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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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Keywords: CODA, machinelearning, deeplearning, 3d tissue matrix, slide images for cell detection optimization, 3d tissue volume, make-cell-detection-mosaic, calculate-image-registration, deconvolve-histological-image, cell detection optimization, cell detection parameter, 3d cell volume, segmented image, sematic segmentation, cell detection, 3d cell coordinate matrix, cell detection algorithm, apply-image-registration, create-downsampled-tif-image, tmc to downsample ndpi, registration on the low resolution, registration to the cell coordinate, using sematic segmentation, mosaic image, images to 10x, resolution image, classified image, manual annotations on the mosaic image, tissue area, cell nuclei, number of cell nuclei, calculate-tissue-w, deep learning function, 1x tif, image, downsample ndpi, manual-cell-count, cell coordinate, tissue, get-nuclear-detection-parameter, deep learning, high resolution, slide image, cell, nuclear coordinate, containing nuclear coordinate, 3d

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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

shorthand in the abstract

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