

OCT Segmentation Manual

Jens Kowal, Pascal Dufour

This manual gives a quick introduction into the OCT Segmentation application in particular it explains how to prepare the OCT data in order to be loaded into the segmentation application and it outlines the existing functionality.

Introduction

The application is a development of the Ophthalmic Technology Group at the ARTORG Center and can be used without restrictions for research purpose. Of course, we ask you to cite our paper if you use the application in your publications:

P. A. Dufour et al. "Graph-Based Multi-Surface Segmentation of OCT Data Using Trained Hard and Soft Constraints." IEEE Trans. Med. Img. 2012.

The application is based on a software framework MARVIN that has been developed within the Ophthalmic Technology Group at the ARTORG Center.

Hardware Requirements

Currently the software runs under Mac OS X 10.7+ or Windows 7 (64Bit). If there is a strong demand for a 32Bit version we might create one in the future.

During the automatic segmentation procedure the application requires about 3GB of memory. Therefore it is advisable to have at least 4GB main memory in your computer. Moreover, the application requires an OpenGL compatible graphic sub system.

Heidelberg OCT Data Export

The OCT systems, currently available on the market, produce a multitude of different data formats. There is no commonly accepted standard to exchange OCT data. DICOM 3.0 might serve as an exchange format for OCT data in the future.

However, due to availability of Heidelberg Engineering OCT's at the clinic we are most often collaborating with, the Inselspital Bern in Switzerland, we focused on the compatibility with the Heidelberg Engineering OCT systems. The standard data exchange format between Heidelberg OCT's is the so-called *e2e* format. This is a binary format whereas the format composition and structure is not freely available for the public.

For research purpose Heidelberg Engineering created an XML exchange format for which the specification is available. We use this XML format to read OCT data into our segmentation application.

The export action can be triggered via the regular export submenu (see Figure 1). The export will create an xml file plus a number of images (depending on the amount of exported data). The export will include always all selected items.

Usually the xml export functionality is not available in a default installation. However, it can be turned on very easily. Open in a text editor the configuration file "*hraviewer.ini*" from your Heidelberg Engineering viewer installation. Add the following two lines to it:

```
[XmlExport]
Workspace=C:\PATH\TO\AN\EXISTING\ DIRECTORY
```

The first line “[XmlExport]” will turn on the xml export facility. The second line controls the target directory for the xml export. You should make sure that the directory listed there exists and that you have the rights to write into it.

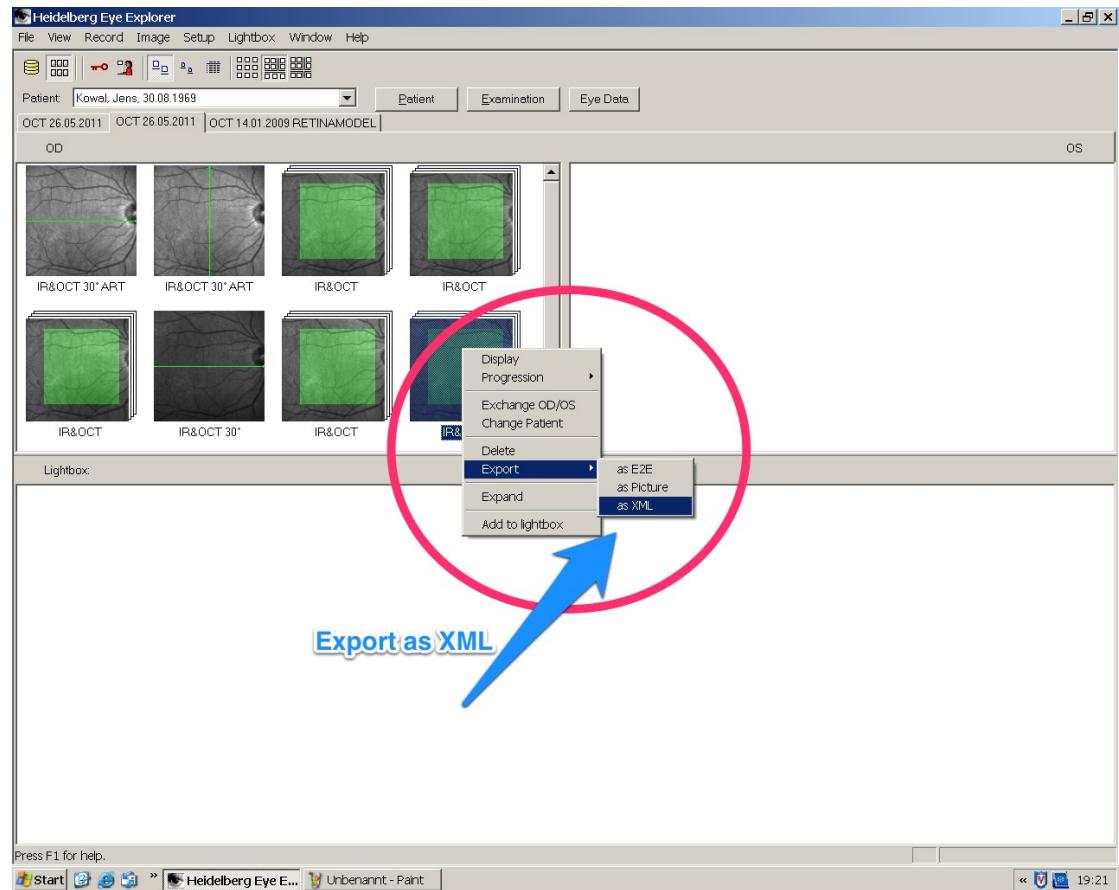


Figure 1: Export menu point to create an xml export

Segmentation Application

The application consist of two main modules the “Patient Manager” and the “OCTSegModule”. You can switch between both modules using the “*Application Module Switcher*” which is the tab bar at the very top of the application.

