DYNAMIC SOCIAL NETWORK MODELING OF DIFFUSE SUBCELLULAR MORPHOLOGIES

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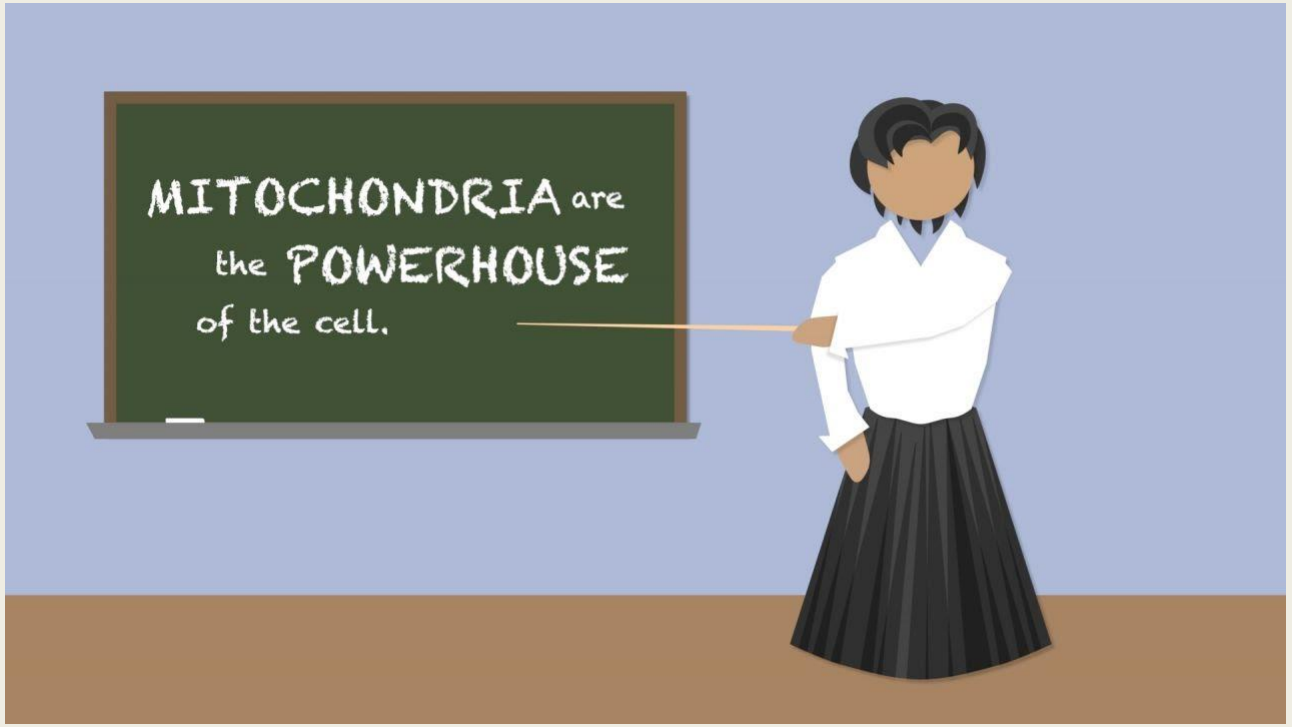
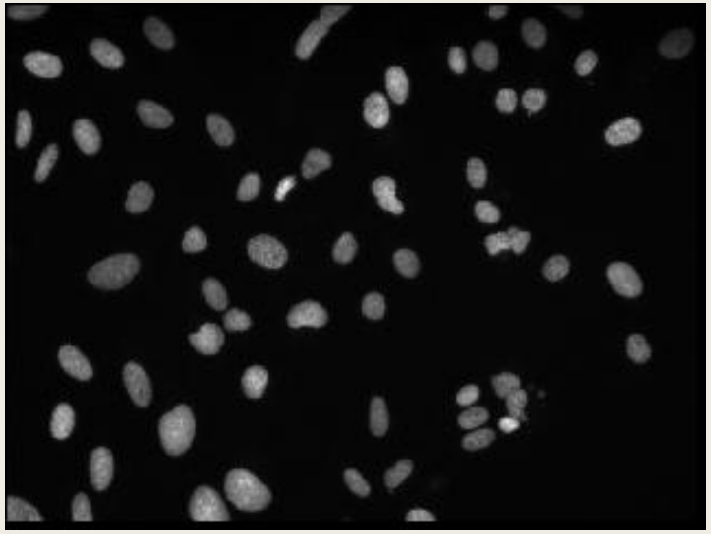
Outline

