

1 Building and Running

GUI version:

The main GUI version of the program will be built and run using the QT Creator¹. To do so one needs to have the Creator, a compiler (preferably g++), cmake² and make³ installed. The following steps then have to be performed to run the program

1. Open the QT Creator.
2. Under "File" select "Open file or project".
3. Navigate to the folder "[BASE]/src/QT/Softwarelab" and open the "CMakeLists.txt" file.
4. One will be prompted to configure the file by selecting a compiler. Make sure the release option is enabled and complete the configuration
5. Select the release option in the bar on the left (where it most likely currently says debug).
6. To build click the hammer symbol on the bottom left or to build and run the play symbol without the bug above the hammer.

Core version:

We henceforth refer to the version without a GUI as the core version. It is not designed to be user-friendly and will need manual coding to accomplish the desired task.

One needs to have the g++ compiler, CMake, and make installed. The following steps need to be performed to build and run this version

1. Open a terminal window in the directory "[BASE]/src/Core/Build".
2. Type "cmake .." and hit enter. If CMake doesn't pick the compiler you intended to use as its default one might need to modify the command to specify a generator. When using MinGW this looks like "cmake .. -G "MinGW Makefiles"". All available generators can be viewed using "cmake -G".
3. Type "make" in the same directory to build the program.
4. Lastly run the program by typing "main.exe". This will execute the commands specified in the "main.cpp" file which needs to be manually set to achieve a task the user wants to fulfill. By default, this will run an example session.

¹<https://www.qt.io/product/development-tools>

²<https://cmake.org/>

³<https://www.gnu.org/software/make/>

2 Documentation

The documentation requires Doxygen⁴ to be installed. To create the documentation

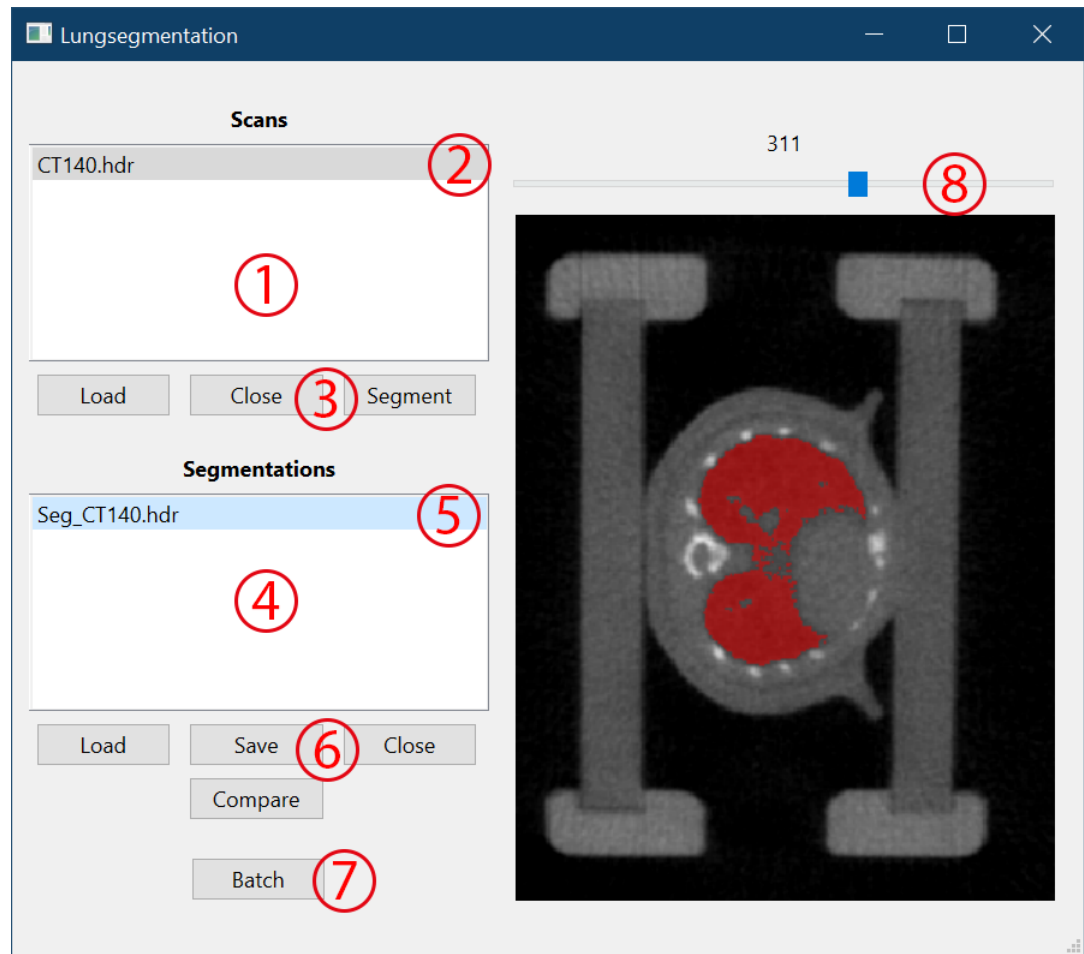
1. Navigate to [BASE]/docs
2. Open a console window in this location
3. Run "doxygen LungSeg.cfg"