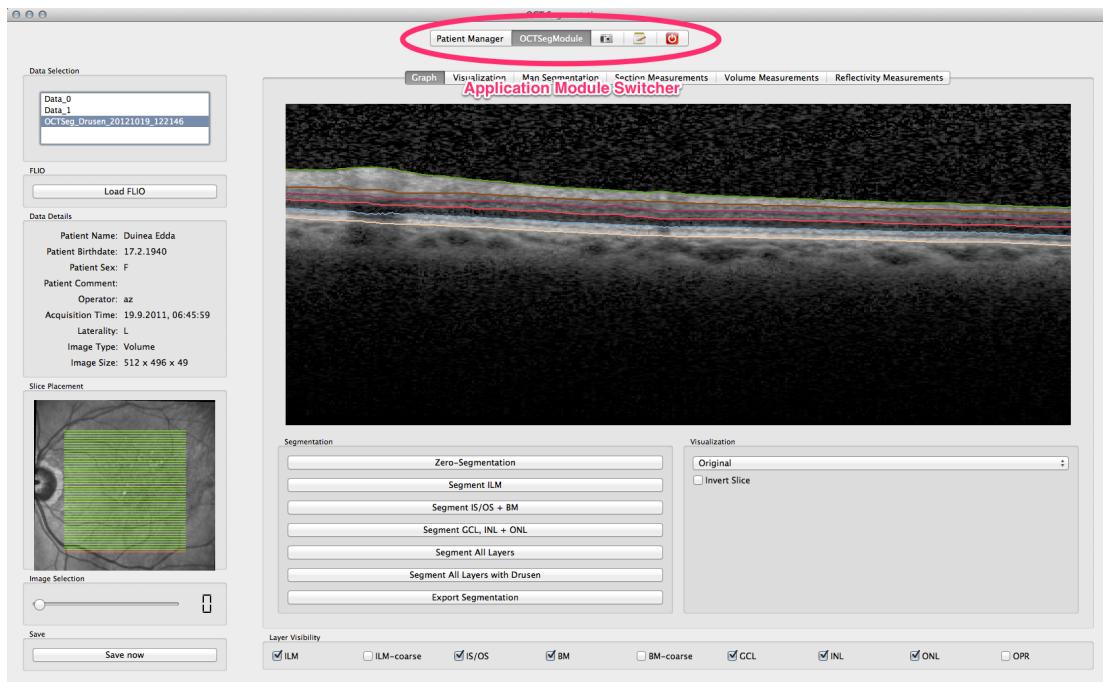


Figure 2: Application main screen

Both modules are explained in the following. Additionally the tab bar contains a button to make screenshots (right to the *OCTSegModule* button), a button to launch the configuration file editor, and the exit button (on the very right end of the tab bar).

As the name suggest the screenshot button enables you to make screen shots of the application. Clicking on it opens a new dialog showing a scaled down picture of the application an to buttons to either save the acquired screenshot or dismiss it. The default location to store the screenshots is the Desktop.

Clicking on the configuration file editor button opens a configuration dialog editor allowing you to change several parameter controlling the behavior of the application. In the remaining part of the manual we will refer occasionally to the configuration editor whenever it is appropriate. For the moment the default values are good to go.

The last button in the tab bar on the right allows you to terminate the application.

Data Loading - Patient Manager

The purpose of the patient manager module is to organize and import data. OCT data are organized by patients and studies. Finally the individual OCT slice stacks are integrated into studies.

You can have as many patients as you want in your patient database.

To import a new OCT image data set click on "New Patient" (see number 1 in Figure 3) first and enter patient specific information as requested in the dialog box that will open. Note: The Patient ID will be assigned automatically.

After creating a new patient you'll have to create a new study, by clicking on "New Study" (see number 2 in Figure 3). In the dialog that will open you can change the Study name or leave it as suggested. Institution name is optional. To finally add an OCT slice stack to the new patient/study combination press the "Add Data" button (see number 3 in Figure 3).

