BrainTrawler Lite: Navigating through a multi-scale multi-modal gene transcriptomics data resource through a lightweight user interface

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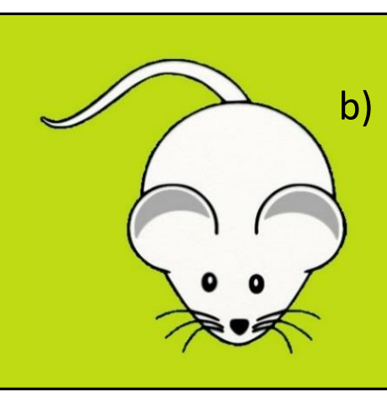
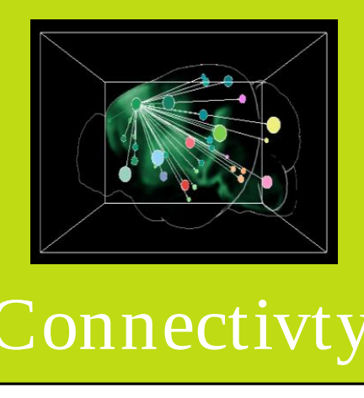
Objective

Joint exploration of behavior, genes and brain structure holds the promise to provide a better understanding of neural circuits than unimodal data analyses. Several consortia provide extensive data resources of different modalities [1-3]. To allow a joint exploration of such existing resources in a common space, we extended BrainTrawler [4], our web-based visual analytics frame work for exploration of neurobiological data of human and mouse, with a selection of publicly available gene expression and connectivity datasets [5]. For an easy navigation through this unique data collection, we additionally created BrainTrawler Lite, a lightweight user interface, which provides a visual overview of gene expression information available across resources.

Data in BrainTrawler[1)]

Data type		
 Gene expression	7x single cell RNA sequencing[2)]	12 x single nucleus RNA sequencing[2)]
	1x in situ hybridization	1x bulk RNA sequencing[2)]
		1x microarray
 Connectivty	Allen Brain Axonal Projections	WU-Minn HCP Resting State Connectome

1) Full data list: https://braintrawler.vrvis.at/docs/data_sources.html
2) Dataset collection is representative of the whole brain of the respective species.

a) Image taken from: https://pngimg.com/image/100728
b) Image taken from: https://getdrawings.com/cute-mouse-drawing

Access

https://braintrawler.vrvis.at/

Interface for dataset coverage

BrainTrawler Lite gives a visual summary of the gene expression information available across resources in the form of an interactive heat map. It shows the distribution of images/samples available for brain regions (columns) and datasets (rows). The darker the color the more data is present, displayed regions or datasets are adjustable. Hoovering over a tile of the heat map shows a summary of the represented data resource for the particular region. This allows easy visual identification of data-subsets of interest for further investigations. Clicking on a tile selects the corresponding data for further explorations on a gene set of interest or genome-wide level.

Hoovering over tile shows summary

Sample Count: 20140
Dataset Category: Bhattacherjee_2019 - Excitatory
BrainRegion: L_Somatomotor areas
Sample Region Annotations: Prefrontal cortex (PFC)
AgeCategories: 2
Phenotypes: 3

Selected tile in orange for further investigations

Expand/collapse parcelation and select regions to be displayed

Select datsets and meta data of interest to be dispalyed

Interface for exploration of gene sets

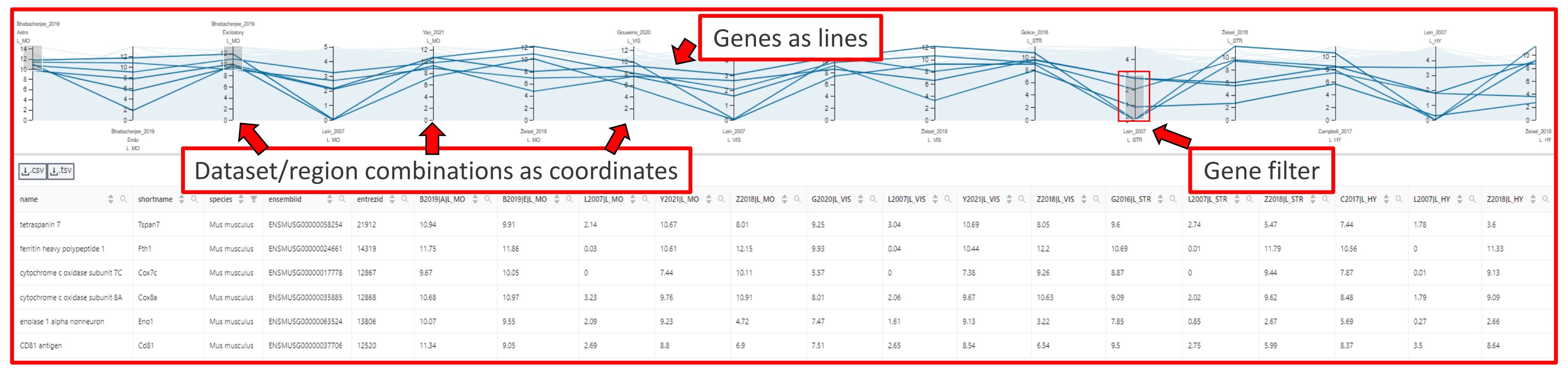
Heat map showing expression of single gene for selected regions/datasets

Select genes to investigate

Small multiples to compare expression of genes

Gene selection can be done by name, based on gene ontology terms or uploaded as a csv file (top). To facilitate exploration of defined gene sets across datasets and regions of interest, expression is shown using heat maps and small multiples. As an example, expression is shown for a gene set of five genes. The bottom right side shows gene expression of the five genes across selected datasets using small multiple heat maps, whereas the bottom left side shows a selected gene with more details. Colors are scaled within each dataset due to limited comparability of absolute values across datasets and range from 0 to maximum expression.

Interface for genome level exploration



Genes as lines

Dataset/region combinations as coordinates

Gene filter

For genome level exploration, parallel coordinates that visualize gene expression of all genes in selected datasets and regions are used. Thereby, each coordinate corresponds to one piece of selected data and the lines represent the genes. Restricting the values a coordinate covers, allows gene filtering, with results shown in a table. This makes parallel coordinates a useful tool to narrow down the genes, which are in the selected value ranges for chosen datasets and regions. The table displays for each filtered gene its name, ensemblID, entrezID and gene expression for each selected region/dataset combination. All generated exploration results can also be exported.

Conclusion

Overall, our extension of BrainTrawler provides neuroscientists simple access to a unique collection of connectivity and gene expression data up to cell-type resolution. The possibility to explore gene expression profiles across datasets of structurally or functionally connected regions of interest may help in hypothesis generation on neural circuits.

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