Self-Supervised Representation Learning for 3D-PLI Reveals Clusters of Characteristic Fiber Structures

Alexander Oberstrass[1], Sascha E. A. Muenzing[1], Markus Axer[1,2], Katrin Amunts[1,3], Timo Dickscheid[1,4,5]

[1]Institute of Neuroscience and Medicine (INM-1), Research Centre Jülich, Jülich, Germany
[2]Department of Physics, University of Wuppertal, Wuppertal, Germany
[3]Cécile & Oskar Vogt Institute for Brain Research, University Hospital Düsseldorf, Düsseldorf, Germany
[4]Helmholtz AI, Research Centre Jülich, Jülich, Germany
[5]Institute of Computer Science, Heinrich-Heine-University Düsseldorf, Düsseldorf, Germany

Contact: a.oberstrass@fz-juelich.de

JÜLICH Forschungszentrum

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Introduction

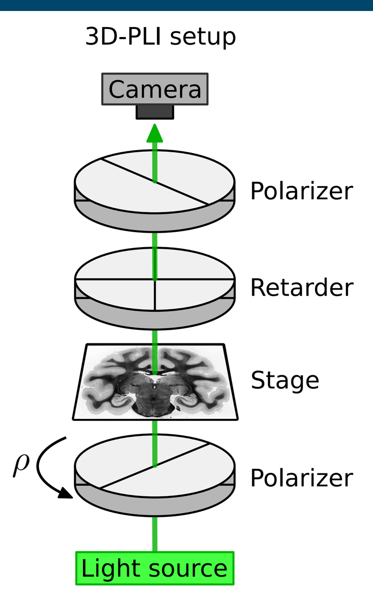
Human brain organization encompasses distinct structural and functional organizing principles, including fiber architecture [1]. Three-dimensional polarized light imaging (3D-PLI) [2] is capable of revealing fine-grained nerve fiber structures in whole brain sections. Manual analysis of 3D-PLI provide an accurate description of fiber architecture [5,6], but are very time consuming. Here, we build on recent advances in **self-supervised learning (SSL) to extract features from 3D-PLI in a fully data-driven way**. We show that such SSL features allow to **identify certain nerve fiber configurations** in 3D-PLI images and fall into **clusters of characteristic fiber architecture**.

