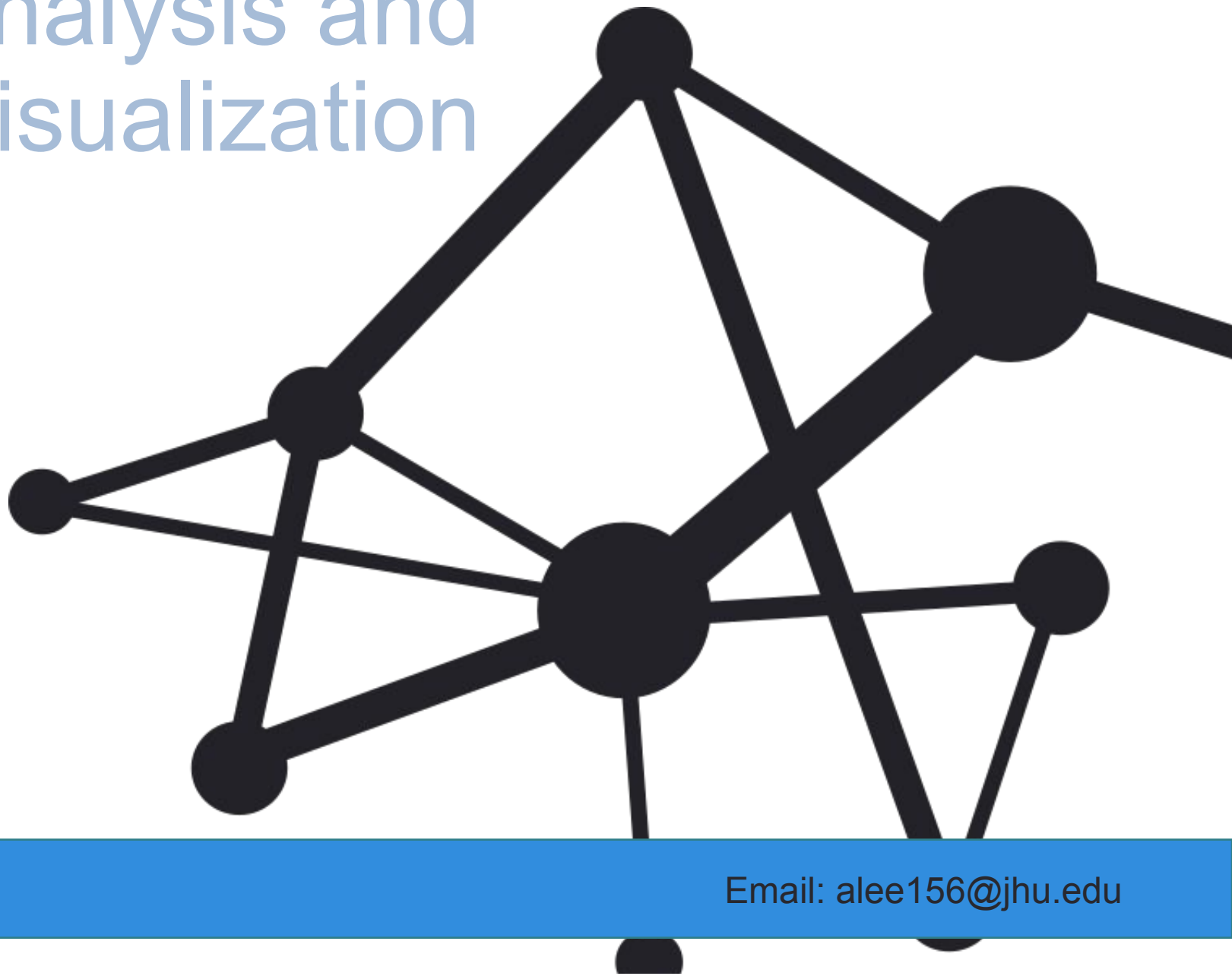
Clviz – Clarity analysis and visualization



Albert Lee, Jon Liu,
Tony Sun, Luke Zhu

Email: alee156@jhu.edu

Clarity

The Clarity technique allows for visualization of brain matter without damaging structural integrity. This allows for unprecedented access to connection and function estimation.

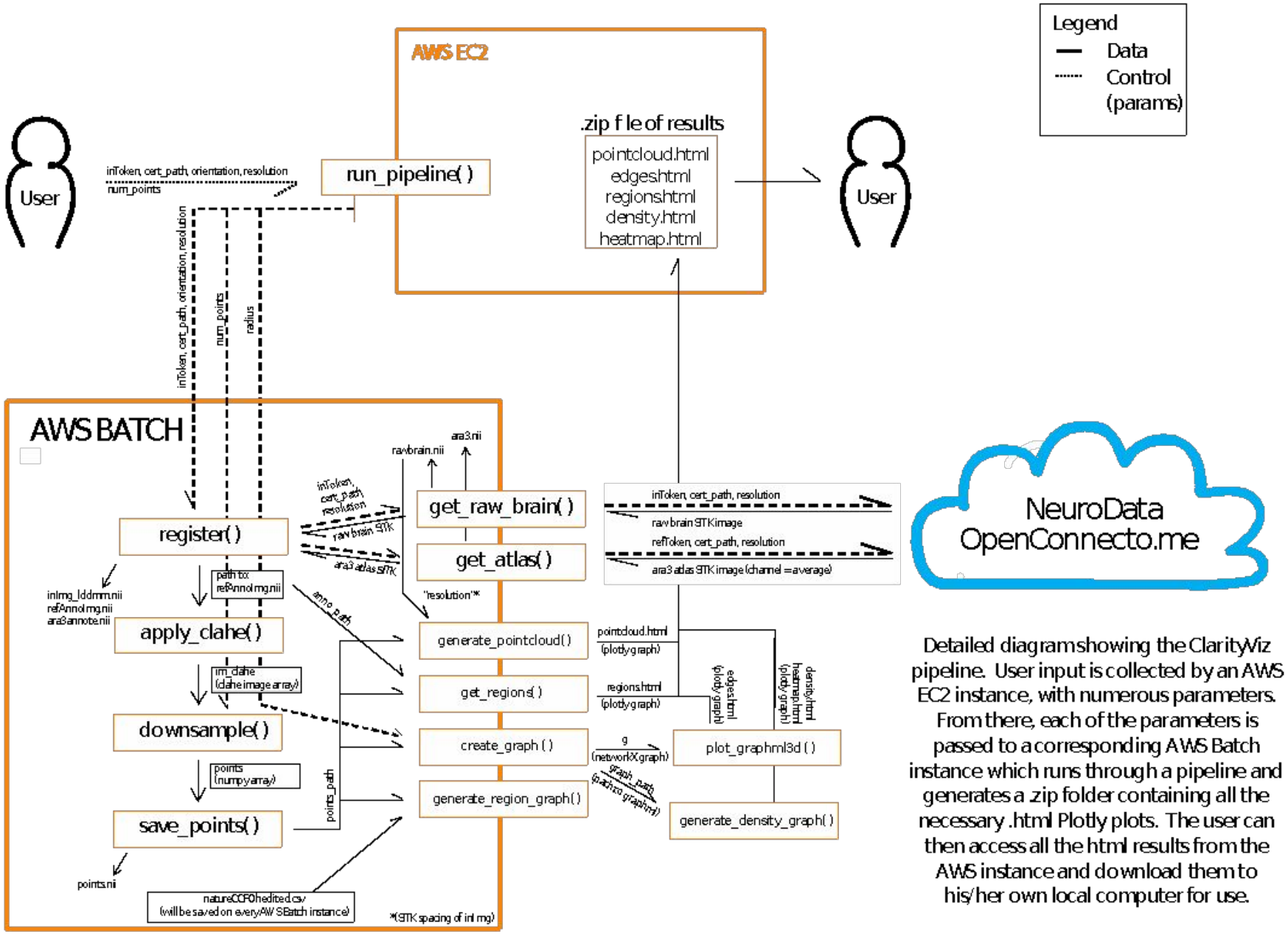
Clarity analysis is underdeveloped

Because Clarity is a relatively new imaging technique, there is a need for the development of high quality pipelines that can easily and quickly analyze and visualize the data.

