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🌐 CODA: shorthand for calling functions | HuBMAP | JHU-TMC V.2

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Protocol status: Working
We use this protocol and it's working

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Abstract

To downsample ndpi or svs images to 10x, 5x, and 1x tifs, use this function:

create_downsampled_tif_images

or try Openslide in python

To calculate registration on the low resolution (1x) images

1. calculate the tissue area and background pixels using this function:

calculate_tissue_ws

2. calculate the registration transforms:

calculate_image_registration

To build a 3D tissue volume using sematic segmentation:

1. generate manual annotations in Aperio imagescope
2. apply the deep learning function to train a model and segment the high resolution (5x or 10x) images:

train_image_segmentation

To apply the registration to segmented images:

apply_image_registration

To build a 3D tissue matrix from registered, classified images:

build_tissue_volume

To build a 3D cell volume containing nuclear coordinates:

1. Build a mosaic image containing regions of many whole-slide images for cell detection optimization:

make_cell_detection_mosaic

2. Manually annotate the mosaic image to get the 'ground-truth' number of cell nuclei:

manual_cell_count

3. Determine cell detection parameters using the manual annotations on the mosaic image:

get_nuclear_detection_parameters

4. Deconvolve the high-resolution (5x or 10x) H&E images before applying the cell detection algorithm:

deconvolve_histological_images

5. Detect cells on the hematoxylin channel of the high-resolution images:

cell_detection

6. Apply the registration to the cell coordinates:

register_cell_coordinates

7. Build a 3D cell coordinate matrix corresponding to the 3D tissue matrix:

build_cell_volume

Part of **SPRINGER NATURE**

shorthand in the abstract

1   Use the above shorthand to facilitate your workflow by using it as a "cheat sheet"