eb_gui/database/HU_conversion/default_CT_calib.hu2rho'

ii. LDR Prostate Test Cases: For LDR prostate test cases, the default CT calibration file is not applicable. Thus, users must select the specific prostate calibration file, located at: 'home/user/eb_gui/database/HU_conversion/prostate_CT.hu2rho'

iii. HDR Breast Test cases: For the these cases, a pre-defined CT calibration is included in eb_gui, derived from a publicly available test [17]. The default file path for the HDR CT calibration is: 'home/user/eb_gui/database/HU_conversion/HDR_Breast_IROCtests.hu2rho'

Please note that the default calibration files listed above are specific to the test cases described in this document. For real patient data, users are encouraged to use their CT scanner calibration file, which can be uploaded via the HU to density table button for more accurate results.

Table 2. CT number to mass density calibration for breast and prostate cases used in this work and included in eb_gui in form of calibration files

Default (LDR Breast) [14]		**LDR Prostate [16]**		**HDR Breast [17]**	
HU	**mass density (g/cm^3)**	**HU**	**mass density (g/cm^3)**	**HU**	**mass density (g/cm^3)**
-3025	0.001	**-832**	0.217	**-1000**	0.00111
-1000	0.001	**-522.8**	0.508	**-992**	0.00121
0	1.008	**-74.2**	0.967	**-976**	0.00131
61.9	1.073	**-34.7**	0.990	**-480**	0.50

1000	1.667	**6.2**	1.018	**-96**	0.95
2000	2.300	**47.8**	1.061	**0**	1.00
3000	2.933	**56.5**	1.071	**48**	1.05
3100	2.999	**244.2**	1.159	**128**	1.10
5000	2.999	**999**	1.575	**528**	1.334
10000	7.365			**976**	1.603
20000	10.0			**1488**	1.85
25000	10.0			**1824**	2.10
				2224	2.40
				2640	2.70
				2832	2.83
				3500	3.555

5.2 Tissue Assignment Scheme

A tissue assignment scheme (TAS) file assigns a tissue composition to each voxel by specifying the mass density for each type of media. This assignment is based on a comparison with voxel densities derived from the previously defined CT calibration file. Essentially, each TAS file maps the patient's contours/organs to the tissues within those contours, along with their associated density thresholds. The default TAS is integrated within eb_gui, and the mass density values for various body regions in prostate test cases are detailed in Table 3. Users can select a TAS from the drop-down box located in the 'import DICOM Virtual Patient Model' tab. The TAS data is stored at the following location: 'home/username/eb_gui/database/tissue_assignment_scheme'

Table 3. The tissue assignment scheme for a prostate case

Region	**Tissue Assignment**	**Elemental Composition (Mass %)**					**Density (g/cm^3)**
		H	**C**	**N**	**O**	**Elements with Z>8**	
Target	Prostate	10.5	8.9	2.5	77.4	Na (0.2), P (0.1), S (0.2), K (0.2)	1.04
	Calcification	0.3	1.6	0.5	40.7	P (18.7), Ca (38.2)	3.06
Bladder	Urinary Bladder (Empty)	10.5	9.6	2.6	76.1	Na (0.2), P (0.2), S (0.2), Cl (0.3), K (0.3)	1.04
Rectum	Rectum	6.3	12.1	2.2	79.0	Na (0.01), P (0.1), Cl (0.1), K (0.1)	0.75
Urethra	Prostate	10.5	8.9	2.5	77.4	Na (0.2), P (0.1), S (0.2), K (0.2)	1.04

5.3 Optional set-up and verification of default files

To ensure the seamless functionality of eb_gui in generating and utilizing input files with egs_brachy without error, we recommend the following steps:

1- Initial Run with 10^7 Histories

In the 'Simulation Options' panel of the 'Run egs_brachy' tab, set the number of histories to 10^7 for the initial run and confirm that the process completes without errors. Afterward, for subsequent runs, use 10^9 histories for breast cases and 10^{10} histories for prostate cases to generate input files. These history counts are selected to maintain target uncertainty below 1%.

2- Mass Energy Absorption Data

For accurate calculations, mass energy absorption data should be provided over a reasonable energy grid (the default is 2000 points). A file named 'brachy_xcom_1.5MeV egsphant.muendat', containing mass-energy absorption coefficients (muen: μ_{en}/ρ) for specific energy values, is included with eb_gui. These data are calculated using the XCOM photon cross section dataset. Alternatively, users can load their own muen file into eb_gui.

3- Source Model Selection

For LDR breast and LDR prostate test cases, select the Pd-103 source (TheraSeed_200) and I-125 source (OncoSeed_6711) [5], respectively. For HDR cases, select the Ir-192 source [7]. All sources are used in a wrapped configuration.

4- Mapping Verification

Verify the mapping between each contour and its corresponding organ based on the selected TAS. For the test cases presented, the **PTV contour** was selected as either the breast or prostate.

5- Contour Priority Verification

Assign priority to each contour. Note that there is no contour priority or mapping for TG-43, as there is only one medium (water).

6- Metallic Artifact Reduction (MAR)

To reduce metallic artifacts, use the threshold replacement values outlined in Table 4 for each LDR test case. These values help correct artifacts arising from the presence of the brachytherapy source during imaging.

Table 4. Threshold values for metallic artifact reduction

	Breast [8]	**Prostate [16]**
Low Threshold	0.8 g cm^{-3}	0.04 g cm^{-3}
High Threshold	1.16 g cm^{-3}	1.1 g cm^{-3}
Replacement Density	0.917 g cm^{-3}	1.04 g cm^{-3}
Radius of the cylindrical replacement region surrounding each seed	5 mm	5 mm

6. A test case simulation step-by-step

This section provides a step-by-step explanation of the simulation for a 3×3×3 grid of seeds in an LDR breast test case. The DICOM files for this test case include an RTPlan file, an RTst file, RTDose file, and a folder containing CT images, which can be accessed at https://github.com/clrp-code/eb_gui.
Before starting the simulation, download the DICOM files for this example, copy them into your virtual system directory, and unzip the files.

