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Combining Probability-guided Contrastive Feature Learning and Graph Neural Networks for Cytoarchitecture Classification in the Human Brain

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The human brain can be subdivided into cytoarchitectonic areas, which are defined based on the spatial organization of neuronal cells, including their distribution, size, type, orientation, as well as their arrangement into distinct cortical layers and columns. Cytoarchitectonic areas are indicators of brain connectivity and function, making them an important building block of multi-modal human brain atlases. They can be analyzed based on high-resolution microscopic scans of histological brain sections obtained by cutting postmortem human brains into thin slices and staining them for cell bodies.

The large inter-individual variability between brains necessitates the analysis of multiple brains to obtain a general picture of the human cytoarchitectonic organization. Modern high-throughput scanners allow large-scale acquisition of microscopic image data, but established cytoarchitecture analysis methods are not suitable for handling the resulting large amounts of data. This motivates the development of methods for automated cytoarchitecture analysis.

We present recent advances in cytoarchitecture analysis methods based on contrastive feature learning and graph neural networks. Our method leverages existing probabilistic cytoarchitectonic brain maps from the Jülich-Brain atlas to formulate a self-supervised contrastive learning objective that promotes the encoding of high-resolution image patches from similar brain areas as similar feature vectors. The resulting cytoarchitectonic feature vectors are then assigned to approximate midsurface meshes of the cortical sheet and processed by graph neural networks for cytoarchitecture classification. The proposed framework efficiently integrates high-resolution image features with brain topology, resulting in improved classification performance.

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