

This Brain Is a Mess:
Inference, Random Graphs, and Biophysics
to Disentangle Neuronal Networks

Kameron Decker Harris
November 30, 2017

Acknowledgements

- **Eric Shea-Brown & team:**

- Josh Mendoza
- Iris Shi
- Doris Voina
- Matt Farrell
- Ali Weber
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- Joel Zylberberg

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- Chris Danforth, Peter Dodds (UVM)
- Ashok Litwin-Kumar, Larry Abbott, Haim Sompolinsky

- **Nino Ramirez & the “respirators:”**

- Tatiana Dashevskiy
- Fred Garcia
- Aguan Wei

- **Stefan Mihalas & Allen Institute “connectors:”**

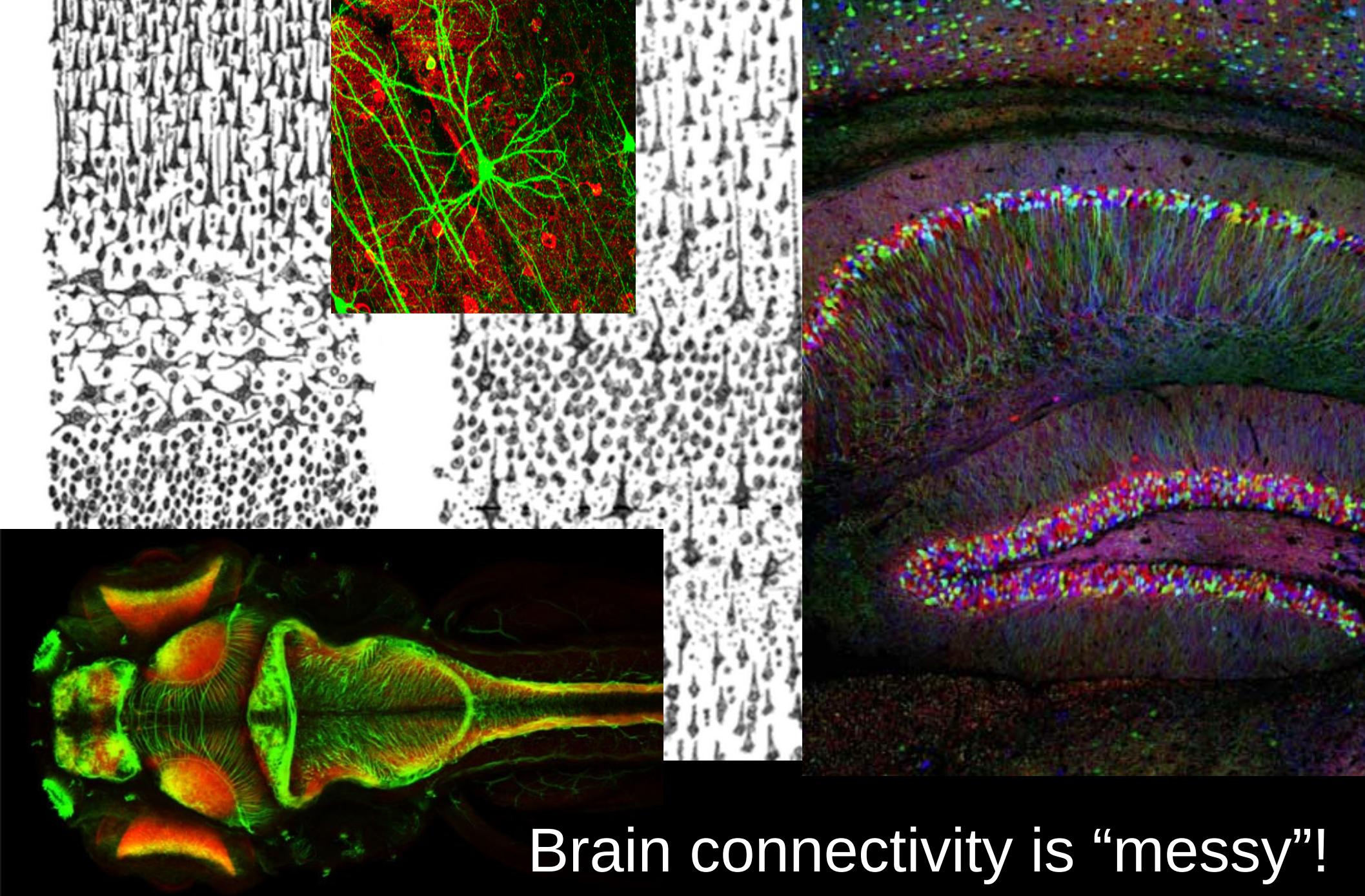
- Joe Knox
- Nile Graddis
- Nick Cain
- David Feng
- Lydia Ng

- **Ioana Dumitriu & the “graphons:”**

- Gerandy Brito
- Thanks also to Marina Meilă

- **UW AMATH:**

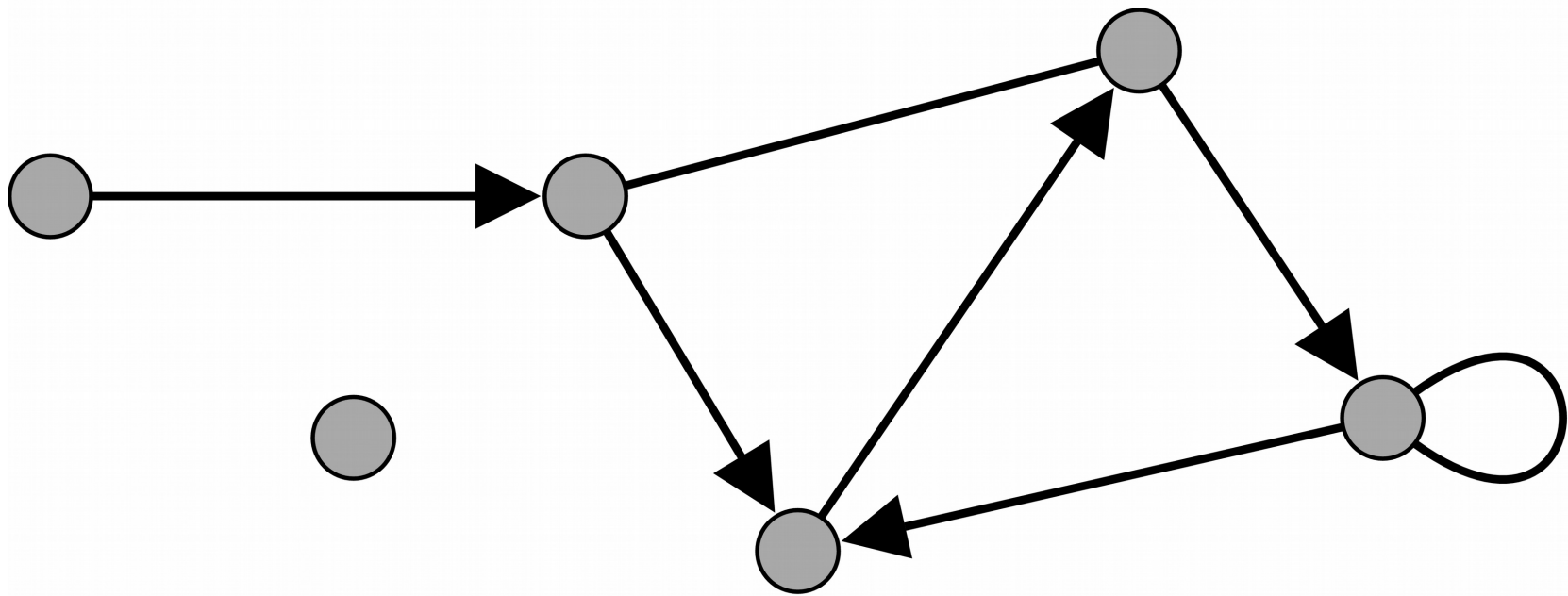
- Keshanie Dissanayake
- Lauren Lederer
- Derek Franz
- Alan Perry
- Tony Garcia
- Everyone else!



Brain connectivity is “messy”!

Credits: Lee et al. (2006) cortical pyramidal cell; Santiago Ramon y Cajal; UCL Zebrafish Group; Tamily Weissman, Jean Livet, Ryan Draft (mouse hippocampus)

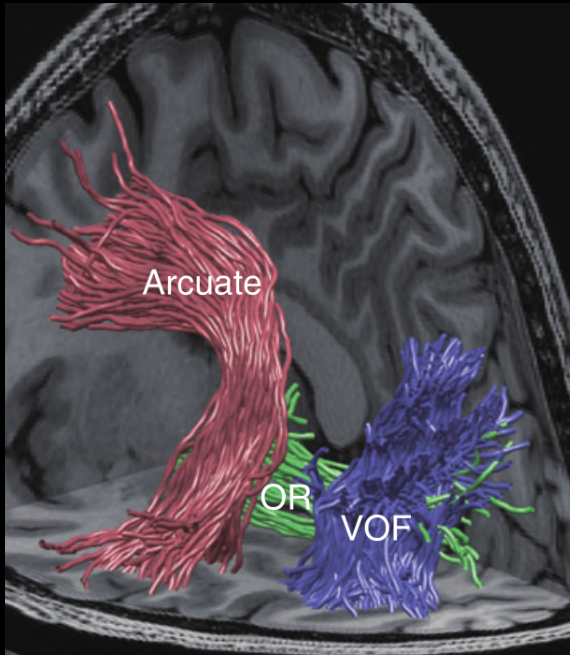
Neuron wiring forms a **network** or **graph**



Structural connectivity data

Structural connectivity data

Diffusion MRI
Macroscopic

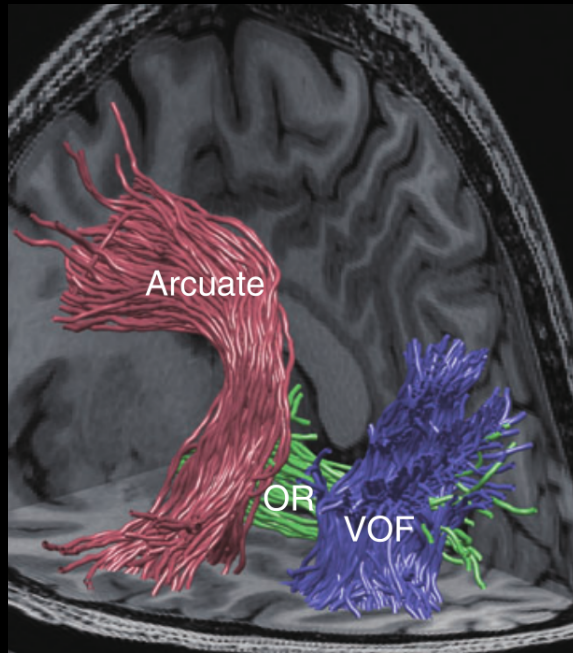


Takemura et al. (2016)

