##BiAMIL

Welcome to the BiAMIL Github repository!

BiAMIL is a tool that predicts gene mutations through pathological images. It is built on bi-directed self-attention multi-instance learning.

This repository contains all the relevant files related to the paper [“BiAMIL: Bi-directed self-attention multi-instance learning for BRCA1/2 gene mutations detection of breast cancer”].

Warning: BiAMIL is currently in a pre-development phase and may contain many bugs. It is recommended that you make copies of all datasets before using this application.

1. ###ROI\_SegByTiles = Automatic ROI segmentation model

--Train\_roi\_model.ipynb = Train the automatically segmentation model.

--Segment\_roi.py = Generate ROI regions based on the automatic segmentation model.

Preprocess\_full\_tiles.ipynb = ROI regions were divided into tiles.

1. ## ColorNorm =Color normalization

get\_snmf.py =Generate non-negative sparse matrix of the WSI.

color\_norm\_multi.py =Normalize the tiles to the target tile.

1. ## Mutaion =Classification using attentionMIL.

--5fold\_train\_breast.py=5-fold cross-validation.

--Slide\_Validation =Validation at the slide level.