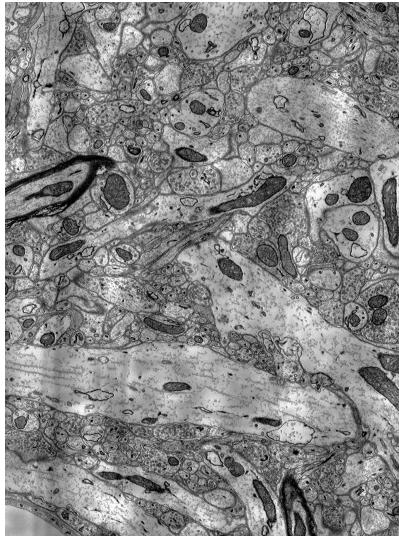


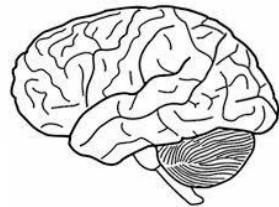
Segmentation of Electron Microscopy Images in Connectomics



Brian Matejek
Advisor: Hanspeter Pfister

Connectomics

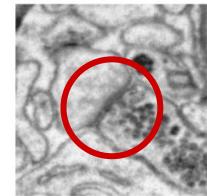
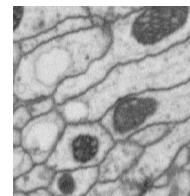
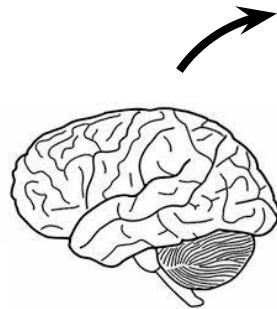
Goal: Extract the wiring diagram from a brain



Connectomics

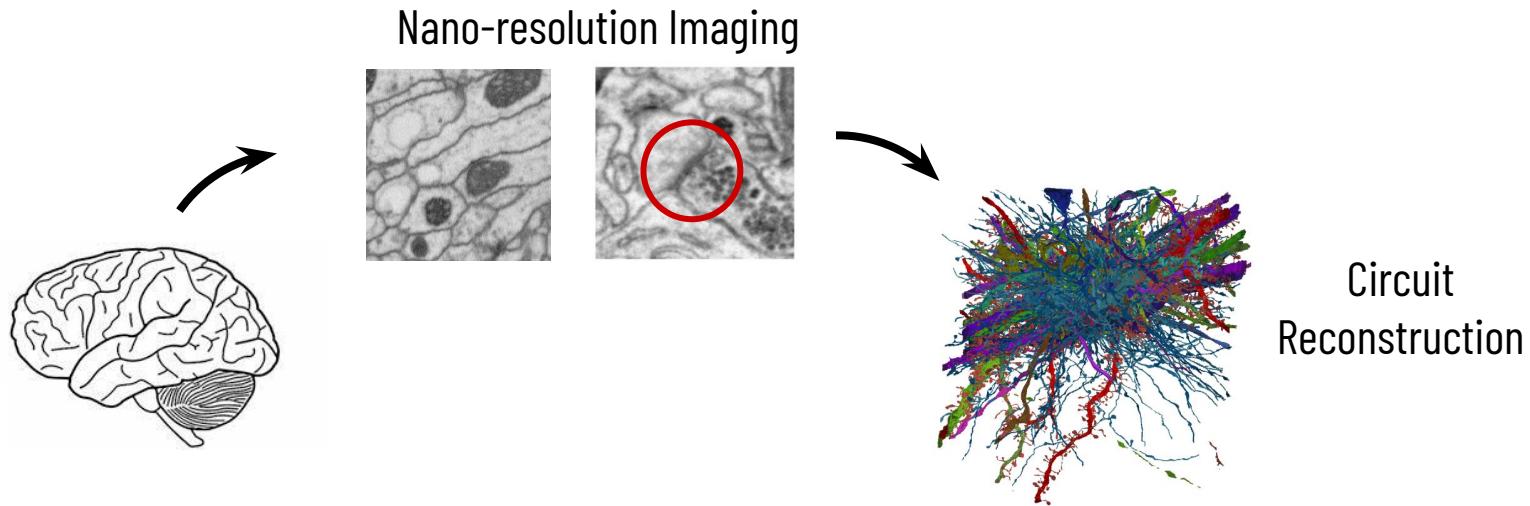
Goal: Extract the wiring diagram from a brain

Nano-resolution Imaging



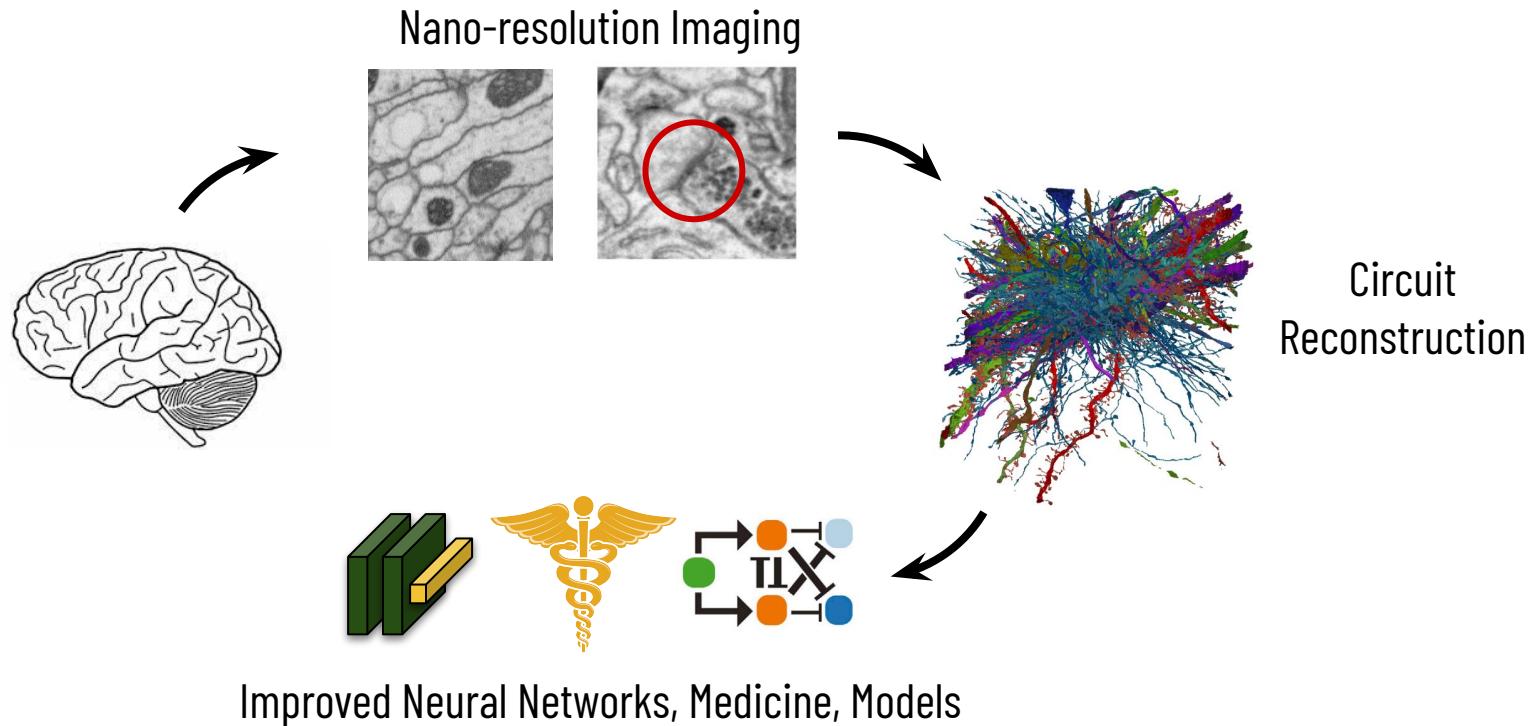
Connectomics

Goal: Extract the wiring diagram from a brain



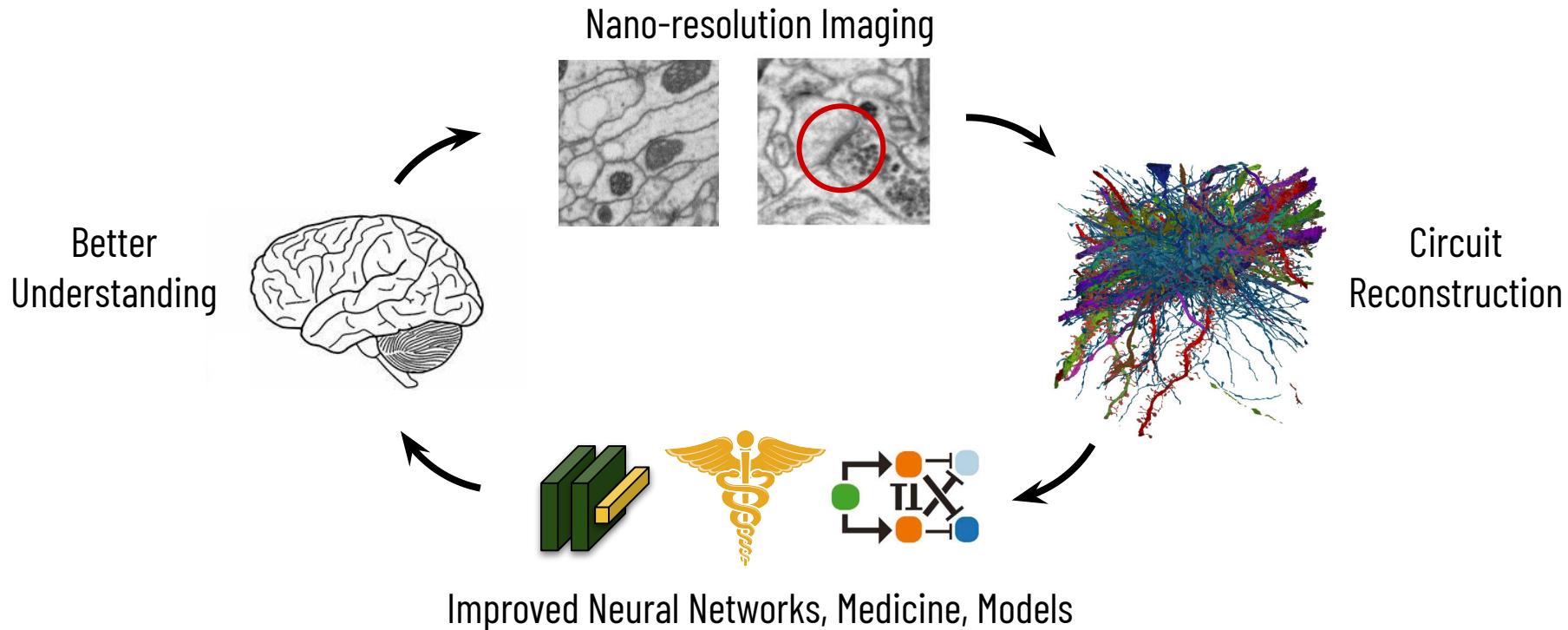
Connectomics

Goal: Extract the wiring diagram from a brain



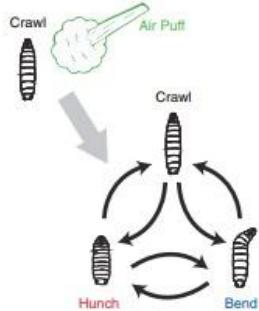
Connectomics

Goal: Extract the wiring diagram from a brain



Connectomics

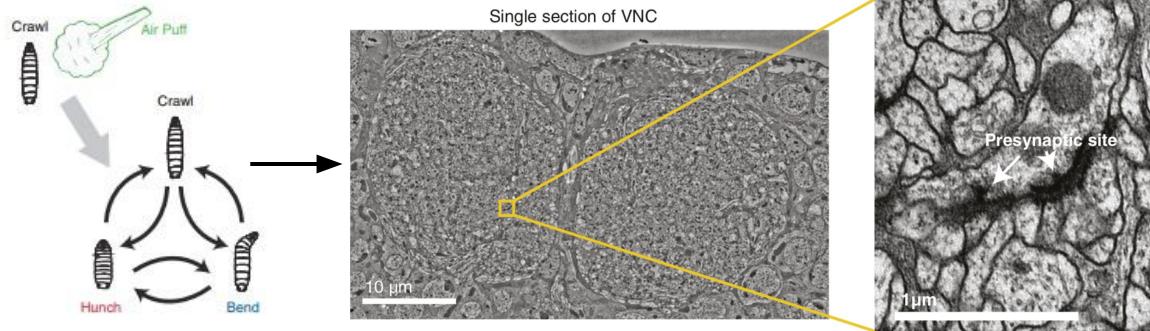
Goal: Extract the wiring diagram from a brain



Behavior

Connectomics

Goal: Extract the wiring diagram from a brain

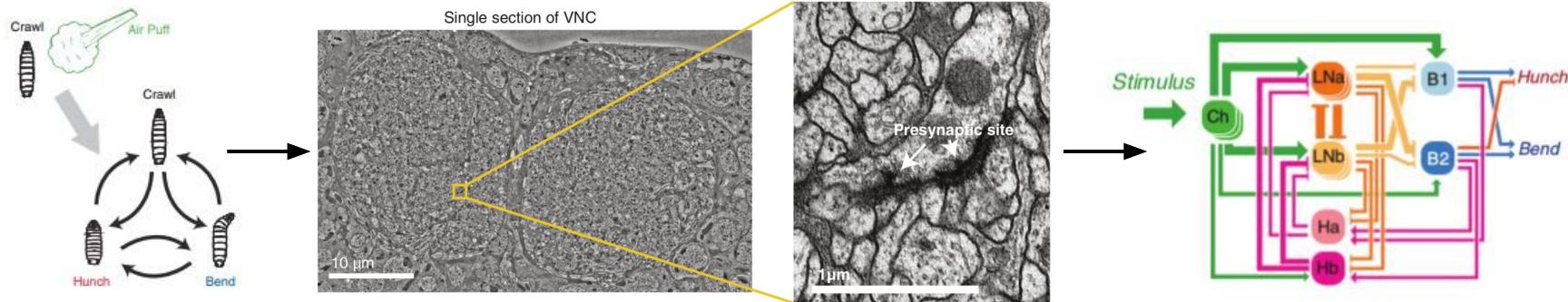


Behavior

Structure

Connectomics

Goal: Extract the wiring diagram from a brain



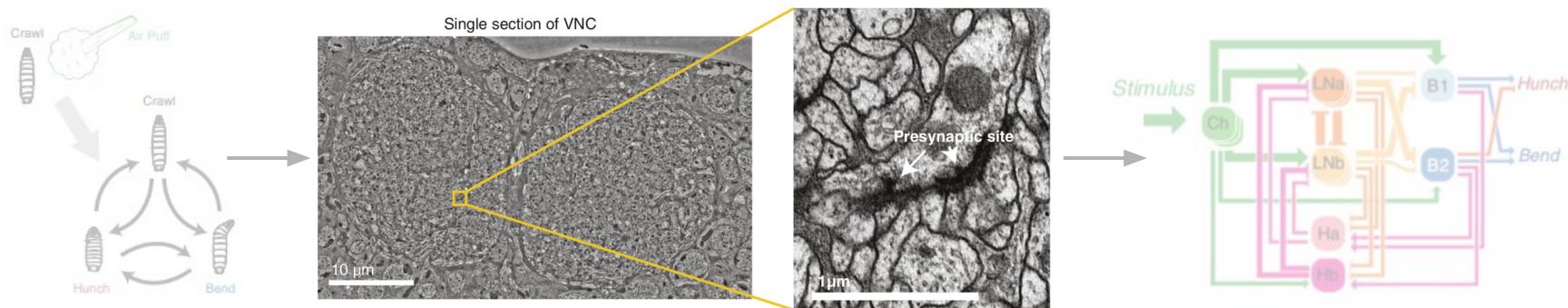
Behavior

Structure

Function

Connectomics

Goal: Extract the wiring diagram from a brain

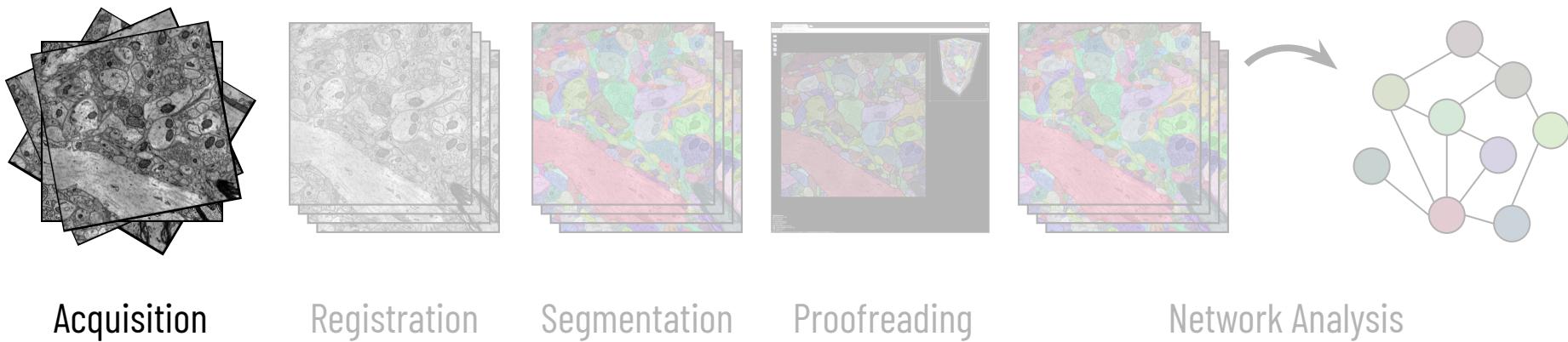


Behavior

Structure

Function

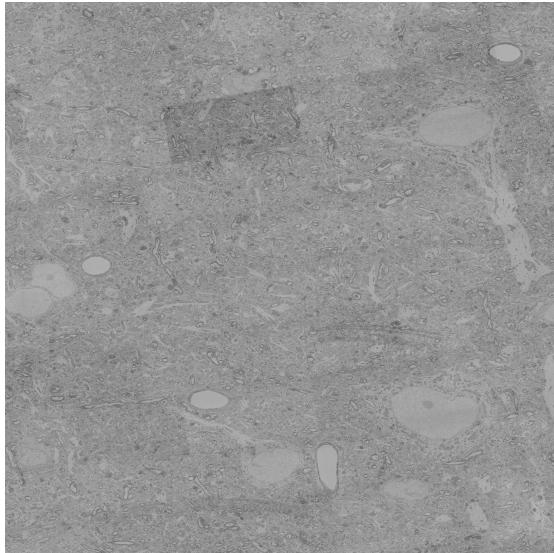
Connectomics Pipeline



Suissa-Peleg et al., Automatic Neural Reconstruction from Petavoxel of Electron Microscopy, *Microscopy and Microanalysis* 2016
Schalek et al., Imaging a 1 mm^3 Volume of Rat Cortex Using a MultiBeam SEM, *Microscopy and Microanalysis*, 2016

Image Acquisition

Multi-beam electron microscopes collect 1 TB of raw image data every hour

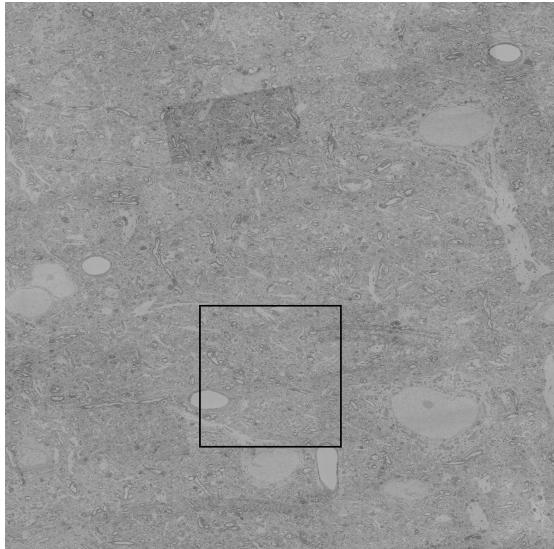


100 μm

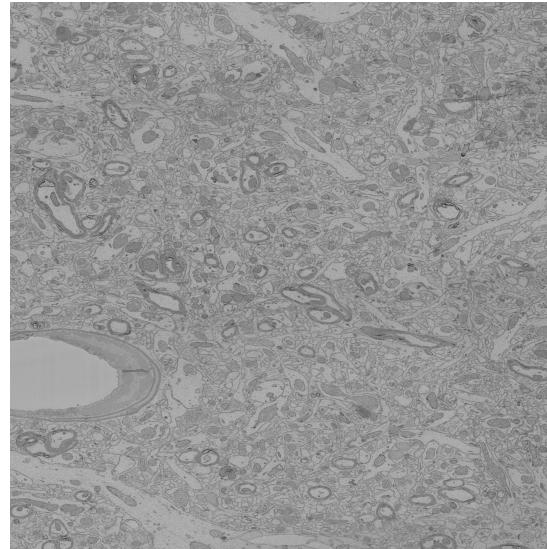
Image Acquisition

Multi-beam electron microscopes collect 1 TB of raw image data every hour

Can image 1 mm^3 of image data (2 PB) in 6 months



100 μm

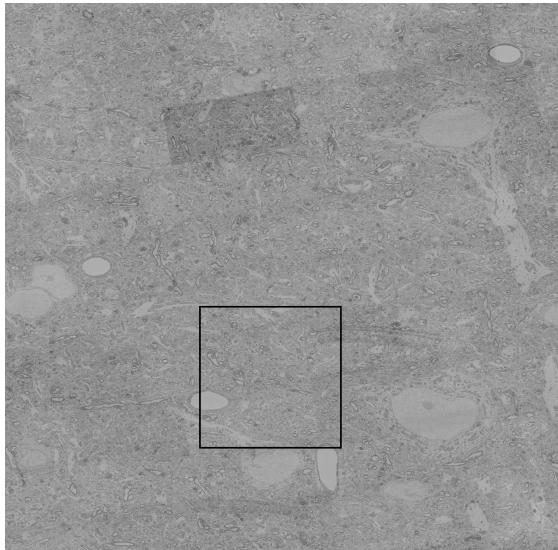


25 μm

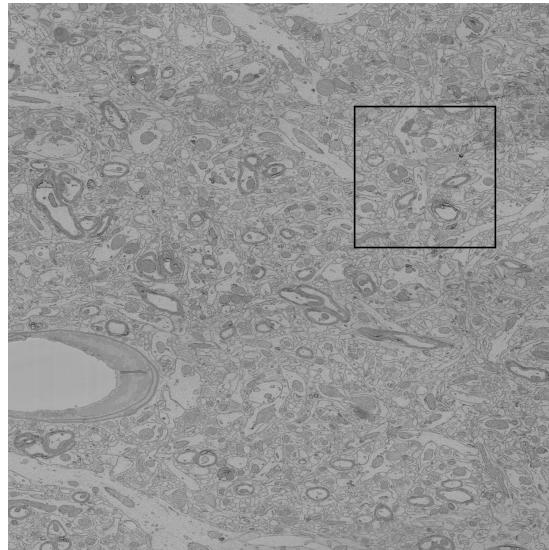
Image Acquisition

Multi-beam electron microscopes collect 1 TB of raw image data every hour

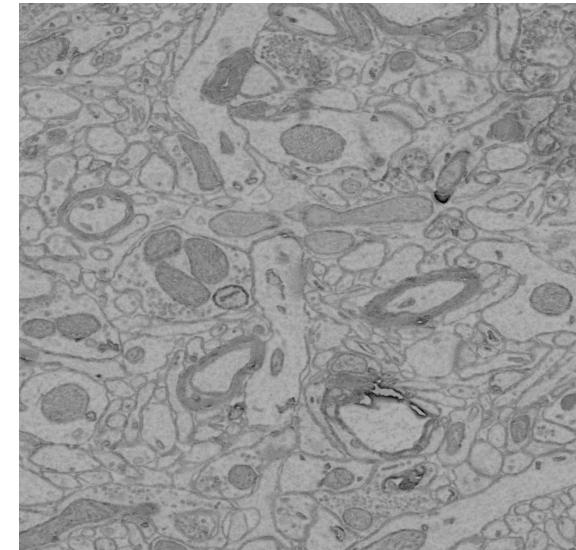
Can image 1 mm³ of image data (2 PB) in 6 months



100 μm

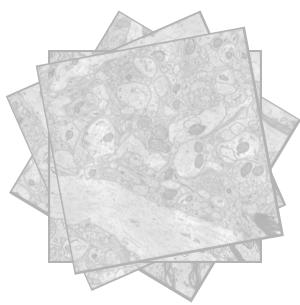


25 μm

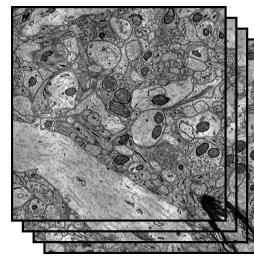


6250 nm

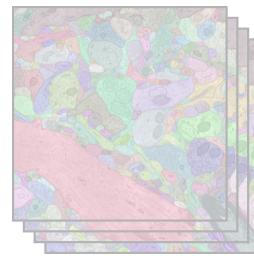
Connectomics Pipeline



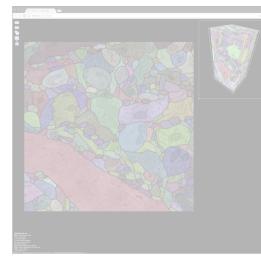
Acquisition



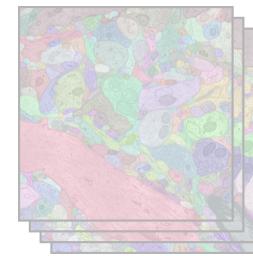
Registration



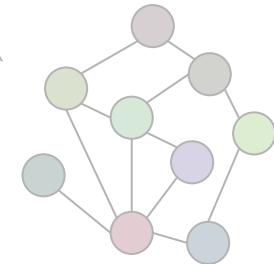
Segmentation



Proofreading

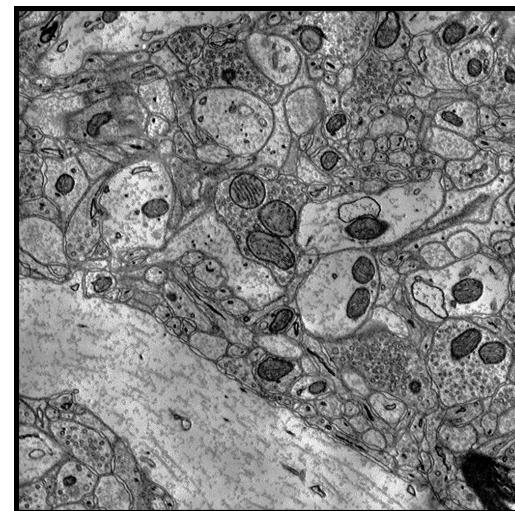
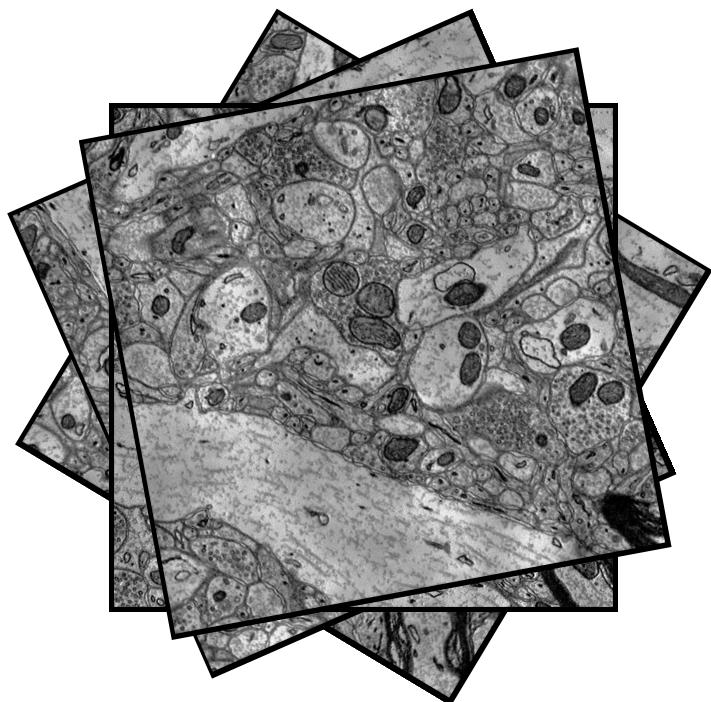


Network Analysis

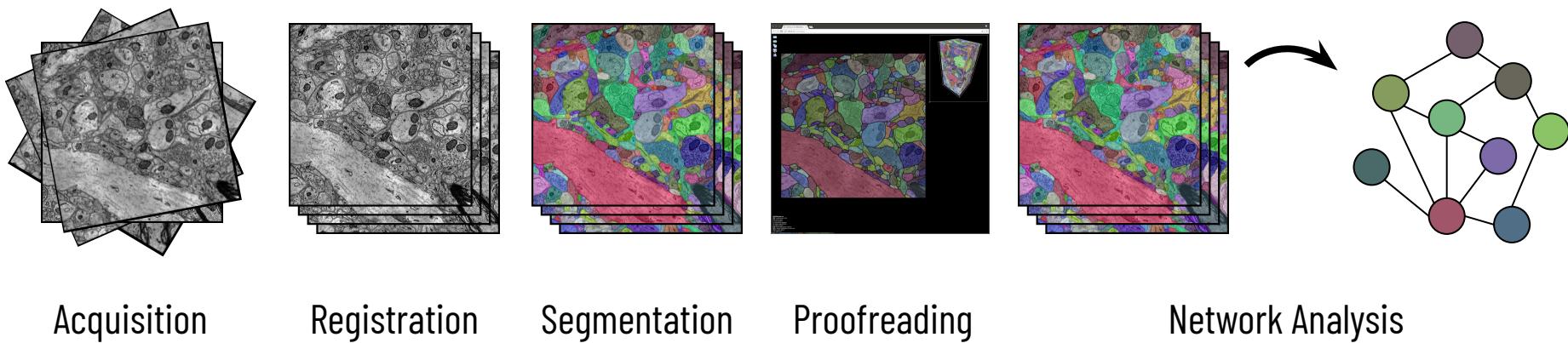


Saalfeld et al., Elastic Volume Reconstruction from Series of Ultra-thin Microscopy Sections, Nature 2012
Khairy et al., Joint Deformable Registration of Large EM Image Volumes: A Matrix Solver Approach, 2018

Registration



Connectomics Pipeline



Nunez-Iglesias et al., Machine Learning of Hierarchical Clustering to Segment 2D and 3D Images, PLoS ONE 2014

Cicek et al., 3D U-Net: Learning Dense Volumetric Segmentation from Sparse Annotation, MICCAI 2016

Januszewski et al., Flood-Filling Networks, 2016

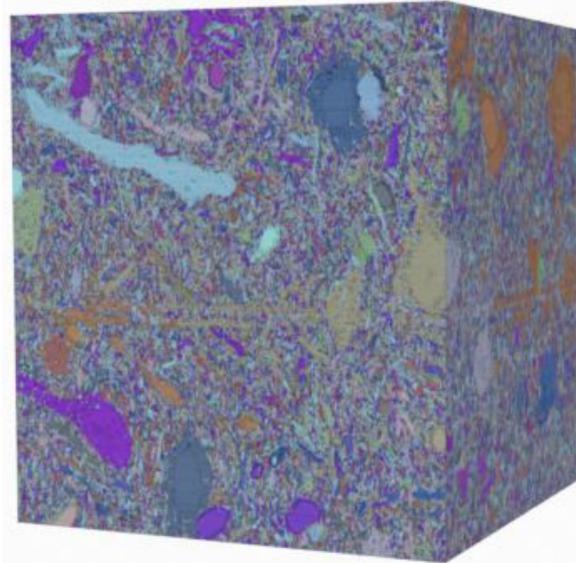
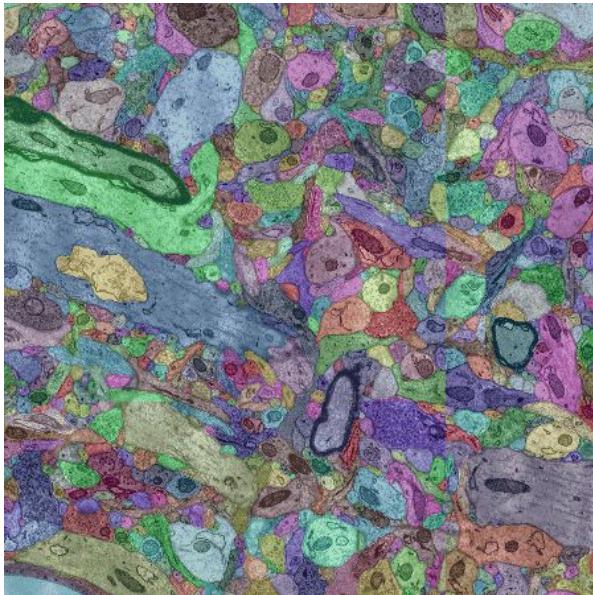
Zeng et al., DeepEM3D: Approaching Human-Level Performance on 3D Anisotropic EM Image Segmentation, Bioinformatics 2017

Pape et al., Solving Large Multicut Problems for Connectomics via Domain Decomposition, ICCV 2017

Lee et al., Superhuman Accuracy on the SNEMI3D Connectomics Challenge, 2017

Label Volumes

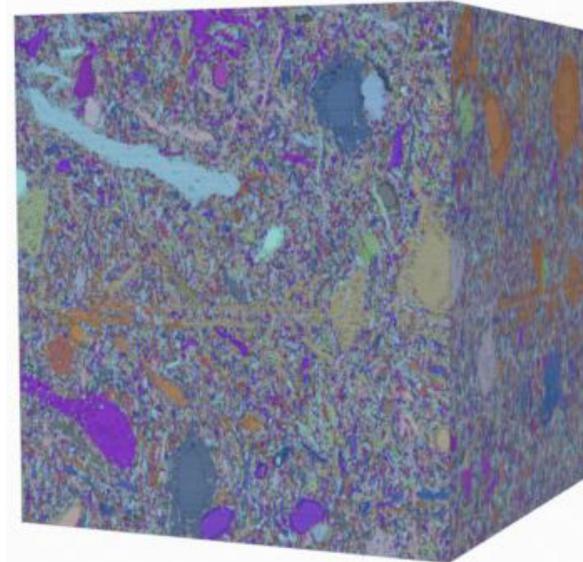
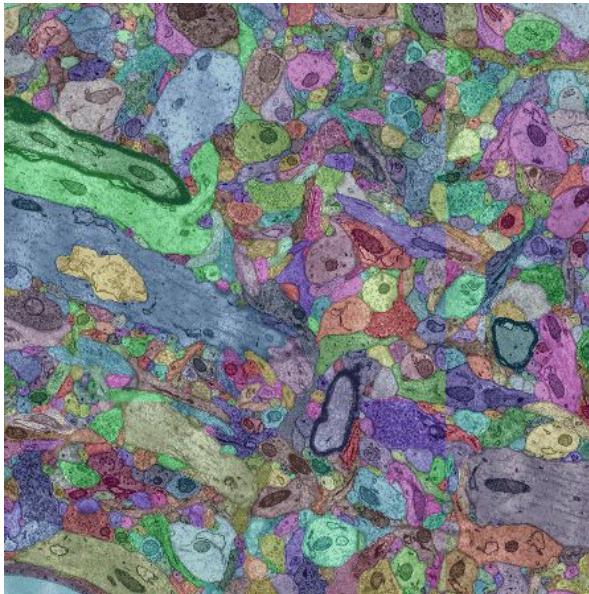
Two voxels have the same label only if they belong to the same neuron



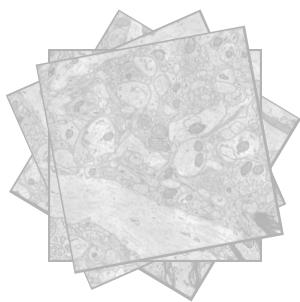
Label Volumes

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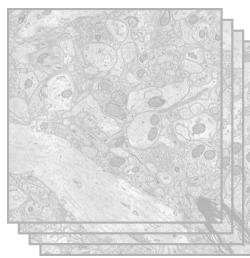
Typically use 64 bits per voxel to label each segment uniquely



