

# Week of 10/9 Deliverables

Team cobalt

# Last week's goals

- ✓ [Jupyter notebook](#) for summing intensity by region of ARA
- ✓ Create [python package](#) for blob detection metrics
- ✓ Write pseudocode for 2 unsupervised algorithms from literature
  - ✓ Ensemble methods
    - ✓ [2D Analysis + 2D Pseudocode](#)
    - ✓ [3D Reconstruction](#)
    - ✓ [Code](#)
  - ✓ FARSIGHT
    - ✓ A benchmarks.md [thing](#)

# Summing intensity by region

- Simple proxy for cell count and can be used as a sanity check
- Notebook [here](#)

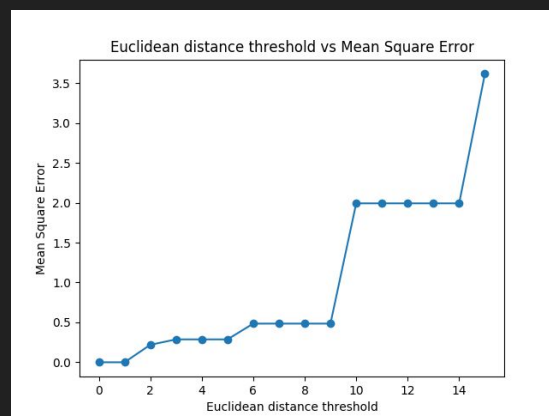
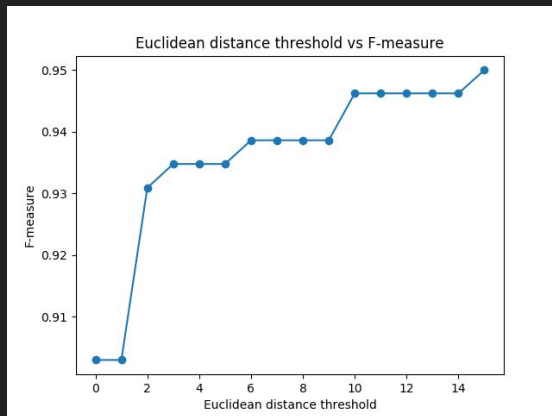
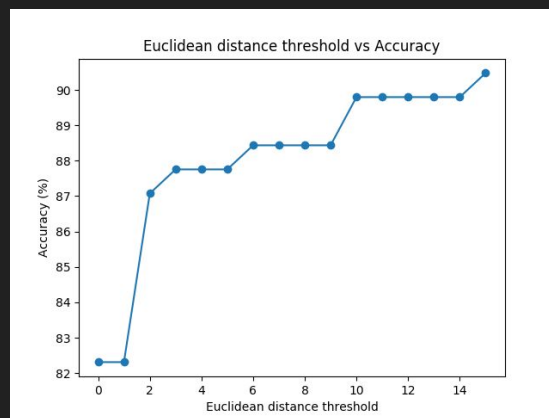
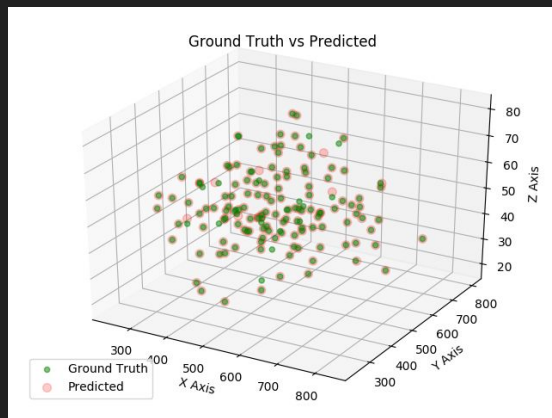
# BlobMetrics Python Package

- Wrote a python package (“BlobMetrics”) to evaluate the results of a blob detector
  - [Usage Documentation](#), [Source Code](#), [Notebook](#)
- In process of making the package pip installable

```
$ pip install blob-metrics
```

- Given the ground truth values and the predicted values the package computes
  - Accuracy
  - Precision
  - Recall
  - F-Measure
  - G-Measure
  - Mean Square Error