Step 0: In the WSL command window, navigate to the eb_gui directory by entering `cd eb_gui` and pressing enter. Then run eb_gui using `./eb_gui`. This will prompt the GUI windows of eb_gui, as shown in Figure 16.

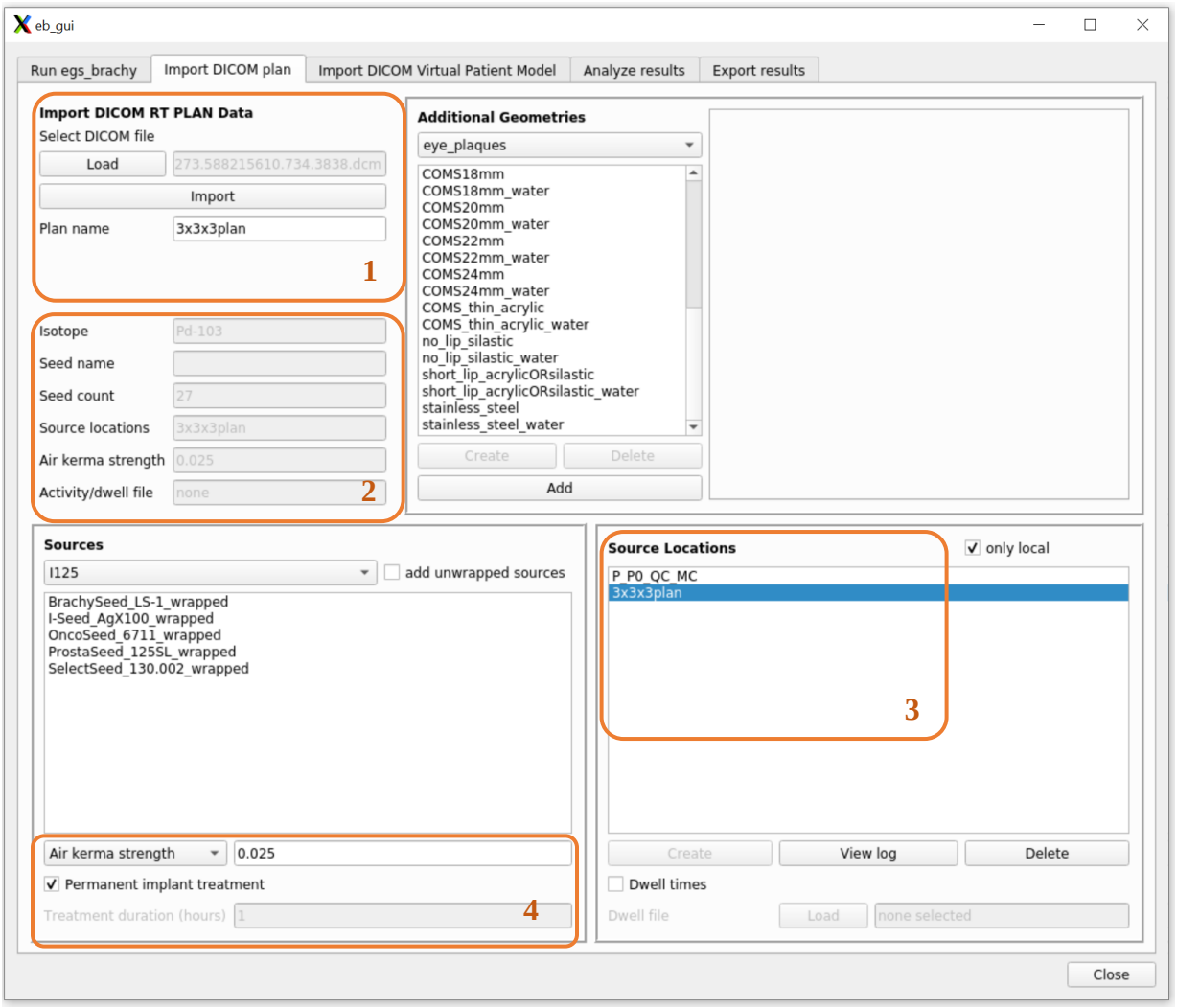


Figure 16. eb_gui window. The orange boxes show panels in the Import DICOM tab

Step 1: Load the RTPlan file in the Import DICOM plan tab, assign it a name (e.g., 3×3×3plan), and click the import button (box 1 in Figure 16).
After loading the RTPlan file, the egsphant creation log will appear, displaying seed information and their positions (Figure 17). Once you close the log file window, the seed data will be populated in box 2 and box 4 (as shown in Figure 16). You will also see the '3×3×3plan' imported file in the Source Location panel (box 3). This log file is saved in the transformation folder, located at 'home/username/EGSnrc_CLRP/egs_home/eb_gui/database/transformation'.

```
------------------------------------------------
Treatment type: MANUAL
Treatment technique: PERMANENT
Treatment time: 2022-09-20 ::
------------------------------------------------
Isotope: Pd-103
Air kerma rate (uGy/h): 2.5
Air kerma strength (Gy*cm^2/h): 0.025
Half-life (h): 407.784
Measurement time: -- ::
Additional seed data:
------------------------------------------------
Found 27 seeds
------------------------------------------------
  1) [   26.414,   12.736,  -23.436]
  2) [   26.414,   12.736,  -24.436]
  3) [   26.414,   12.736,  -25.436]
  4) [   25.414,   12.736,  -23.436]
  5) [   25.414,   12.736,  -24.436]
  6) [   25.414,   12.736,  -25.436]
  7) [   27.414,   12.736,  -23.436]
  8) [   27.414,   12.736,  -24.436]
  9) [   27.414,   12.736,  -25.436]
 10) [   27.414,   11.736,  -23.436]
 11) [   27.414,   11.736,  -24.436]
 12) [   27.414,   11.736,  -25.436]
 13) [   26.414,   11.736,  -23.436]
 14) [   26.414,   11.736,  -24.436]
 15) [   26.414,   11.736,  -25.436]
 16) [   25.414,   11.736,  -23.436]
 17) [   25.414,   11.736,  -24.436]
 18) [   25.414,   11.736,  -25.436]
 19) [   25.414,   13.736,  -23.436]
 20) [   25.414,   13.736,  -24.436]
 21) [   25.414,   13.736,  -25.436]
 22) [   26.414,   13.736,  -23.436]
 23) [   26.414,   13.736,  -24.436]
 24) [   26.414,   13.736,  -25.436]
 25) [   27.414,   13.736,  -23.436]
 26) [   27.414,   13.736,  -24.436]
 27) [   27.414,   13.736,  -25.436]
------------------------------------------------
```