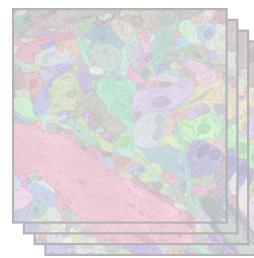
Connectomics Pipeline



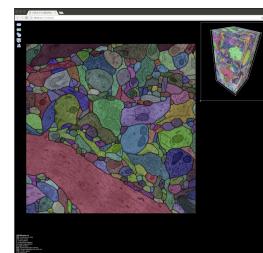
Acquisition



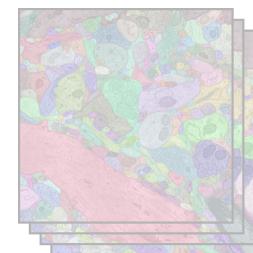
Registration



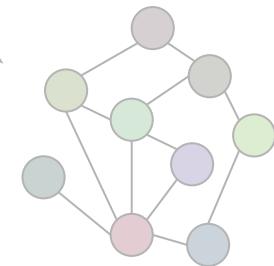
Segmentation



Proofreading



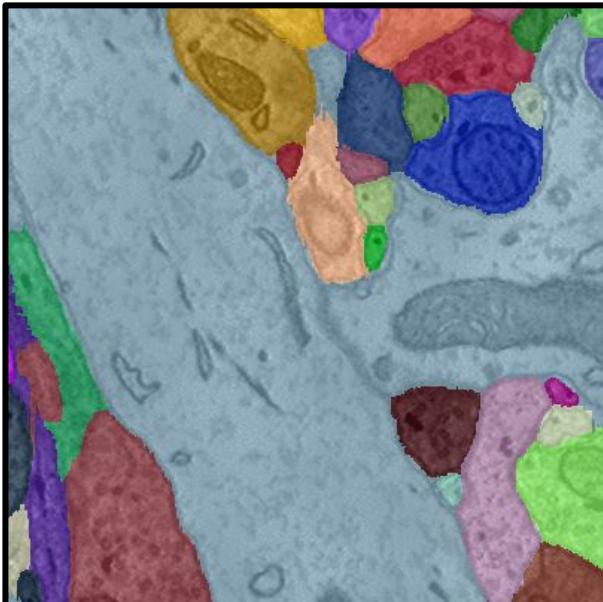
Network Analysis



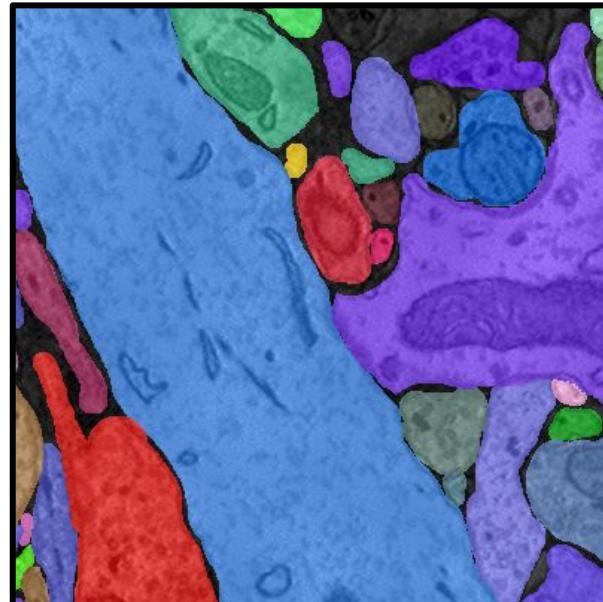
Haehn et al., Design and Evaluation of Interactive Proofreading Tools for Connectomics, IEEE VIS 2014
Zung et al., An Error Detection and Correction Framework for Connectomics, NIPS 2017
Haehn et al., Guided Proofreading of Automatic Segmentations for Connectomics, CVPR 2018

Merge Errors

Automatic Segmentation

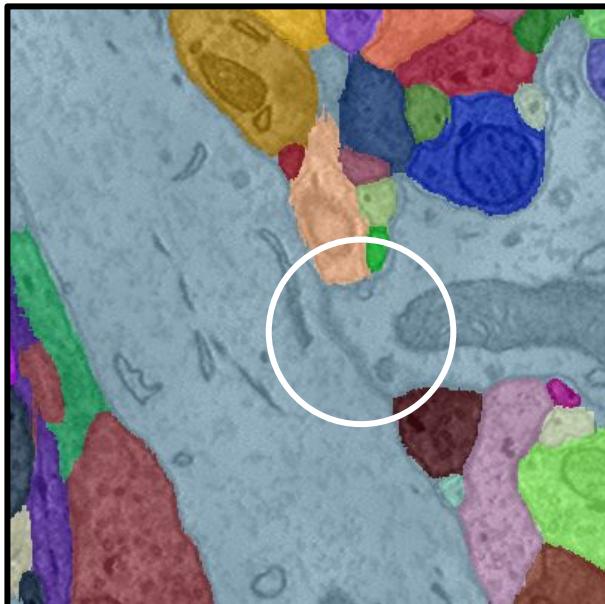


Ground Truth

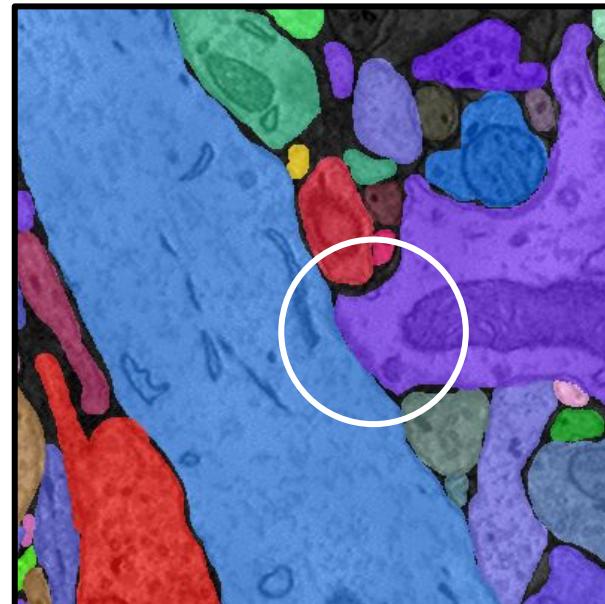


Merge Errors

Automatic Segmentation

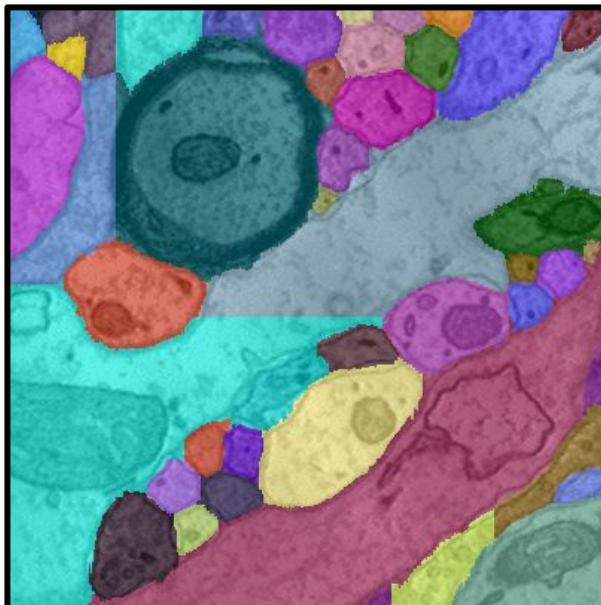


Ground Truth

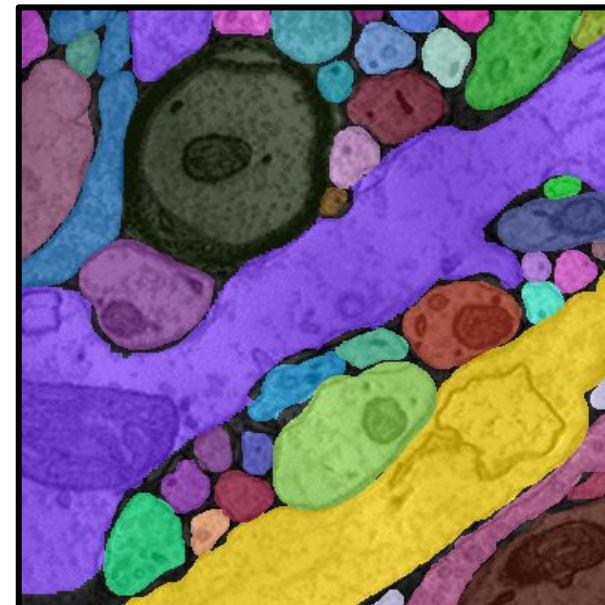


Split Errors

Automatic Segmentation

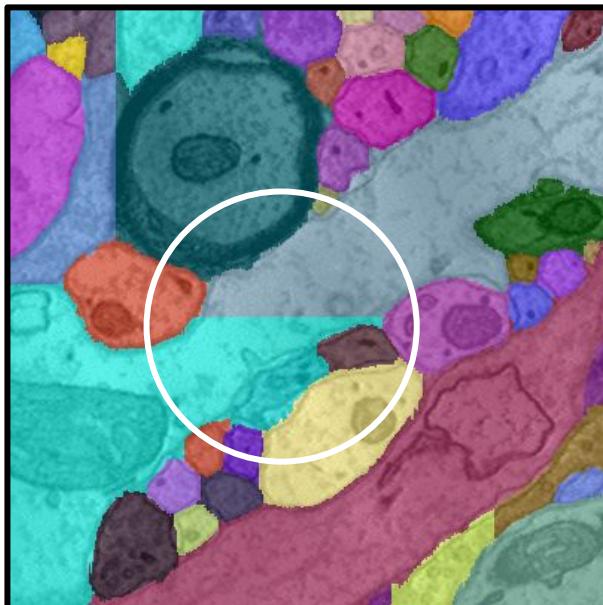


Ground Truth

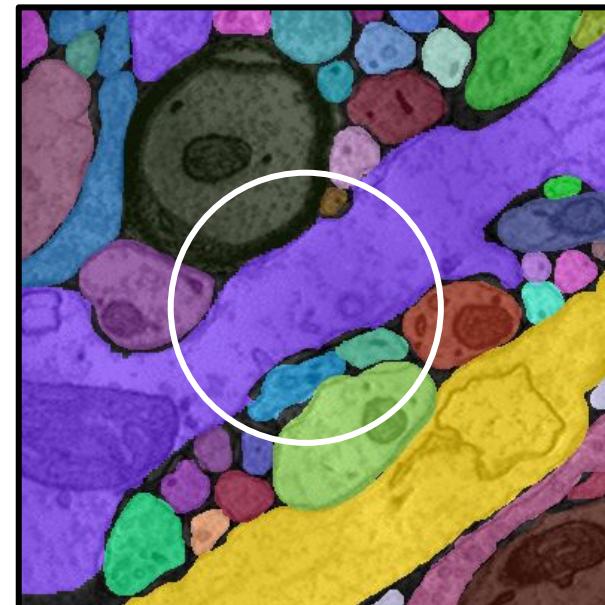


Split Errors

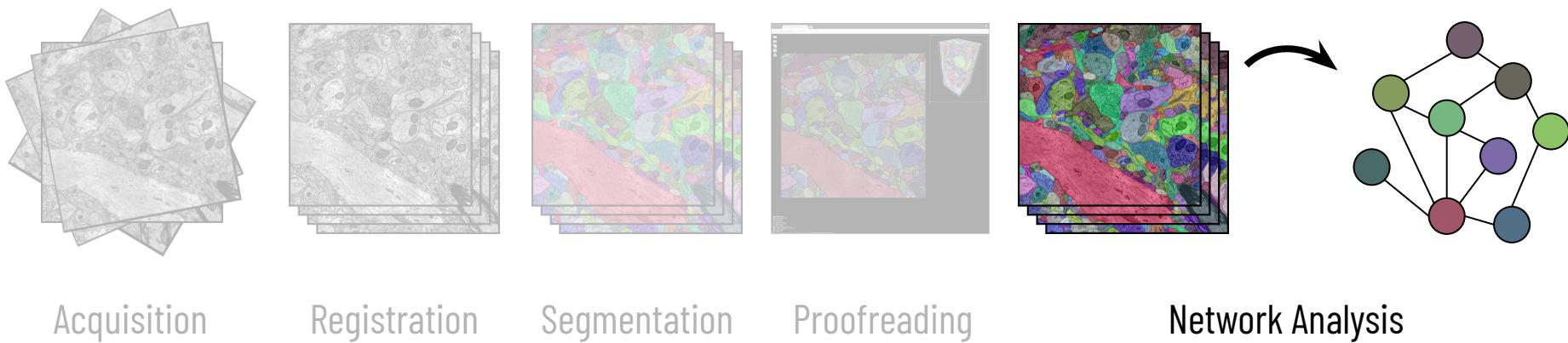
Automatic Segmentation



Ground Truth



Connectomics Pipeline



Acquisition

Registration

Segmentation

Proofreading

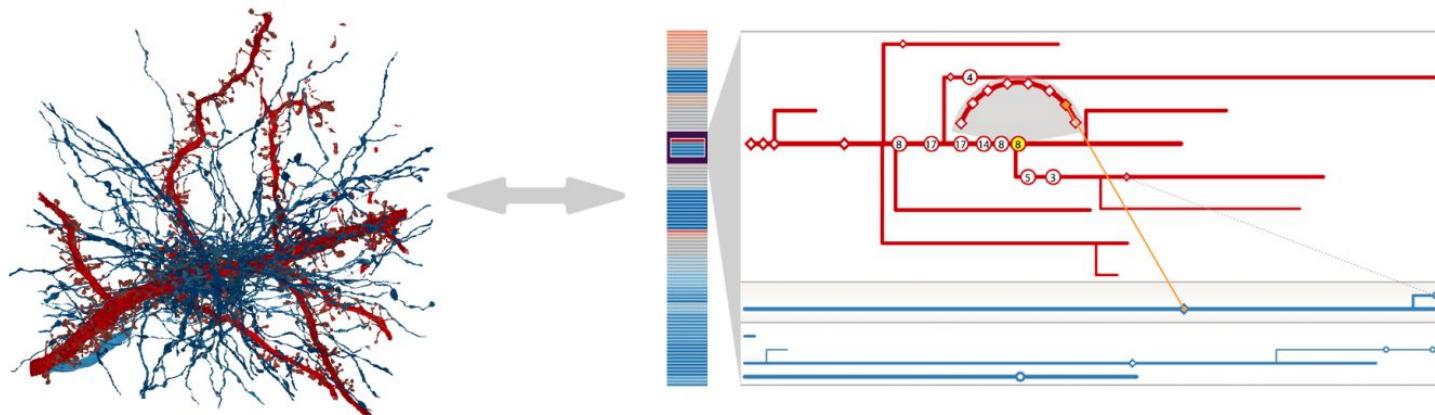
Network Analysis

Sorger et al., neuroMAP - Interactive Graph-Visualization of the Fruit Fly's Neural Circuit, BioVIS 2013

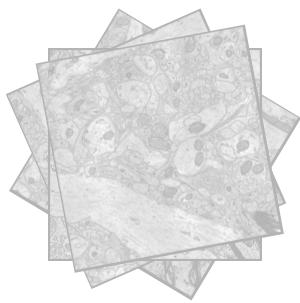
Al-Awami et al., NeuroLines: A Subway Map Metaphor for Visualizing Nanoscale Neuronal Connectivity, IEEE VIS 2014

Haehn et al., Scalable Interactive Visualization for Connectomics, MDPI Informatics 2017

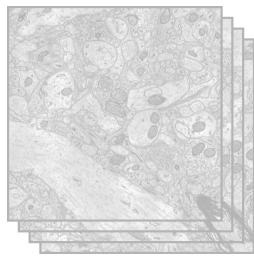
Network Analysis



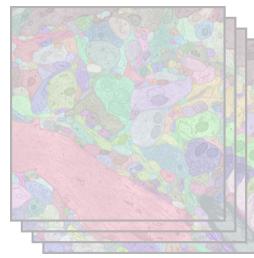
Connectomics Pipeline



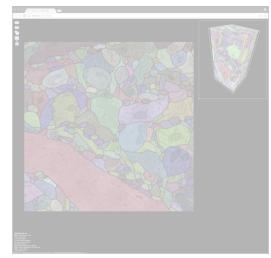
Acquisition



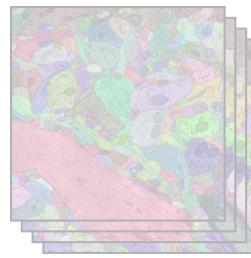
Registration



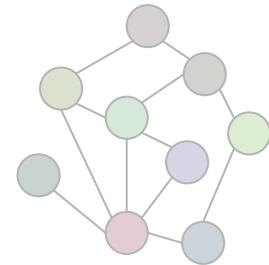
Segmentation



Proofreading

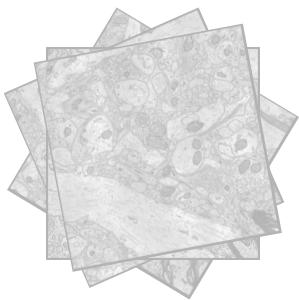


Network Analysis

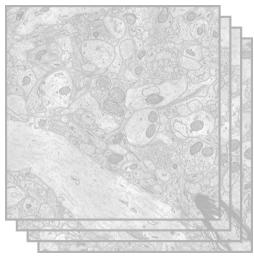


Connectomics Pipeline

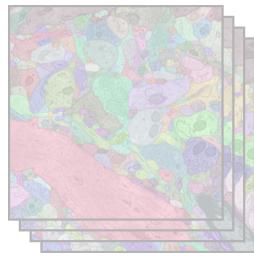
Compression



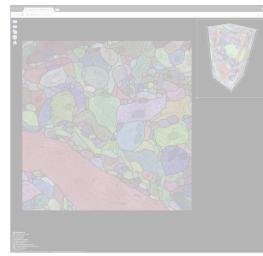
Acquisition



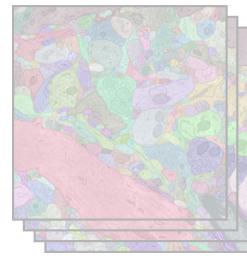
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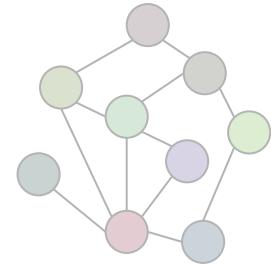
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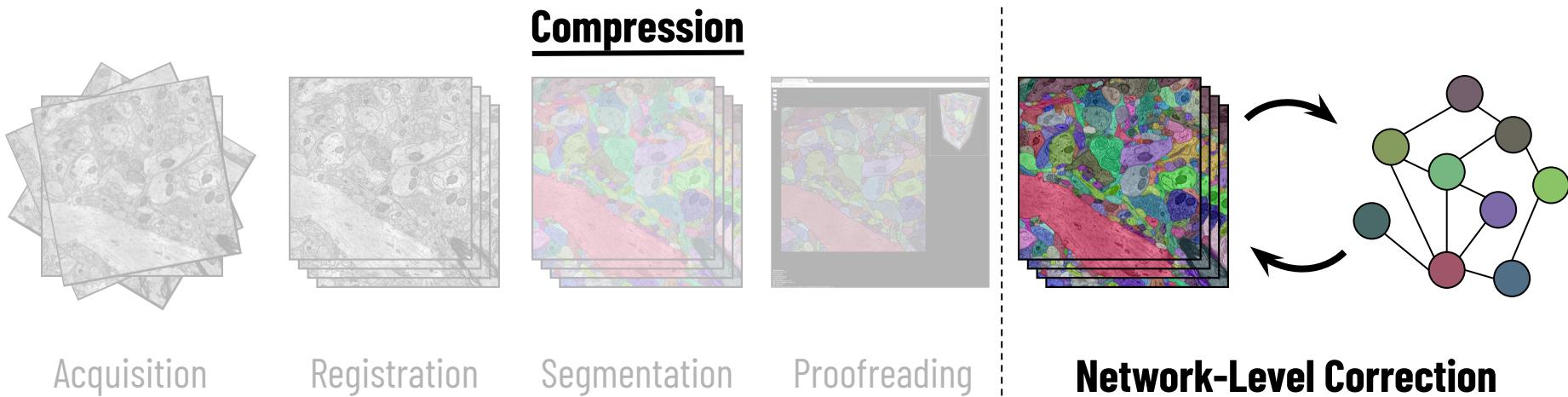
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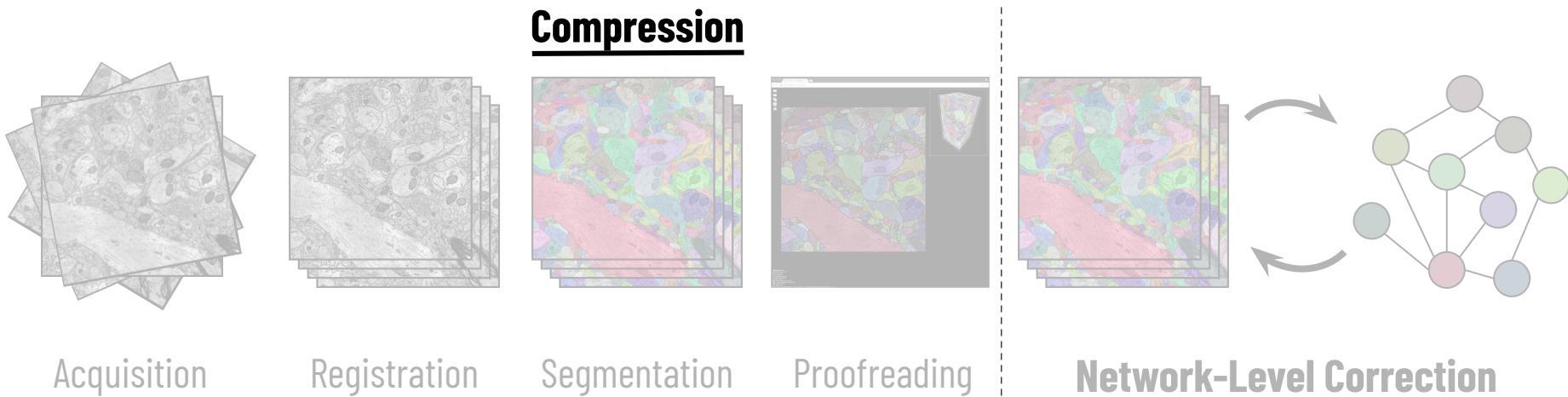
Network Analysis



Connectomics Pipeline

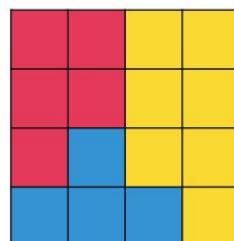


Connectomics Pipeline



Compresso: Efficient Compression of Segmentation Data for Connectomics

Brian Matejek, Daniel Haehn, Fritz Lekschas, Michael Mitzenmacher, Hanspeter Pfister



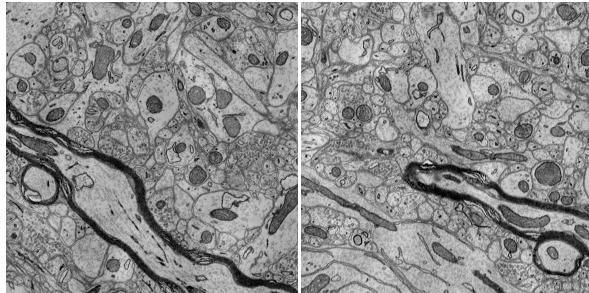
0	1	2	3
4	5	6	7
8	9	10	11
12	13	14	15

$$\sum_{i=0}^{n-1} \mathbb{I}(i)2^i$$

$$2^1 + 2^5 + 2^8 + 2^9 + 2^{10} + 2^{14} + 2^{15} = 50978$$

Increasing Scales of Challenge Datasets

SNEMI

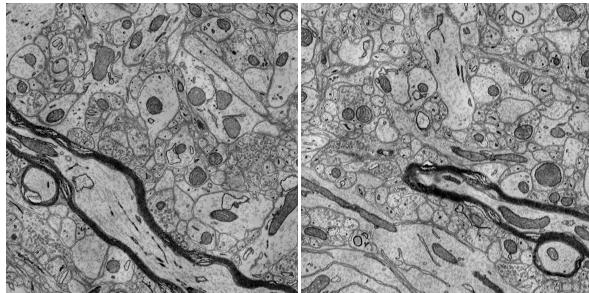


210 MB

2013

Increasing Scales of Challenge Datasets

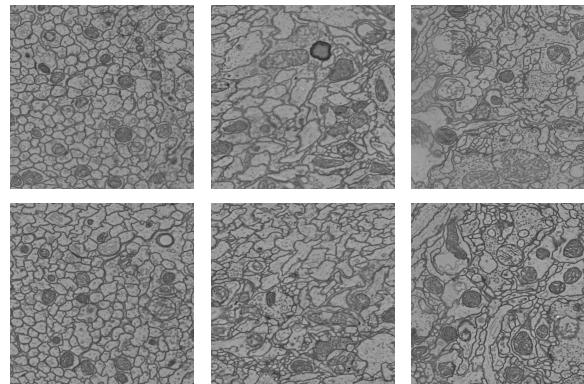
SNEMI



210 MB

2013

CREMI

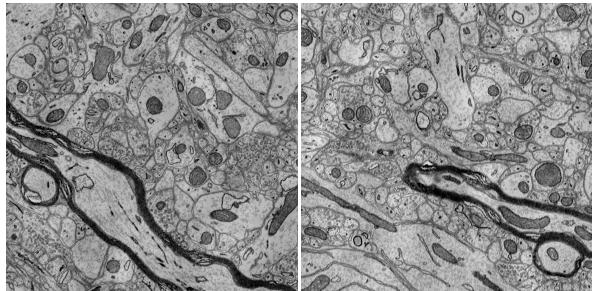


1.2 GB

2016

Increasing Scales of Challenge Datasets

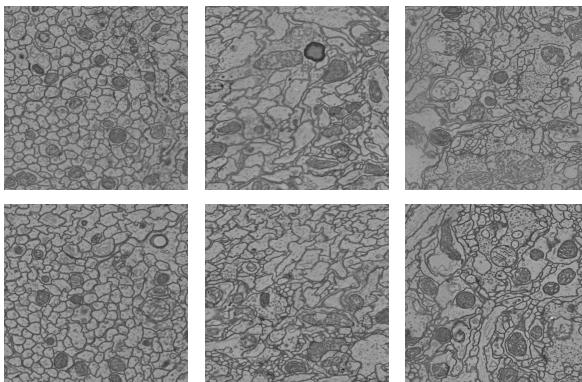
SNEMI



210 MB

2013

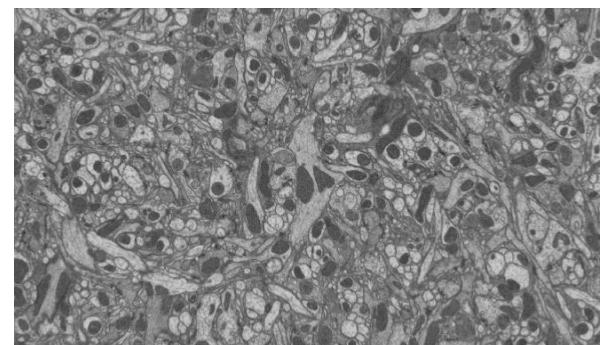
CREMI



1.2 GB

2016

FIB-25

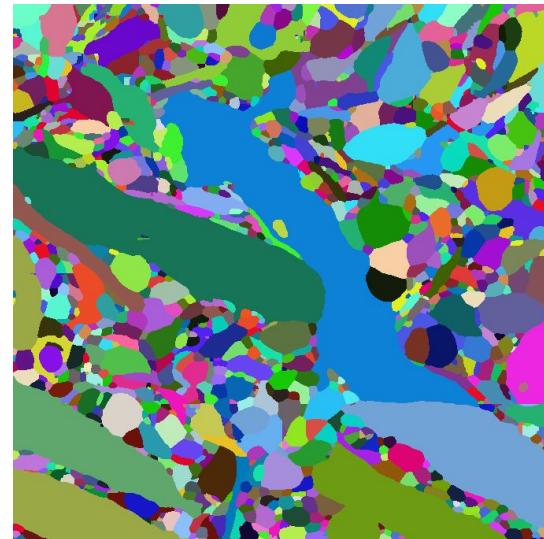


15.7 GB

2017

Connectomics Label Volumes

Large invariant regions without natural relationships between labels

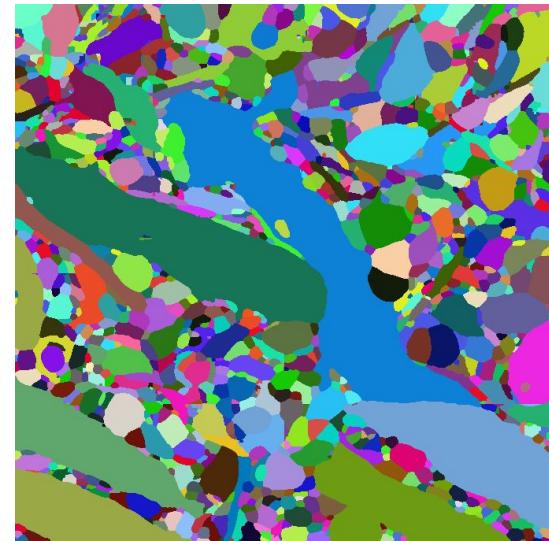


Existing Compression Schemes

General-purpose compression schemes

BZ2, GZIP, LZMA, LZW, ZLIB, etc.

Not optimized for these unique label volumes



Existing Compression Schemes

General-purpose compression schemes

BZ2, GZIP, LZMA, LZW, ZLIB, etc.

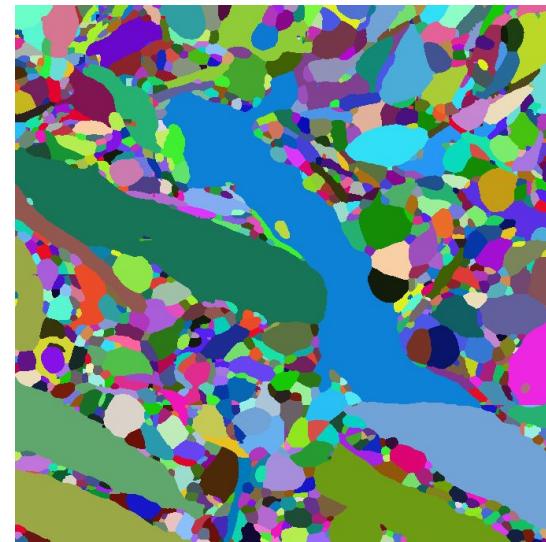
Not optimized for these unique label volumes

Image compression schemes

JPEG, JPEG2000, PNG, etc.

Rely on frequency reduction and value prediction

Not useful with large invariant regions



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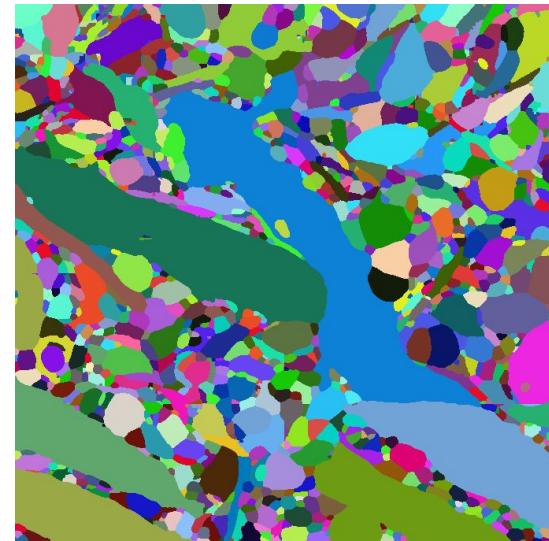
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Video compression schemes

H.264, H.265, MPEG, etc.

Color space optimizations do not translate



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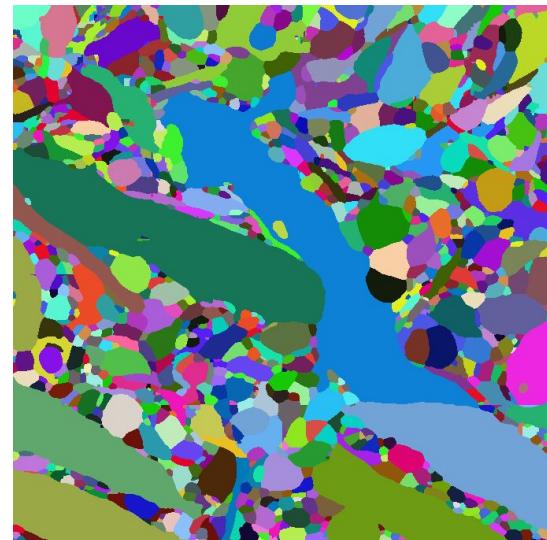
Video compression schemes

H.264, H.265, MPEG, etc.

