

Intuitive access to spatially linked brain activity and transcriptomic data using BrainTrawler

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Introduction

Spatial patterns in the brain transcriptome follow broad trends in the brain network architecture, which can be used to study the molecular mechanisms of functional connectivity [1]. To investigate this, multimodal data at different resolutions needs to be fused. However, the sophisticated pre-processing and data fusion workflows involved often require the expertise of computer scientists. “BrainTrawler” is a web-based neuroscience data exploration framework that allows researchers to skip these workflows by providing an extensive database of integrated transcriptomic and neuroimaging data along with powerful query options [2,3]. Here, we present an extension to BrainTrawler that includes dedicated workflows to link volumetric brain activity data, such as fMRI, perfusion MRI or cFos imaging, to our existing transcriptomic database. This allows researchers to interactively generate hypotheses about the relation between molecular brain organization and macro-scale measures of brain (dys)function.

Investigate Group-Level Trends

Brain function in patient and control groups or treatment groups is commonly investigated using volumetric brain activity data such as fMRI. BrainTrawler now supports group-wise activation comparisons in arbitrary regions of interest (ROIs) at a glance. To explore a dataset, users search arbitrary ROIs for high or specific activity. ROI selections are reflected in the 2D and 3D views, as shown in fig. 3a. Searches return individual measurements ranked by (specific) expression in a tabular format, as depicted in fig. 3b. Each measurement is labeled with a task/treatment group and can be reassigned interactively. To effectively communicate group-wide activity distributions inside the ROI, BrainTrawler uses violin plots, as displayed in fig. 3c. This visualization approach enables researchers to quickly identify key characteristics and differences in large functional studies.

