

SPM Anatomy Toolbox

Version 3.0

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For general questions and comments regarding cytoarchitectonic mapping please contact Prof. Katrin Amunts (k.amunts@fz-juelich.de)

References for the SPM Anatomy toolbox:

Eickhoff S, Stephan KE, Mohlberg H, Grefkes C, Fink GR, Amunts K, Zilles K. A new SPM toolbox for combining probabilistic cytoarchitectonic maps and functional imaging data. *NeuroImage* 25(4), 1325-1335, 2005

Eickhoff, S.B.; Heim, S.; Zilles, K.; Amunts, K. Testing anatomically specified hypotheses in functional imaging using cytoarchitectonic maps. *NeuroImage* 32(2), 570-582, 2006

Eickhoff SB, Paus T, Caspers S, Grosbras MH, Evans A, Zilles K, Amunts K. Assignment of functional activations to probabilistic cytoarchitectonic areas revisited. *NeuroImage* 36(3), 511-521, 2007

References for probabilistic cytoarchitectonic mapping

Zilles K, Amunts K. Centenary of Brodmann's map – conception and fate. *Nature Reviews Neuroscience* 11(2): 139-145, 2010 Amunts K, Schleicher A, Zilles K. Cytoarchitecture of the cerebral cortex – more than localization. *Neuroimage* 37: 1061-1065, 2007

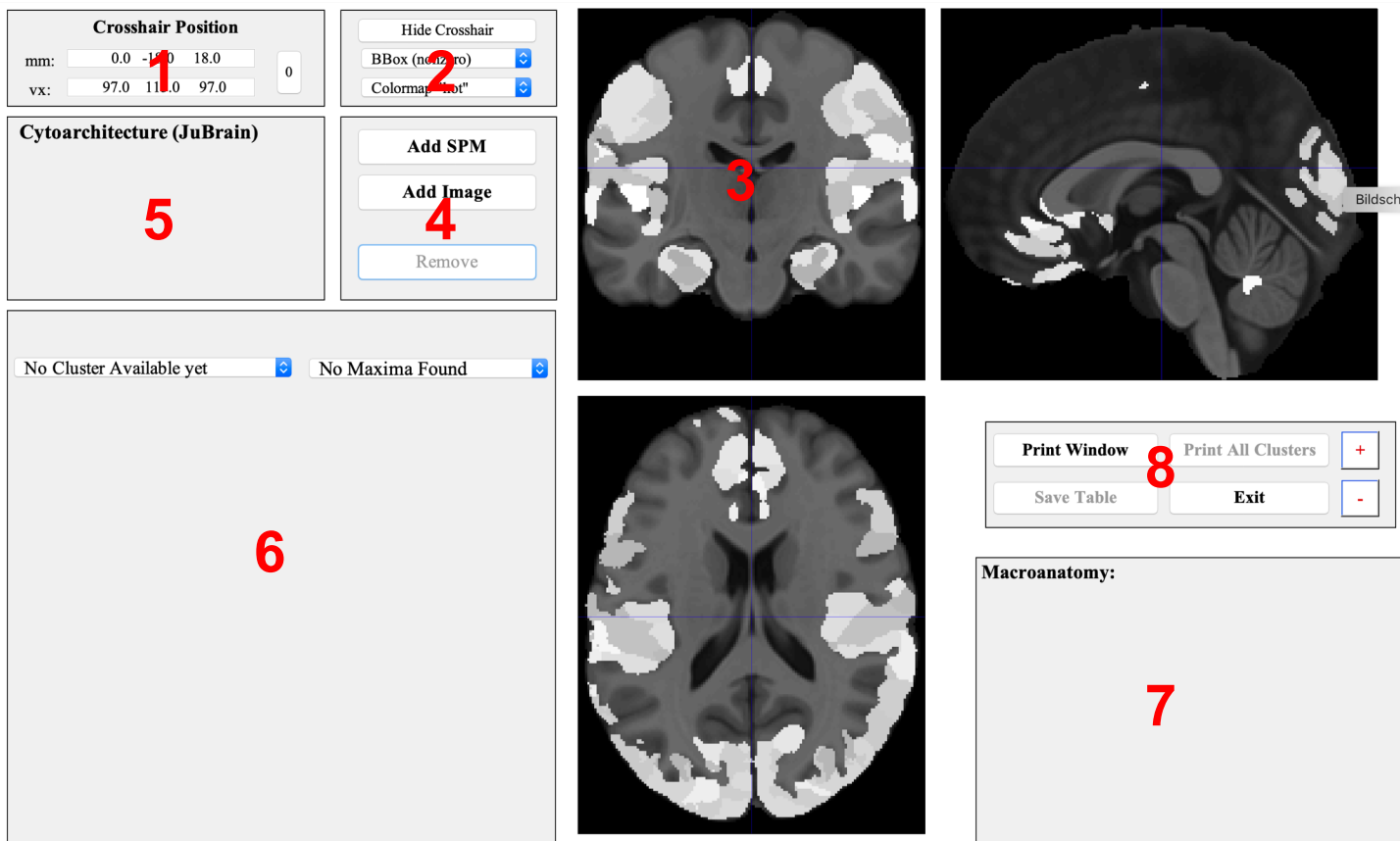
Zilles K, Schleicher A, Palomero-Gallagher N, Amunts K. Quantitative analysis of cyto- and receptor architecture of the human brain. In: *Brain Mapping: The Methods*, J. Mazziotta and A. Toga (eds.), p. 573-602, 2002