Color space optimizations do not translate

Neuroglancer compression scheme

Specifically designed for label volumes



Neuroglancer

Specifically designed for label volumes

Exploits homogeneity by creating small blocks with N labels

Reduces local entropy to $\log_2(N)$

Lookup tables decode the values $[0, N)$ to the original 64-bit labels

Blocks are typically 8x8x8 voxels each



Google Open Source

<https://opensource.google.com/projects/neuroglancer>

Compression

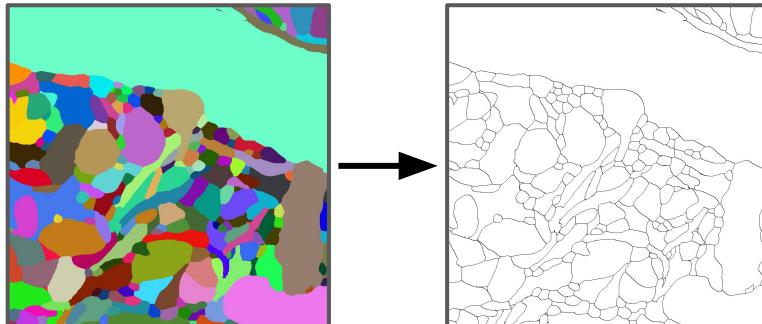
Compresso Overview

Lossless compression

Compresso Overview

Lossless compression

Decouple per-segment shapes and per-pixel labels

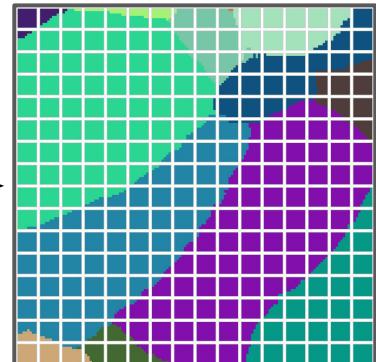
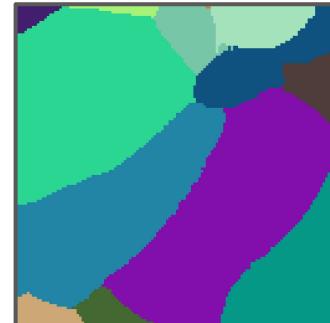
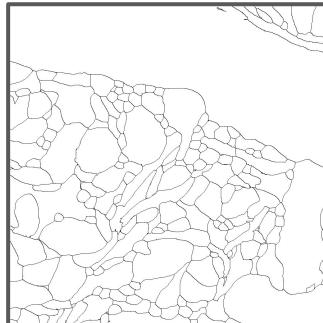
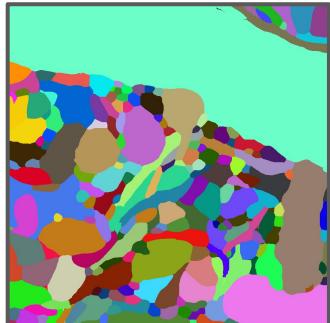


Compresso Overview

Lossless compression

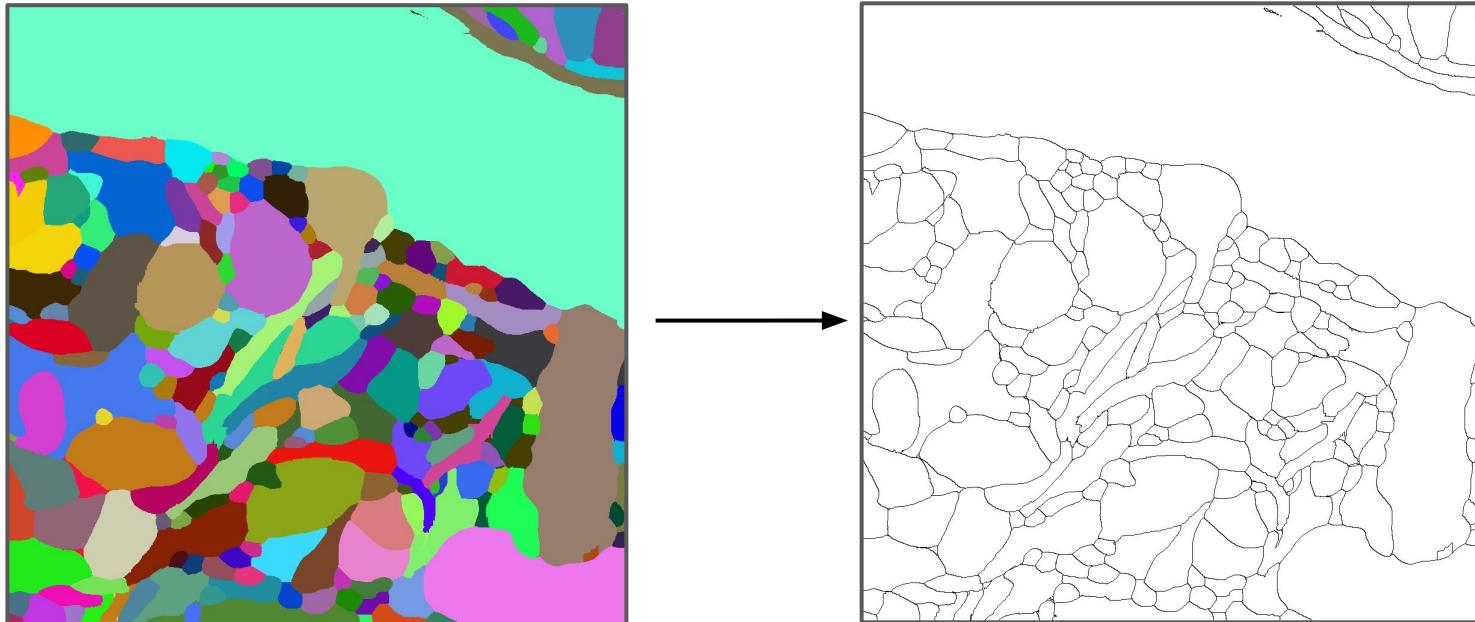
Decouple per-segment shapes and per-pixel labels

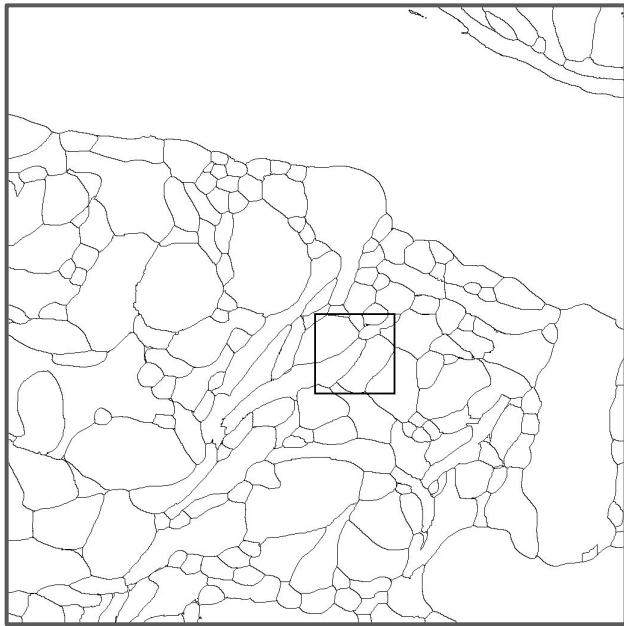
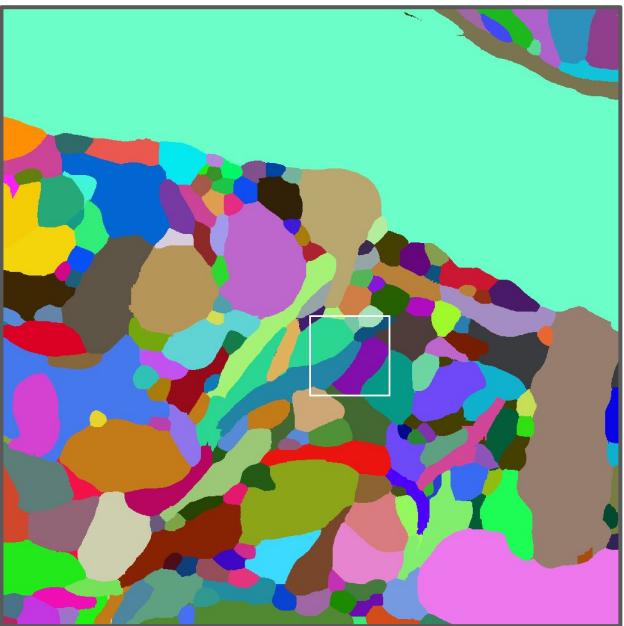
Divide the volume into non-overlapping congruent 3D windows



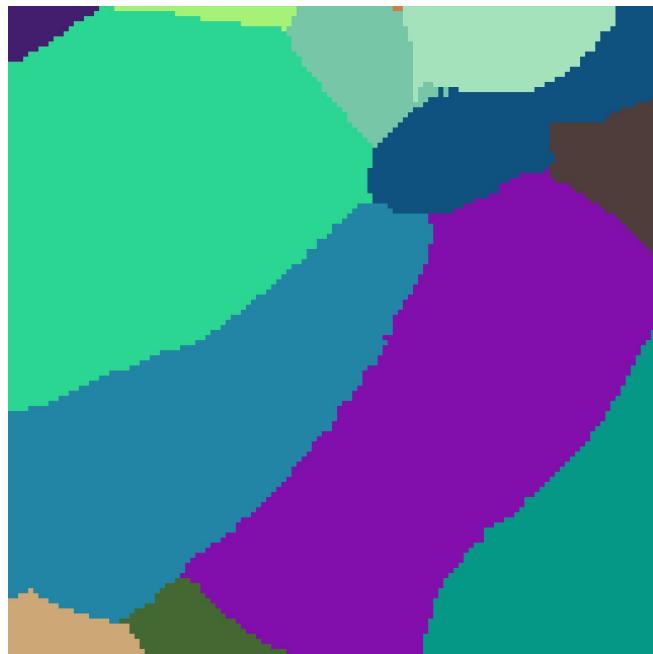
Boundary Map Generation

A pixel (x, y, z) is 1 if its neighbor $(x + 1, y, z)$ or $(x, y + 1, z)$ belongs to a different segment



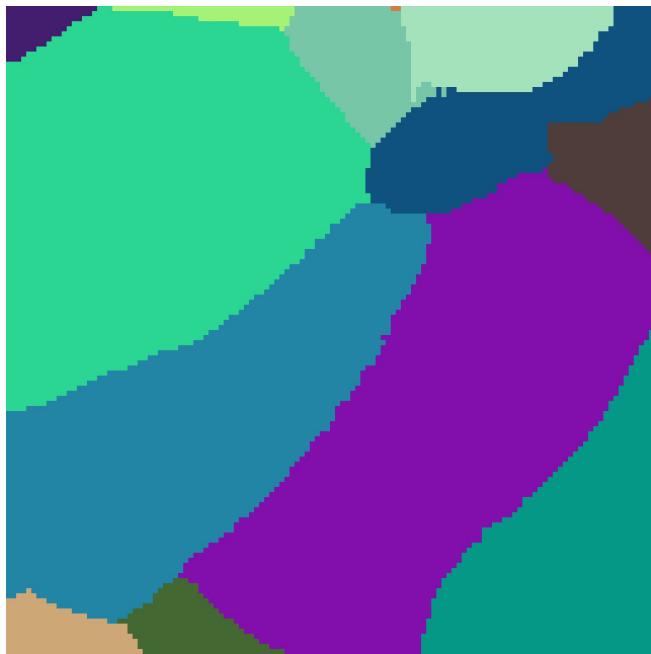


Boxed region divided into congruent windows

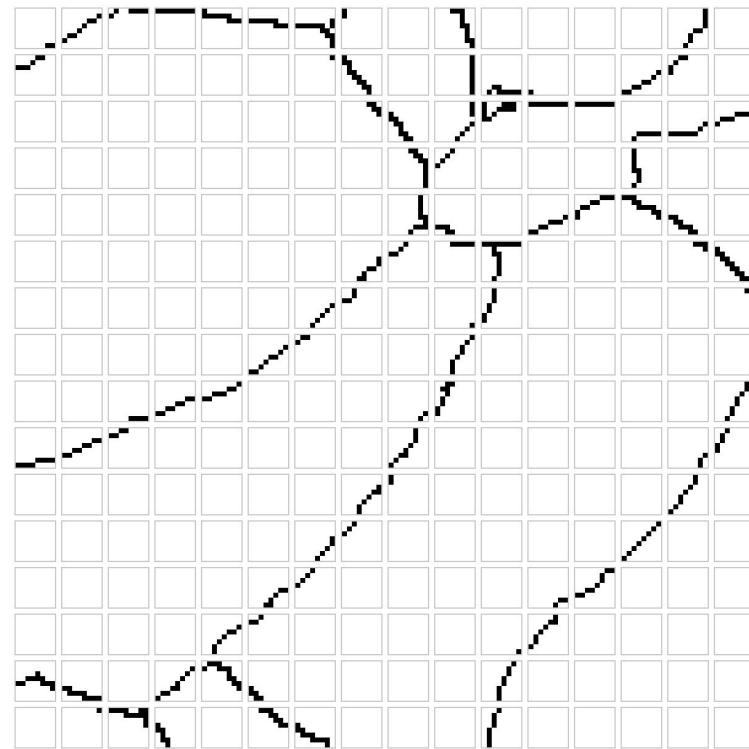
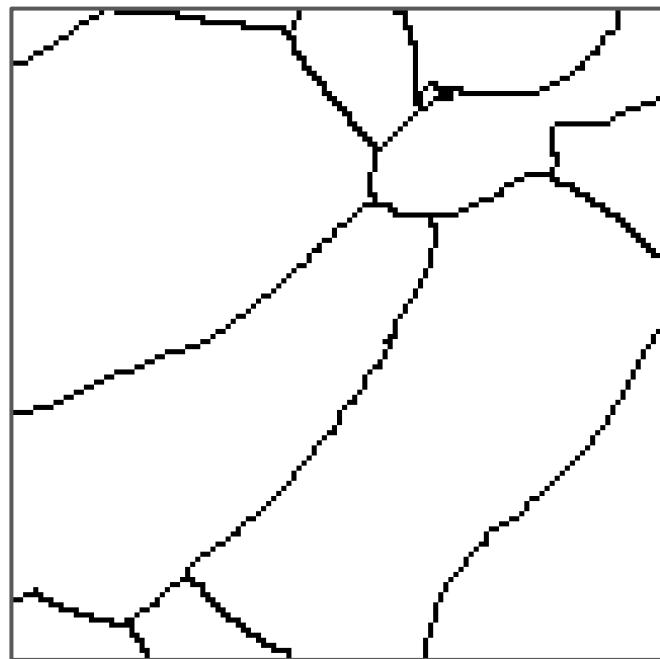


Boxed region divided into congruent windows

Each window is $8 \times 8 \times 1$ voxels

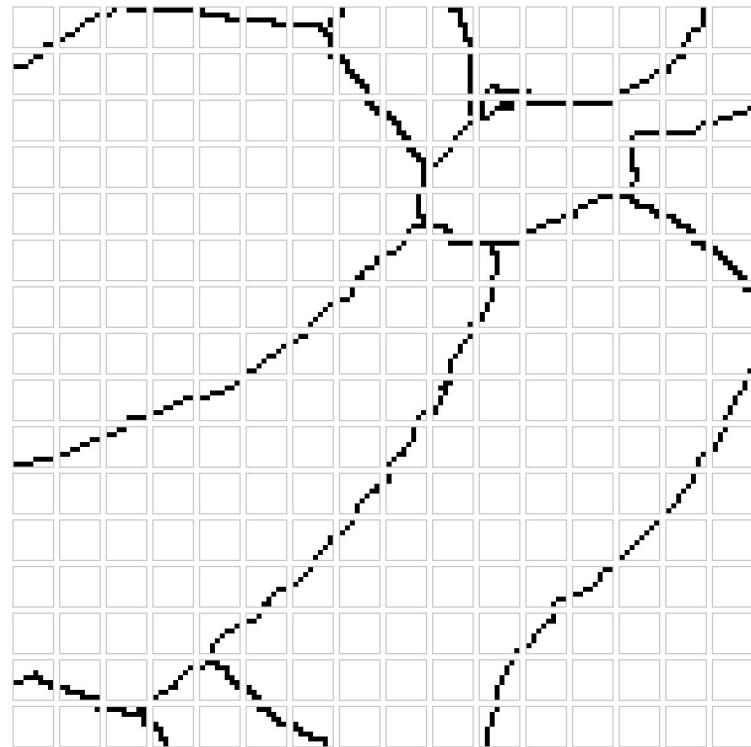
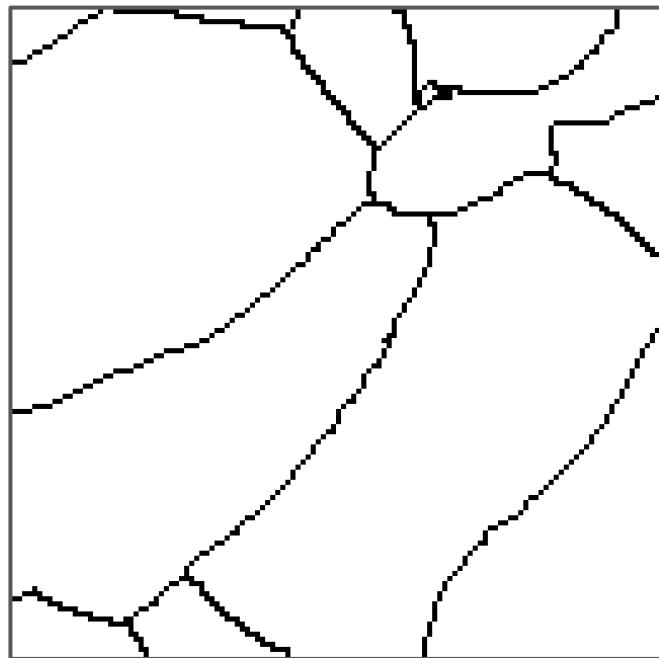


Accompanying boundary map

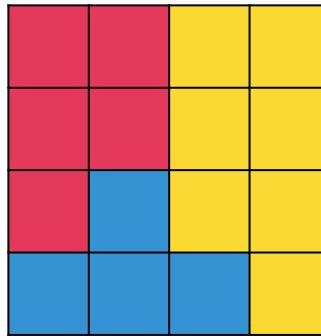


Accompanying boundary map

Goal: Store one 64-bit integer per window



Assigning Values to Windows

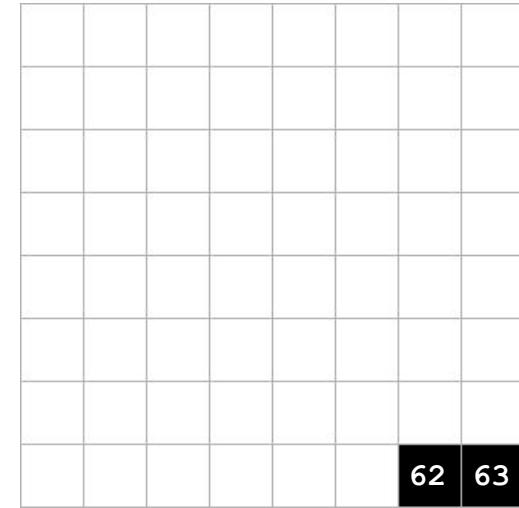
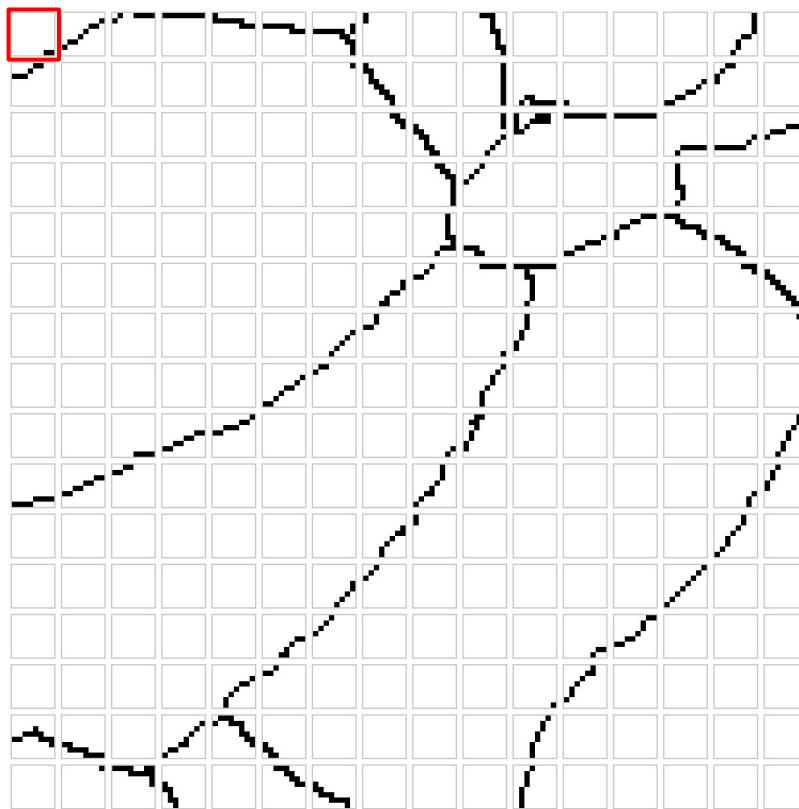


0	1	2	3
4	5	6	7
8	9	10	11
12	13	14	15

$$\sum_{i=0}^{n-1} \mathbb{I}(i)2^i$$

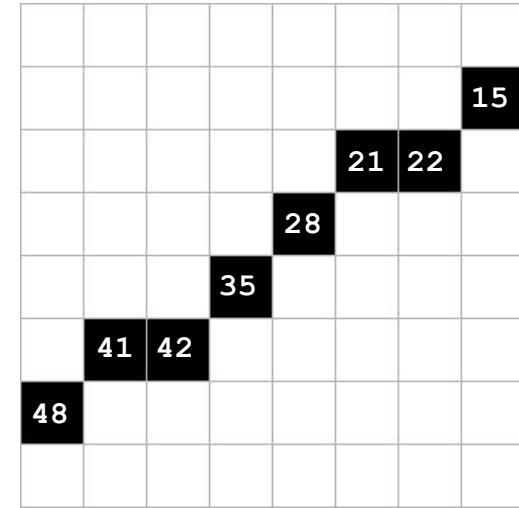
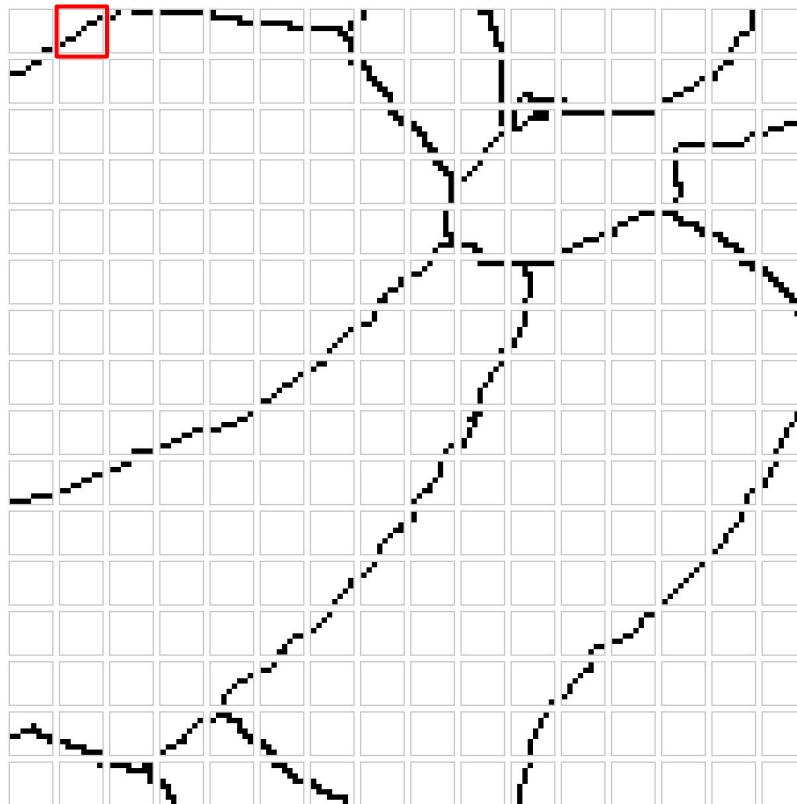
$$2^1 + 2^5 + 2^8 + 2^9 + 2^{10} + 2^{14} + 2^{15} = 50978$$

Boundary Encoding



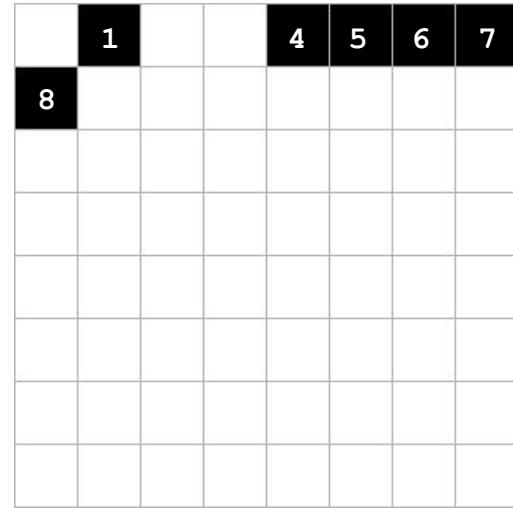
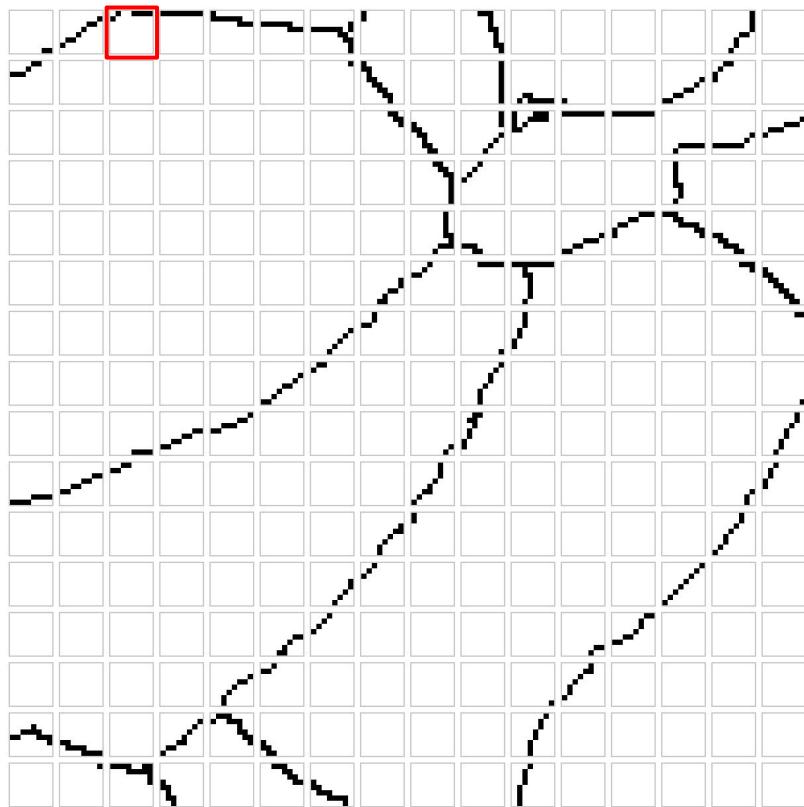
$$2^{62} + 2^{63} = 13835058055282163712$$

Boundary Encoding



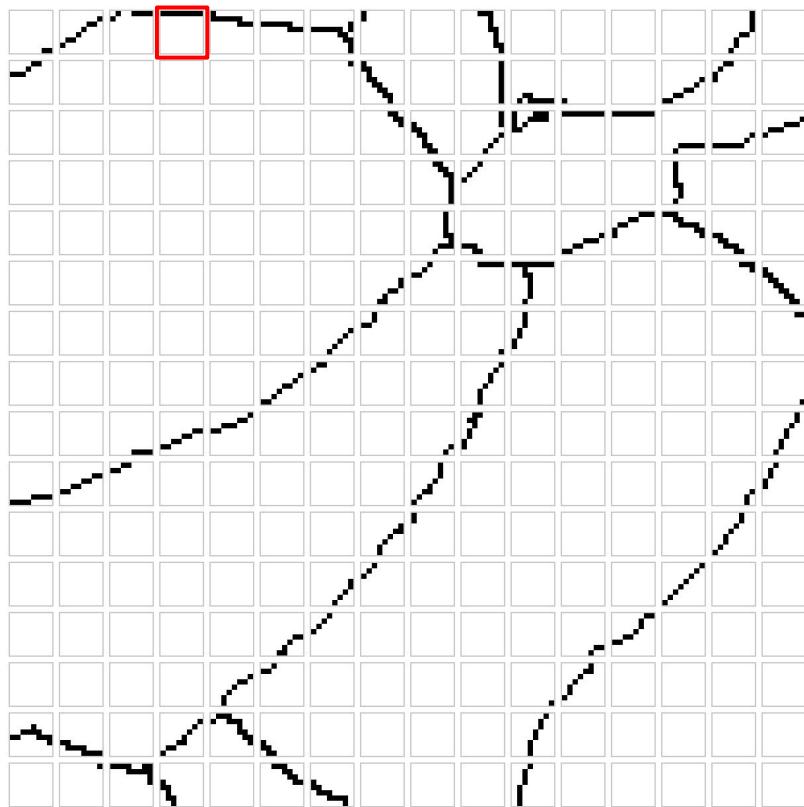
$$2^{15} + 2^{21} + 2^{22} + 2^{28} + 2^{35} + 2^{41} + 2^{42} + 2^{48} = \\ 288106680975360$$

Boundary Encoding



$$2^1 + 2^4 + 2^5 + 2^6 + 2^7 + 2^8 = 498$$

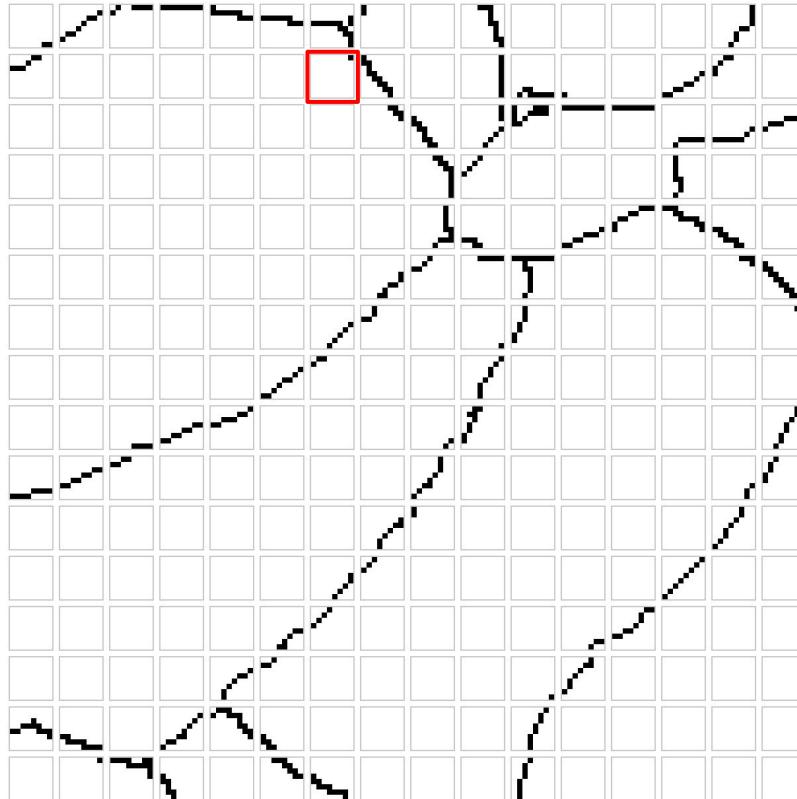
Boundary Encoding



0	1	2	3	4	5	6	7

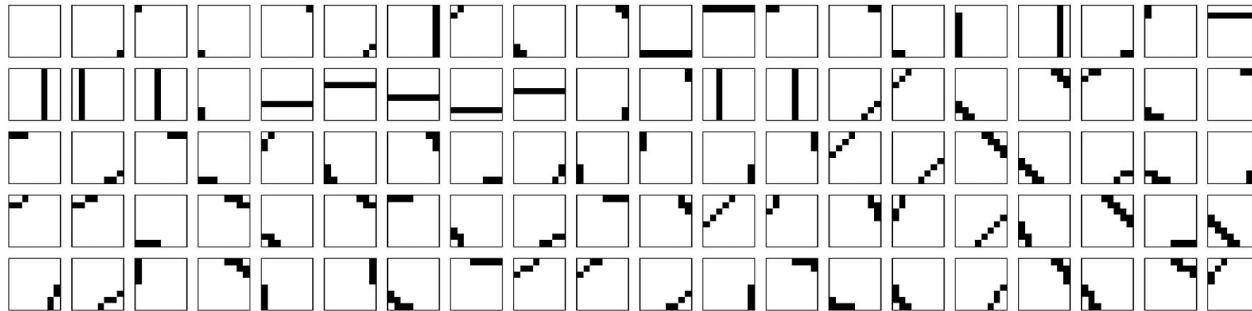
$$2^0 + 2^1 + 2^2 + 2^3 + 2^4 + 2^5 + 2^6 + 2^7 = 255$$

Boundary Encoding



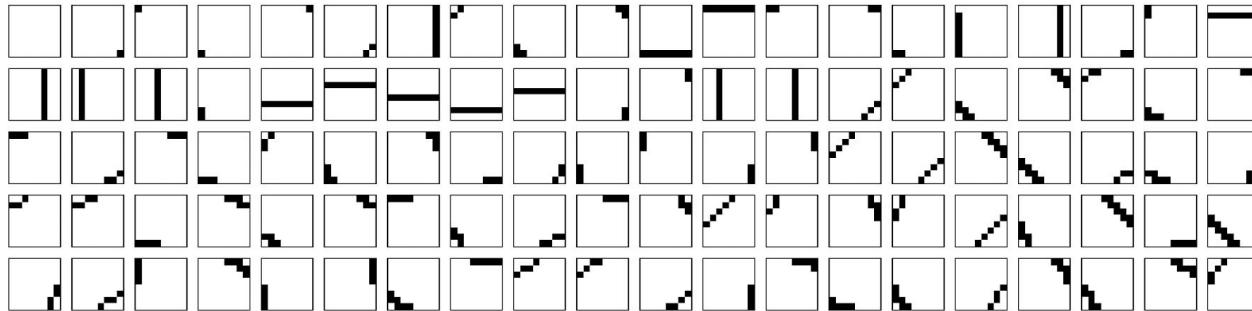
13835058055282163712
288106680975360
498
255
14696193
3762225152
9259612355635970048
257
0
9277485877618024504
0
0
0
0
580982358589603968
0
460848
0
0
0
0
0
128
•
•
•

Window Repetition



These 100 windows account for over 82% of all windows on a representative connectomics dataset

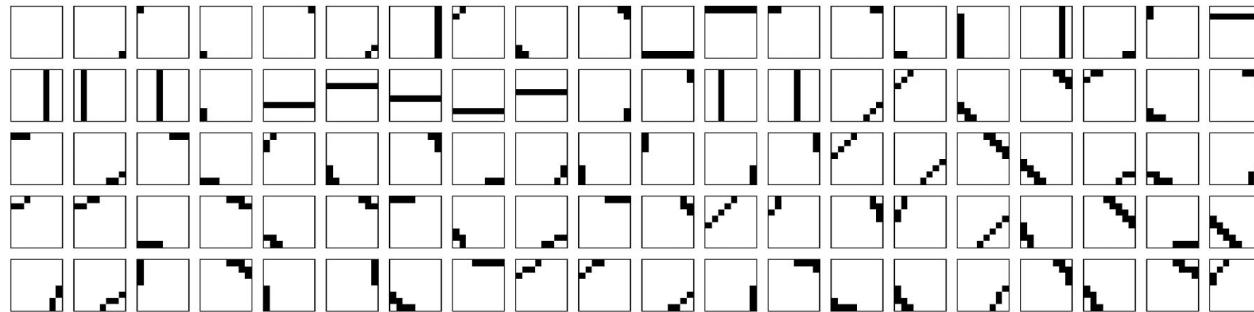
Window Repetition



These 100 windows account for over 82% of all windows on a representative connectomics dataset

Typically there are only 100,000 unique windows in a given label volume

Window Repetition



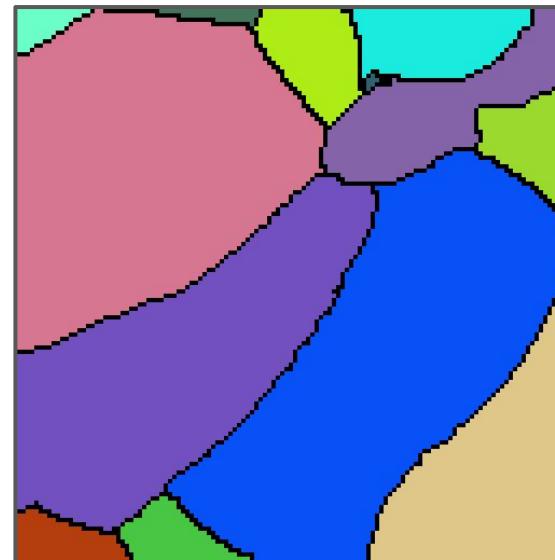
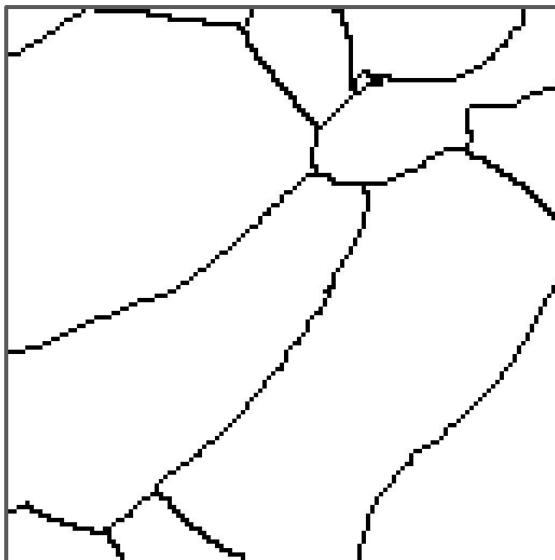
These 100 windows account for over 82% of all windows on a representative connectomics dataset

Typically there are only 100,000 unique windows in a given label volume

Map window values to this smaller subset to use 3 bytes per window

Compressing Per-Pixel Labels

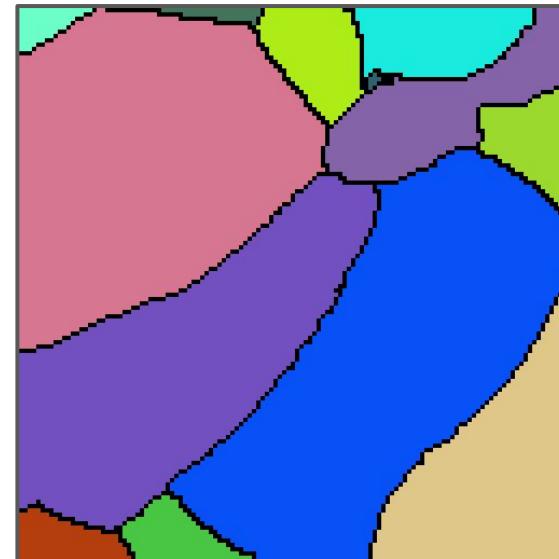
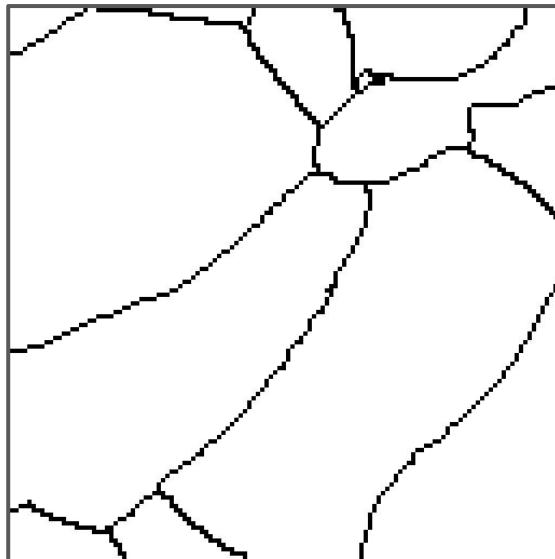
Goal: Store one 64-bit label per component



