Tissue Segmentation by Machine Learning and Classical Methods on Multi-Modal X-ray Imaging

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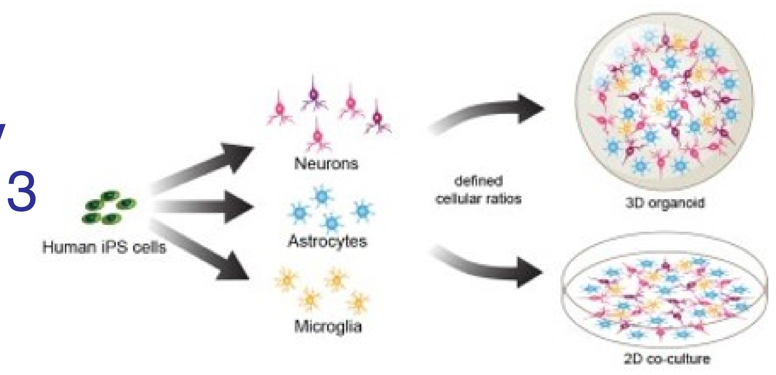
AIM

Brain organoids are tissues cultured in-vitro from human stem cells. They recreate a 3 dimensional structure of the brain.

Organoids can be used in various research areas such as : neurodevelopmental studies, disease modeling or drug screening.

The instrumentation provided by ESRF beamlines ID16A and ID13 allows to image such structures at the nanoscale.

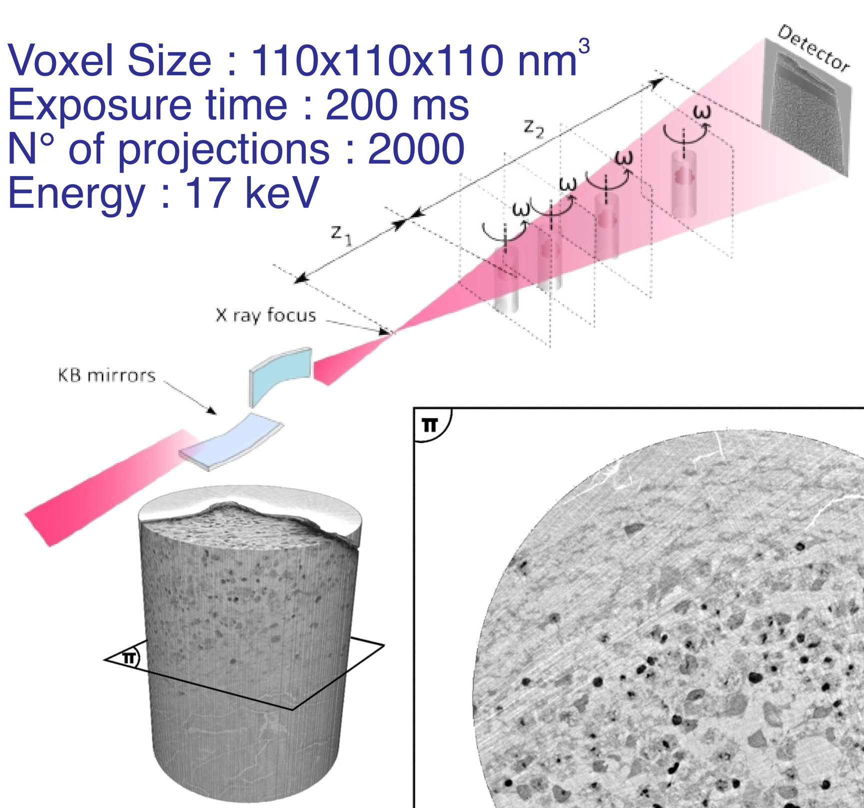


The aim of this project is to develop machine learning workflows to segment the provided data for futher analysis.