The documentation will appear in the folder.

⁴<https://doxygen.nl/>

3 Overview of User Interface

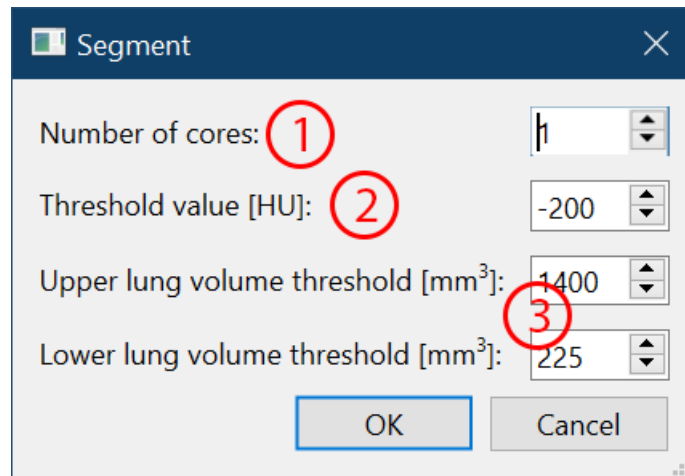
Main Window



1. A list of all open scans will appear here. The user can select the one they want to operate on.
2. An example of a selected scan. This scan will be displayed on the right. The user can double-click it to rename it.
3. The available options to perform on scans. Load will prompt the user to select whether or not they want to scale or blur and then to select a scan in a file browser. Close and Segment both operate on the currently selected scan. For more information on the segment, options look in section 4.

4. A list of all open segmentation for the current scan. These are coupled to the scan so will only show those segmentations that belong to the currently selected scan.
5. An example of a selected Segmentation. This will be overlayed over the scan on the right. Double-clicking will allow the user to rename to segmentation and specify the classes they want to display as a comma-separated list of numbers.
6. All options for the segmentations. All except for Load will again work only on the selected segmentation.
7. This button will enter the user into Batch-Mode. For more on this view section 4.
8. On the right a slice of the currently selected scan will be displayed. Overlayed over it will be the selected segmentation. The slider controls which slice is viewed.

Segment Window

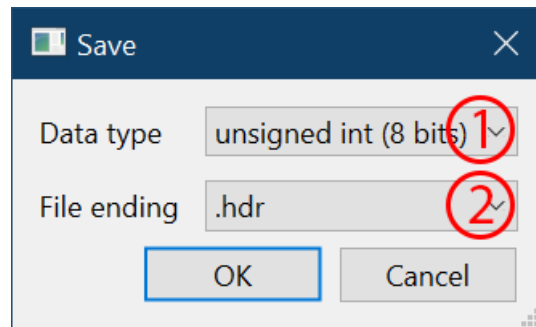


Upon clicking the segment button in the Main window this window appears. It is used to set the parameters for the segmentation.