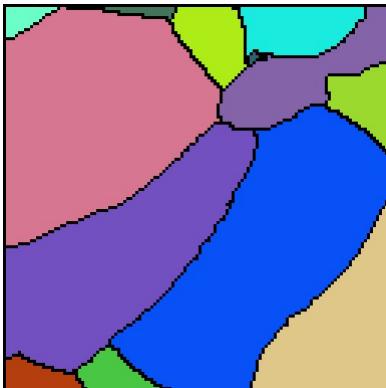
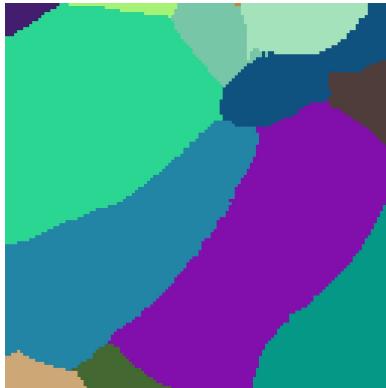
Compressing Per-Pixel Labels

Goal: Store one 64-bit label per component

Solution: Identify continuous regions using a connected components algorithm

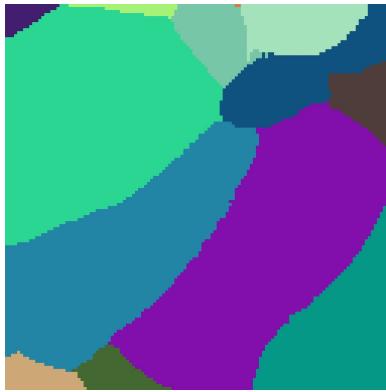


Per-Pixel Label Encoding

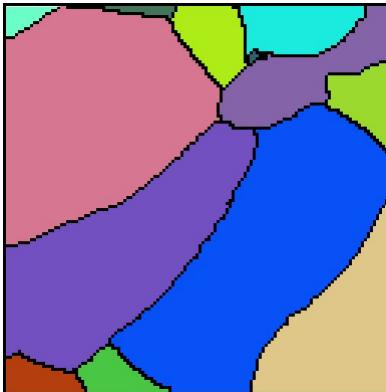


1 \longrightarrow 1381

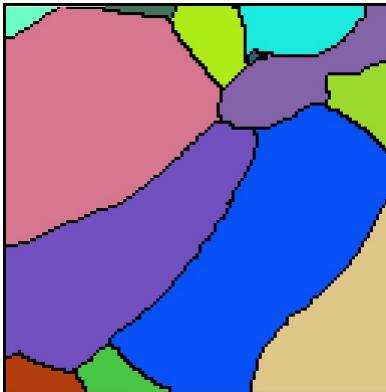
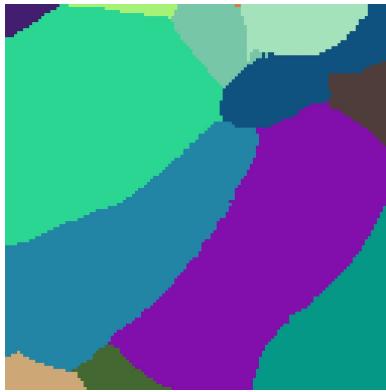
Per-Pixel Label Encoding



1  →  1381
2  →  836

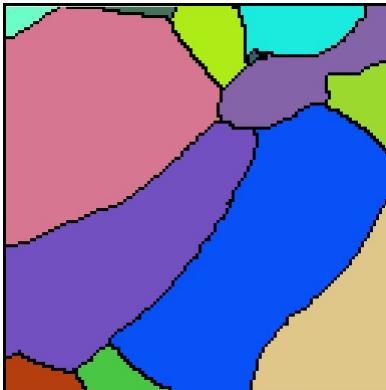
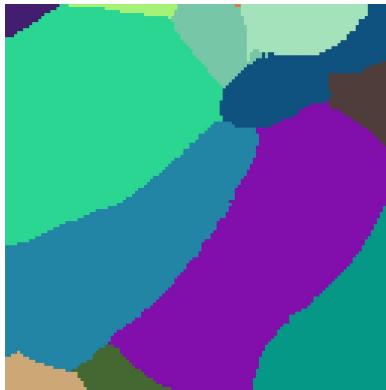


Per-Pixel Label Encoding



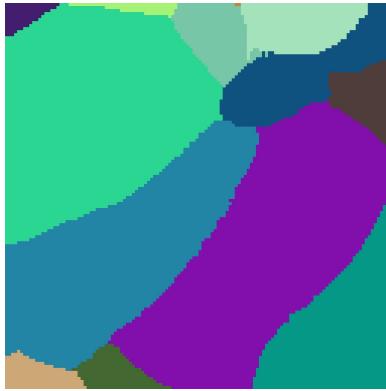
1	■	→	■	1381
2	■	→	■	836
3	■	→	■	538

Per-Pixel Label Encoding

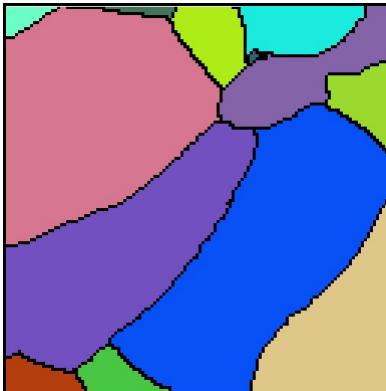


1		→		1381
2		→		836
3		→		538
4		→		1617

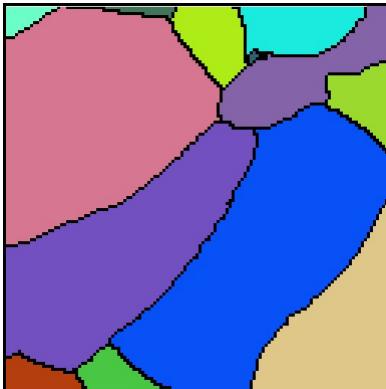
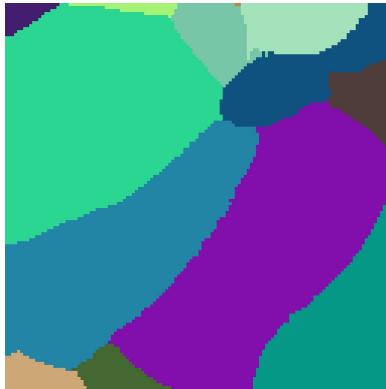
Per-Pixel Label Encoding



1	→	1381
2	→	836
3	→	538
4	→	1617
5	→	1709

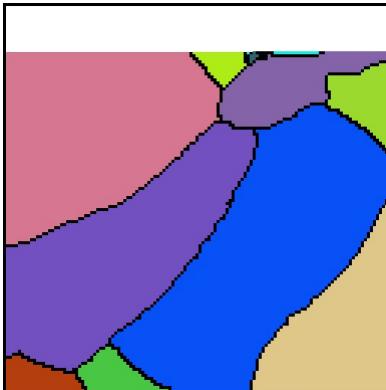
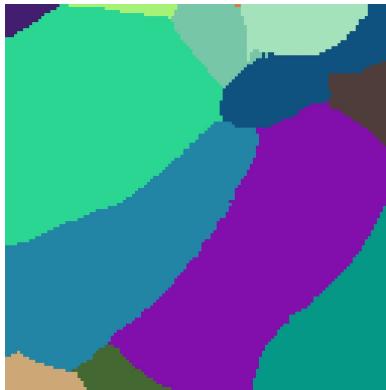


Per-Pixel Label Encoding



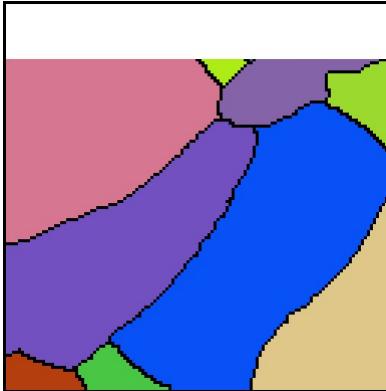
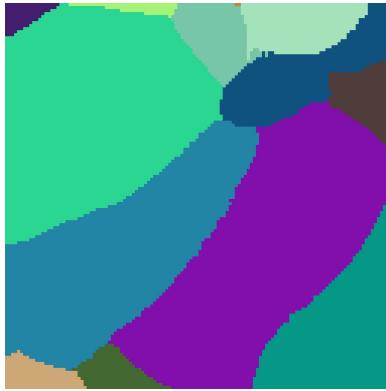
1	→	1381
2	→	836
3	→	538
4	→	1617
5	→	1709
6	→	1688

Per-Pixel Label Encoding



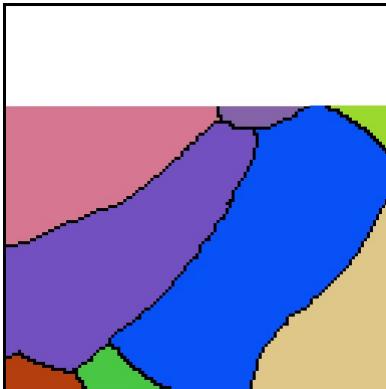
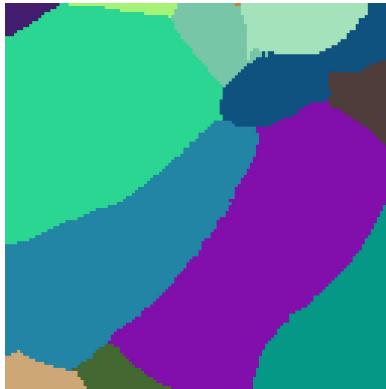
1	■	→	■	1381
2	■	→	■	836
3	■	→	■	538
4	■	→	■	1617
5	■	→	■	1709
6	■	→	■	1688
7	■	→	■	1617

Per-Pixel Label Encoding



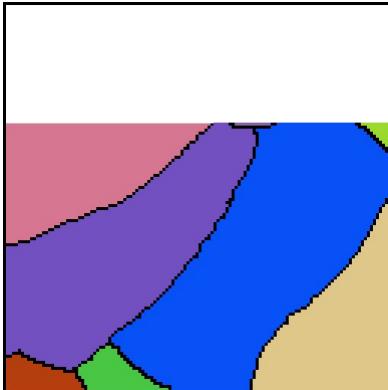
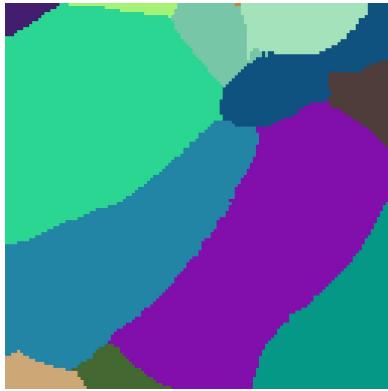
1	■	→	■	1381
2	■	→	■	836
3	■	→	■	538
4	■	→	■	1617
5	■	→	■	1709
6	■	→	■	1688
7	■	→	■	1617
8	■	→	■	1619

Per-Pixel Label Encoding



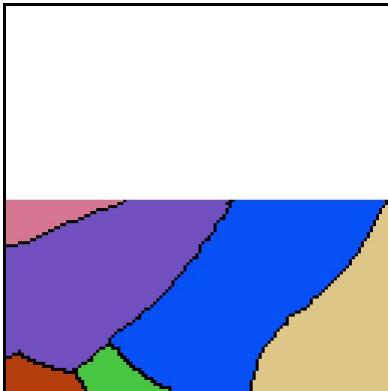
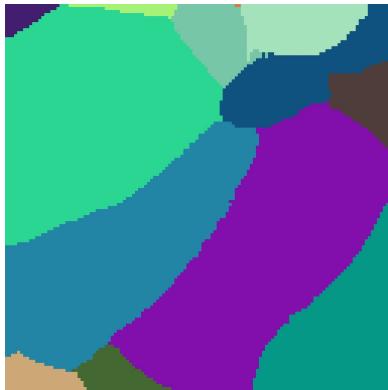
1	■	→	1381
2	■	→	836
3	■	→	538
4	■	→	1617
5	■	→	1709
6	■	→	1688
7	■	→	1617
8	■	→	1619
9	■	→	1020

Per-Pixel Label Encoding



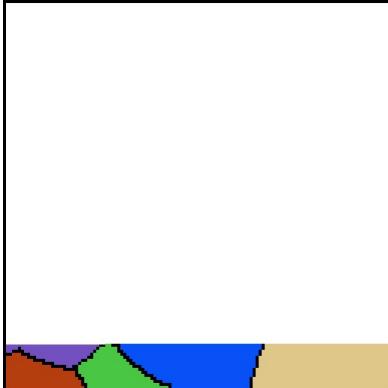
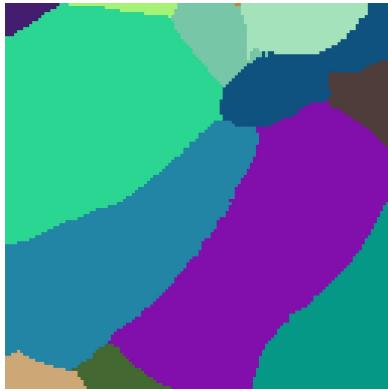
1	■	→	■	1381
2	■	→	■	836
3	■	→	■	538
4	■	→	■	1617
5	■	→	■	1709
6	■	→	■	1688
7	■	→	■	1617
8	■	→	■	1619
9	■	→	■	1020
10	■	→	■	827

Per-Pixel Label Encoding



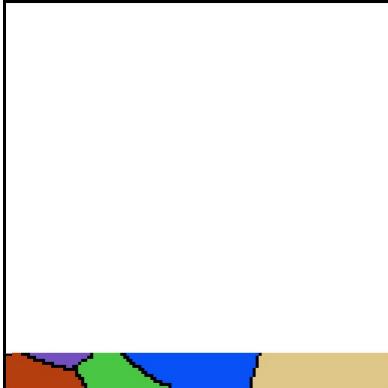
1	■	→	■	1381
2	■	→	■	836
3	■	→	■	538
4	■	→	■	1617
5	■	→	■	1709
6	■	→	■	1688
7	■	→	■	1617
8	■	→	■	1619
9	■	→	■	1020
10	■	→	■	827
11	■	→	■	1723

Per-Pixel Label Encoding



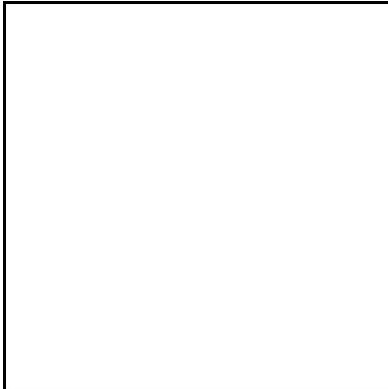
1	■	→	■	1381
2	■	→	■	836
3	■	→	■	538
4	■	→	■	1617
5	■	→	■	1709
6	■	→	■	1688
7	■	→	■	1617
8	■	→	■	1619
9	■	→	■	1020
10	■	→	■	827
11	■	→	■	1723
12	■	→	■	1246

Per-Pixel Label Encoding



1	■	→	■	1381
2	■	→	■	836
3	■	→	■	538
4	■	→	■	1617
5	■	→	■	1709
6	■	→	■	1688
7	■	→	■	1617
8	■	→	■	1619
9	■	→	■	1020
10	■	→	■	827
11	■	→	■	1723
12	■	→	■	1246
13	■	→	■	1258

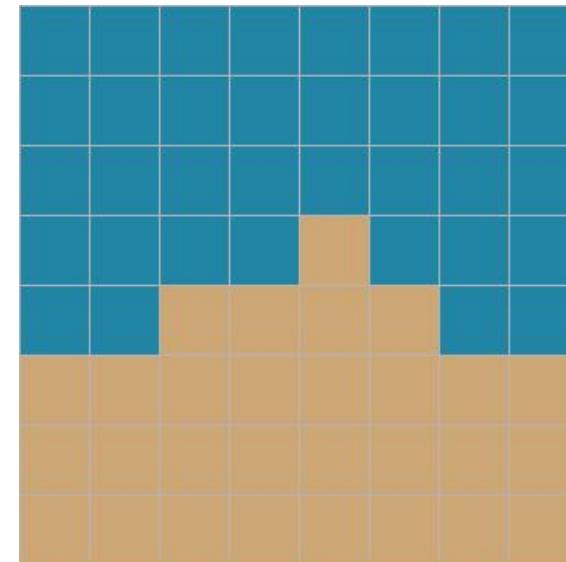
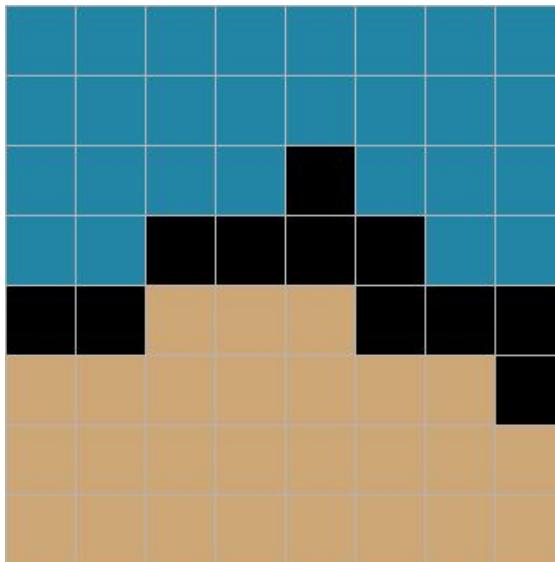
Per-Pixel Label Encoding



1	■	→	■	1381
2	■	→	■	836
3	■	→	■	538
4	■	→	■	1617
5	■	→	■	1709
6	■	→	■	1688
7	■	→	■	1617
8	■	→	■	1619
9	■	→	■	1020
10	■	→	■	827
11	■	→	■	1723
12	■	→	■	1246
13	■	→	■	1258

Indeterminate Locations

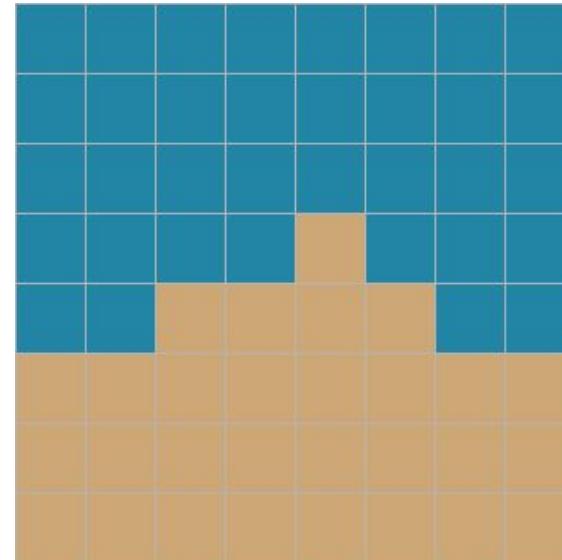
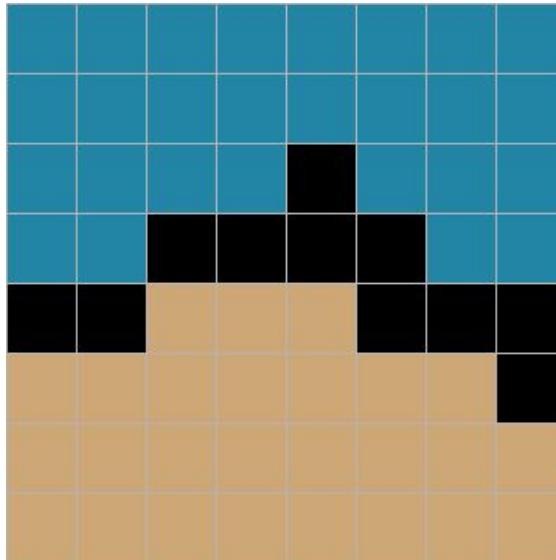
So far, we assumed the boundary map and connected component mapping is enough for decompression



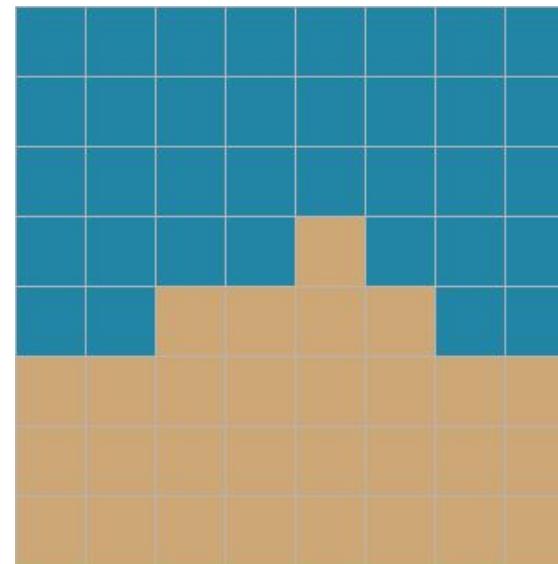
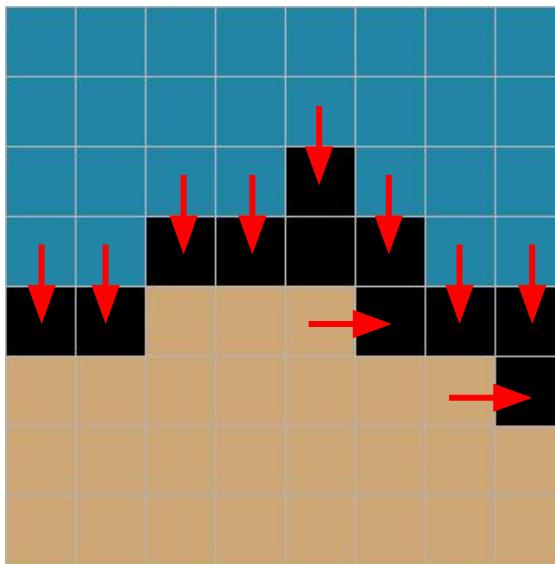
Indeterminate Locations

So far, we assumed the boundary map and connected component mapping is enough for decompression

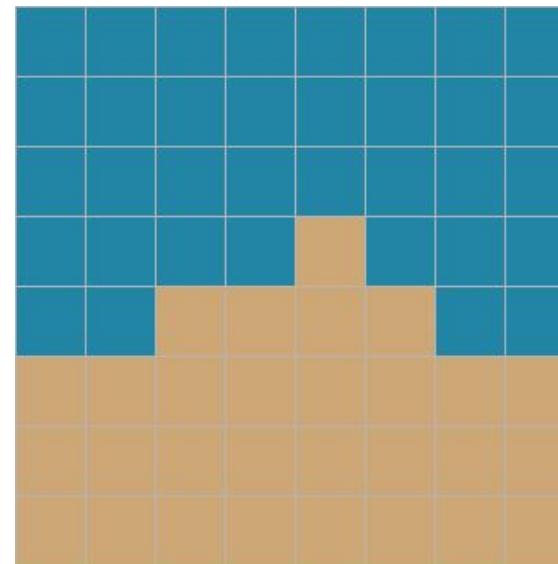
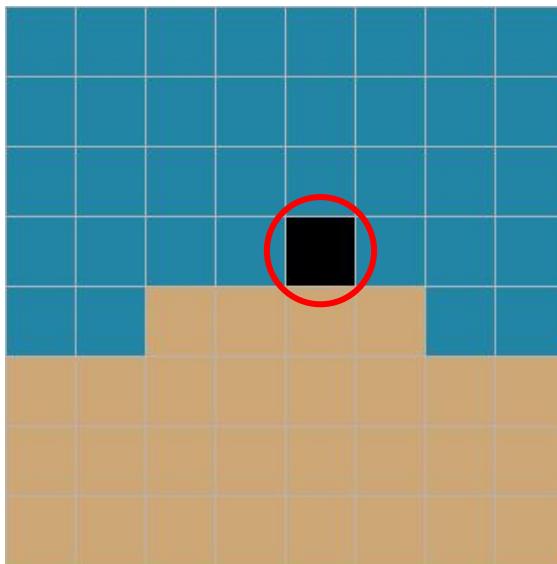
One additional corner case to consider:



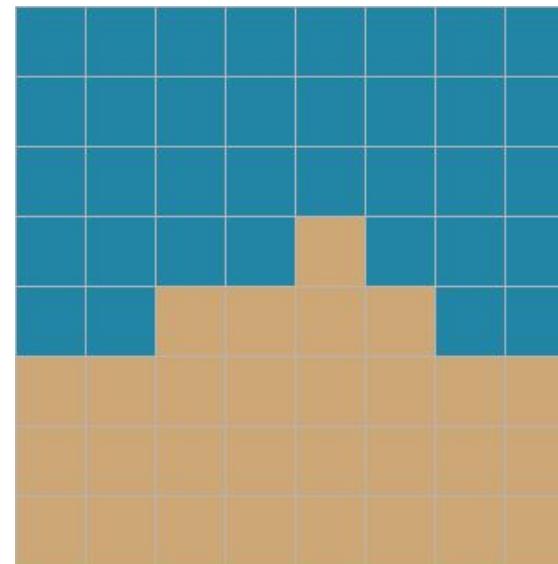
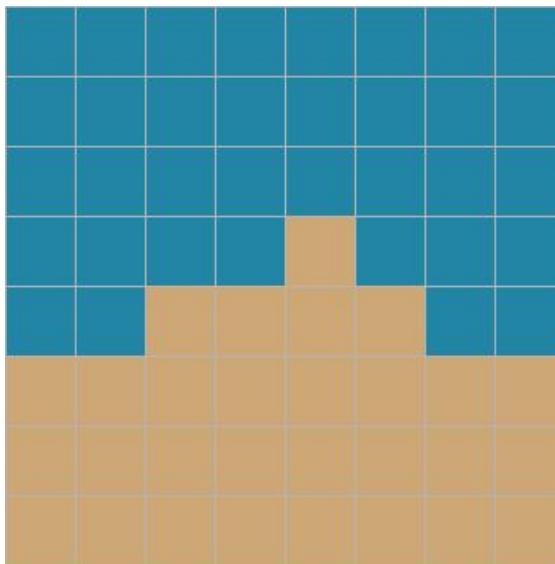
Indeterminate Locations



Indeterminate Locations



Indeterminate Locations



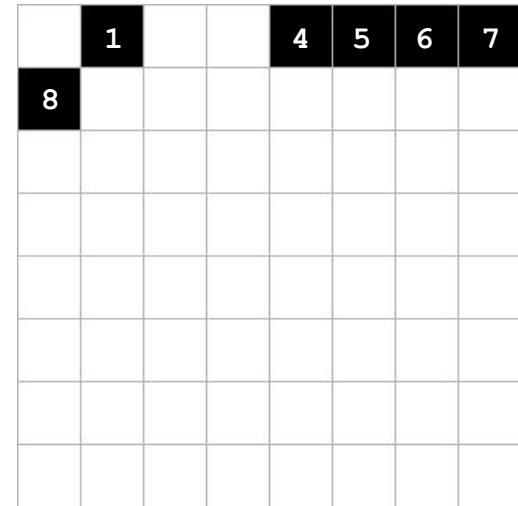
Decompression

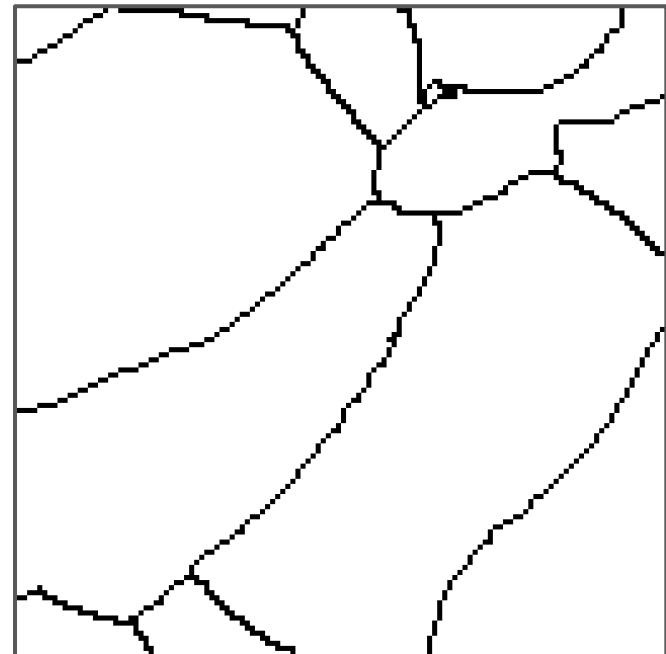
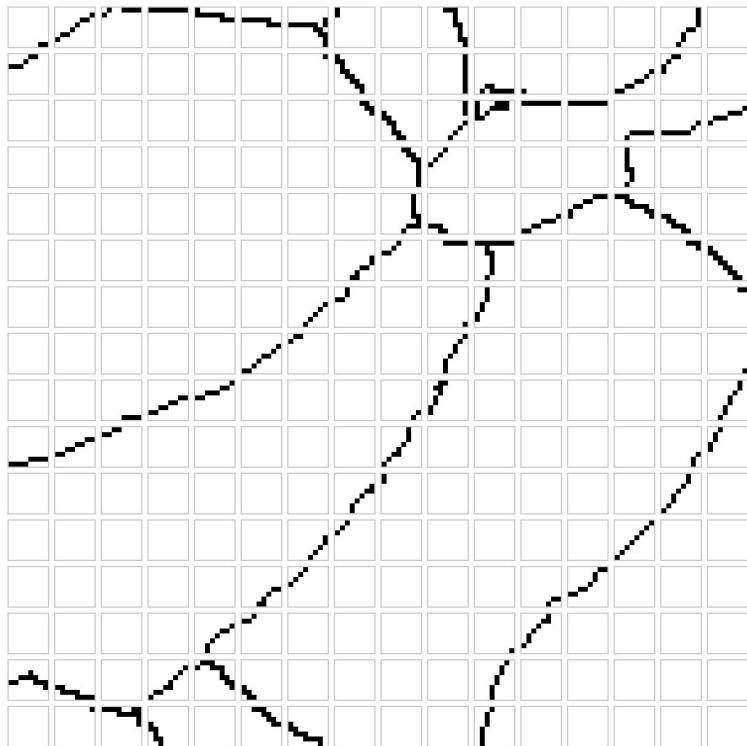
Decompressing Boundary Map

```
13835058055282163712
 288106680975360
    498
    255
  14696193
 3762225152
9259612355635970048
    257
    0
9277485877618024504
    0
    0
    0
    0
  580982358589603968
    0
  460848
    0
    0
    0
    0
    0
    0
  128
  •
  •
  •
```

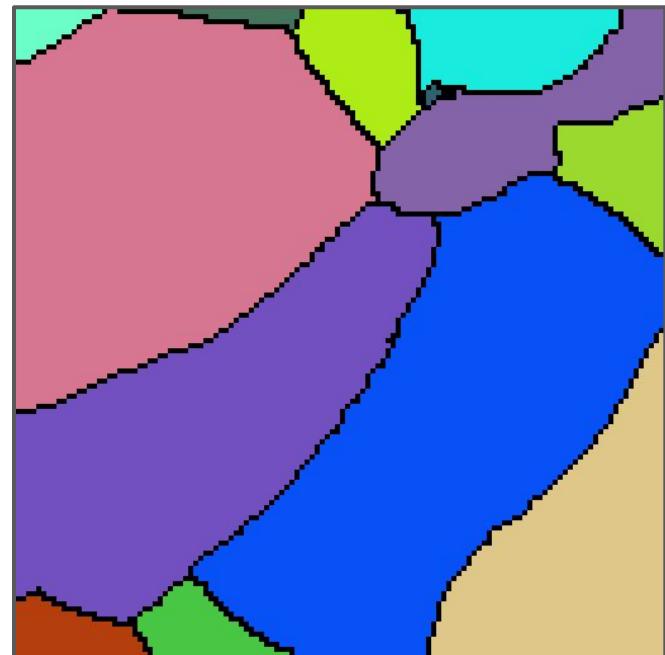
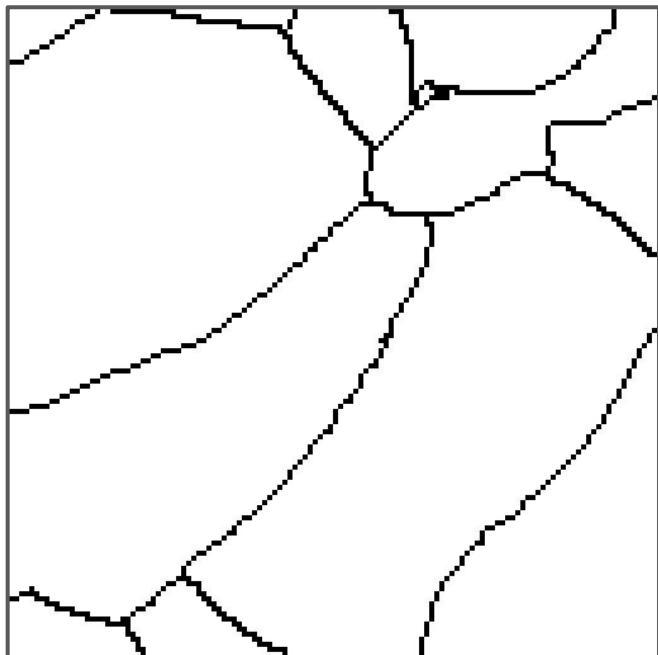
Decompressing Boundary Map

Decompressing Boundary Map

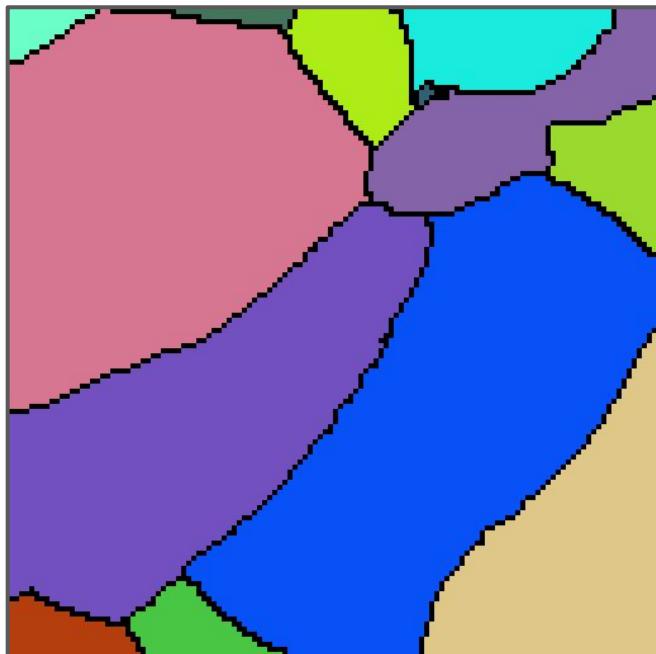




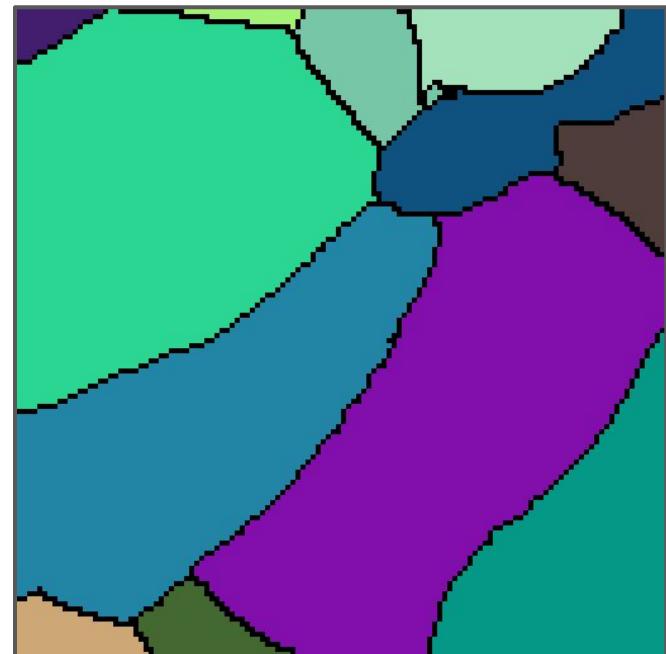
Decompressing Per-Pixel Labels



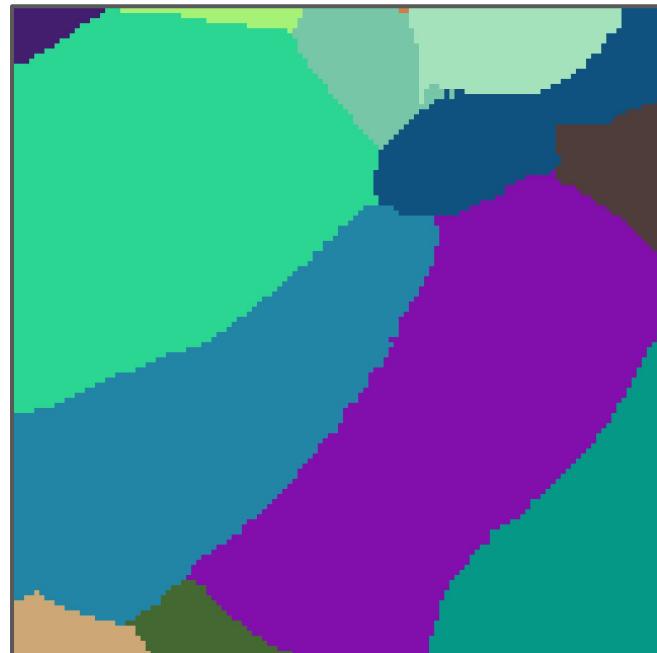
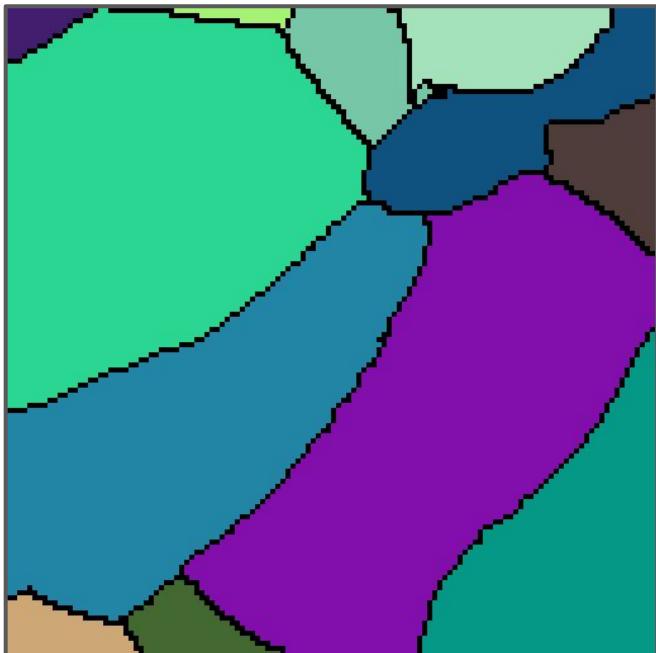
Decompressing Per-Pixel Labels