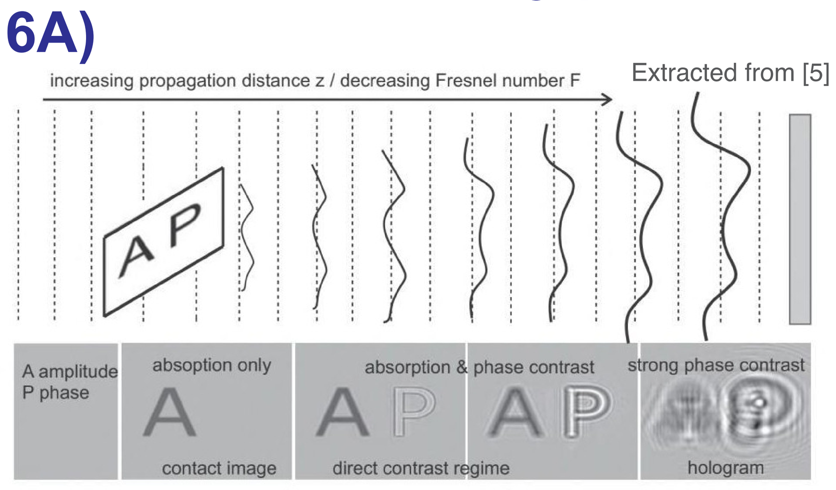
Imaging modalities

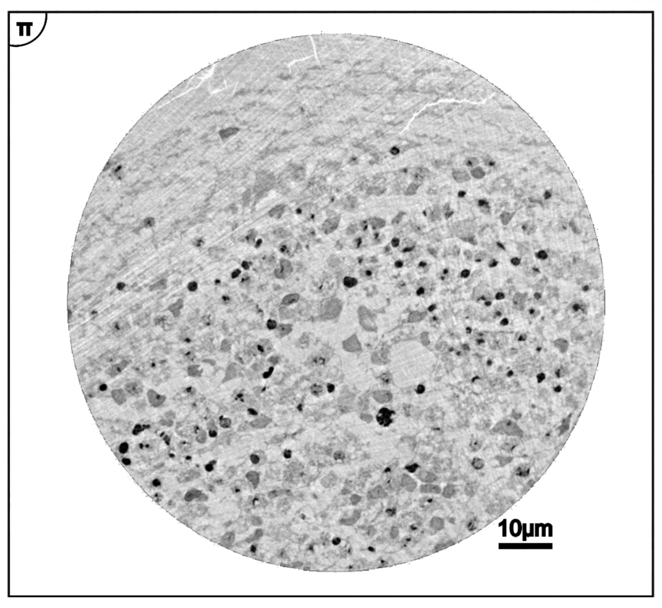
XNH: 3D reconstructed volumes of unstained tissues by phase-contrast tomography (Beamline ID16A)

Voxel Size : 110x110x110 nm^3
Exposure time : 200 ms
N° of projections : 2000
Energy : 17 keV



Extracted from [5]

