

Joined interactive exploration of genetic, functional and network data of the brain

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Recent advances in neuro-imaging allowed big brain-initiatives and consortia to create vast resources of brain data that can be used by researchers for their own projects. Understanding the relationship between genes, structure, and behavior is one of the driving questions of neurocircuit research. This requires fusion of spatial data at varying resolutions such as whole brain gene expressions, structural and functional connectivities, as well as non spatial data like gene lists related to behavior. Current analytical workflows in neuroscience involve time-consuming manual aggregation of the data and only sparsely incorporate spatial context to operate continuously on different scales.

We propose a framework to explore heterogeneous neurobiological data in an integrated visual analytics workflow. This allows experts to embed and explore their own experimental data in the context of public data resources. On-demand queries on volumetric gene expression and connectivity data enable an interactive dissection of networks, with billions of edges, in real-time, and based on their spatial context. Relating data to the hierarchical organization of common anatomical atlases allows experts to compare multimodal networks on different scales. This is supported by anatomy-driven layouts to make the networks more comprehensible. Additionally, 3D visualizations have been optimized to accommodate domain experts' needs for publishable network figures.

To evaluate our approach, case studies and expert interviews were conducted. We demonstrate the relevance of our approach for neuroscience by identifying fear-related functional neuroanatomy in mouse, which is investigated in current research. Further, we show its versatility by comparing multimodal brain networks linked to autism, even across species between mouse and human.

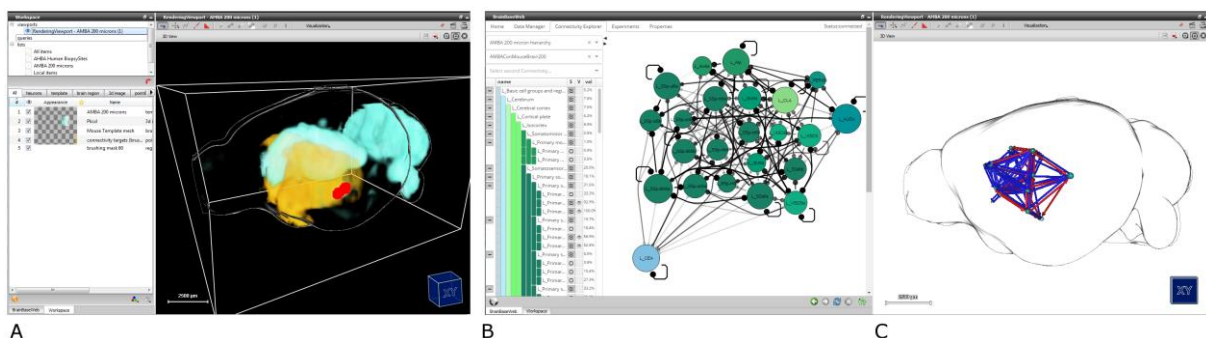


Figure 1: An integrated workflow for visual analysis of neurobiological data. A: 3D volume rendering of an anatomical template with volumetric gene-expression data (cyan), combined with structural connectivity (orange) outgoing from a selected region (red). B: 2D graph embedding showing functional connectivity based on hierarchical brain regions (selected region and structural connectivity), C: 3D visualization of the graph