

1 Ilastik Troubleshooting

1.1 What We Still Need To Do:

As I mentioned in the Jupyter notebook (which can be found under our main repo, in the Tony folder, titled IlastikRawandHistEqFear199Data.ipynb and linked [here](#)), we want to detect membrane boundaries to quantify the number of cells in a region.

Ilastik has a built in counting tutorial that does pretty much what we want (linked [here](#)) but it unfortunately ONLY takes 2D data (I tried running it with 3D data and it threw all sorts of assertions).

1.2 Figuring Out Errors in Probability Mapping

Currently, my object probability mapping is blank (see Jupyter notebook), meaning that despite having generated objects in my classifier, my classifier is finding no objects in the input data.

As I discussed in the Jupyter notebook, this process involves troubleshooting the classifier I built and figuring out if it was either the classifier that's the problem (which I think is unlikely given that it's finding objects in my trial data), or if the problem lies in how I'm using the headless display to generate results.

Again, I mention in the notebook about trying to use the built-in batch import functionality, but the functionality is for all intents and purposes not working as intended (there are Github issues on the Ilastik page documenting the exact problems I ran into).

1.3 Interpreting Trial Results

Another thing to note is that the objects I'm generating (see ipynb) are significantly larger than I'd like. While I am finding a couple bright points, I don't seem to be able to find as many as there actually are. This is probably due to the fact that my features aren't as robust as they should be, and that I can work on tuning all the sigmas more appropriately.

That being said, it's interesting to note that the histogram equalized version of the brain generated much better (and many more) objects than did the raw data - the contrast increase definitely helped pick out relative bright points for the classifier.