# Large-scale Deep Learning for Cytoarchitecture **Classification in the Human Brain** BrainComp workshop 2022 - 21.09.2022

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HELMHOLTZA



Human Brain Project



## **Building a Human Brain Atlas for Cytoarchitecture**



Brodmann, 1909

Amunts et al., 2020



# **Histological Human Brain Sections**

- **Postmortem** human brains
- Fixate and **cut** into histological sections
  - 6000-8000 sections per brain
  - Thickness:  $20 \mu m$
- Stain for **cell bodies**
- Microscopic imaging at  $1 \mu m$  pixel resolution
- Cerebral cortex: Outer layer of the cerebrum





## Cytoarchitecture

- **Cytoarchitecture:** Distribution, shape, and type of neuronal cells
- Organization into cortical layers
- Regional differences define **cortical areas**
- Indicators for **connectivity** and **function**





# **Cytoarchitectonic Brain Mapping**

- Brain mapping: Identify cytoarchitectonic areas
- Gold standard method: Schleicher et al., 1999
  - Statistical image analysis
  - Reproducible and observer-independent
  - Time intensive: ≥ 30-60 min/section/area
- Goal: Automated cytoarchitectonic mapping to enable large-scale cytoarchitecture analysis
- Train deep neural networks to predict areas from images





# **Distributed Deep Learning on HPC**

- Dataset size
  - Large images: ~80,000×100,000 px (> 8 GB)
  - Many images: 6000-8000 images per brain
  - Large patches: 2048×2048 px/patch (4mm<sup>2</sup>@2µm/px)
- Technical challenges
  - I/O: Random access to patches → flash-based storage
  - **Preprocessing:** Augmenting large image patches → **CPUs**
  - **Training:** Data parallel deep learning → **GPUs**







# **Distributed Deep Learning on HPC**







## Application 1: Supporting Cytoarchitectonic Mapping with Deep Learning

- Goal: Interactive workflow to support brain mapping
- Idea: Train specialized models using few annotations
  - Provide annotation on every n-th brain section
  - Train model on pairs of adjacent annotated sections
  - Apply model to fill the gaps between annotations
- Web interface for visualization, annotation, configuration

C. Schiffer et al., Convolutional neural networks for cytoarchitectonic brain mapping at large scale, NeuroImage 240, 2021, DOI: 10.1016/j.neuroimage.2021.118327.





### 3D Cytoarchitectonic Maps in the EBRAINS Multilevel Human Brain Atlas





## **Application 1: Computational requirements**

- Users define and submit training and prediction jobs
- Training and prediction on **JURECA-DC**, each job using...
  - Four A100 GPUs (4 × 40GB)
  - 64 MPI ranks, four threads per rank (256 total)
- Number of models depends on area size (≤ 20)
- Runtime: 10-15min → Interactive use

C. Schiffer et al., Convolutional neural networks for cytoarchitectonic brain mapping at large scale, NeuroImage 240, 2021, DOI: 10.1016/j.neuroimage.2021.118327.





## **Application 2: Contrastive Cytoarchitectonic Feature Learning at Large Scale**

- Goal: General model for cytoarchitecture classification
- Approach: Contrastive learning
  - Learn features by comparison
  - Make features of similar images similar
  - Make features of dissimilar images dissimilar
- Similarity based on labels or probabilities
- Learned features enable classification and clustering

C. Schiffer et al., Contrastive Representation Learning For Whole Brain Cytoarchitectonic Mapping In Histological Human Brain Sections, ISBI, 2021, DOI: 10.1109/ISBI48211.2021.9433986.



before training



after training



## **Application 2: Computational requirements**

- Challenge: Large batch size for comparison
- Training on **JURECA-DC**
- Contrastive training configuration
  - 64 A100 GPUs (16 nodes)
  - **1024 MPI ranks**, four threads per rank (4096 total)
  - 16 images per GPU (total GPU memory: 2.5 TB)
  - Total data read: ≥ 155 TB
  - **Runtime:**  $\geq$  6h
- Methods using more data in development

C. Schiffer et al., Contrastive Representation Learning For Whole Brain Cytoarchitectonic Mapping In Histological Human Brain Sections, ISBI, 2021, DOI: 10.1109/ISBI48211.2021.9433986.



before training



after training



## Application 3: Graph Neural Networks for Cytoarchitecture Classification

- Previously: Classify individual images
  - Ill-defined: Classification often requires context
  - Directly providing context (e.g., 3D) is **infeasible**
- Idea: Model brain as a graph
  - Coarse brain reconstruction to obtain a mesh/graph
  - Assign image features to graph nodes
  - Apply graph neural networks (GNNs) to classify nodes
- Improves performance by combining high-resolution image features with context encoded in the graphs

C. Schiffer et al., 2D Histology Meets 3D Topology: Cytoarchitectonic Brain Mapping with Graph Neural Networks, MICCAI, 2021, DOI: 10.1007/978-3-030-87237-3\_38.







cytoarchitectonic features



annotations







## **Application 3: Computational requirements**

- Currently: Pre-computed features
- Training on **JURECA-DC**
- Graph neural network training configuration
  - 8 A100 GPUs (2 nodes)
  - 128 MPI ranks, four threads per rank (256 total)
  - **Runtime:** 20 120 min
  - Pre-computed attributed graphs: ~60 GB
- End-to-end feature and graph learning in development

C. Schiffer et al., 2D Histology Meets 3D Topology: Cytoarchitectonic Brain Mapping with Graph Neural Networks, MICCAI, 2021, DOI: 10.1007/978-3-030-87237-3\_38.





### Future work

- Advanced feature learning methods
  - Use non-annotated data (self-supervised learning)
  - Compute requirements grow linearly with data
- End-to-end feature and graph learning
  - End-to-end learning
  - Enable data augmentation for robustness
  - Potentially combination with contrastive learning
  - Challenge: I/O and compute requirements grow exponentially with model depth

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