



# Data-Driven Brain Staining

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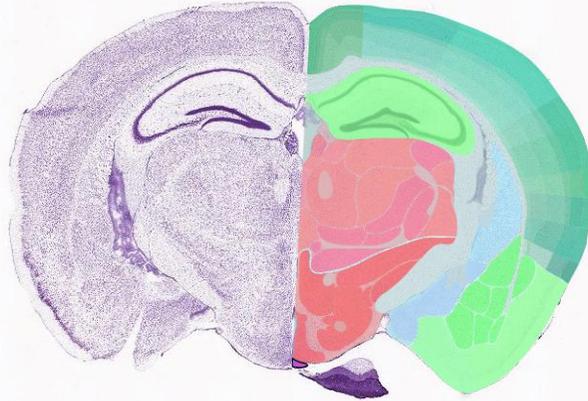
OIST



ALLEN INSTITUTE  
for BRAIN SCIENCE  
Fueling Discovery

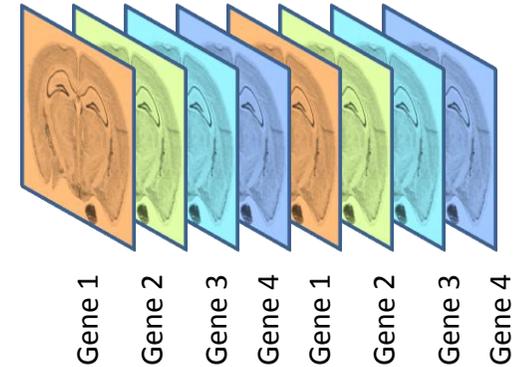
Recognizing neural structures from stained brain is a difficult task that requires both a skilled and an experienced eye. Often, some regions and nuclei are not clearly defined and missed even by experts. Different staining methods can be used to better recognize different neural structures.

The goal of this project is to suggest a staining method that is both descriptive and informative, such that the regions in the stained left hemisphere could be as easily interpretable as the colored sketch of the right hemisphere.



Using in situ hybridization staining with multiple colors on the same tissue is possible. However, multi color staining is limited to only a small number of different markers.

Therefore, the challenge is to find the **best small set of markers** whose combined expression is most informative over all brain regions.



~4,000  
Coronal  
genes

Mouse energy  
matrix

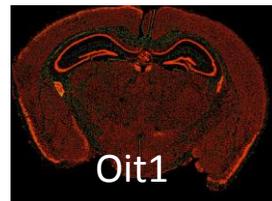


Sparse  
PCA

~50,000  
Voxels (3d pixel)

The small set of “Orthogonal genes” is identified using the registered mouse brain data. *Sparse Principal Component Analysis* is used to find genes whose **combined expression pattern** holds most of the spatial variance.

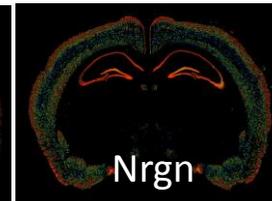
- The four “Orthogonal genes” identified are: *Oit1*, *Syt1*, *Nrgn* and *Nsf*.
- Some notable spatial features: *Oit1* expression pattern is highly expressed across the brain, much like nissel staining; *Syt1* expression in the hippocampus is limited to only the dentate gyrus; *Nrgn* expression pattern makes it is easy to differentiate between cortical layers.
- These four markers applied to the same tissue each with a different color will make it easier to recognize different brain structures and layers.



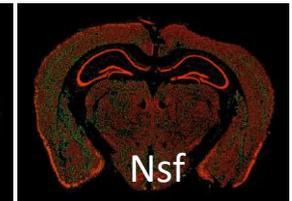
Oit1



Syt1



Nrgn



Nsf