APR 01, 2024

OPEN ACCESS

DOI:
dx.doi.org/10.17504/protocols.io.5qpvoknkbl4o/v1

Protocol Citation: Kyu Sang Han, Pei-Hsun Wu, Joel Sunshine, Ashley Kiemen, Sashank Reddy, Denis Wirtz 2024. CODA: shorthand for calling functions | HuBMAP | JHU-TMC. **protocols.io** https://dx.doi.org/10.17504/protocols.io.5qpvoknkbl4o/v1

MANUSCRIPT CITATION:
Kiemen, A.L., Braxton, A.M., Grahn, M.P. *et al.* CODA: quantitative 3D reconstruction of large tissues at cellular resolution. *Nat Methods* **19**, 1490–1499 (2022). https://doi.org/10.1038/s41592-022-01650-9

CODA: shorthand for calling functions | HuBMAP | JHU-TMC

Kyu Sang Han[1], Pei-Hsun Wu[1], Joel Sunshine[2], Ashley Kiemen[2], Sashank Reddy[2], Denis Wirtz[1,2]

[1]Johns Hopkins University; [2]Johns Hopkins Medicine

Human BioMolecular Atlas Program (HuBMAP) Method Development Community

TMC - Johns Hopkins University

Kyu Sang Han
Johns Hopkins University

License: This is an open access protocol distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited

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

Created: Mar 28, 2024

Last Modified: Apr 01, 2024

PROTOCOL integer ID: 97516

Keywords: CODA, machinelearning, deeplearning

Funders Acknowledgement:
Institute of Arthritis and Musculoskeletal and Skin Diseases
Grant ID: U54AR081774
National Cancer Institute
Grant ID: U54CA143868

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