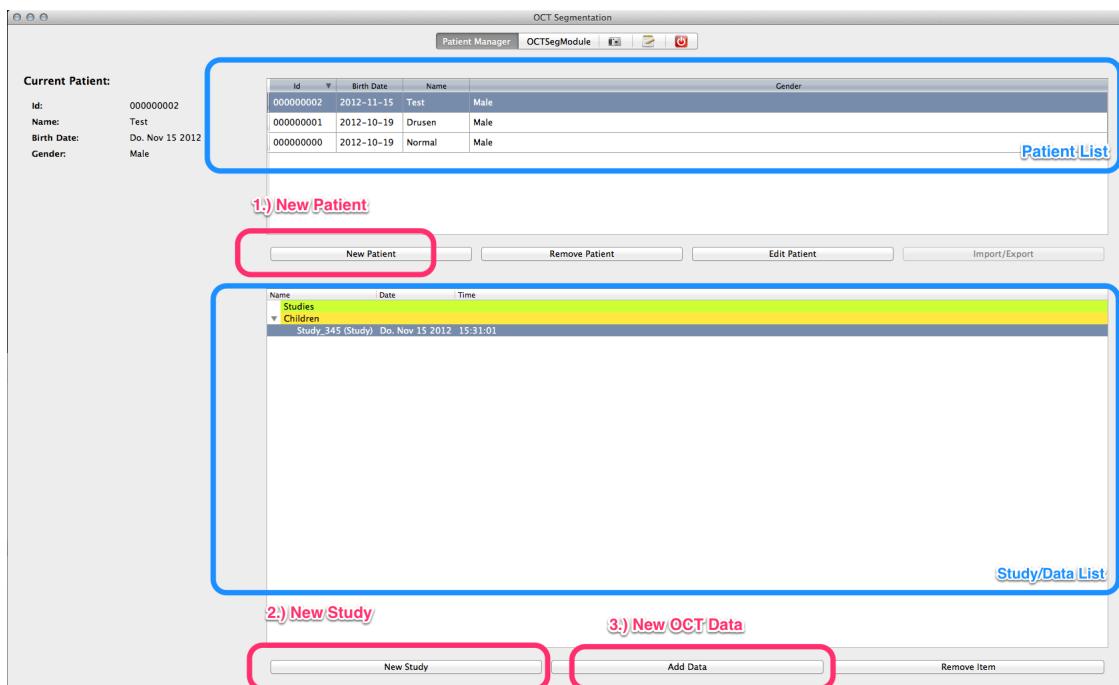


Figure 3: Patient Manager Module

Clicking on the *Add Data* button will open a Dialog box shown in Figure 4. This dialog window lets you normally choose the type of data that you want add. Currently within this application only OCT data are of concern therefore this is the only type you can select here.

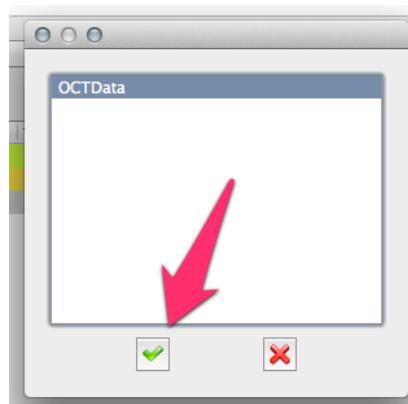


Figure 4: Choose Data Type Dialog

To proceed click on the green checkmark. A new dialog will open where you can provide a name for OCT data (green arrow in Figure 5) - you can also proceed with the suggested name. Clicking on the green plus sign will bring up a file dialog that lets you choose the data to be added (see Figure 6).

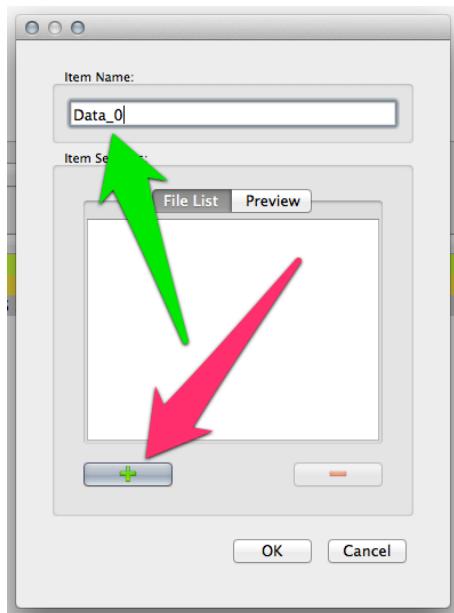


Figure 5: Add Data Dialog

With the File Dialog navigate to the directory where you exported the OCT from the Heidelberg Engineering system and select the xml File (double click on it or select it and click open). The File Dialog will close and the list view in the Add Data Dialog will be updated with the OCT data just added.