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Atlas & Assignment Tool

ROI Tool

Atlas & Assignment Tool



- 1) **Coordinate panel**
Showing and changing the crosshair position
- 2) **Figure settings**
Modifying the display of the orthogonal sections
- 3) **Orthogonal sections**
Showing the MNI152 template in the background with the JuBrain Maximum Probability Map in lighter greyx
- 4). **Overlay controls**
Load or remove an SPM map or an image overlay
- 5) **JuBrain Voxel Assignment**
Cytoarchitectonic information for the crosshair location
- 6) **JuBrain Cluster assignment**
Cytoarchitectonic information per overlay-cluster + Navigation through the overlay (SPM map, image)
- 8) **Macroanatomical panel**
Assignment of the crosshair position and the current overlay cluster (if applicable) to the Harvard-Oxford macroanatomical atlas
- 7) **Control panel**
Various controls including the change of font size (+ / - buttons)

Coordinate panel

Cross-hair position in MNI152 (world) space

Cross-hair position in MPM voxel space

Changing the coordinates (confirmed by ↵)

moves the cross-hair and updates the voxel assignment

Crosshair Position				
mm:	0.0	-18.0	18.0	0
vx:	97.0	115.0	97.0	

Move cross-hair to origin

Figure settings

Hide Crosshair	
BBox (nonzero)	⬇
Colormap "hot"	⬇

Toggle cross-hairs on / off (not affecting behavior)

Zoom in/out focused on the cross-hair location

Change the colormap of an overlay
(not affecting the atlas & template display)

Control panel

Cycle through all clusters and save a screen-shot

Screen-shot

Save JuBrain

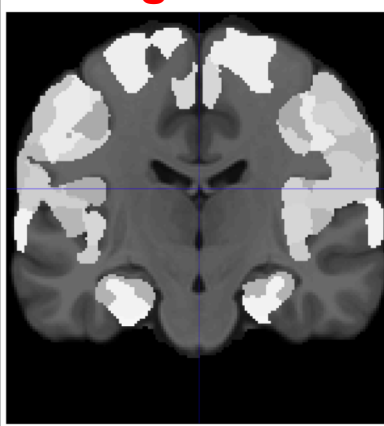
assignment for all clusters as tsv

Print Window	Print All Clusters	+
Save Table	Exit	-

Increase font size

Decrease font size

Orthogonal sections



In dark grey, the (non-linear) MNI152 template is shown, light grey represents the assignment to histological areas based on the JuBrain Maximum Probability Map. This map assigns each voxel to the most likely histological area at that position.

Overlays, e.g., findings from functional or structural imaging studies may be overlaid on this map and are shown using the color-scale defined in the figure settings panel.

Clicking on any of the three sections changes the cross-hair position to that location. In this process, the coordinate panel, the JuBrain voxel assignment and the macroanatomical information is updated.

Overlay controls



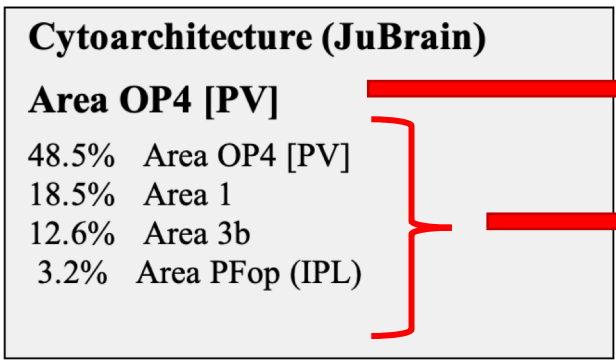
Bring up the SPM contrast manager, allowing you to define, evaluate and threshold contrasts

