Breakout Session 6: Track B

Retinal Circuitry - Improving AI Readiness of Existing Retinal Connectomes

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Retinal Circuitry - Improving AI Readiness of Existing Retinal Connectomes

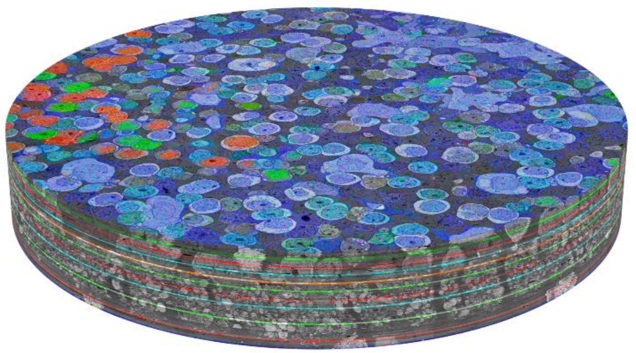
Presenter: James Anderson

PI: Bryan Jones

NOT-OD-22-67

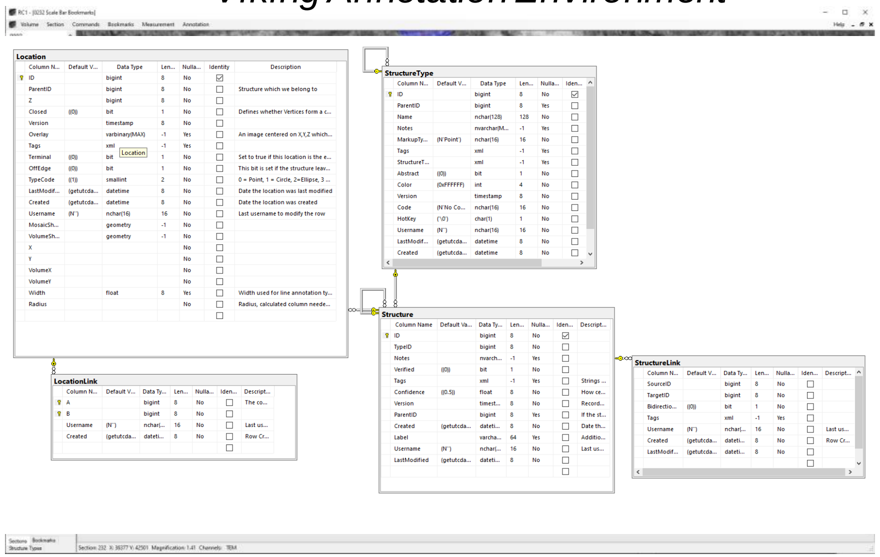
Connectomics Workflow

Volume Construction

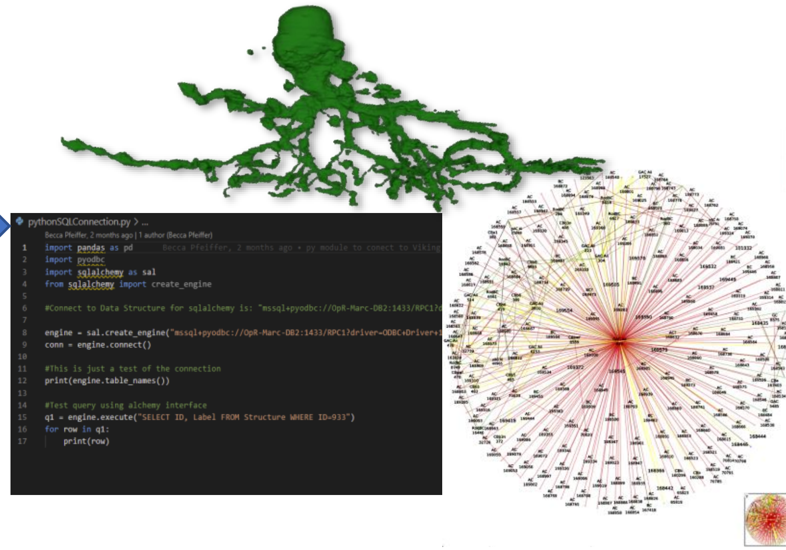


- ssTEM (70-90nm sections)
- 2.18nm/px resolution
- Interleaved small molecule labeling

Viking Annotation Environment



Analysis



Comparative Neuroanatomy

RC1
Rabbit retinal connectome
Status: Open
Database Annotations: ~1.3 million

RC2
Mouse retinal connectome
Status: Active
Database Annotations: ~500k

RC3
Primate (Macaque) retinal connectome
Status: Captured
Database Annotations: N/A