Figure 17. 3x3x3plan.log file containing radioactive information and seeds positions

Step 2: Go to the '*Import DICOM Virtual Patient Model*' tab, click on the '*import CT directory*' (box1 in Figure 18), select the CT images folder, and provide a name for the phantom (e.g., 3×3×3Phantom).

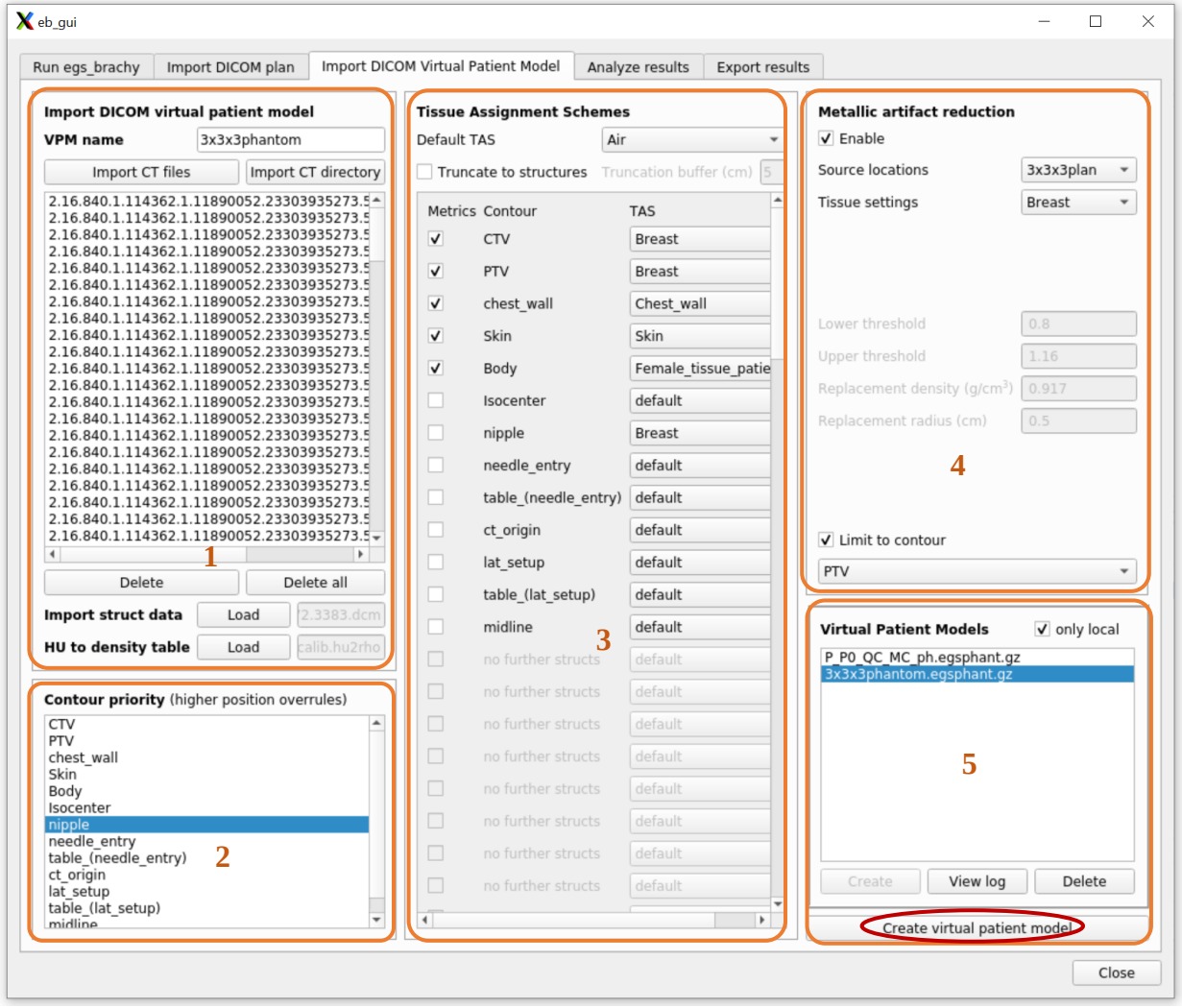


Figure 18. Import DICOM Virtual Patient Model tab

Step 3: In the '*Import struct data*' section, load the RTstruct file, which contains DICOM structure data. Also, load 'default_CT_calib.hu2rho' in the *HU to density table* (box 1 in Figure 18).

Step 4: The contour priority panel will be filled with the contour names as shown in box 2 (Figure 18). Adjust the priority according to the following order for breast cases (left side has higher priority).

High Priority: Breast (PTV)→ Skin→ Chest wall→ Ribs → Heart→ Lung: Low Priority
Note: For prostate cases, use the following priority order:
High Priority: Urethra → Prostate → Rectum→ Bladder: Low Priority

Step 5: In the '*Tissue Assignment Schemes*' panel, select the *Default TAS* as Air. Then assign other regions as shown in box 3 (Figure 18).

Step 6: *Enable* the MAR and choose *3×3×3Plan* from the *Source Locations* drop-down box. Set the Tissue setting to 'Breast'. To restrict the MAR to the 'PTV', check the box for 'Limit to contour' and select 'PTV' from the drop-down options, as illustrated in Figure 18 (box 4).