A 3 click pipeline for visualization and analysis

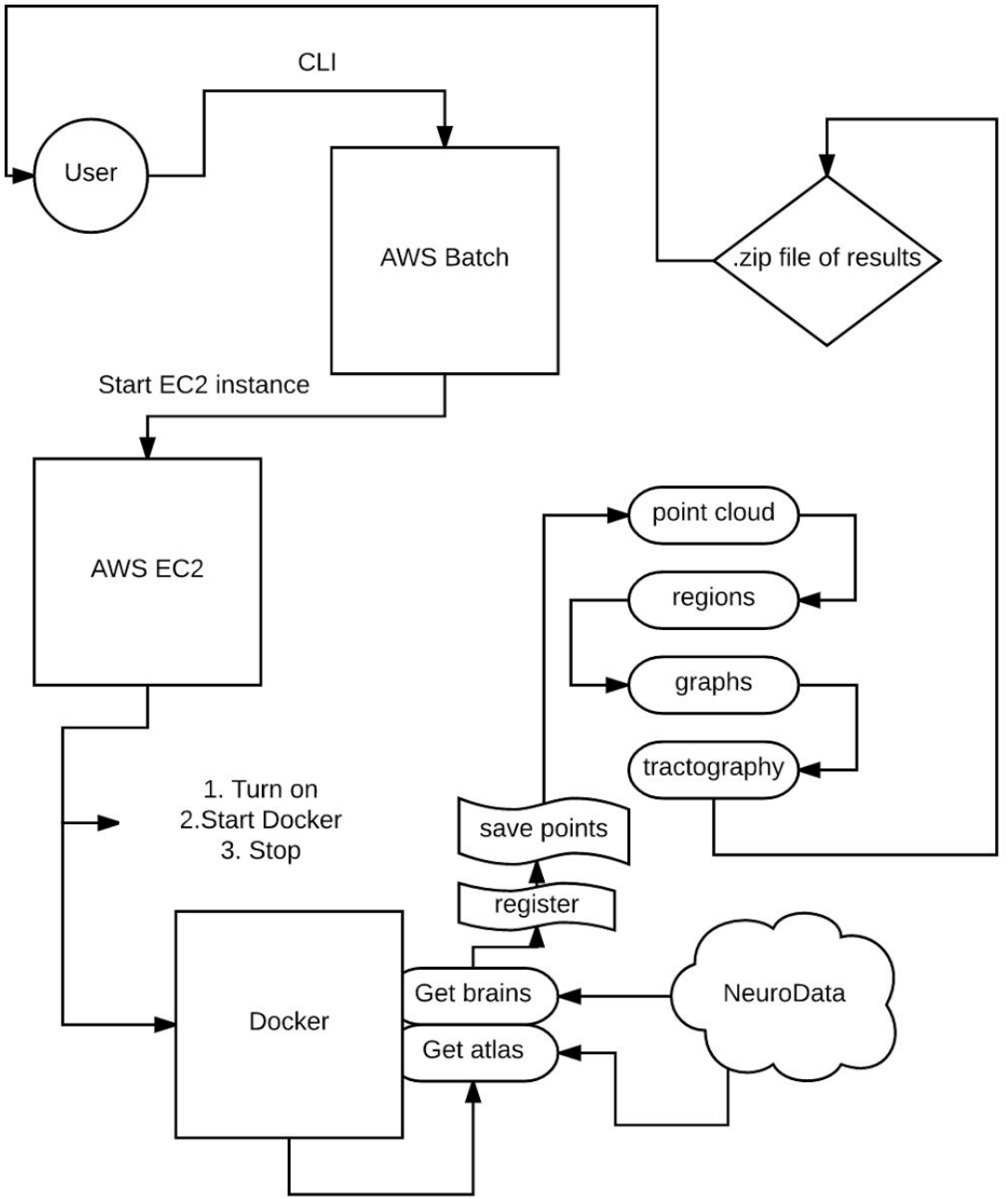
We developed an open-source visualization and analysis pipeline which is packaged to be able to be used on any modern operating system (OSX, Windows, Linux). The pipeline is implemented as a cloud-computing web service that is highly scalable.

Connectomics at Scale



Detailed diagram showing the ClarityViz pipeline. User input is collected by an AWS EC2 instance, with numerous parameters. From there, each of the parameters is passed to a corresponding AWS Batch instance which runs through a pipeline and generates a .zip folder containing all the necessary .html Plotly plots. The user can then access all the html results from the AWS instance and download them to his/her own local computer for use.

clviz pipeline


CLI
User
AWS Batch
.zip file of results
Start EC2 instance
AWS EC2
point cloud
regions
graphs
tractography
1. Turn on
2.Start Docker
3. Stop
save points
register
Docker
Get brains
Get atlas
NeuroData

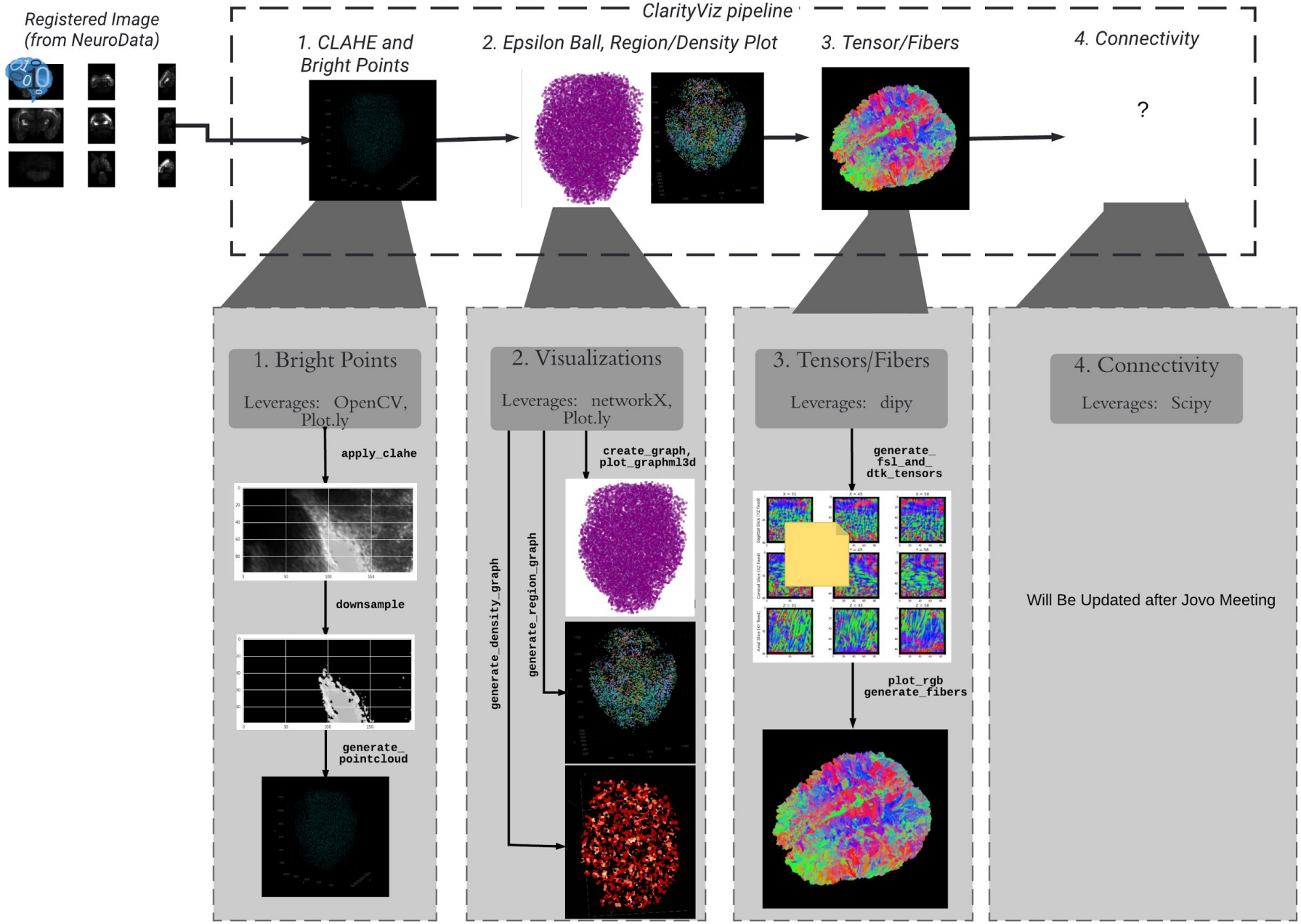
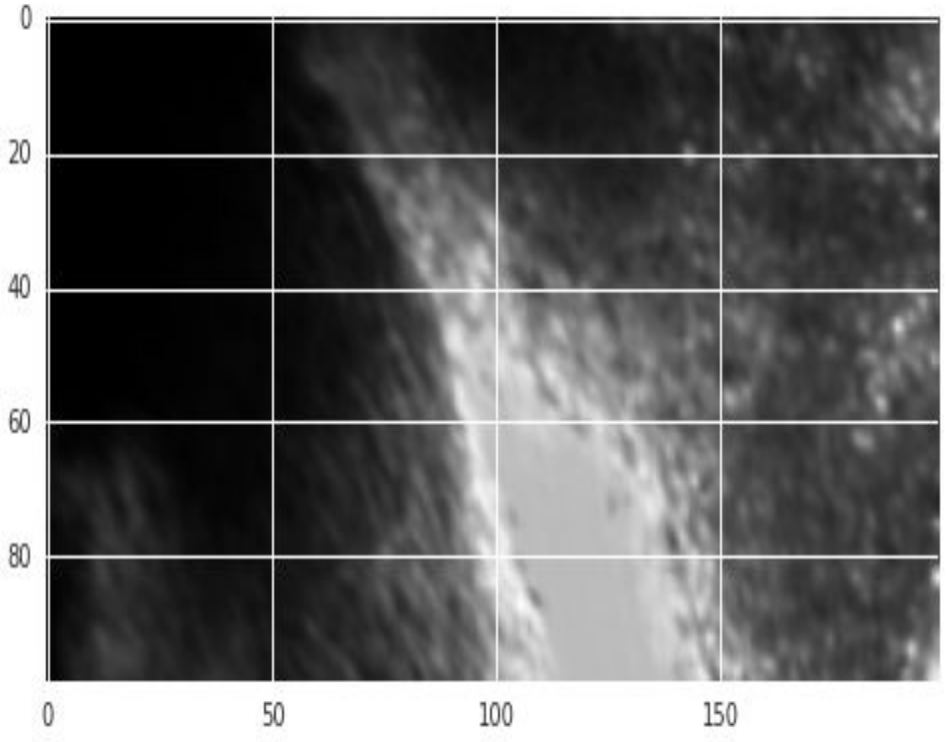
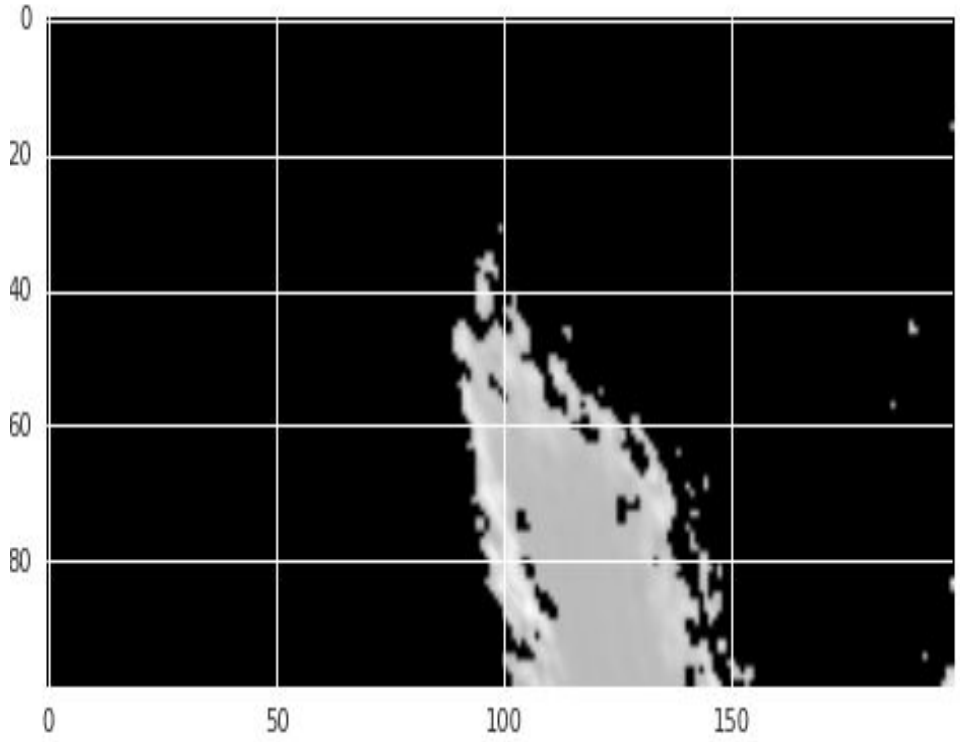