Pathoconnectomics

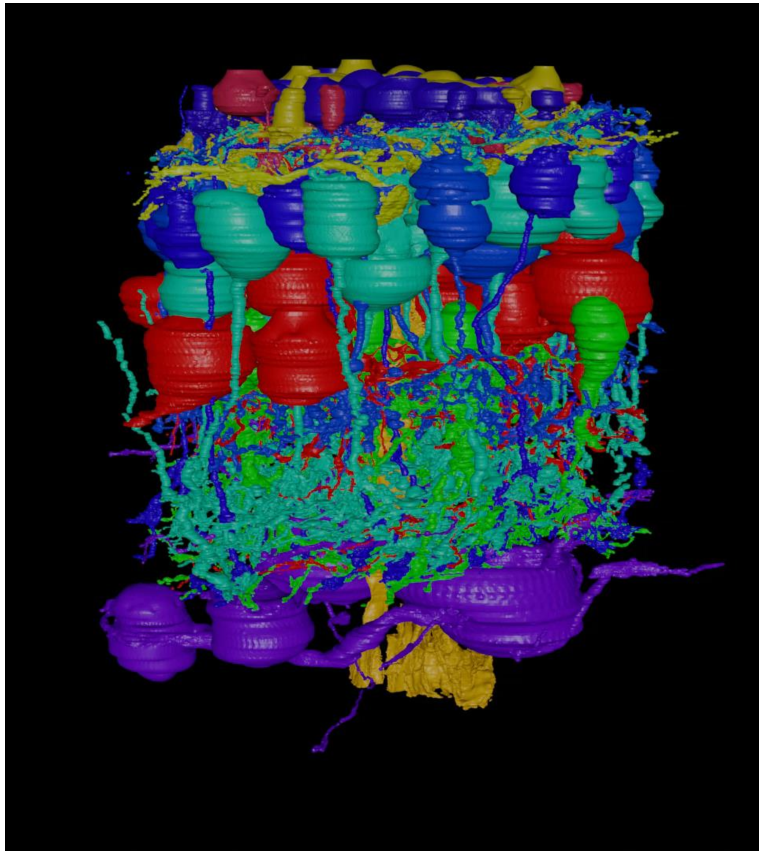
RPC1
Pathoconnectome from 10mo rabbit model of Retinitis Pigmentosa (Phase 1 retinal degeneration)
Status: Open
Database Annotations: ~280k

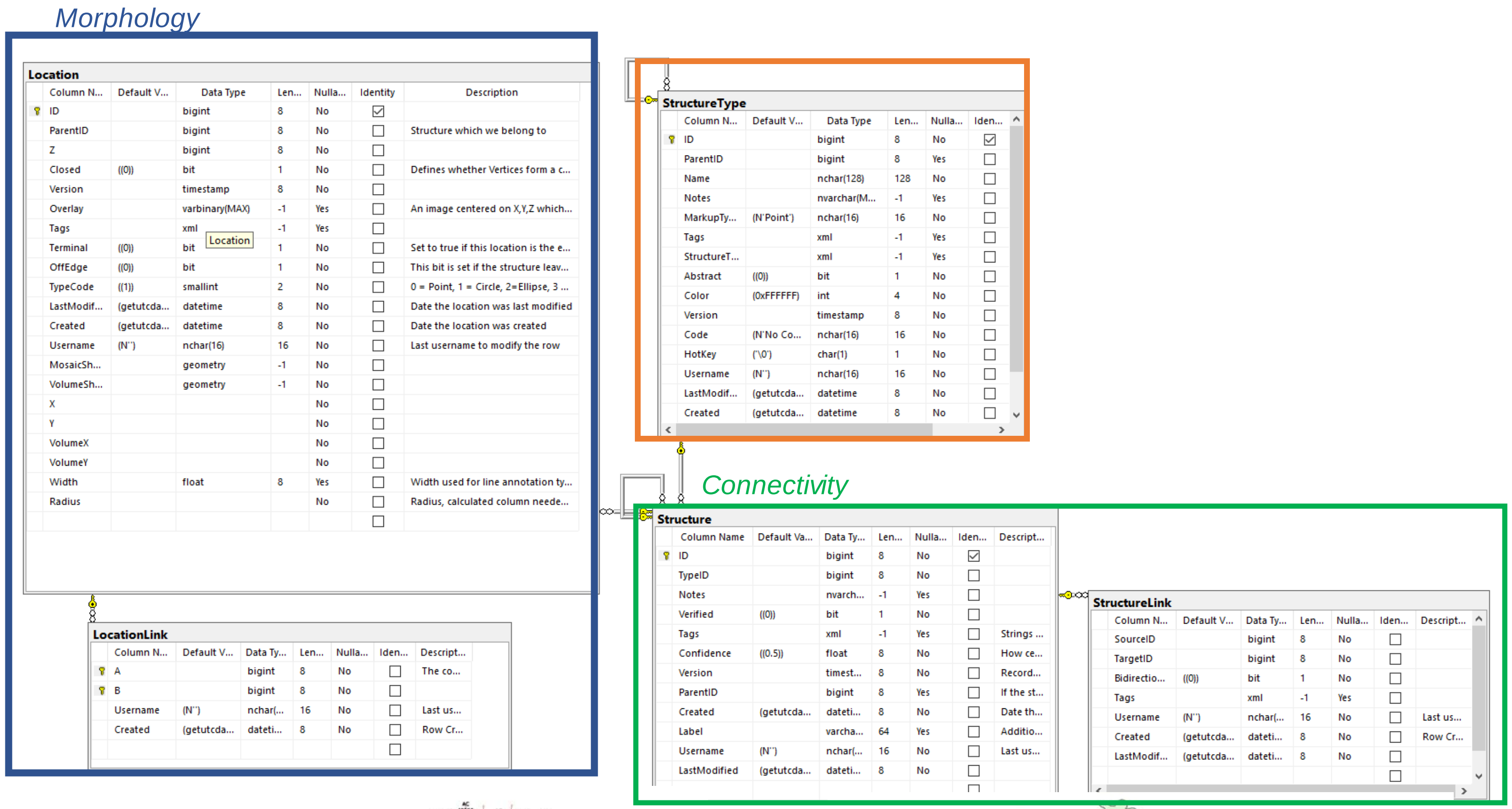
RPC2
Pathoconnectome from 2yo rabbit model of Retinitis Pigmentosa (Phase 2 retinal degeneration)
Status: Active
Database Annotations: ~100k

