E4 Project: MALIS

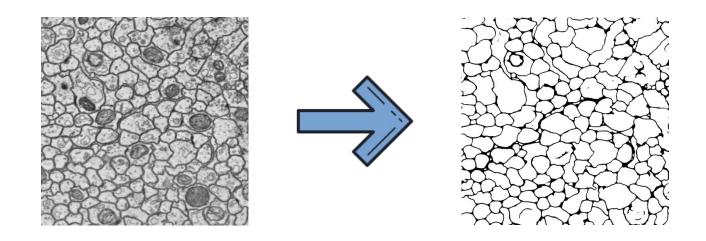
Work available at : *github.com/garridoq/malis-project*

Supervisor: Laurent NAJMAN

Quentin GARRIDO Tiphanie LAMY-VERDIN Raphaël LAPERTOT Josselin LEFEVRE Annie LIM

Introduction

Drosophila connectome segmentation

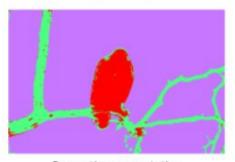


⇒ Brain architecture

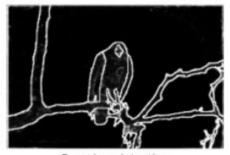
Image segmentation



Original image



Semantic segmentation



Boundary detection



Object detection

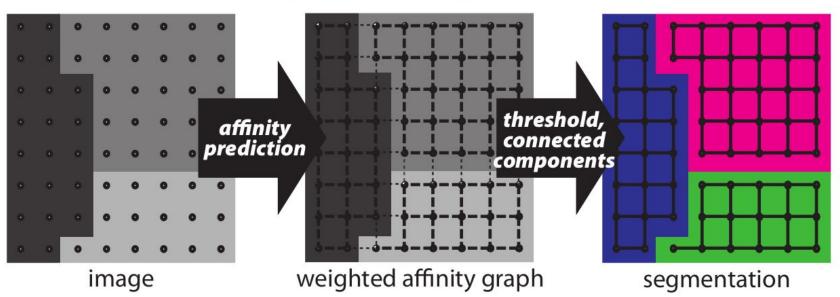
Summary

- Method's presentation
- Our implementation
- Results
- Project organization

Method's presentation

S. Turaga et al., "Maximin affinity learning of image segmentation," 2009

segmentation algorithm



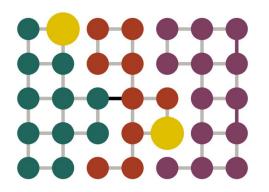
How to predict affinity?

Various methods:

- Distance between pixels
- Any kind of classifier that is smooth
- Neural Networks

Rand Index

$$1 - RI(\hat{S}, S) = {N \choose 2}^{-1} \sum_{i < j} |\delta(s_i, s_j) - \delta(\hat{s}_i, \hat{s}_j)|$$



Belong to same object?

 $\begin{array}{cc} {\rm Predicted} & {\rm Truth} \\ {\rm Yes} & {\rm No} \end{array}$

Computing the Maximin affinity

- Maximin path :
$$P_{ij}^* = \arg\max_{P \in \mathcal{P}_{ij}} \min_{\langle k,l \rangle \in P} A_{kl}$$

- Maximin affinity :
$$A_{ij}^* = \max_{P \in \mathcal{P}_{ij}} \min_{\langle k,l \rangle \in P} A_{kl}$$

Property: Any path in a MST is a Maximin path

Computing the Maximin affinity

First paper approach:

Process:

- Pick a single pair of random pixels i,j
- Find the maximin affinity between them



Data from the MST is not used fully

J. Funke et al., "Large Scale Image Segmentation with Structured Loss Based Deep Learning for Connectome", July 2019.

Computing the Maximin affinity

Second paper approach: Constrained MALIS

We want to compute a loss over all pairs of points, which gives us:

$$L(s, a) = \sum_{u,v \in F} l(\delta(u, v), a(mm(u, v))).$$

This can be reduced to a quasilinear computation:

$$w_P(e) = |\{(u, v) \in F^2 \mid \delta(u, v) = 1, \ e = \min(u, v)\}|.$$

 $w_N(e) = |\{(u, v) \in F^2 \mid \delta(u, v) = 0, \ e = \min(u, v)\}|.$

$$L(s, a) = \sum_{e \in MST(G)} w_P(e)l(1, a(e)) + w_N(e)l(0, a(e))$$

Constrained Malis loss

Computing wp and wn:

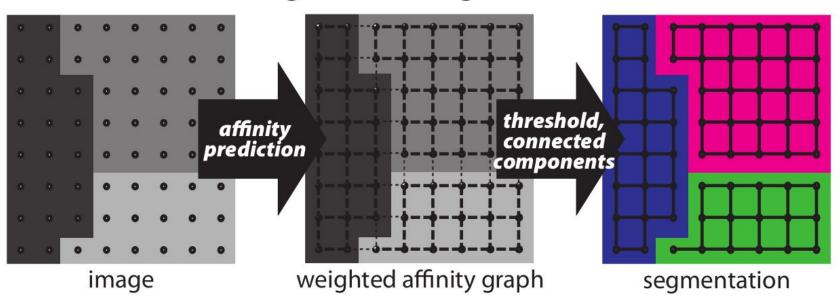
Adding an edge e to our MST merges two trees T_1 and T_2

Then
$$w_p=\sum_{i\in\{1,...k\}}|V^i_{T_1}||V^i_{T_2}|$$

$$w_n=\sum_{i\neq j\in\{1,...k\}}|V^i_{T_1}||V^j_{T_2}|=|V_{T_1}||V_{T_2}|-w_p$$

MALIS' method

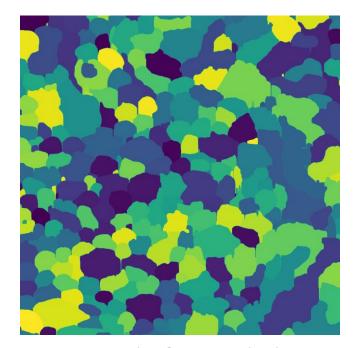
segmentation algorithm



Additional post processing

Examples

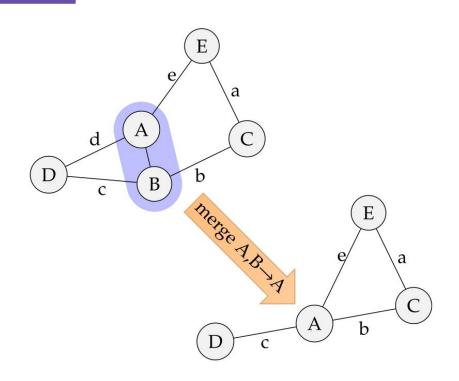
- Watershed
- Watershed + deletion of small regions
- Mumford Shah + cut
- Watershed + agglomeration (as used in the improved version of MALIS)



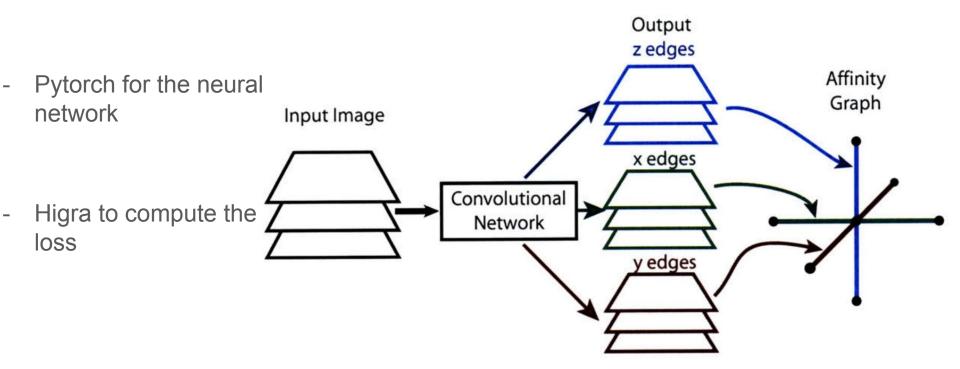
Result of a watershed

Agglomeration of objects

- Compute a Region Adjacency Graph
- Edge values are the affinity between both objects
- Merge object with smallest edge value between them