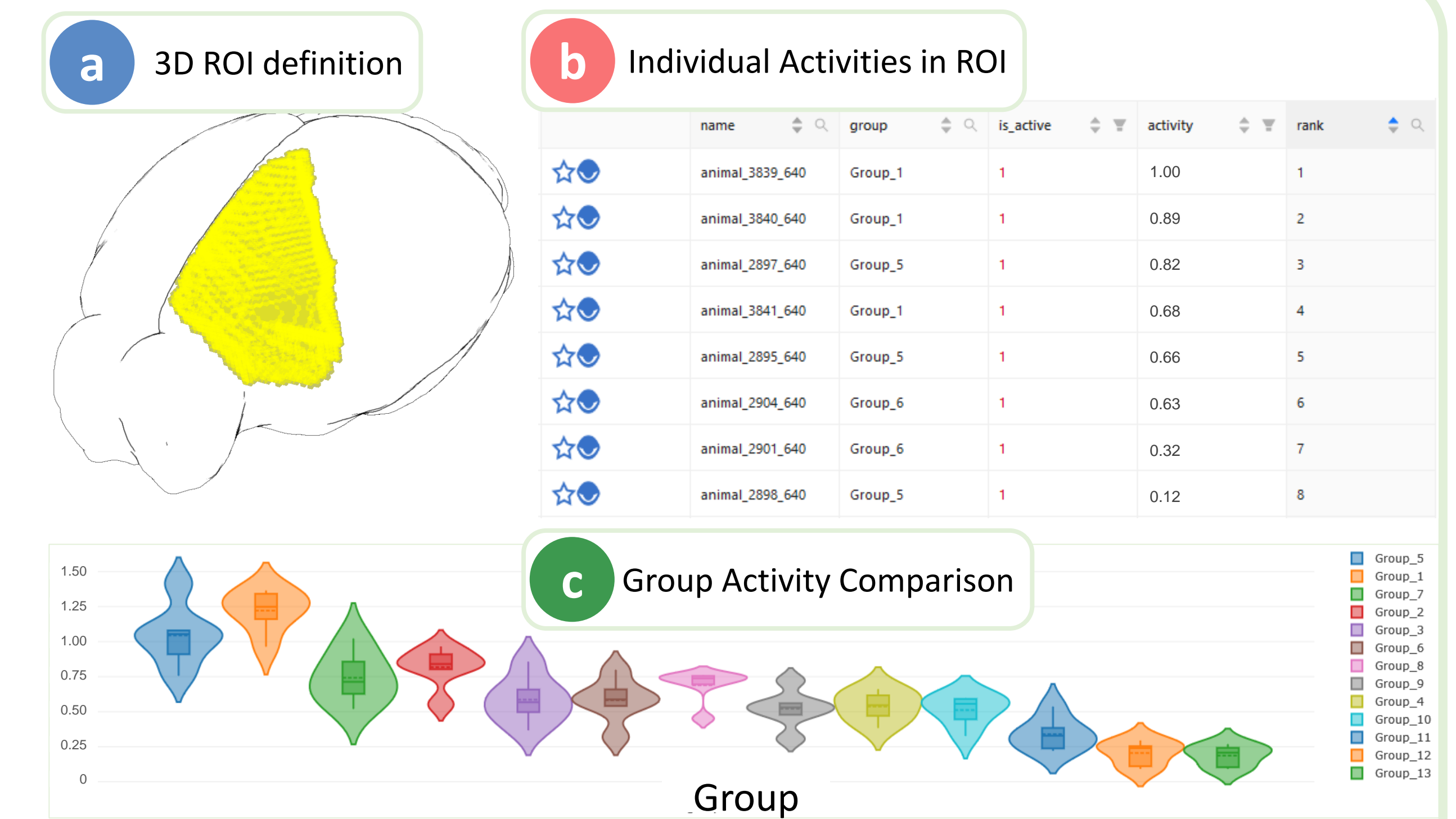


Figure 3: Exploration of activity datasets in BrainTrawler.