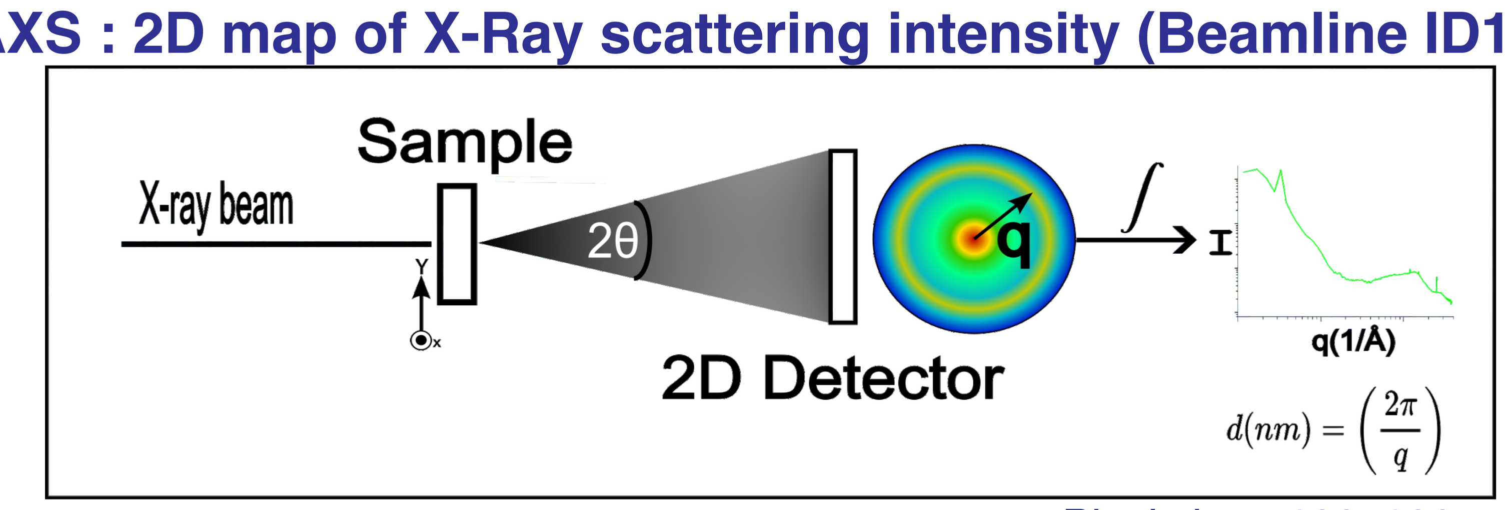




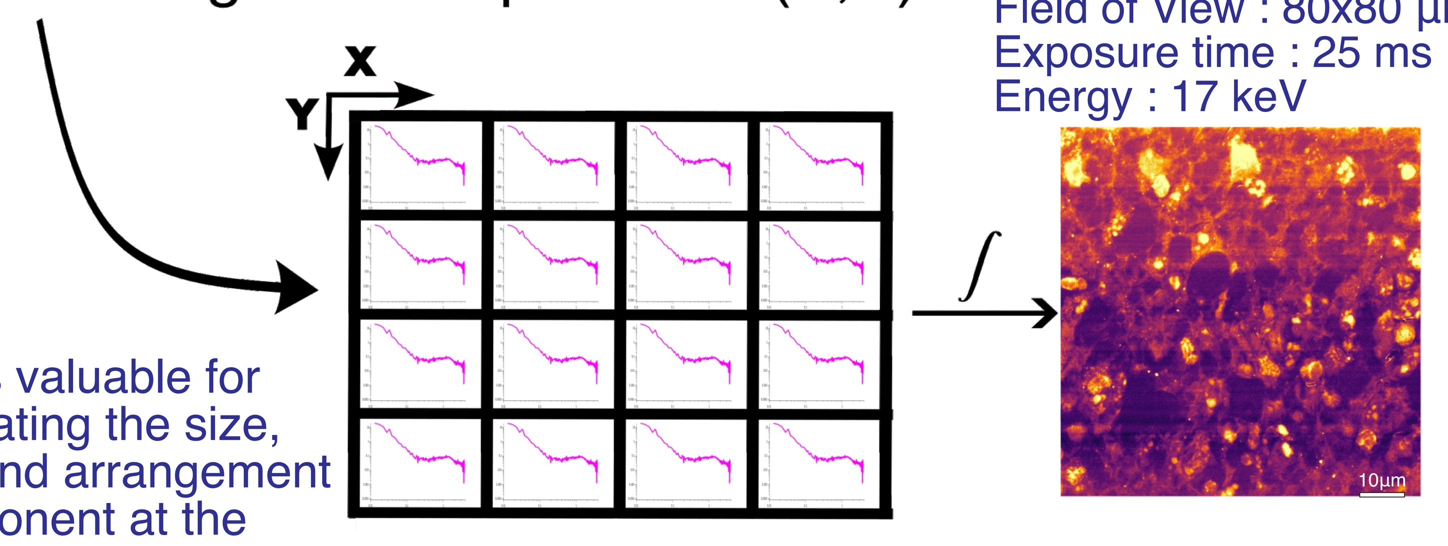
Thanks to the high coherence of the synchrotron beam, X-ray Nano Holotomography can map the electron density in a sample with a resolution at the nano scale.