1-3 mm
Undirected
Non-destructive

Structural connectivity data

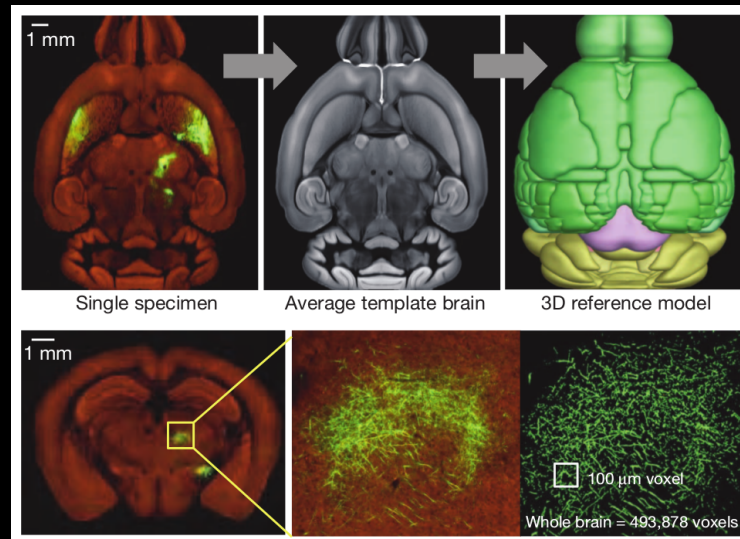
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Tracing & tomography
Mesoscopic



Oh et al. (2014)

10-100 μm
Directional
100's of neurons

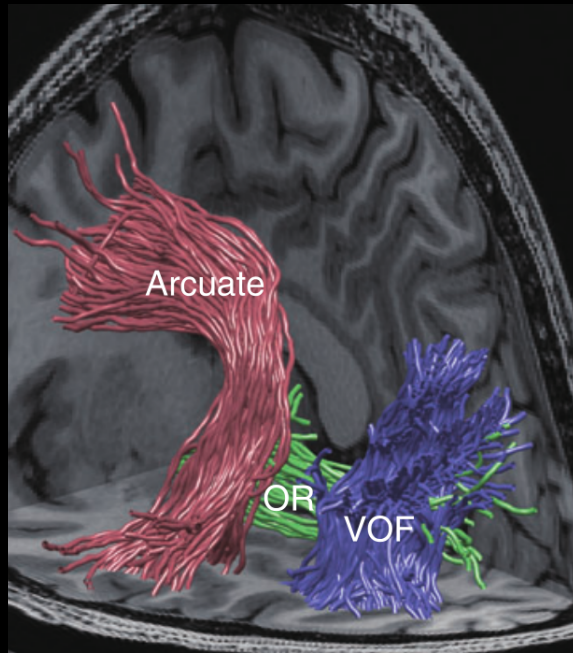
Increasing resolution



All require algorithms!

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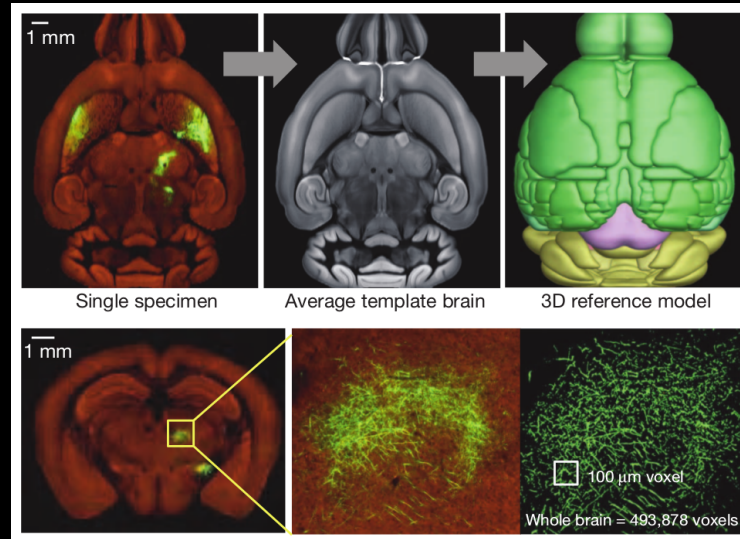
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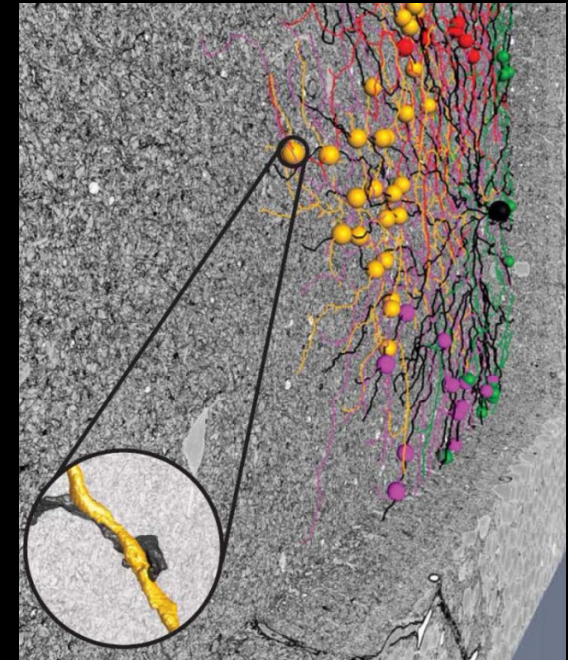
Tracing & tomography Mesoscopic



Oh et al. (2014)

10-100 μm
Directional
100's of neurons

Electron Microscopy Microscopic



Kleinfeld et al. (2011)

10 nm
Neurons & synapses

Increasing resolution

All require algorithms!

Connectivity questions

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1) How do we infer mesoscopic connections?

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Machine learning for neuronal network data

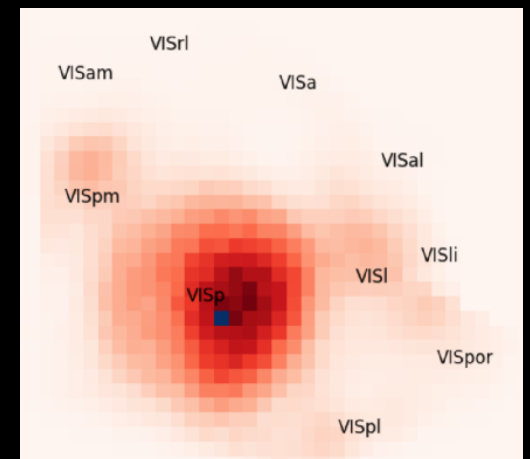
Published as:

Harris, Mihalas, Shea-Brown.

“Nonnegative spline regression of incomplete tracing data reveals high resolution neural connectivity.”

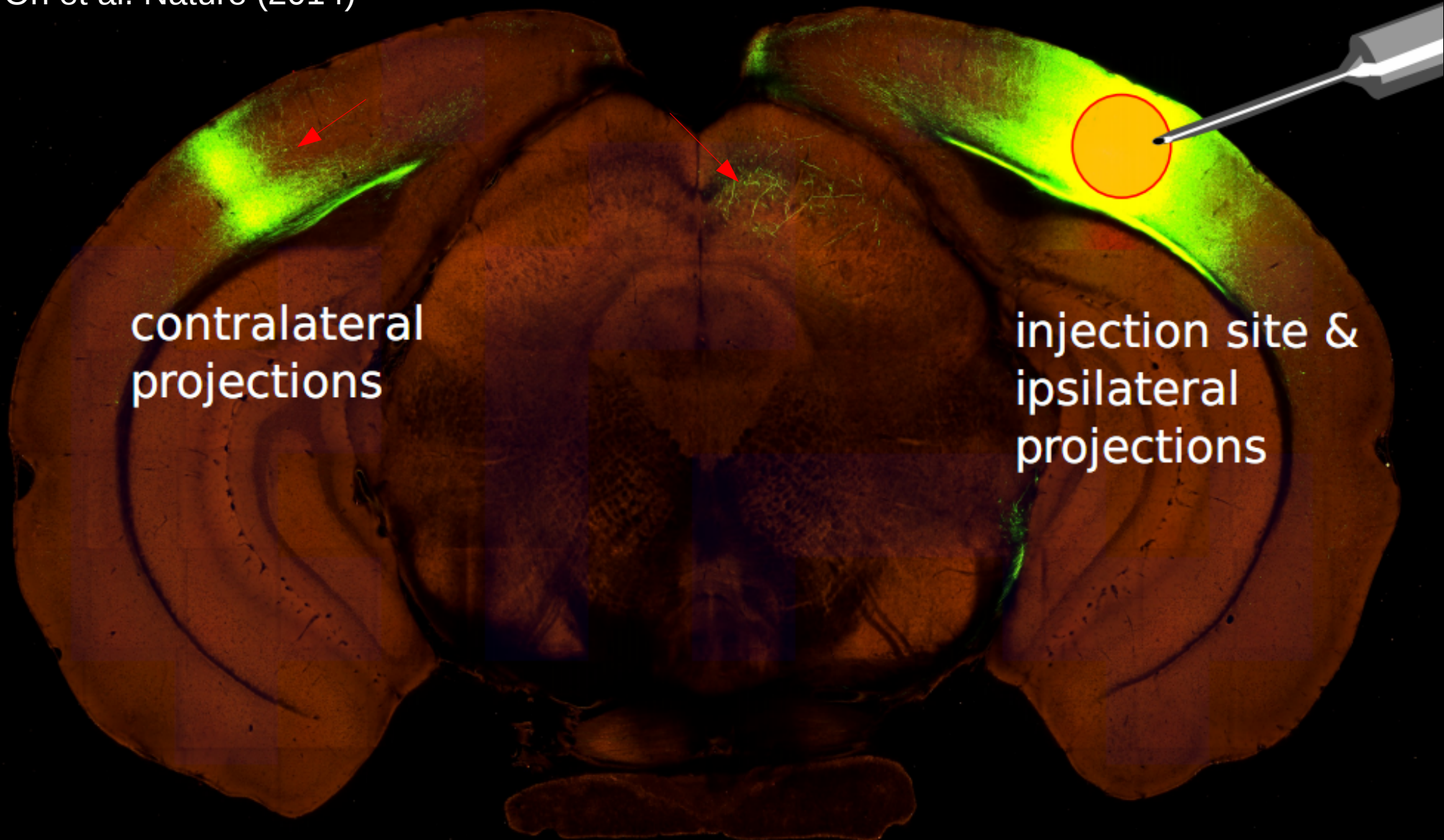
In proceedings of NIPS. 2016.

