**Synopsis**

This document relates to the Matlab GUI known as Section Extractor and provides instructions on its usage. It does not attempt to explain the image processing methodology used for segmentation.

This program provides a means to automatically crop tissue sections from images generated using the QBI brightfield and fluorescence slide scanners. The slide scanners generate images with sizes on disk which prohibit them being opened at full resolution in any other image processing package other than Imaris. This creates a problem because the files are unwieldy making it slow to copy the image of the whole slide to the QBI fileserver or an external storage device. This GUI uses a file-to-file process so that neither the full image of the slide or the tissue section being cropped is ever loaded fully into memory. Tissue sections are automatically detected in the image by the GUI and a means is provided to crop all sections or a user selection and the final image can a single channel or can be made to crop all channels present in the input image. Additionally the user can choose to crop at full resolution or a scaled-down image of the tissue section can be generated. The output format is TIFF.

1. Identify the slide scanner image

A preview of the selected channel is displayed here

Segment a brightfield or fluorescence image

Identify a slide image for processing
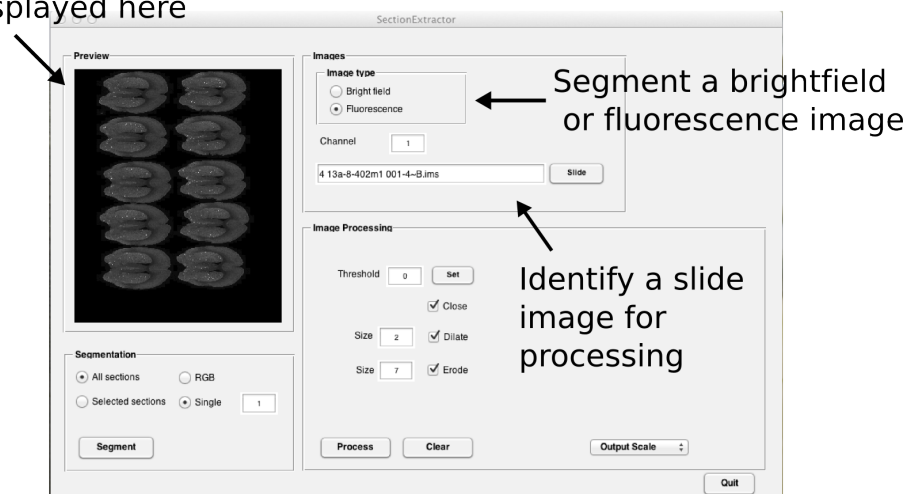
Use the button marked "Slide" to select the slide scanner image to be processed; the name will appear in the adjacent text-box. A preview of the channel identified by the text-box labelled "Channel" is shown in the preview on the right. This channel will be used for the image segmentation routine. Channel 1 is selected by default. To use a different channel type the channel number (starting at 1) in the text-box.

2. Image segmentation
Automatic detection of the tissue sections is performed by simply thresholding of the image and locating the so-called connected components in the image. A scaled-down version of the image is used for this process.

A threshold level is provided by the user either by typing a number in the text-box labelled "Threshold" or by using a simple GUI that can be accessed by pushing the button labelled "set".
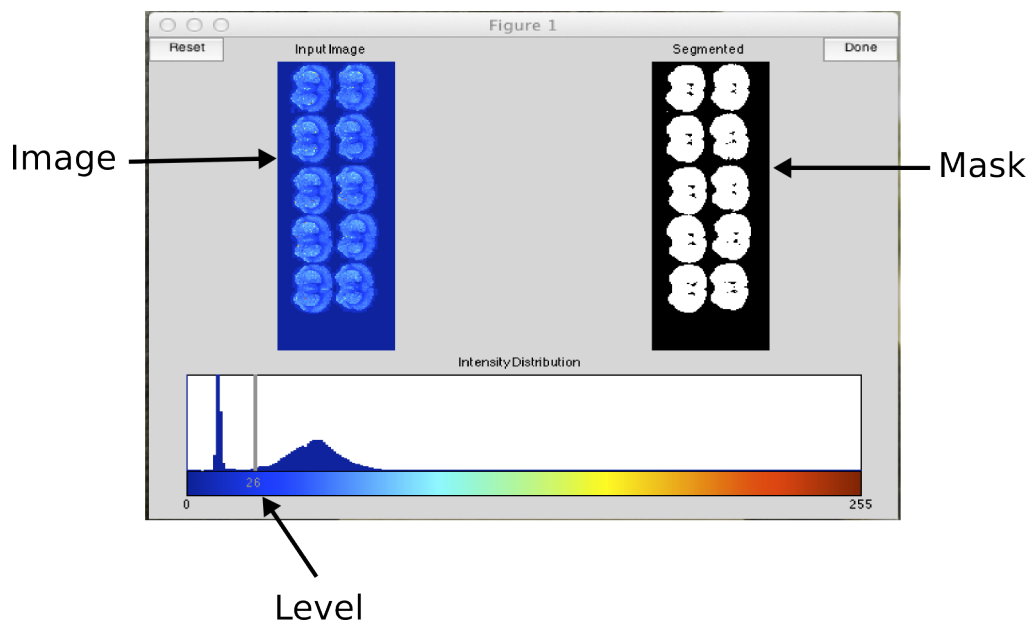
The check-box indicate the image processing to be carried out on the mask generated by applying the threshold. The option to "close" performs a closing operation on the image that will remove any small holes. Dilation is a process that grows a region to fill larger gaps. The text-boxes marked "size" and "iterations" allow the user to set a size for the structuring element and the number of iterations used when dilating the image.

If the tissue sections are close to one another erosion can be used to separate the sections into individual objects. Erosion shrinks the size of the individual objects. Again the text-boxes are used to set the size of the structuring element and number of iterations used to erode the image.

The selected image processing routines are applied by pushing the button marked "Process". After processing the coordinates of the top-left-hand corner and size of the region marked for segmentation are displayed in the list box (x y w h). Selecting one or more of the regions in the list box marks the section being segmented with a red square on the preview image.

A number of options are available for the output TIFF. The user can select individual (or multiple) sections or all detected sections can be segmented. The output can be an RGB image or a single plane selected by entering the channel number in the text-box. The output image can be a full resolution image or can be scaled down using the popup menu (options of 1, 2, 4, 8, 16, 32 and 64 can be selected).

Preview of segmented regions

Segment all sections or selected and output an RGB or a single plane

Scaling factor of output image