Overview

The goal of this software package is to make machine learning predictions of brain microenvironment viscosity based on cellular images.

Step 1. Pre training

For pre training, the model will be trained only on image data of microglia. Specifically, the model will be given images of microglia with a patch removed. The goal of the model will be to determine which of the presented patches is the most likely to be the one removed from the image.

Step 2. Finetuning

For fine-tuning, the model will have to predict the local viscosity of the microenvironment based on input microglia images.

Modules:

**Image class**

This will be a Python class, from dataclass, that tracks the images of interest

**Data IO:**

load\_tif

def: function to load in tif files to be used for ML. Part of loading should include using the validate\_im function to ensure the image can be used

inputs: file\_path: string

outputs: loaded file

load\_npy

def: function to load in npy files to be used for ML. Part of loading should include using the validate\_im function to ensure the image can be used

validate\_im:

Def: function to validate the input image will work for the given workflow. Should check the shape of the image, ensure it isn’t empty, etc

**Data preprocessing:**

Train\_test\_split:

Def: Method to split images into training, testing, and validation, based on criteria such as “random”, “by slice,” “by animal.” If there are different conditions it should also ensure there is an even split.

Create\_positive\_pairs

Create\_negatie\_pairs

**Deep learning model class:**

Model class

Forward pass

Backward pass

**Loss function calculations:**

Contrastive learning calculations

**Output visualizations:**

**Helper/utility functions:**