Dual Spatial Data Linking

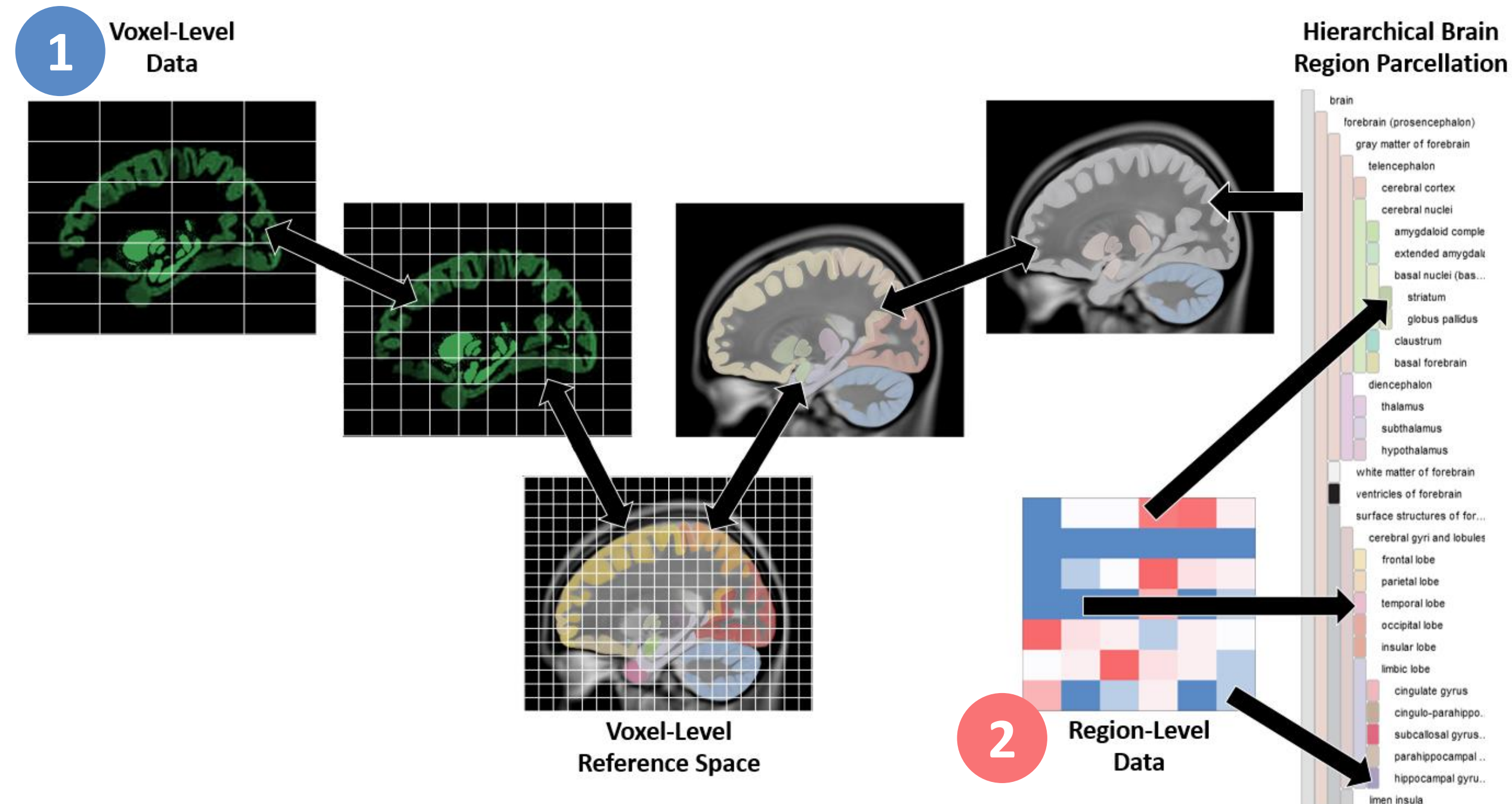


Figure 1: Dual spatial data linking approach in BrainTrawler.

BrainTrawler uses a dual approach for linking spatial data, as depicted in fig. 1: (1) Imaging data is registered to MNI 152 space (human) / Allen mouse brain CCF v3 (mouse). Then, the data is resampled to fit the reference space resolution. (2) Data on brain region level resolution, e.g. scRNA seq. data, is mapped from its native region ontology to the Allen Human/Mouse Brain Atlas. It is then mapped to the reference space using the brain region parcellation.