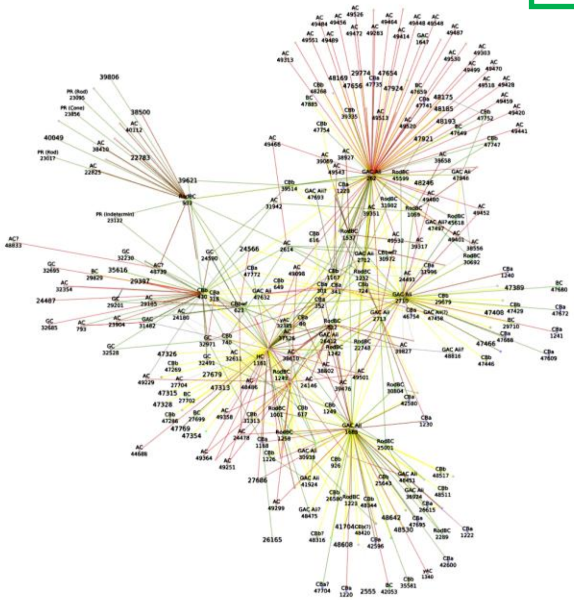
RPC3
Pathoconnectome from 4yo rabbit model of Retinitis Pigmentosa (Phase 3 retinal degeneration)
Status: Captured
Database Annotations: N/A

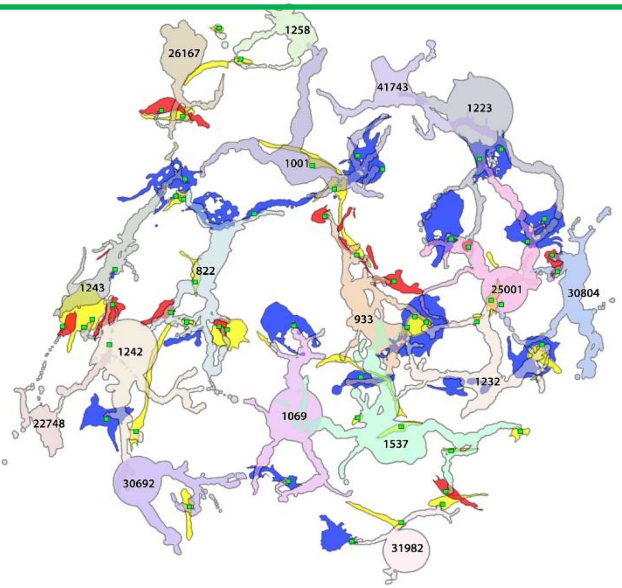
Database Features:

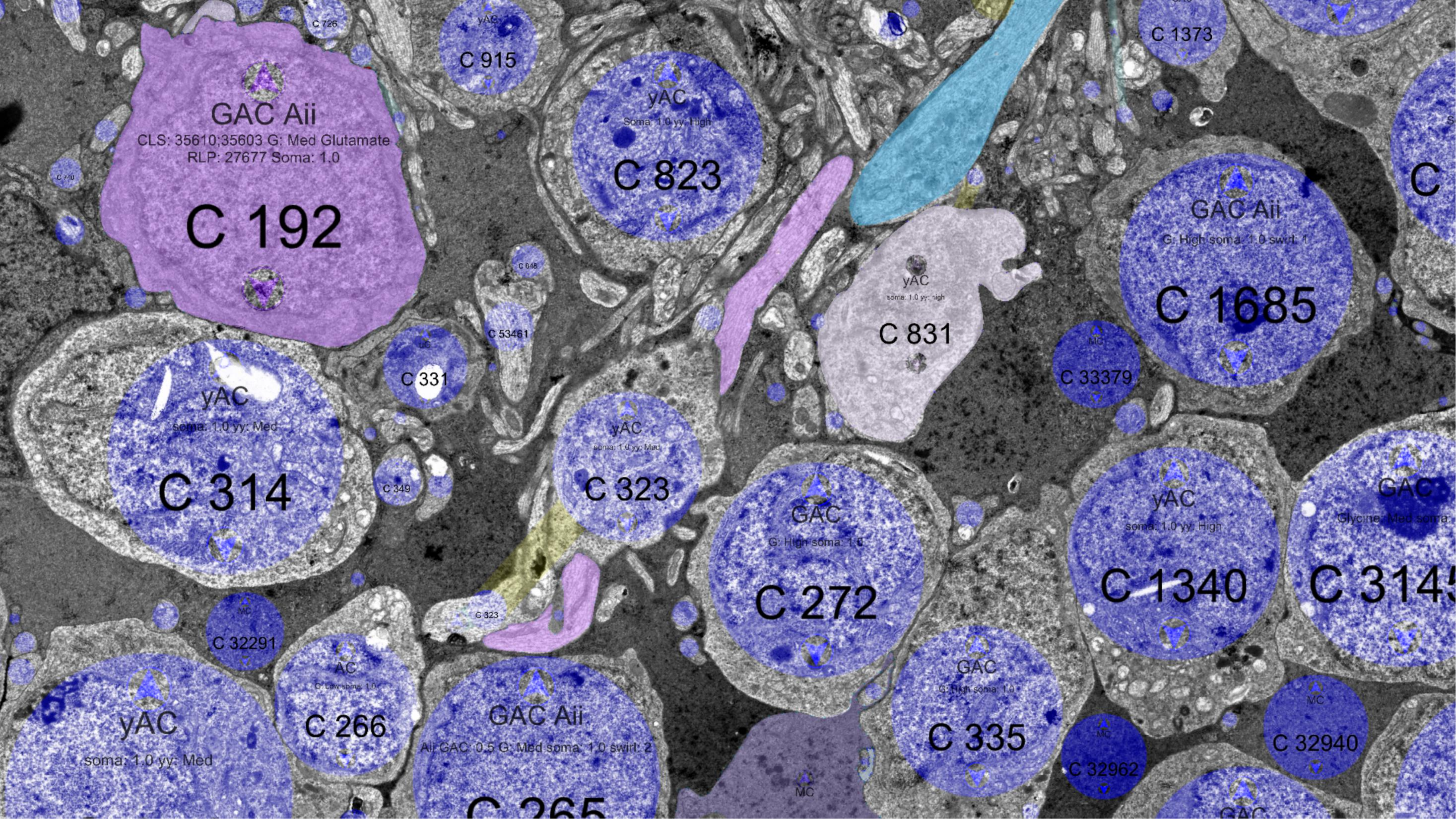
- SQL reduces development cost and maintenance. Very mature tools.
- Flexible addition of new structures
- Geometry columns encode annotations. Spatial queries within SQL. Enables encoding any geometric shape.
- Hierarchy describes relationships of biological structures (Parent=Cell, Child=Subcellular structures)
- Size, shape, and position are encoded in every annotation
- Morphology and connectivity are encoded in separate but relatable graphs. Allowing efficient querying.