1	→	1381
2	→	836
3	→	538
4	→	1617
5	→	1709
6	→	1688
7	→	1617
8	→	1619
9	→	1020
10	→	827
11	→	1723
12	→	1246
13	→	1258



Decompressing Per-Pixel Labels



Variable 3D Window Sizes

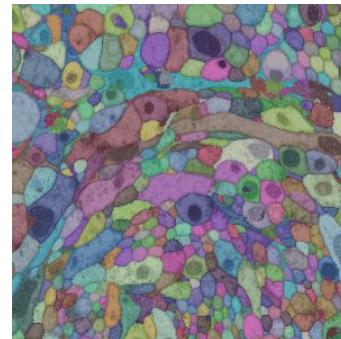
Compresso can use different sized windows depending on the input data

Variable 3D Window Sizes

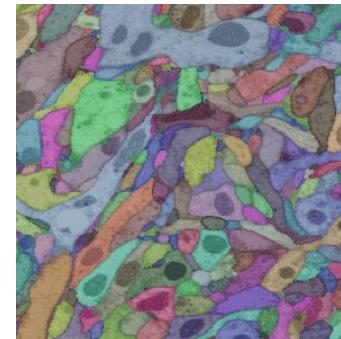
Compresso can use different sized windows depending on the input data

4x4x4 windows outperform 8x8x1 windows by 12.5% on an isotropic dataset

Isotropic Data

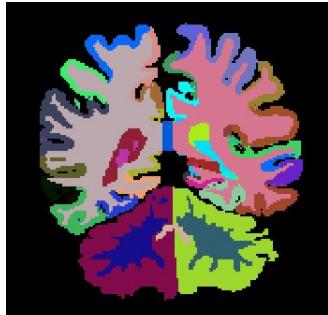


XY-plane



YZ-plane

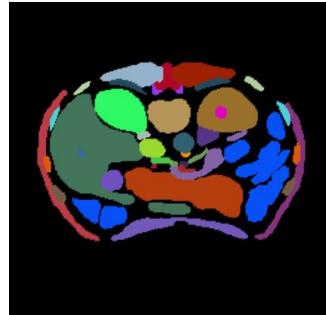
Extends to Other Segmentation Datasets



SPL Brain Atlas



SPL Knee Atlas



SPL Abdominal Atlas



Berkeley Segmentation
Dataset



PASCAL Visual Object
Classes Dataset

Results

Two Stage Compression with LZMA

Follow Compresso with a general-purpose compression scheme such as LZMA

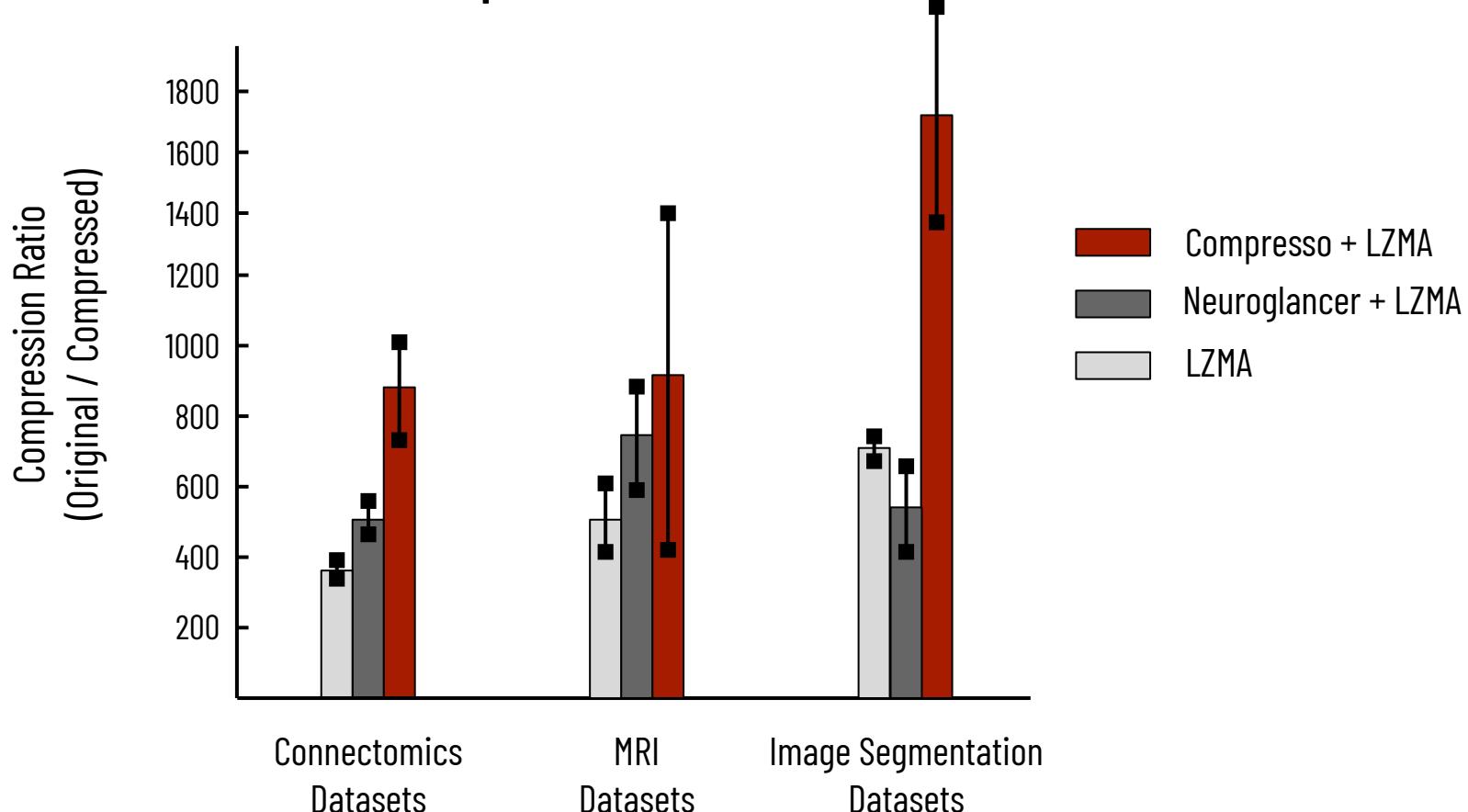
Two Stage Compression with LZMA

Follow Compresso with a general-purpose compression scheme such as LZMA

LZMA uses complex models for probability predictions of bits

Dataset	Uncompressed	Neuroglancer + LZMA	Compresso + LZMA
AC3 Mouse cortex, EM	1.26 GB	550x	771x
AC4 Mouse cortex, EM	838.86 MB	479x	660x
CREMI A, B, C Drosophila brain, EM	1.56 GB	465x, 629x, 496x	804x, 1158x, 899x
L. Cylinder Mouse cortex, EM	10.07 GB	425x	889x
SPL Brain Atlas T1/T2-weighted MRI	135.27 MB	764x	645x
SPL Knee Atlas MRI	249.56 MB	1172x	1562x
SPL Abdominal Atlas CT	59.24 MB	417x	482x

Compression Ratio



Method	Compression Speed	Decompression Speed
LZMA	9.89 MB / s	366.13 MB / s
Neuroglancer + LZMA	43.80 MB / s	164.32 MB / s
Compresso + LZMA	131.15 MB / s	206.60 MB / s

Complexity

P is the number of pixels; N is the number of distinct window values; X and Y are the size of the x and y dimensions of the input data; and α is the inverse Ackermann function.

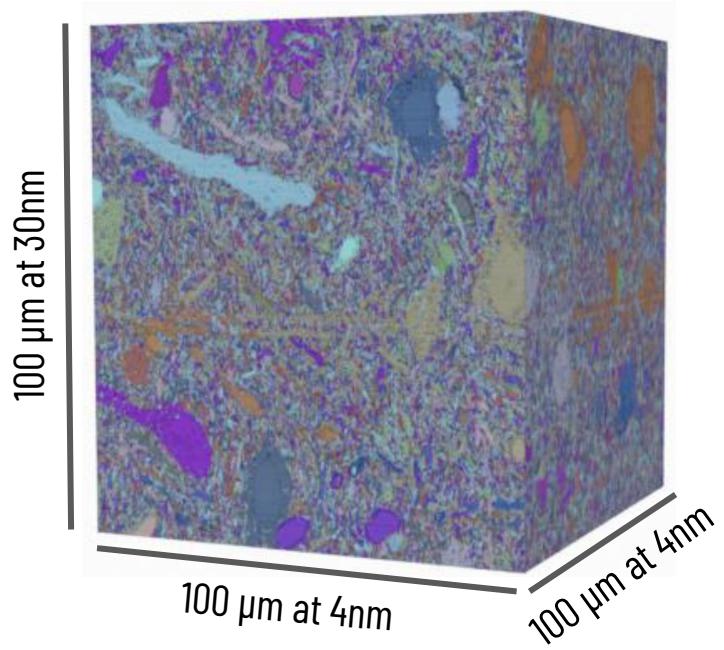
Compression:

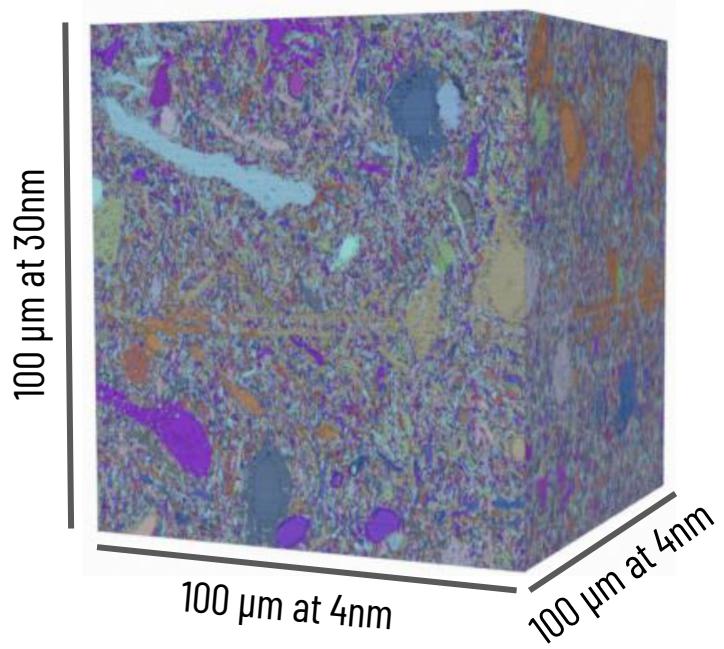
$$O(P(1 + \alpha(XY)) + N \log N)$$

Decompression:

$$O(P(1 + \alpha(XY)))$$

Compression of 100 microns cubed

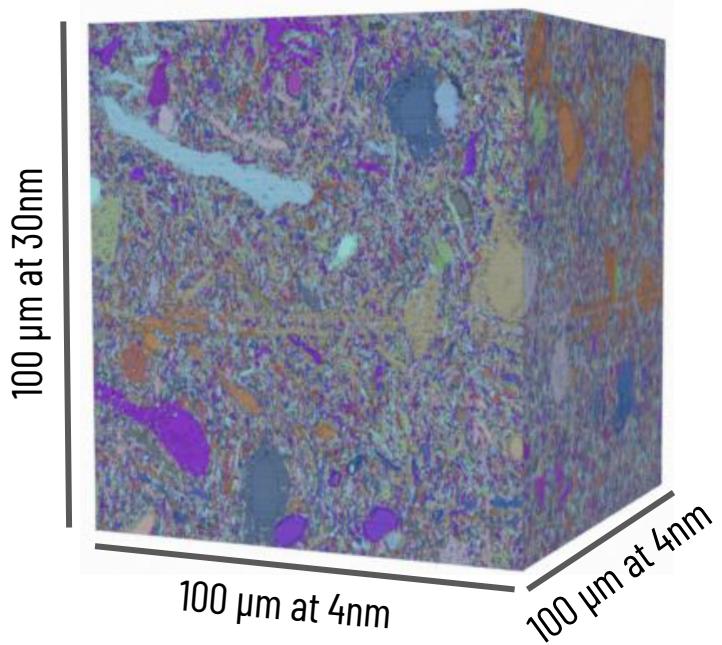




Uncompressed:

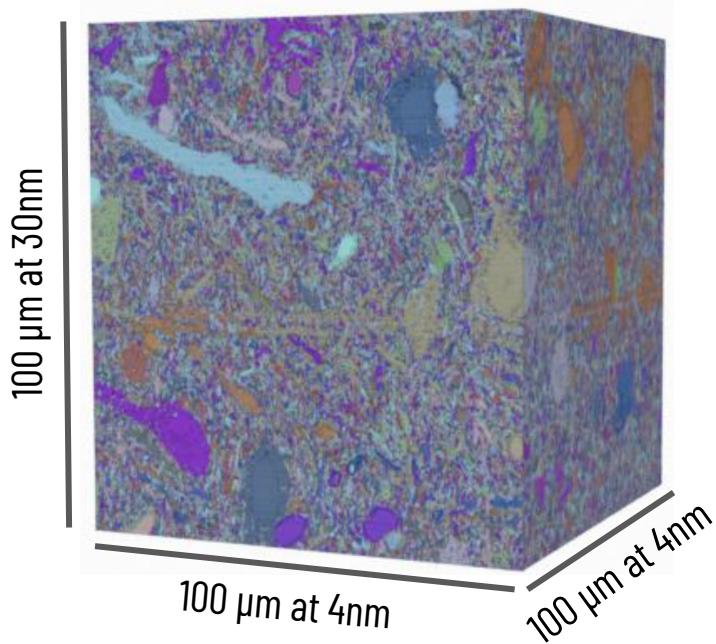
19.25 terabytes

Compression of 100 microns cubed



Uncompressed:	19.25 terabytes
With Compresso + LZMA:	25.94 gigabytes
Ratio:	742x

Compression of 100 microns cubed



Uncompressed: 19.25 terabytes

With Compresso + LZMA: 25.94 gigabytes

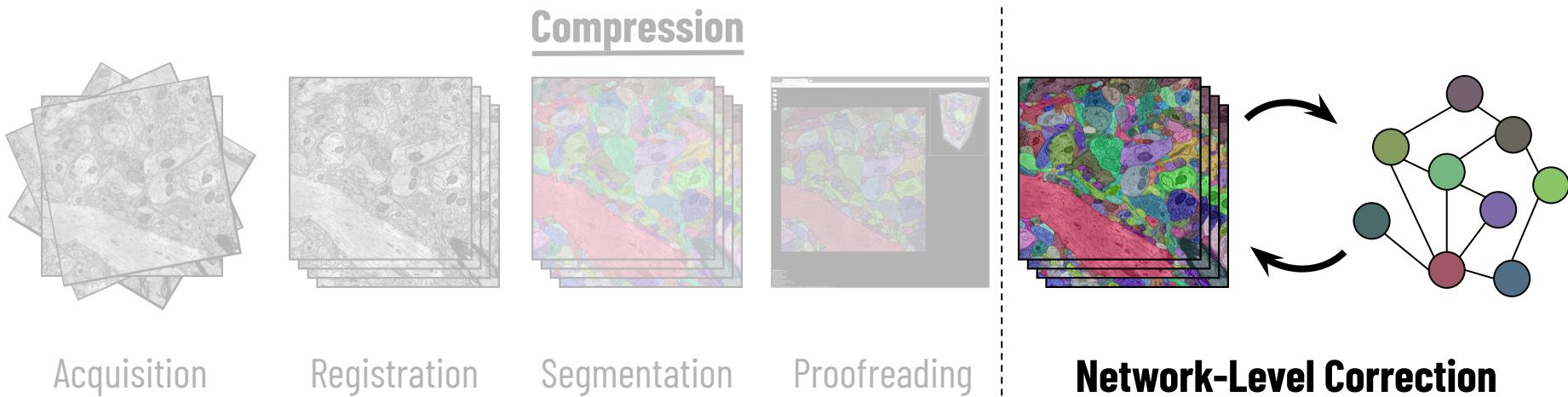
Ratio: 742x

AWS Storage Costs (S3 Standard Storage):

Uncompressed: \$442.75 / month

Compressed: \$0.60 / month

Connectomics Pipeline

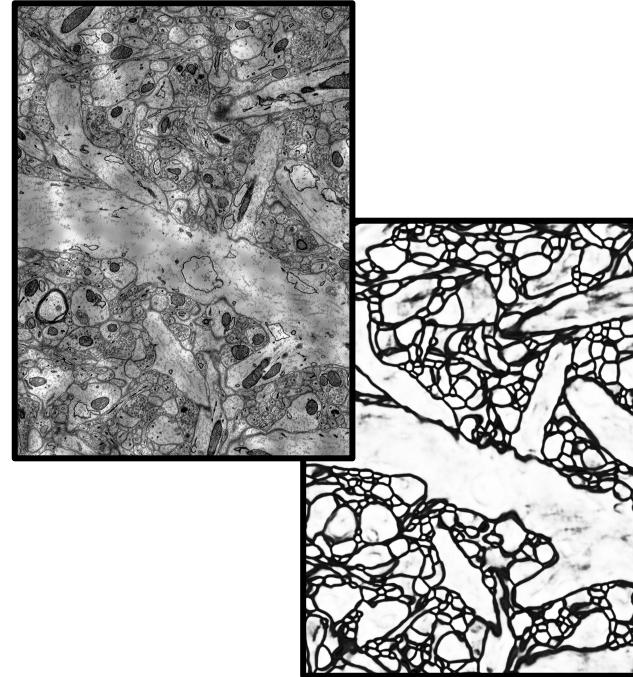
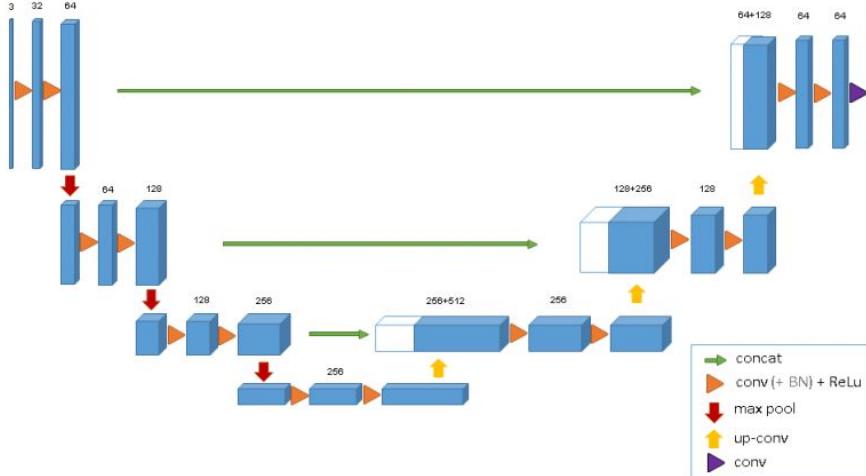


Biologically-Constrained Region Merging for Connectome Reconstruction

Brian Matejek, Daniel Haehn, Donglai Wei, Toufiq Parag, Hanspeter Pfister

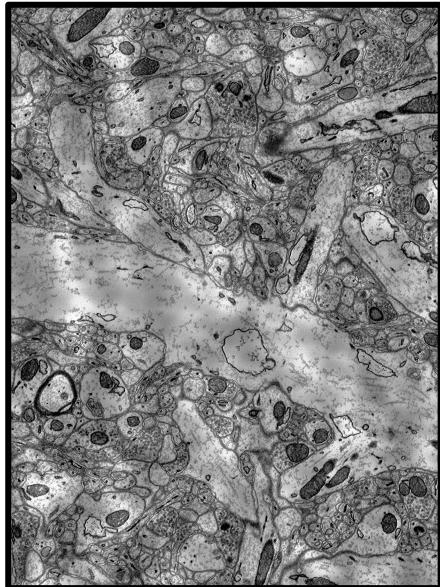


U-Net



Ronneberger et al., U-Net: Convolutional Networks for Biomedical Image Segmentation, MICCAI 2015
Cicek et al., 3D U-Net: Learning Dense Volumetric Segmentation from Sparse Annotation, MICCAI 2016

3D Watershed on Affinities



Zlateski et al., Image Segmentation by Size-Dependent Single Linkage Clustering of a Watershed Basin Graph, 2015

Funke et al., A Deep Structured Learning Approach Towards Automating Connectome Reconstruction from 3D Electron Micrographs, 2017

Zeng et al., DeepEM3D: Approaching Human-Level Performance on 3D Anisotropic EM Image Segmentation, Bioinformatics 2017

Context-Aware Delayed Agglomeration

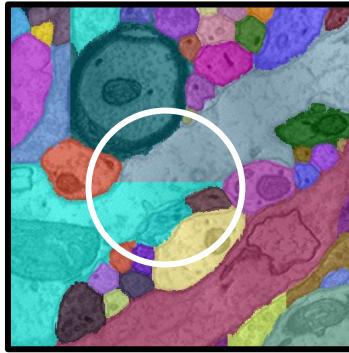


Nunez-Iglesias et al., Machine Learning of Hierarchical Clustering to Segment 2D and 3D Images, PLoS ONE, 2013

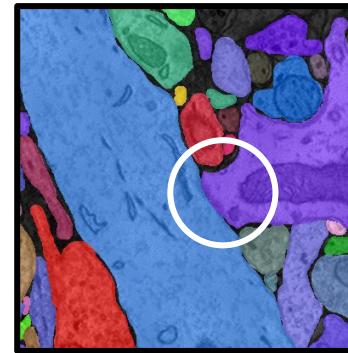
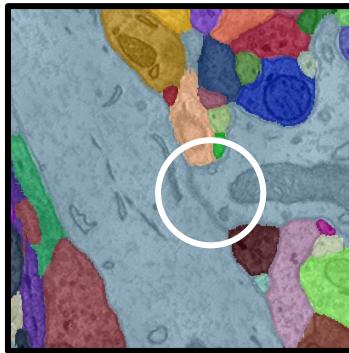
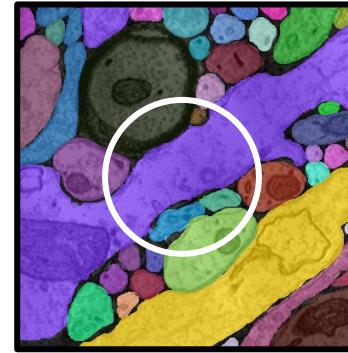
Parag et al., A Context-Aware Delayed Agglomeration Framework for Electron Microscopy Segmentation, PLoS ONE 2015

Errors

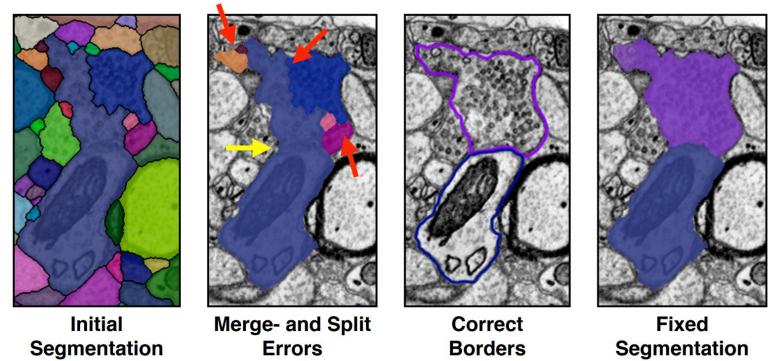
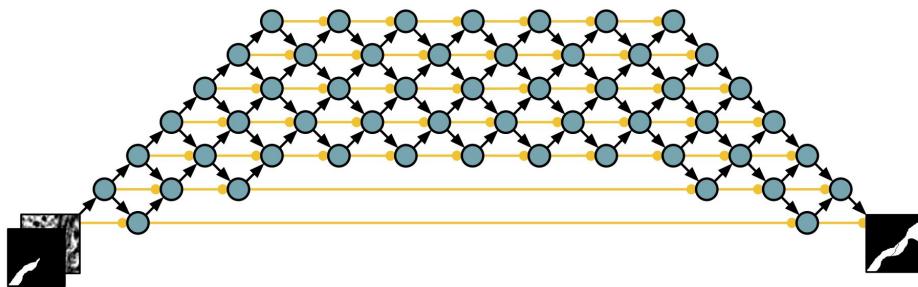
Automatic Segmentation



Ground Truth



Proofreading and Error Correction

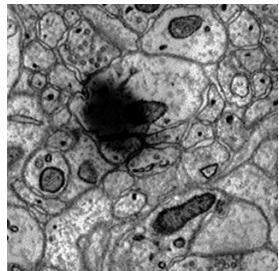


Zung et al., An Error Detection and Correction Framework for Connectomics, NIPS 2017

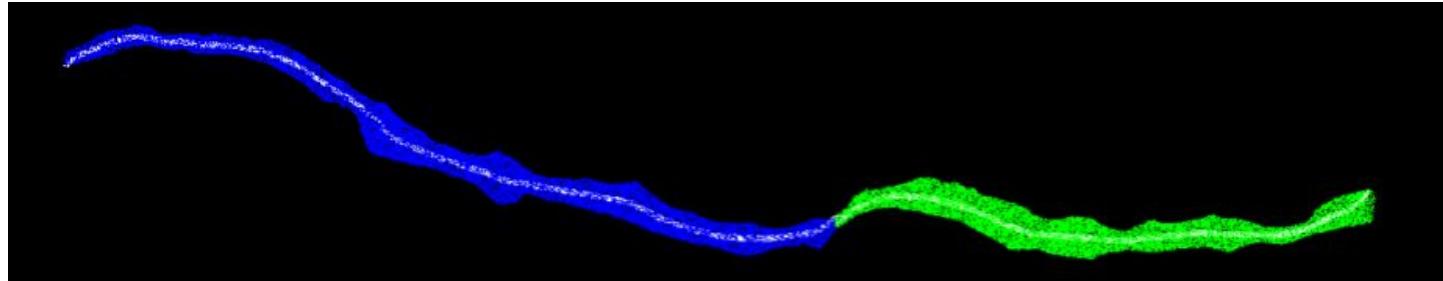
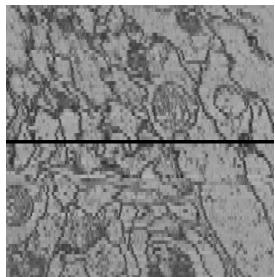
Haehn et al., Guided Proofreading of Automatic Segmentations for Connectomics, CVPR 2018

Need for Global Context

Stained Images

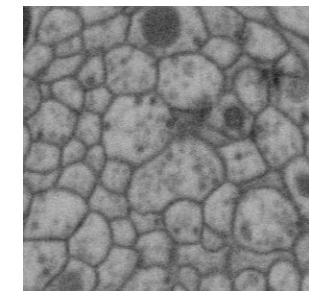
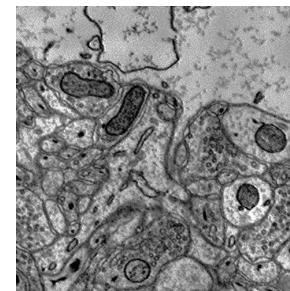
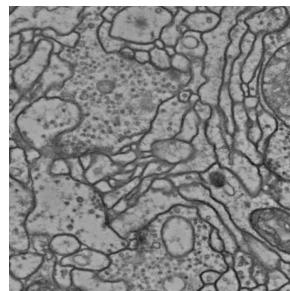
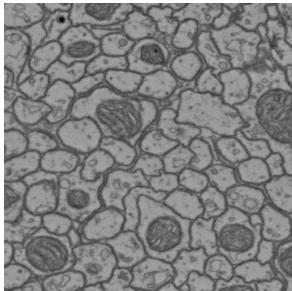


Missing Sections

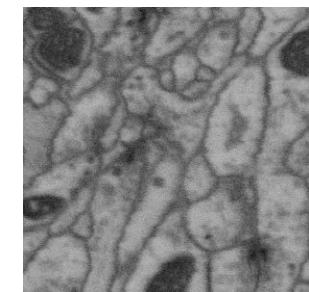
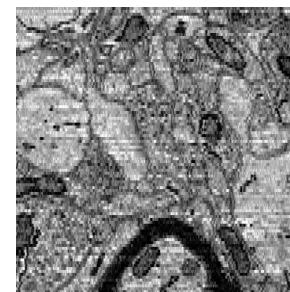
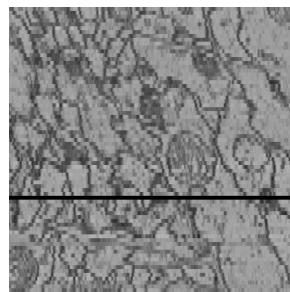
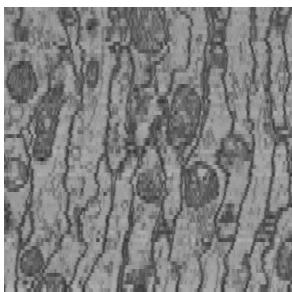


Variable Image Data

xy-slice



yz-slice



Cremi Vol. A

Drosophila melanogaster

4 x 4 x 40 nm³ / vx

Cremi Vol. C

Drosophila melanogaster

4 x 4 x 40 nm³ / vx

Kasthuri

Mouse

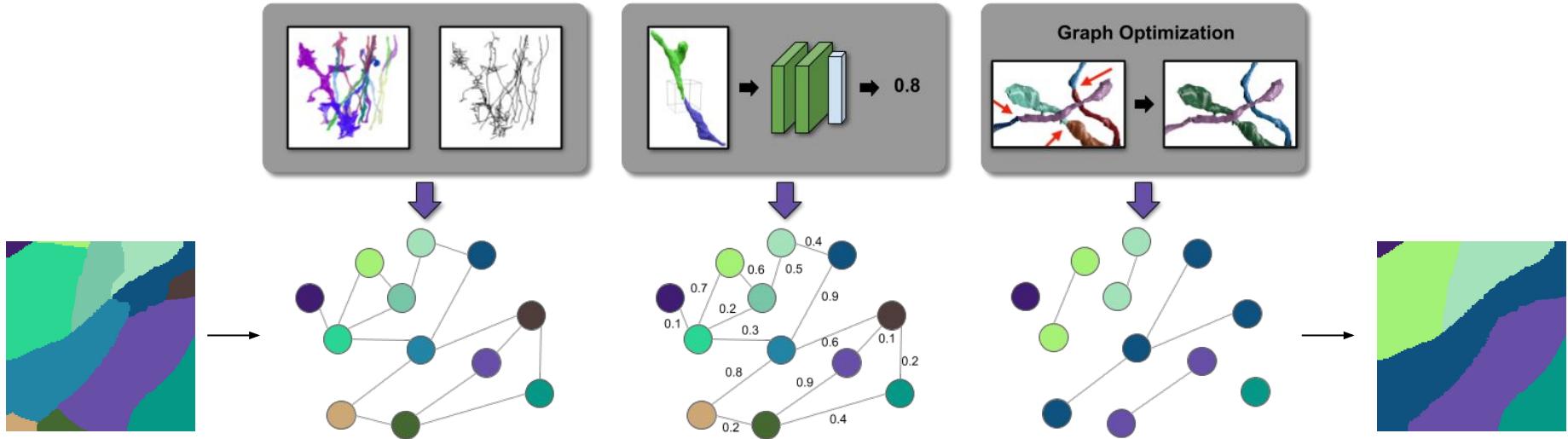
6 x 6 x 30 nm³ / vx

FlyEM

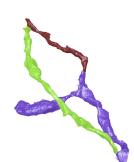
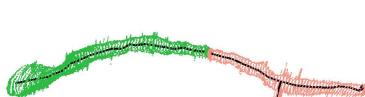
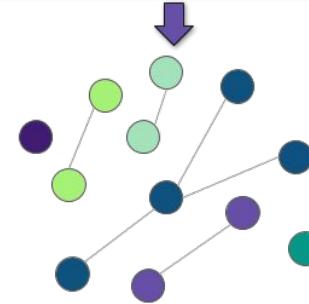
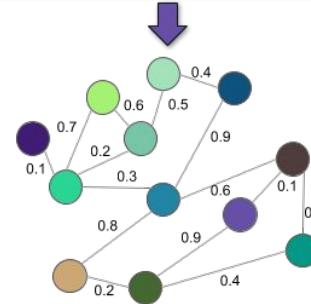
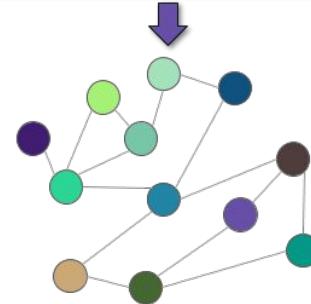
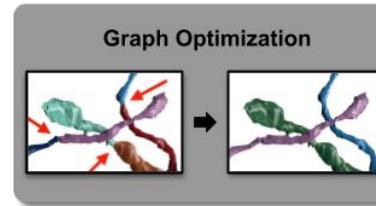
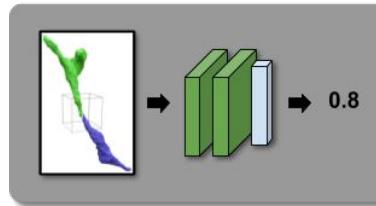
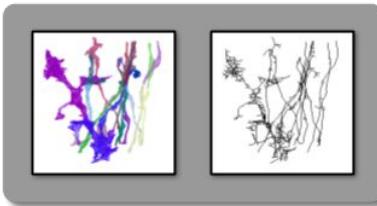
Drosophila melanogaster

10 x 10 x 10 nm³ / vx

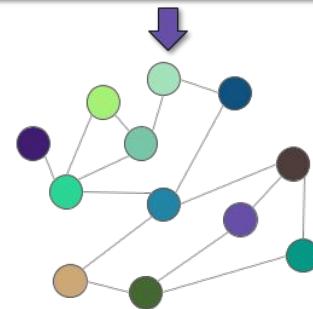
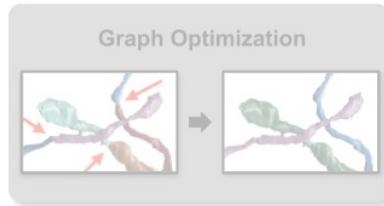
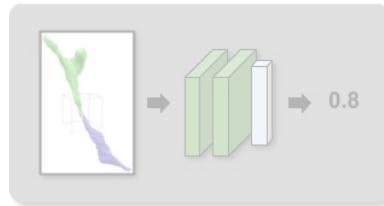
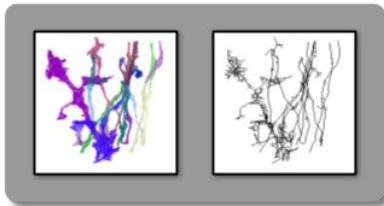
Proposed Region Merging



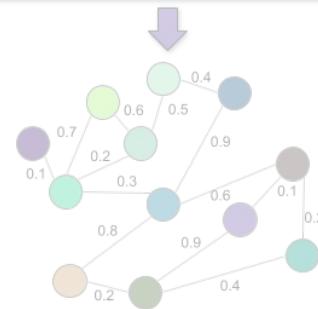
Proposed Region Merging with Biological Constraints