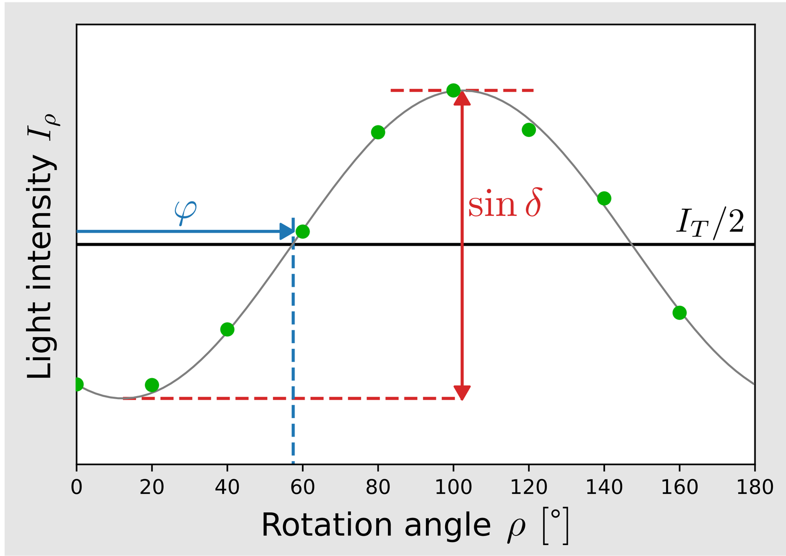
3D-PLI

3D-PLI measures maps of

- **Transmittance I_T**
- **Direction φ**
- **Retardation $\sin(\delta)$**

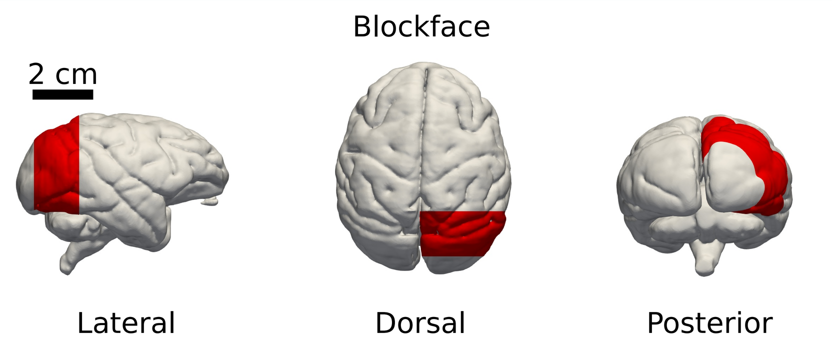
The **Fiber orientation** displays Direction and Inclination (derived from Retardation) in HSV color space.

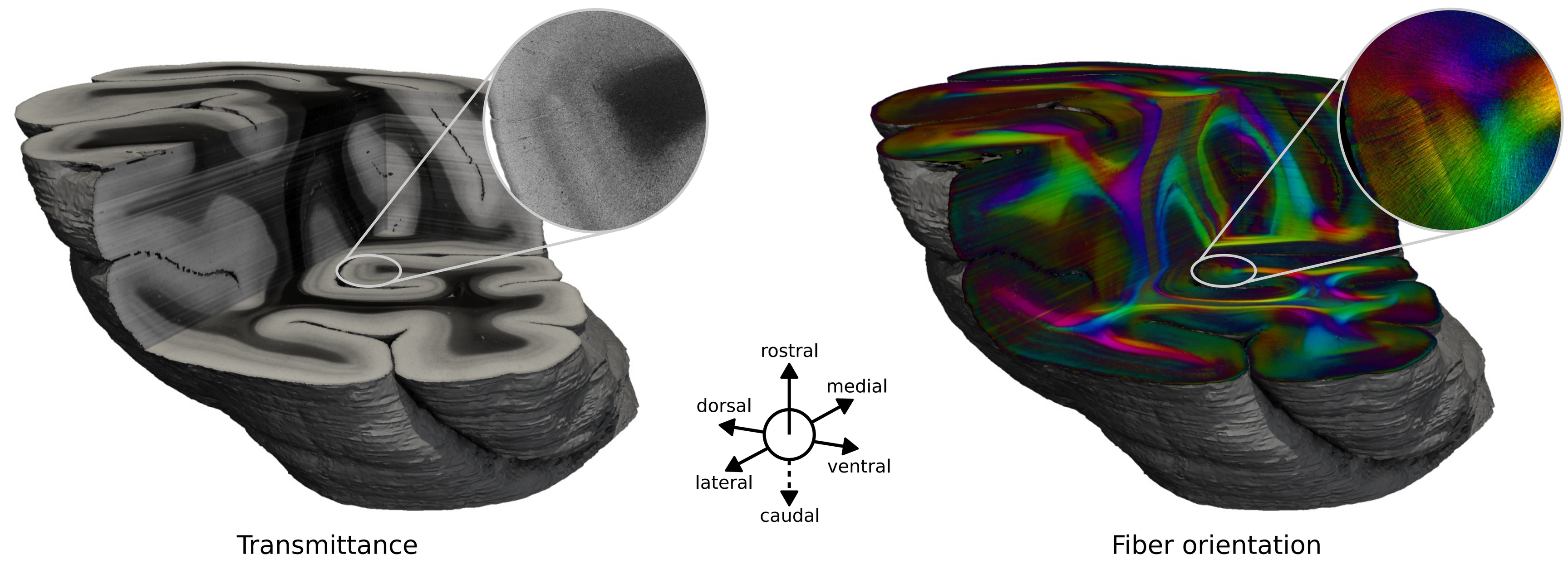




Vervet Monkey Occipital Pole

We analyze a stack of **234 coronal sections** of the **right occipital pole** of a **Vervet monkey brain**. All sections were aligned to their blockface images [2] using non-linear deformation fields.