Ongoing work with Joe Knox and others at Allen Institute

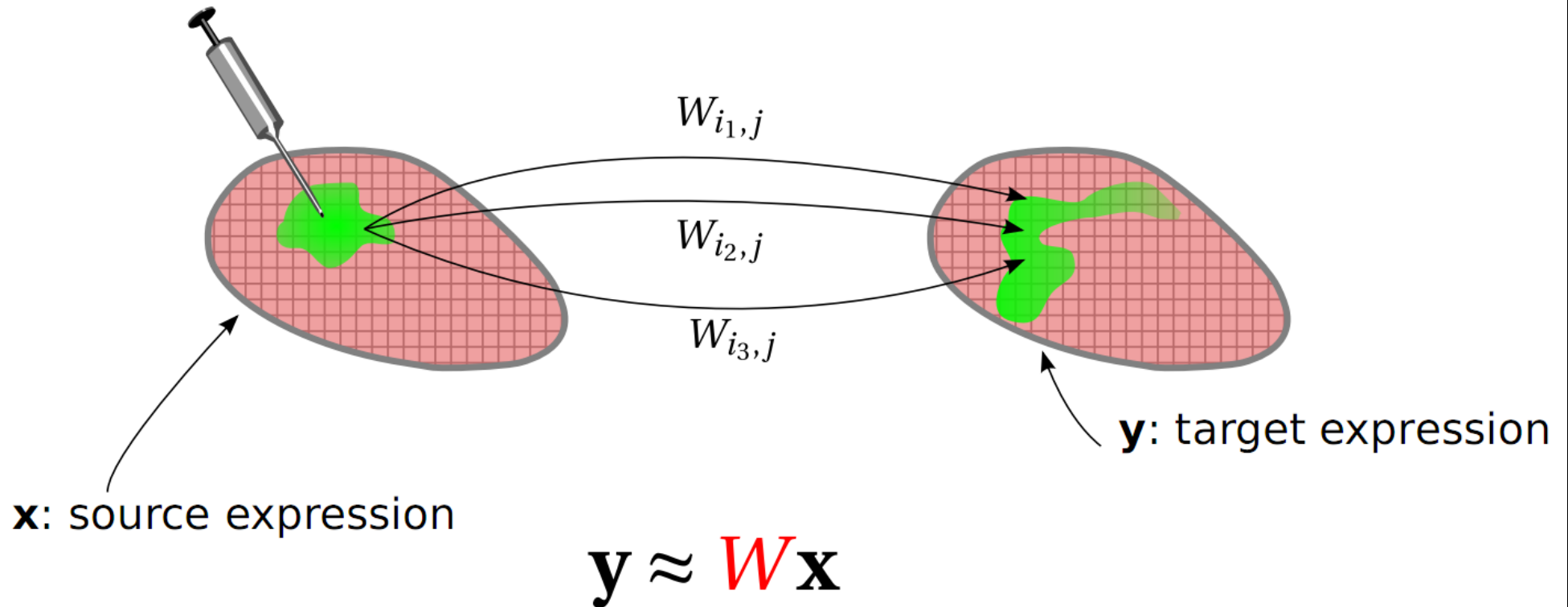


Mesoscale viral tracing experiments Allen Institute for Brain Science (AIBS)

Oh et al. Nature (2014)



Model connectivity as a matrix



Challenges for inference:

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- 1) Injection sites do not cover whole brain; model is underdetermined

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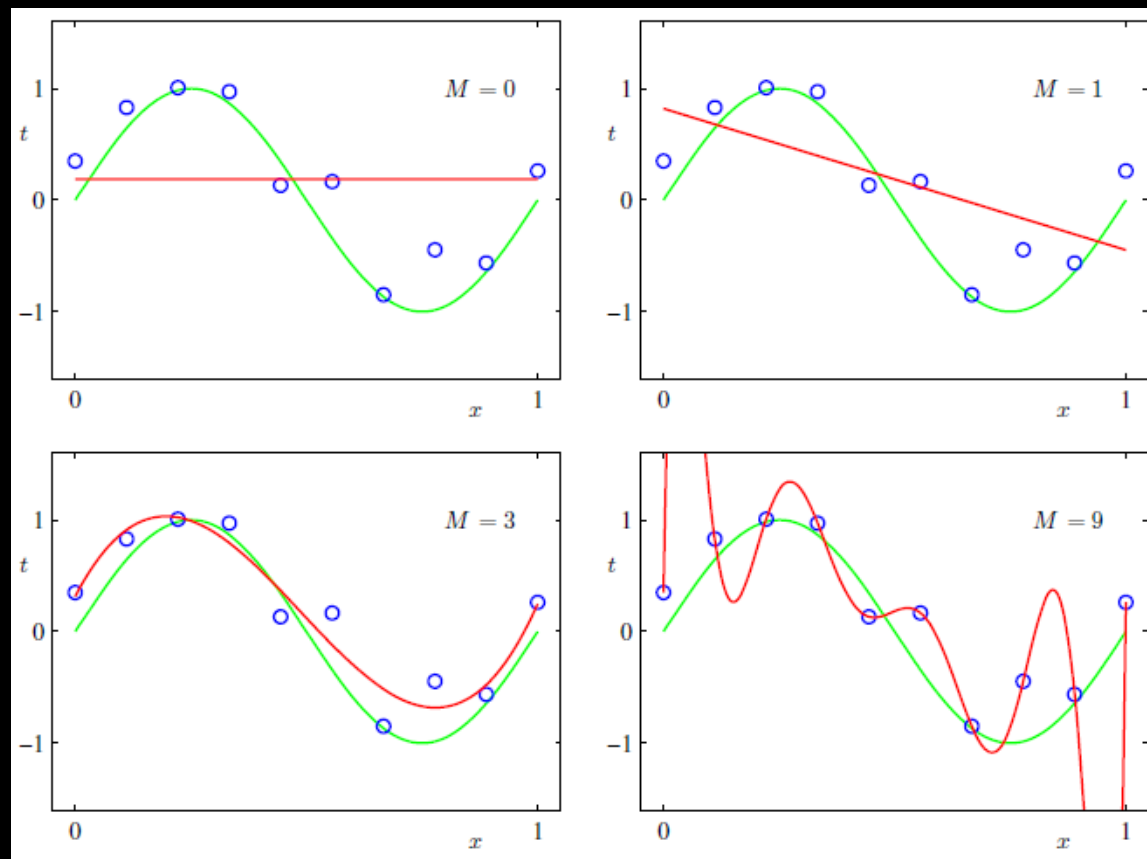
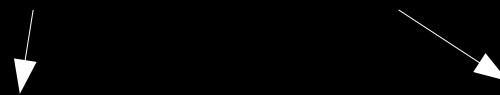
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Challenges for inference:

- 1) Injection sites do not cover whole brain; model is underdetermined
 - Fill in gaps with smoothing regularizer
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Regularization prevents over-fitting

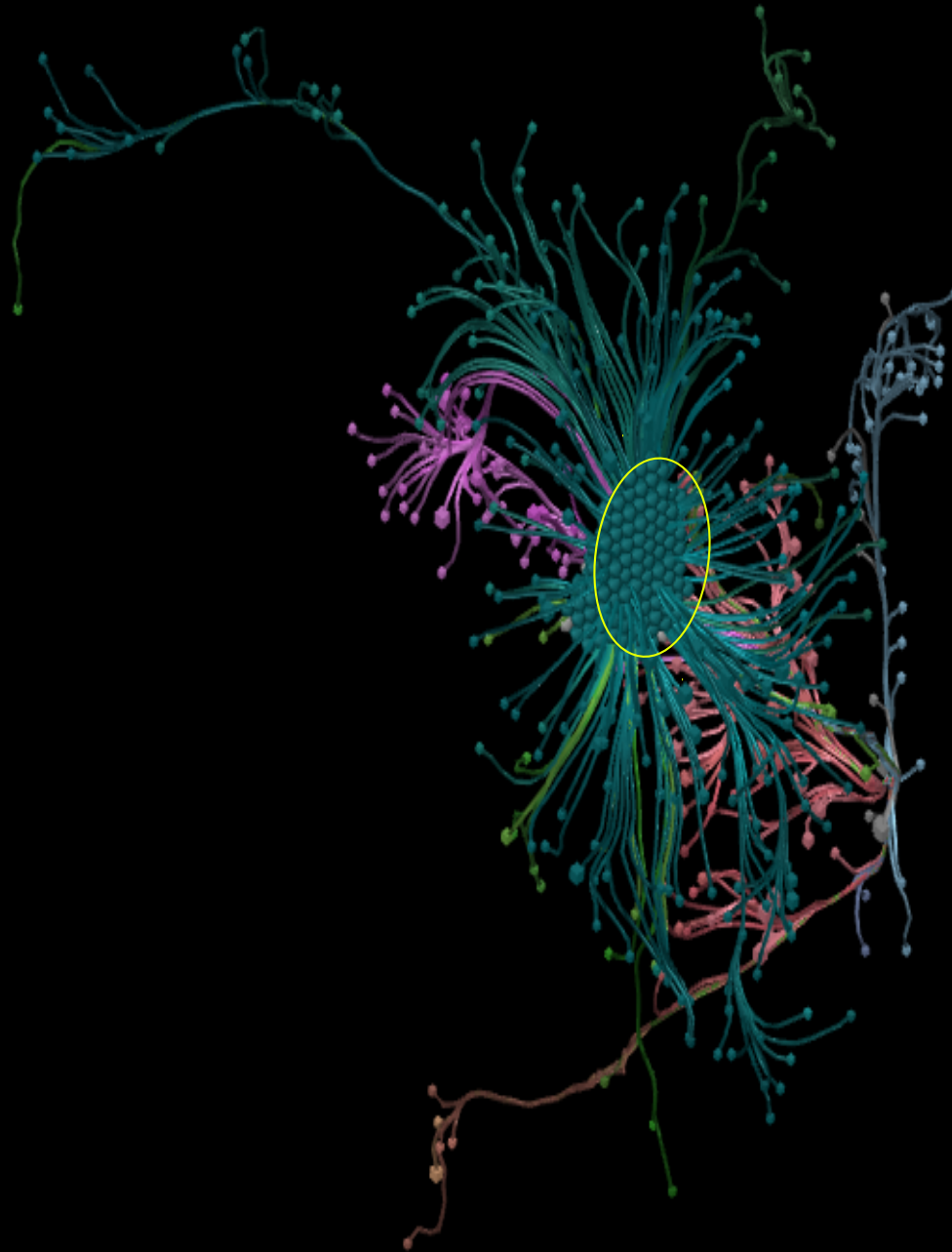
High bias (underfit)



Just right

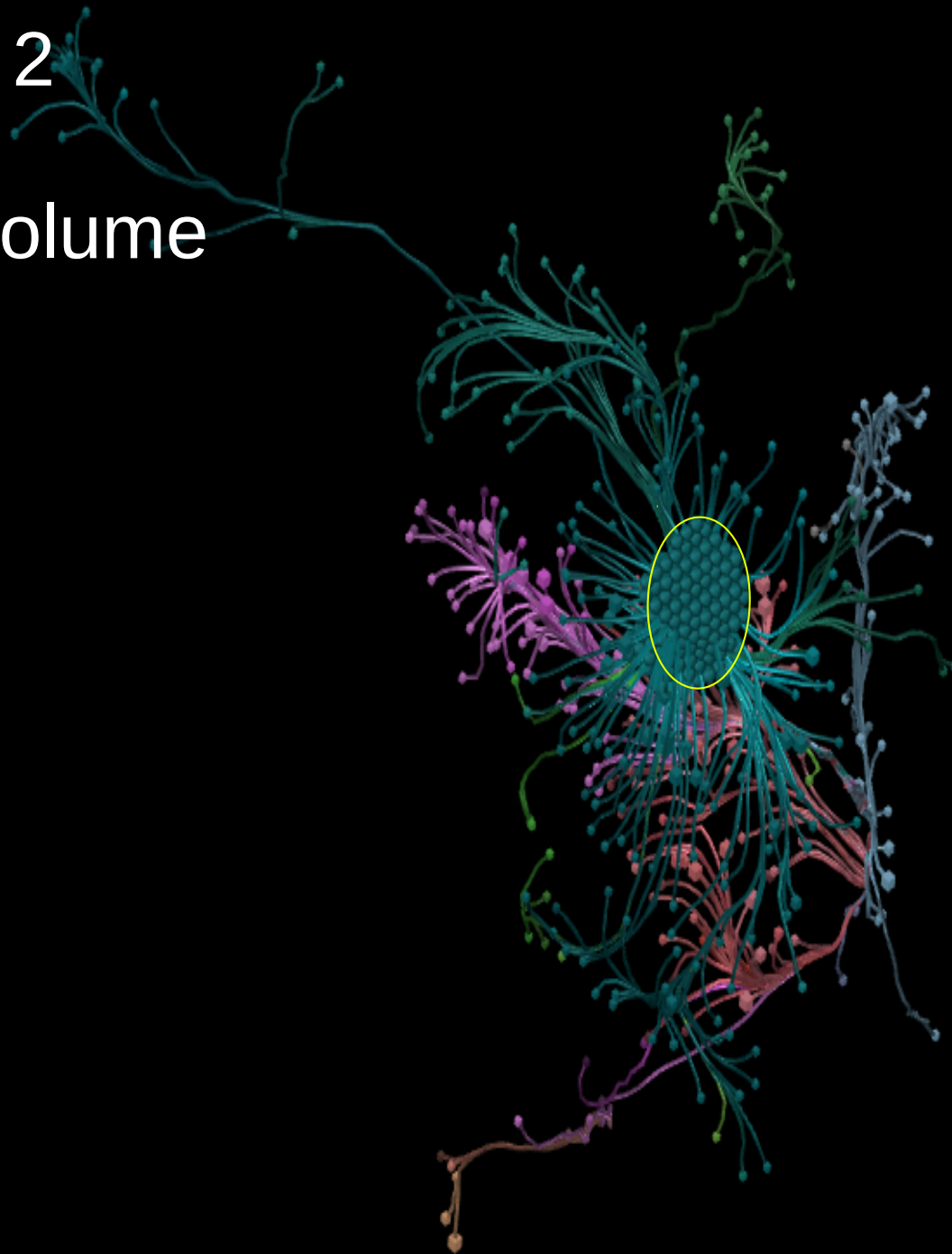
High variance
(overfit)