Our implementation

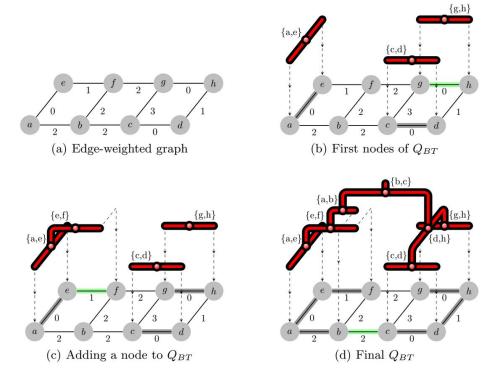


Using a MST and a BPT

The BPT contains all the data for computing

$$w_p = \sum_{i \in \{1, \dots k\}} |V_{T_1}^i| |V_{T_2}^i|$$

and w_n



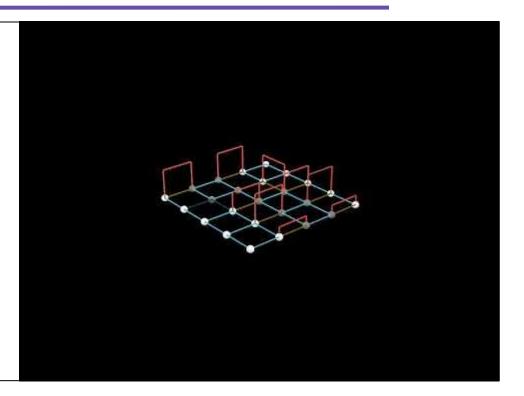
Visualizing the construction of the MST & BPT

Light blue: Low affinity

Dark blue: High affinity

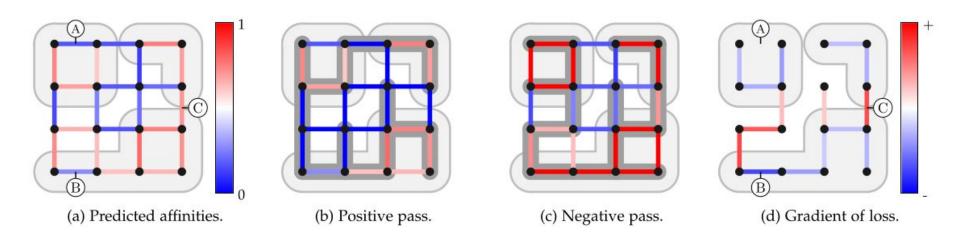
Yellow: Maximum Spanning Tree

Red: Binary Partition Tree



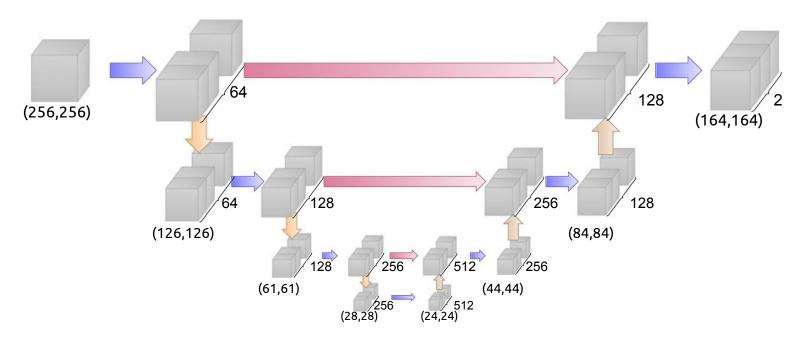
Two pass loss

$$L(s, a) = \sum_{e \in MST(G)} w_P(e) l(1, a(e)) + w_N(e) l(0, a(e))$$



J. Funke *et al.*, "Large Scale Image Segmentation with Structured Loss Based Deep Learning for Connectome", July 2019. ¹⁸