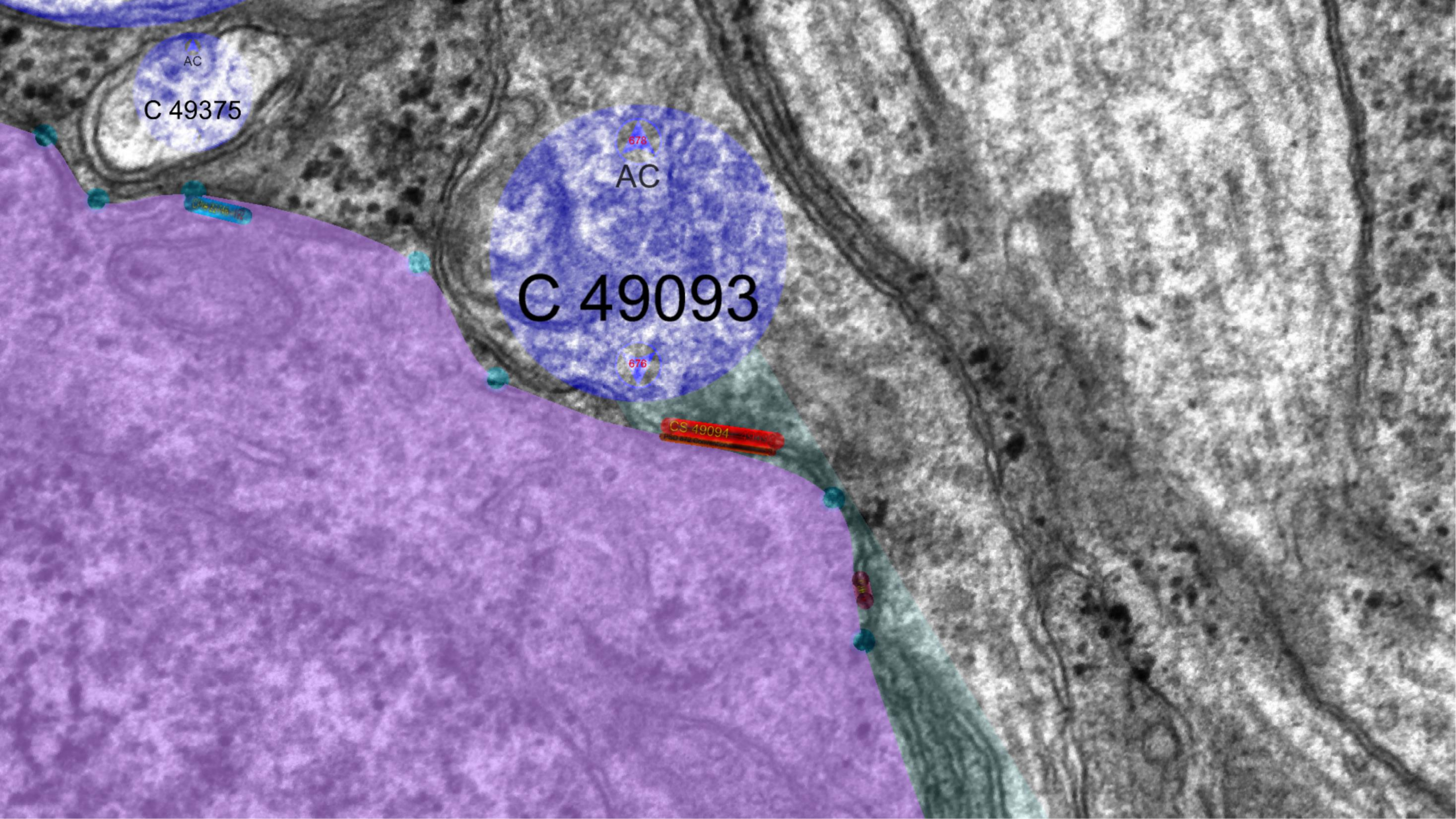




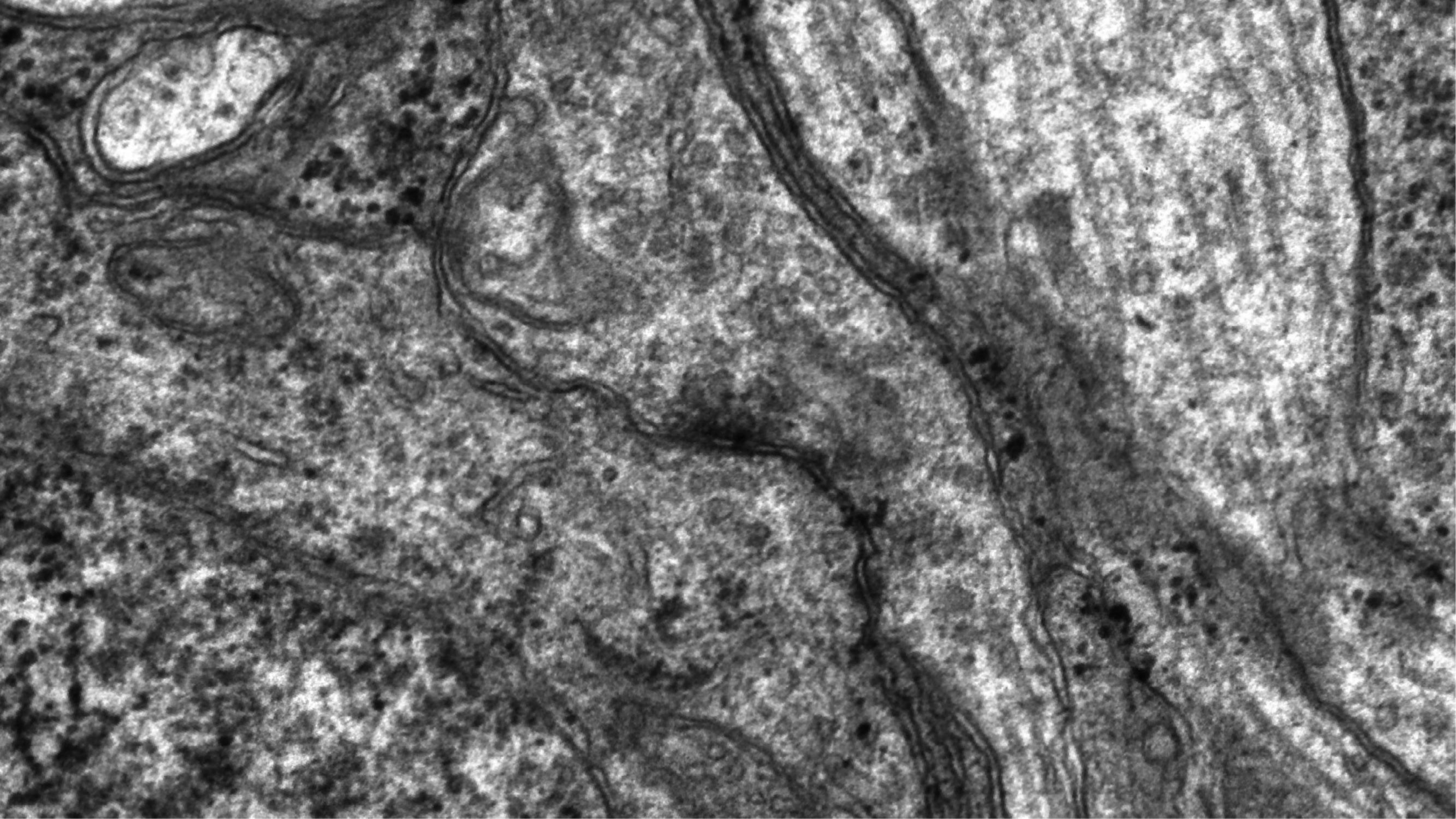




GAC Aii
CLS: 35610;35603 G: Med Glutamate
RLP: 27677 Soma: 1.0
C 192
C 726
yAC
C 915
yAC
Soma: 1.0 yy: High
C 823
C 1373
C 648
yAC
C 831
GAC Aii
G: High soma: 1.0 swirl: 1
C 1685
C 53461
C 331
C 33379
yAC
soma: 1.0 yy: Med
C 314
C 349
yAC
C 323
GAC
G: High soma: 1.0
C 272
yAC
soma: 1.0 yy: High
C 1340
GAC
Glycine: Med soma
C 3145
C 323
C 32291
AC
C 266
yAC
soma: 1.0 yy: Med
GAC Aii
Aii GAC: 0.5 G: Med soma: 1.0 swirl: 2
GAC
G: High soma: 1.0
C 335
C 32962
C 32940
MC



AC
C 49375
678
AC
C 49093
676
CS 49094



Data Sharing

Primary Goal: Make it simple for collaborators to access our combined annotation and image data to create machine learning algorithms to augment volume annotation efforts.

