Report for Segmentation Results

Functionality

The function *Segmentation → Export Results* exports the results of the automatic retinal layer segmentation of a SPECTRALIS OCT scan into a tab separated text file. Positions for each layer are exported in relative coordinates, as distance in nanometers to image top for each A-scan line.

The format of the text file is described in detail in chapter "Data Structure" below.

Save formats

Offered file save formats are Microsoft® Excel™ (.xls) or text file (.txt). The name of the file created by this function can be chosen by the user.

When choosing .xls file format, a file format warning is (correctly) issued when first opening the file in Excel™. After import of the file by clicking "Yes" and saving as Excel™ worksheet, the warning will not appear again.
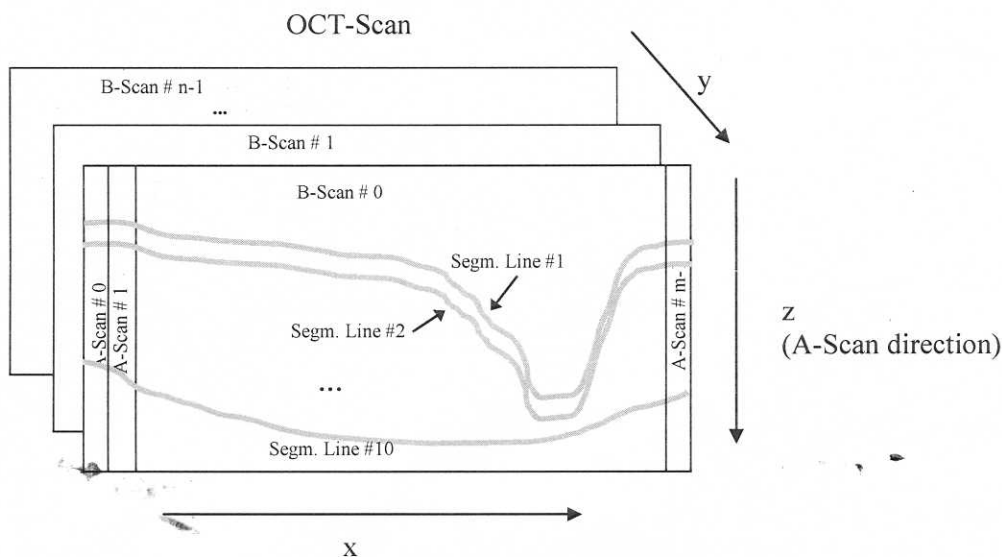
Coordinate System and Dimensions

The following diagram shows the naming conventions for the coordinate system and the dimensions of an OCT-Scan.

Each OCT-Scan consists of n B-Scans ($n = 1 \ldots 241$).

Each B-Scan consists of m A-Scans ($m = 384 \ldots 1536$).

Therefore, each segmentation line consists of m sample points ($m = 384 \ldots 1536$).

Each A-Scan consists of l samples ($l = 496$).

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File Layout

Layout of the text file:

Header	

```
┌─────────────────────────┐
│        Header           │
├──┬──────────────────┬───┤
│  │ Line Name.Position│   │ ⎫
├──┴──────────────────┴───┤ ⎪
│    Result at Position   │ ⎪
├──┬──────────────────┬───┤ ⎬ Segmentation results
│  │ Line Name.Position│   │ ⎪
├──┴──────────────────┴───┤ ⎪
│    Result at Position   │ ⎪
├─────────────────────────┤ ⎪
│           ...           │ ⎭
└─────────────────────────┘
```

The file is in plain text format and consists of the following components:

- Two lines of file header, containing field names (e.g. "First name") in the first line, and the corresponding patient and image information in the second.

- The header is followed by the segmentation results, each consisting of two lines. The first line contains the name of the layer/boundary and the number of the corresponding A-Scan, i.e. pixel X-position. Format is <name>.<x-pos>, e.g. RPE.123. The second line holds the corresponding z-position of the respectively boundary found by the segmentation.

- When multiple results were exported simultaneously (multiple images were selected for export in Heyex), the first block is followed by an empty line, then the information from the next image as described above, and so on.