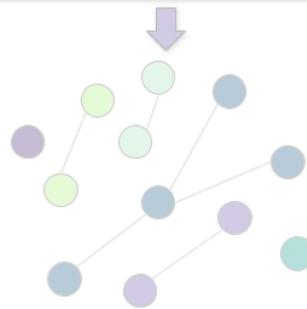
Goal: Construct a graph with as few extra edges as possible



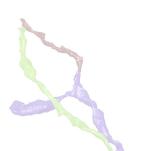
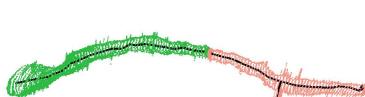
Geometric Priors



Learned Constraints



Topological Restrictions



Adjacency Graphs

Every segment in the label volume receives a node

Segments with a pair of neighboring voxels receive an edge between the corresponding nodes

Adjacency Graphs

Every segment in the label volume receives a node

Segments with a pair of neighboring voxels receive an edge between the corresponding nodes

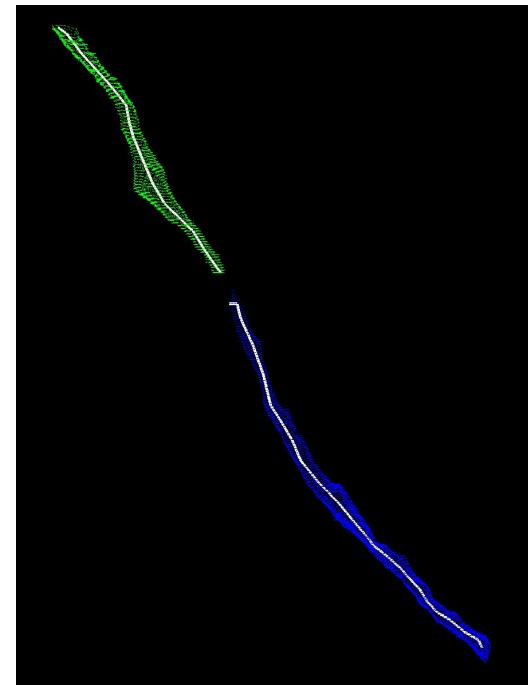
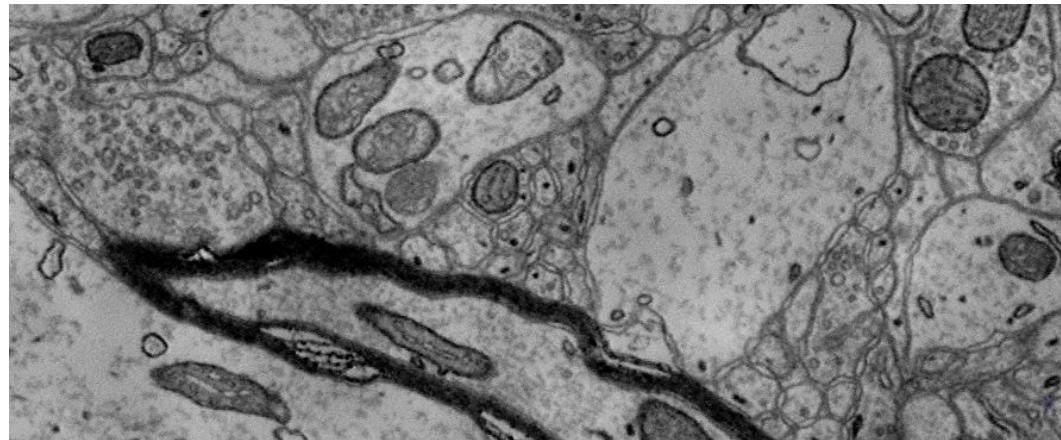


Typical Segment

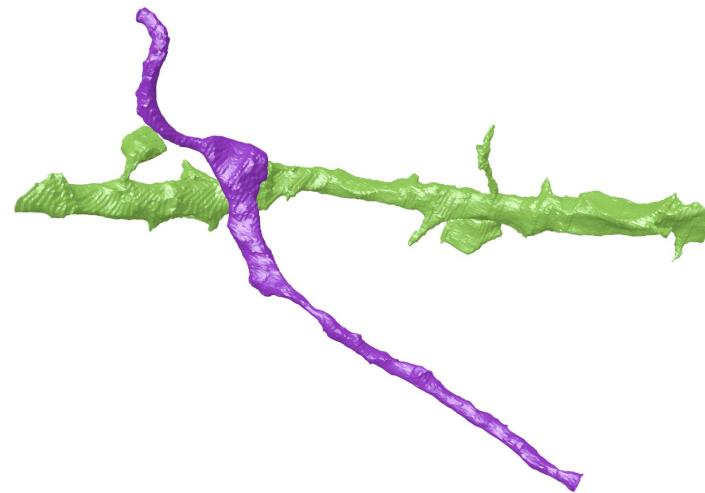
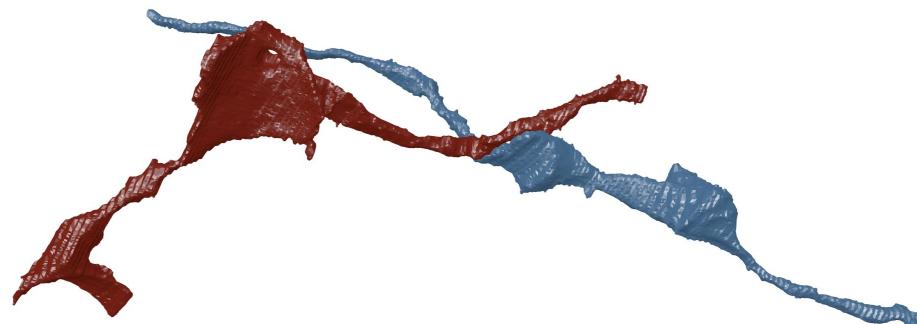


103 Adjacent Neighbors

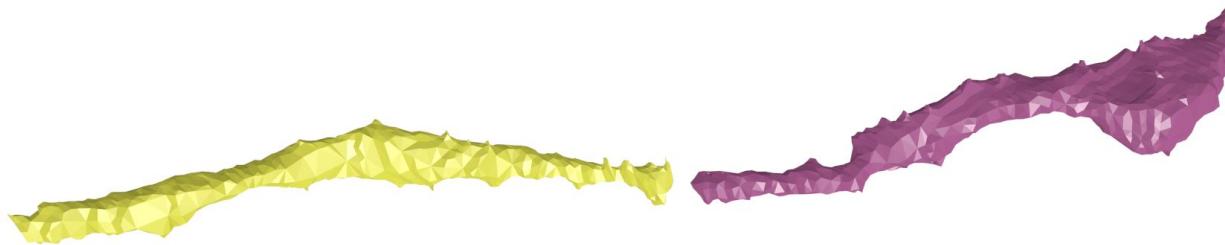
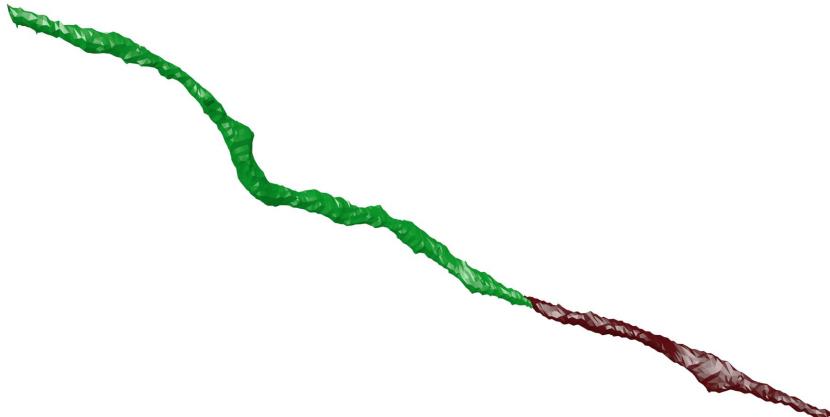
Non-Adjacent Split Errors



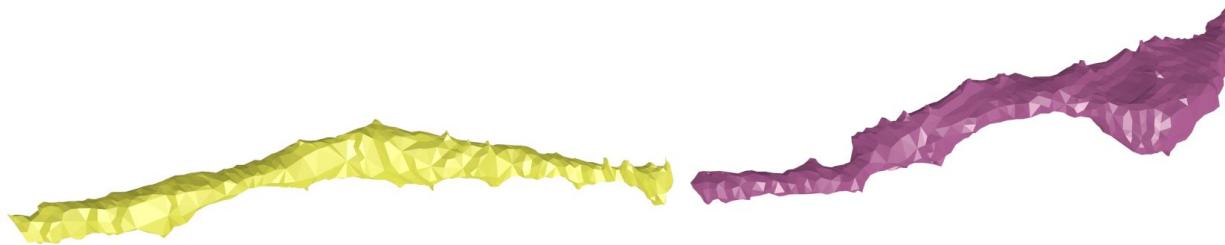
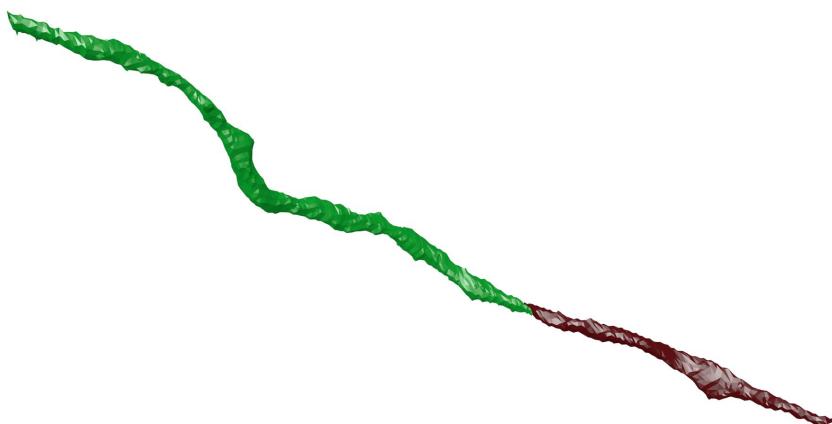
Correctly Segmented



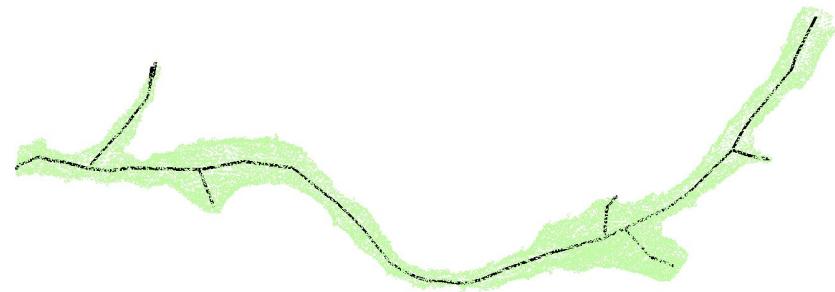
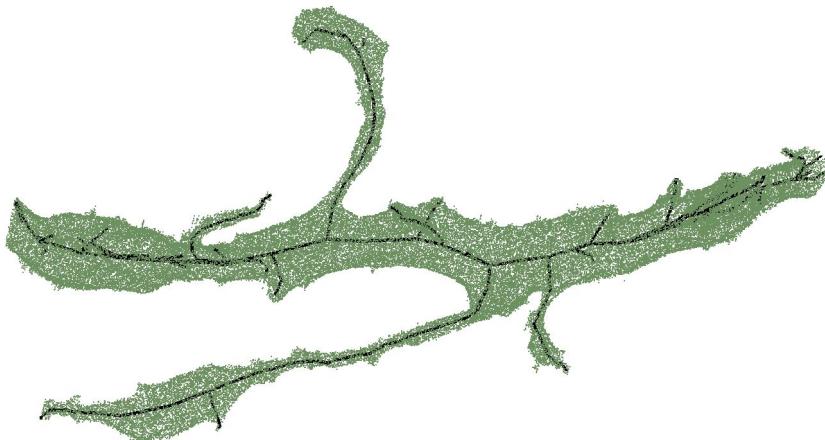
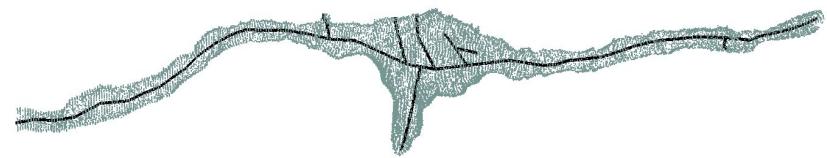
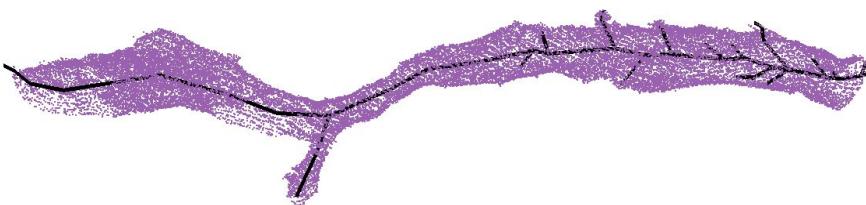
Incorrectly Split



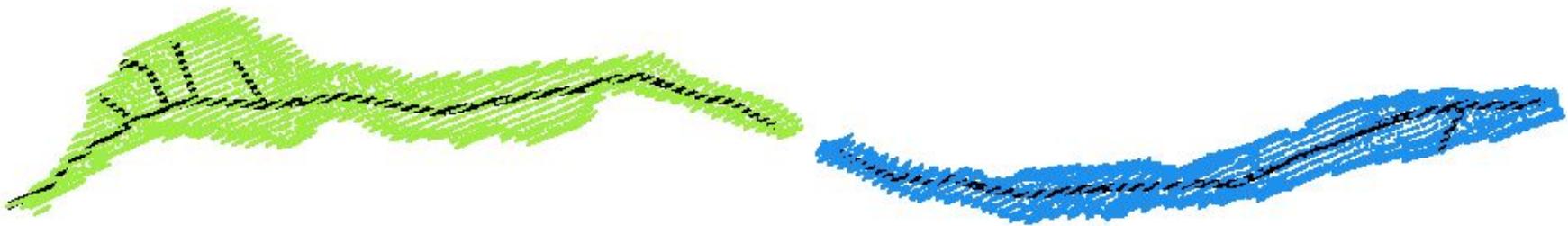
Incorrectly Split



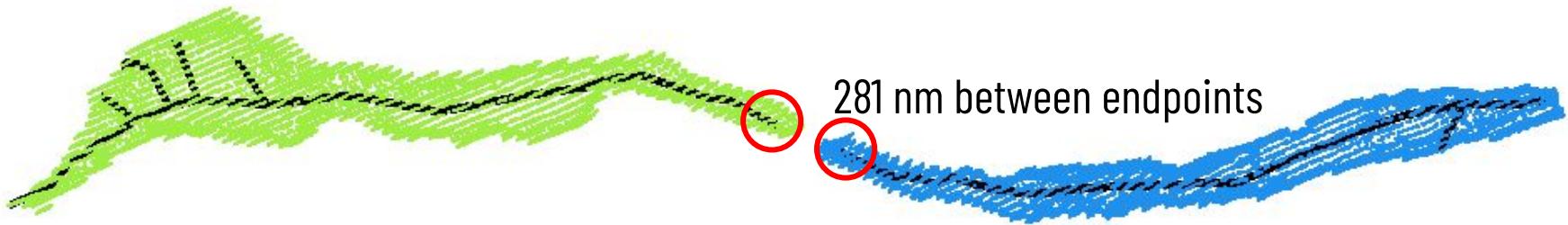
Skeletonization



Merge Candidate



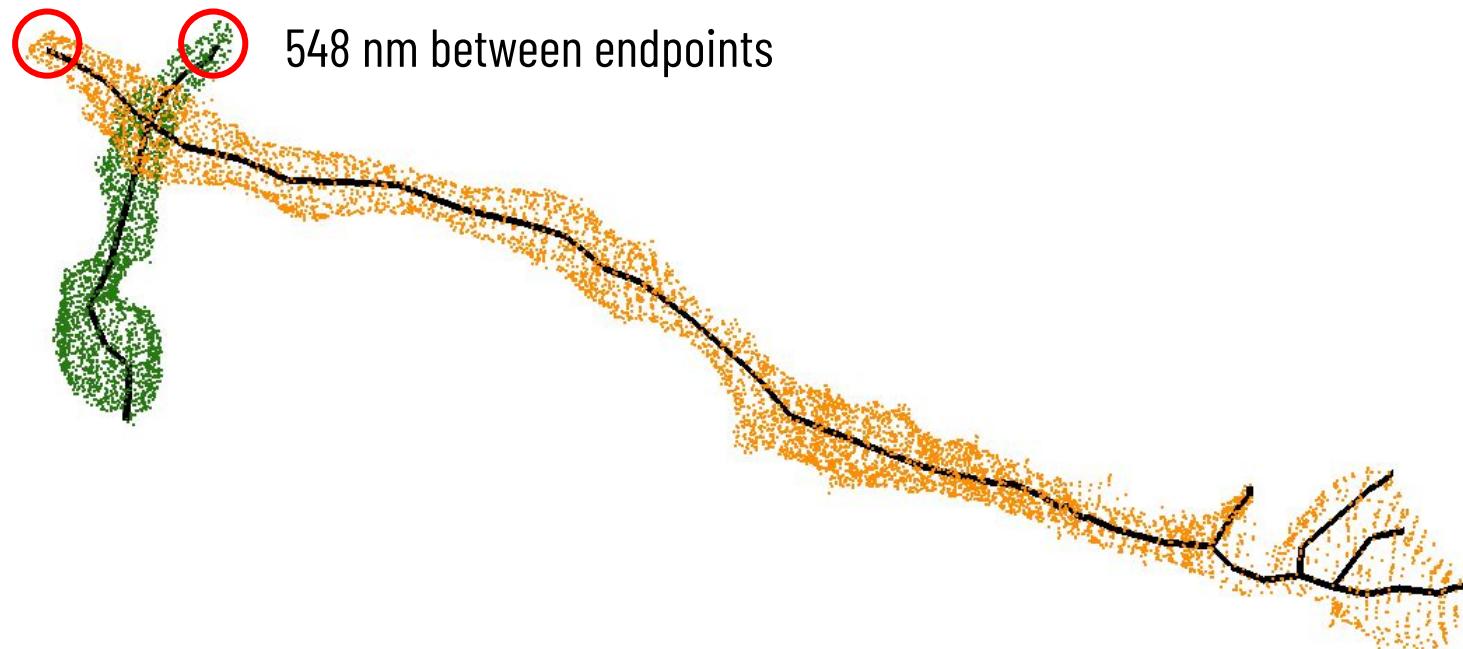
Merge Candidate



Pruned Candidate



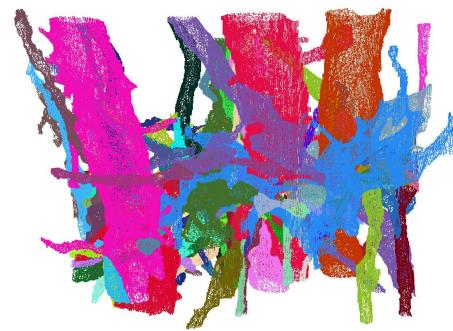
Pruned Candidate



Number of Edges



Typical Segment



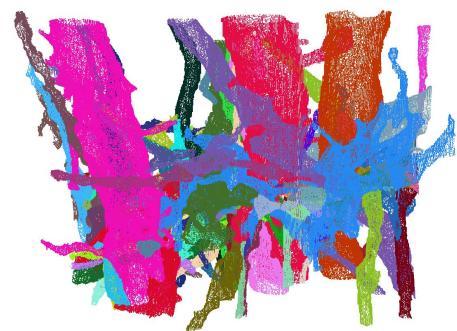
103

Before

Number of Edges

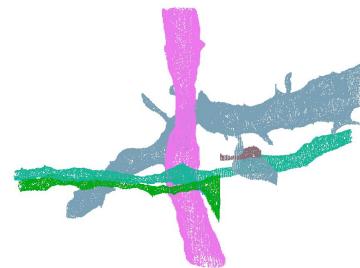


Typical Segment



103

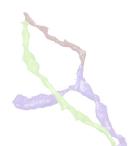
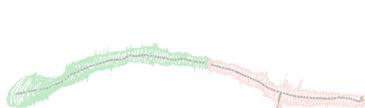
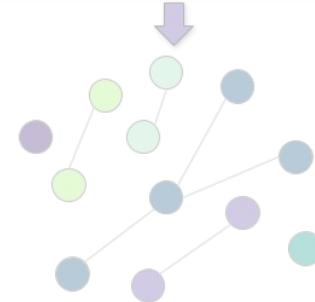
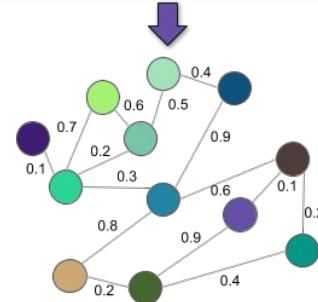
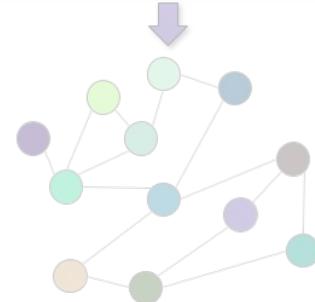
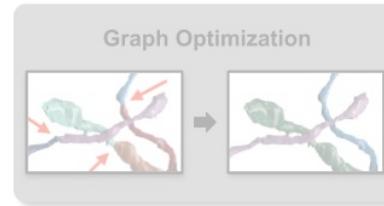
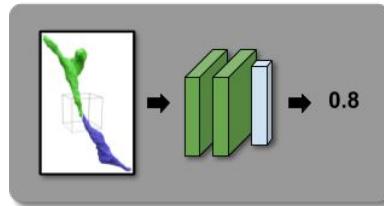
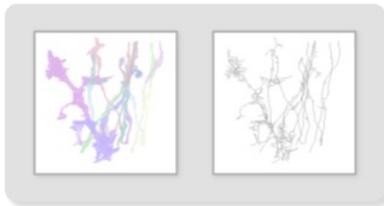
Before



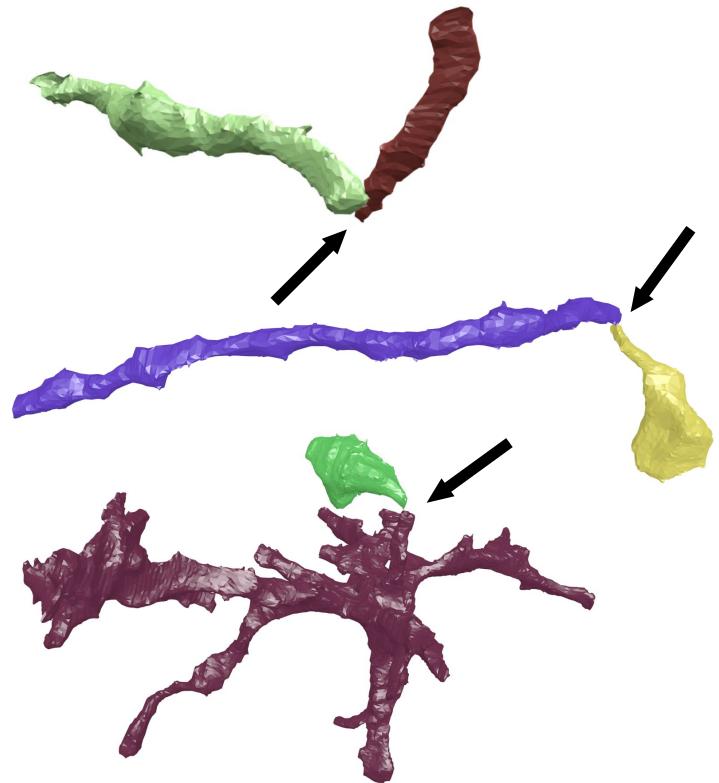
5

After

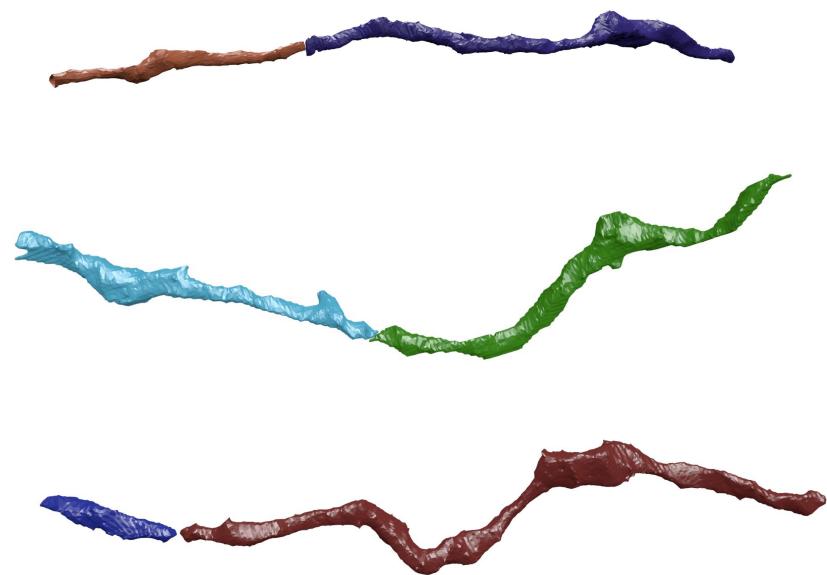
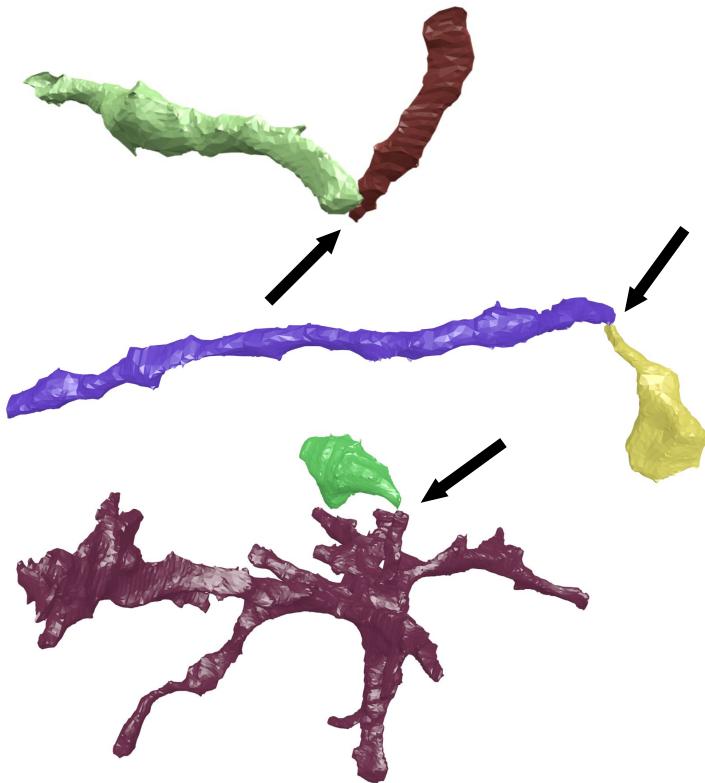
Goal: Populate edge weights for the graph



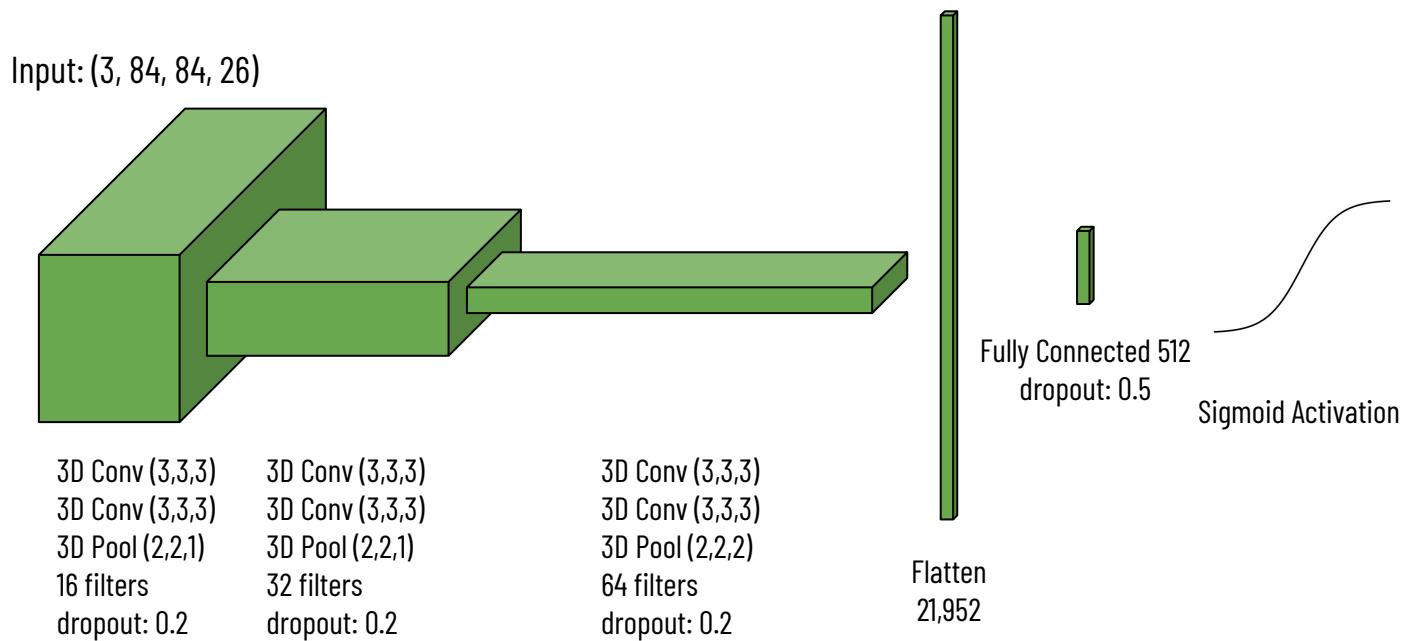
Learned Constraints



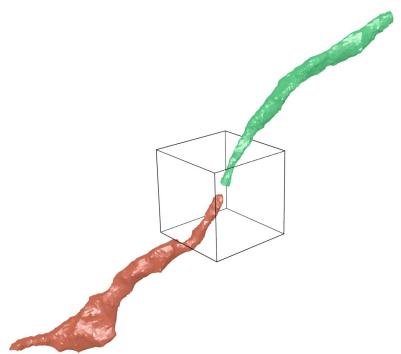
Learned Constraints



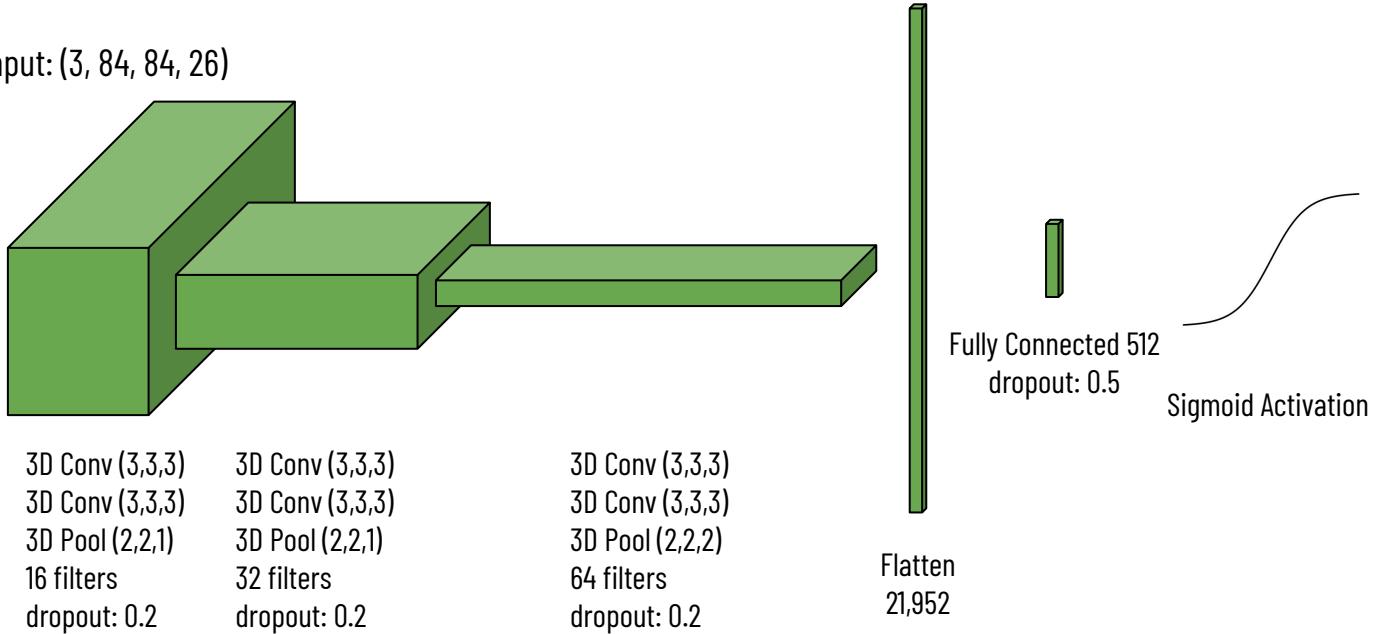
Architecture and Training Parameters



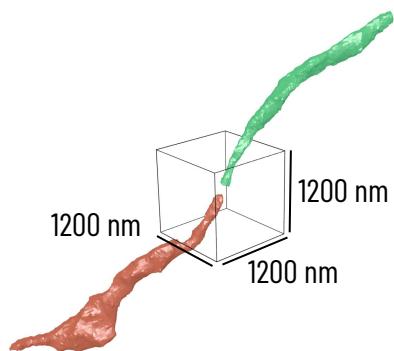
Architecture and Training Parameters



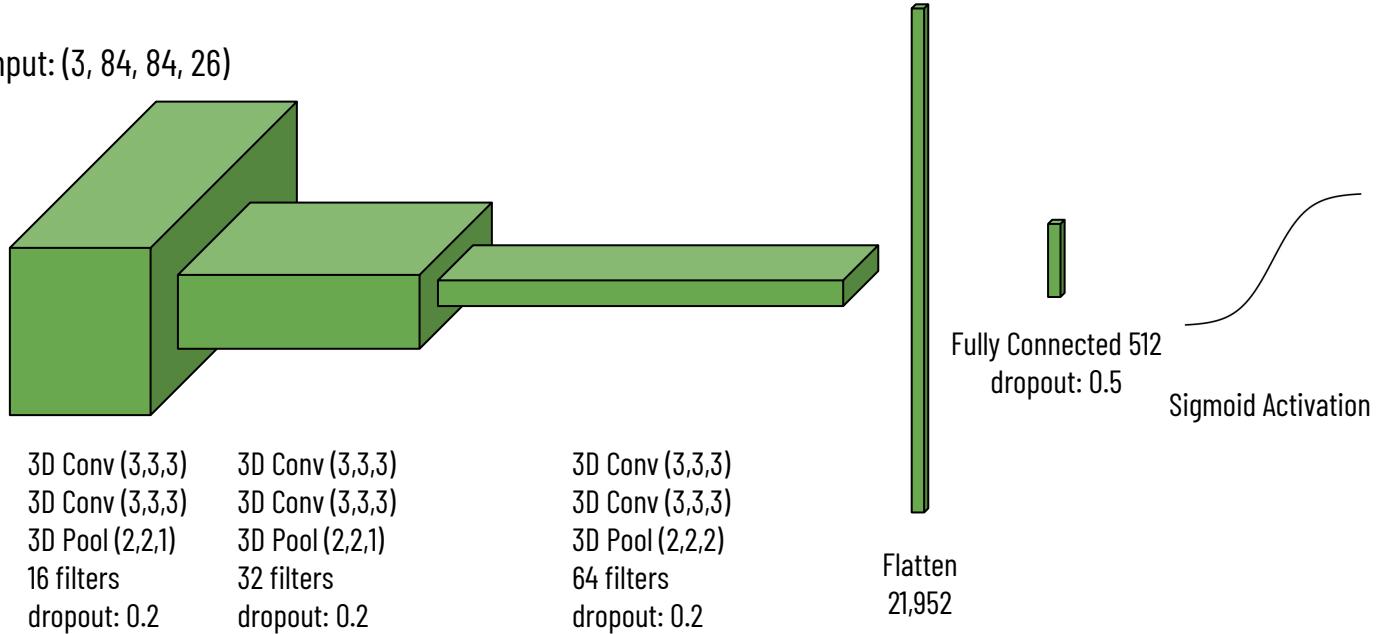
Input: (3, 84, 84, 26)