Injection 1 into VISp



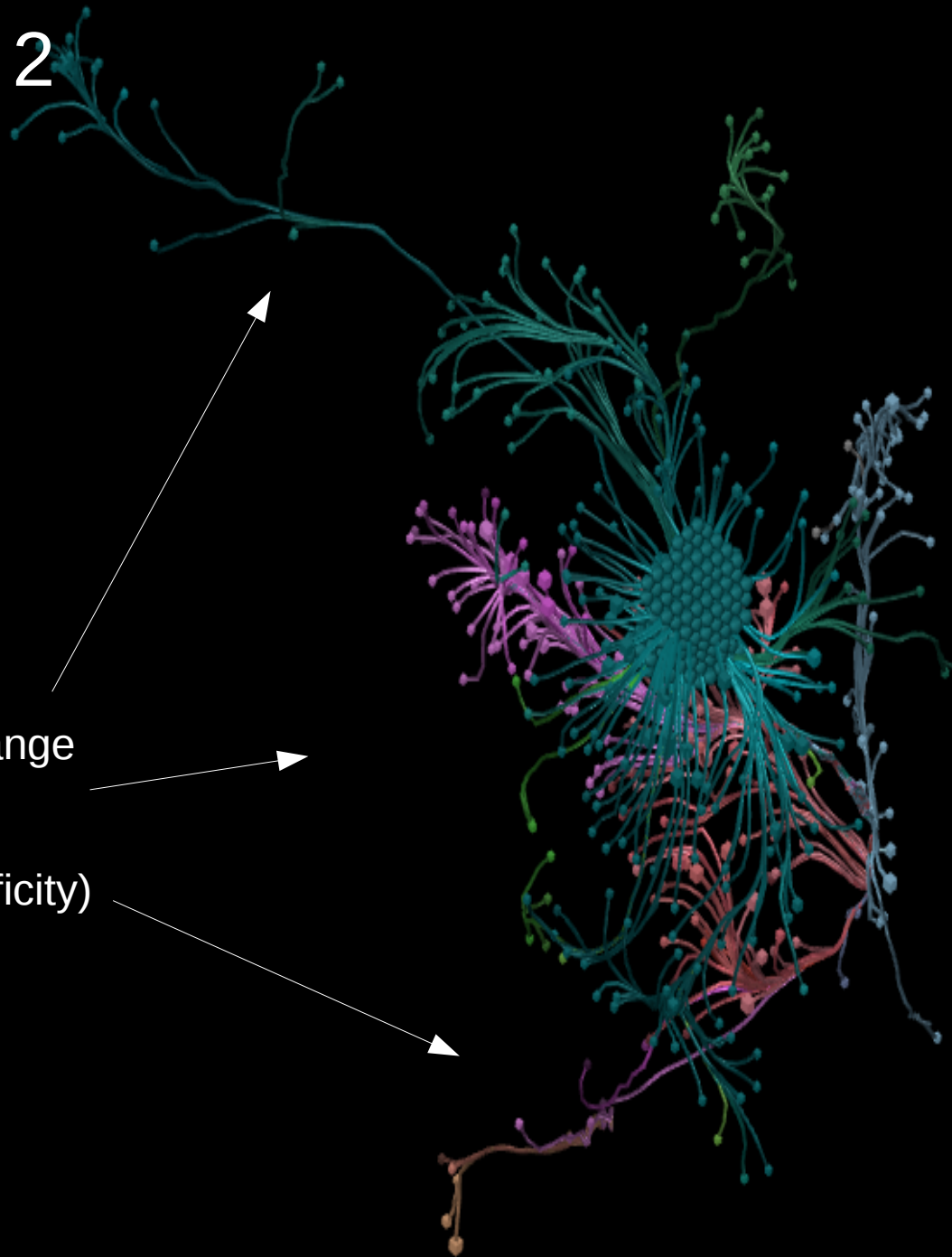
Images made with
AIBS Brain Explorer

Injection 2
Nearby
Similar volume

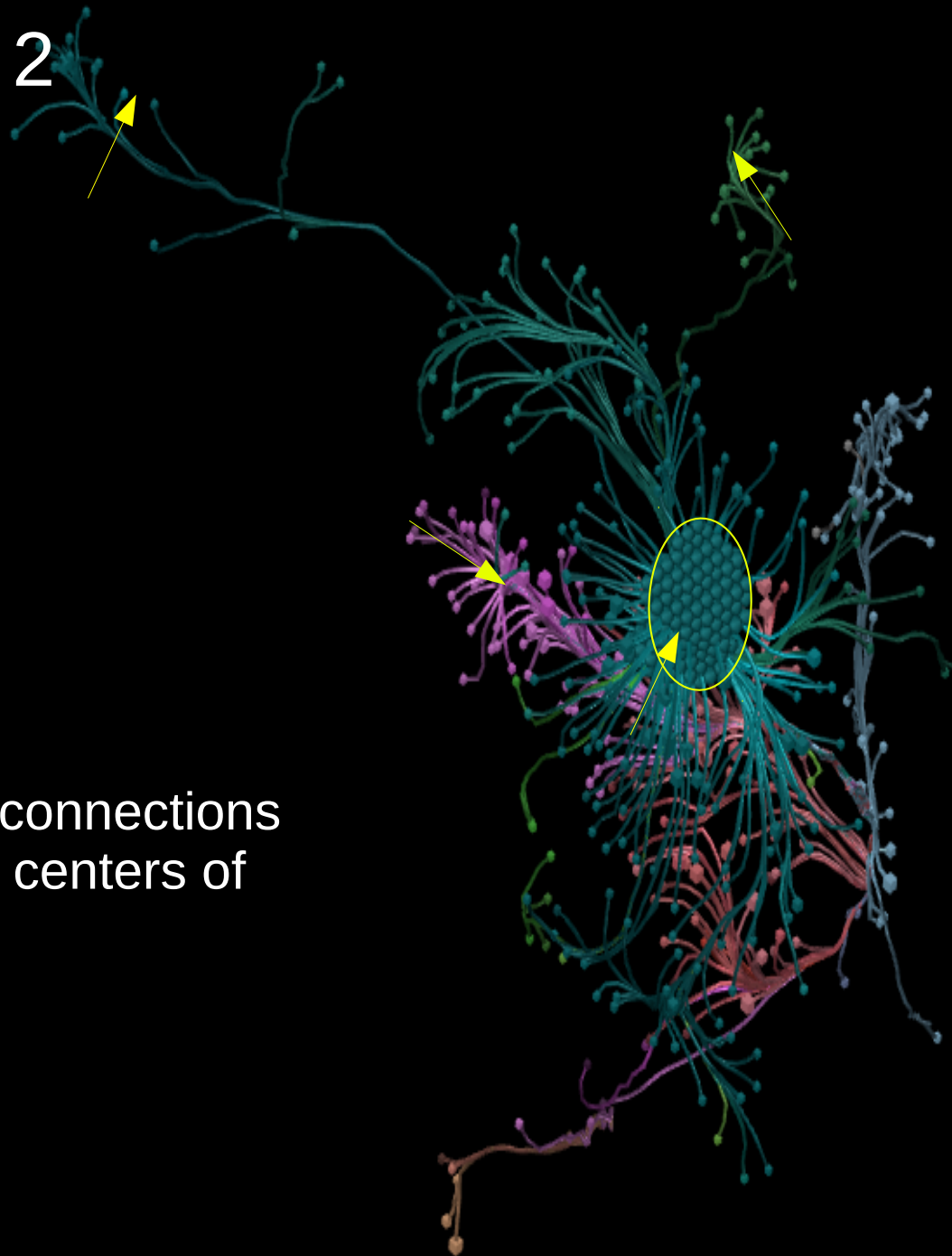


Injection 2

Same long-range
clusters of
projections
(region specificity)