Registered Image
(from NeuroData)
ClarityViz pipeline
1. CLAHE and
Bright Points
2. Epsilon Ball, Region/Density Plot
3. Tensor/Fibers
4. Connectivity
?
1. Bright Points
Leverages: OpenCV, Plot.ly
apply_clahe
downsample
generate_
pointcloud
2. Visualizations
Leverages: networkX, Plot.ly
create_graph,
plot_graphml3d
generate_density_graph
generate_region_graph
3. Tensors/Fibers
Leverages: dipy
generate_
fsl_and_
dtk_tensors
plot_rgb
generate_fibers
4. Connectivity
Leverages: Scipy
Will Be Updated after Jovo Meeting

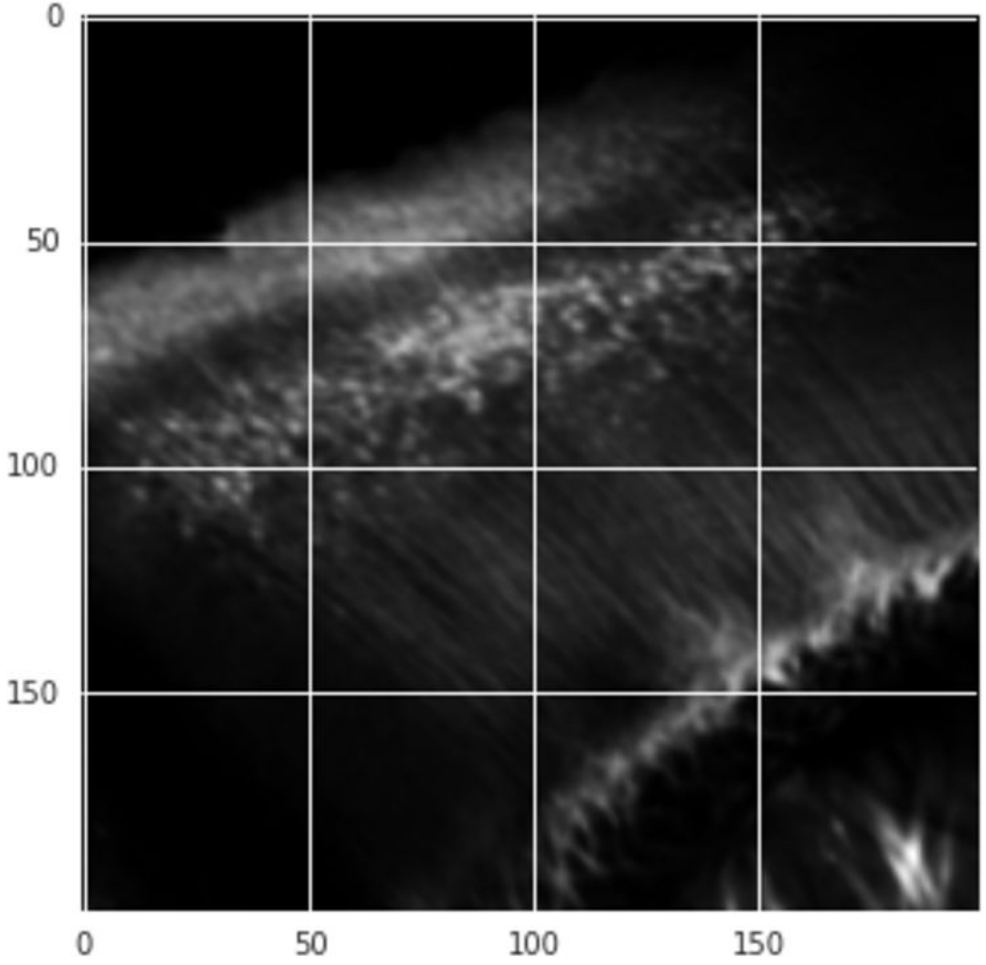
Image Preprocessing

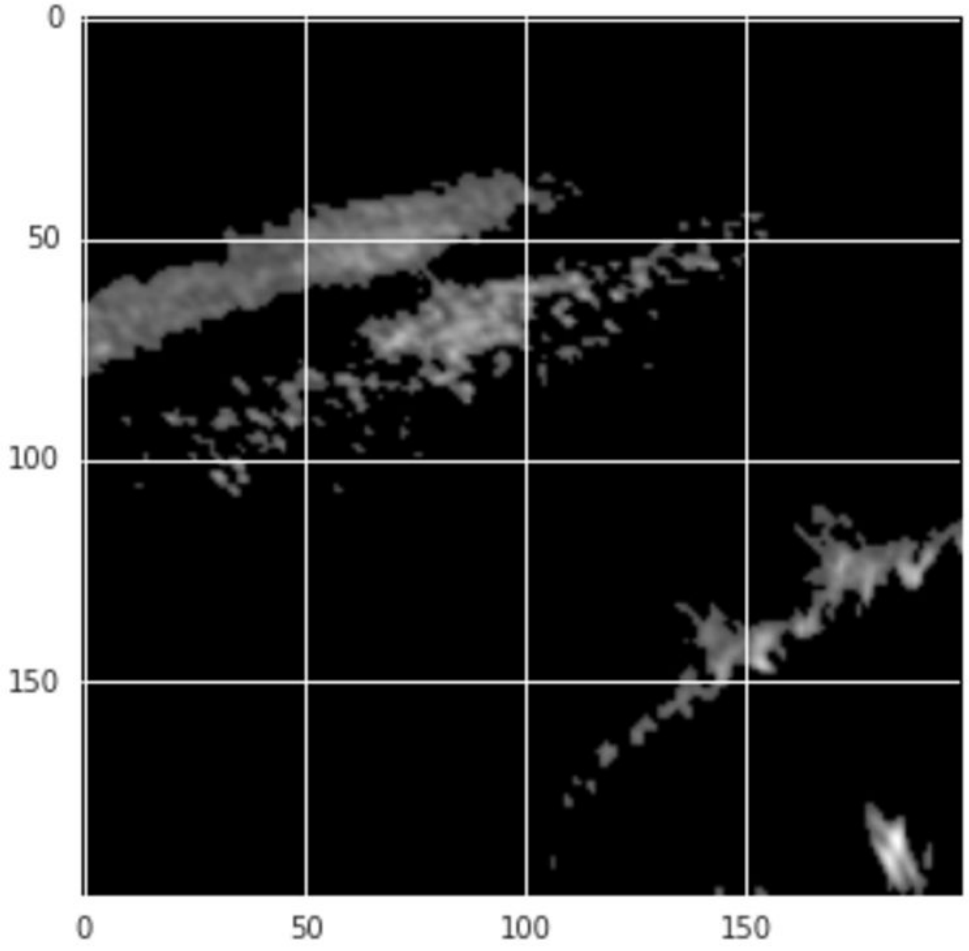
Find Locally Brightest Points in High Background Setting