This technique requires two reconstruction steps :
1) Phase retrieval
2) Tomographic reconstruction

SAXS : 2D map of X-Ray scattering intensity (Beamline ID13)



Scanning the Sample in 2D (X,Y)

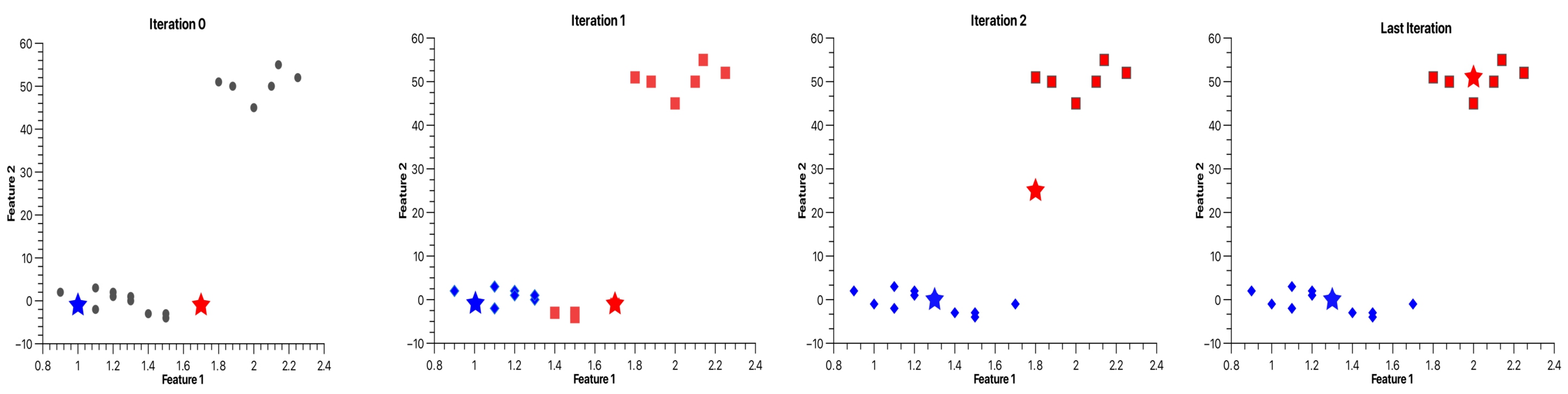


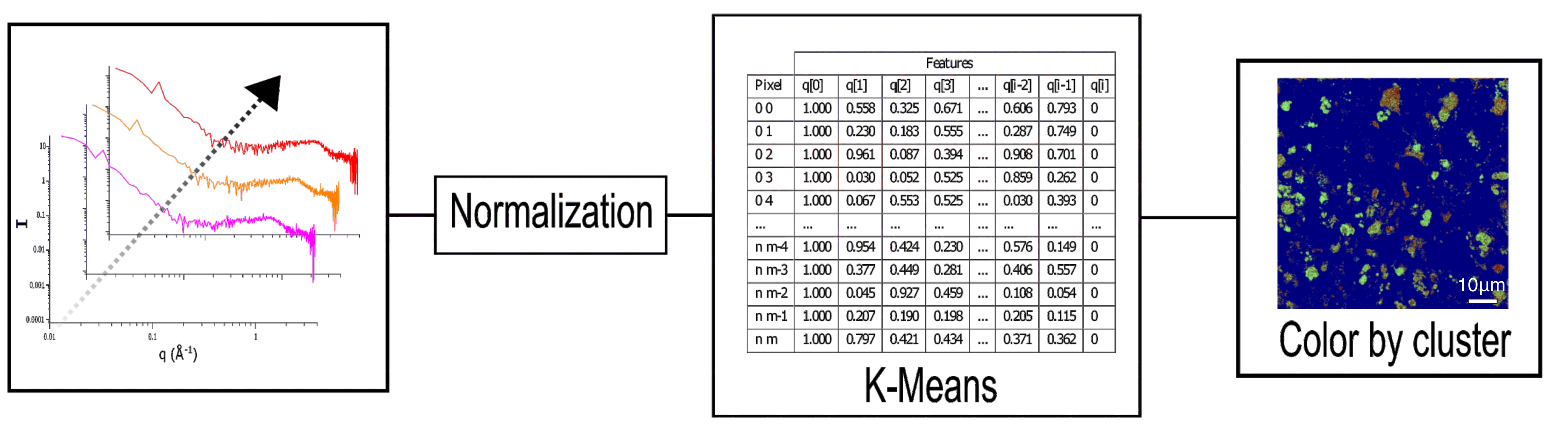
Pixel size : 100x100 nm^2
Field of View : 80x80 μm^2
Exposure time : 25 ms
Energy : 17 keV