Step 7: Click on *Create virtual patient model* (red oval in Figure 18). A window will appear, indicating that the phantom has been successfully created. You will then see the '*3×3×3phantom.egsphant.gz*' file in the *Virtual Patient Model panel* (box 5). The egsphant creation log file will display the following information: Media contour and TAS data, HU to density conversion data, Metallic artifact reduction applied to any voxels, etc. Both egsphant.gz and log files can be found at:
'home/username/EGSnrc_CLRP/egs_home/eb_gui/database/egsphant'.
You can unzip the egsphant.gz file and open it in Notepad.

Step 8: In the '*Run egs_brachy*' tab, from the list below the '*Virtual Patient Models*' (Figure 19, box 1), select the '*3×3×3phantom.egsphant.gz*'.

Step 9: In the '*Sources'* panel (Figure 19, box 2), ensure that the option "add unwrapped sources" is unchecked. Then, select Pd103 from the drop-down list and choose 'TheraSeed_200_wrapped'.

Step 10: In the *Source Locations* (Figure 19, box 3), select *3×3×3plan*.

Step 11: Provide a name in the '*Simulation Options*' panel (Figure 19, box 4), e.g., *3×3×3TestCase*. **Note: the term "preview" is reserved for eb_gui, so avoid using it in any naming.**

Step 12: Set the histories to 10^7 for testing (since the test case does not have the complexity of real patients, 10^7 histories are sufficient).

Step 13: Click on '*Run egs_view*' to check the geometry of your simulation.

Step 14: Leave other option as default and click on '*Run egs_brachy*' (Figure 19, box 4).

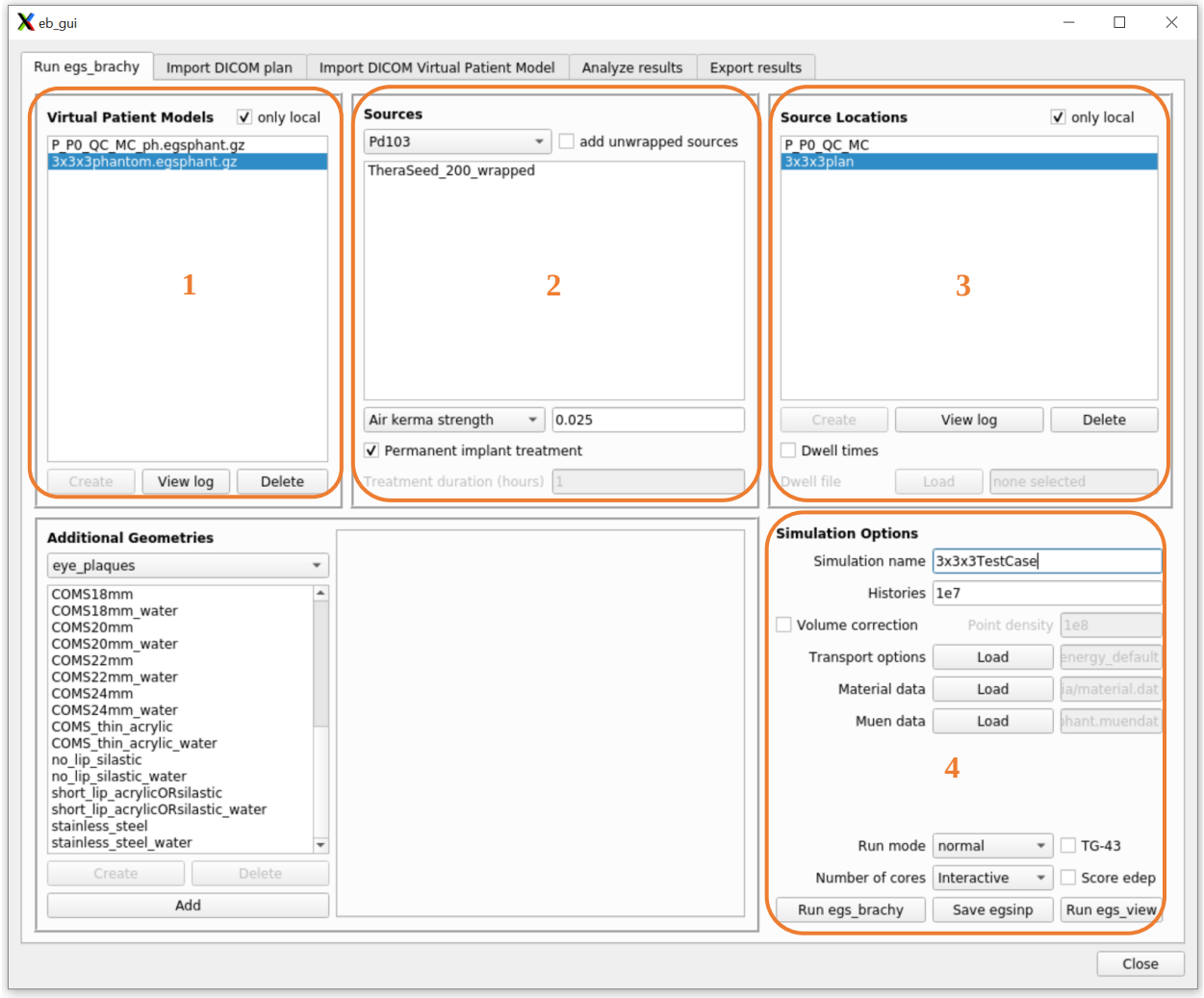
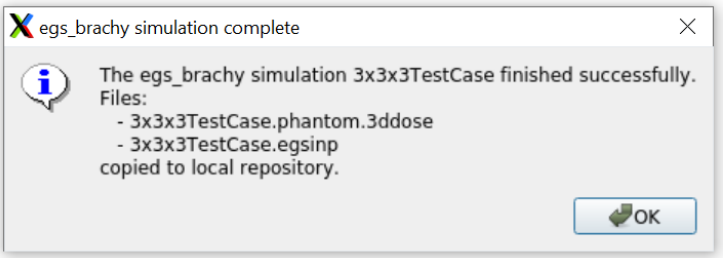


Figure 19. Run egs_brachy tab

After completing the simulation, a prompt will appear confirming the successful completion of the simulation, as shown below. Click on the ‘Save ‘button to save the console output, and then click on the ‘Close’ button to exit the console.