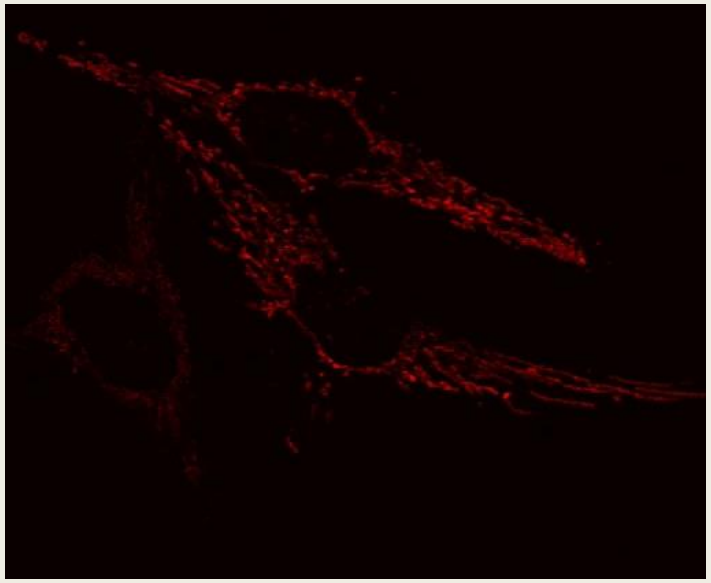
- Background
  - *Image Processing*
  - *Biology*
- Proposed Pipeline
  - *Segmentation Process*
  - *Node Generation*
  - *Edge Weight Calculations*
- Network Analysis
- Future Work



Background

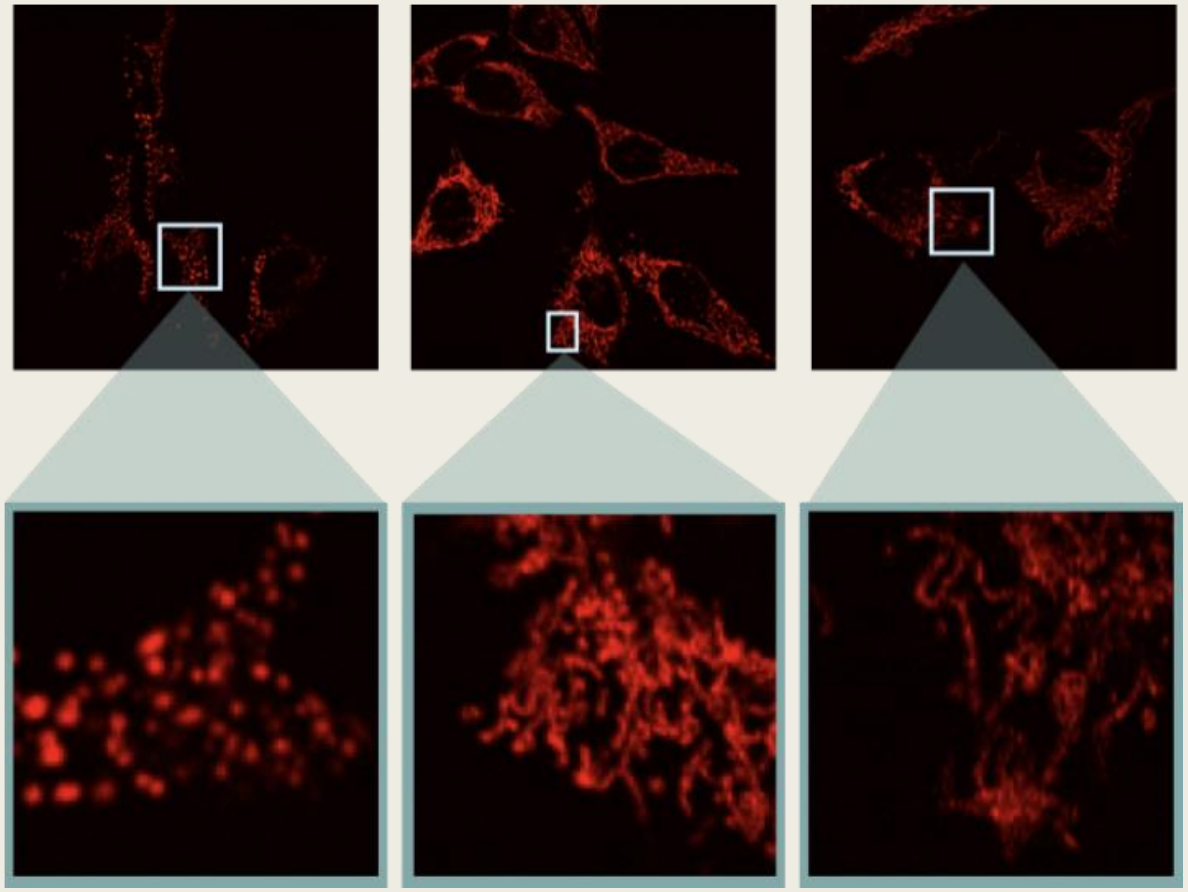
- Microscopy has lead to widespread biomedical image data
- Many techniques have arisen to segment, track, and quantify this new data
- These advances are too heavily focused on ‘solid’ structures like nuclei, or cell bodies
- We aim to fill the gap in software focused on diffuse patterns induced by mitochondria or actin