# BlobMetrics Python Package - Visualization



# Identified unsupervised algorithm

- Estimation of Small Blob Detection based on Local Convexity, Intensity and shape information
  - Pre-processing involves identifying blob candidate regions based on local convexity.
  - Regional blobness and regional flatness is extracted and HDoG (Hessian-based Difference of Gaussian) is applied
- Hysteresis Thresholding
  - The hysteresis mode uses a hysteresis loop to provide a more connected result. Any pixel above the upper threshold is turned white.
  - The surround pixels are then searched recursively. If the values are greater than the lower threshold they are also turned white.
  - The expected result is that there are many fewer specks of white in the resulting image.

# Ensemble Methods implementation

- [2D Segmentation](#)
- [3D Reconstruction](#)

## Algorithm

### Pseudocode:

#### Inputs:

- img\_stack
- z\_dim, y\_dim, x\_dim

#### Psuedocode:

For every z\_slice in the image stack:

1. Adaptive Threshold
2. Otsu's binarization to get binary image
3. Perform morphological erosion with kernal of radius of 5 voxels
4. Perform morphological opening with kernal of radius of 5 voxels
5. Get connected components using union-find
6. Compute centroids of each component

TODO: k-means for segmentation refinement

## 3D Reconstruction

### Pseudocode

#### input:

- z\_comps: a collection of components for all the z slice

#### pseudocode:

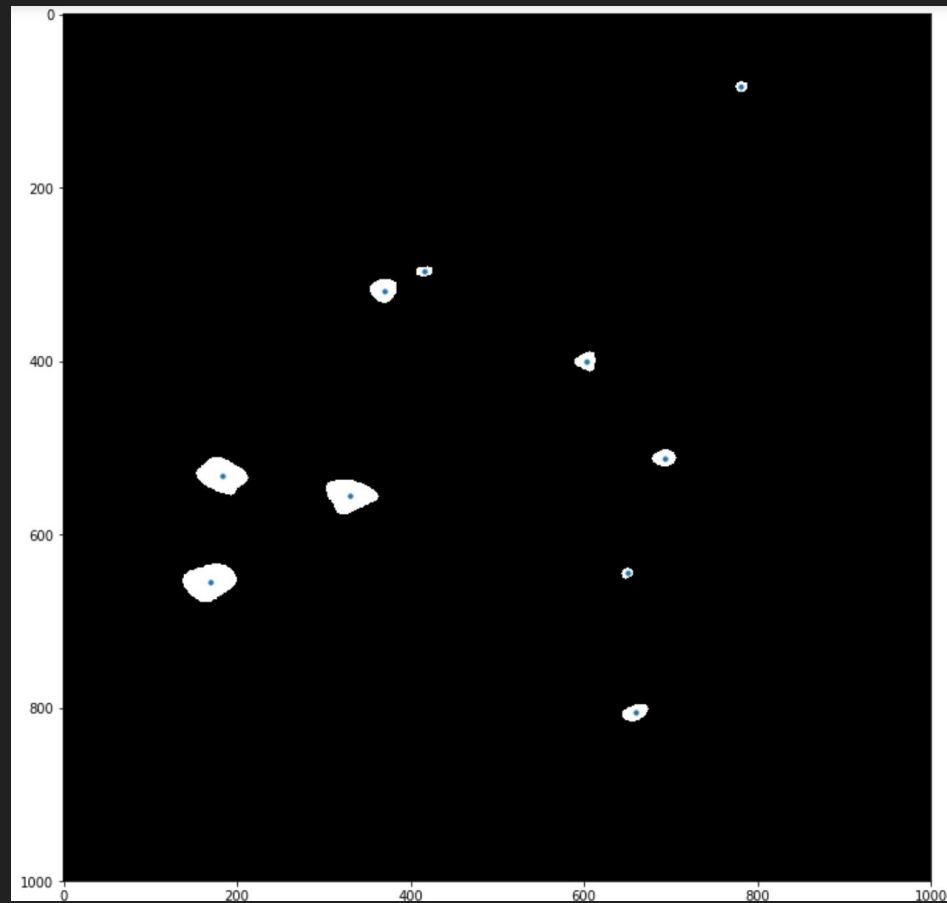
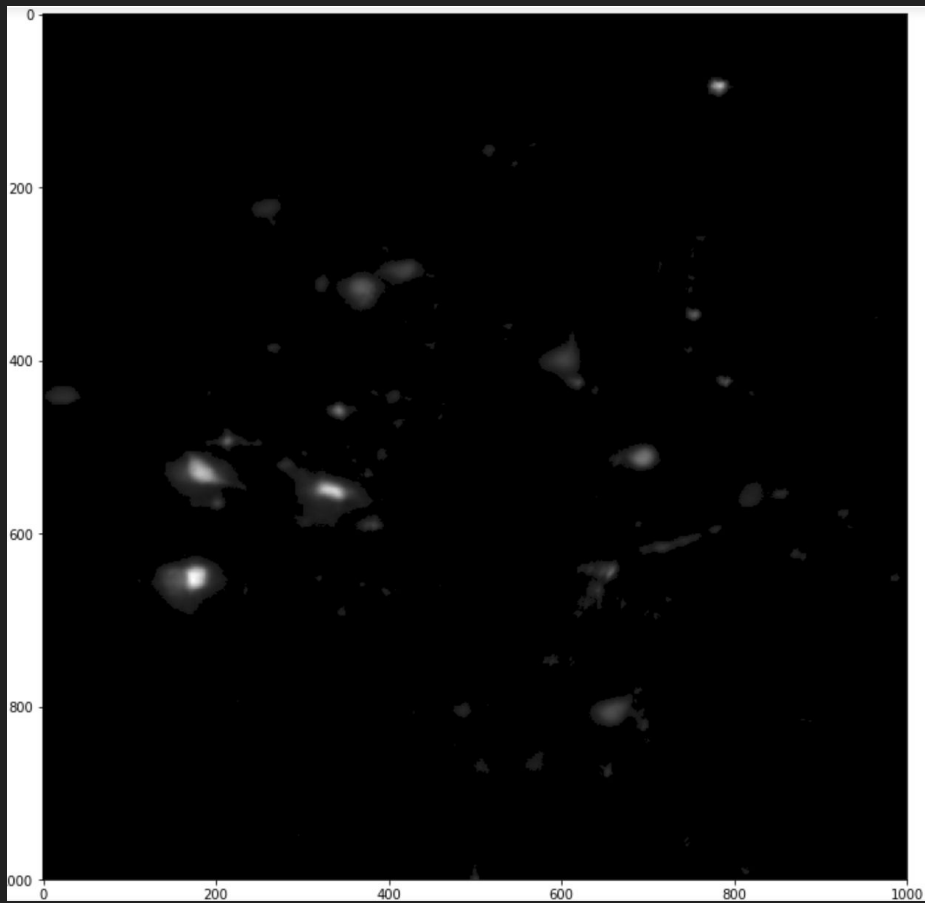
for each set of components for each z slice: for each component in this set:

1. If nearest centroids in z planes above and below the current plane are within a specified x-y radius, then current centroid is a part of that blob, so put it in that blob's collection