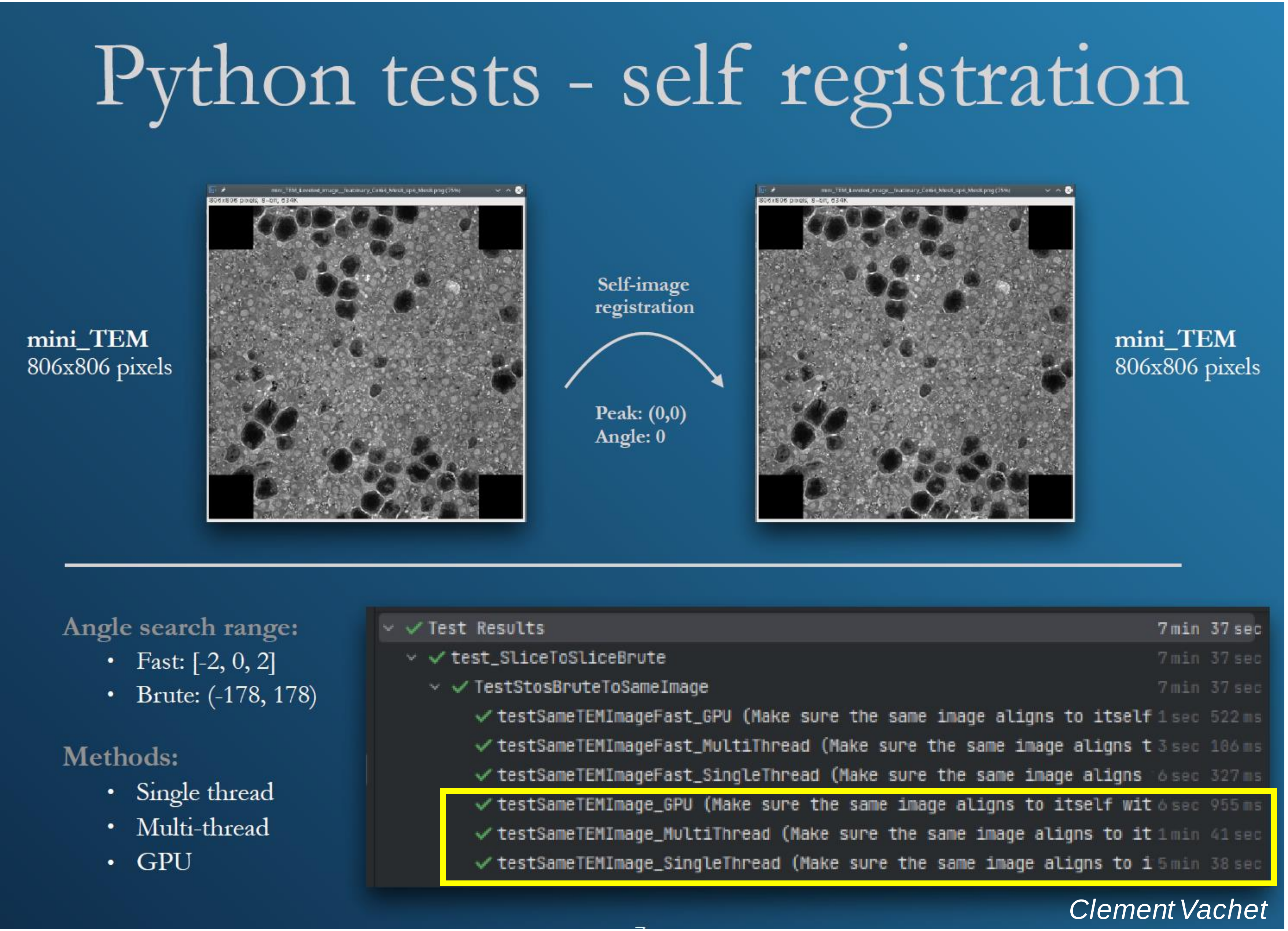
Annotations:

- OData works great for sharing annotations:
  - http://websvc1.connectomes.utah.edu/RC1/OData/
- Queryable, Readable directly into a Browser, Spreadsheet, or programming API
- Spatial data is plain text Open Geospatial Consortium format. Libraries exist to interpret it

Images:

- The goal is to ease accessibility for the image processing lab.
- Viking uses client GPU to perform transforms. Moving processing from client to server simplifies the client experience.
- Real-time transformation has been an advantage for adjusting volume registration during annotation phase.
- Attempts to share images:
  - 1st Approach : Client exports region-of-interest to disk
  - 2nd Approach : Cached RC1 volume available via HTTP, ex: http://storage1.connectomes.utah.edu/RC1VolumeRegisteredV2/RC1/234/Tiles/001/X160_Y049.png
  - 3rd Approach : Web API (Stopped at prototype due to performance issues)
  - 4th Approach : A stack of numpy arrays, either shipped in the mail or a long download

Progress Towards Goal: CuPy proof-of-concept



Registration requirements:
- FFT
- Random Number Generation
- Image Labeling
- Arithmetic
- Convolution

Assembly Requirements:
- Delaunay triangulation
- Texture mapping

Registration Speed

GPU	< 7 sec
Multi-core	101 sec

GPU is 14x faster at Registration!