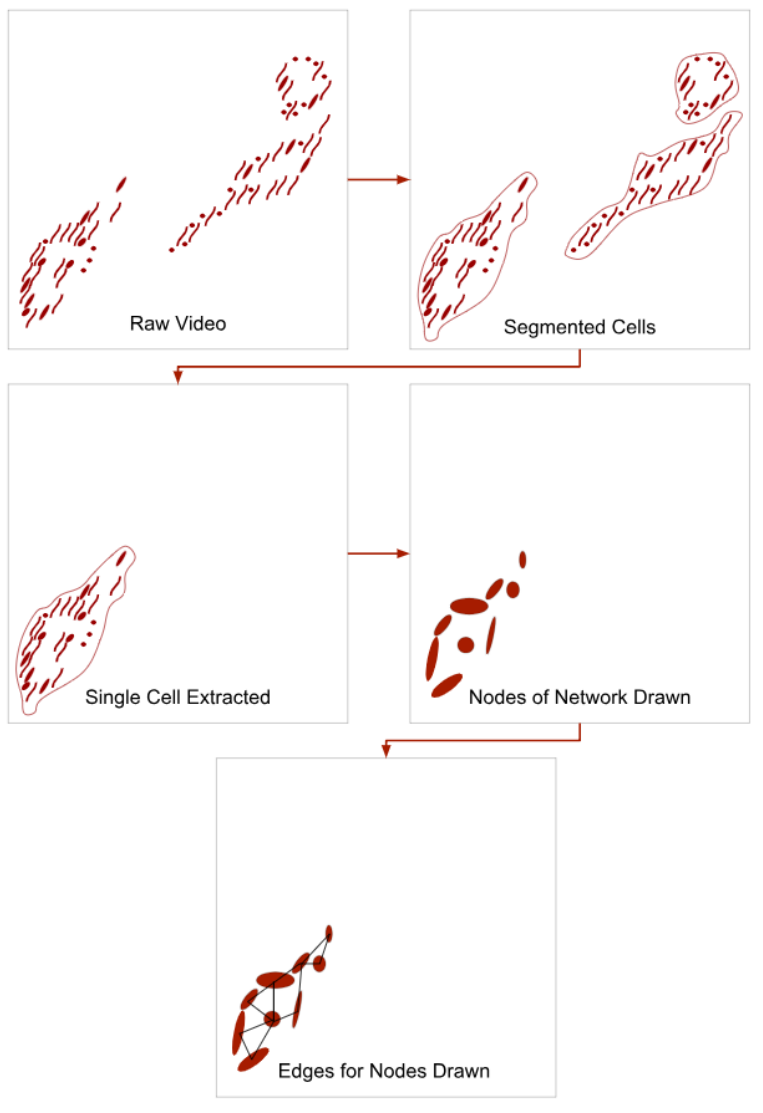
Mitochondrial Behavior

- Our data consists of three categories
- Wild Type: the natural topology of the protein structure
- Fragmented: isolated high concentration areas induced by LLO
- Hyperfused: a stringy fused together form of the wild type topology induced by mdivi-1
- These are the categories on which we condition our network analysis