Add an overlay image from a nifti-file.
Premultiply: Multiply all image values by a scalar
Hight threshold: Evaluated after pre-multiplication
Extent threshold: In voxels (native image space)

Remove the current overlay (only one overlay can be shown at any time)

Overlays need to be in MNI152 space and are resampled to the template resolution (1 mm isotropic)

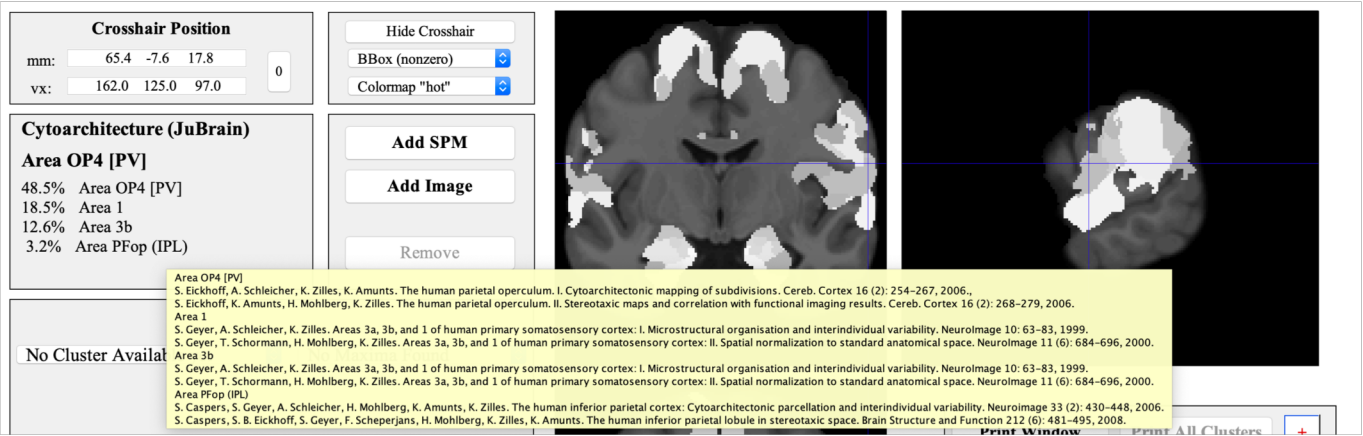
JuBrain Voxel Assignment



“Hard” assignment based on the Maximum Probability Map (MPM)

Full description: probabilities for all histological area found at this position

Information in this panel pertain (only) to the voxel at the cross-hair position



Pointing the cursor on the name of a cytoarchitectonic area and keeping it there for ~1 second reveals the references describing the cytoarchitectonic mapping of this histological area.

JuBrain Cluster assignment

This will update the *JuBrain Voxel Assignment* panel for information on maxima location



Use this menu to jump to the different clusters.
Coordinates indicate the location of the cluster maximum

Use this menu to jump to the different peaks (local maxima) within a cluster.
Values in parenthesis indicate the overlay value (e.g., T / Z statistic).

Comparison between the current cluster and the JuBrain MPM
Overlap is provided relative to cluster and area (in brackets) volume (Eickhoff et al., 2005)

Average probability for each JuBrain area at the location of the cluster relative to its full probability map
Higher values indicate a location more towards the center of the area (cf. Eickhoff et al., 2007)

Image: timing [u=0.0, k=0]

(618 vox): -38 / -12 / +60 (7.61): -38 / -12 / +60

Assignment based on Maximum Probability Map

11.8% in Area 3b [5.8 activated]

7.2% in Area 1 [3.4 activated]

4.0% in Area 4p [3.3 activated]

3.9% in Area 4a [1.7 activated]

3.5% in Area 2 [1.6 activated]

Probability exceedance (under cluster vs. entire map)

1.51 [1.35; 1.73] for Area 4p

1.49 [1.40; 1.55] for Area 3b

1.24 [1.16; 1.33] for Area 1

0.90 [0.82; 0.97] for Area 2

0.75 [0.72; 0.79] for Area 4a

Top probabilities at peak voxels (union)

0.99 for Area 1

0.92 for Area 3b

0.77 for Area 2

0.46 for Area 4a

Union of the probability values for each area at the location of the local maxima
High values indicate that at least one peak was most likely located in the respective area give histological variability

The **Macroanatomical panel** follows the same layout
It is concurrently updated when a new cluster / maximum is selected