SAXS is valuable for investigating the size, shape and arrangement of component at the nanoscale

Results : Unsupervised Methods

K-Means Clustering [1]



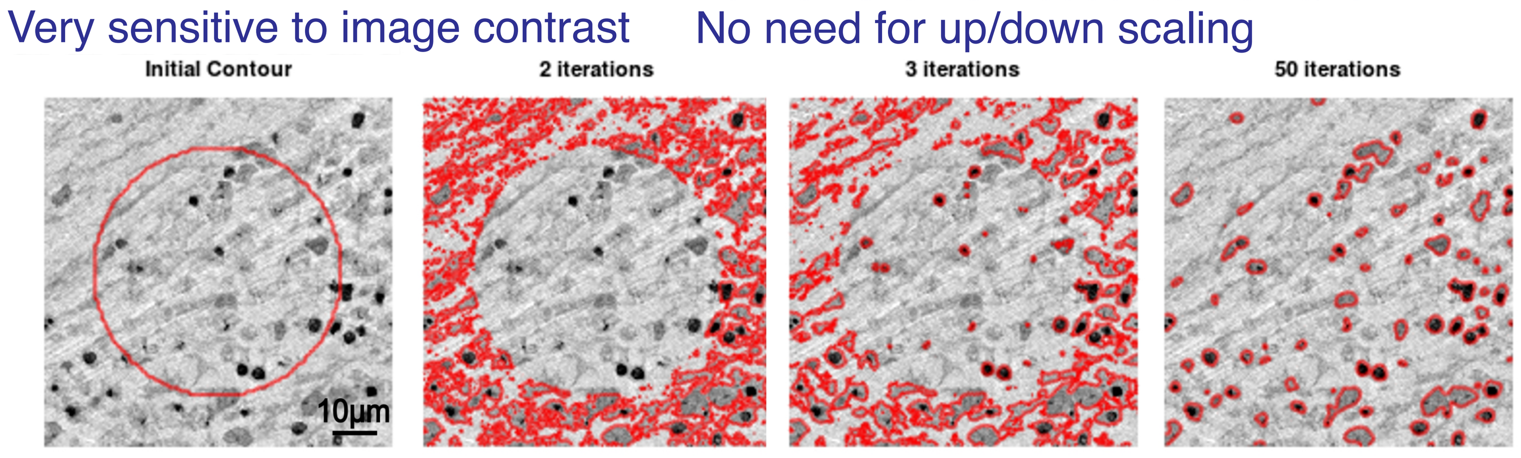


Results : Manual Processing

Chan-Vese Segmentation [2]

