Graphing Directional Connectivity in FMRI

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https://neuromatch.io/

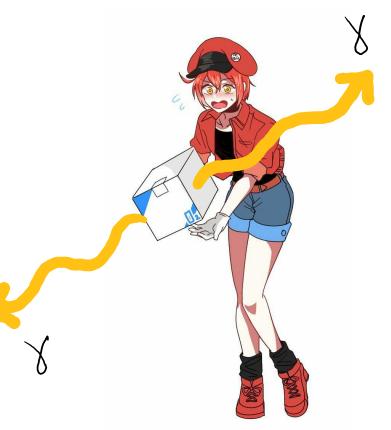
What is FMRI?

Functional Magnetic Resonance Imaging

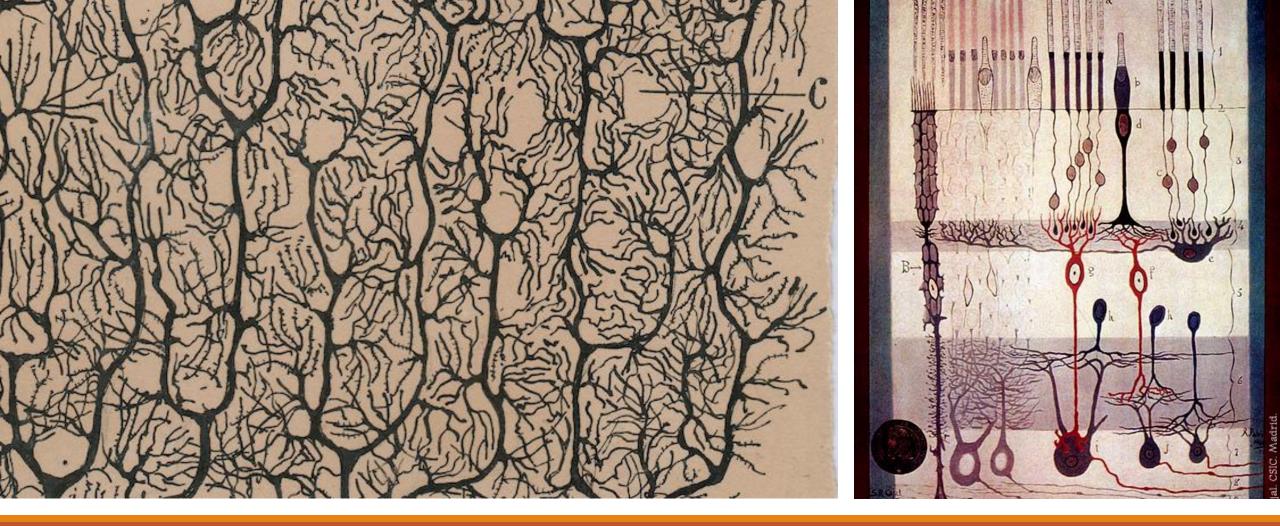
Measures BOLD signal : Blood Oxygen Level Dependent Signal

Highly sensitive to motion (currently limits clinical use to neurosurgery)

Assumes areas with high relative blood oxygen levels are currently active



Red Blood Cell Carrying Oxygen: Cells at Work! (Linden Films)



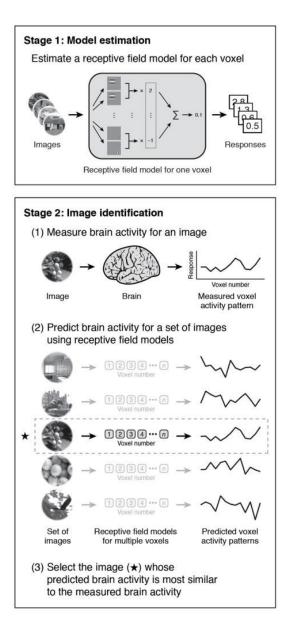
Ramon y Cajal versus Golgi – late 1800s

If nerves use electrical signals where's the switch that determines which way signals go?