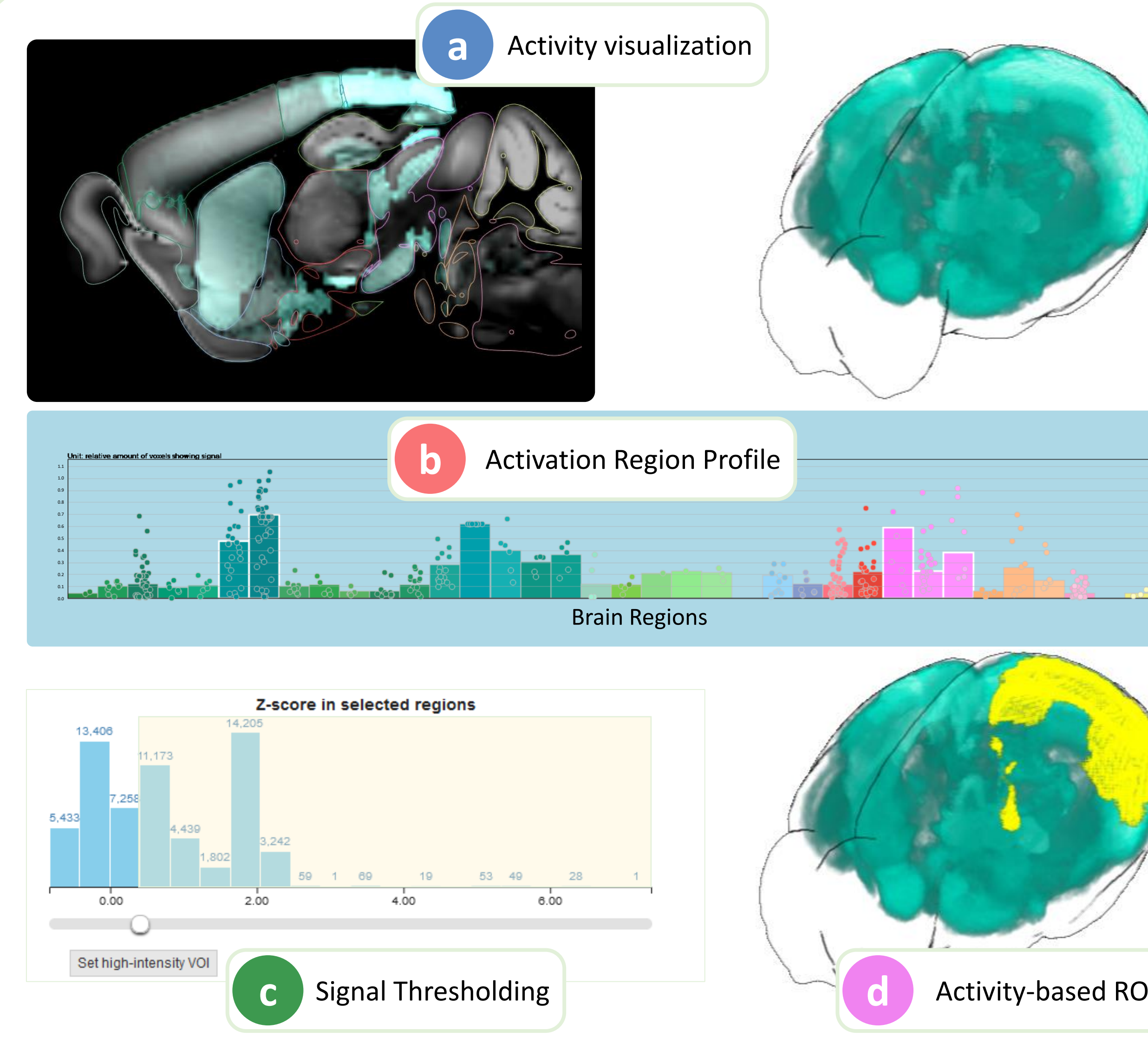


Figure 2: Generation of activity-based ROIs in BrainTrawler.

