

# M1. CEREBROVIZ: AN R PACKAGE FOR ANATOMICAL VISUALIZATION OF SPATIOTEMPORAL BRAIN DATA

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**Background** Spatiotemporal transcriptomic profiling has provided insight to the patterning of gene expression throughout the human brain from early fetal development to adulthood. When combined with the prior knowledge about a disease's age at onset and region-specificity, these expression profiles have provided the necessary context to both strengthen putative gene-disease associations and infer new associations. While a wealth of spatiotemporal expression data exists, there are currently no tools available to programmatically visualize this data within the anatomical context of the brain, thus limiting the intuitive interpretation of many of these findings.

**Methods** We present cerebroViz, an R package to map spatiotemporal brain data to scalable vector graphic diagrams of the human brain. Our tool allows rapid generation of publication-quality figures that highlight spatiotemporal trends in the input data, all while striking a balance between usability and customization. cerebroViz is generalizable across datasets and currently supports visualization of thirty brain regions found in datasets such as BrainSpan, GTEx, and RoadMap Epigenomics.

**Results** cerebroViz is capable of producing publication-quality SVG diagrams of the human brain. These diagrams may be used in publications, posters, and presentations. Multiple diagrams can be generated in a time series for creating movies or gif images with other tools to loop across time points, thus creating a dynamic visual representation of the expression profile. cerebroViz creates diagrams for a variety of uses. Our tool can also be used to highlight key similarities and differences between expression profiles of any two genes, time points, isoforms, replicates, or any quantifiable brain data at a regional resolution. For example, while common use of cerebroViz pertains to transcriptomic data, it may also be used to visualize methylation or histone modification levels in different brain regions.

**Discussion** Our tool provides programmatic visualization of spatiotemporal brain data. Visualizing this data within the anatomical context of the brain allows enhanced interpretability of spatiotemporal data such as gene expression profiles.

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