Brain Network is like River Deltas

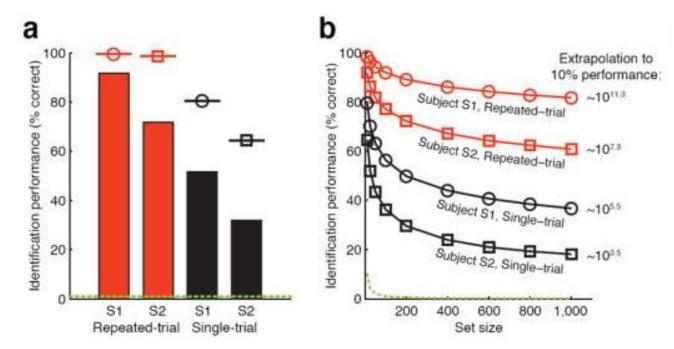


https://nasaviz.gsfc.nasa.gov/11759

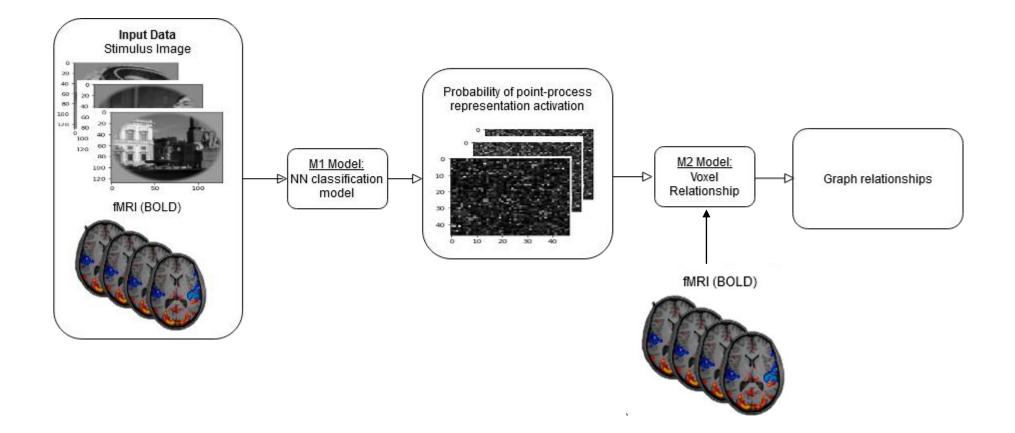


Identifying natural images from human brain activity Kay et. al. (2008)

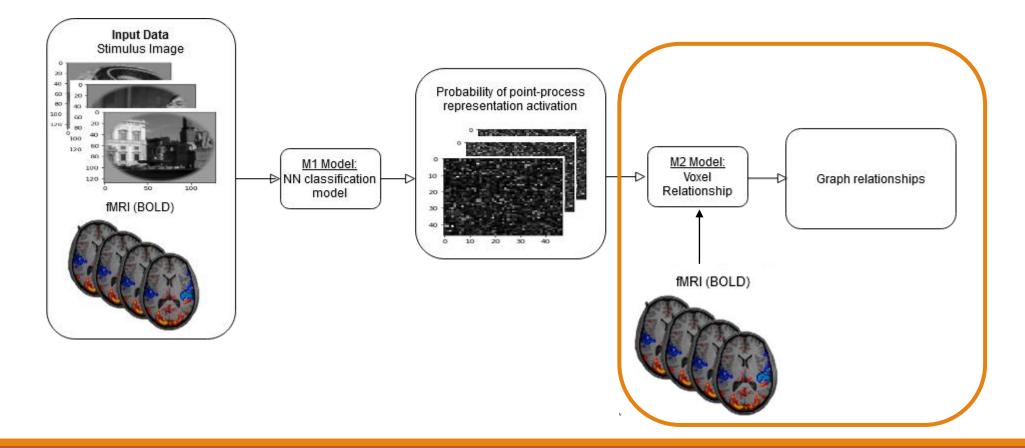
Data Available at <u>https://crcns.org/data-sets/vc/vim-1/about-</u> vim-1