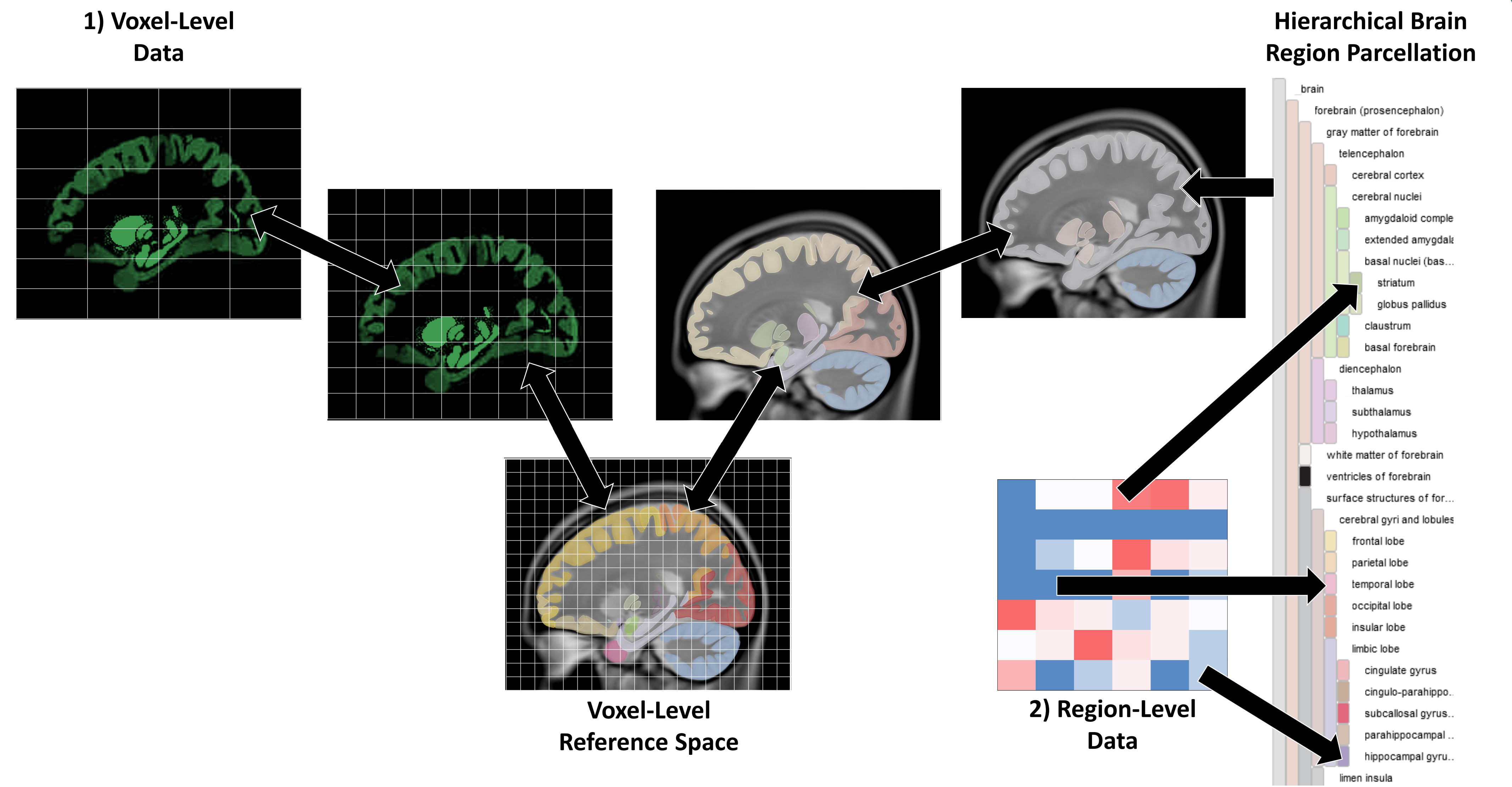