Progress Towards Goal: GPU Implementation with CuPy

CuPy

CuPy is a NumPy/SciPy open-source array library
for GPU-accelerated computing with Python

Transforms	single CPU	multi CPU	partial GPU	full GPU
Rigid_NoRotation	✓	✓		✓
Rigid	✓	✓		✓
Centered Similary	✓	✓		✓
MeshWithRBFFallback	✓	✓	✓	
GridWithRBFFallback	✓	✓	✓	

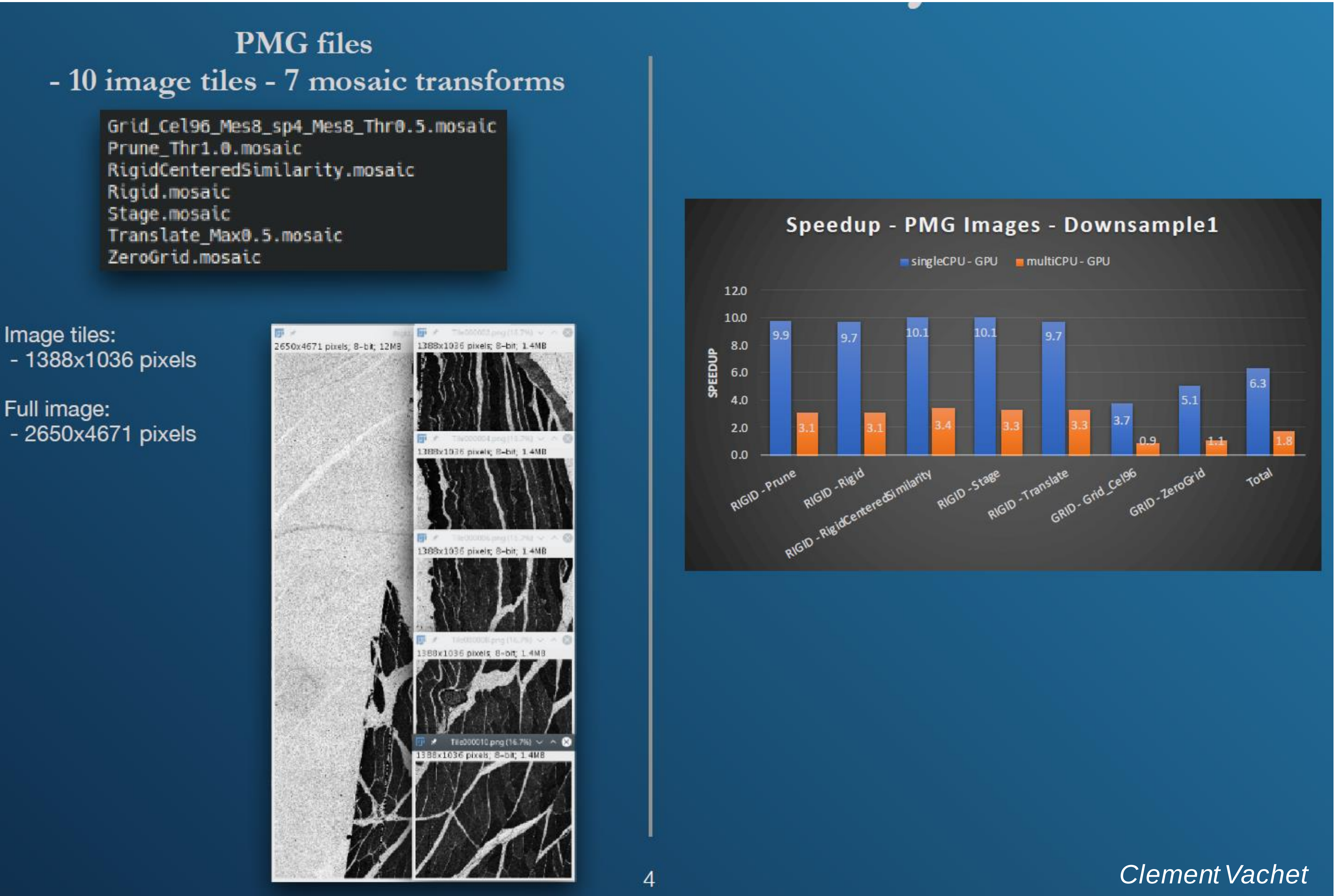
Implementation for assembly transforms

Note: some transform components (e.g. triangulation) haven't yet been implemented in CuPy

Clement Vachet

- CuPy lacked the LinearNDInterpolator function necessary for a full GPU implementation.
- The function was pulled into the next CuPy release two weeks ago
- Our CuPy version will be fully implemented upon next official cupy release

Progress Towards Goal: Tile Assembly



- Ignore the blue bar results.
- Yellow multi-core comparison ran on an 8-core desktop system.
- Beyond missing LinearNDInterpolate I suspect moving memory between CPU and GPU is a significant time cost. Most likely optimizable.