Our Pipeline



Our Pipeline



Point Process (Tagliazucchi et. al. (2011)

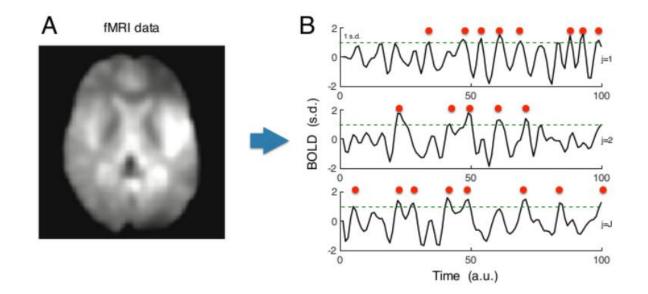


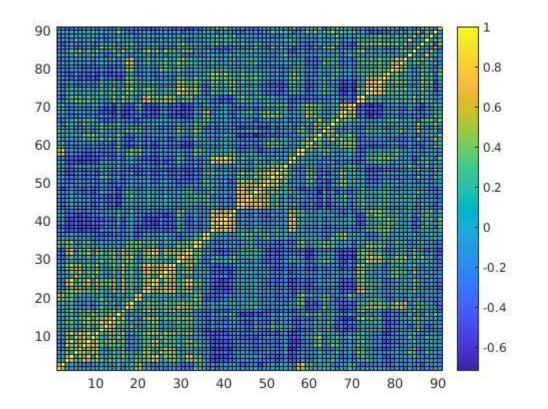
FIGURE – Time points are selected at the upward threshold crossings or the peaks of the signal (filled circles). Adapted from I. Cifre el at. 2020.

https://doi.org/10.1016/j.neulet.2010.11.020

The Trouble with Pearson Correlation

$$r = rac{\sum \left(x_i - ar{x}
ight) \left(y_i - ar{y}
ight)}{\sqrt{\sum \left(x_i - ar{x}
ight)^2 \sum \left(y_i - ar{y}
ight)^2}}$$

r(i,j) = r(j,i) gives limited network information

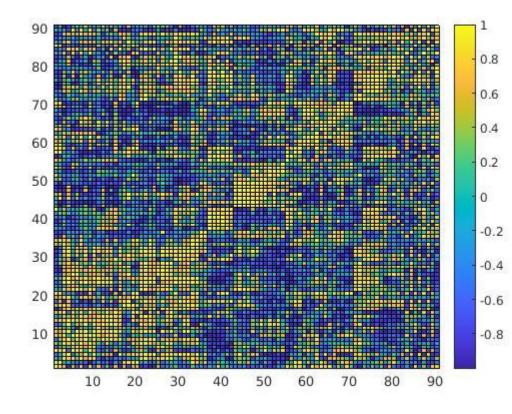


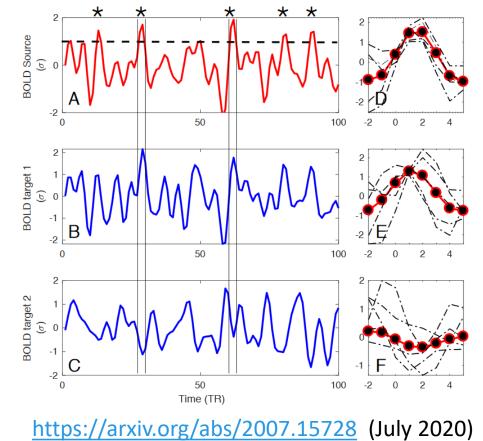
90 ROI using automatic anatomical labeling: <u>https://www.oxcns.org/aal3.html</u>