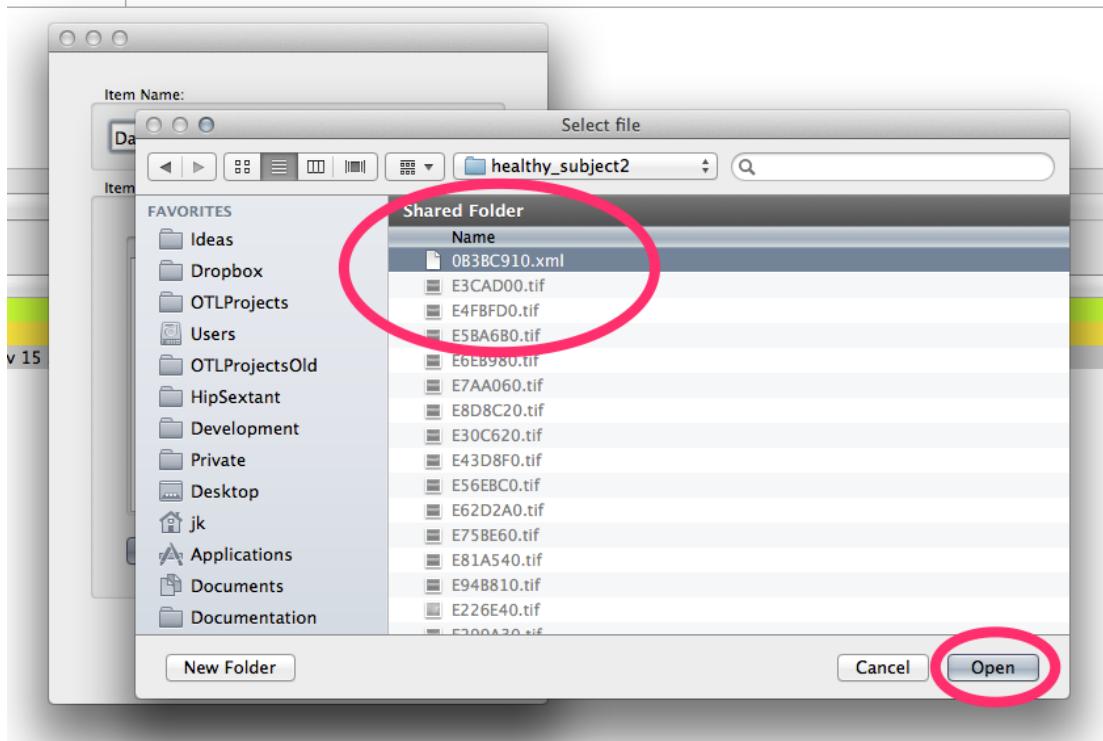


Figure 6: File Dialog to select the OCT Data

After clicking Ok in the Add Data Dialog the xml File will be parsed and if the export contains several studies it will let you choose one study. Click Ok to close the selection dialog.

Before we proceed with the actual segmentation some general remarks to the patient data handling:

- All patients known to the application will be shown in the upper list view marked in blue as *Patient List* (see Figure 3).
- The created studies for a particular patient are listed in a tree like structure together with the data they encapsulate (shown with a blue mark entitled "*Study Data List*" see lower part of Figure 3).
- You can edit some patient information by clicking on the *Edit Patient* button.
- You can remove Patients by clicking on the Remove Patients button.
- You can add multiple studies to a particular patient and you can have multiple OCT image data within one study.
- Throughout the application we use the concept of a "Current Patient" and a "Current Study"/"Current Data". This means each edit/remove action in the Patient Manager is always in relation the selected items in each of the two list views. Moreover, later in the Segmentation Module only data of the currently selected Study are available for segmentation. If you want to segment OCT's from a different study or from a different patient you have to go back to the "Patient Module" and select the respective Patient/Study in the related list views.
- **IMPORTANT:** Currently we do not copy OCT image data around while importing them into the database of the application. This means if you delete/move the data from the location where you have added them the application won't find them again, e.g. if you have them on a USB stick add them by navigating to the USB stick during the Add Data step and if you unplug the USB stick the application will fail to access the data. A save approach would be to copy the data into a location of your file system where they can stay permanently. In the future we might change this behavior.

Segmentation

With a study selected in the study view we can proceed to the Segmentation Module by clicking on the respective button in the tab bar. The application will look like shown in Figure 7. The list view highlighted in Figure 7 shows all OCT data items of the study currently selected. Double clicking on one OCT slice stack will enable it for the segmentation procedure.

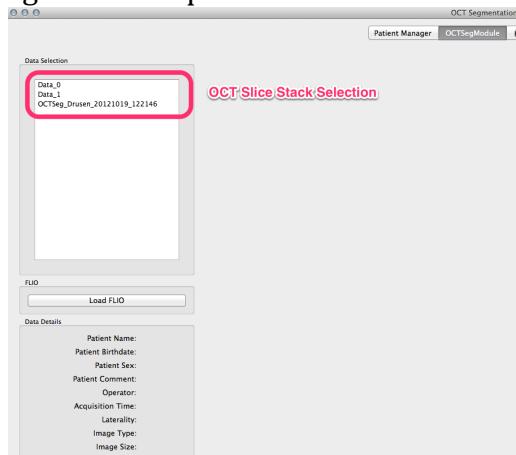


Figure 7: OCT Segmentation Module without data loaded.

The data will be loaded and some preprocessing steps will be performed (anisotropic diffusion).

Thereafter the slice stack is shown in the application as illustrated in Figure 8.