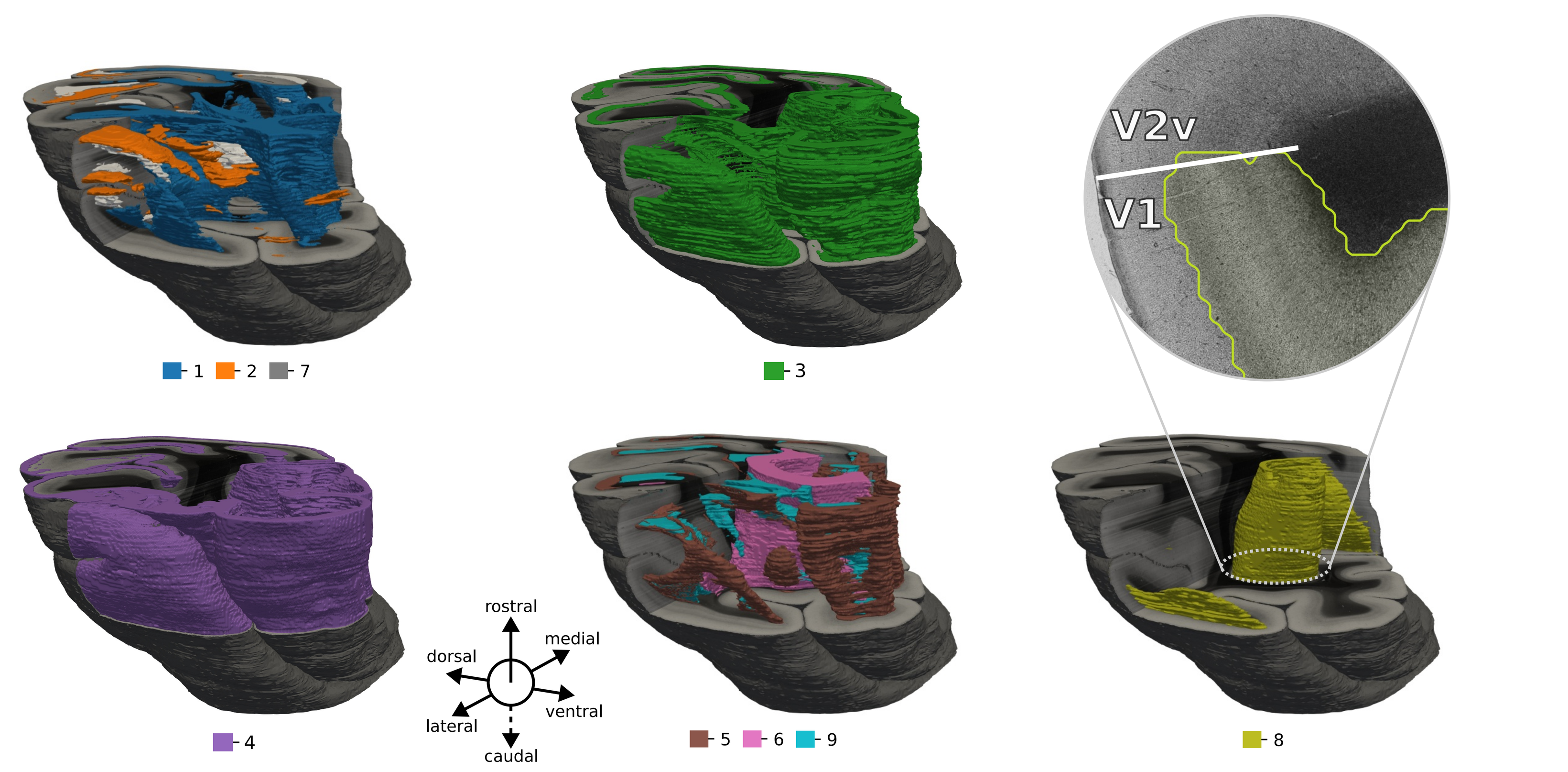




Spatial Consistent Clusters in 3D

- Cross section consistency as **mean IoU** of agglomerative cluster assignments **between neighboring sections**.
- Clusters of **SSL features have higher consistency** compared to clusters of 3D-PLI parameter histograms.