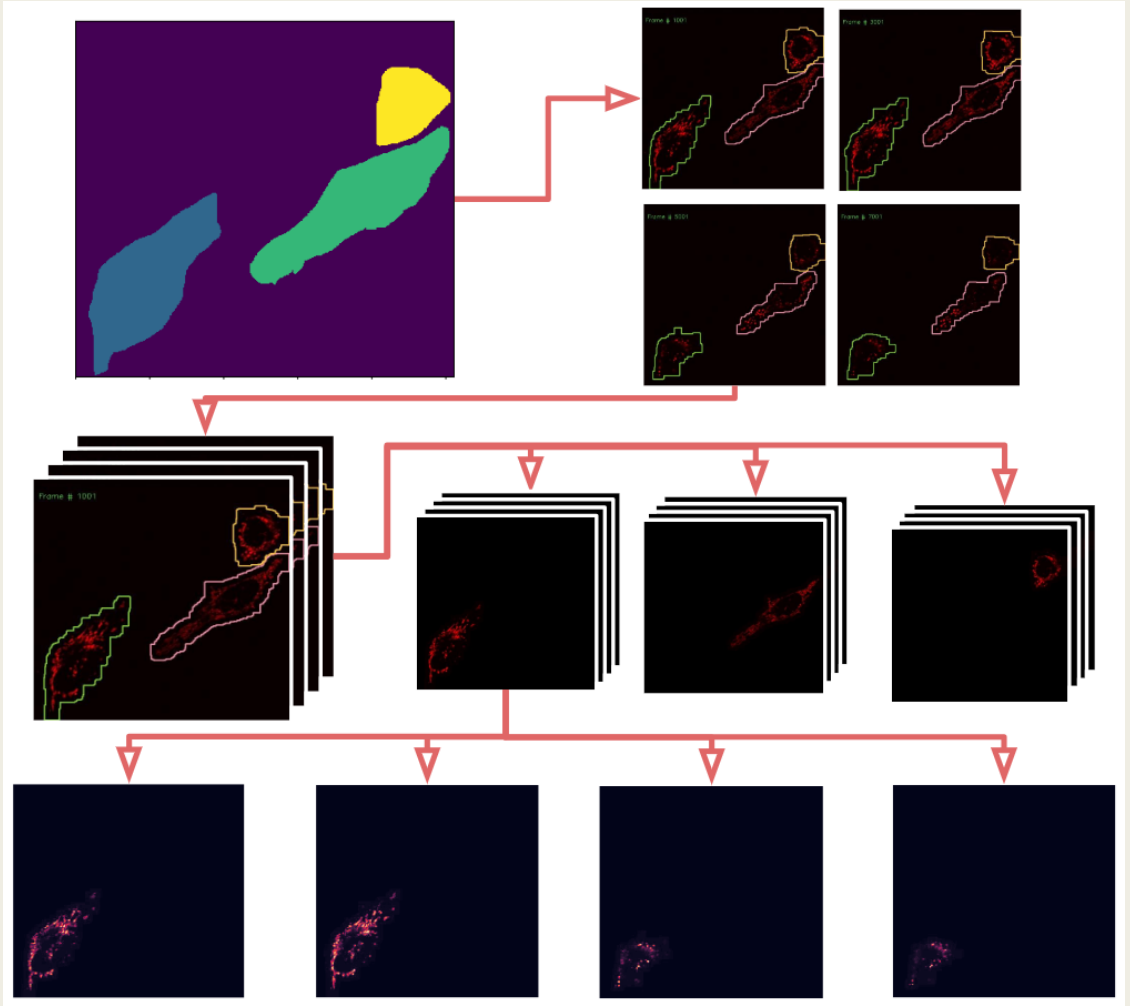
Pipeline

- We aim to autonomously segment each cell
- We apply a Gaussian Mixture Model to determine nodes of our network analogue
- With nodes determined we apply a pseudo-distance metric to determine edges and weights for the network
- At which point we use network metrics to quantify the behavior of each protein structure