1. The number of cores will specify on how many threads the segmentation will be run. The default here is 1.
2. The threshold value will allow the user to modify the brightest color value of a voxel that will still be considered to possibly be part of the lung.
3. The upper and lower volume thresholds are used to specify the physical volume range a lung can be in. When the user runs into problems with

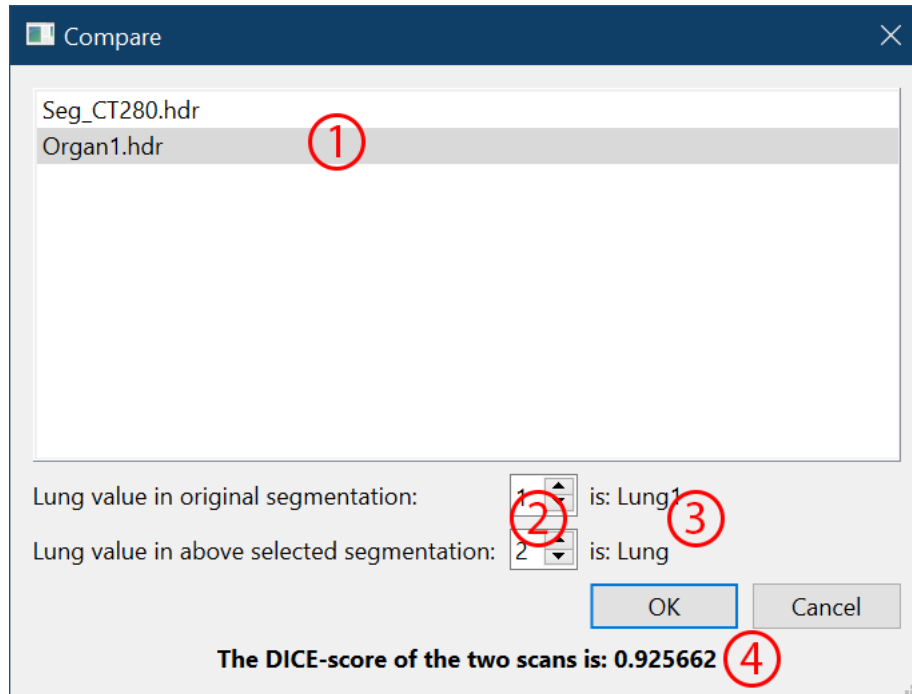
wrong positive segmentation the lower threshold is a good parameter to change first.

Save Window



1. The user can specify the data type that is used to save a scan. This should usually not be changed as unsigned int8 will (almost always) be big enough to save everything lossless and create the smallest files.
2. The user can select whether to save the segmentation as a ".nii" or ".hdr/.img" file here.

Compare Window



Upon clicking the compare button in the main window this window will open. It allows the user to compare a second segmentation to the originally selected segmentation in the main window.

1. The same list as in the main window of all available segmentation. Here the user will select the second scan to compare to the original.
2. As a single segmentation file may contain multiple classes (e.g Bone, Lung, Liver,...) the user will have to select a class number here.
3. If there exists a .cls-file for the segmentation the name of the selected class will be displayed here. Otherwise, it can be a bit of a guessing game to find the correct number for the class.
4. After running the comparison the result is displayed here.

Batch Window

The screenshot shows the 'Batch' window with the following elements and annotations:

- 1**: 'Load' button
- 2**: 'Names of the scans to be read:' text box containing 'CT140.hdr, CT280.hdr'
- 3**: 'Expected number of lungs:' dropdown menu set to 'Mixed'
- 4**: 'Include subdirectories:' checkbox, which is checked
- 5**: 'Check number of files' button
- 6**: List box showing scan results, including 'Found 1 lung(s) in the scan: C:/Users/setta/Desktop/SEP_Data/Presentation/Batch/M01_048h/CT280.hdr' and 'Found 1 lung(s) in the scan: C:/Users/setta/Desktop/SEP_Data/Presentation/Batch/M01_072h/CT280.hdr'

Other visible elements include: 'Batch' title bar, 'OK' and 'Cancel' buttons, a green progress bar at 100%, and a status bar at the bottom.

The batch window contains all settings for the batch mode. Many of these are already explained in the segment window and save window sections. The unique ones are

1. Similarly to load the user is asked to select the operating path. However here a directory is selected instead of a file. The batch mode will consider

all files in the directory.

2. To specify the files to work on the user has to give the names of the wanted files as a comma-separated list with file extensions as seen in the picture.
3. Here the user can set how many lungs they expect to find in the scans. This setting is not used for the segmentation itself but only to highlight non-conforming results in the output seen in 6.
4. Does the user want to work in only the selected directory or all sub-directories of it?
5. Before running the actual batch mode the user might want to know how many files they selected with the parameters they set. This can be achieved using this button.
6. The progress of the run can be tracked here. If there are more or fewer lungs than expected found in a scan it will be highlighted in red here to easily identify them and possibly run again manually.