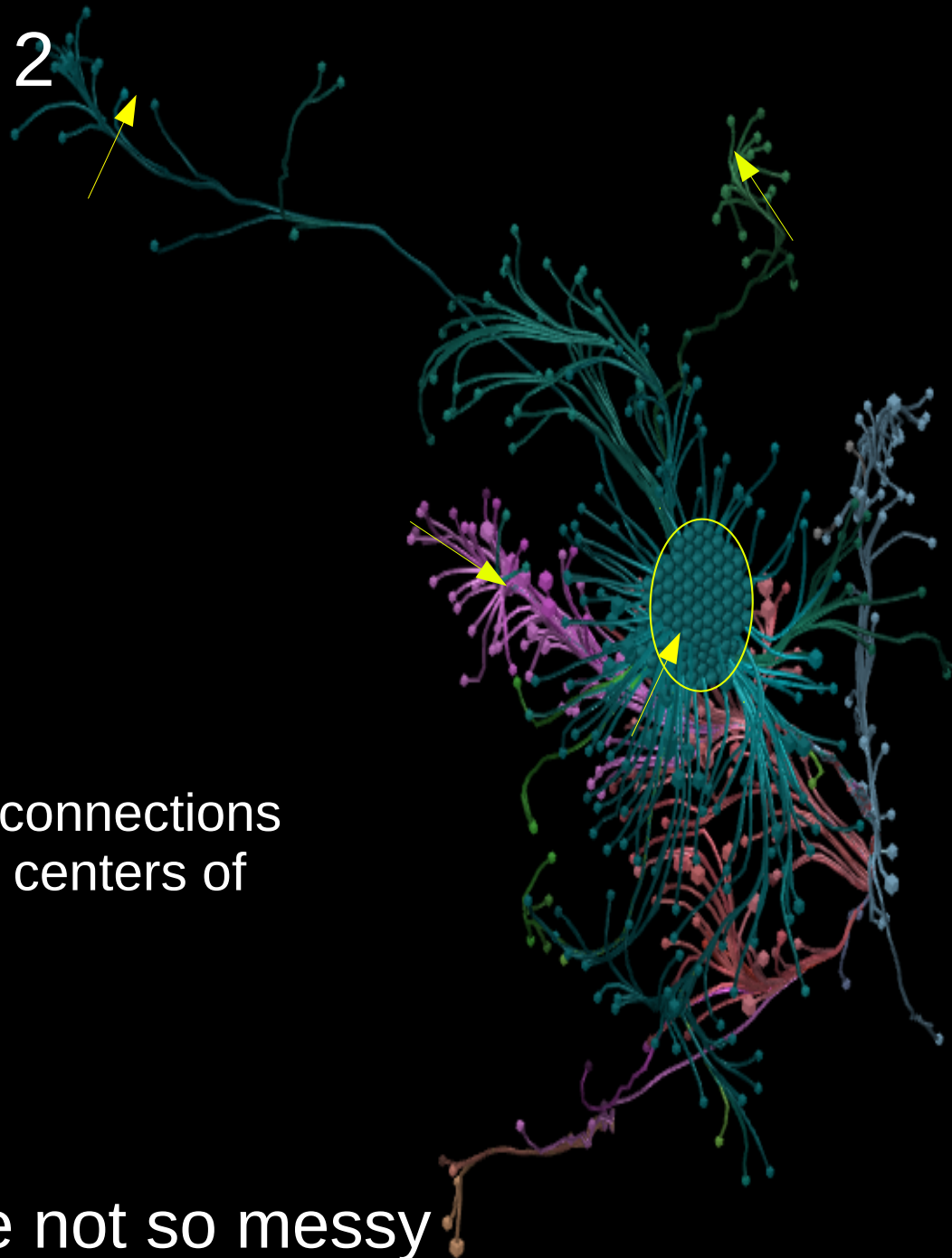


Injection 2



Long-range connections
have shifted centers of
mass

Injection 2



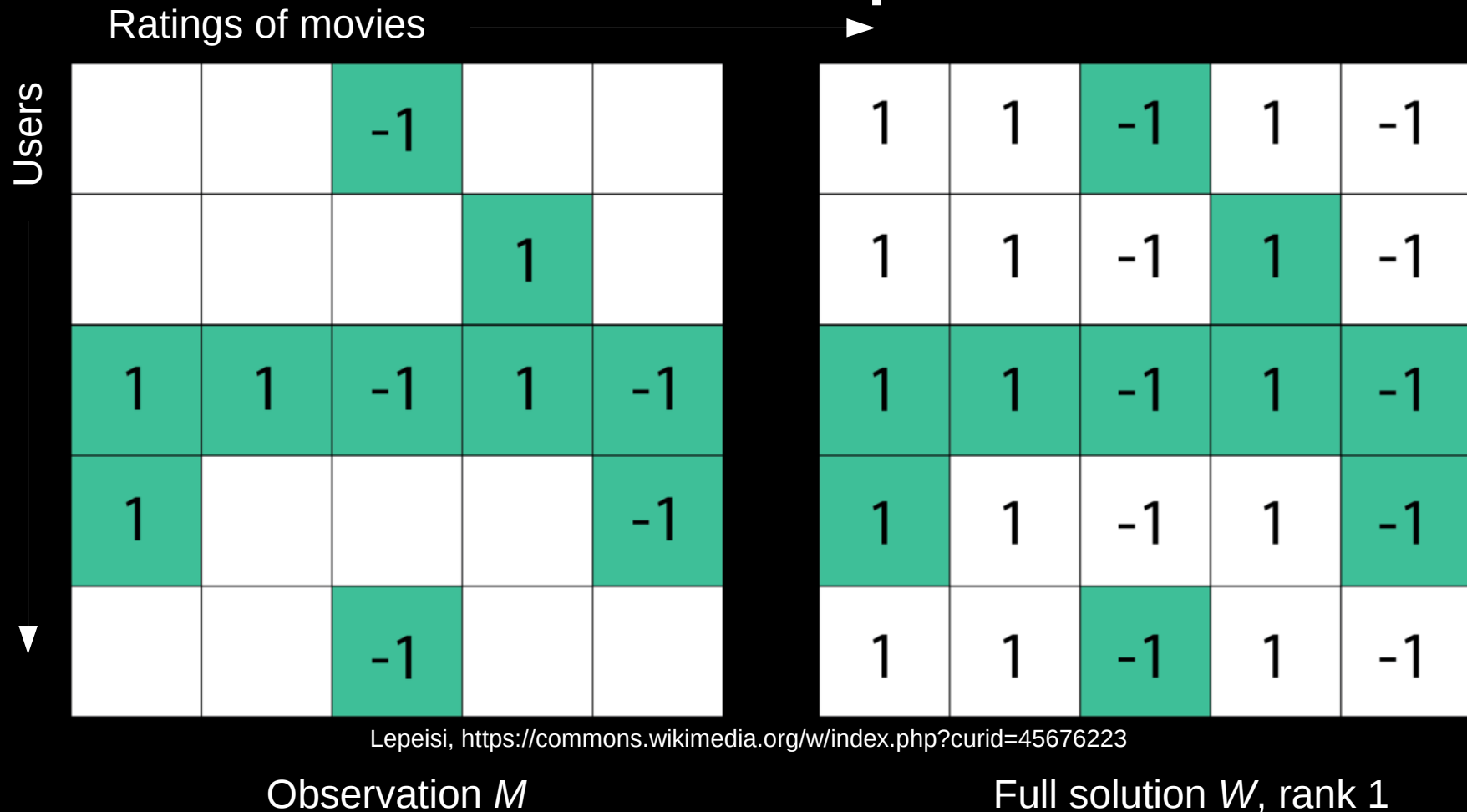
Long-range connections
have shifted centers of
mass

Mesoscale not so messy
Smoothness assumption is reasonable

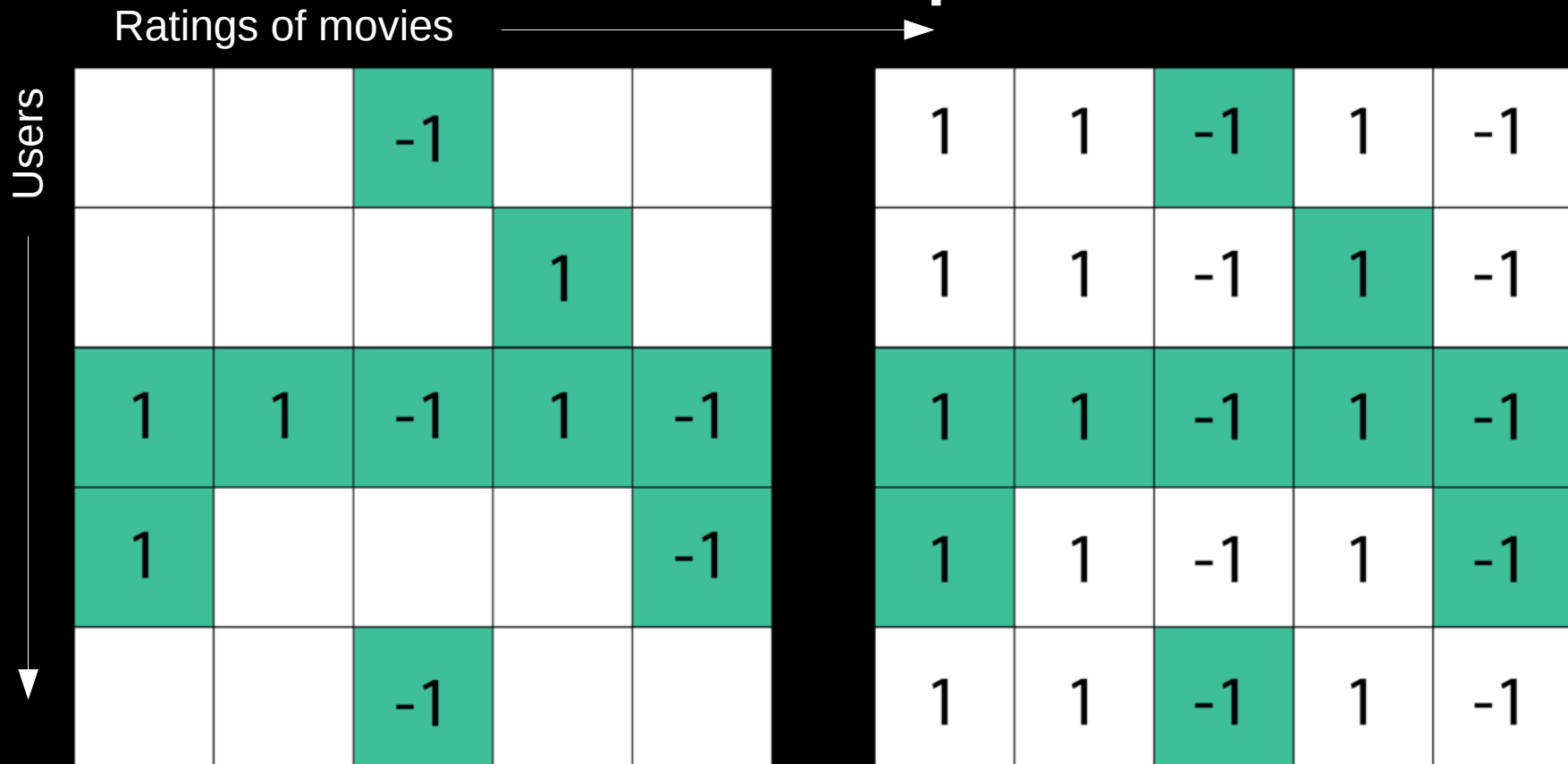
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 - Ignore unknown residuals
- 3) Dimensionality of unknown W

Netflix challenge: matrix completion



Netflix challenge: matrix completion



Lepeisi, <https://commons.wikimedia.org/w/index.php?curid=45676223>

Observation M

Full solution W , rank 1

$$\min_W \|W\|_* \quad \text{where} \quad \boxed{P(W - M) = 0}$$

Complexity of W

Match W to data M where observed

Challenges for inference:

- 1) Injection sites do not cover whole brain; model is underdetermined
 - Fill in gaps with smoothing regularizer
- 2) Projection strength unknown at injection site
 - Ignore unknown residuals
- 3) Dimensionality of unknown W
 - Make $W = UV$ low rank

Both regularization and compression

Spline regression model of connectome

- Find W nonnegative that minimizes the expression

$$\|P(WX - Y)\|_F^2 + \lambda \|L(W)\|_F^2$$

Goodness of fit
(loss)

Roughness penalty
(regularization, prior)

Spline regression model of connectome

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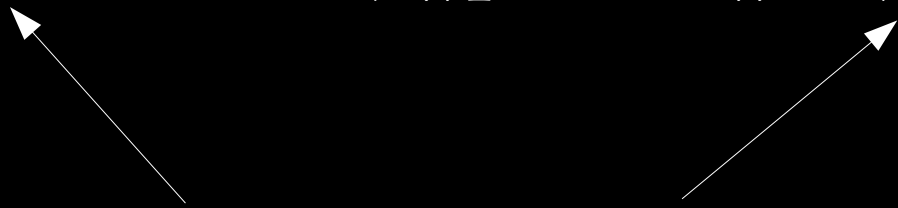
Squared Frobenius norms = sum of squares of matrix entries
= Gaussian noise model

Spline regression model of connectome

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Unknown weight matrix



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Injection data

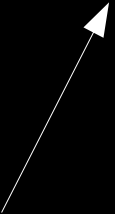


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Projection data



Spline regression model of connectome

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Deals with holes in data, just like **matrix completion**

Ignores residuals in injection sites

Spline regression model of connectome

- Find W nonnegative that minimizes the expression

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Controls strength of smoothing

Spline regression model of connectome

- Find W nonnegative that minimizes the expression

$$\|P(WX - Y)\|_F^2 + \lambda \|L(W)\|_F^2$$


Laplacian “roughness” of W

Can respect region boundaries

6-dimensional!