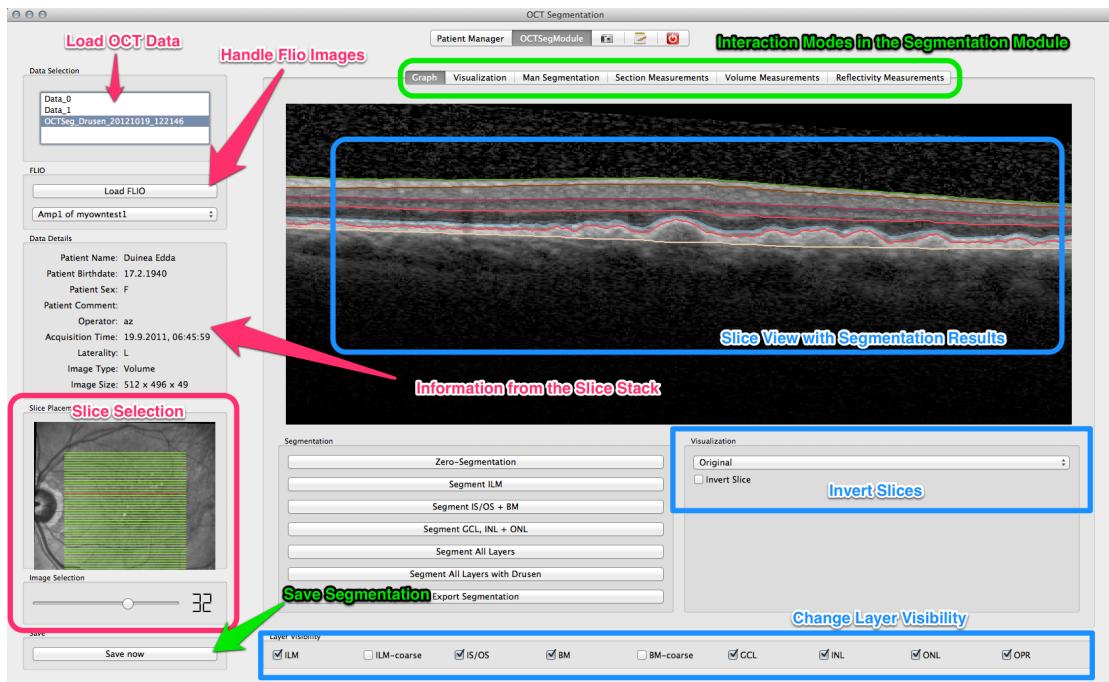


Figure 8: Segmentation - Automatic Segmentation View

The Segmentation module provides 6 different interaction modes. You can switch between them using the tab bar highlighted green in Figure 8. Two modes ("Graph" and "Man Segmentation") allow for segmenting an OCT slice stack automatically or manually respectively, one mode ("Visualization") is to visualize the OCT slice stack together with its segmentation results in 3D, additionally three different measurement modes are available ("Section Measurement", "Volume Measurement", "Reflectivity Measurement").

Automatic Segmentation

The Automatic Segmentation will be activated by clicking on the "Graph" button in the interaction mode tab bar (highlighted in green in Figure 8).

The automatic segmentation procedure ranges always over all images in the slice stack.

The button group "Segmentation" underneath the slice view allows to control the segmentation procedure. The first button in that group "Zero Segmentation" can be used to reset an existing segmentation.

In general you can choose between segmenting all layers together or individually.

"Segment ILM" will selectively segment the internal limiting membrane.

"Segment IS/OS + BM" will segment inner outer segment interface and Bruch

membrane. "Segment GCL + INL/ONL" will segment ganglion cell layer and the inner nucleus layer (INL), and outer nucleus layer (ONL).

NOTE: If you segment the layer individually it is of importance to do it in the right order 1.)ILM; 2.)IS/OS + BM; 3)GCL + INL/ONL.

"Segment all Layers" performs a segmentation of all layers. "Segment all Layers with Drusen" does basically the same but the segmentation of the inner/outer segment interface layer (IS/OS) and the outer PE/RPE complex layer (OPR) is less constrained by the statistical model which allow them to better follow potential pathologies in that area. However, it might take a bit longer (35sec versus 90sec on my computer).

After each segmentation step the segmented layer will show up in the slice view. You can browse over individual slices by using the slider ("Image Selection") highlighted in Figure 8 in the lower left part of the application window. The individual layer are color coded in the slice view. You drag and zoom the slice in the slice viewer if you want to look for particular details.

The layer can be turned on/off individually using the checkboxes grouped as "Layer Visibility" at the bottom of the application window.

The segmentation should be able to handle regular slice stacks containing several slices as well as single slices - both of the central retina.

For slice stacks consisting of several slices the segmentation algorithm does not segment the slices individually it will rather find an optimal segmentation result over all slices together. That is the reason for the rather large amount of main memory the application will occupy during the segmentation step.

Segmentation of OCT's centered around the optic nerve is not yet supported because we don't have yet a statistical model for it.

The Checkbox "Invert Slice" (located in the lower right part of the segmentation view) inverts the color mapping of the slice view. The selection box above allow visualization of different steps of the image processing queue of the slices.

The button "Save now" stores the current segmentation result. Stored segmentations will show up in the selection view in the upper right area of the application window. They can be re-loaded like a regular slice stack for subsequent inspections. They have the creation date and time in their names encoded.