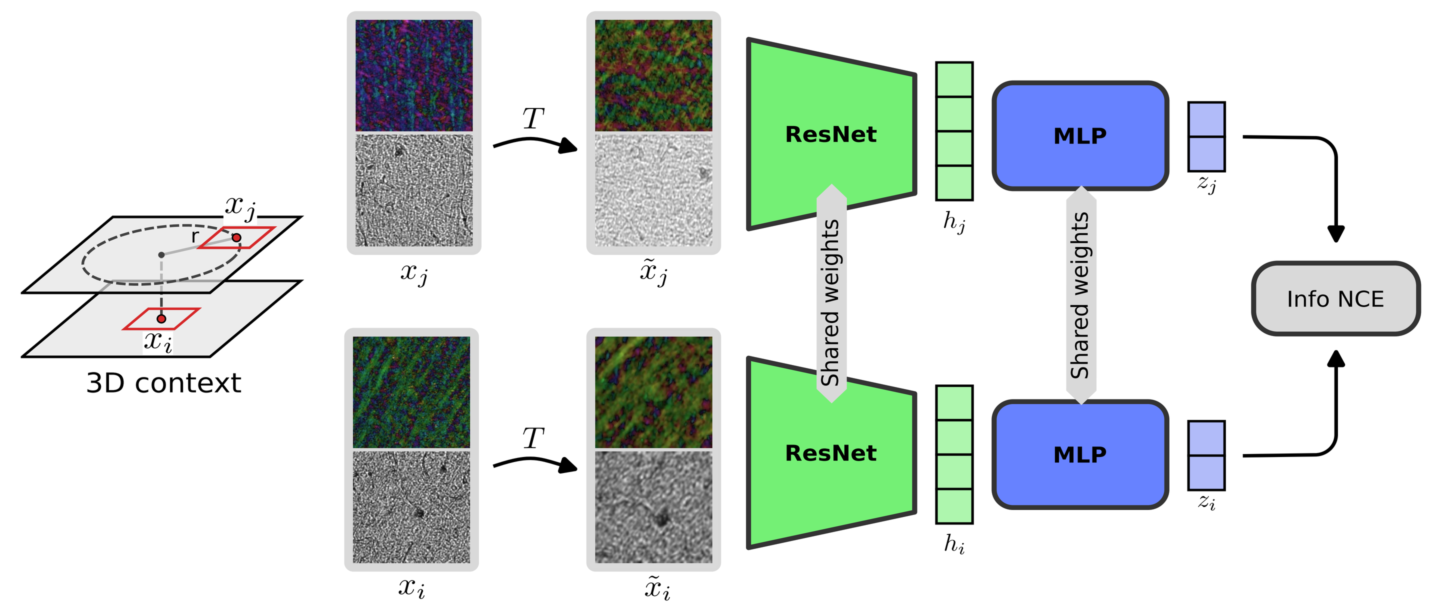
Clusters	Histogram	SSL
2	**0.95**	0.94
5	0.65	**0.80**
9	0.53	**0.71**
21	0.36	**0.58**



Volume renderings of clusters demonstrate their spatial consistency across sections and **highlight certain fiber configurations**:

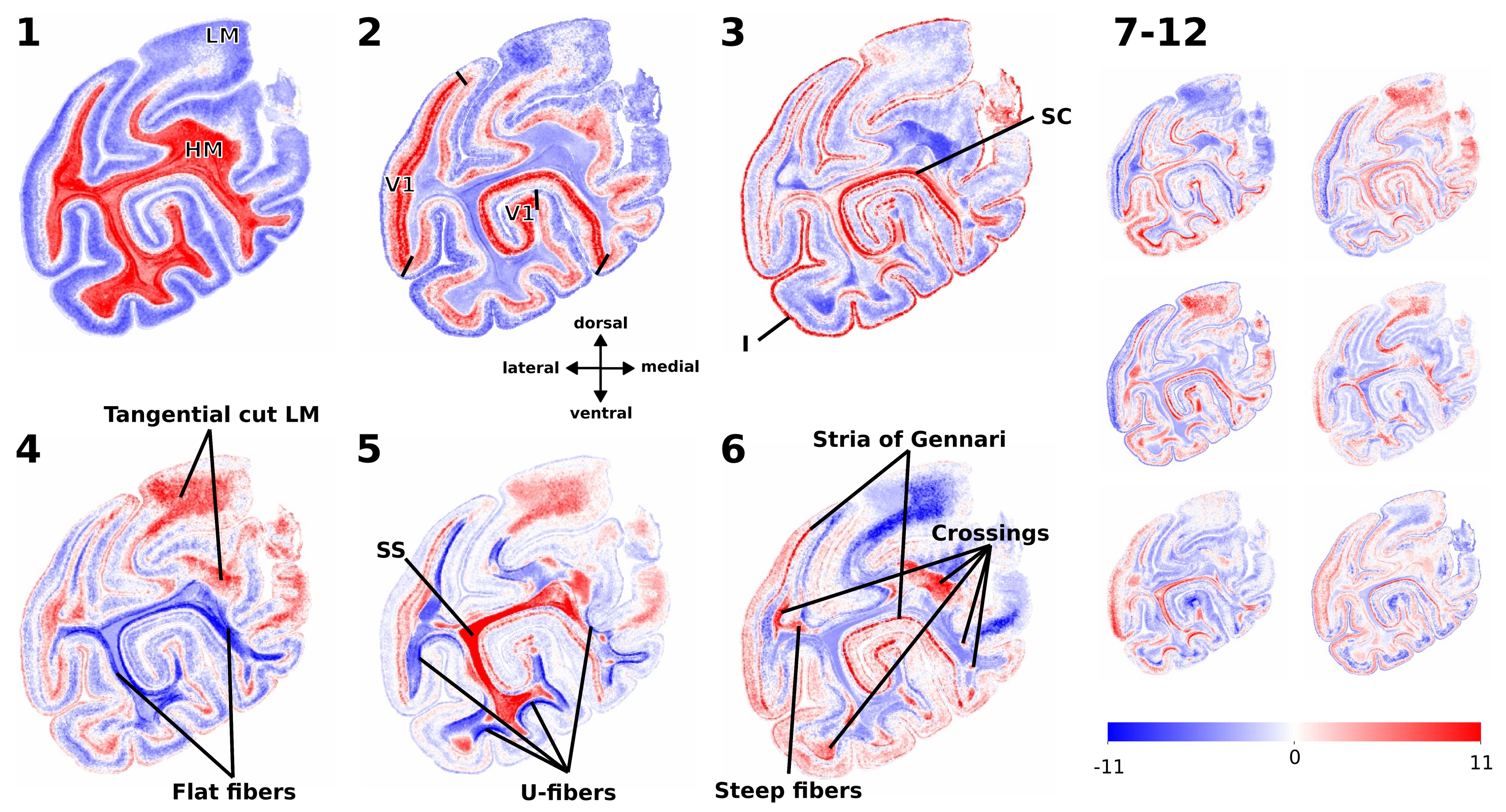
- Flat HM (1)
- Tangential cut LM (2, 7)
- Inner cortical layers (3)
- Outer cortical layers (4)
- Steep fibers or crossings (5, 9)
- Roughly the SS and surrounding fibers (6)
- Layers IVb - VI of primary visual area V1 (8)

3D Context Contrastive Learning



- Build on **SimCLR** [3] **contrastive learning framework**
- **Utilize 3D context** of sections from the reconstructed 3D-PLI volume
- Use **3D-PLI specific data transformations *T***
- Reduced ResNet-50 [4] extracts **256 features h_i** for patches of 166µm

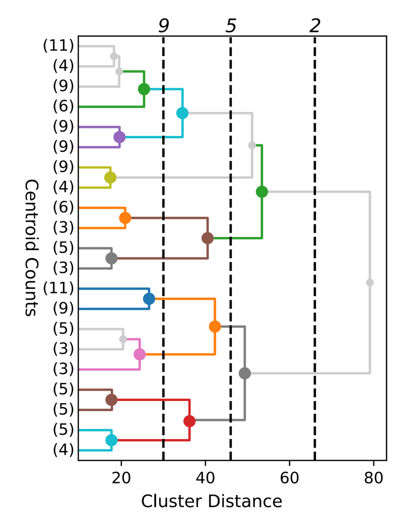
PCA



Project learned features onto **12 PCA components** with 60% explained variance. The maps of projections **highlight fundamental anatomical principles:**

- Low/high myelination (LM, HM)
- Primary visual area (V1)
- Cortical layer I
- Stria of Gennari
- Stratum calcarinum (SC)
- Stratum sagittale (SS)
- U-fibers
- Tangential cut LM
- Flat fiber bundles
- Steep fibers/ crossings