Spline regression model of connectome

- Find W nonnegative that minimizes the expression

$$\|P(WX - Y)\|_F^2 + \lambda \|L(W)\|_F^2$$

Problem is convex:

unique global solution and **standard methods to find it**

We found W for mouse visual cortex

- 7497 x 7497 matrix fit with 28 injections
- **Marked improvement** over regional model:

– Regional model:	48% regional	107% voxel
– Voxel model:	16% regional	33% voxel

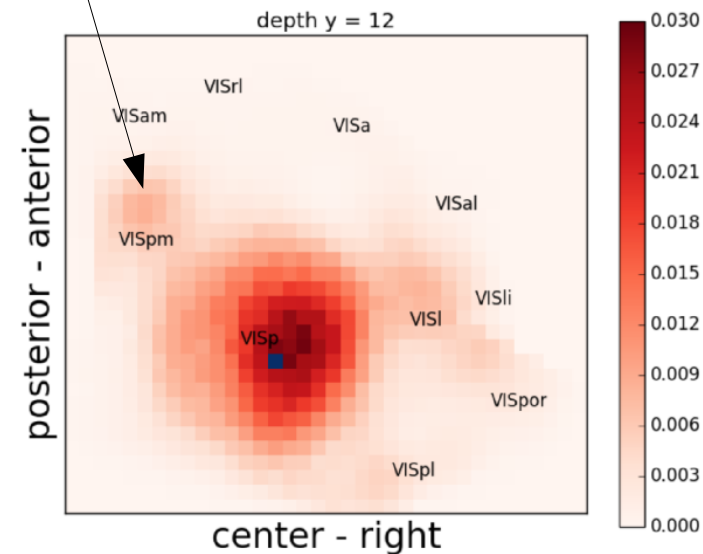
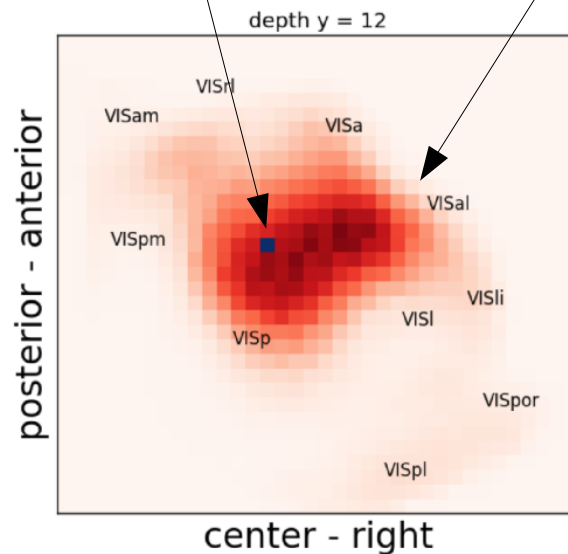
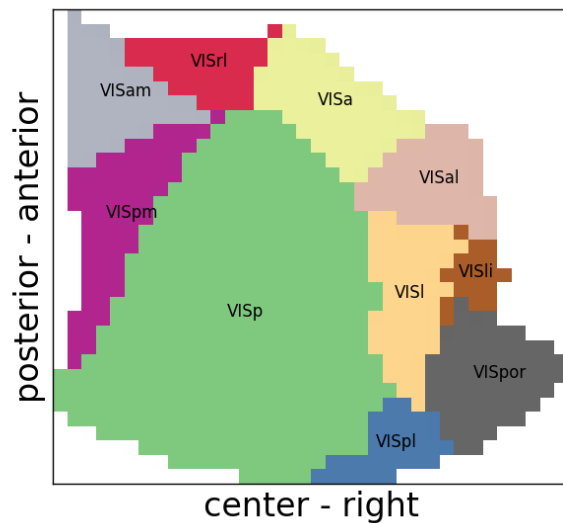
$$\frac{\|Y_{\text{pred}}\|^2}{\frac{1}{2}\|Y_{\text{pred}}\|^2 + \frac{1}{2}\|Y_{\text{true}}\|^2}$$

Applied to visual cortex we see hints of retinotopy

Maps of retinal (visual) space between areas

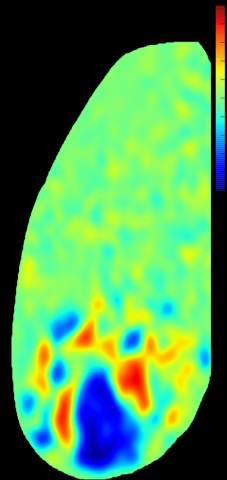
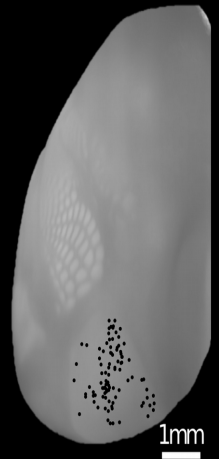
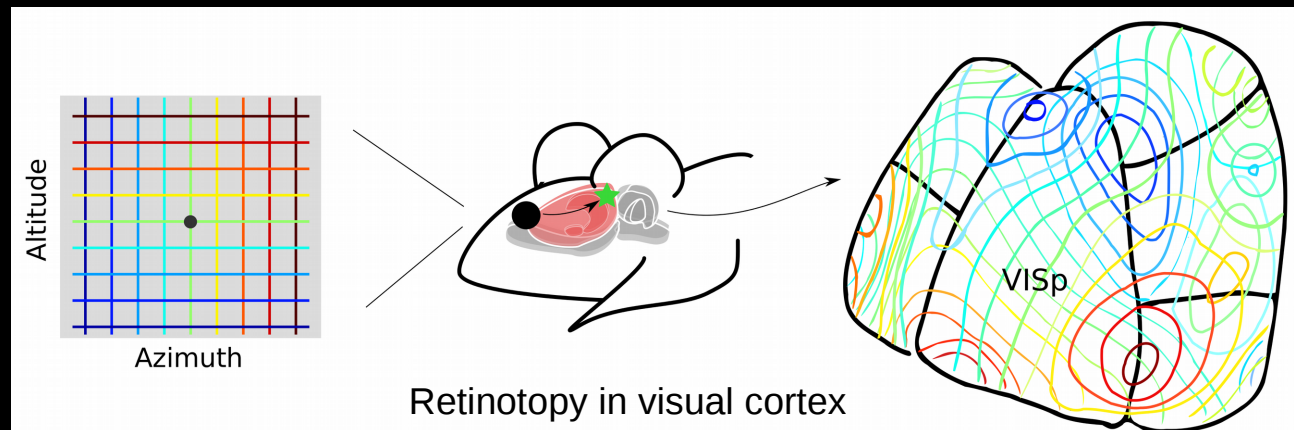
Source voxel

“Blobby” projections move with source



Spatial connectivity opens exciting scientific directions

- Comparable to neuron activity data
 - e.g., [Kim et al. Cell Reports \(2016\)](#), “Crystal Skull”
- Topography between regions (retinotopy, tonotopy, etc.)
- Cell-type specific data: E/I, layers, etc.
- Connectivity-defined regions?



Zhuang, et al.
eLife (2017)

Conclusions: mesoscopic inference

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- New spatial inference method tailored to data

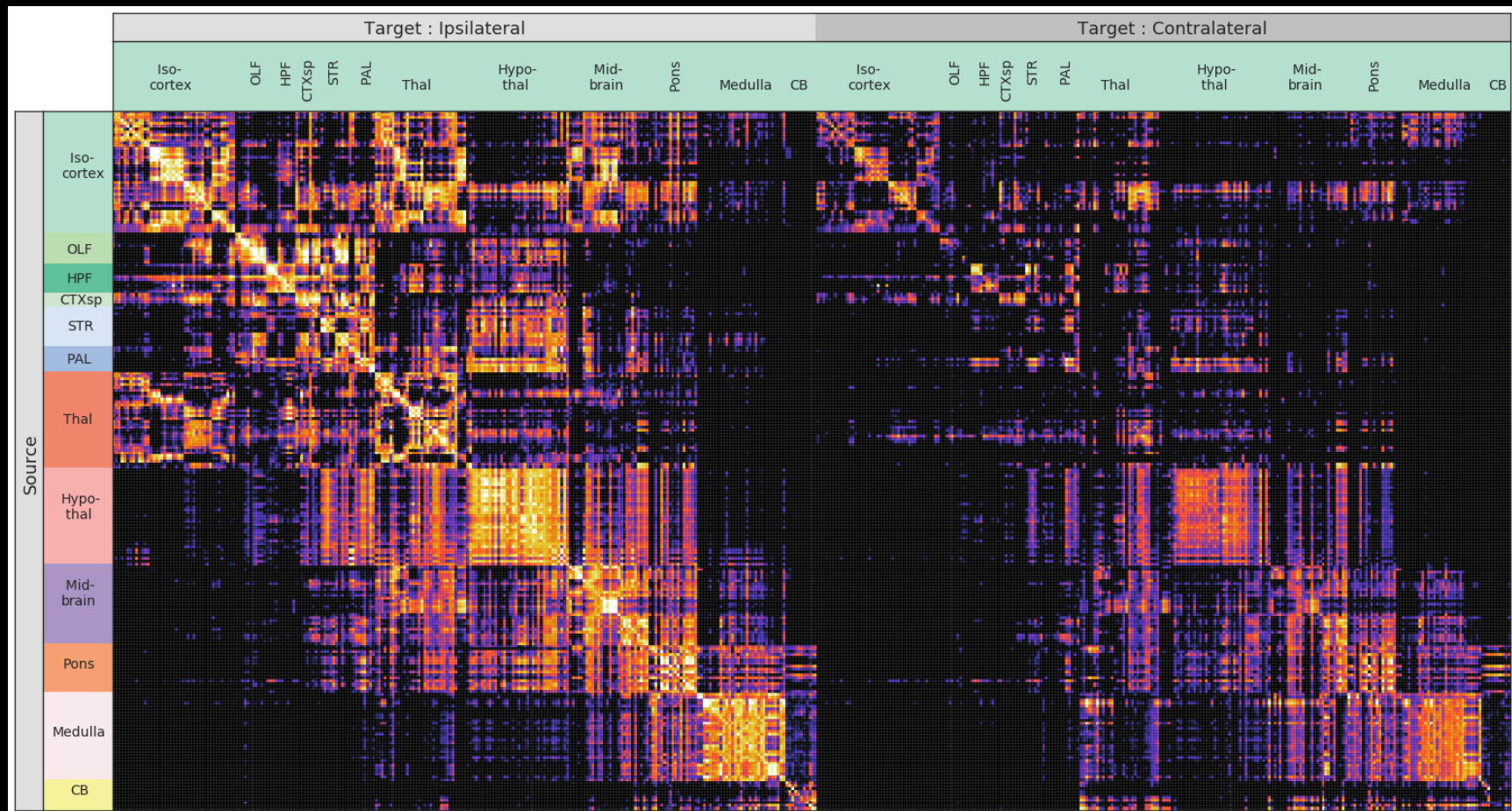
Conclusions: mesoscopic inference

- New spatial inference method tailored to data
 - More predictive than before

Conclusions: mesoscopic inference

- New spatial inference method tailored to data
 - More predictive than before
 - Improves regional models, too!

Joe Knox (AIBS)

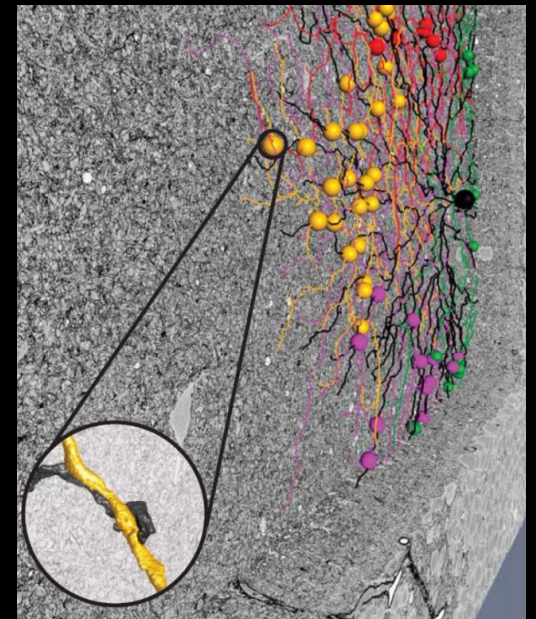


Connectivity questions

- 1) How do we infer mesoscopic connections?
- 2) **What are good microscopic models?**
- 3) How does connectivity affect brain dynamics?