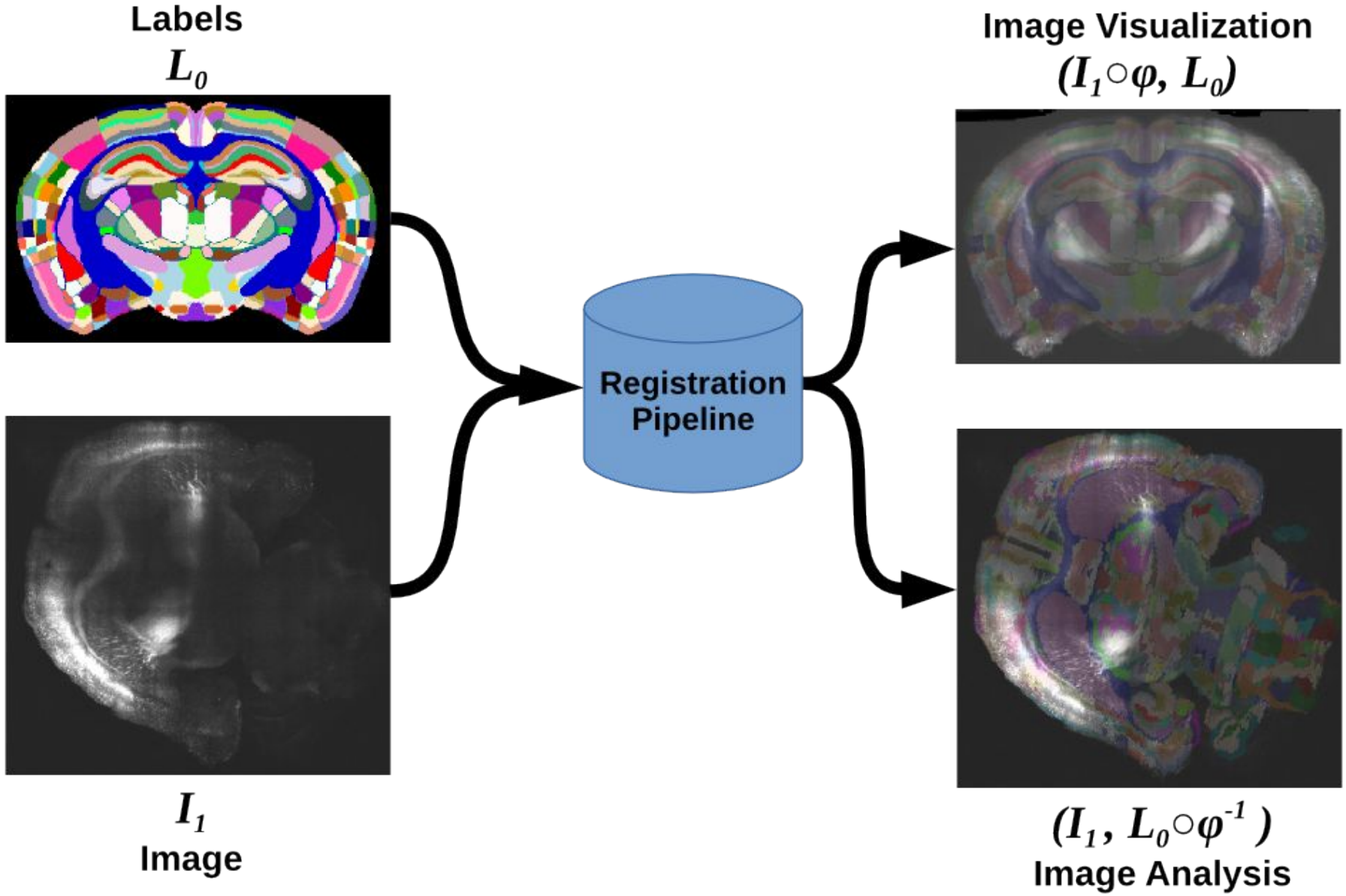


Find Locally Brightest Points in Low Background Setting

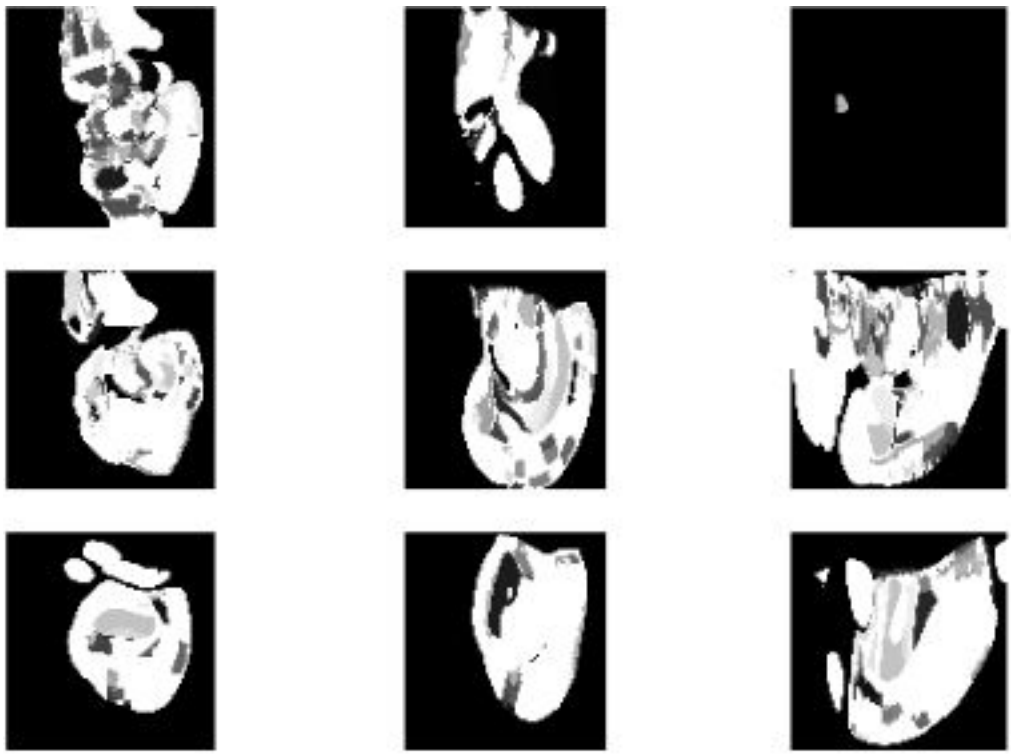




Registration

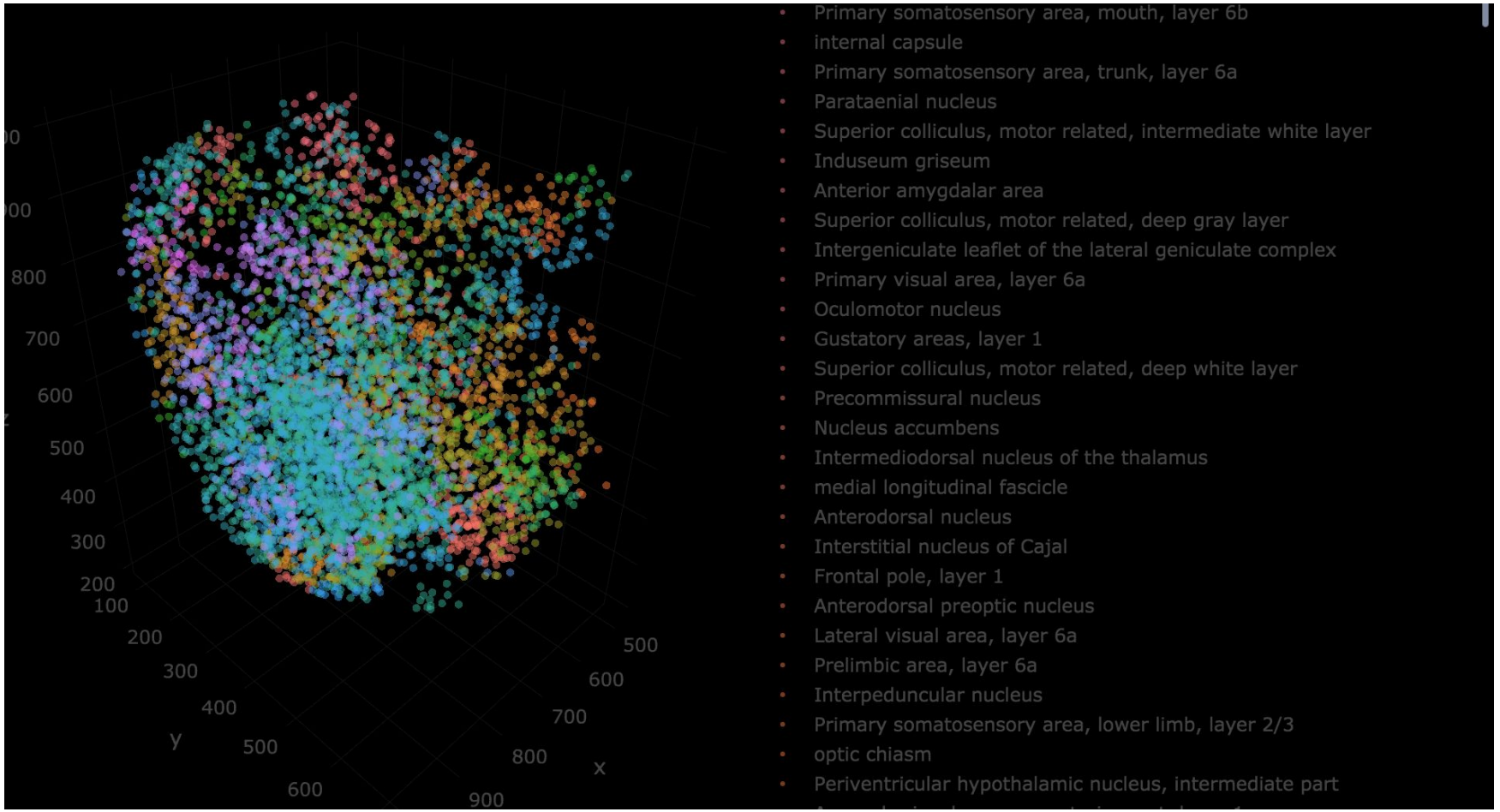

Labels
L_0
I_1
Image
Registration Pipeline
Image Visualization
$(I_1 \circ \varphi, L_0)$
$(I_1, L_0 \circ \varphi^{-1})$
Image Analysis

