

Histo-cloud / segment WSI (testing)

The SegmentWSI tool on devathena.rc.ufl.edu provides an easy-to-use interface for segmenting whole slide images using deep learning. In this guide, we will walk you through the steps to segment a whole slide image using the SegmentWSI tool.

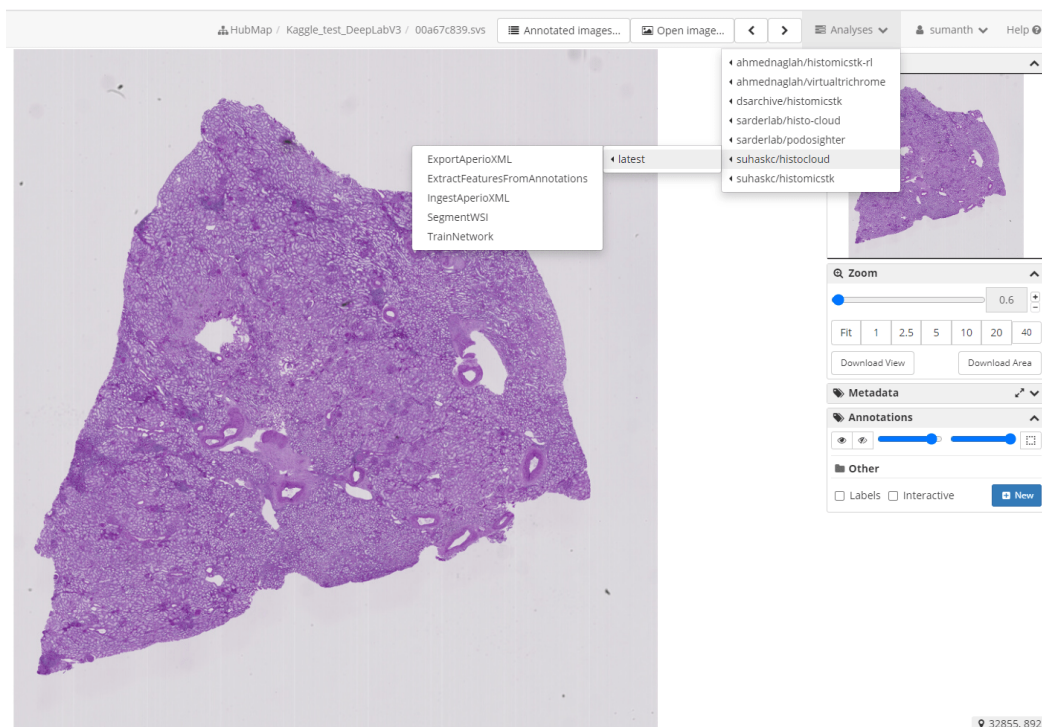
Go to devathena.rc.ufl.edu to access the Digital Slide Archive and click on 'Register' if you are a new user or 'Log In' if you have an existing account.

Upload / Access a Whole Slide Image

- Click 'Collections' on the menu to the left to access collections of whole slide images a whole slide image.
- To create a new collection of whole slide images go to 'Collections' and click on 'Create collection', for this you need authorization / admin access.

SegmentWSI

- On the Whole slide image to segment click on 'Open in HistomicsUI' and it opens a new tab with the selected whole slide image in HistomicsUI.
- Click on Analyses dropdown, select 'suhaskc/histocloud' -> latest -> 'SegmentWSI'.



- This will open a new popup on the left-hand side of the screen, where you can input the necessary parameters for the segmentation job.

Parameters

IO

- Input Image: Select the input whole slide image you wish to segment. You can choose multiple images using a regular expression such as "*.svs".
- Select an existing segmentation model or upload a new model in zip format under 'Input Model File - Zip file'.

- Finally, specify the output glomeruli annotation file where the segmented annotations will be saved.

IO ^

Input Image

Input image

00a67c839.svs
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Input Model File - (zip file)

A zip file containing Tensorflow model-files and metadata for the deeplab segmentation network

model-Glomeruli-11-13-20
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Output Glomeruli Annotation File

Output annotation file (*.anot) containing glomerular annotations

Segment WSI-outputAnnotationF
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Heatmap Output

- The 'Heatmap Output' section allows you to save the network logits (probabilities) as heatmap layers. Specify the heatmap stride, which is the additional downsample applied to the saved heatmaps.

Heatmap Output ^

Save the network logits (probabilities) as heatmap layers.

Save heatmaps

Heatmap stride

The additional downsample (applied by striding the logits) applied to the saved heatmaps.

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WSI Analysis

- In the 'WSI Analysis Parameters' section, you can specify the parameters for the analysis.
- The 'Analysis tile downsample' is the downsample rate at which the analysis should be performed with respect to the full resolution.
- The 'Analysis tile size' is the tile size for blockwise analysis in pixels, and 'Tile stride' is the stride used for overlapping patches during analysis in

pixels.

- 'Remove Patch border' specifies the size of the patch border that is discarded prior to stitching to remove edge artifacts.
- The 'Analysis batch Size' is the batch size for processing WSI patches, and the 'Minimum object Size' is the minimum size in pixels of objects detected by the analysis.
- The 'Annotation contour approximation epsilon' specifies the amount of approximation used to simplify the predicted boundaries. It is recommended not to set this above a value of 0.01, and uses the Douglas-Peucker Algorithm.
- Finally, you can specify the ID of the GPU to use for the analysis.

WSI Analysis ^

Analysis tile downsample
The downsample rate at which the analysis should be performed w.r.t. full resolution

Analysis tile size
Tile size for blockwise analysis (pixels)

Tile stride
The stride used for overlapping patches during analysis (pixels)

Remove patch border
The size (pixels) of the patch border which is discarded prior to stitching - removes edge artifacts (this requires sufficient patch overlap)

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Analysis batch size

The batch size for processing WSI patches

Minimum object size

The minimum size in pixels of objects detected by the analysis - a value of 0 does not remove small objects

Annotation contour approximation epsilon

The amount of approximation used to simplify the predicted boundaries - we don't recommend setting this above a value of 0.01 (uses the Douglas-Peucker Algorithm)

GPU

The ID of the GPU to use for analysis

Once you have specified all of the necessary parameters, click 'Submit' to run the job. The SegmentWSI tool will begin segmenting the input whole slide image(s) and saving the annotated glomeruli segmentation to the output file. You can check the status of the segmentation under Jobs section.

Segment WSI



Segments structures from a whole-slide image

Reload

Submit

Jobs



- ✓ [Segment WSI on ff339c0b2.svs](#)
- ✓ [Segment WSI on e464d2f6c.svs](#)
- ✓ [Segment WSI on bacb03928.svs](#)
- ✓ [Segment WSI on a14e495cf.svs](#)
- ✓ [Segment WSI on 9e81e2693.svs](#)
- ✓ [Segment WSI on 5d8b53a68.svs](#)
- ✓ [Segment WSI on 5274ef79a.svs](#)
- ✓ [Segment WSI on 1eb18739d.svs](#)
- ✓ [Segment WSI on 0749c6ccc.svs](#)
- ✓ [Segment WSI on 00a67c839.svs](#)