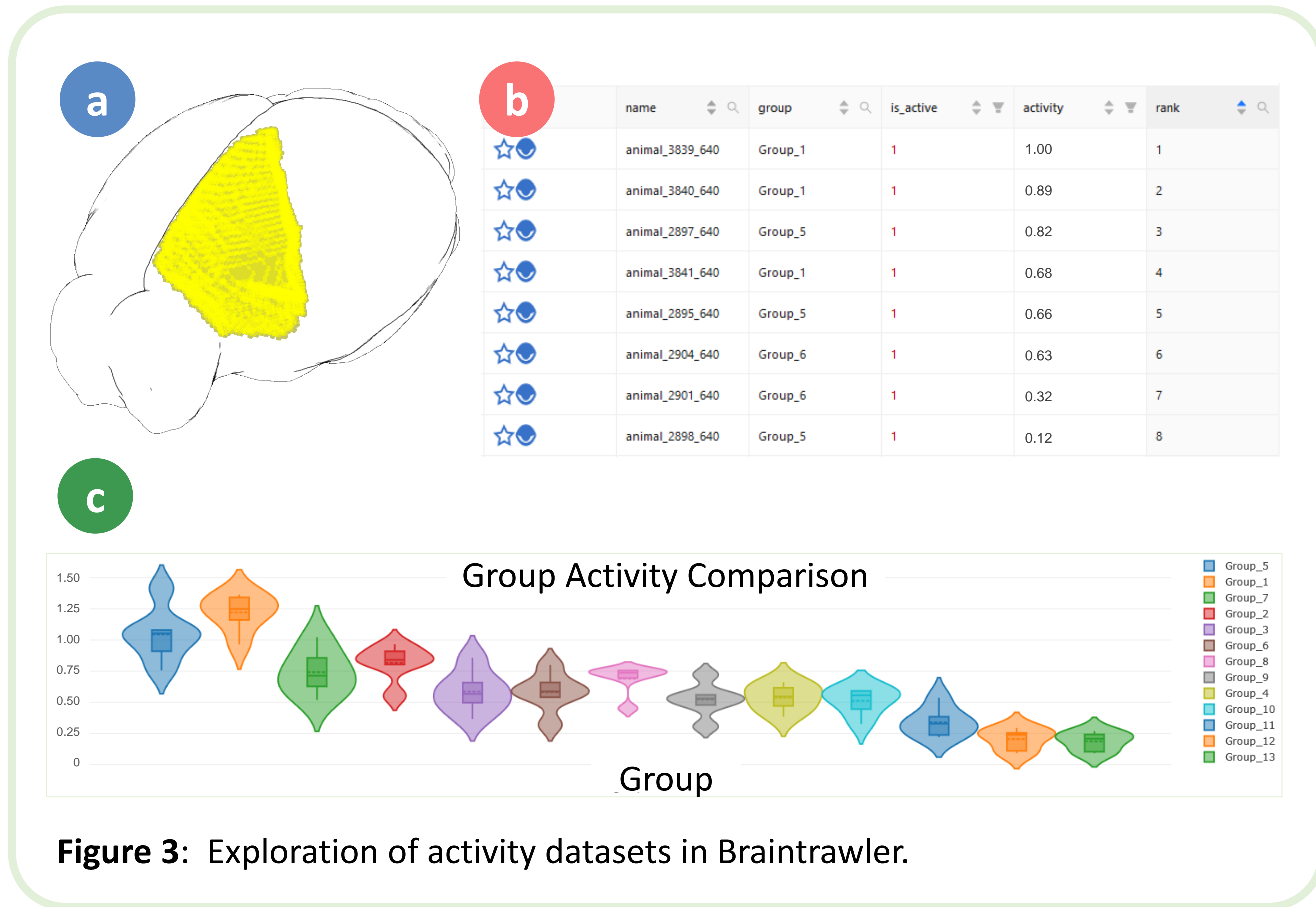
Create Custom ROIs from Activity Data