Step 15. In the '*Analyze Results*' tab, choose the '*Preview*'. From the drop-down list next to VPM, select your virtual model (it has *.egsphant.gz extension). Click on '*Render*', preferably checking the '*Live render*' option. Initially, you will see a black square; now click on '*reset*' button at the top of this panel. The CT preview will appear, and you can move between slices using the mouse wheel or adjusting the z-depth.

Step 16. From the drop-down list in front of '*Colour map*', select the dose file (*.3ddose) and wait for it to be loaded. Click on '*Render*'. If you have already checked the '*Live render*' option, the dose distribution will be automatically mapped over the image. Figure 20 shows an example of the colormap view of a slice at z-depth of -25.6 cm.

Step 17. From the *legend* drop-down list (shown in a blue box in Figure 20), select 'Colour map' to display the range of dose over the image.

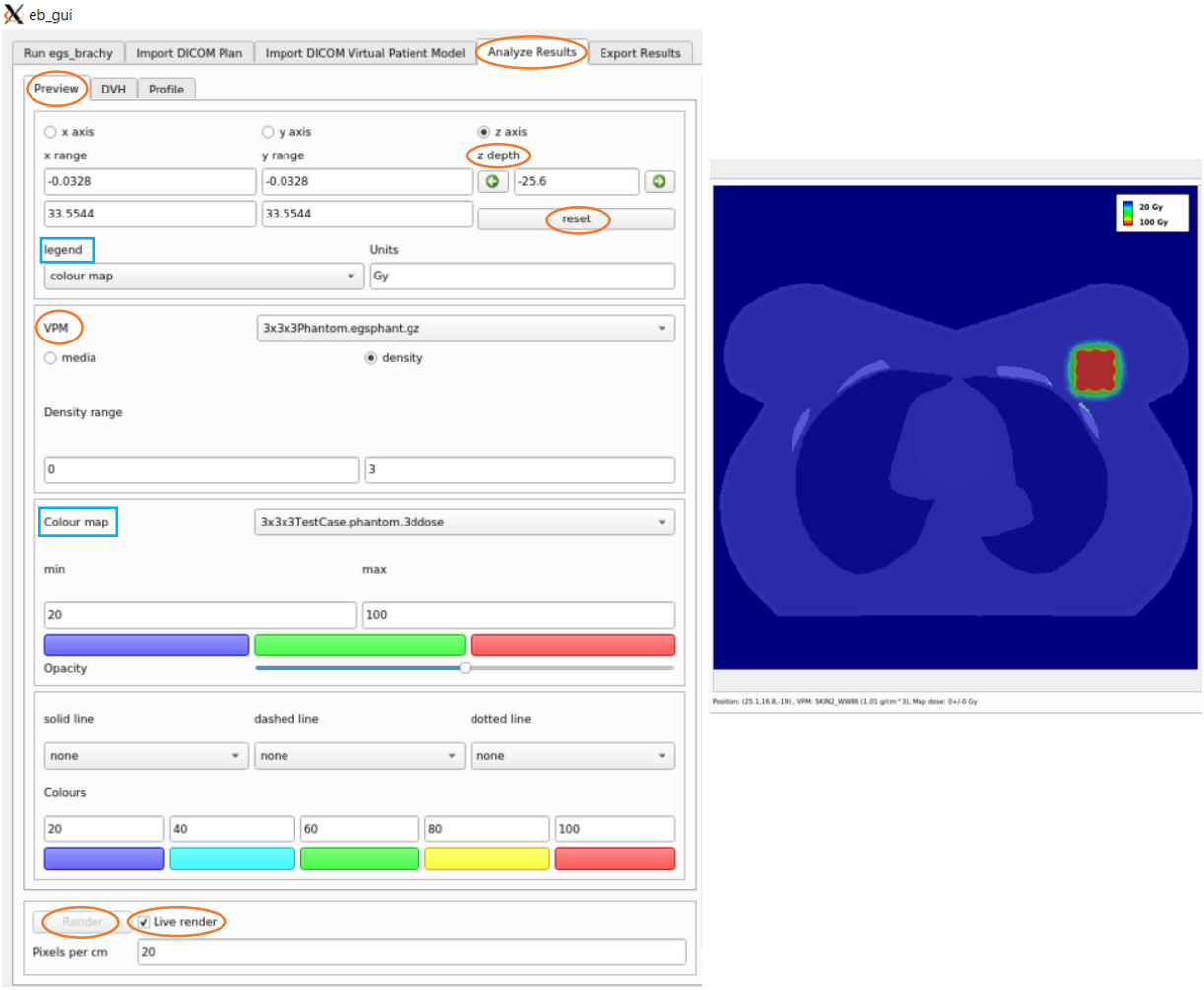


Figure 20. Preview of Virtual model and dose distribution for the LDR breast test case.

Step 18. Select the '*DVH'* tab. From the drop-down list under '*Virtual patient model*', select the virtual model (3x3x3Phantom.egsphant.gz), as shown in Figure 21.

Step 19. Choose the CTV mask (3x3x3phantom.CTV.mask.egsphant.gz) from the '*Structure'* drop-down list.

Step 20. Load the dose distribution (3x3x3TestCase.phantom.3ddose) in the '*Doses'* section.

Step 21. Click on '*Render'* to plot the DVH. Figure 21 shows the DVH limited to 400 Gy using '*Max dose'* option.