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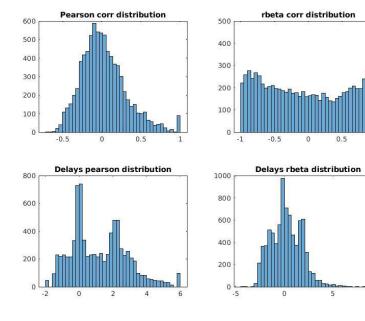
Solution: Event Triggering

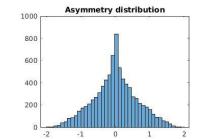
rBeta: resting BOLD event triggered averages





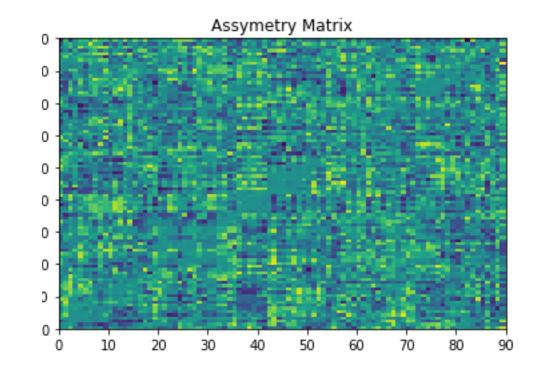
Asymmetry



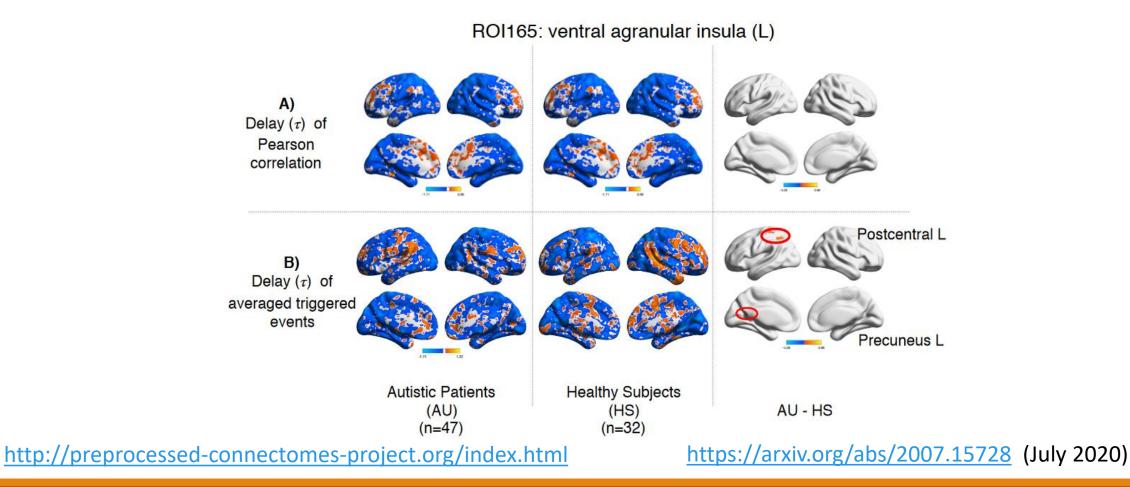


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10



Adding Time Delays



Parallelized

Over 25,000 voxels of interest (attributed to cortical regions)

produces 335 million undirected comparisons

700 million pair-wise comparisons.

Ordinary linear Pearson correlation : 1 h 14 min, 20 threads and 30 GB of memory

rBeta calculation took 18 h using 22 threads and 30 GB of memory producing 10 GB of floats per trial



Code Availability

Matlab Version: https://github.com/remolek/NFC

-has machinery for rbeta and rbeta delays

-slower

Python and Parallelized Version: https://github.com/gdbassett/rbeta

- -has machinery for rbeta, rbeta delays in progress
- -faster 😳

Can be installed from the test pypi server with:

python3 -m pip install --index-url https://test.pypi.org/simple/ --no-deps --upgrade rbeta