Compute Centroid of all centroids associated with a blob

return list of blob centroids

# 2D Blob Detection





# Yousef's automatic cell detection pseudo code

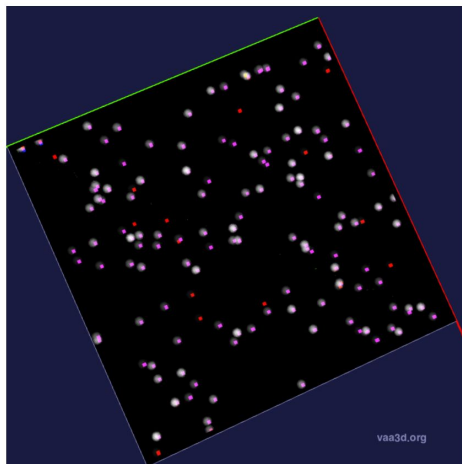
- In-depth description:  
[https://github.com/NeuroDataDesign/clarity-f17s18/blob/master/docs/jyim6/Automatic%20nuclei%20segmentation%20pipeline%20\(Yousef\).md](https://github.com/NeuroDataDesign/clarity-f17s18/blob/master/docs/jyim6/Automatic%20nuclei%20segmentation%20pipeline%20(Yousef).md)
- Yousef's algorithm is actually a pipeline of running multiple algorithms to do cell detection and segmentation
- The data medium: histopathology cells are also different than ours. We detail the steps of the algorithm relevant to us:
  - a. **Binarization/Threshold:** Fit the data to a bimodal poisson mixture model, i.e. find the threshold parameter. Get the bi-modal poisson PDF for whether a cell is in the foreground or not
  - b. **Labeling/large blob detection:** Run a max-flow/min-cut algorithm to discover the connected components (i.e. large blobs)
  - c. **Edge detection:** Run the multiscale LoG for different scales and construct a response map.
  - d. **Cell/small blob detection:** Find the local maximas in the response map.
  - e. **Cell segmentation:** Run watershed or some clustering algorithm to do an initial cell segmentation.
- The rest of the steps in the actual pipeline include refining the cell segmentation and doing a graph coloring

# Benchmarking

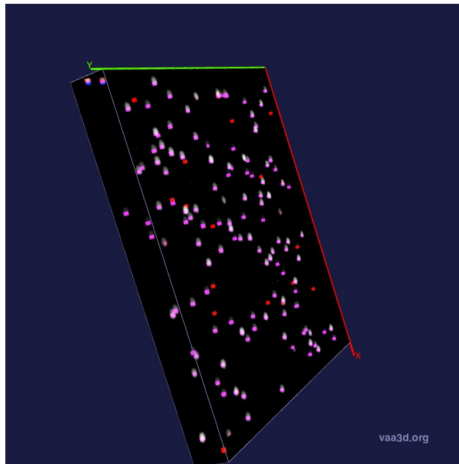
- More in depth: [https://github.com/NeuroDataDesign/clarity-f17s18/blob/master/docs/jyim6/week6\\_deliverables.md](https://github.com/NeuroDataDesign/clarity-f17s18/blob/master/docs/jyim6/week6_deliverables.md)

faded\_147\_randomized\_cells\_random\_intensity

Front



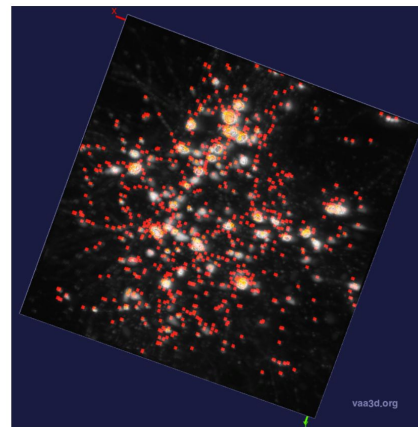
Side



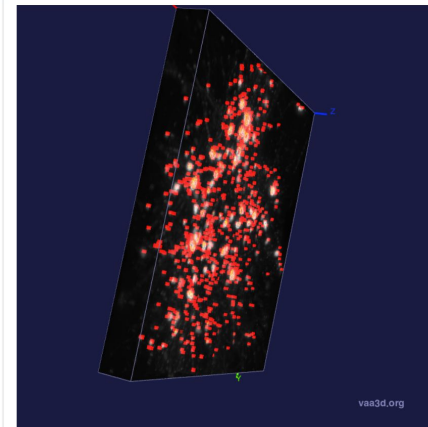
- Precision: 88%
- Recall: 100%

s3617\_cutout

Front



Side



# Next week

- Determine how to remove inhomogeneity in light sheet images (for registration)
- Identify 1 paper for each of the following in cell detection workflow:
  - Preprocessing
  - Thresholding/binarization
  - Edge detection/blob detection
  - Clustering /refinement
- Implement algorithm in this [paper](#)
- Make blob-metrics pip installable