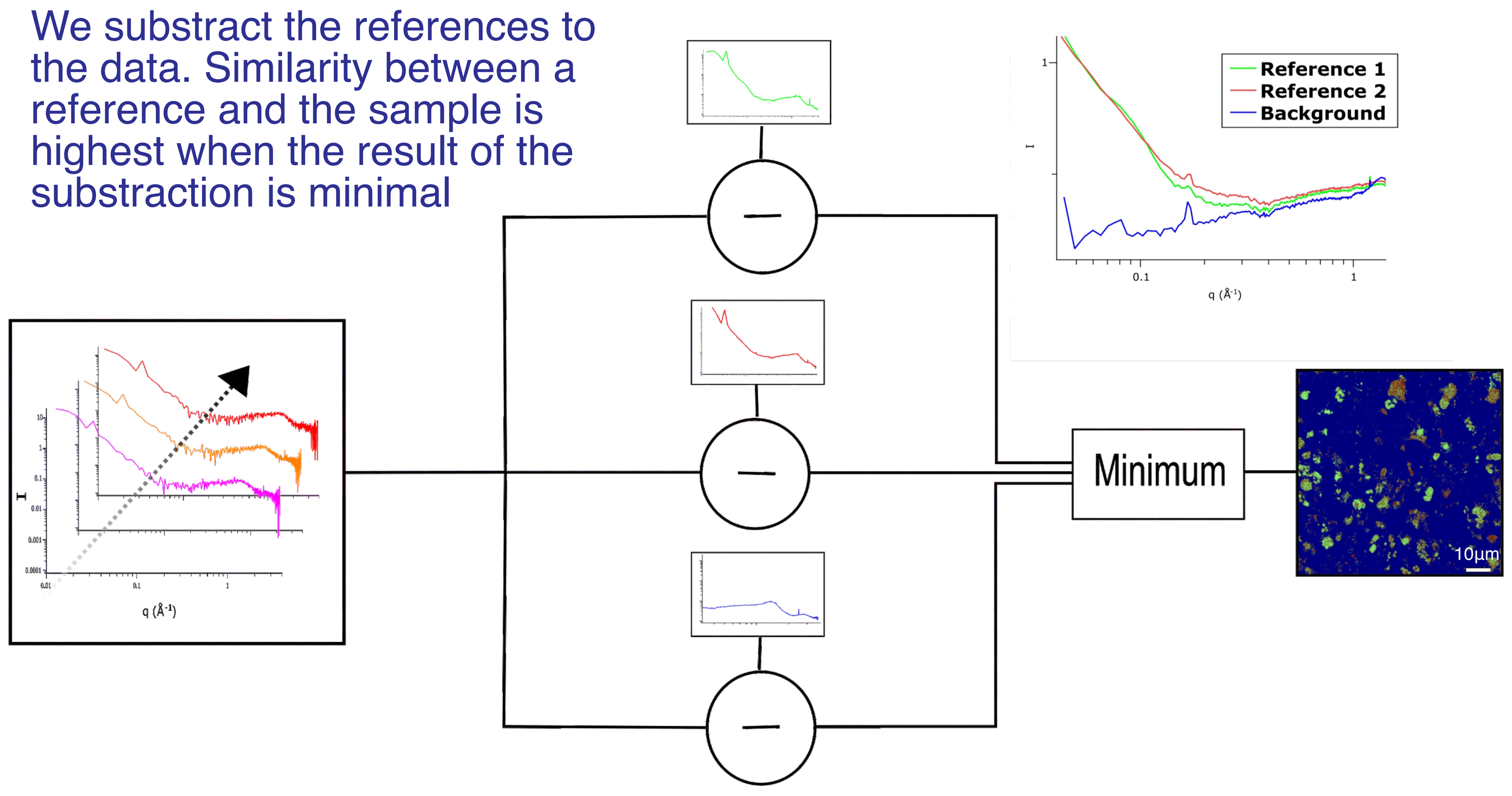
Cons :
Not based on AI
Very sensitive to image contrast