Docs



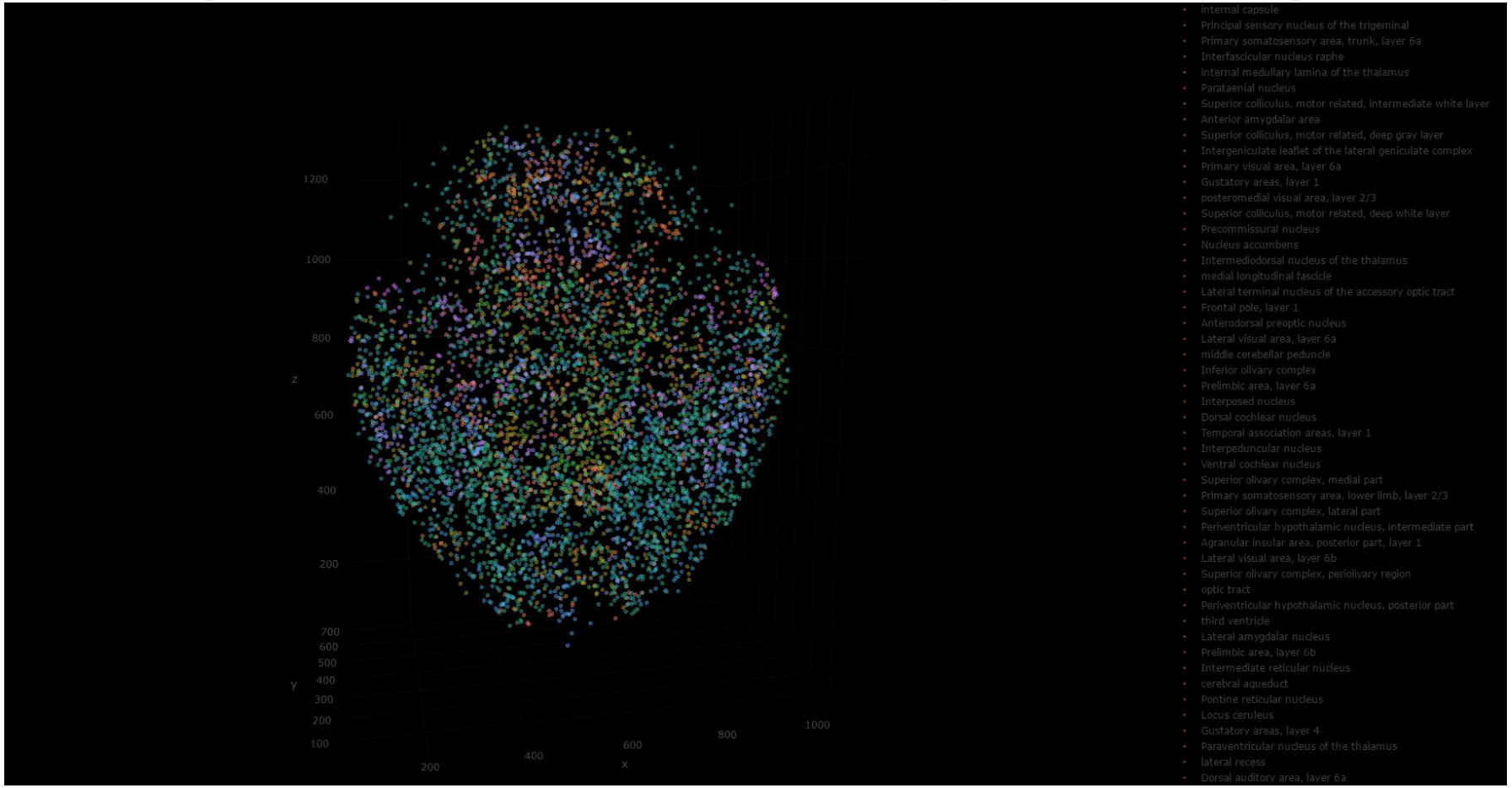
Region Graph

Interactive 3D Plot of 10,000 Brightest Points (s275)



- Each dot is one of the 10,000 brightest points
- Dots are colored by region
- Can interactively select/unselect any region
- Mousing over dot provides region name and 3D coordinate (in ARA space)
- Link to interactive plot in cloud

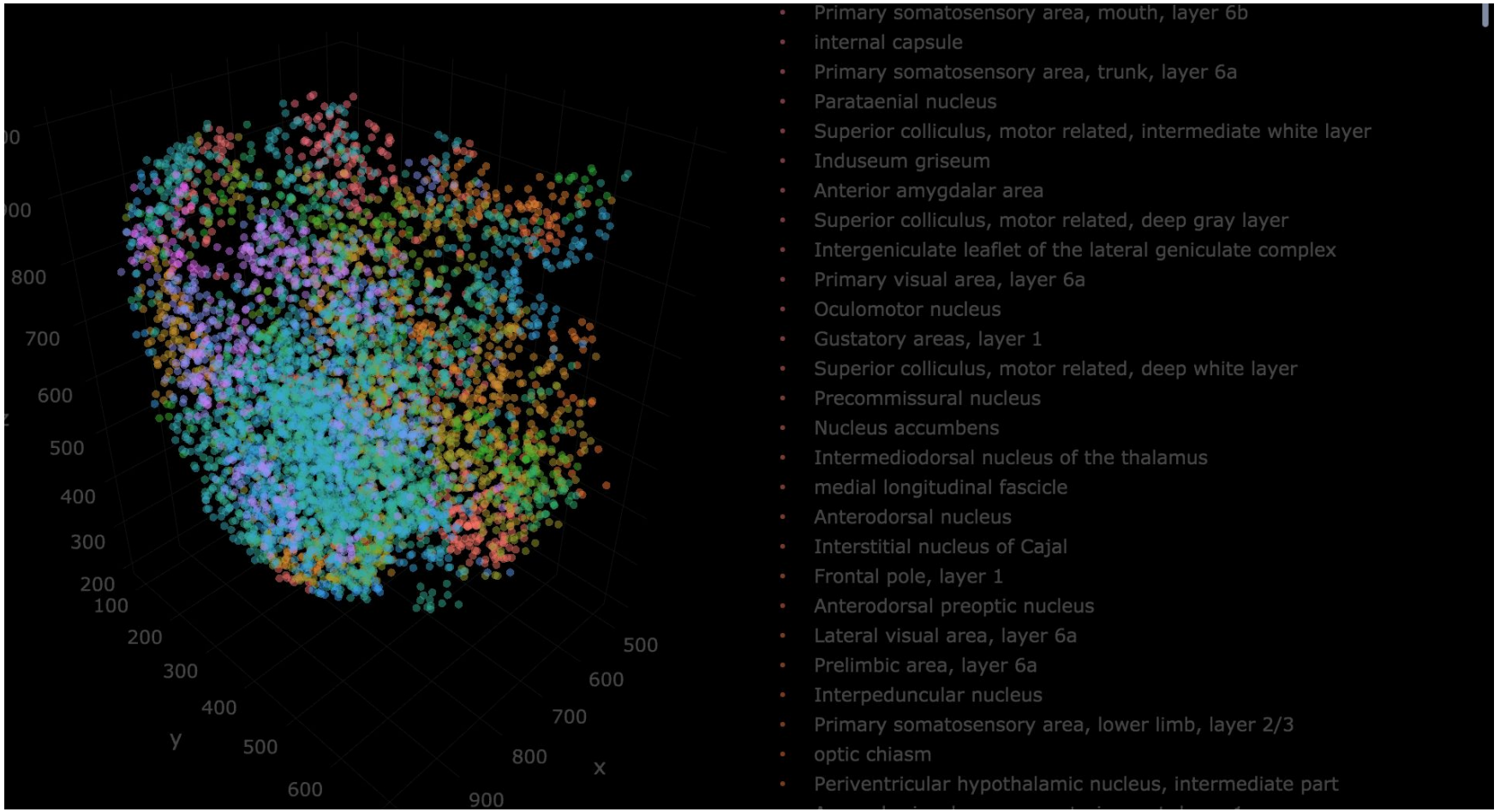
Interactive 3D Plot of 10,000 Brightest Points (s3617)



- Each dot is one of the 10,000 brightest points
- Dots are colored by region
- Can interactively select/unselect any region
- Mousing over dot provides region name and 3D coordinate (in ARA space)
- Link to interactive plot in cloud

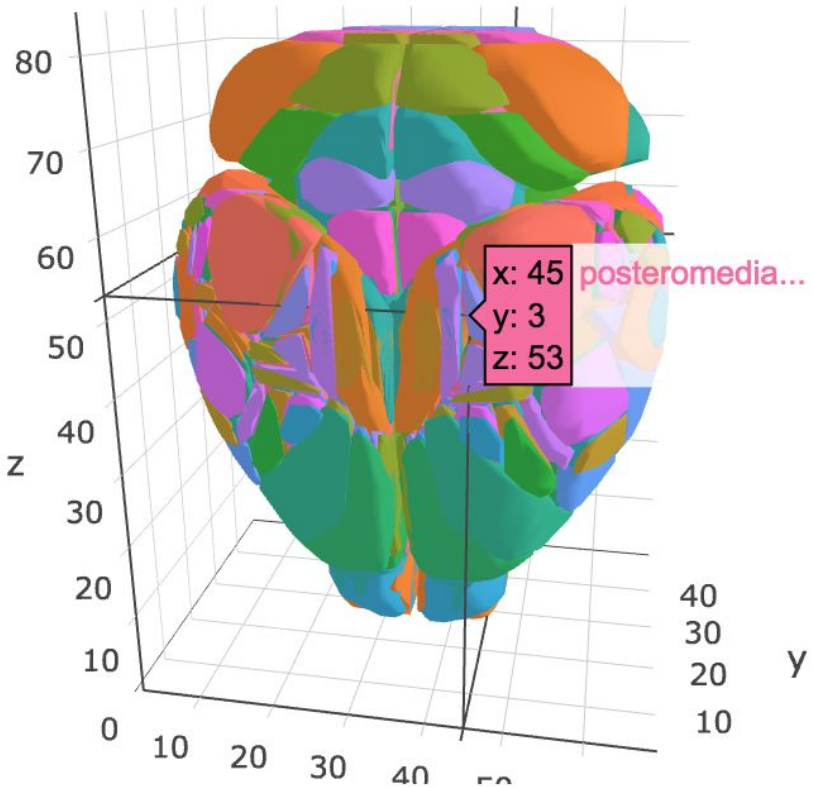
Brightest Centroids and Mesh

Interactive 3D Plot of 10,000 Brightest Points (s275)