Manual Segmentation

The manual segmentation mode (activated via the button "Man Segmentation") allows to refine an existing segmentation. The basic interaction is the same as for the automatic segmentation.

To change manually a segmented contour you have to first select the contour that you want change using the selection list highlighted in Figure 9 in blue.

Inside the viewer you drag the selected contour to the desired position using the mouse. The mouse is visualized as a cross with surrounding square. The color of

the square correlates always with the color of the currently selected layer (e.g. in Figure 9, layer that will be changed is ILM shown in green therefore the surrounding square is green as well).

Additionally, each manual segmentation interaction creates an item on the undo stack (shown in green in Figure 9). You can use this to undo the last potentially faulty manual segmentations.

"Save now" allows you to explicitly store the refined segmentation result. Manual changes in the slice viewer always affect the current slice only - this means if you want to propagate the changes to the adjacent slices as well you have to repeat the manual refinement for each affected slice.

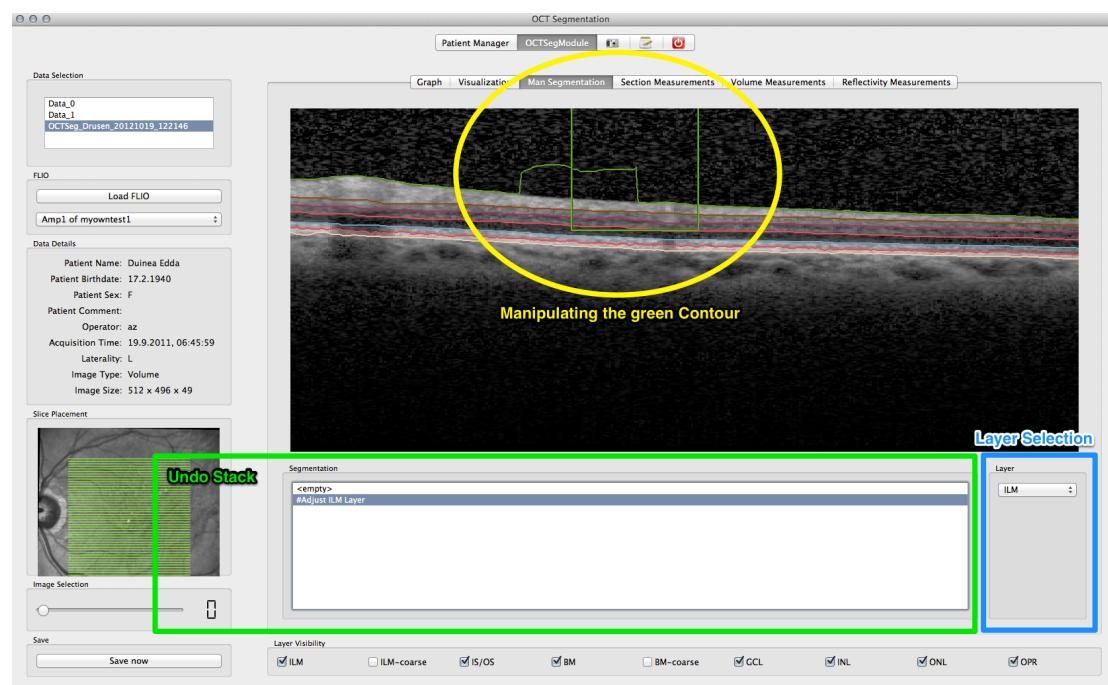


Figure 9: Manual Segmentation Screen

Measurements

Section Measurements

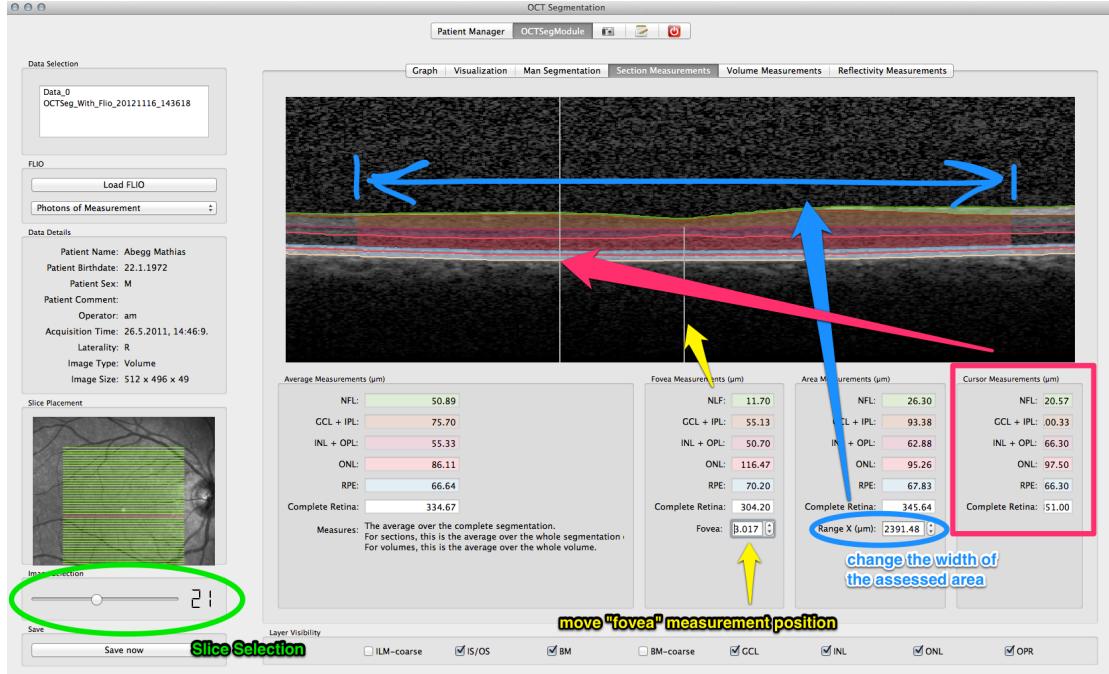


Figure 10: Section Measurement Screen

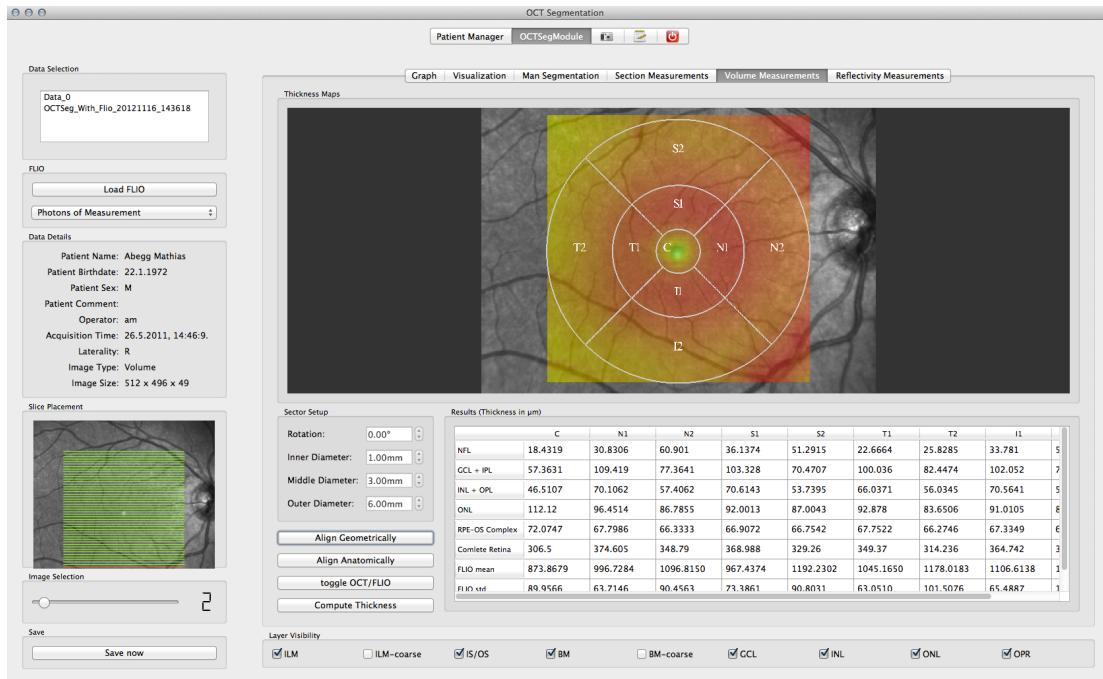
The section measurement uses an existing segmentation to perform measurements on the currently displayed slice out of the slice stack. If you change the slice (using the slice selection, highlighted in green in Figure 10) the measurements will be updated. The section measurements are grouped in four individual measurement scopes (see the four group boxes located in the lower half of the main screen):

1. **Average Measurements:** Average distance measurements over the complete segmentation of the current slice.
2. **Fovea Measurements:** Punctual distance measurement at the fovea. The position where the current fovea measurement is assessed is indicated with a grey vertical line (see yellow arrow in Figure 10). The horizontal position of the line can be adjusted using the spin-box entitled “Fovea” (yellow arrow in Figure 10).
3. **Area Measurements:** Area measurement is an average distance measurement covering only the area with the semi transparent colored overlay. The width of the area can be controlled with blue highlighted spin-box entitled “Range X” (see Figure 10). The area is always centered around the fovea measurement line shown in gray. This means you can move the measured area horizontally by changing the Fovea position (see previous point). If you move the area or change the width the values are updated automatically.
4. **Cursor Measurements:** Assesses the current layer thicknesses at the position of the cursor (cursor position indicated by the gray line passing vertically across the whole image). If you move the cursor the values are updated automatically.