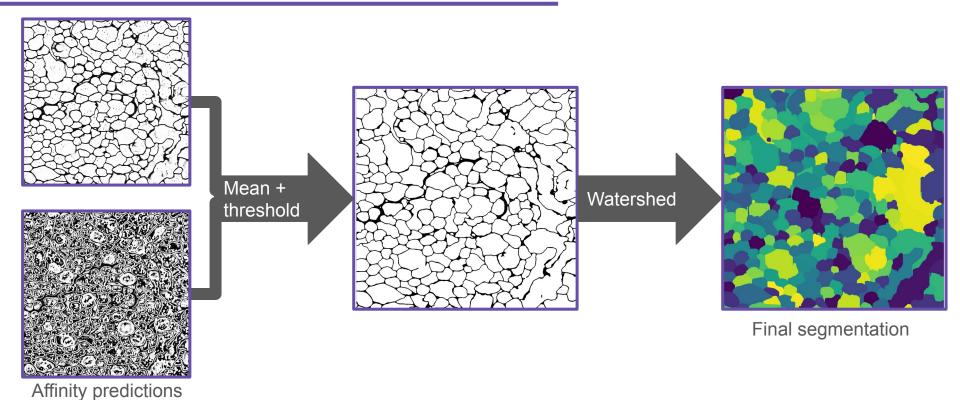
Results: U-net architecture



Architecture used for the experiments

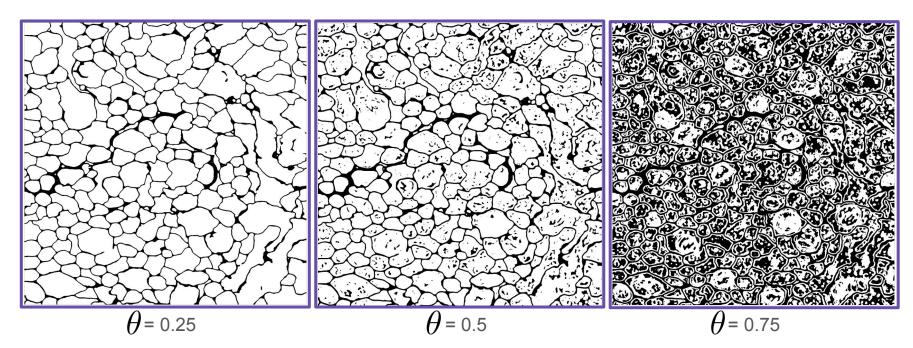
J. Funke *et al.*, "Large Scale Image Segmentation with Structured Loss Based Deep Learning for Connectome", July 2019. ¹⁹

Results: Post processing used



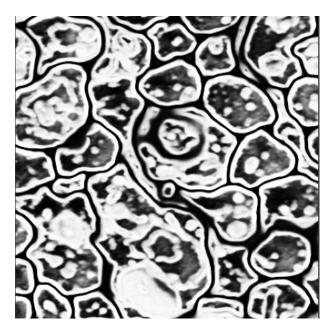
Results: Post processing used

Influence of threshold value

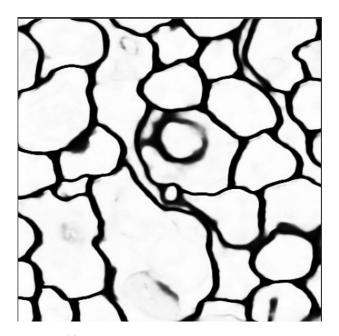


Discrepancies between affinities

Prediction difference between X and Y axis:

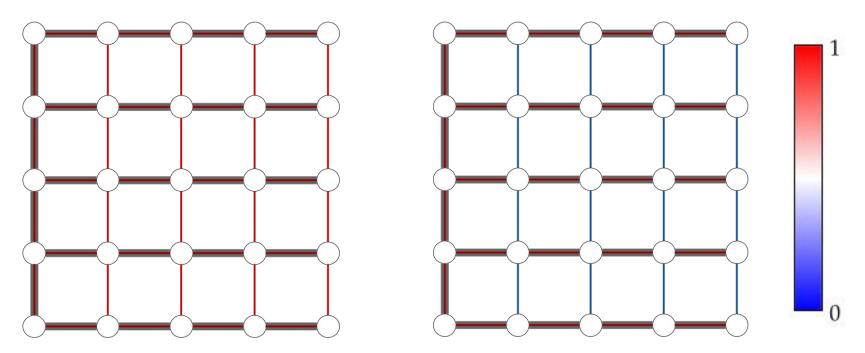


Affinity along the x axis



Affinity along the y axis

Graphs with the same MALIS loss



Both are valid, and give the same loss, but the left one is more desirable

Results: CREMI dataset

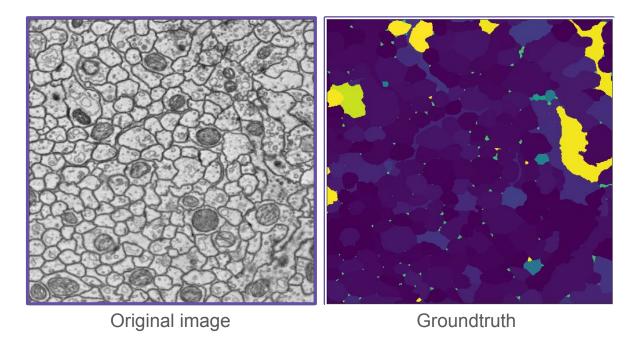
Dataset presentation:

Image size : 1250x1250x125

Number of images used: 1

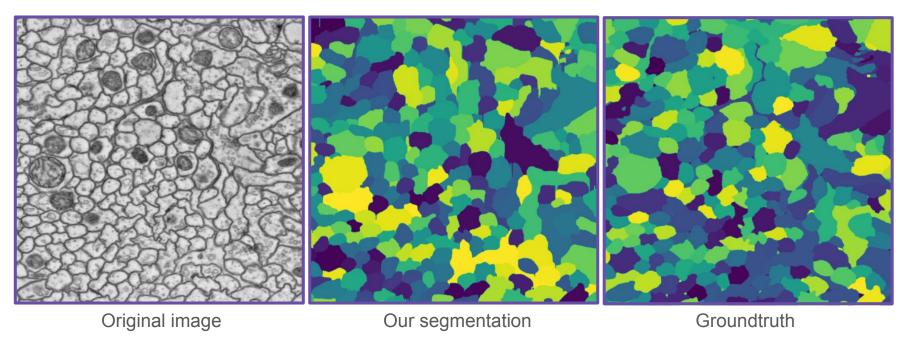
Split train/test: 100/25

Evaluation using a python 2 library



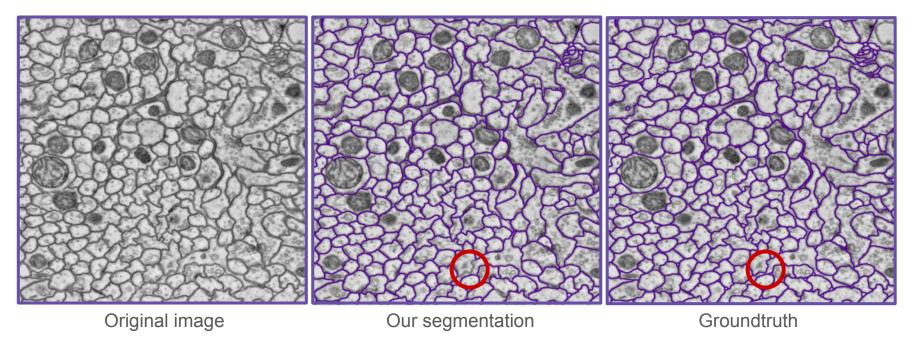
Results: CREMI dataset

Example results: CREMI volume A (Test set)



Results: CREMI dataset

Example results: CREMI volume A (Test set)



Results: Metrics used

Rand index:

$$R(X,Y) = {N \choose 2}^{-1} \sum_{i < j} |\delta(X_i, X_j) - \delta(Y_i, Y_j)|$$

VOI merge and split:

$$VOI(X,Y) = \underbrace{H(X|Y)}_{\text{VOI split}} + \underbrace{H(Y|X)}_{\text{VOI merge}}$$

CREMI score:

$$CREMI = \sqrt{VOI(X,Y) \times (1 - R(X,Y))}$$

Results: CREMI dataset Training set

Numerical results

	Rand index	VOI merge (lower is better)	VOI split (lower is better)	CREMI score (lower is better)
FCN + MALIS	0.61	1.25	1.03	0.94
U-Net	0.58	0.91	0.52	0.78
U-Net MALA	0.83	0.46	0.54	0.42

Results: CREMI dataset Test set

Numerical results

	Rand index	VOI merge (lower is better)	VOI split (lower is better)	CREMI score (lower is better)
FCN + MALIS	0.53	1.57	1.38	1.18
U-Net	0.52	1.07	0.47	0.87
U-Net MALA	0.80	0.50	0.57	0.46
SOTA (in 3D)	0.89	0.115	0.339	0.221

Project organization

- Meetings (Hangouts)
- Weekly reports
- Trello
- Jupyter notebooks
- Social networks





Difficulties encountered

- Scientific papers
- Basic knowledge
- Higra
- PyTorch
- Quarantine



Conclusion

Work available at : github.com/garridoq/malis-project