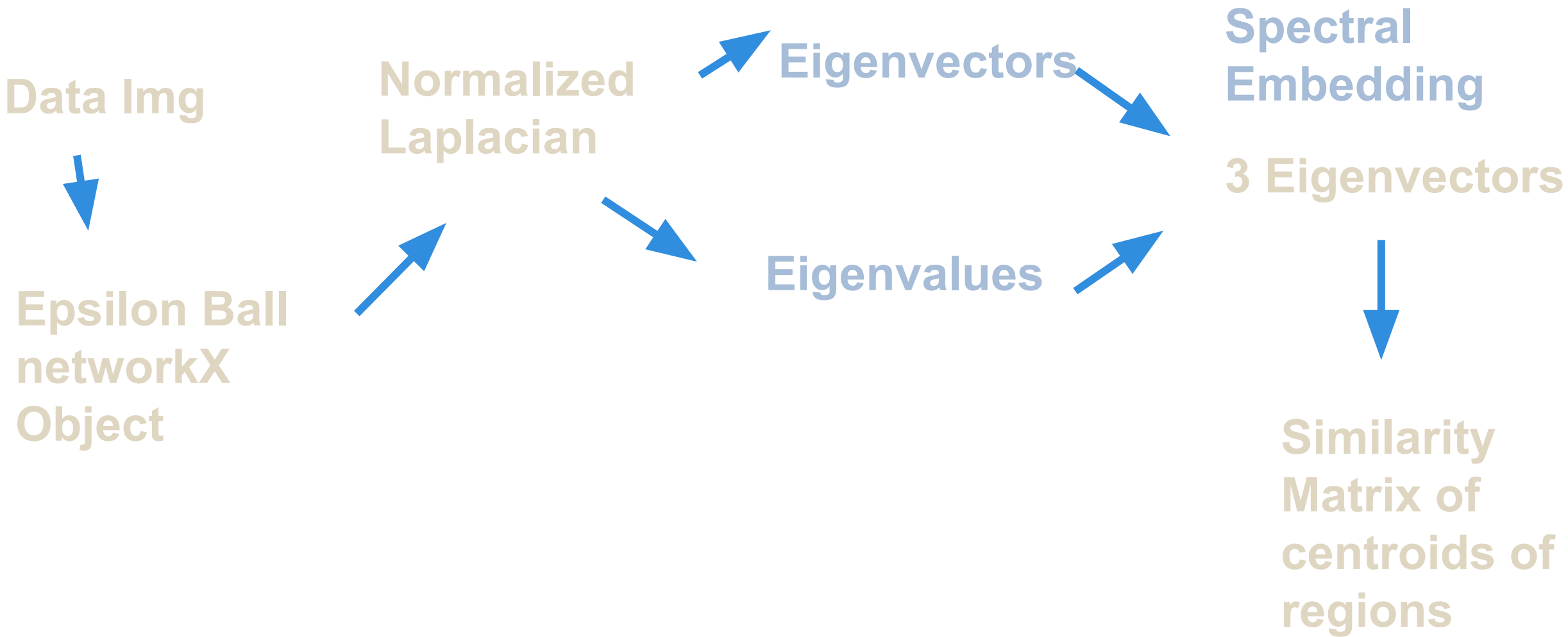
- Each dot is one of the 10,000 brightest points
- Dots are colored by region
- Can interactively select/unselect any region
- Mousing over dot provides region name and 3D coordinate (in ARA space)
- Link to interactive plot in cloud

Interactive 3D Plot of ROI Meshes: opacity implies # of bright spots



- Opacity of mesh is proportional to # of locally bright spots
- Mousing over dot provides region name and 3D coordinate (in ARA space)
- Dots are colored by region
- Link to Jupyter notebook making plots
- Link to interactive plot in cloud
- Link to hemisphere with medial view

Connection Estimation

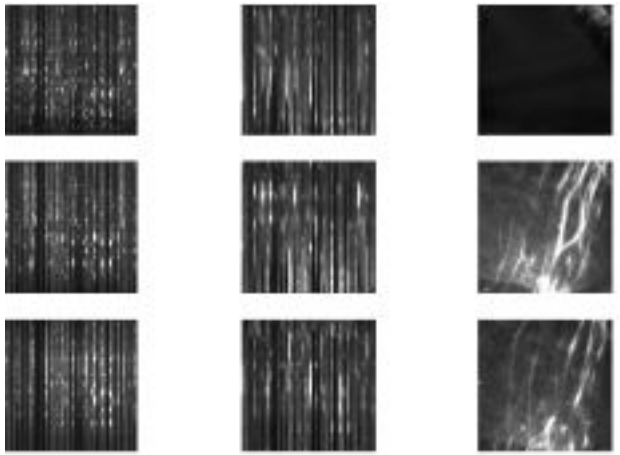

Data Img
Epsilon Ball networkX Object
Normalized Laplacian
Eigenvectors
Eigenvalues
Spectral Embedding
3 Eigenvectors
Similarity Matrix of centroids of regions

Docs

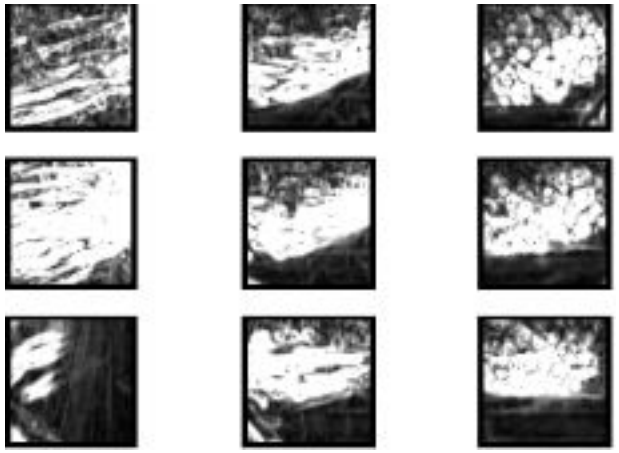
Current Progress:

- Generated epsilon ball graph and density plots.
- Have a methodology and sample code on test data for connectivity of sample data.
- In process of generating a general connectivity estimate for real data.

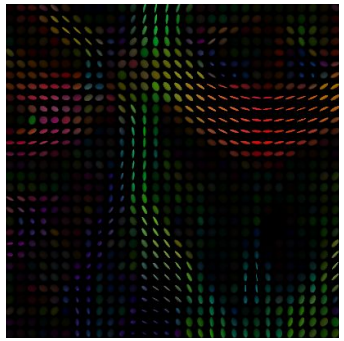
Tensor Estimation



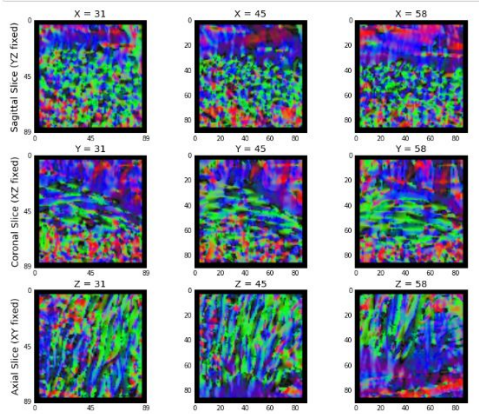
Data Img



Mask



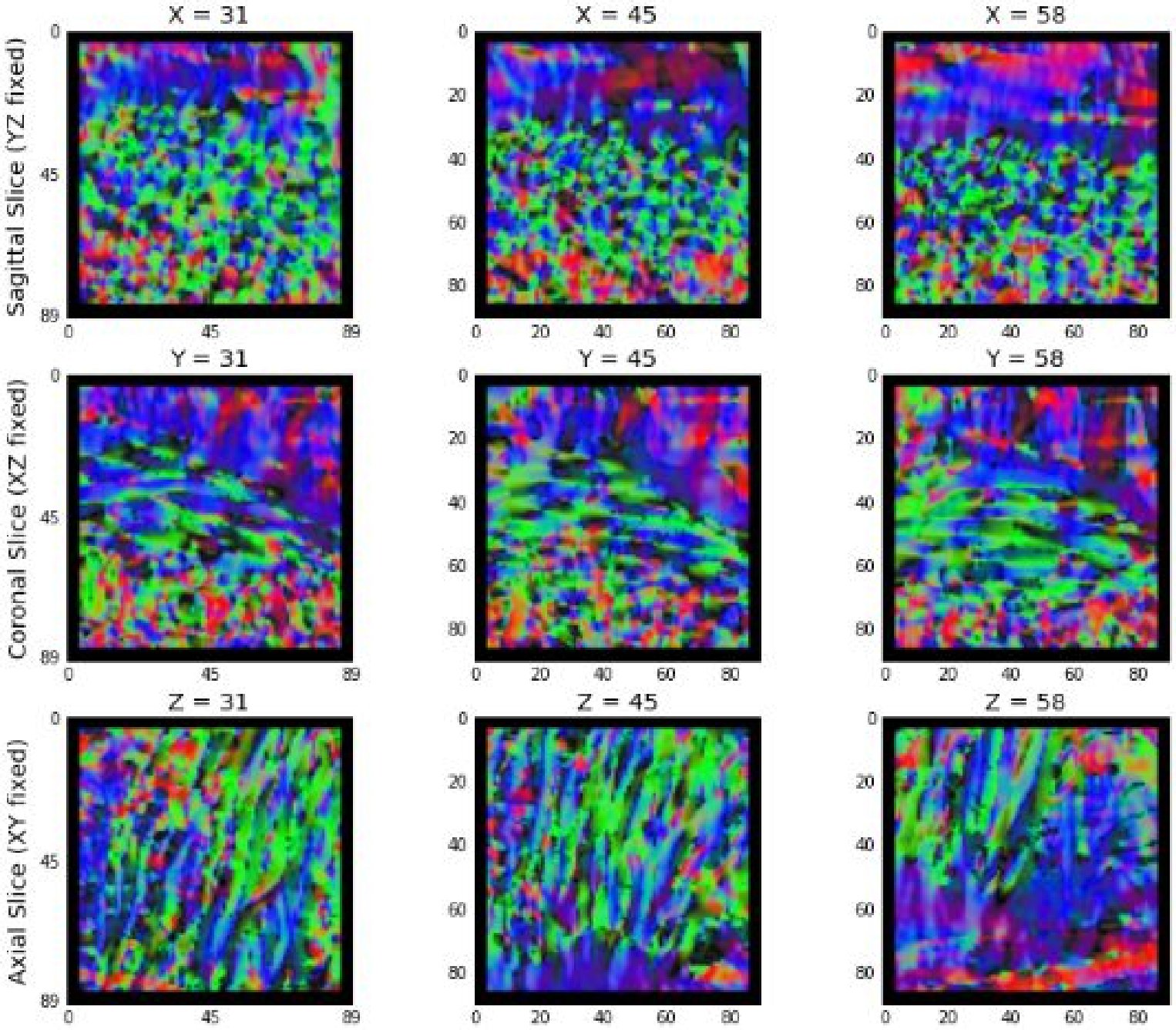
Tensors



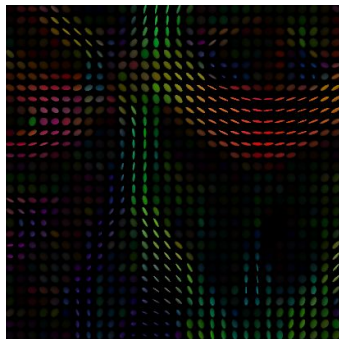
QA

Input
Intermediate
Output

Docs


X = 31
X = 45
X = 58
Y = 31
Y = 45
Y = 58
Z = 31
Z = 45
Z = 58
Sagittal Slice (YZ fixed)
Coronal Slice (XZ fixed)
Axial Slice (XY fixed)
0
20
40
45
60
80
89

