**Importing Images and Cell Morphology into the Database**

Starting in June 2024, we will be importing all scientific images of retinas, cells, and brains into the datajoint database. We are starting with images of retinal cells. This also includes their morphology data from the tracing and flattening software.

Doing this sucessfully requires care and attention to detail with file naming and data entry!

In general these are the steps:

1. Make a folder for your import and check that all the files in there are named correctly and have the same settings. What I mean by the same settings is that the number of channels of the images and their meaning (which is a cell fill, which is ChAT, etc.) must be the same for everything in the folder. It’s totally fine if you have taken different images with different settings, but you need to make a separate loading folder for each batch.

2. Load the raw images. Depending on how many and how big they are, this may take a while. Please do this on a machine connected via ethernet. The office PC and rig machines should all work for this.

3. Load the morphology data from the arborData.mat files that are created by RGCMorphologyAnalyzer. This step also requires careful folder structure, but it is very quick and can be done from your own machine.

A few notes before we get started:

1. Any cell recorded in Symphony for which you have an image must be curated BEFORE starting this process. When the Curator runs, it makes an entry in the table sln\_cell.Cell (and also in sln\_cell.RetinalCell). These are required for correctly assigning images to cells. If you forget this step, the importer will assume that a matching cell does not exist, and it will create a new cell. This will be a mess to untangle, so please try to avoid this error!

2. As impied above, there is a distinction between a cell entry (sln\_cell.Cell and sln\_cell.RetinalCell) and a cell recorded in Symphony (which has an entry in sln\_symphony.ExperimentCell). The importers are built to handle cells for which there is no corresponding symphony data. This is totally fine. They will be created as new sln\_cell.Cell entries, each with a with unique cell\_unid. If you do things correctly in the importer, they will also be associated with the correct animal (sln\_animal.Animal) and eye (sln\_animal.Eye).

3. The mapping between cells and images does not need to be 1:1 in either direction. A single image can be linked to multiple cells, since we often take images with more than one cell in them, and a single cell can be mapped to multiple images (e.g. if we took a 2P and a confocal image of the same cell).

4. Stitching needs to be done in FIJI before the import process. You will be importing the stitched image as a single image, not the parts. However, as you will see below, you will need to keep the parts around during the import process.

5. The importer should handle 3 kinds of files: (A) .nd2 files from a Nikon scope, (B) .tif files from ScanImage recorded on the rigs, (C) .tif composite files from FIJI that are made by stitching (whether initially from .nd2 of .tif).

**Import Steps**

1. Decide which kind of batch import you want to do: by tissue or by cell.

By tissue: Your folder will be for a single eye. This makes the most sense for eyes in which you imaged a lot of cells, individually, on a confocal.

By cell: Your folder will have a subfolder for each cell named by its Symphony name (e.g. 050224Ac3). Of course, this only works if every cell in the folder has a corresponding (CURATED!) Symphony recording.

Of course, you can mix and match. For example, if you did an experiment on a rig and recorded 5 cells in Symphony but then imaged 6 cells because the last one died before you could get any Symphony data, I would suggest the following. First, do a “by cell” import for the first 5 cells. Then do a “by tissue” import for the last cell by putting it in its own folder.