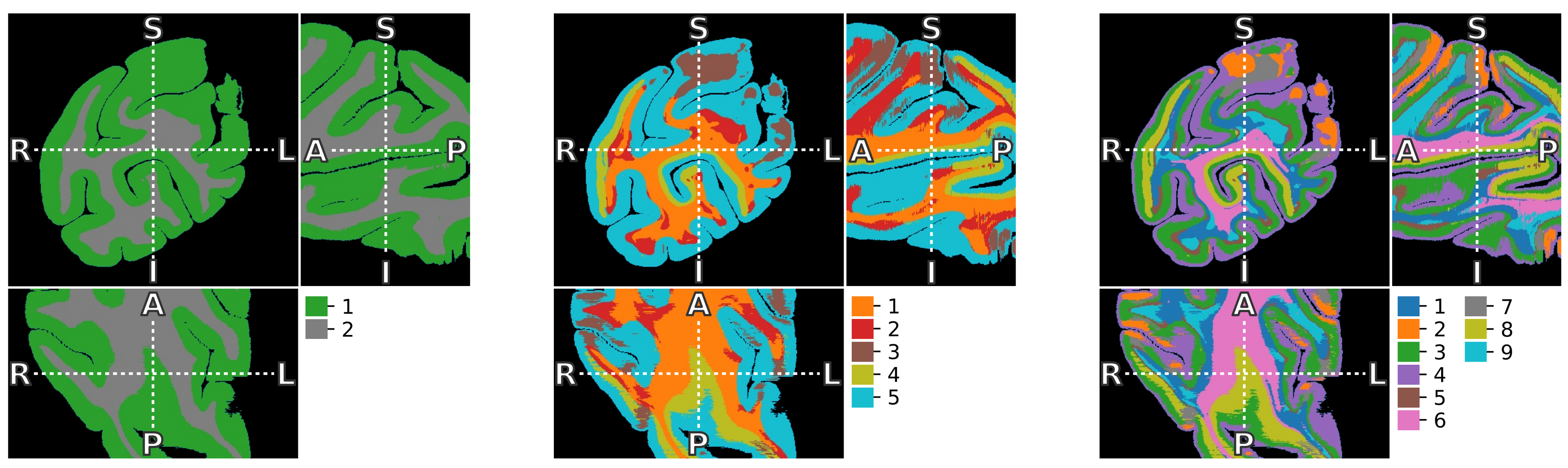
Hierarchical Clustering



We first reduce 16M data points to 128 k-Means centroids. The centroids serve as the basis to **calculate a dendrogram using agglomerative clustering**.

Left: Dendrogram of clusters getting merged shows hierarchy of clusters

Bottom: Agglomerative clustering results of the initial 128 k-Means centroids for 2, 5 and 9 clusters



Conclusions

The proposed method **enables the extraction of features that are sensitive to different configurations of fiber architecture** observed in 3D-PLI and **form spatially consistent clusters**. It can directly be applied to 3D reconstructions of other brain regions, species, and modalities. Future work will explore how the features can be used for data-driven analysis and segmentation of fiber structures.

References

[1] Amunts, K. (2020), "Julich-Brain: A 3D probabilistic atlas of the human brain's cytoarchitecture", Science, vol. 369, no. 6506, pp. 988–992, doi: 10.1126/science.abb4588.
[2] Axer, M. (2011), "High-Resolution Fiber Tract Reconstruction in the Human Brain by Means of Three-Dimensional Polarized Light Imaging", Frontiers in Neuroinformatics, vol. 5, 2011, doi: 10.3389/fninf.2011.00034.
[3] Chen, T. (2020), "A Simple Framework for Contrastive Learning of Visual Representations", in International Conference on Machine Learning, Nov. 2020, vol. 119, pp. 1597–1607.
[4] He, K. (2016), "Deep Residual Learning for Image Recognition", in 2016 IEEE Conference on Computer Vision and Pattern Recognition (CVPR), Jun. 2016, pp. 770–778. doi: 10.1109/CVPR.2016.90.
[5] Takemura, H. (2020), "Anatomy of nerve fiber bundles at micrometer-resolution in the vervetmonkey visual system", eLife, vol. 9, p. e55444, Aug. 2020, doi: 10.7554/eLife.55444.
[6] Zeineh, M. (2017), "Direct Visualization and Mapping of the Spatial Course of Fiber Tracts at Microscopic Resolution in the Human Hippocampus", Cerebral Cortex, vol. 27, no. 3, pp. 1779–1794, doi: 10.1093/cercor/bhw010.

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