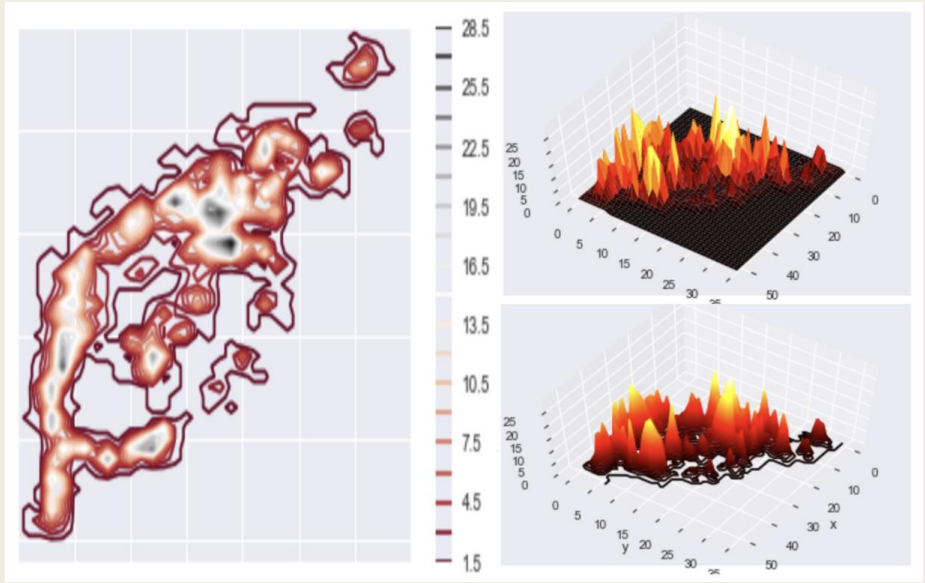
Segmentation

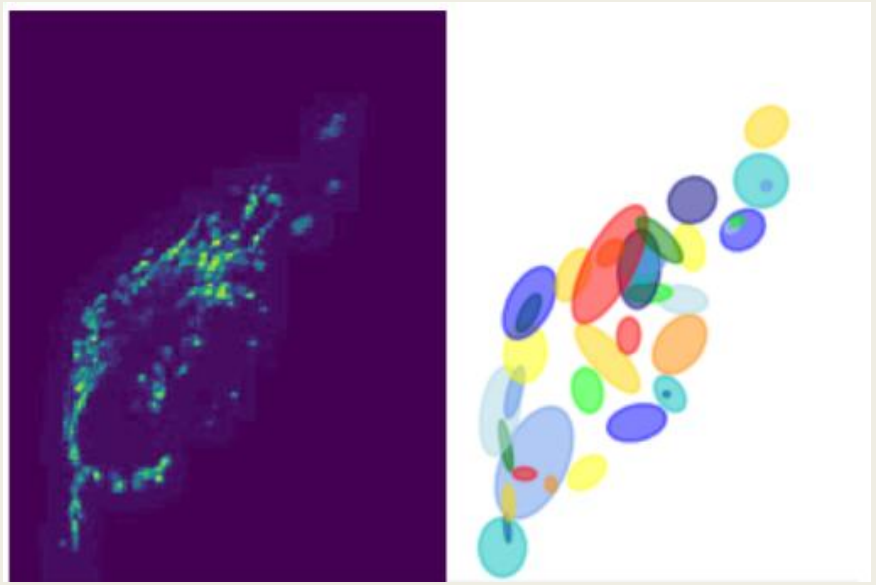
- To avoid bias we separate each cell
- Due to the diffuse structure and tight region boundaries we primed the segmentation process with hand drawn masks
- Using a iterative process of dilation and erosion of each mask we deform each mask to follow each cells morphological changes
- This process outputs cell masks for each frame which allow us to pull out a single cell for network fitting.