Zooming in with random graphs

In preparation:
Brito, Dumitiru, Harris.
“Spectral gap in random bipartite biregular
graphs and its applications.”

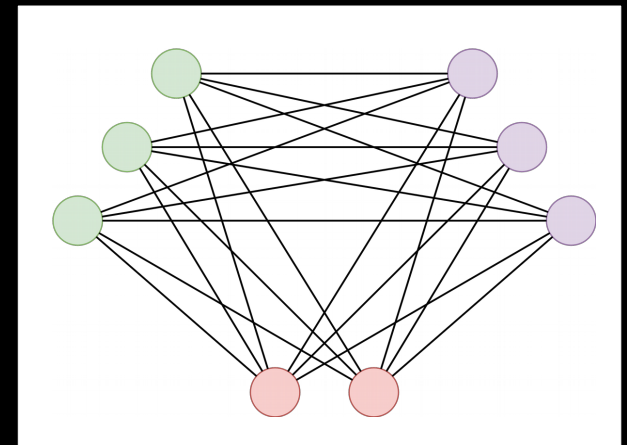
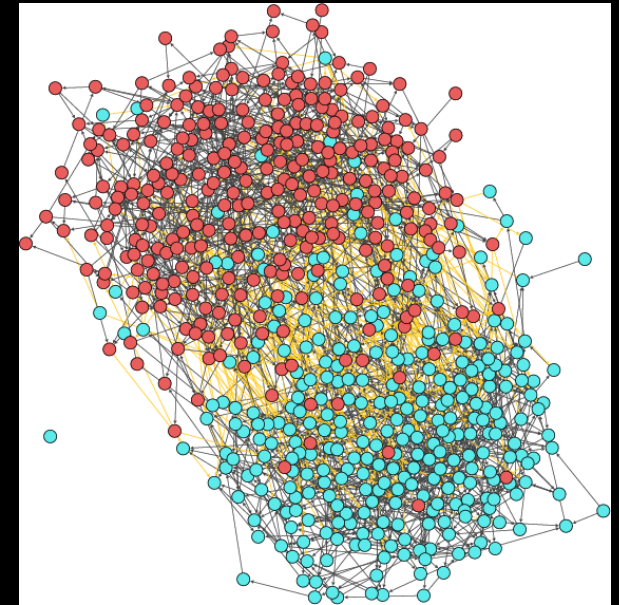


Kleinfeld et al. (2011)

Random graphs can match measurable microscopic features

Joshua Mendoza

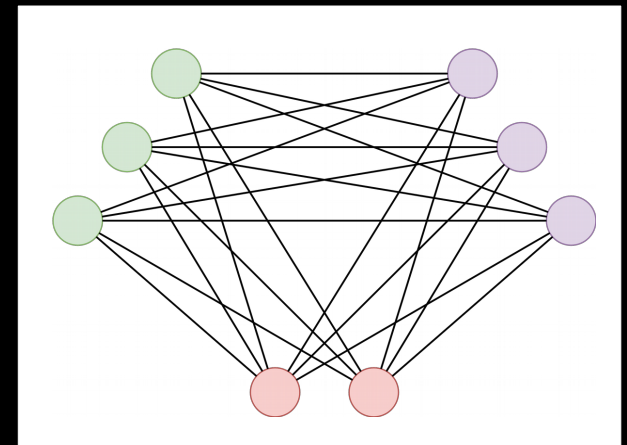
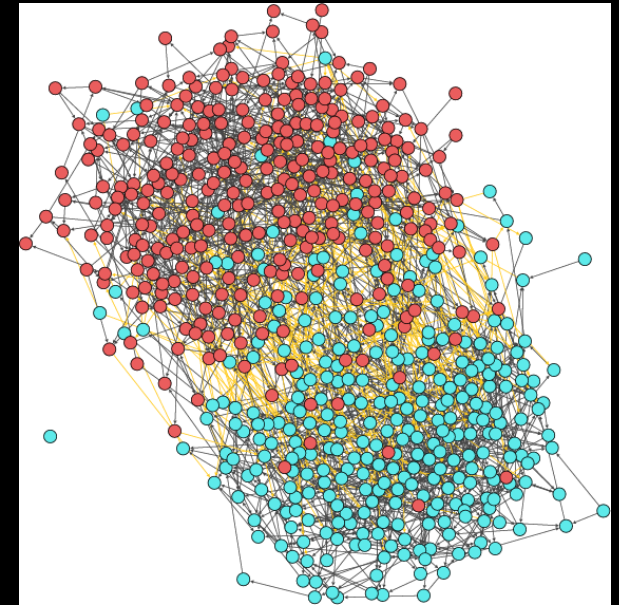
- Example statistics:
 - Average # connections (degree)
 - Number of cycles
 - Other subgraph counts



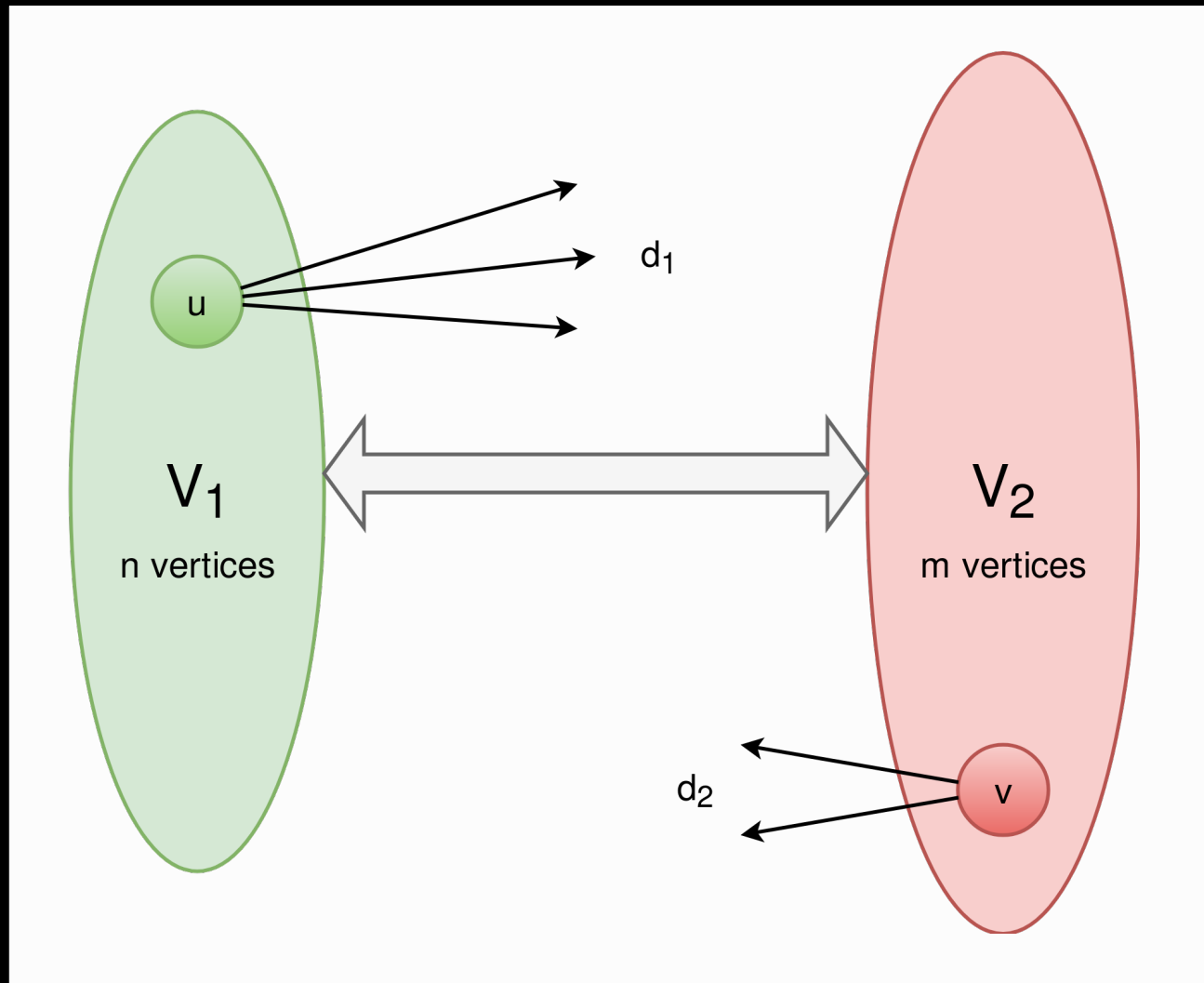
Random graphs can match measurable microscopic features

Joshua Mendoza

- Example statistics:
 - Average # connections (degree)
 - Number of cycles
 - Other subgraph counts
- Community structure
 - Block models
 - Multi-partite graphs



Bipartite, biregular random graphs



Fixed d 's mean these graphs are **very sparse**

We found a spectral “gap!”

- $\lambda_1 \gg \lambda_2 \rightarrow$ **expander**

Extends past work for d-regular graphs:

Friedman (2003, 2004)

Alon (1986)

Bordenave (2015)

Angel, Friedman, Hoory (2015)

Marcus, Spielman, Srivastava (2013)

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 - Random walks
 - Community detection & spectral clustering
 - Error correcting codes
 - Matrix completion

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Hold that thought!

Friedman (2003, 2004)

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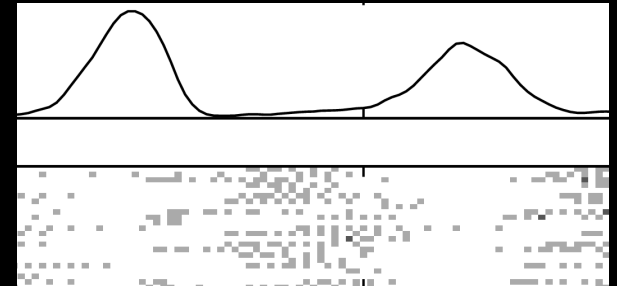
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Effects of sparsity on rhythm generation



Published as:

Harris, Dashevskiy, Mendoza, Garcia III, Ramirez, Shea-Brown.

“Different roles for inhibition in the rhythm-generating respiratory network.”

J Neurophys 118(4), 2070-2088. 2017.

Litwin-Kumar, Harris, Sompolinsky, Abbott.

“Optimal synaptic connectivity.”

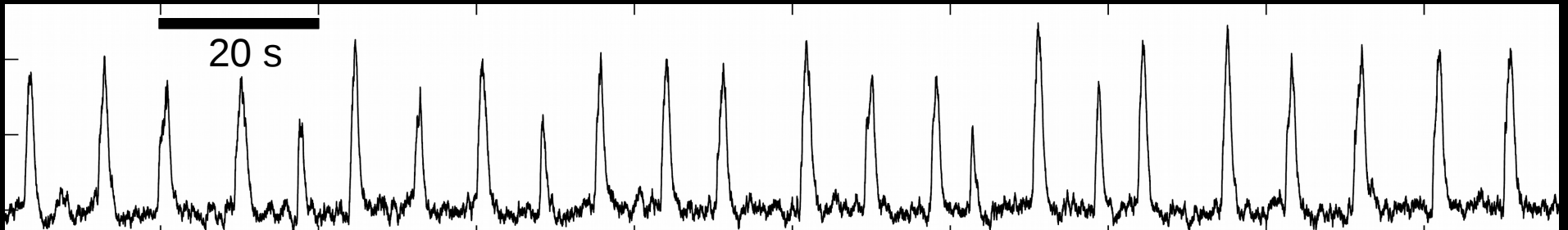
Neuron 93, 1153-1164. 2017.