Fiber Tractography

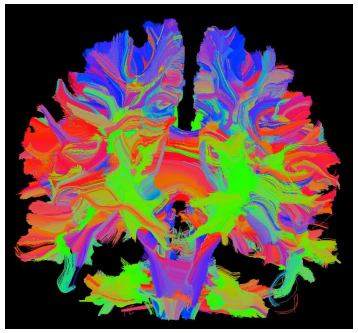


Tensors

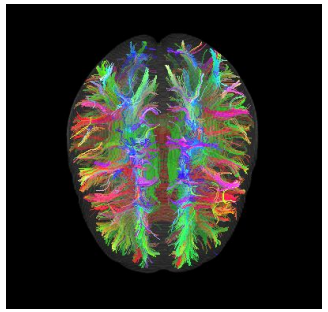
t_{fa}

FA thresh

Mask



Fibers



QA

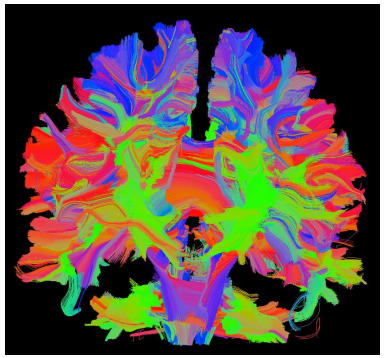
Input
Intermediate
Output

Docs

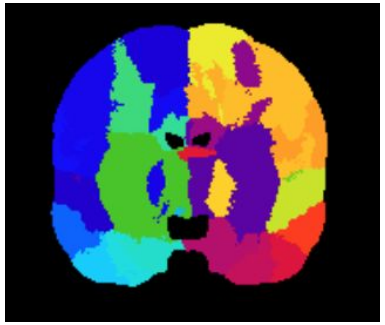
Rest of the slides are in progress

All slides past this point are Greg’s

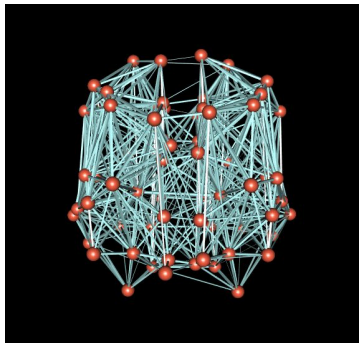
Graph Estimation



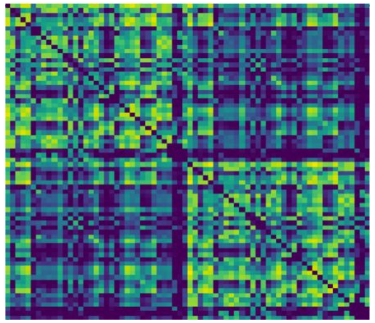
Fibers



Parcellation



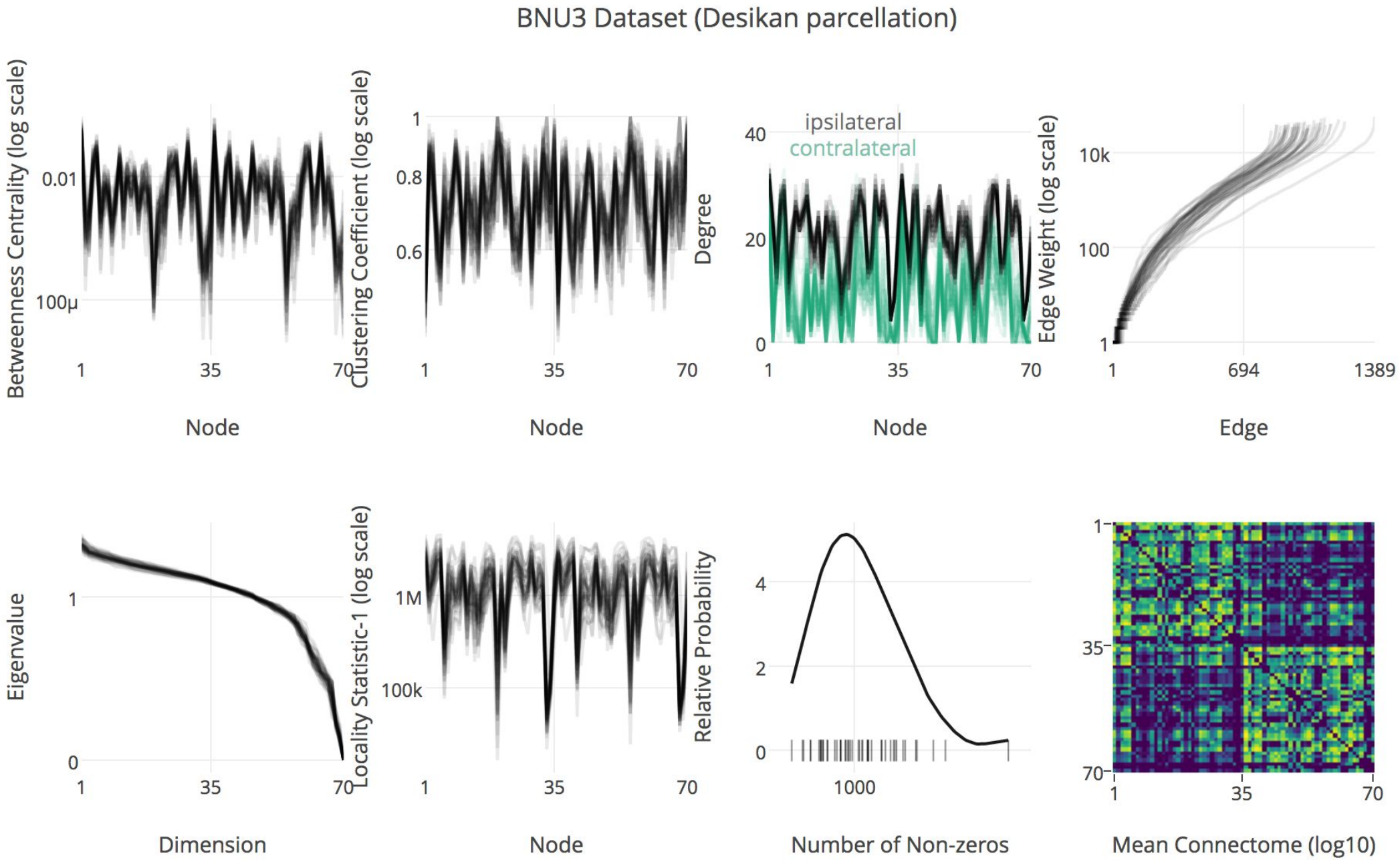
Connectome



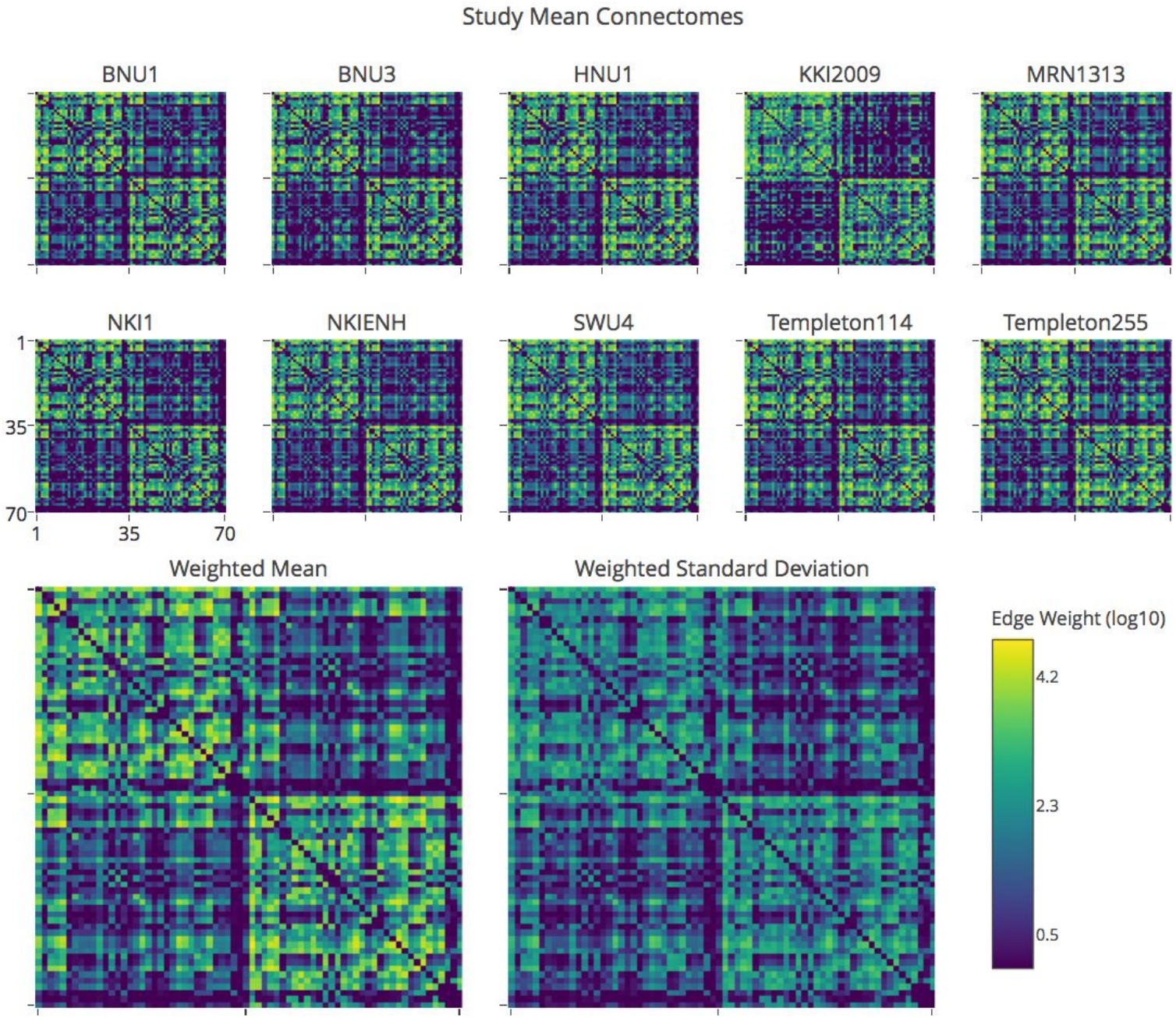
QA

Input
Intermediate
Output

Docs


BNU3 Dataset (Desikan parcellation)
Betweenness Centrality (log scale)
0.01
100µ
1
35
70
Node
Clustering Coefficient (log scale)
1
0.8
0.6
1
35
70
Node
Degree
ipsilateral
contralateral
40
20
0
1
35
70
Node
Edge Weight (log scale)
10k
100
1
1
694
1389
Edge
Eigenvalue
1
0
1
35
70
Dimension
Locality Statistic-1 (log scale)
1M
100k
1
35
70
Node
Relative Probability
4
2
0
1000
Number of Non-zeros
1
35
70
1
35
70
Mean Connectome (log10)

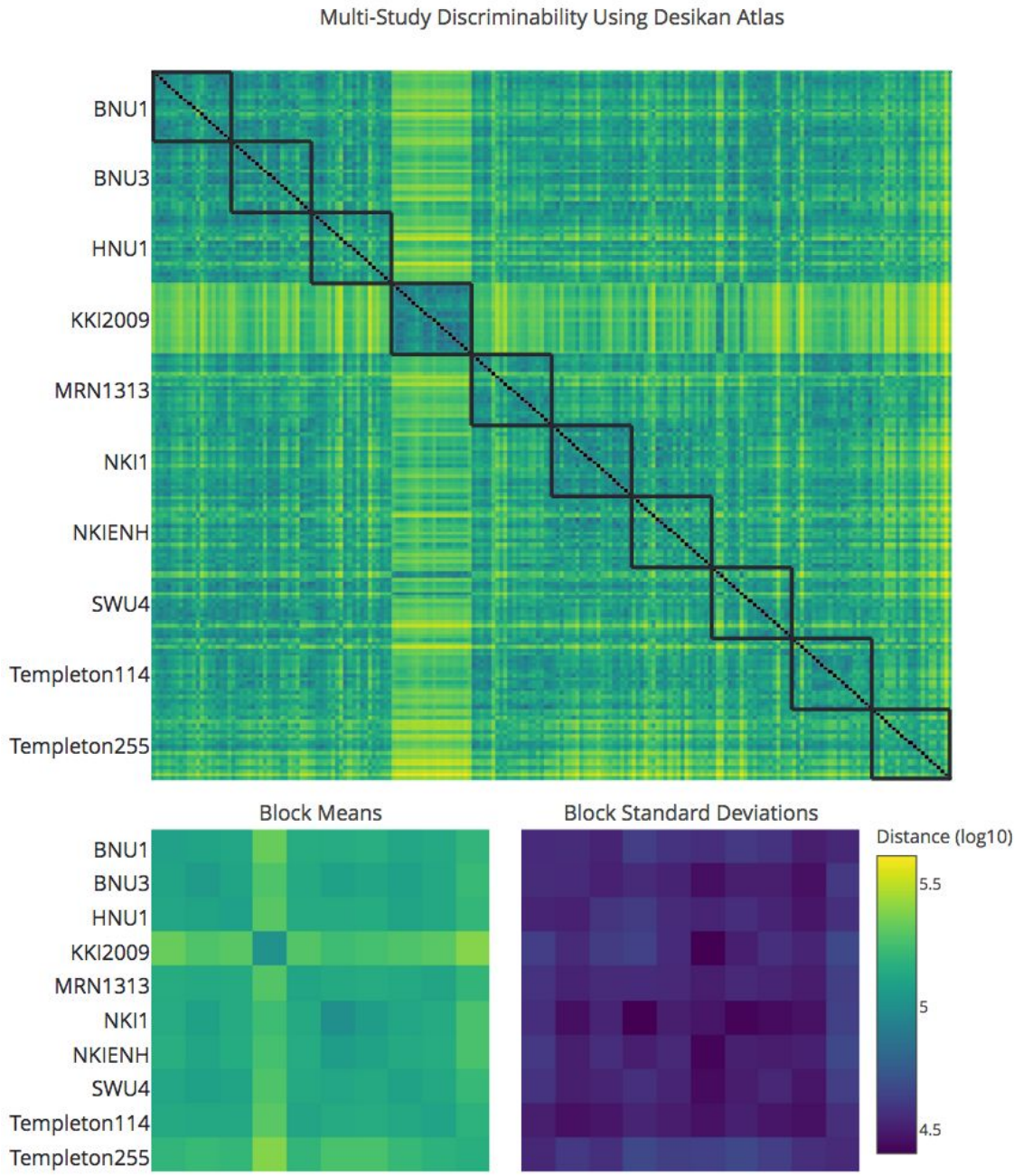
Datasets are Qualitatively Similar



Datasets are Significantly Quantitatively Different

Discriminability = 0.632 (chance = 0.363)

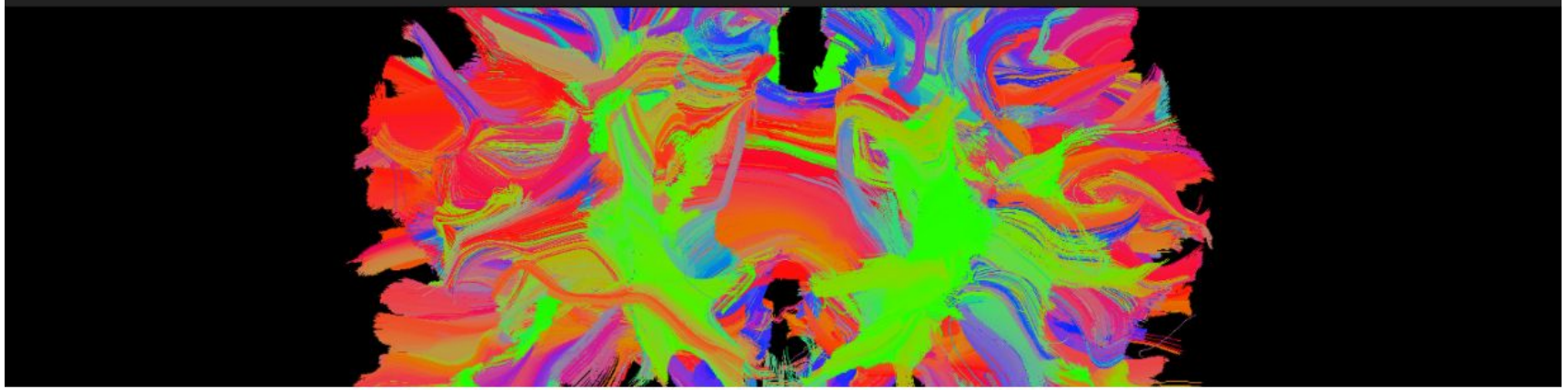
While different datasets are qualitatively similar, they are quantitatively different



One-Click Deployment of clviz

```
ndmg_cloud participant --bucket mrneurodata --bidsdir /data/BNU1/ \