Mixture Model

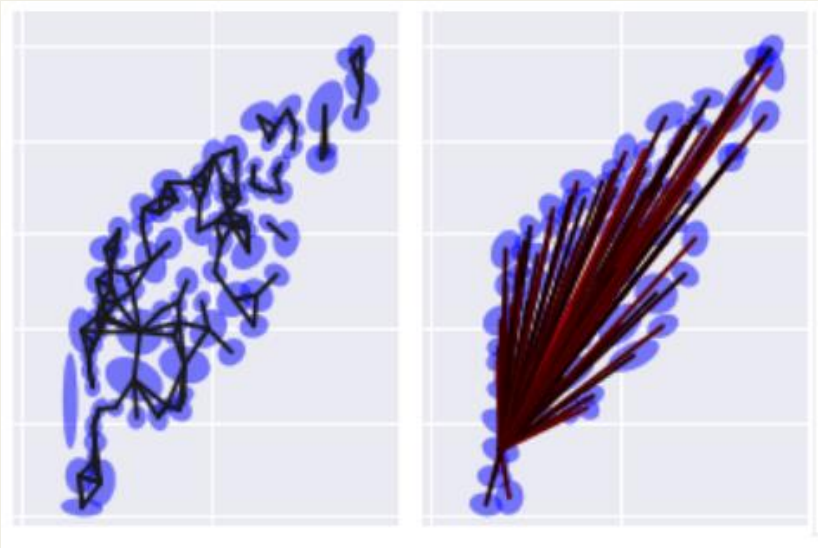
- Finds nodes to characterize the locale of mitochondria within the structure
- We determine the number of nodes by counting local maxima of the image
- We convert each cell to a discrete probability distribution
- We then fit SciKit Learn's Gaussian Mixture Model to our image
- Each component becomes a node
- Each frame is then fit by the GMM using the previous frame's model parameters