To effectively link activation peaks to other spatial data, BrainTrawler allows users to define ROIs directly from activation signals. This workflow starts with loading an activation image into the viewer (fig. 2a). Activity is also summarized in a region profile (fig. 2b) for additional anatomical reference. To start ROI generation, users can select a set of brain regions in the profile. A thresholding dialogue shows the voxel-wise activity distribution in the selected regions as a histogram (fig. 2c). All voxels with a higher activity than the selected threshold are collected in an ROI. The resulting activity-based ROI can then be used to query the extensive transcriptomic and connectivity database of BrainTrawler. Figure 2d shows an example activity-based ROI.

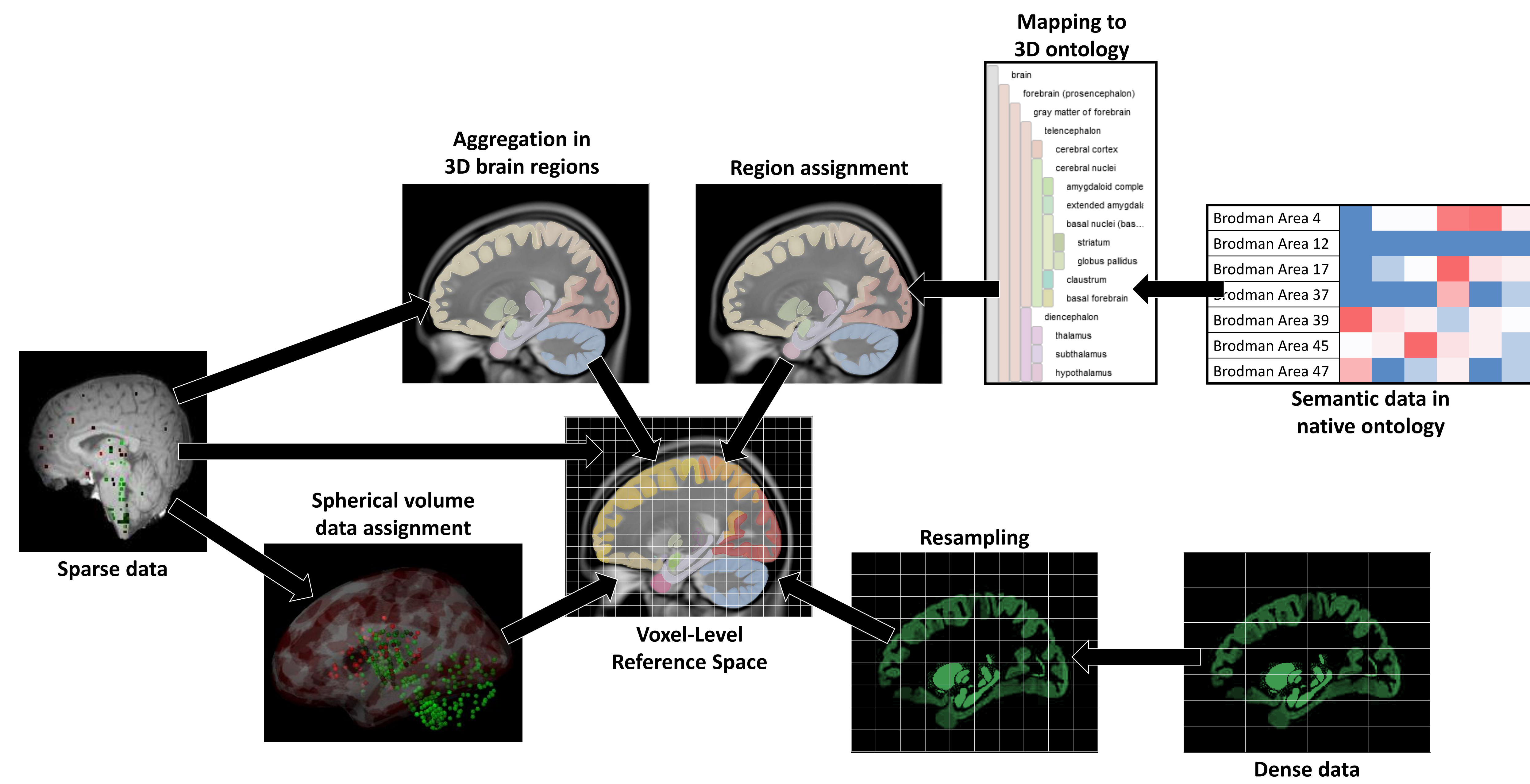
Conclusion

By adding support for volumetric brain activity data in BrainTrawler, we enable quick comparisons between task/treatment groups and detailed investigations of behavior and brain function in the multimodal context of activation, gene expression and connectivity. To the best of our knowledge, BrainTrawler is now the only interactive brain data exploration tool that allows the investigation of brain-wide single-cell transcriptomics data based on functional constraints.

[1] Fornito (2019). Bridging the Gap between Connectome and Transcriptome. Trends in Cognitive Sciences, 23(1), <https://doi.org/10.1016/j.tics.2018.10.005>
 [2] Ganglberger (2019). BrainTrawler: A visual analytics framework for iterative exploration of heterogeneous big brain data. Computers and Graphics, 82, <https://doi.org/10.1016/j.cag.2019.05.032>
 [3] Ganglberger (2024). BrainTACO: an explorable multi-scale multi-modal brain transcriptomic and connectivity data resource. Communications Biology, 7(1), <https://doi.org/10.1038/s42003-024-06355-7>



expression	sample_mri_0	sample_mri_1	sample_mri_2
12.494	74	96	29
11.688	129	78	81
12.743	85	96	19
0.7693	94	102	26
0.7876	145	75	66
10.950	128	92	36
12.494	146	88	61
11.688	98	95	33
12.743	125	90	36



Mapping to 3D ontology