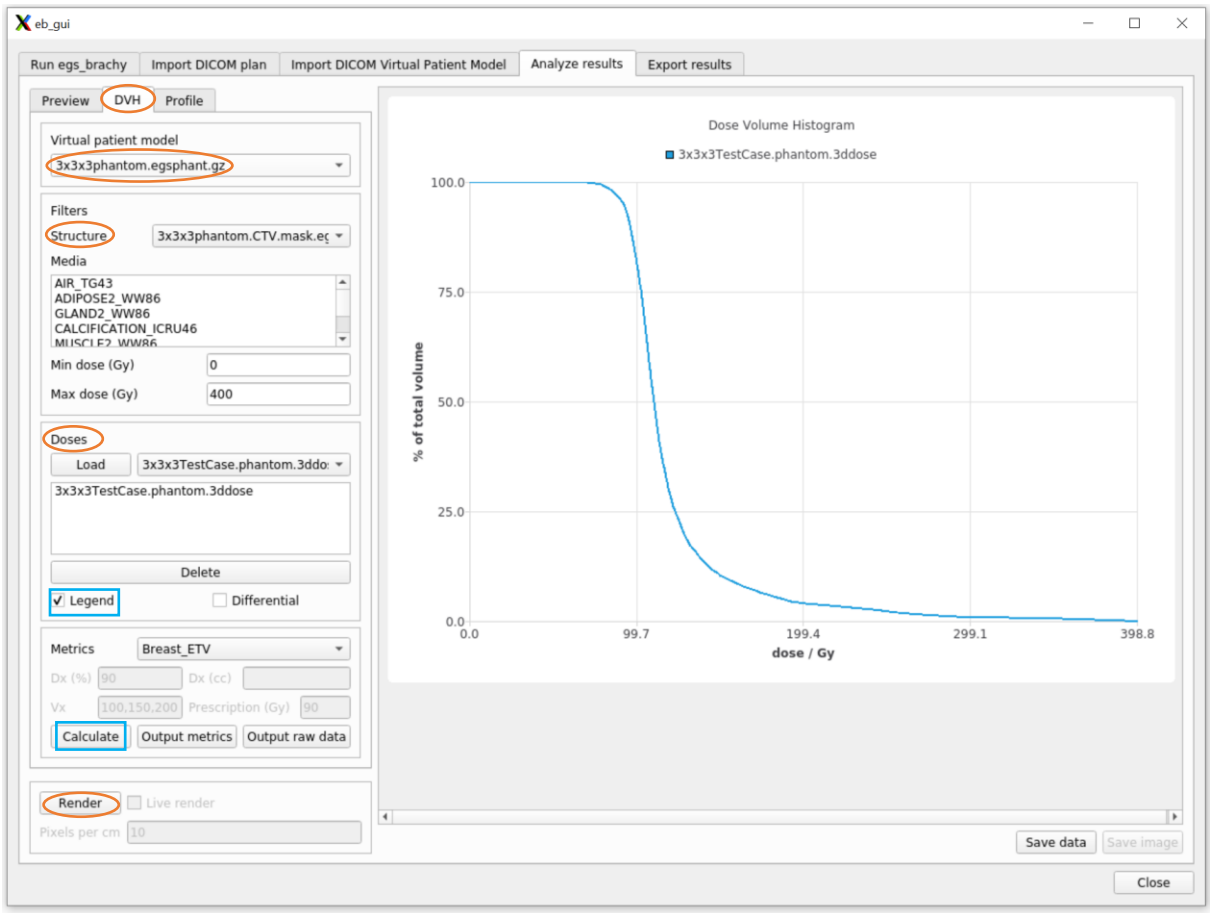


Figure 21. DVH of the *example* test case for CTV contour

Step 22. Next to '*Metric'* in *DVH* tab, select Breast_ETV and click on '*Calculate'*. You can also Output the data. The dosimetric data will be displayed in the log page, as shown in Figure 22.

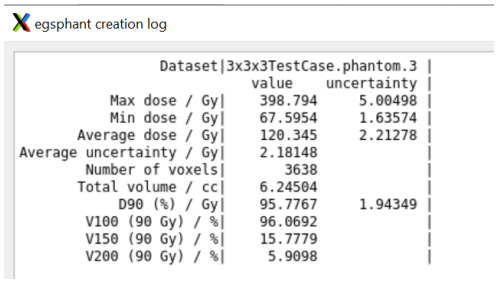


Figure 22. Dosimetric metrics for the LDR breast test case

Step 23. Go to the '*Profile'* tab and load the dose file.

Step 24. Return to the '*Preview'* tab (Figure 20) to copy the x, y, and z range from there. In the coordinate section, paste the start and stop points for each axis.

Step 25. Click on '*Render'* to plot the line profile of the dose based on the selected coordinates.

