Label-free imaging of architectural order and its analysis with deep learning

Syuan-Ming Guo[1,*], Li-Hao Yeh[1], Ivan E. Ivanov[1], Bryant B. Chhun[1], Zhenqin Wu[2], M. Keefe[3], Galina Schmunk[3], James Zou[2], Tomasz Nowakowski[3], Shalin B. Mehta[1,*]

[1]Chan Zuckerberg Biohub, San Francisco, CA 94158, USA

[2]Stanford University, Stanford, CA 94305, USA

[3]University of California, San Francisco, CA 94143, USA

[*]Correspondence: syuan-ming.guo@czbiohub.org, shalin.mehta@czbiohub.org

Abstract:

Emergence of architectural order among interacting components is a defining characteristic of living systems. Scalable and unbiased imaging of architecture remains challenging, especially in primary cells and tissues that are difficult to label genetically. Label-free imaging provides facile visualization of structures and reports intrinsic physical properties. Advances in deep learning are beginning to enable quantitative analysis of structures seen in label-free images.

We describe joint optimization of polarization-resolved label-free imaging and deep learning to map architectural order [1] and employ it to study the human brain architecture and interaction of primary neuronal cells. Human tissue is not only scarce but cannot be easily manipulated. Immunolabeling of primary tissue is time-consuming, can introduce sample-to-sample variation, and is not compatible with live imaging. We visualize diverse structures in human brain tissue by mapping optical properties of density, birefringence, orientation, and scattering. We acquire training data by multiplexed imaging of label-free signatures and fluorescent reporters of specific structures. We report computationally efficient variants of U-Nets to predict tract distribution and cell types from intrinsic optical properties of the tissue. Our approach leads to predictive models that generalize to tissue sections not used in the training data. Our approach significantly increases the throughput at which information about brain cytoarchitecture can be acquired from scarce brain tissue samples. We expect that computational label-free imaging will be especially valuable when applied to archival tissue material.

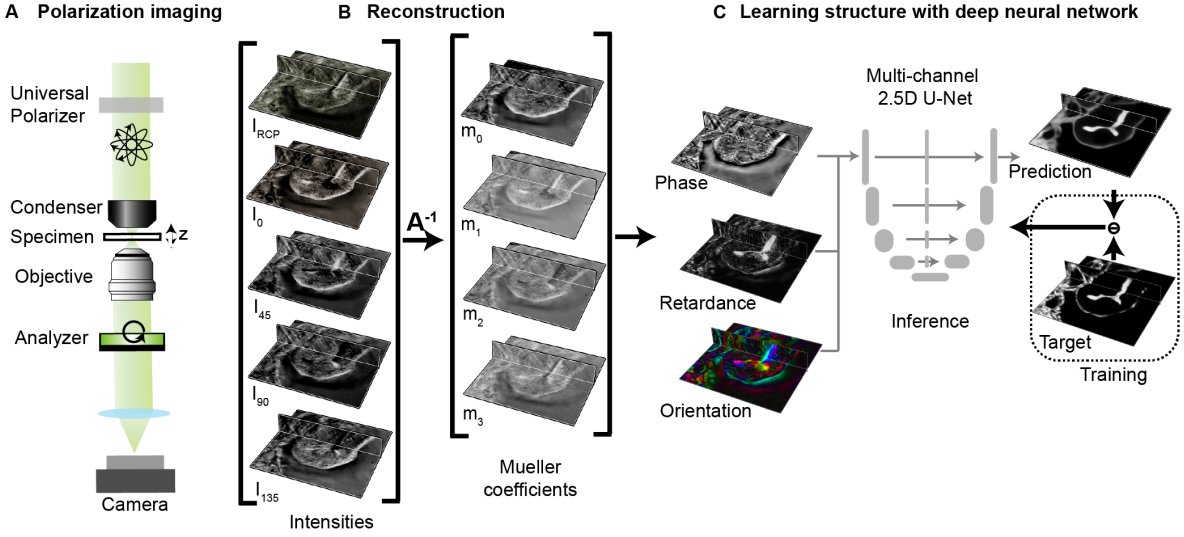

Figure 1. Computational imaging of density and anisotropy without label (A and B) and analysis of specific structures with supervised learning (C).

References

[1] S.-M. Guo, L.-H. Yeh, J. Folkesson et al., bioRxiv, 631101, 2019.