The units for all shown measurements are μm . In each of the four groups the field complete retina gives the overall height of the retina. The color-coding

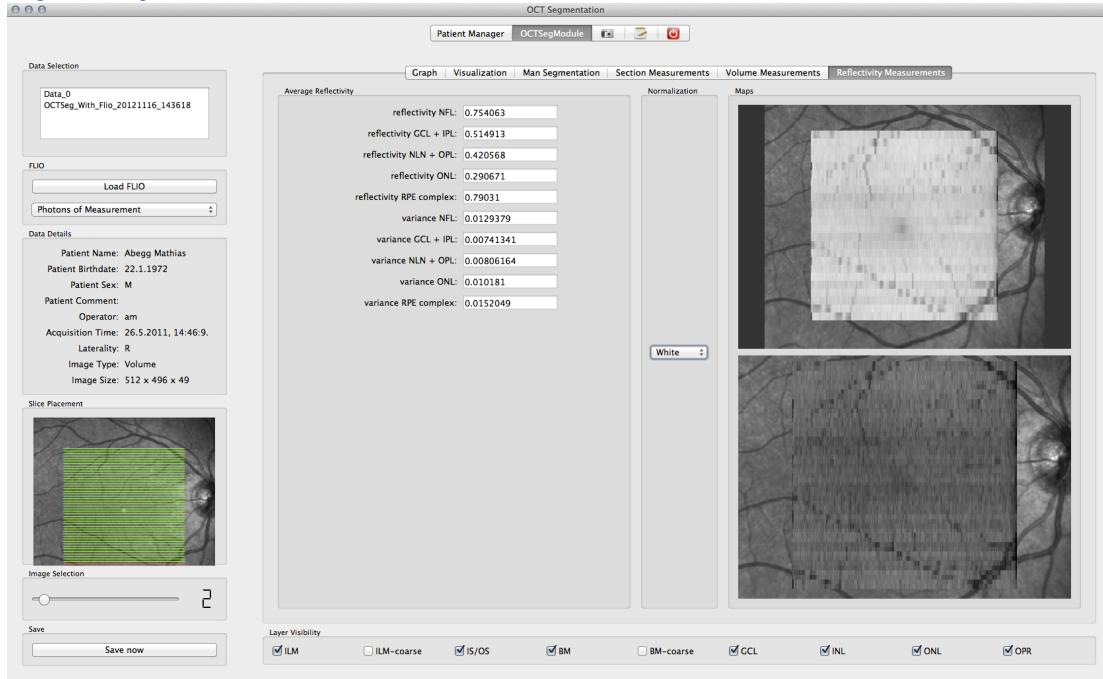
shown in the image view correlates with the background color in the individual fields.

Volume Measurements



still to come...

Reflectivity Measurements



still to come...

Visualization

Is just a 3D viewer with some interactions like rotation, zoom, pan that shows the relation of the localizer image, the OCT slides, the segmented contours (shown as surfaces) and eventually a loaded Flio Image. See Figure 11 for details.

Layer visibility can be toggled, flio image position can changed (just the z-axis). You can browse through the OCT Slices using the slider.

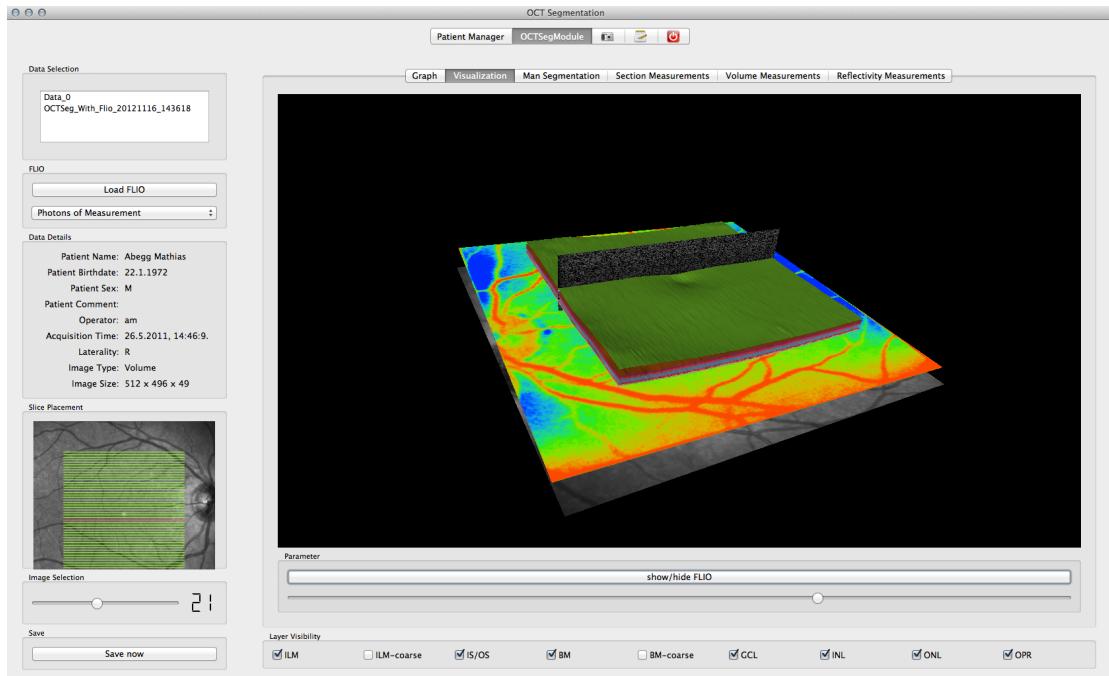


Figure 11: 3D Visualization Mode