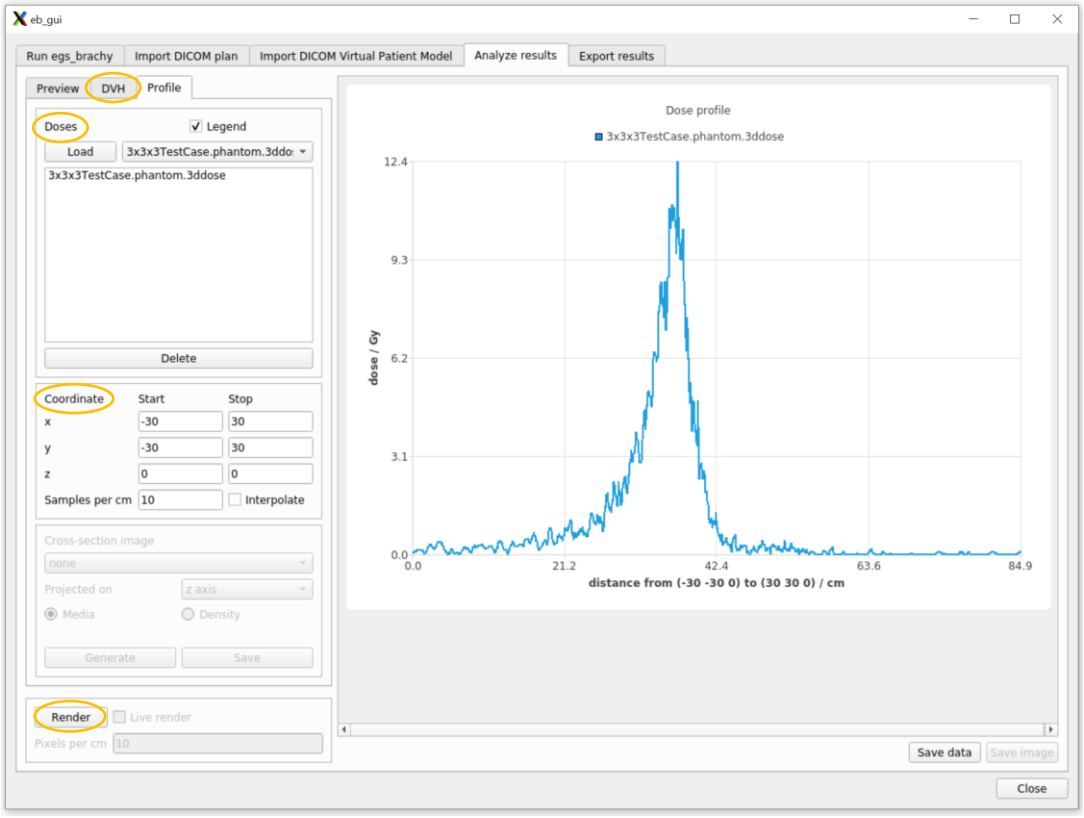


Figure 25. Dose profile of the test case

Step 26. Go to the '*Export Results*' tab.

Step 27. In the left panel, select the '*Dose Distribution*' and click on '*Output RT Dose*' to save it as a DICOM file. A save page will prompt you to select the directory. Provide a name and click 'Save'. Two files with the *.dose and *.error extensions will be saved in DICOM format at the selected directory.

Step 28. In the right-hand panel, select the '*Patient Geometry*', '*Source Positions*', and '*Dose'* files. The section below contour will be filled automatically, but you need to set the '*Metrics'* (shown in the Figure 26) and select the DVH and differential data you want to output.

Step 29. Click on '*Output all data*'. It will prompt you to select a directory to save the data. A progress bar will appear as the data is being saved. Once completed, all the data listed in Figure 27 will be available in that directory.

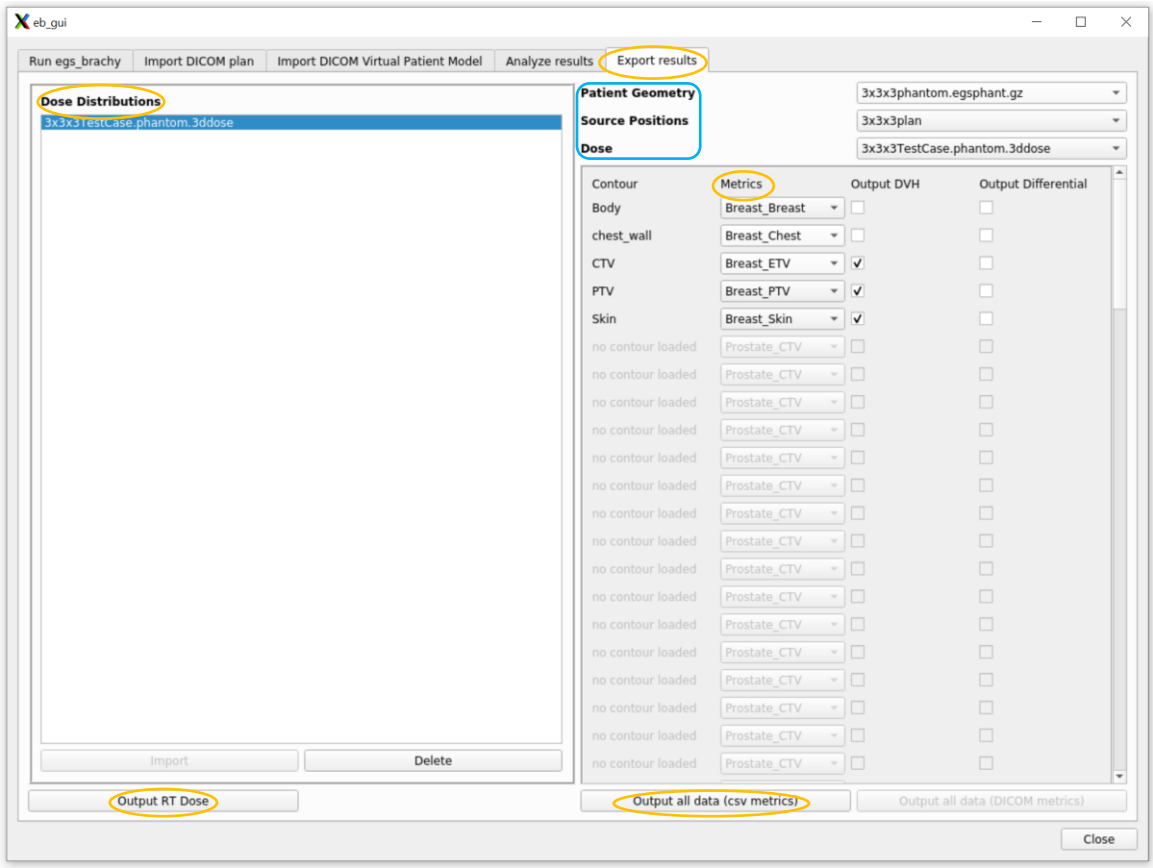
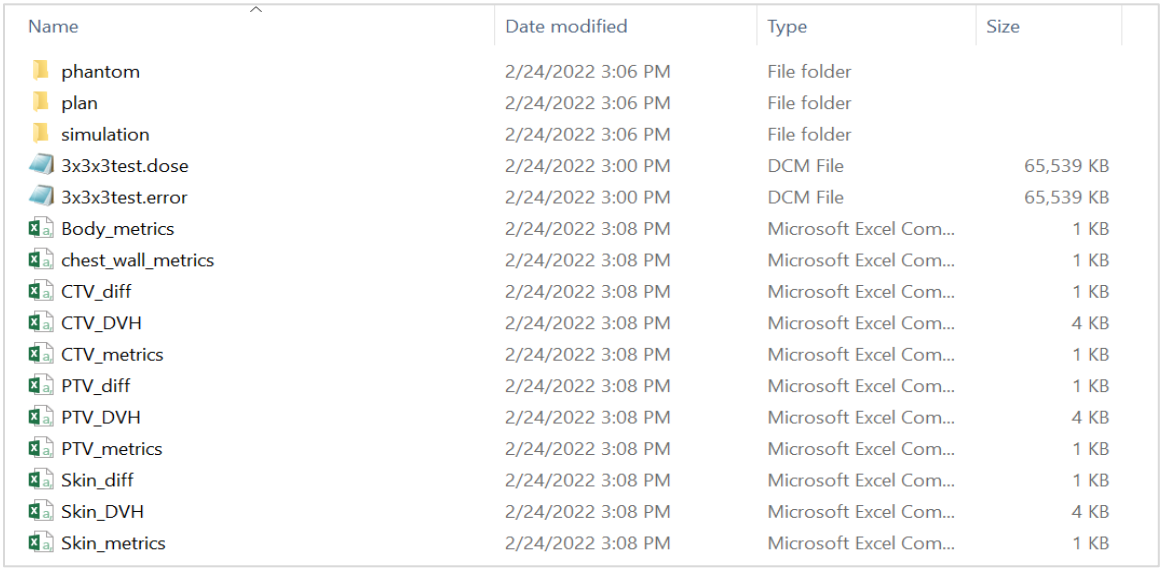


