A revised toolbox for combining probabilistic cytoarchitectonic maps and functional imaging data

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Authors:

Simon B. Eickhoff[1], Svenja Caspers[2], Guillaume Flandin[3], Martina Minnerop[4], Claudia R. Eickhoff[5], Timo Dickscheid[1], Peter Pieperhoff[1], Hartmut Mohlberg[1], Karl Zilles[1], Katrin Amunts[1]

Institutions:

[1]Institute of Neuroscience and Medicine (INM-1, INM-7); Forschungszentrum Jülich, Jülich, Germany, [2]Institute of Anatomy I, Heinrich Heine University Duesseldorf, Duesseldorf, Germany, [3]Wellcome Centre for Human Neuroimaging, UCL Queen Square Institute of Neurology,, London, United Kingdom, [4]Center for Movement Disorders and Meuromodulation, Heinrich-Heine University Düsseldorf, Düsseldorf, Germany, [5]Clinical Neuroscience and Medical Psychology, Medical Faculty, Heinrich Heine University, Duesseldorf, Germany

Introduction:

The idea of corresponding topographic distinctions between function, connectivity and (micro-) structure is critical to the concept of a cortical area (Eickhoff et al., 2018). Establishing the relationship between functional and structural neuroimaging findings on the one hand and cytoarchitecture of the human brain on the other hand enables a comprehensive view on regional differentiation. It is, however, complicated by the fact that the former is assessed in-vivo while the latter may only be investigated post-mortem. To address these challenges, the SPM Anatomy Toolbox was released in 2004 and has since become a widely used tool for integrating histological data on brain cytoarchitecture and neuroimaging results (Eickhoff et al., 2005). Roughly five years after the last substantial update of the software, we here present a completely rewritten and substantially improved version 3.0 of the (SPM) Anatomy Toolbox. The toolbox is relying on data from cytoarchitectonic mapping in ten post-mortem brains, resulting in 3D probabilistic maps of cortical areas and subcortical structures (JuBrain atlas; Amunts and Zilles, 2015).

Methods:

All cytoarchitectonic maps are now provided in MNI152 space instead of the MNI single subject space, improving compatibility with in-vivo imaging data.

The GUI is now provided by a dedicated window rather than a modification of the SPM graphics window, providing space for additional information (including macro-anatomical allocation through the Harvard-Oxford probabilistic atlas, Desikan et al., 2006).
The code-base has been completely rewritten and simplified, with most actions and information now being represented through the GUI objects to increase speed and flexibility. Information on cluster allocation is stored and hence does not have to be re-computed.
Given the recent growth in coverage of the JuBrain atlas, the previous storage of the probabilistic cytoarchitectonic maps as (uncompressed) image files resulted in large disk-usage and slow performance. v3.0 stores all data in a sparse format within a single MAT-file, resulting in a much smaller footprint and faster execution. Individual probabilistic maps will be shared through the Human Brain Project website.
Functionality for creating binary VOIs based on the Maximum Probability Map representations of individual cytoarchitectonic areas was revised into a much more flexible GUI allowing for group-wise selections and integrated with the functions to extract per-area data from user-defined files. ToolTip references to histological papers are now provided throughout the software

Results:

Screenshots are presented in figure 1 and 2. From a user perspective, the introduced changes result in three main improvements: 1) No more confusion between reference spaces, as the JuBrain Anatomy toolbox now works in the space that is used by SPM and FSL. 2) A cleaner interface providing more detailed information. 3) A substantial improvement in speed allowing real-time navigation. The new toolbox moreover offers an increased number of structures and will be tightly synchronized with other data repositories, e.g., the "Human Brain Atlas" of the HBP (https://www.humanbrainproject.eu /en/explore-the-brain/atlases/).

