

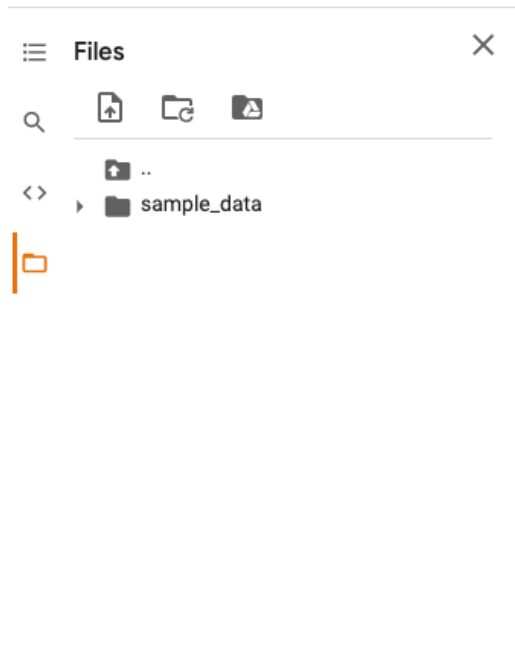
## How to run the Maddox cell segmentation pipeline

### Preprocessing

1. Tile the full image into 512x512 tiles by running the jupyter script (tile)

### Running the trained model

1. Open the colab file and load the .zip file of your data under Files>content



2. Download the trained model to your gdrive (/content/gdrive/MyDrive) or specify the location
3. Run the colab notebook. This will save the full stitched version of the model output (in 2D) to the specified out directory.

### Post Processing

1. First process the raw output by running the jupyter script and separating the boundary and inside classes. This should give you two sets of images, one for only the boundaries and one for only the insides.
2. Run the CellProfiler pipeline to clean up the model prediction and identify all cells (mdxPost).
3. To convert the prediction back to 3D, run the jupyter script. This will open up the 3D stack on napari viewer.