Pros :
Low CPU/GPU Resource Demand
No need for up/down scaling



Reference based classification

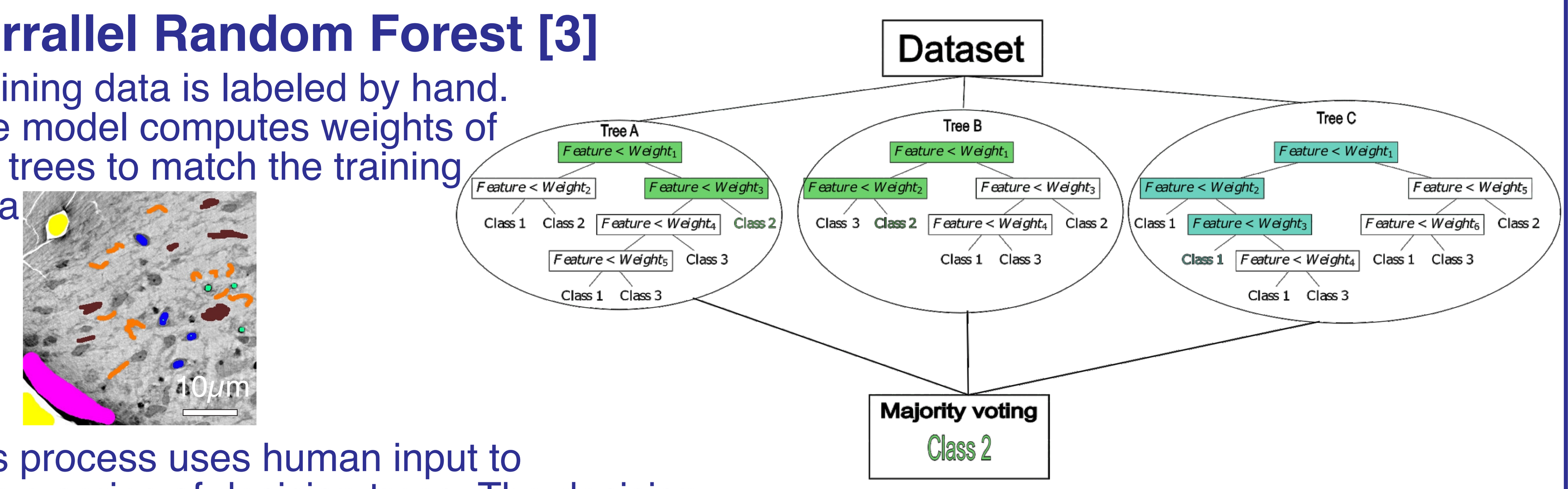
We substract the references to the data. Similarity between a reference and the sample is highest when the result of the substraction is minimal



Results : Supervised Methods

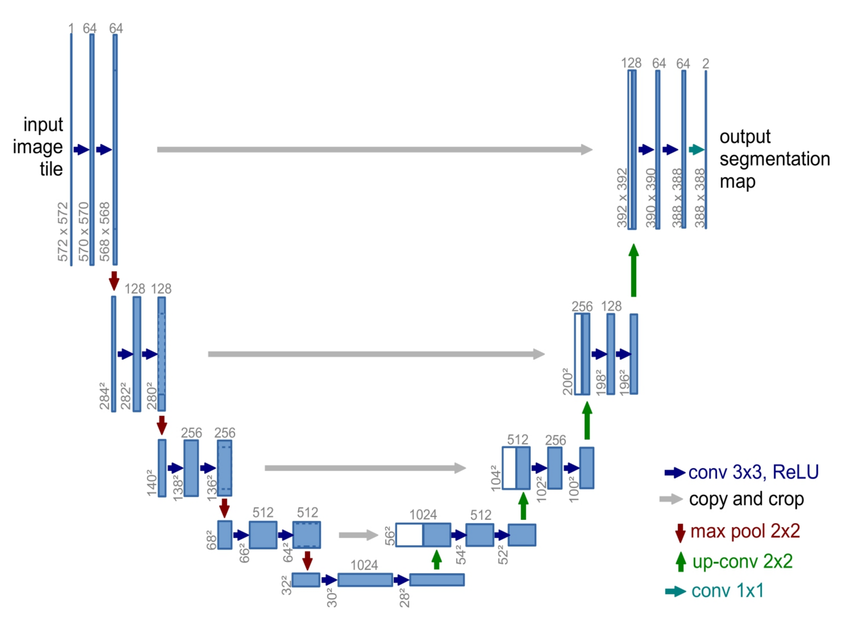
Parrallel Random Forest [3]