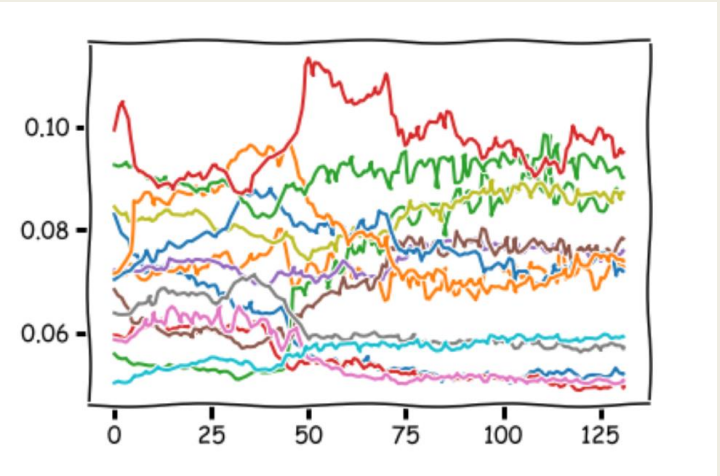
Affinity Functions

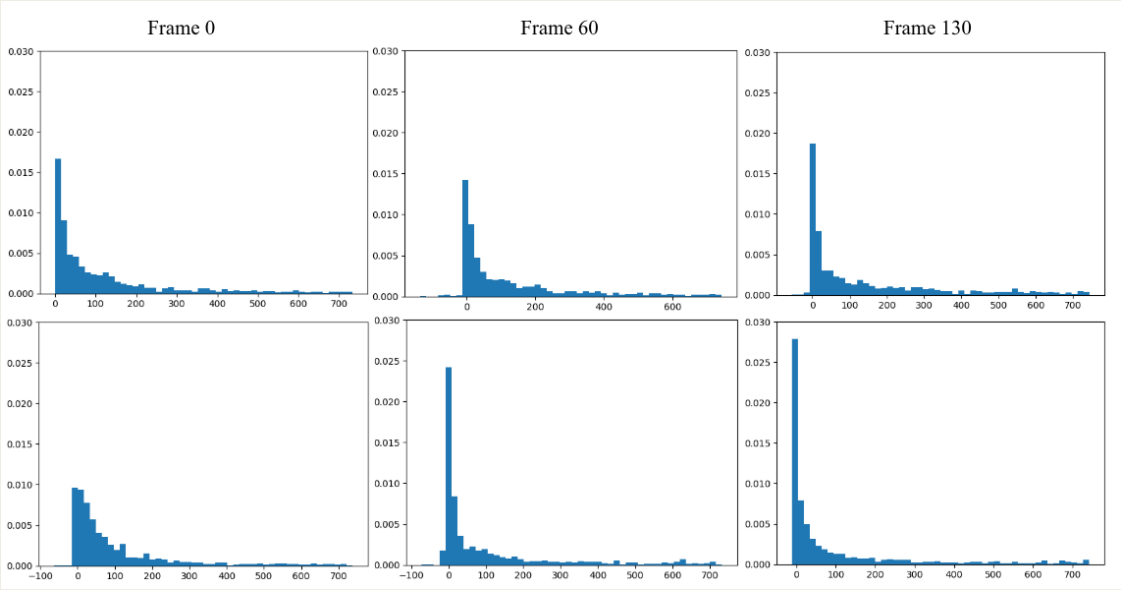
- Early distance based metrics
  - *Simple and quick*
  - *Doesn't account for variance*
- Probability Based Metric
  - *A -> B = A(μ(B))*
  - *Directionally accounts for variance*
  - *assymetric*
- Kullback-Leibler Divergence
  - *Psuedo-distance metric for probability distributions*
  - *assymetric*
- Jensen-Shannon Divergence
  - *Based on KL Divergence*
  - *symmetric*



Network Analysis

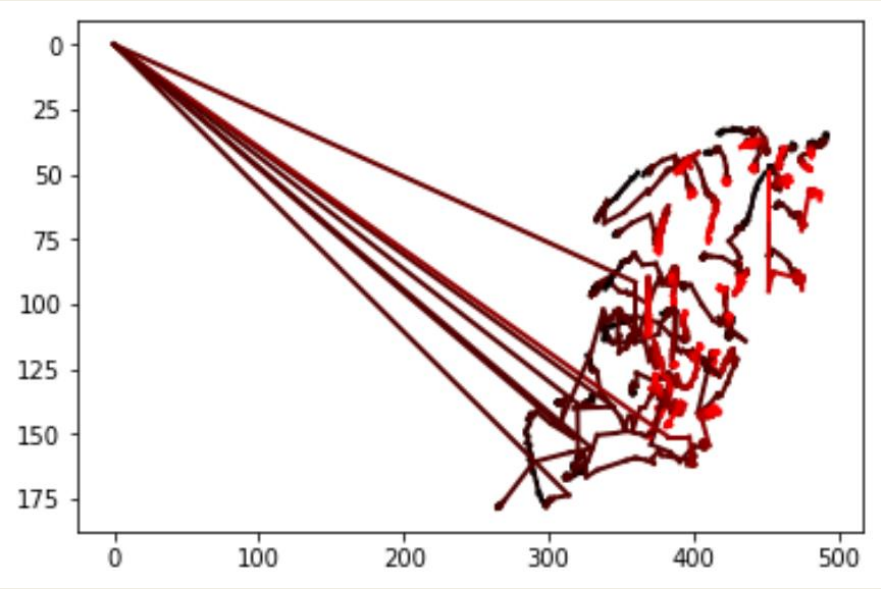
- Connectivity Based
  - *Look at the number and weight of connections in the network*
- Page Rank
  - *Estimates the Eigenvectors of each component in an asymmetric network*
- Future work
  - *Spectral Clustering*
  - *Network Characteristics (centrality, density, etc)*





Conclusions and Future Work

- We are able to infer some biological behaviors from properties of our network analogues
- We intend to have a fully autonomous segmentation step
  - *Powered by a Dense FCN*
- We are looking into the pros and cons of each affinity function
- We are continuing forward with new forms of Network Analysis
- We are working to implement our own Gaussian Mixture Model for Node determination



Thank You

Also Here is a link to the paper in the proceedings of SciPy:

http://conference.scipy.org/proceedings/scipy2018/Andrew_Durden.html