Progress and Ongoing Efforts

Tools

- Every critical path now utilizes CuPy (with the one exception discussed). Passes unit tests.
- Have support to export a stack of full resolution numpy files
- Waiting for next cupy version to fully test with GPU at scale

Docker Distribution

- Docker is simple to deploy and gives us easy access to our university high-performance computing center. This provides easier access to the command-line tool that can export registered volumes and will allow clients to run the Web Service locally for performance.
- All but one tool required to take images from capture to a 3D numpy array now run in a single docker image.
- We have contracted Kitware to port the remaining legacy C++ ITK-based tool to a web image to complete the docker image.

Web Service

- In progress.
- GPU performance determines if we revisit the original on-the-fly web service prototype or rely upon pre-generated images.

Legacy Data

- Original registered RC1 images available via HTTP are being copied into a stack of numpy arrays.
- RC1 raw data is now compatible with the latest code. Going from imported data to a registered volume is a great stress test for the new GPU code.

MarcLab for Connectomics:

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Unmet CuPy Contributor:

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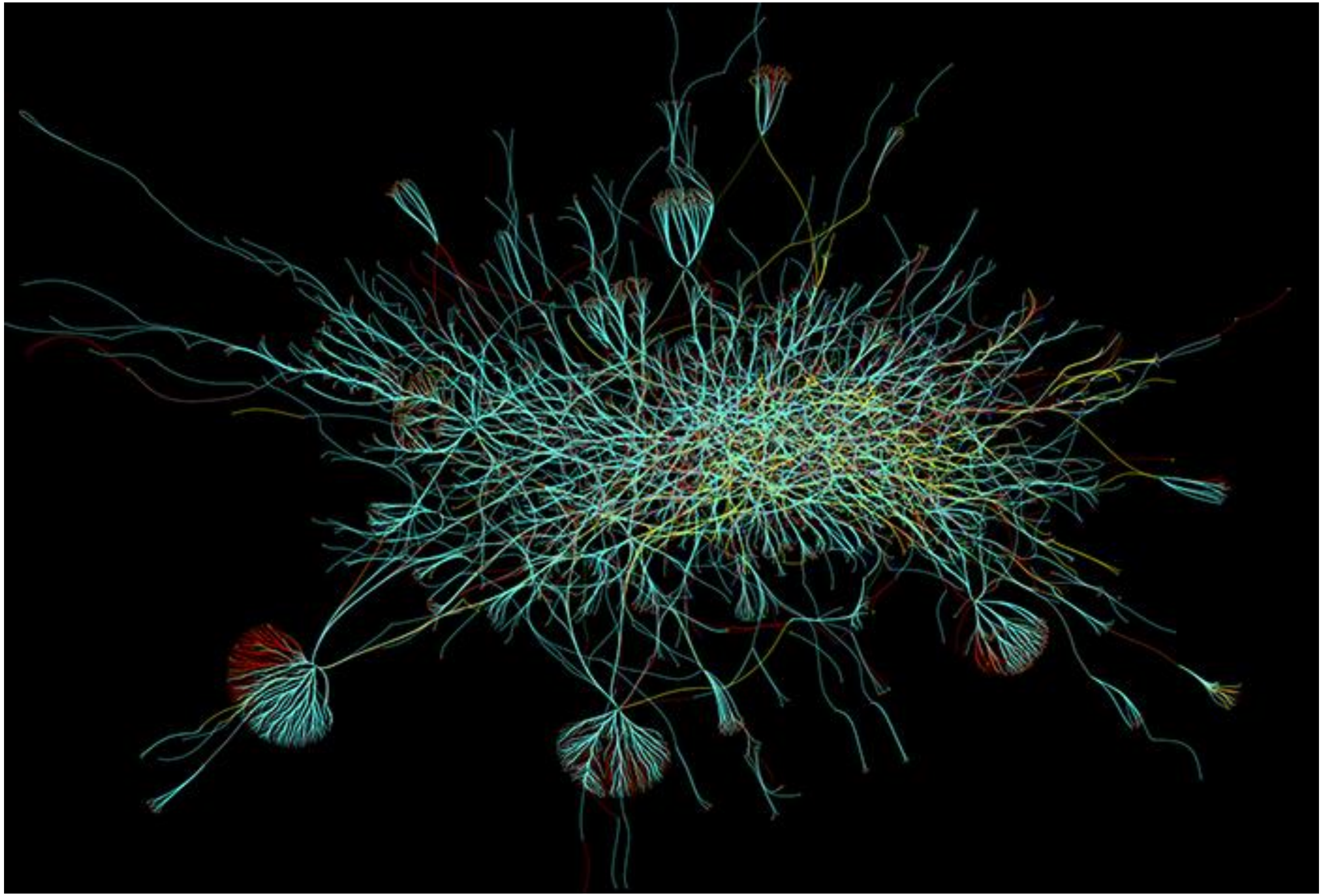
(LinearNDInterpolator Author)



National Eye Institute

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