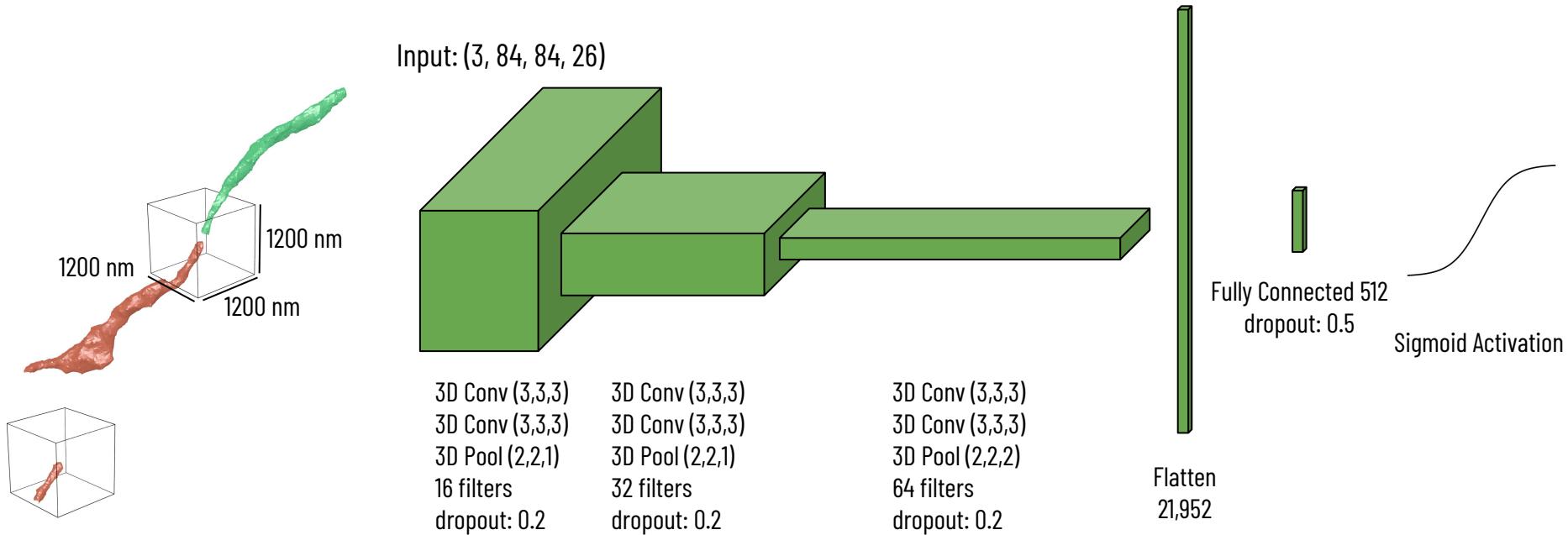
Architecture and Training Parameters



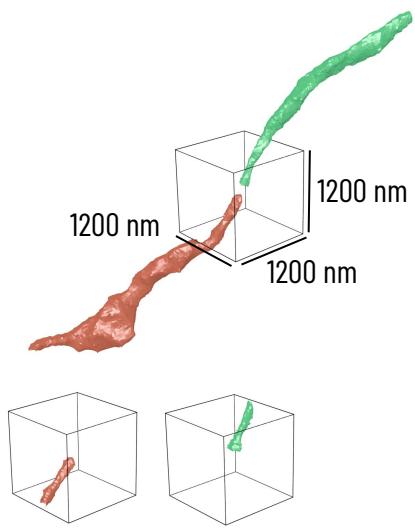
Input: (3, 84, 84, 26)



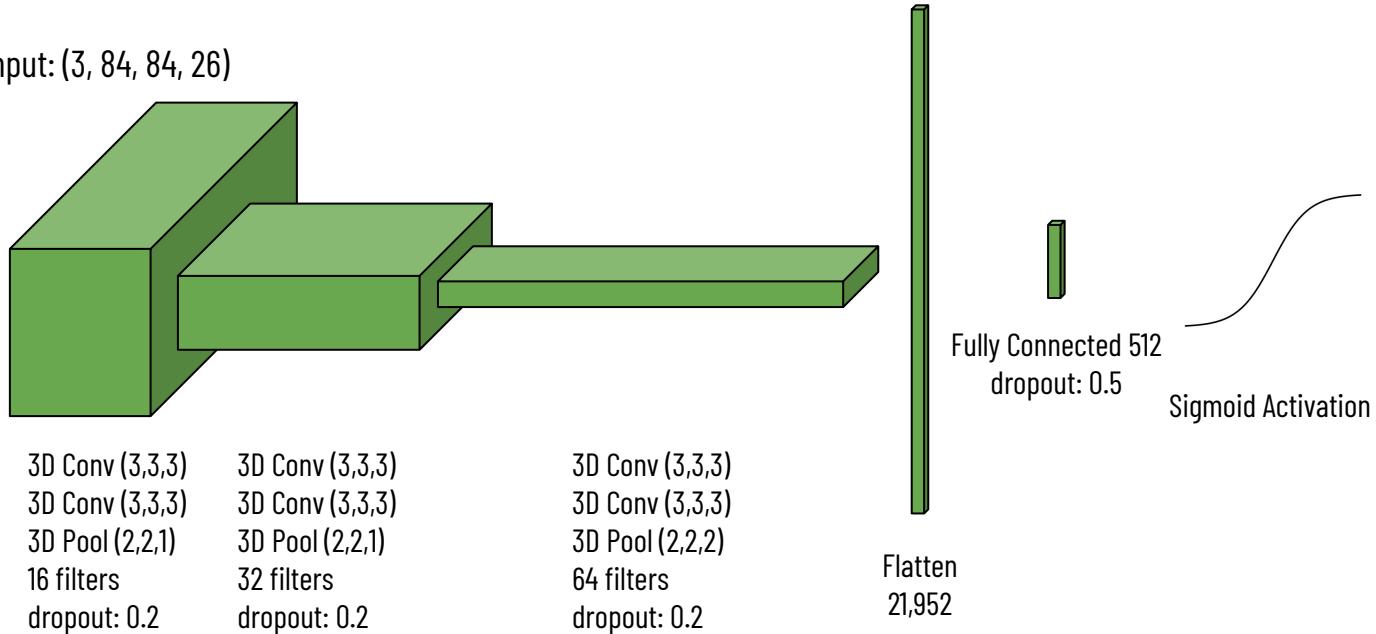
Architecture and Training Parameters



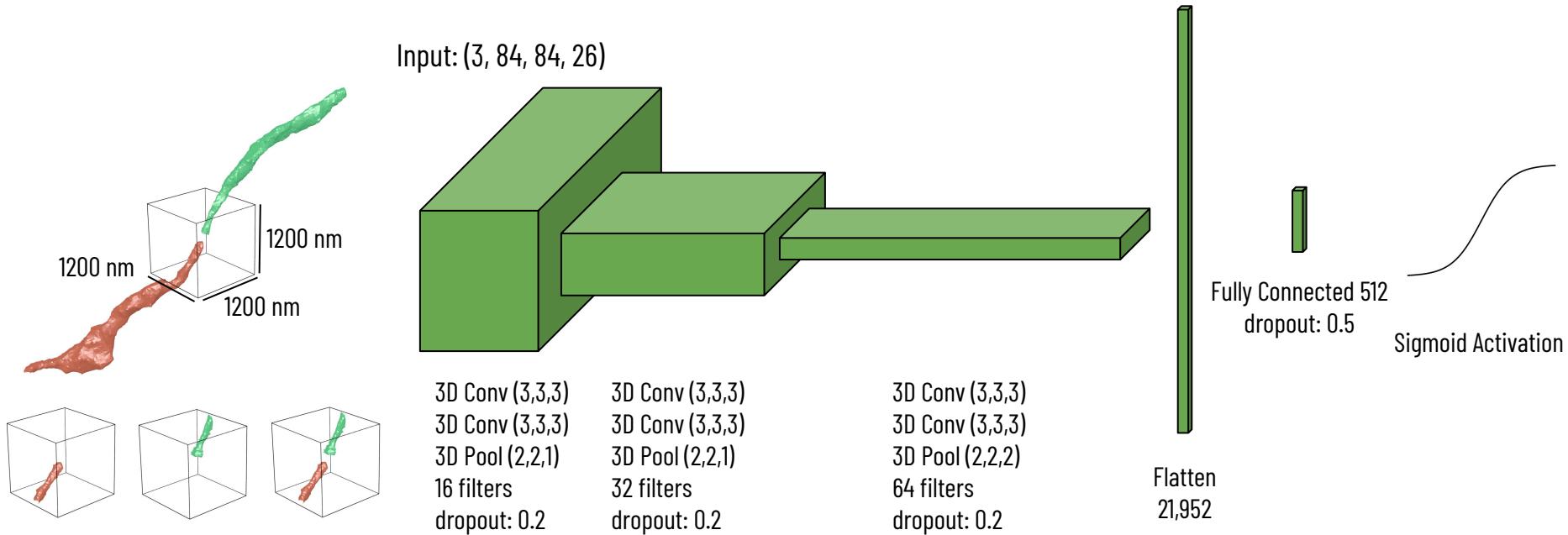
Architecture and Training Parameters



Input: (3, 84, 84, 26)



Architecture and Training Parameters



Parameters

Parameters	Values
Loss Function	Mean Squared Error
Optimizer	SGD with Nesterov Momentum
Momentum	0.9
Initial Learning Rate	0.01
Decay Rate	$5 * 10^{-8}$
Activation	LeakyReLU ($\alpha = 0.001$)
Kernel Sizes	$3 \times 3 \times 3$
Filter Sizes	$16 \rightarrow 32 \rightarrow 64$

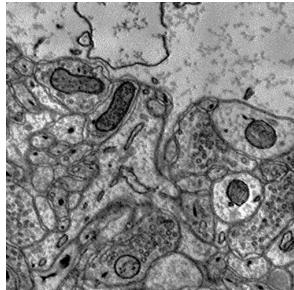
Table 1: Training parameters.

Architectures

Depth	Input Size	No. Parameters	Output Size	Accuracy	Precision	Recall
3	(3, 18, 52, 52)	1,101,553	(64, 3, 3, 3)	91.30	58.06	92.81
3	(3, 20, 60, 60)	2,313,969	(64, 4, 4, 4)	92.41	61.70	92.41
3	(3, 22, 68, 68)	4,312,817	(64, 5, 5, 5)	92.33	61.49	92.34
3	(3, 24, 76, 76)	7,294,705	(64, 6, 6, 6)	93.51	65.78	93.13
3	(3, 26, 84, 84)	11,456,241	(64, 7, 7, 8)	95.38	74.43	92.34
3	(3, 28, 92, 92)	16,994,033	(64, 8, 7, 8)	91.87	59.70	94.22
3	(3, 30, 100, 100)	24,104,689	(64, 9, 9, 9)	92.01	60.24	93.75
4	(3, 28, 92, 92)	1,404,913	(128, 2, 2, 2)	91.70	60.24	85.94
4	(3, 32, 108, 108)	2,650,097	(128, 3, 3, 3)	92.80	64.28	86.88

Table 2. The results of various network architectures trained on the Kasthuri data.

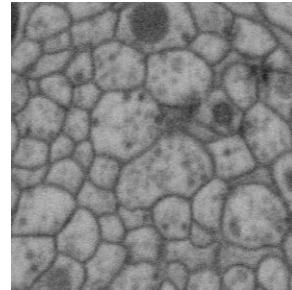
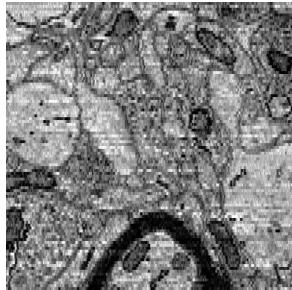
Independent of Image Data



Kasthuri

Mouse

$6 \times 6 \times 30 \text{ nm}^3 / \text{vx}$



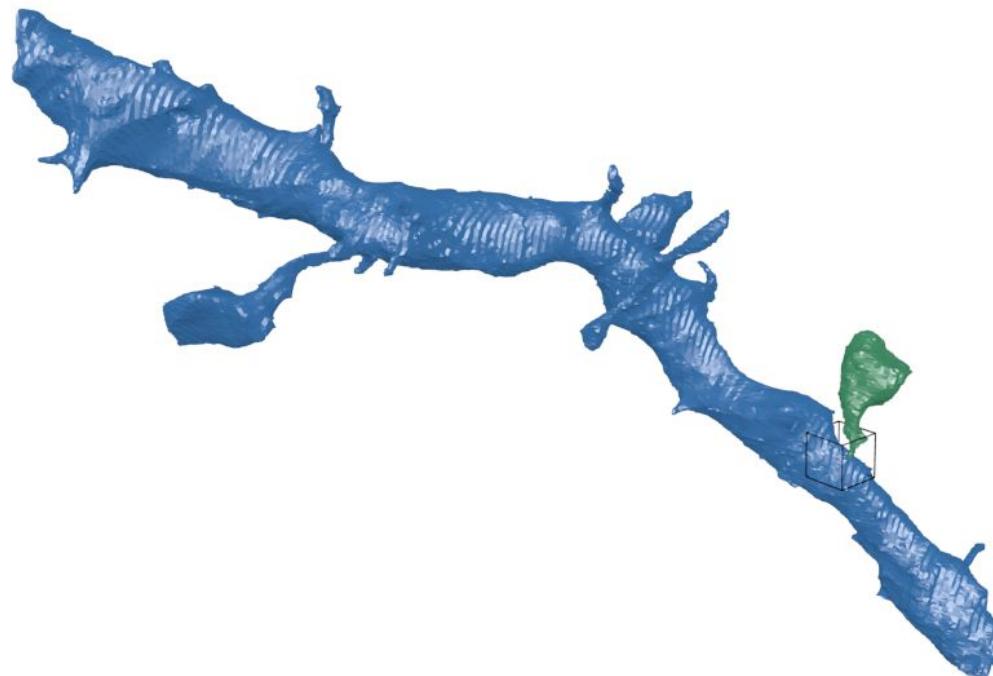
FlyEM

Drosophila melanogaster

$10 \times 10 \times 10 \text{ nm}^3 / \text{vx}$

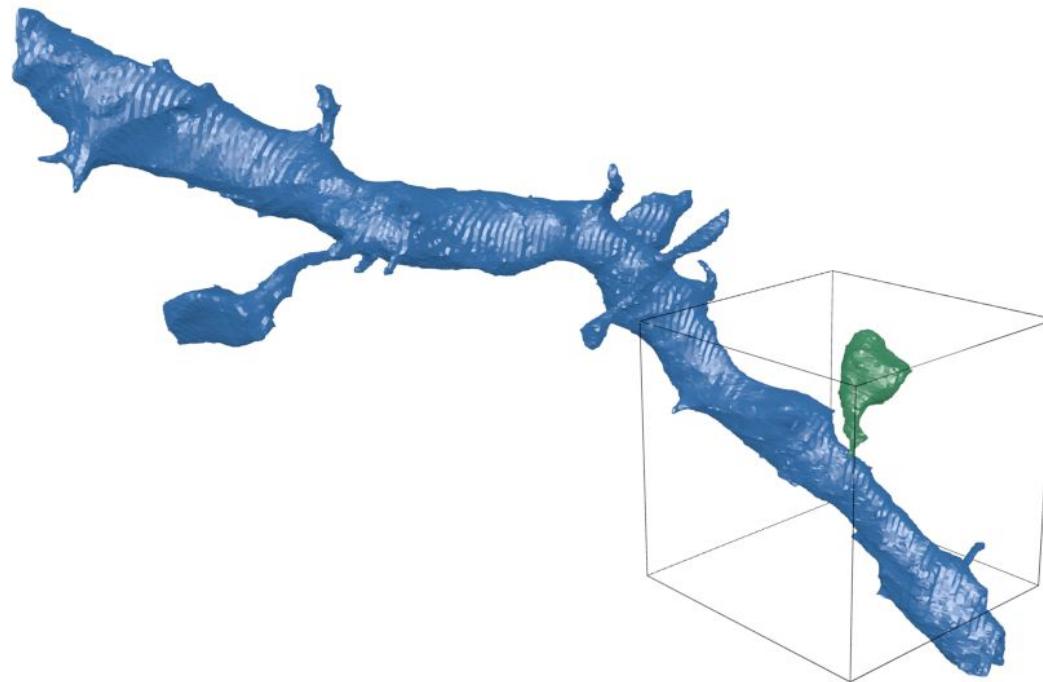
Regions of Interest

Too small and there is not enough local context



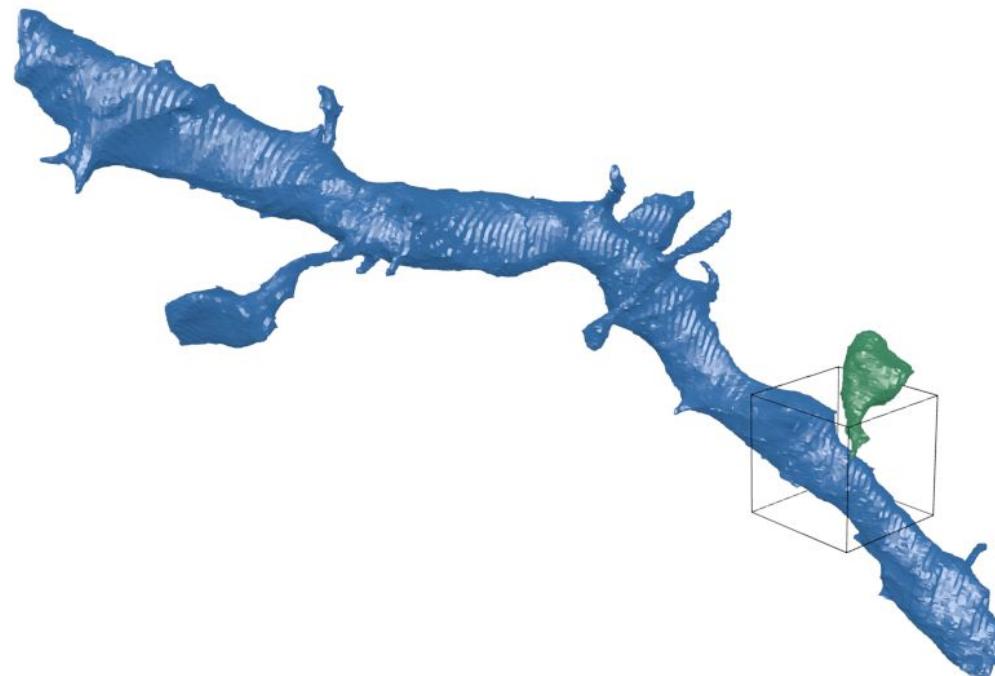
Regions of Interest

Too large and unnecessary detail inhibits learning



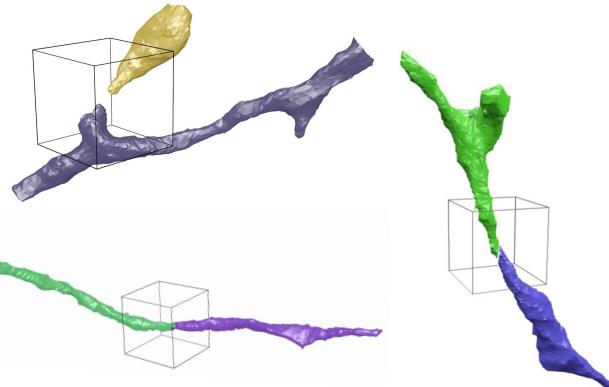
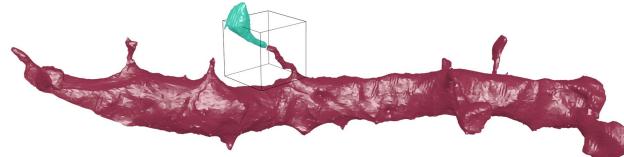
Regions of Interest

Found that cubes of size $1200 \times 1200 \times 1200 \text{ nm}^3$ work well



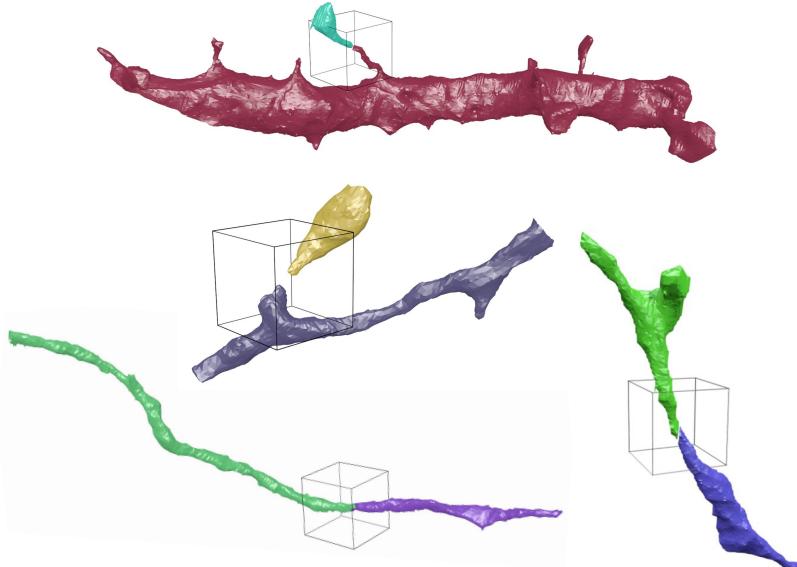
Input Examples

Should Merge

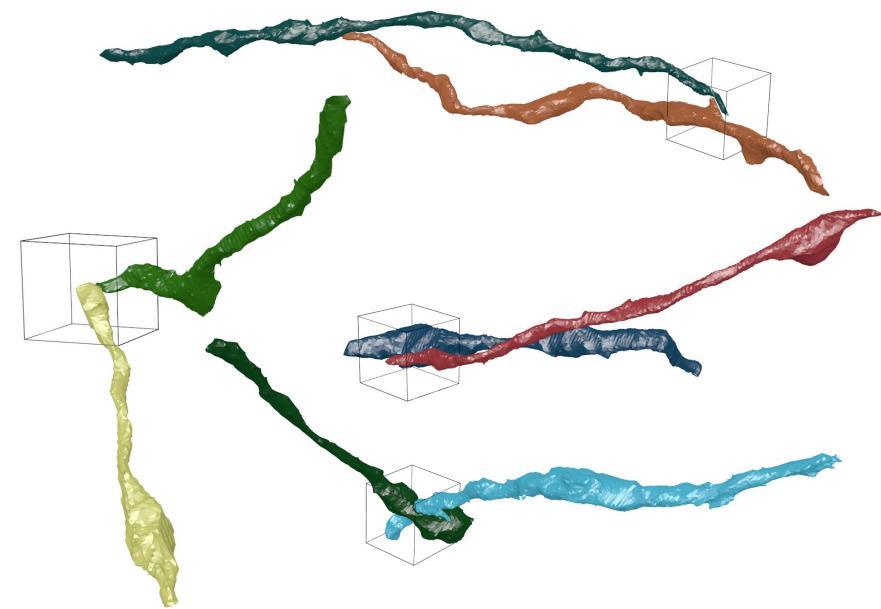


Input Examples

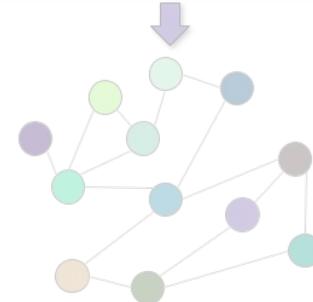
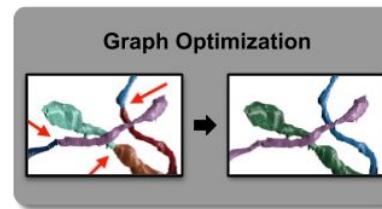
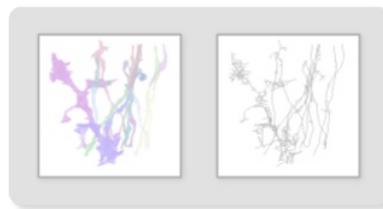
Should Merge



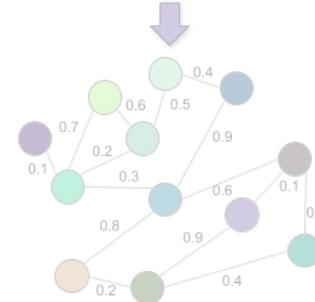
Should Not Merge



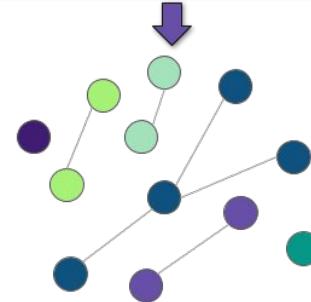
Goal: Partition the graph into individual neurons



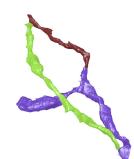
Geometric Priors



Learned Constraints



Topological Restrictions



Multicut

Reformulate the segmentation problem as a multicut graph partitioning one

Multicut

Reformulate the segmentation problem as a multicut graph partitioning one

The final number of segments is not predetermined

Multicut

Reformulate the segmentation problem as a multicut graph partitioning one

The final number of segments is not predetermined

Guarantees a globally consistent solution

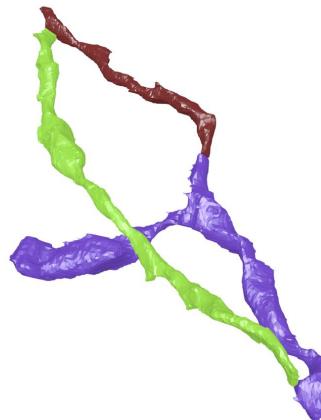
Multicut

Reformulate the segmentation problem as a multicut graph partitioning one

The final number of segments is not predetermined

Guarantees a globally consistent solution

Enforce topological constraints on neurons



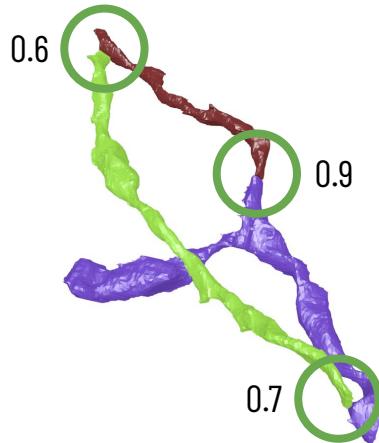
Multicut

Reformulate the segmentation problem as a multicut graph partitioning one

The final number of segments is not predetermined

Guarantees a globally consistent solution

Enforce topological constraints on neurons



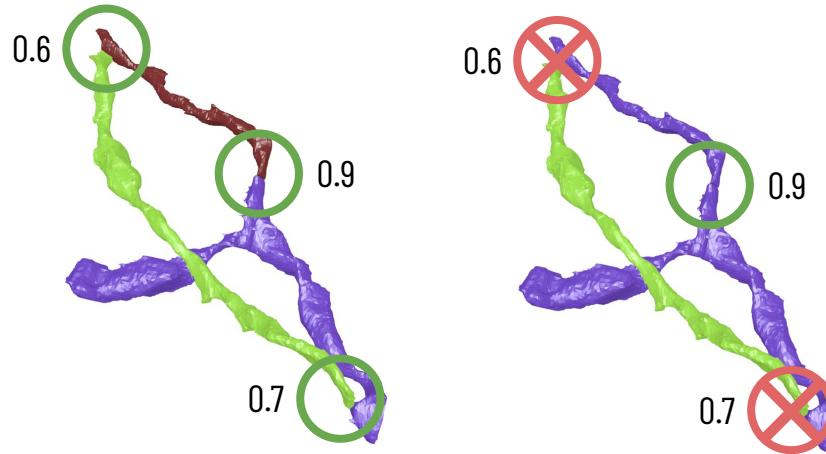
Multicut

Reformulate the segmentation problem as a multicut graph partitioning one

The final number of segments is not predetermined

Guarantees a globally consistent solution

Enforce topological constraints on neurons



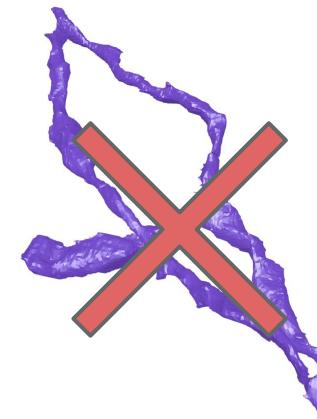
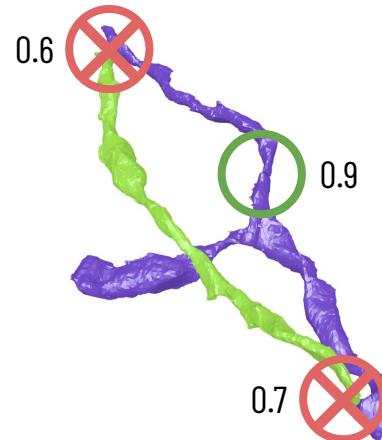
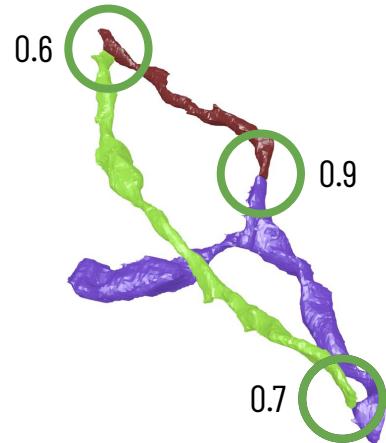
Multicut

Reformulate the segmentation problem as a multicut graph partitioning one

The final number of segments is not predetermined

Guarantees a globally consistent solution

Enforce topological constraints on neurons



Multicut

Reformulate the segmentation problem as a multicut graph partitioning one

Multicut

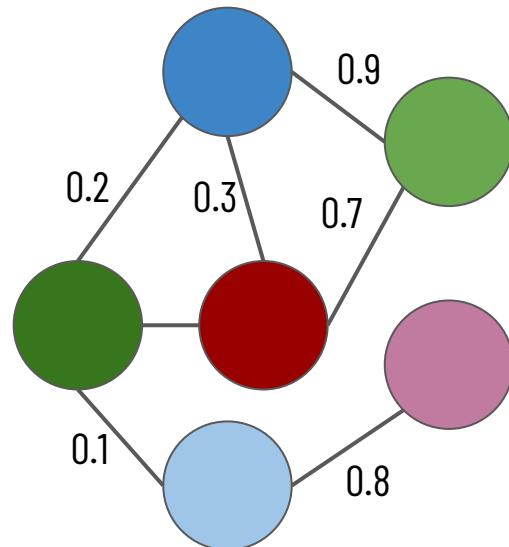
Reformulate the segmentation problem as a multicut graph partitioning one

Guarantees a globally consistent solution

Multicut

Reformulate the segmentation problem as a multicut graph partitioning one

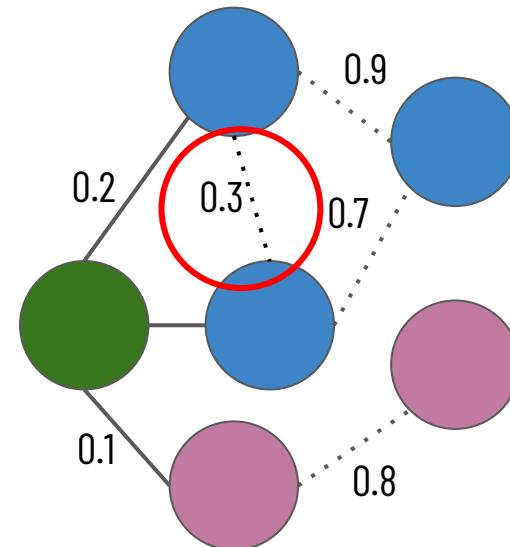
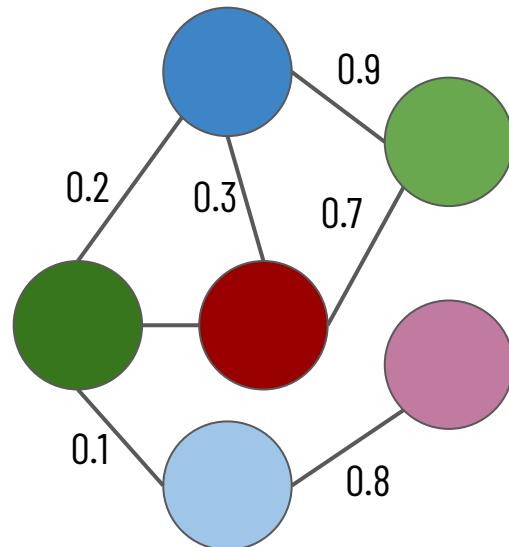
Guarantees a globally consistent solution



Multicut

Reformulate the segmentation problem as a multicut graph partitioning one

Guarantees a globally consistent solution



Multicut

Reformulate the segmentation problem as a multicut graph partitioning one

Guarantees a globally consistent solution

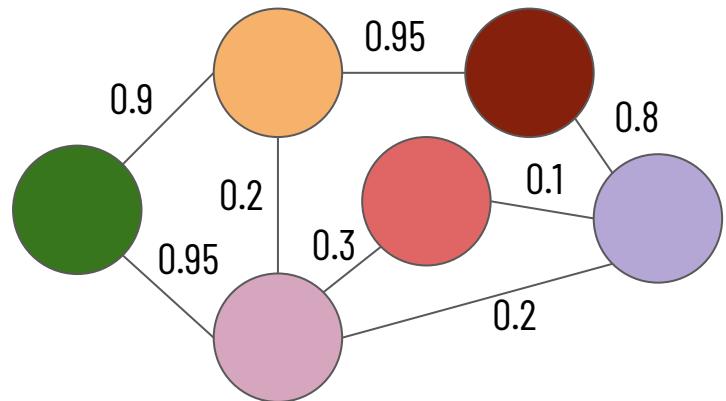
The final number of segments is not predetermined

Lifted Multicut Extension

Costs associated with segmenting any pair of nodes

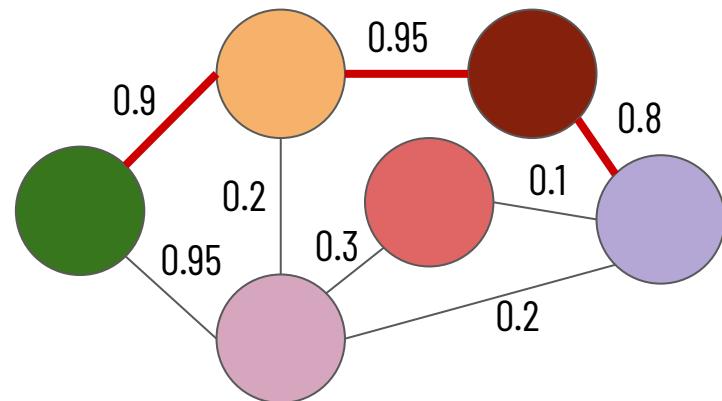
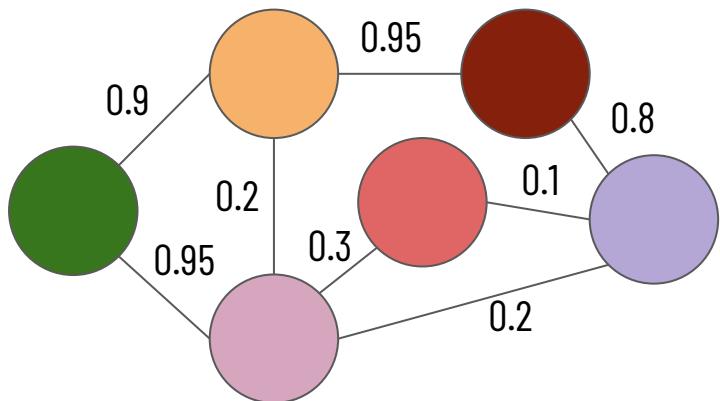
Lifted Multicut Extension

Costs associated with segmenting any pair of nodes



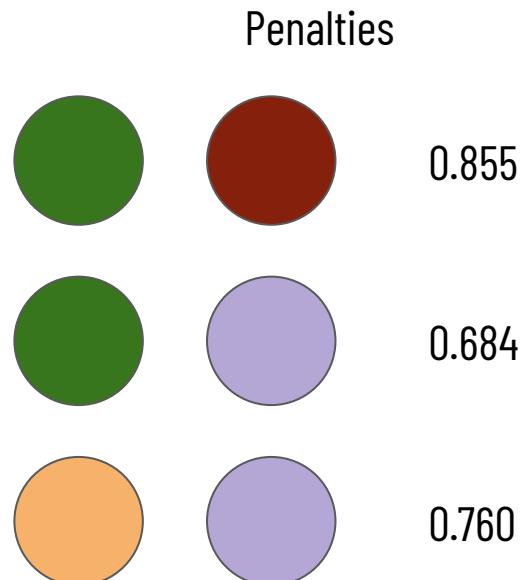
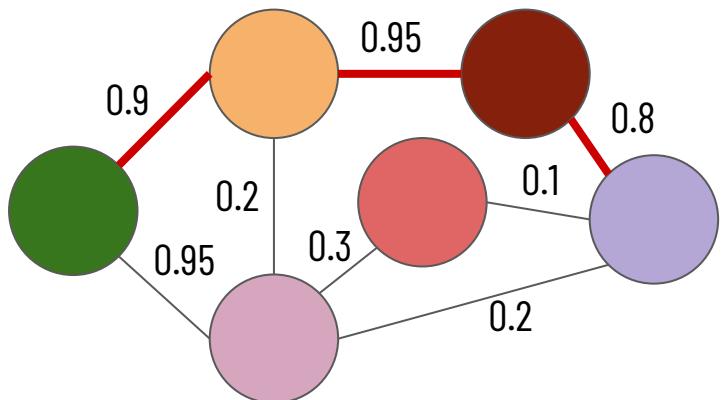
Lifted Multicut Extension