Data Structure

This section gives an overview over all the data that is written in the report. An example in detail can be found at the end.

File Header

The following information is exported alongside the segmentation results:

Abbreviation	Description
LastName	Last name of the patient
FirstName	First name of the patient
DOB	Date of birth of the patient
PatientID	Unique ID of the patient in the data base (if given)
Eye	Which eye was examined, i.e. 'L' or 'R'
ImageID	Unique ID of the image in the data base (always given)
ExamDate	Date when the segmented image was acquired
ExamTime	Time when the segmented image was acquired
AQMVersion	Version of the Spectralis OCT acquisition module (if given)
Quality	Image quality rating (if given)
ARTMean	If Automatic Real Time (ART) was used, and if yes, with how many images (if given)

Segmentation Data
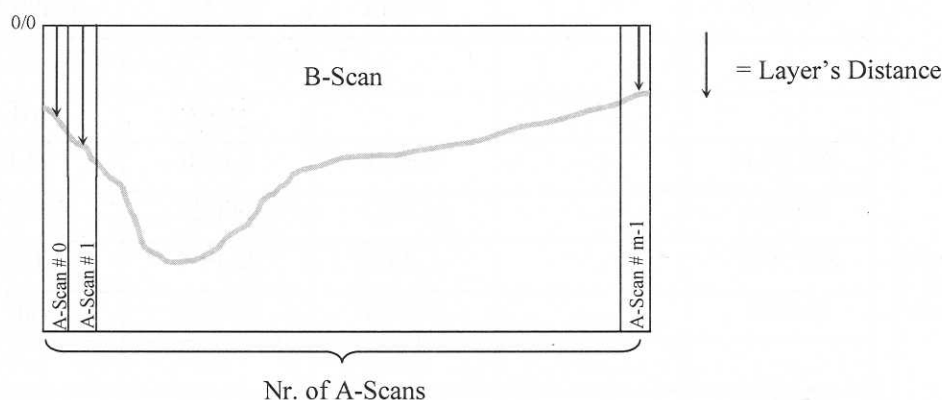
All segmentation lines are given as a vector of distances from the upper image border at each X position (see figure above).

Although the distance information for each pixel is internally calculated as floating point numbers (e.g. 123.456 µm for line 7, pixel 321), writing out of these numbers is dependent on the local language settings. For example, in American English, the above example would be written as 123.456 µm, but in German, it would be written 123,456 µm, with a comma as a separator instead of a period.

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Therefore, each Z position is given as an integral value in *nanometers (nm)*.

1000 nanometer equal 1 µm, so in the above example 123456 would be written. To convert the values back to µm positions, they have to be divided by 1000.

If the segmentation fails locally or a boundary is not present at a position, e.g. outside of the image area, the term "n/a" is written out.

Please note:

The single layer distances to the image top border depend on the manual alignment of the acquisition device relative to the eye. So, the single position values do not comprise any meaningful information. Only the *differences* between boundary positions are meaningful. For example, the position of the RPE minus the position of the ILM (RPE - ILM) gives the thickness of the retina, but no spatial position information.

Example File

This is an example how a file could look like if imported into Excel.

LastName	FirstName	...	ImageID	...	
Doe	John	...	339.0		
ILM.1	ILM.2	ILM.3	...	ILM.768	
123456	125893	130124	...	465924	
NFL.1	NFL.2	NFL.3	...	NFL.768	Image 1
n/a	n/a	167427	...	503845	
...	...	...	...	...	
RPE.1	RPE.2	RPE.3	...	RPE.768	
338843	341596	344347	...	849183	
Doe	John	...	339.2	...	
ILM.1	ILM.2	ILM.3	...	ILM.768	
123456	125893	130124	...	465924	
NFL.1	NFL.2	NFL.3	...	NFL.768	Image 2
n/a	156301	167427	...	503845	
...	...	...	...	...	
RPE.1	RPE.2	RPE.3	...	RPE.768	
338843	341596	344347	...	849183	

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