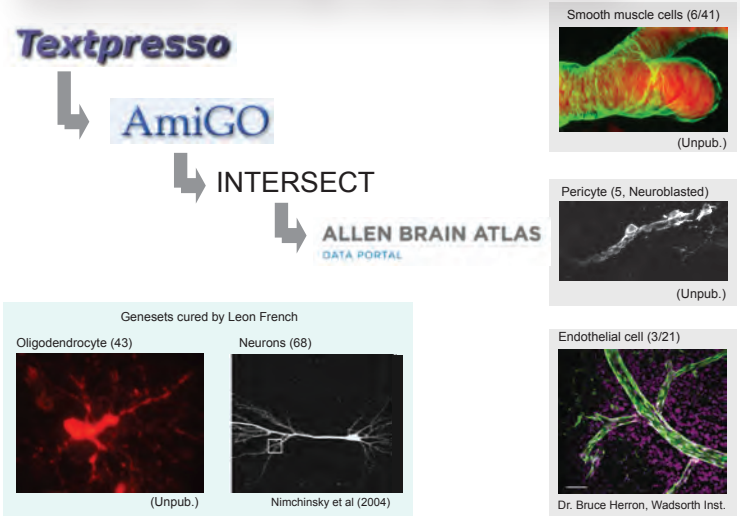
Whole-brain Neurovascular Interface genetic fabric

Pablo Blinder, Phd - Neuroscience Department Tel-Aviv University - pb@post.tau.ac.il

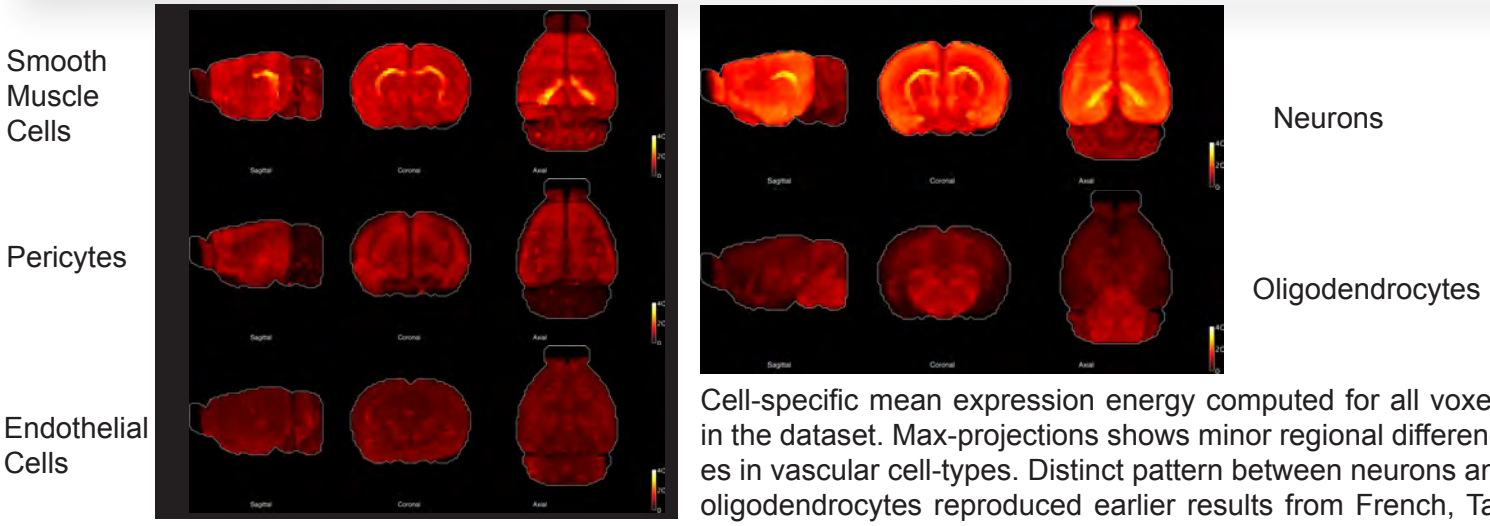
Proper brain function depends on continuous supply of oxygen and nutrients to active areas. This process is mediated by the coordinated activity of interneurons, astroglia, pericytes and smooth muscle cells; an ensemble commonly referred as the neurovascular unit. Here, I surveyed the correlated changes in cell-specific genetic markers across the entire mouse brain.

Expression energy max-projection



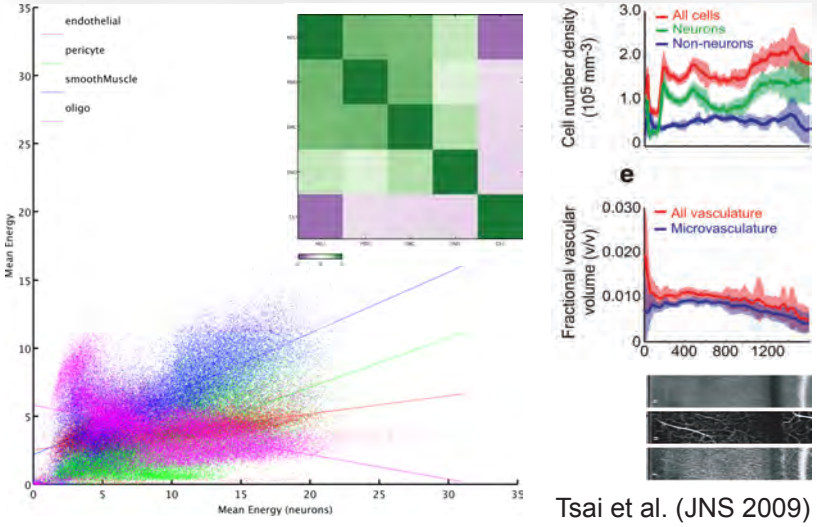
Cell-specific and non overlapping gene set where compiled from a semi-automated literature search. Texpresso was used to generate an initial list of candidate genes. Human and mouse gene nomenclature discrepancies where resolved with AmiGO. The non-overlaping subset of each candidate list was selected by sequential intersections with available tools (Intersector). The final set used was restricted by the coronal gene expression data at the ABA database. Enclosed in parentheses is the number of genes used for each cell type.

Expression energy max-projection



Cell-specific mean expression energy computed for all voxels in the dataset. Max-projections shows minor regional differences in vascular cell-types. Distinct pattern between neurons and oligodendrocytes reproduced earlier results from French, Tan and Pavlidis (2011).

All-voxel x cell-type cross correlation



Tsai et al. (JNS 2009)

Scatter-plots of for all voxel's mean energy per cell type show positive correlation between neurons, smooth-muscle cells(highest), pericytes and endothelial cells (lowest). The negative correlation with oligodendrocytes reproduces existing results as above. Inset, a cell by cell correlation matrix. Interestingly the correlation between neurons and endothelial cells pins on the existing histological correlates between cortical neurons and the vasculature (Tsai et all, JNS 2009).