Costs associated with segmenting any pair of nodes



Lifted Multicut Extension

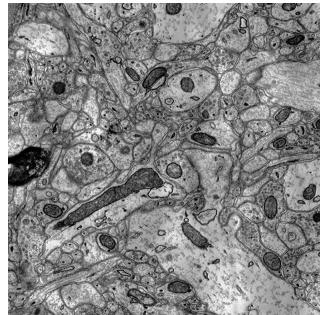
Costs associated with segmenting any pair of nodes



Results

Datasets

Training Data



Kasthuri Vol. 1

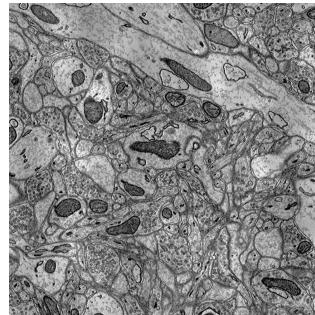
Mouse

$6 \times 6 \times 30 \text{ nm}^3 / \text{vx}$

$1335 \times 1809 \times 338 \text{ vx}$

$8.01 \times 10.85 \times 10.14 \mu\text{m}^3$

Testing Data



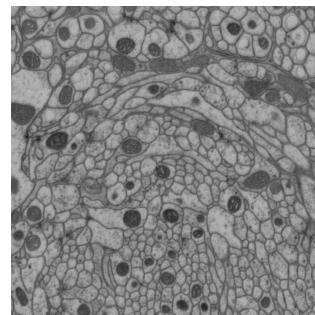
Kasthuri Vol. 2

Mouse

$6 \times 6 \times 30 \text{ nm}^3 / \text{vx}$

$1336 \times 1809 \times 338 \text{ vx}$

$8.02 \times 10.85 \times 10.14 \mu\text{m}^3$



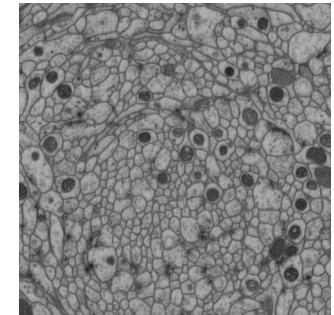
FlyEM Vol. 1

Drosophila melanogaster

$10 \times 10 \times 10 \text{ nm}^3 / \text{vx}$

$999 \times 999 \times 998 \text{ vx}$

$9.99 \times 9.99 \times 9.98 \mu\text{m}^3$



FlyEM Vol. 2

Drosophila melanogaster

$10 \times 10 \times 10 \text{ nm}^3 / \text{vx}$

$999 \times 999 \times 999 \text{ vx}$

$9.99 \times 9.99 \times 9.99 \mu\text{m}^3$

Split Variation of Information

Measure of entropy between segmentation and ground truth

Split Variation of Information

Measure of entropy between segmentation and ground truth

VI Split: Increases if two voxels from the same neuron have different labels



Split Variation of Information

Measure of entropy between segmentation and ground truth

VI Split: Increases if two voxels from the same neuron have different labels



VI Merge: Increases if two voxels from different neurons have the same label



Split Variation of Information

Measure of entropy between segmentation and ground truth

VI Split: Increases if two voxels from the same neuron have different labels

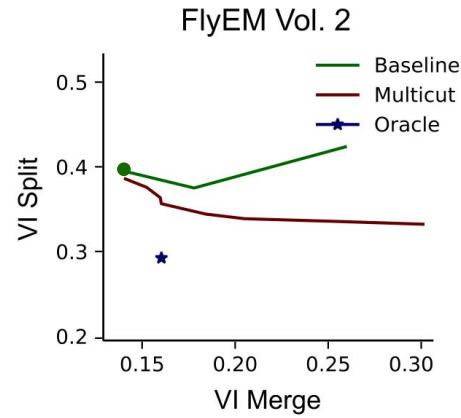
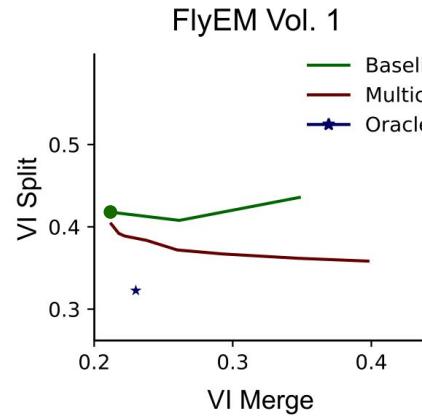
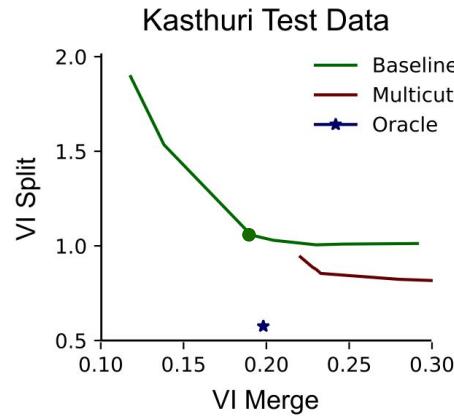


VI Merge: Increases if two voxels from different neurons have the same label



Total Variation of Information = VI Split + VI Merge

Variation of Information

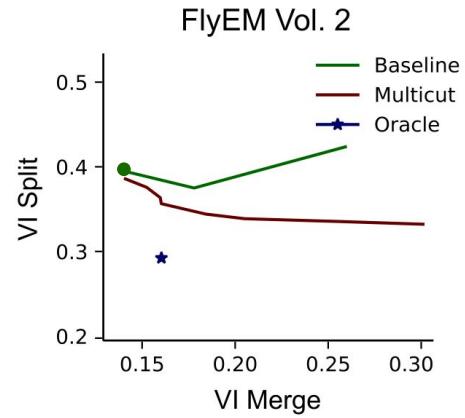
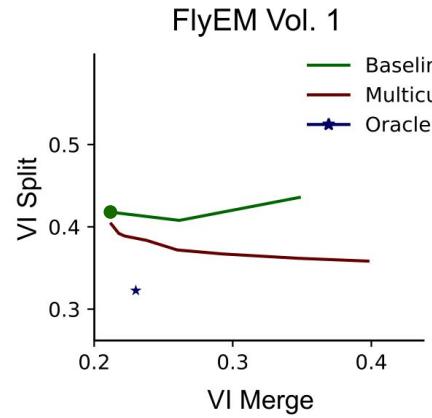
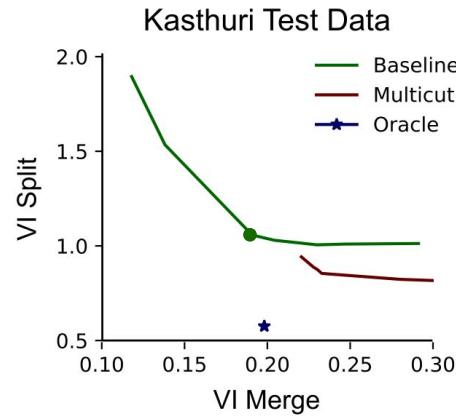


Baseline curve is generated by varying an agglomeration parameter in the Neuroproof algorithm

Green dot represents the input segmentation

Oracle correctly partitions the graph that we extract from the input segmentation

Variation of Information



Total VI Improvement:

10.4%

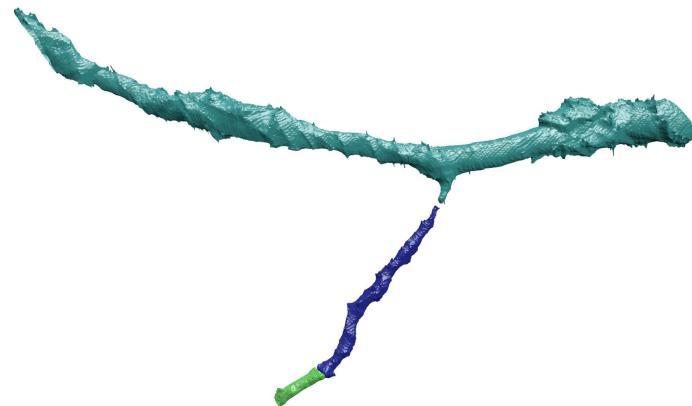
8.9%

5.4%

Qualitative Results



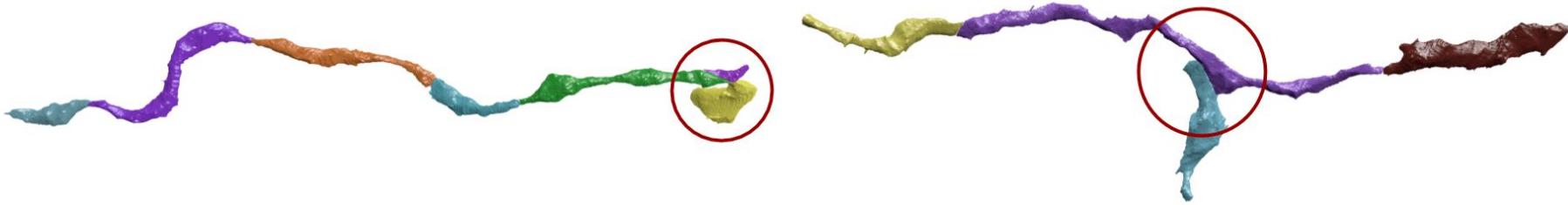
Qualitative Results



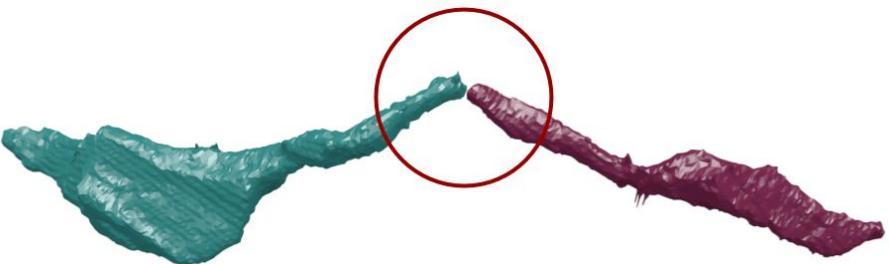
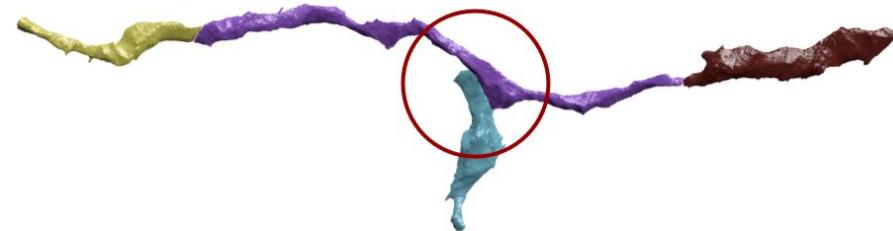
Qualitative Results



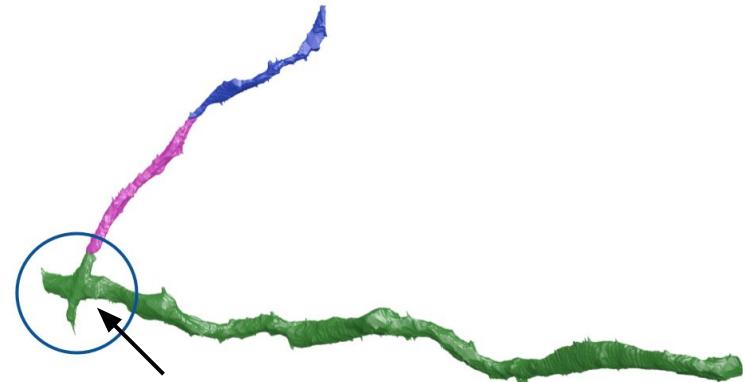
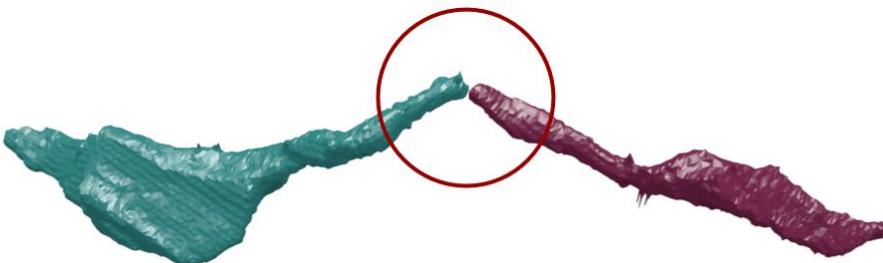
Failure Cases



Failure Cases

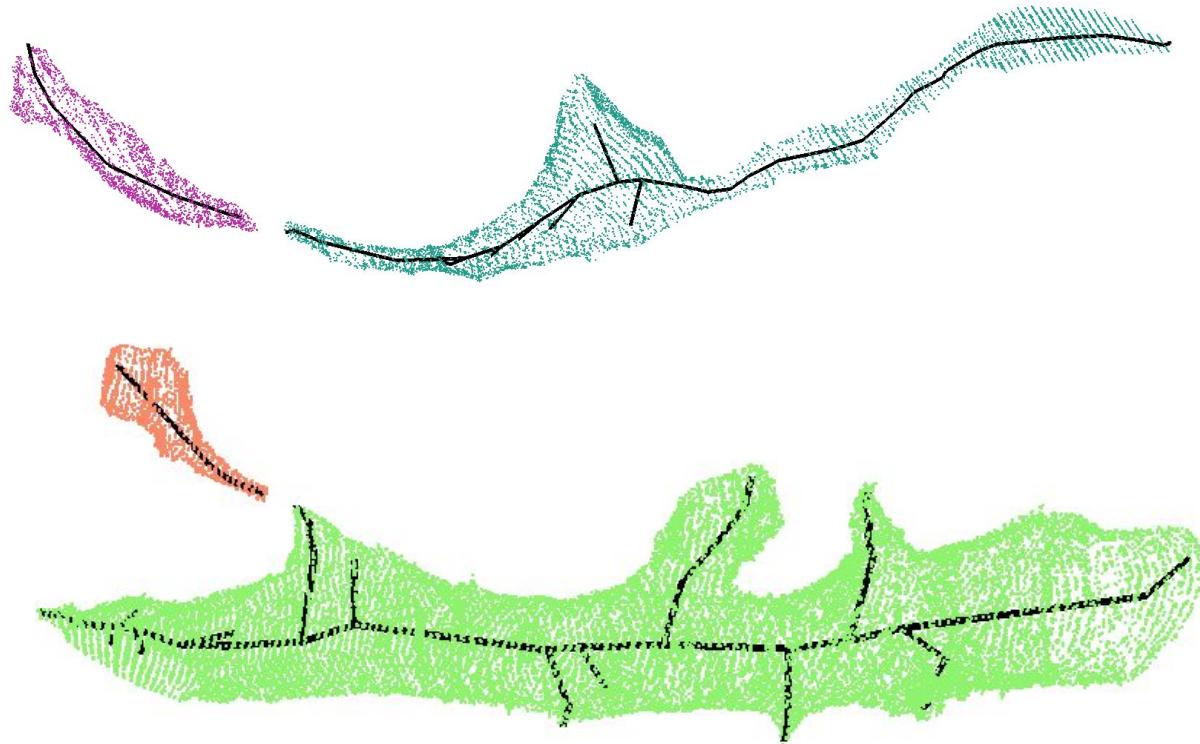


Failure Cases

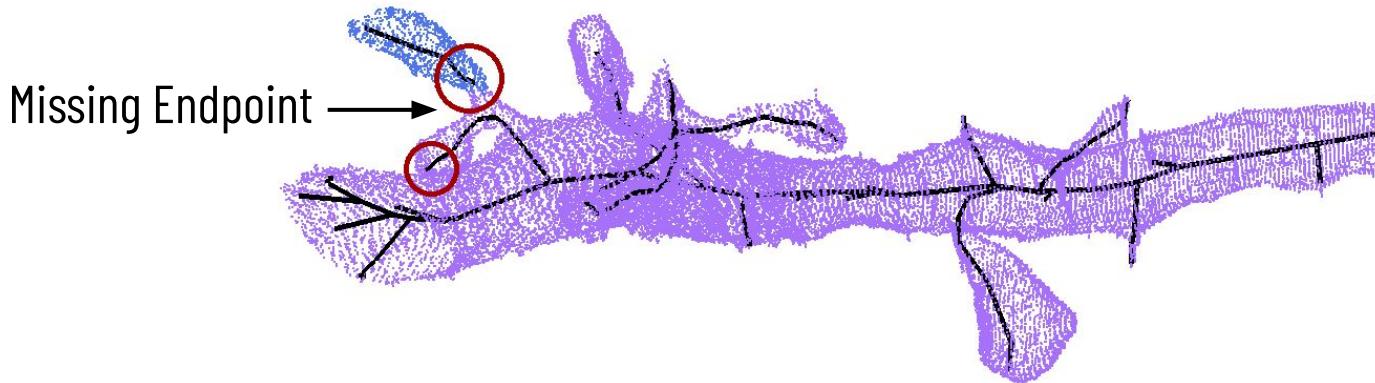
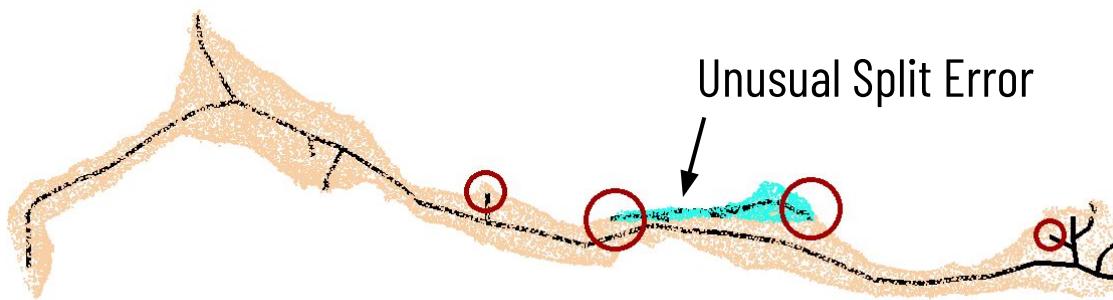


Error in Input Segmentation

Graph Pruning



Failure Cases

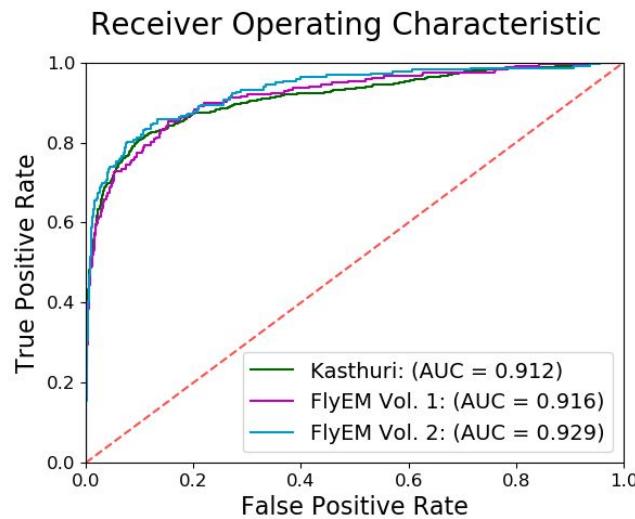


Graph Extraction Results

Table 1: The results of our graph pruning approach compared to the baseline graph with all adjacent regions. We show the number of true merge locations (e.g., 974) compared to total number of edges in the graph (e.g., 25,798) for each case. The number of missed splits corresponds to the number of split errors that our method misses compared to an adjacency matrix.

Dataset	Segment Adjacency	Skeleton Pruning	Missed Splits	Gained Edges
Kasthuri	974 / 25,798	764 / 6,218	307	97
FlyEM Vol. 1	304 / 15,949	212 / 4,578	105	13
FlyEM Vol. 2	298 / 17,614	197 / 4,366	120	19

CNN Results



Accuracies:

Kasthuri	90.4%
FlyEM Vol. 1	94.4%
FlyEM Vol. 2	95.2%

Multicut Results

Table 2: Precision, recall, and accuracy changes between CNN only and CNN paired with graph-optimized reconstructions for the training and three test datasets. The combined method results in better precision and accuracy. The lifted multicut extension provides very slight improvements in recall and accuracy over these three datasets.

Dataset	Multicut			Lifted Multicut		
	Δ Precision	Δ Recall	Δ Accuracy	Δ Precision	Δ Recall	Δ Accuracy
Kasthuri	31.94%	-36.24%	0.71%	-1.01%	0.60%	0.02%
FlyEM Vol. 1	40.87%	-42.37%	1.26%	0.35%	0.85%	0.04%
FlyEM Vol. 2	27.80%	-44.95%	0.33%	0.54%	0.92%	0.04%

Running Times

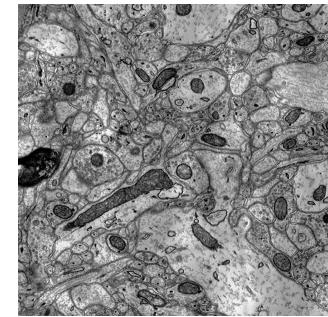
Skeletonization: 0.56 seconds per segment on average

Graph Extraction: 31 seconds

CNN Inference: 124 seconds

Multicut: 37 seconds

~45 minutes



Kasthuri Vol. 1

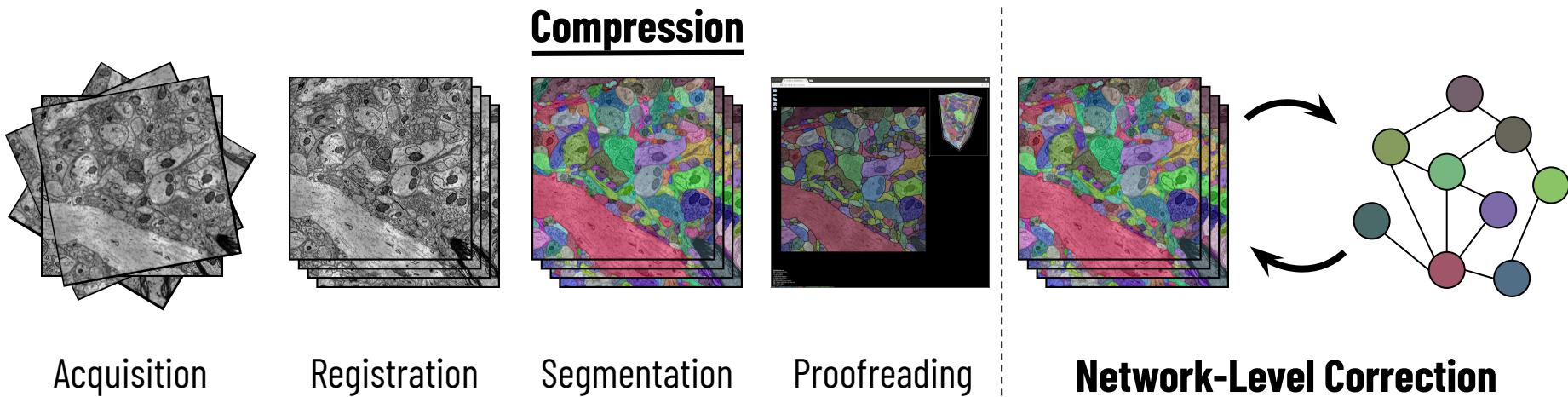
Mouse

$6 \times 6 \times 30 \text{ nm}^3 / \text{vx}$

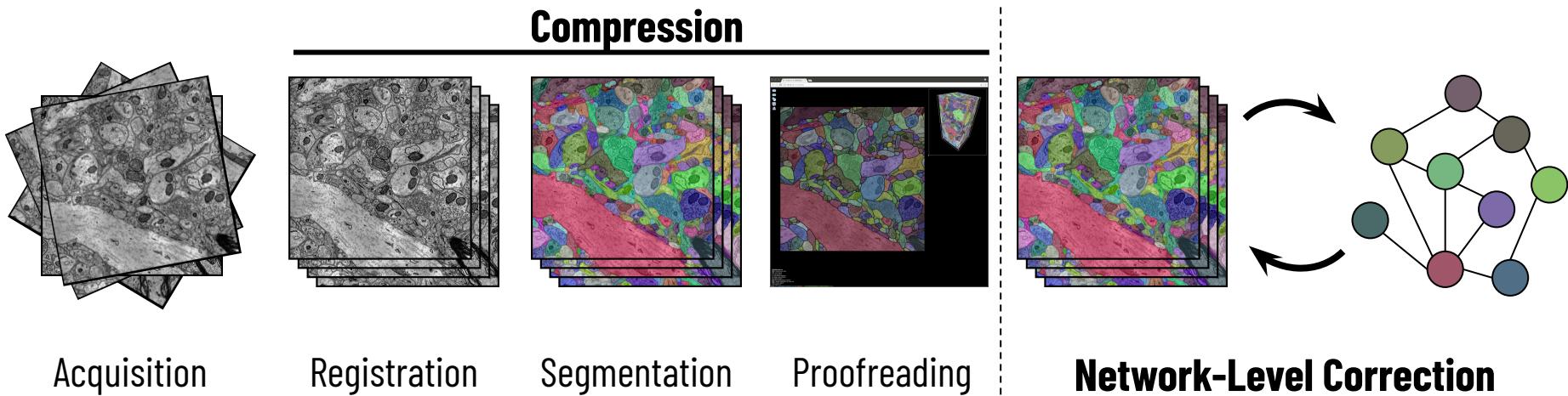
$1335 \times 1809 \times 338$

$8.01\mu\text{m} \times 10.85\mu\text{m} \times 10.14\mu\text{m}$

Connectomics Pipeline

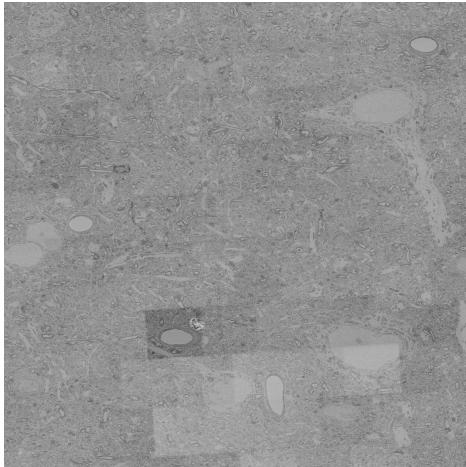


Connectomics Pipeline



Compression Future Work

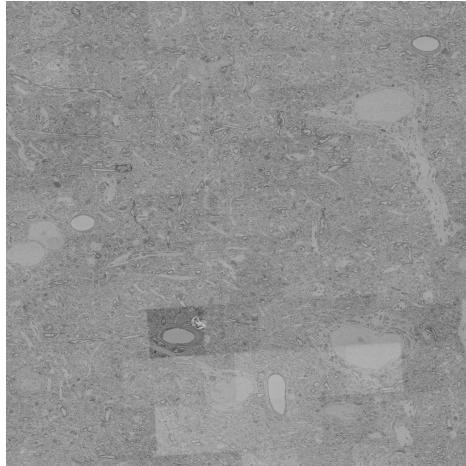
Specialized compression techniques for raw images (currently use JPEG 2000)



Compression Future Work

Specialized compression techniques for raw images (currently use JPEG 2000)

Use convolutional neural networks to improve compression of images

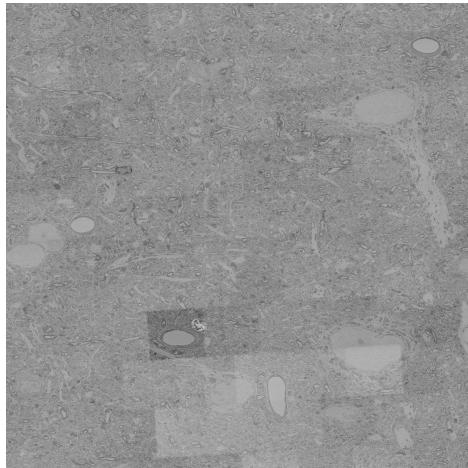


Compression Future Work

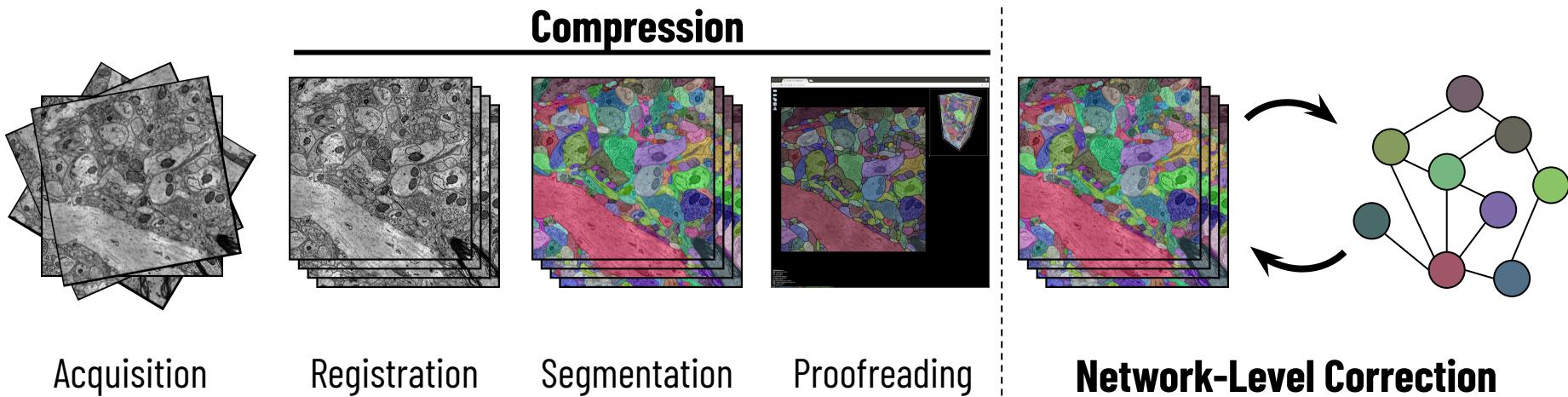
Specialized compression techniques for raw images (currently use JPEG 2000)

Use convolutional neural networks to improve compression of images

Add random access to Compresso for smoother real-time visual analysis of large datasets

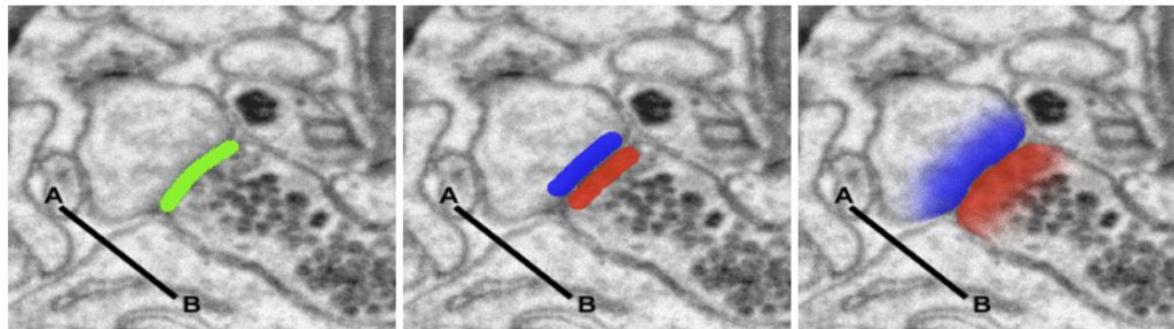


Connectomics Pipeline



Additional Biological-Constraints

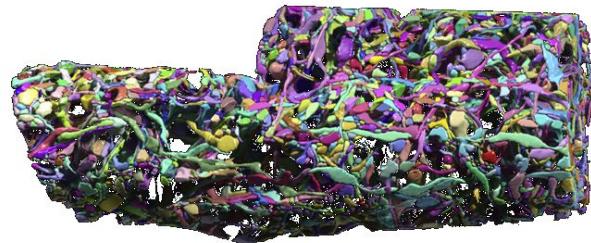
Use synaptic information to prevent dendrites and axons from merging



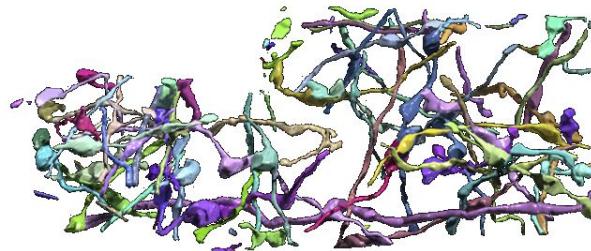
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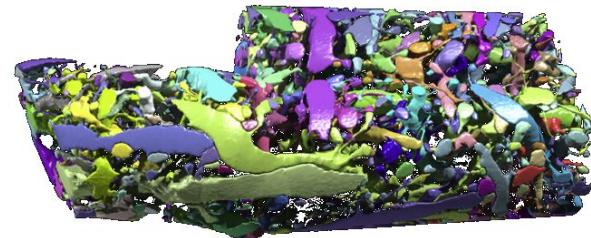
Classify neuron types to prevent inhibitory and excitatory neurons from merging



Excitatory Axons



Inhibitory Axons



Dendrites

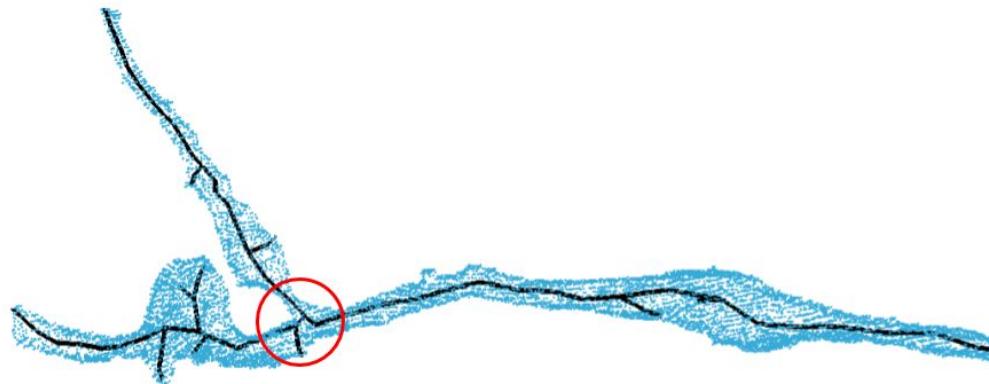
Address Merge Errors

Currently difficult because the number of potential split candidates grows quickly

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Use skeletons to quickly locate potential merge errors

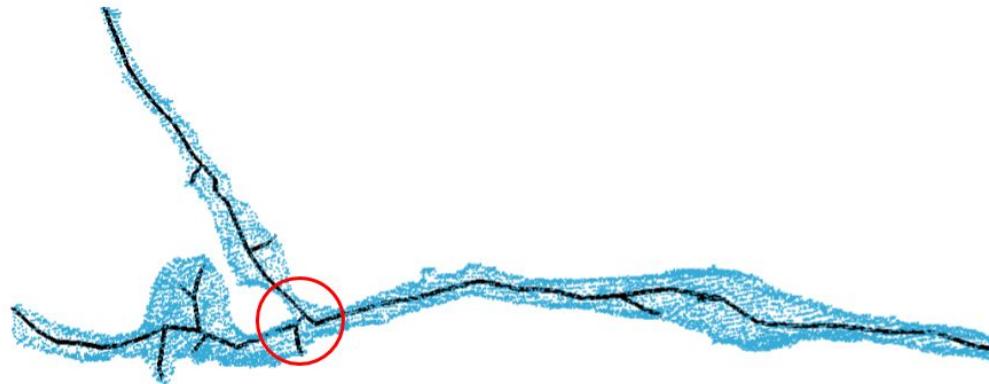


Address Merge Errors

Currently difficult because the number of potential split candidates grows quickly

Use skeletons to quickly locate potential merge errors

Divide segments with a watershed algorithm and use existing CNN



Thank you!

Questions?