PageRank Algorithm

https://graph-tool.skewed.de/

Cool Review Article: Farahani et. al Front. Neurosci., 06 June 2019 | https://doi.org/10.3389/fnins.2019.00585

executed using graph-tool PageRank function (form of eigenvector centrality)

V1 activation probabilities as personalization dictionary

•Weights from rbeta analysis gives transition probabilities

Resting data from Kay lead in / lead out times as initial PR's

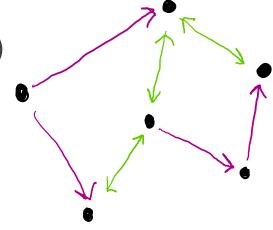
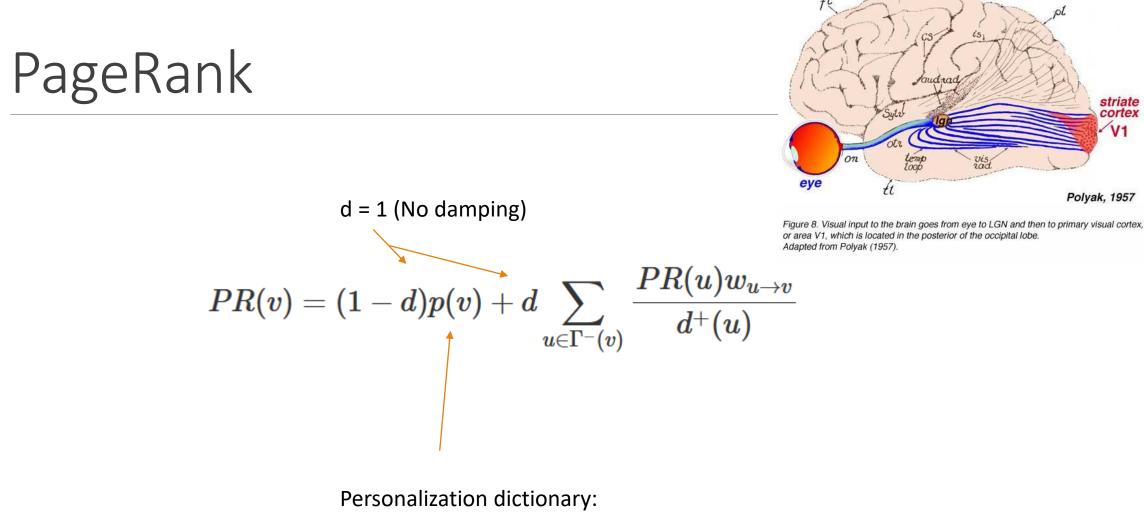


