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CODA (part 1): setting up environment and preparing sample dataset | HuBMAP | JHU-TMC

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Human BioMolecular Atlas Program (HuBMAP) Method Development Community

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ABSTRACT

CODA workflow part 1. setting up environment and preparing dataset

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

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Software requirements

1. MATLAB MATLAB (mathworks.com)
   Image processing toolbox Image Processing Toolbox - MATLAB (mathworks.com)
   Deep learning toolbox Deep Learning Toolbox - MATLAB (mathworks.com)
   MATLAB - Resnet50 model MATLAB resnet50 (mathworks.com)
2. Aperio ImageScope Aperio ImageScope (leicabiosystems.com)
3. FIJI ImageJ Fiji Downloads (imagej.net)

Download Source code

4 Codes are available at the following GitHub: CODA Github Repository

Download Sample dataset

5 Here, we discuss application to a sample dataset “lungs”, containing 150 serial histological images. Download the sample dataset (serial images and sample annotations) here: Lung Sample Dataset on Google Drive

6 Images are .ndpi format and were scanned at 20x magnification (approximately 0.5 micron / pixel resolution), spaced 10 micron apart. Save the images in a local drive folder (e.g. **\\Users\Ashley\Documents\lungs).**

7 Filenames for each image should be created such that tissue sections are read consecutively by Matlab. Therefore, include zero-padding in numerical indices.

CORRECT FILENAMES: **lungs_001.ndpi, lungs_002.ndpi, ..., lungs_011.ndpi**
INCORRECT FILENAMES (no zero padding): **lungs_1.ndpi, lungs_2.ndpi, ..., lungs_11.ndpi**

Create downsampled copies of high-resolution images

8 The function **create_downsampled_tif_images** will create downsampled copies of the .ndpi files by directly loading each high-resolution images in tiles and down sampling it to the desired pixel resolutions.

9 First, decide the resolution of the images you want to create. Here, we create images of 1 micron / pixel, 2 microns / pixel, and 10 micron / pixel resolution:

ds=[1 2 10];

10 Next, decide on the name of the output folders for each of the downsampled images you create. Here, we will save the images downsampled to 1 micron / pixel in a folder named “10x”, the images downsampled to 2 micron / pixel in a folder named “5x,” and the images downsampled to 10 micron / pixel in a folder named “1x.”

subfolders=["10x" "5x" "1x"];

11 Finally, call the function: **create_downsampled_tif_images(pth,ds,subfolders);**

12 Using this function, you will make two subfolders within the original folder containing the .ndpi images. One subfolder named “10x” containing the 20x images downsampled by a factor of 2. The other subfolder named “1x” containing the 20x images downsampled by a factor of 20. Most calculations will be performed on these tif images. Note: here we use 10x and 1x for example, but other resolutions could be created as desired.

pth10x=[pth,'10x'];
pth1x=[pth,'1x'];
****Note: If this code fails due to memory constraints on your computer, try python Openslide.**