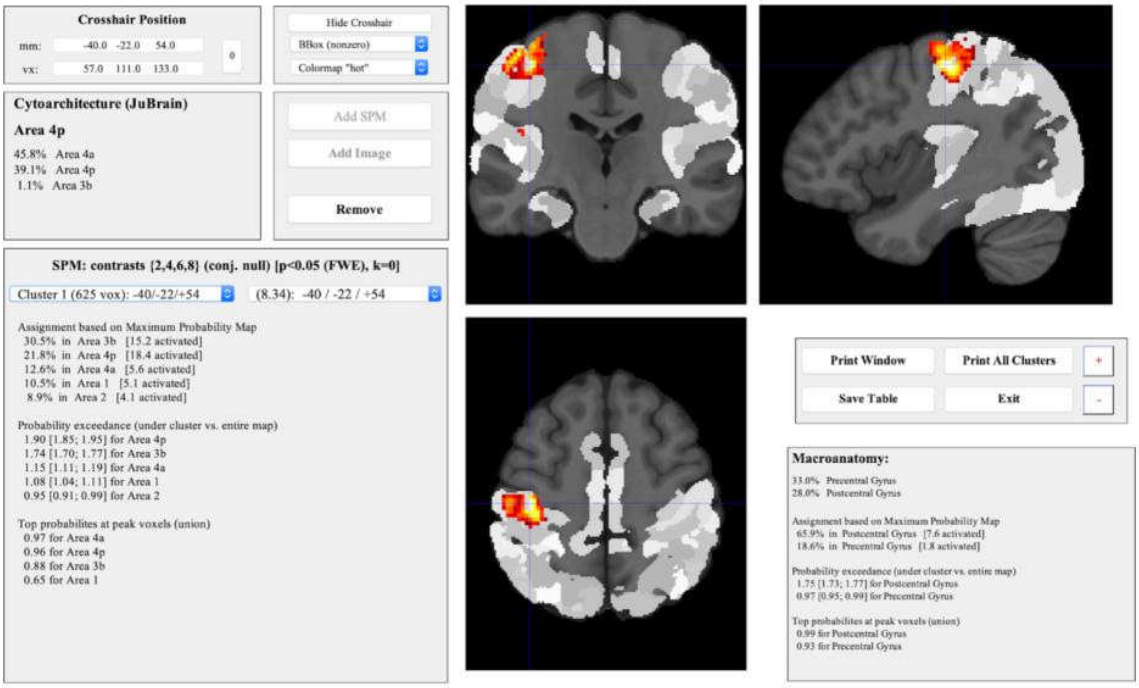

Figure 1. The new main GUI providing information on the cytoarchitectonic areas and macro-anatomical structures found at the current cross-hair position as well as detailed per-cluster assignment of the functional overlay.

Figure 2. The new GUI for ROI generation and ROI based analysis

Conclusions:

Following a series of more gradual changes, v3.0 of the JuBrain (SPM) anatomy toolbox represents a major remake of the entire software, keeping all functionalities that were offered in the past but providing a substantially improved usability. The beta-version of v3.0 of the JuBrain Anatomy is currently available for download at https://fz-juelich.sciebo.de/s/REcsqsgIKtmauNb. In the future, this link will provide access to release candidates while the "official", stable releases will be available through a dedicated web-page of the Forschungszentrum Jülich as well as the HBP neuroinformatics platform.

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Informatics:

Brain Atlases [1]
Databasing and Data Sharing

Neuroanatomy:

Anatomy and Functional Systems
Cortical Cyto- and Myeloarchitecture [2]

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Atlasing
Data Organization
Other - Cytoarchitecture

1|2Indicates the priority used for review

My abstract is being submitted as a Software Demonstration.

No

Please indicate below if your study was a "resting state" or "task-activation" study.

Other

Healthy subjects only or patients (note that patient studies may also involve healthy subjects):

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Was any human subjects research approved by the relevant Institutional Review Board or ethics panel? NOTE: Any human subjects studies without IRB approval will be automatically rejected.

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Not applicable

Please indicate which methods were used in your research:

Postmortem anatomy
Computational modeling

Provide references using author date format

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