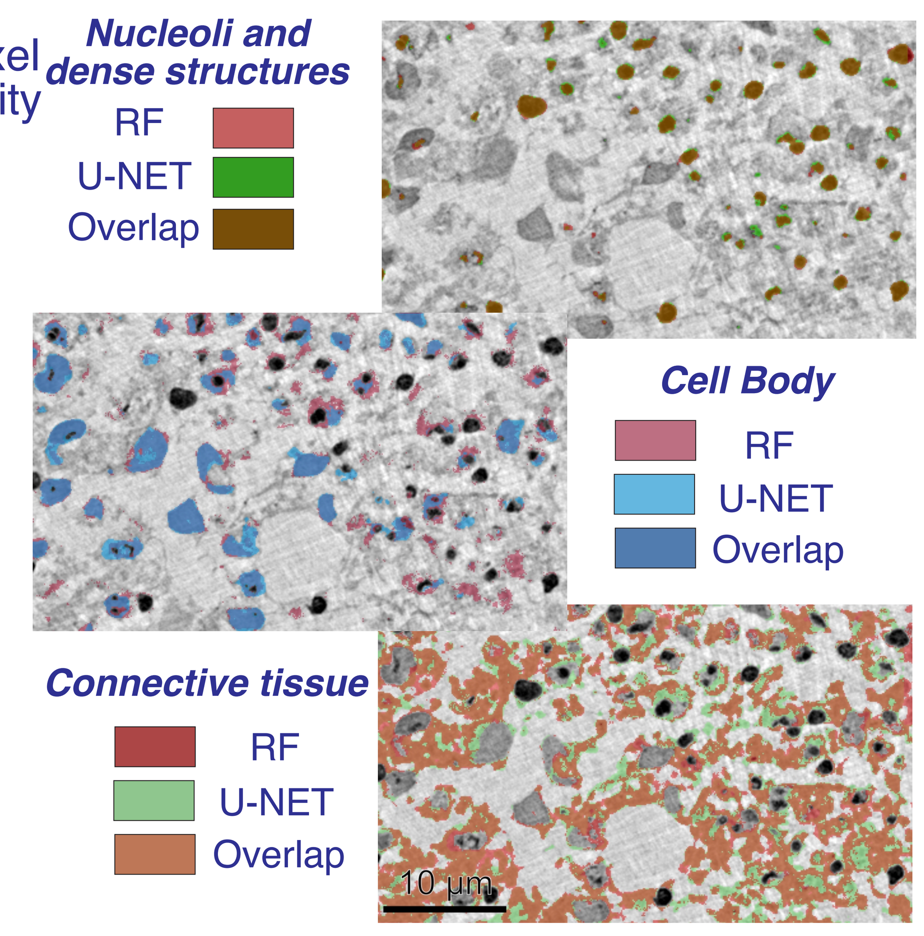
Training data is labeled by hand. The model computes weights of the trees to match the training data



This process uses human input to train a series of decision trees. The decision trees compare various features of the input pixel to the weights. The class is assigned by majority voting of all the trees in the forest

U-Net Deep Learning Model [4]





Acknowledgment

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References

[1]F. Pedregosa *et al.*, *Journal of Machine Learning Research*, vol. 12, no. 85, pp. 2825–2830, 2011.
[2]T. Chan and L. Vese, Springer Berlin Heidelberg, 1999, pp. 141–151. doi: 10.1007/3-540-48236-9_13.
[3]S. Berg *et al.*, *Nature Methods*, Sep. 2019, doi: 10.1038/s41592-019-0582-9.
[4]O. Ronneberger, P. Fischer, and T. Brox, 2015, doi: 10.48550/ARXIV.1505.04597.
[5] T. Salditt, T. Aspelmeier, and S. Aeffner, De Gruyter, 2017.doi: 10.1515/9783110426694.
[6] K. Joppe, J.-D. Nicolas, T. A. Grünewald, M. Eckermann, T. Salditt, and P. Lingor, Biomed. Opt. Express, vol. 11, no. 7, p. 3423, Jul. 2020, doi: 10.1364/BOE.389408.
[7] M. A. Lancaster and J. A. Knoblich, Nat Protoc, vol. 9, no. 10, pp. 2329–2340, Oct. 2014, doi: 10.1038/nprot.2014.158.
[8] M. A. Lancaster and J. A. Knoblich, Science, vol. 345, no. 6194, p. 1247125, Jul. 2014, doi: 10.1126/science.1247125.
[9] J. C. da Silva et al., Optica, vol. 4, no. 5, pp. 492–495, May 2017, doi: 10.1364/OPTICA.4.000492.
[10] M. Eckermann et al., Proceedings of the National Academy of Sciences, vol. 118, no. 48, p. e2113835118, 2021, doi: 10.1073/pnas.2113835118.

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