Figure 26. Export Results tab showing the metrics setting for the breast test case



Name	Date modified	Type	Size
phantom	2/24/2022 3:06 PM	File folder	
plan	2/24/2022 3:06 PM	File folder	
simulation	2/24/2022 3:06 PM	File folder	
3x3x3test.dose	2/24/2022 3:00 PM	DCM File	65,539 KB
3x3x3test.error	2/24/2022 3:00 PM	DCM File	65,539 KB
Body_metrics	2/24/2022 3:08 PM	Microsoft Excel Com...	1 KB
chest_wall_metrics	2/24/2022 3:08 PM	Microsoft Excel Com...	1 KB
CTV_diff	2/24/2022 3:08 PM	Microsoft Excel Com...	1 KB
CTV_DVH	2/24/2022 3:08 PM	Microsoft Excel Com...	4 KB
CTV_metrics	2/24/2022 3:08 PM	Microsoft Excel Com...	1 KB
PTV_diff	2/24/2022 3:08 PM	Microsoft Excel Com...	1 KB
PTV_DVH	2/24/2022 3:08 PM	Microsoft Excel Com...	4 KB
PTV_metrics	2/24/2022 3:08 PM	Microsoft Excel Com...	1 KB
Skin_diff	2/24/2022 3:08 PM	Microsoft Excel Com...	1 KB
Skin_DVH	2/24/2022 3:08 PM	Microsoft Excel Com...	4 KB
Skin_metrics	2/24/2022 3:08 PM	Microsoft Excel Com...	1 KB

Figure 27. Folders and files in different formats saved in a selected directory

Congratulations, you have successfully completed your first simulation using eb_gui!

7. HDR simulation procedure

To Simulate an HDR case, follow the same steps outlined for an LDR case as explained in the previous section up to step 10.

Step 10: In the '*Source Locations*' (Figure 19, box 3), select the HDR case plan. Then, in the '*Dwell times*' section, upload the dwell time by clicking Load. The eb_gui will open the path to dwell time files. Select the file with the same name as the plan file chosen for the Source Location.

Step 11: Provide a name in the '*Simulation Options*' panel (Figure 19, box 4), e.g., HDRTestCase.

Step 12: Set the number of histories to 10^7. Note that the HDR test case requires fewer histories, but this may result in a longer simulation time.

Step 13. Change the '*Transport option*' to 'High_energy_default' by clicking Load and selecting the new transport file.

Step 14. Leave other options as default unless you have new material. If so, select your material and muen files.

Step 15. Select *superposition* as the 'Run mode' and click on '*Run egs_brachy*' (Figure 19, box 4).

Continue with the subsequent steps outlined for the LDR case to analyze the results of the HDR simulation.

Try your own test cases!

Users are encouraged to use the IROC Houston test cases, which are available at the: Imaging and Radiation Oncology Core --IROC Website (mdanderson.org)
To access these, go to the IROC website, click on *Brachy Sources*, navigate to *Source Registry*, then select *Model-Based Dose Calcs*. Finally, click on the red box labeled *Click for Cases*.

Below is a quick overview of all test cases. For more detailed information on these test cases, refer to Ballester *et al* [18].

Test case	Information
Test case 1	A single Ir-192 source is positioned at the center of a water cube with a side length of 51.1 cm.
Test case 2	A single Ir-192 source is positioned at the center of a water cube with a side length of 20.1 cm, which is then surrounded by an outer cube of air with a side length of 51.1 cm.
Test case 3	This case involves a single Ir-192 source in a medium similar to Test Case 2, but the source is offset laterally by 7 cm from the center and positioned 3.05 cm away from the surface of the water cube.

8. Constraints and future directions

The current version of eb_gui does not yet support the simulation of applicators for HDR brachytherapy applications, and its benchmarking and validations are currently limited to specific treatment types. Further clinical validation and real-world feedback from practitioners will be essential to refine and optimize its performance. Expanding source libraries, applicator models, and integrating eb_gui more directly with treatment planning systems are key areas for future development.

Future work will also focus on commissioning eb_gui for a broader range of brachytherapy scenarios, including LDR treatments and other applications that can be modeled using egs_brachy, such as ocular brachytherapy and electronic brachytherapy. The software already enables users to access any source or patient geometry available in the egs_brachy library, which will facilitate its use in a wide range of clinical applications going forward.

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