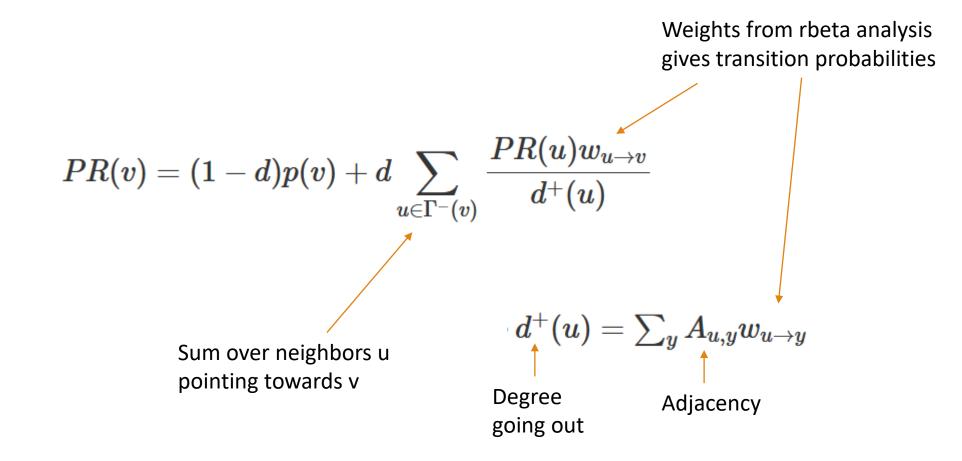
Image: Webvision Matthew Schmolesky



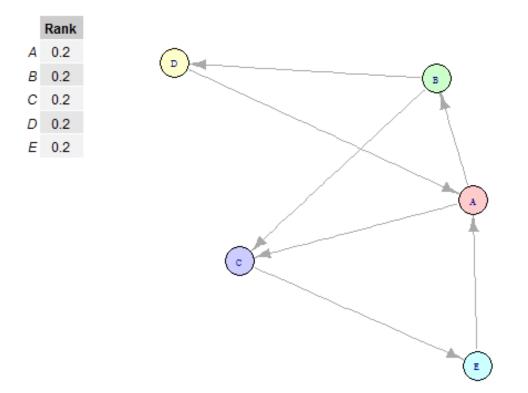
V1 Activation Probability

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PageRank



Page Rank of the nodes at start



From:

Google Page Rank, Power Iteration and the Second EigenValue of the Google Matrix Sandipan Dey 2 Jan 2017

Constructing Graph to pass into PageRank

g = Graph()

ROI1 = g.add_vertex()

ROI2 = g.add_vertex()

...loop over all regions of interest

Edge = g.add_edge(ROI1, ROI2)

...loop to form all to all connectivity. Unimportant edges will just have low weights g.save("excitatory.xml.gz")

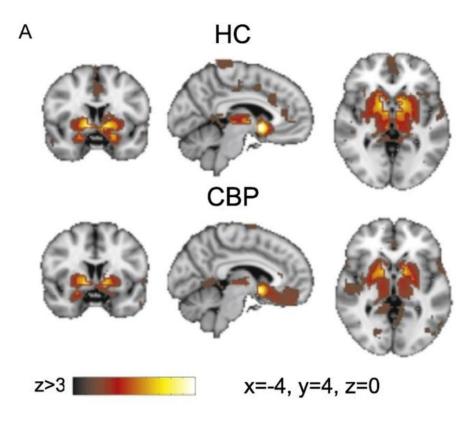
```
g2 = load_graph("excitatory.xml.gz")
```

```
# create personalization dictionary from M1
personalization dict = dict(zip(self.roi idx, prediction))
#pred weights = nx.pagerank(M1, personalization=personalization dict, weight=weight, nstart=self.resting state)
prediction = self.ml predictions[1, :]
personalization dict = dict(zip([str(k) for k in self.roi idx], prediction)) <-----
personalization = self.ml ex.new vertex property("float")
for node id in self.ml ex.get vertices(): # iterate through vertices
    name = self.ml ex.vp.name[node id] # get the 'name' node property map value for node
    if not name in ['source', 'destination']:
       v = self.ml ex.vertex(node id)
        try:
            personalization[v] = personalization dict.get(name, 0) +
        except:
           print(v, name)
            raise
predictions ex = pagerank(self.ml ex, pers=personalization, weight=self.ml ex.ep.weight, damping=0.0)
pred ex dict = dict(zip(list(self.ml ex.vp.name), list(predictions ex)))
```

Total weight combines activation and depletion weights

Clinical Applications

- •fMRI currently limited to planning neurosurgery due to motion constraints
- •Functional Ultrasound possible replacement for fMRI
- •Aid in communication for paralysis patients
- •Help eliminate bias as a diagnostic tool as data sets expand



Conclusion

•We have produced efficient, scalable ways to process large amounts of fMRI data

Improvements on directional correlation based on BOLD signal using rBeta

- BOLD data is highly self correlated but has a lot of 0's
 - BOLD signal can be shrunk to point process
 - Is there value in higher resolution then ?
 - Looking at cortical regions of interest and down-sampling may help produce a manageable amount of data.

•Future: add additional nodes to the graph along slower edges to lag the iteration of data