  --jobdir scratch/ --credentials ~/credentials.csv --dataset BNU1
```

Science in the Cloud (SIC)



A Framework for Extensible Science

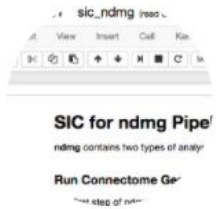
Exploiting scientific containers, cloud computing, and cloud data services, we present a framework for performing and communicating scalable, reproducible, and extensible science in the cloud. We show the capability to compute massive amounts of data parallelly in the cloud, and run a web service that enables intimate interaction and demonstration with the tools and data presented. We hope this model will inspire the community to produce reproducible and, importantly, extensible results which will enable us to collectively accelerate the rate at which scientific breakthroughs are discovered, replicated, and extended.

Read our paper @ GigaScience arXiv

Try our Demo!

Try out SIC!

Running as a persistent Jupyter notebook, our demonstration walks through the ndmg pipeline and quality control.



Fork our Code

Download either the frozen-for-publication or up-to-date versions of our code and try sic yourself!

- GigaDB archive

Use the Cloud

Our pipeline is integrated with a variety of platforms, and has been used to process a variety of datasets in the cloud. We encourage you to pull on one of these threads.

Authors

Kiar, G; Gorgolewski, K, J; Kleissas, D; Gray Roncal, W; Litt, B; Wandell, B; Poldrack, R A; Wiener, M; Vogelstein, R J; Burns, R; Vogelstein, J T

Demo

In Progress