

How to integrate cytoarchitectonic and receptor data in a human brain model and how to apply it to functional studies

Nicola Palomero-Gallagher

Institute of Neuroscience and Medicine INM-1, Research Centre Jülich, Jülich,

Karl Zilles

Institute of Neuroscience and Medicine INM-1, Research Centre Jülich, Jülich,
and

Dept. of Psychiatry, Psychotherapy and Psychosomatics, RWTH University Aachen,
Germany

Structural and functional MRI data are the main sources for the related information on the living human brain in present neuroimaging. However, these data provide a resolution between 100µm and several mm, which is far above the resolution of microscopic studies of cytoarchitecture and fibre anatomy as well as receptor architecture. The latter three approaches can only be performed in post mortem brains, but provide, beside a superior spatial resolution, the anatomical ground truth and are indispensable for a precise and reliable, multimodal and multiscale parcellation of the human brain. Moreover, functional data are also provided at multiple scales reaching from LFPs to gross description of functional domains based on respective databases and meta-analyses. How to integrate these different scales and modalities?

We will present a strategy which allows this integration in a widely used common reference space, i.e. the Montreal Neurological Institute (MNI) space for the human brain. Cytoarchitectonic maps are presented in 3D as continuous probability maps or maximum probability maps, and multireceptor data can be assigned to these areas. Furthermore, the cytoarchitectonic maps can be seen in the JuBrain atlas and used as masks in the Anatomy Toolbox to identify data based on fMRI or provided by meta-analyses.