Sparsity is good for
“classifier” circuits

Breathing arises in the brainstem

- The “pre-Bötzinger Complex”

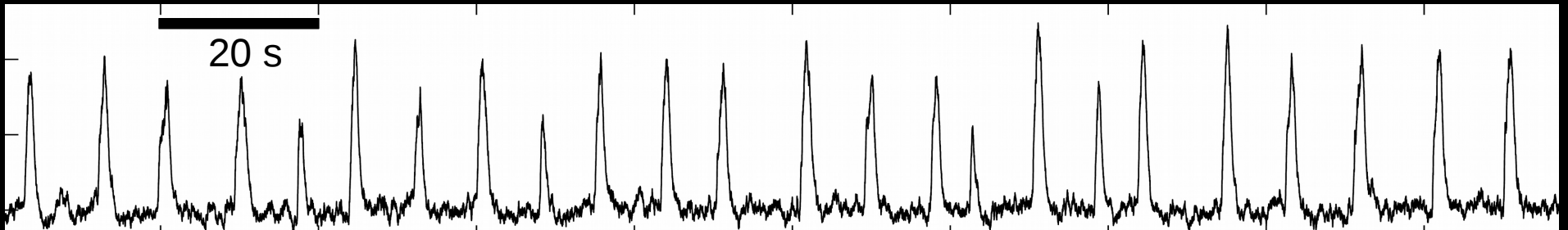


Important related papers:

Smith et al. 1991
Ramirez & Richter 1996
Rekling & Feldman 1998
Feldman et al. 2013

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 - Bursting, tonic spiking, and quiescent E / I cells

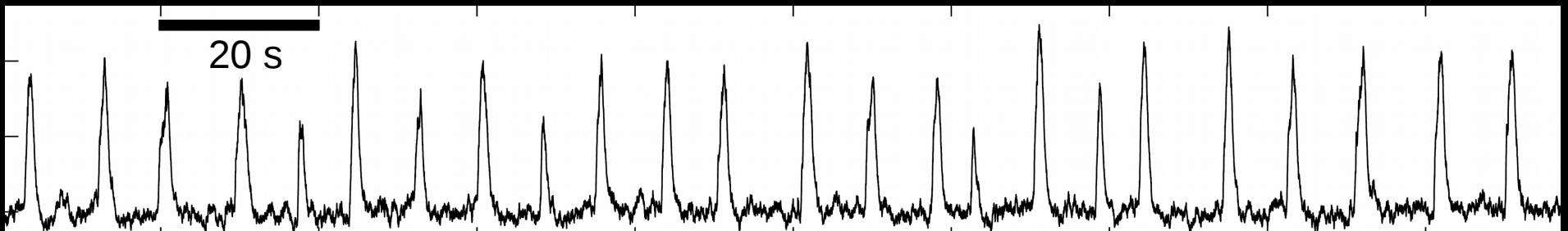


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 - Synchronized population bursts via excitation



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Why do you get expiratory cells?

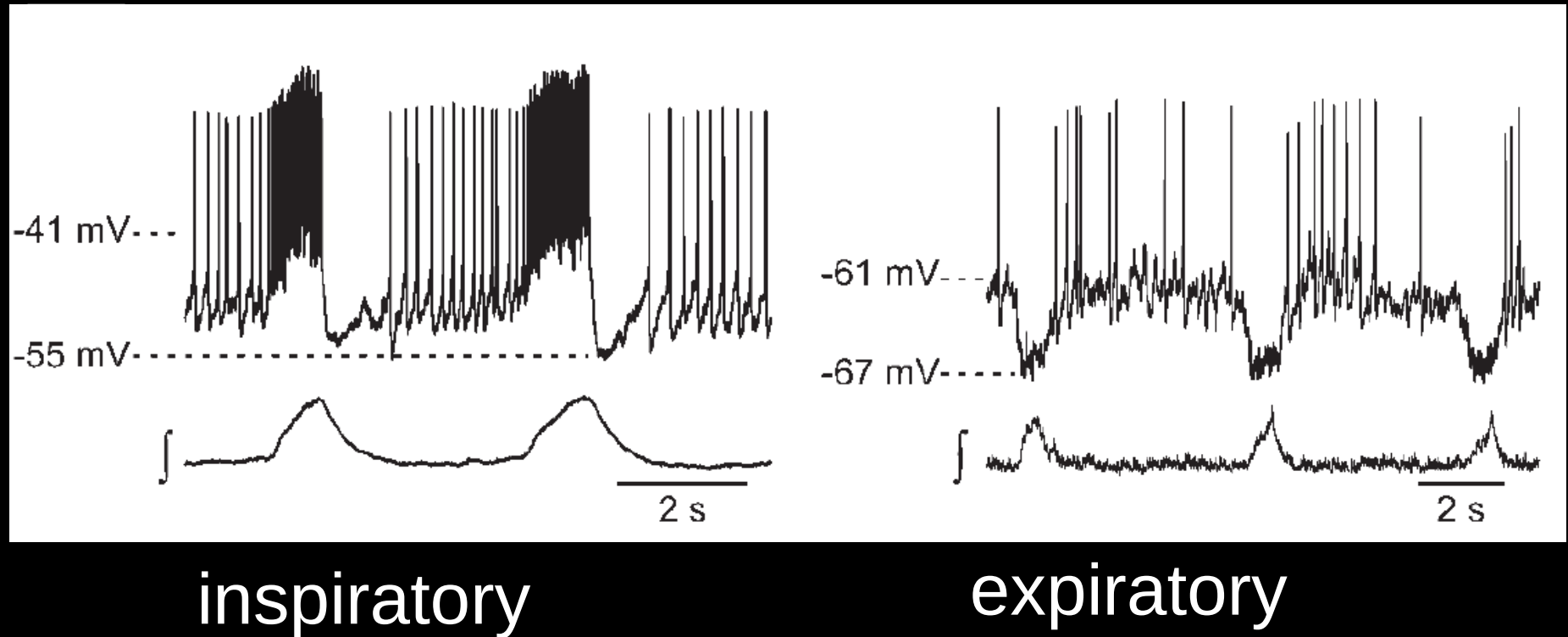
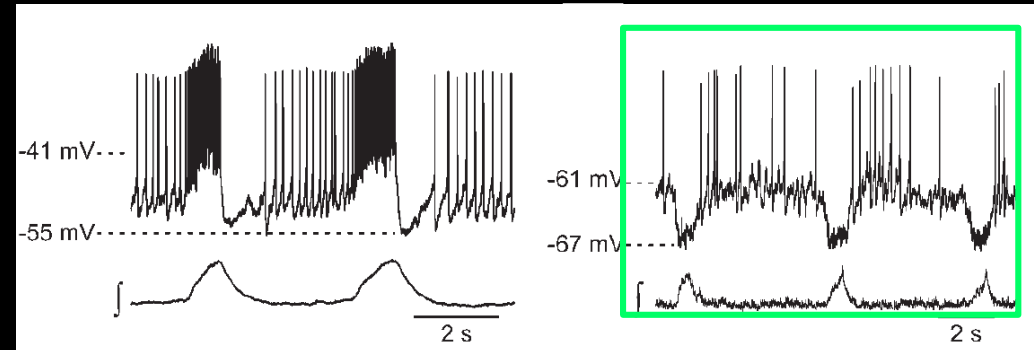


Figure from:
Lieske, Thoby-Brisson, Telgkamp, Ramirez (2000)

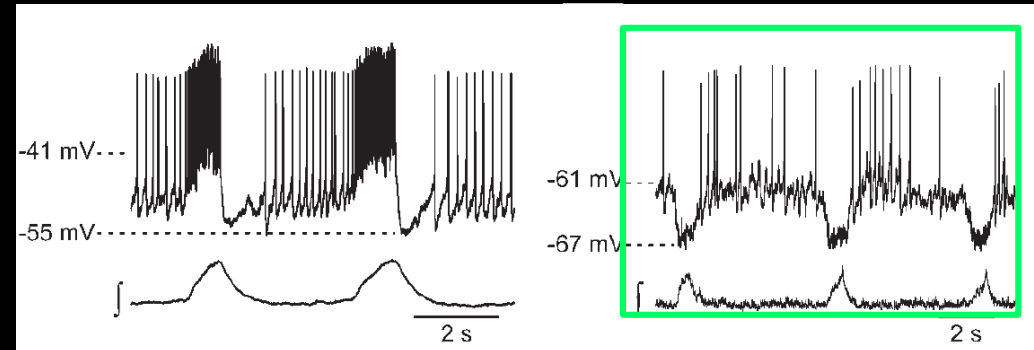
Why do you get expiratory cells?



inspiratory cell

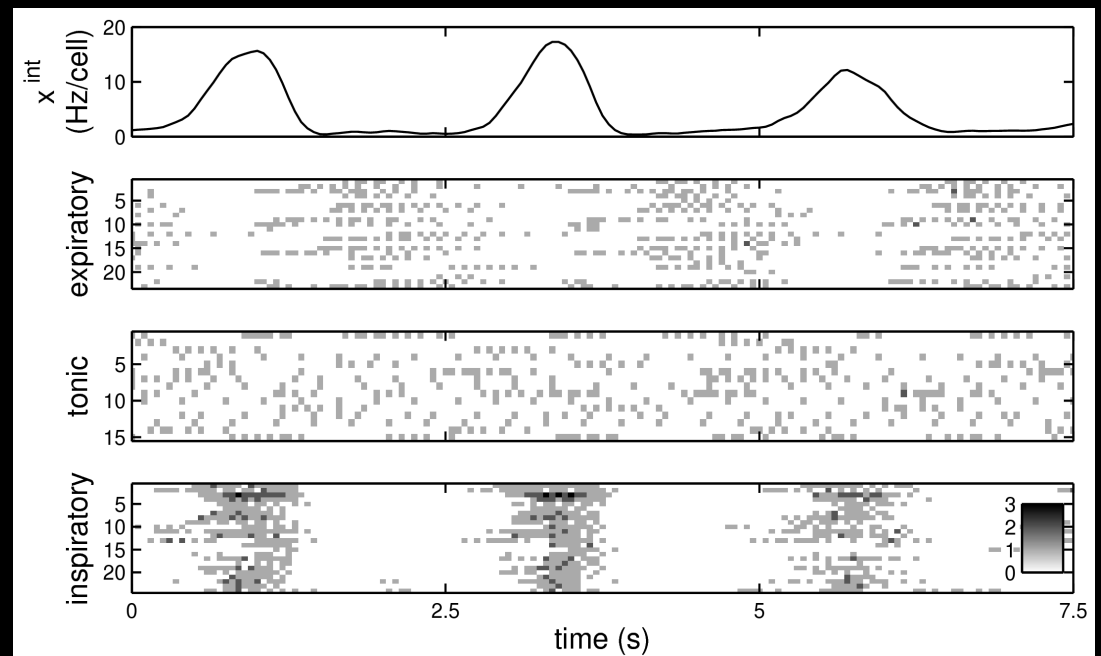
expiratory

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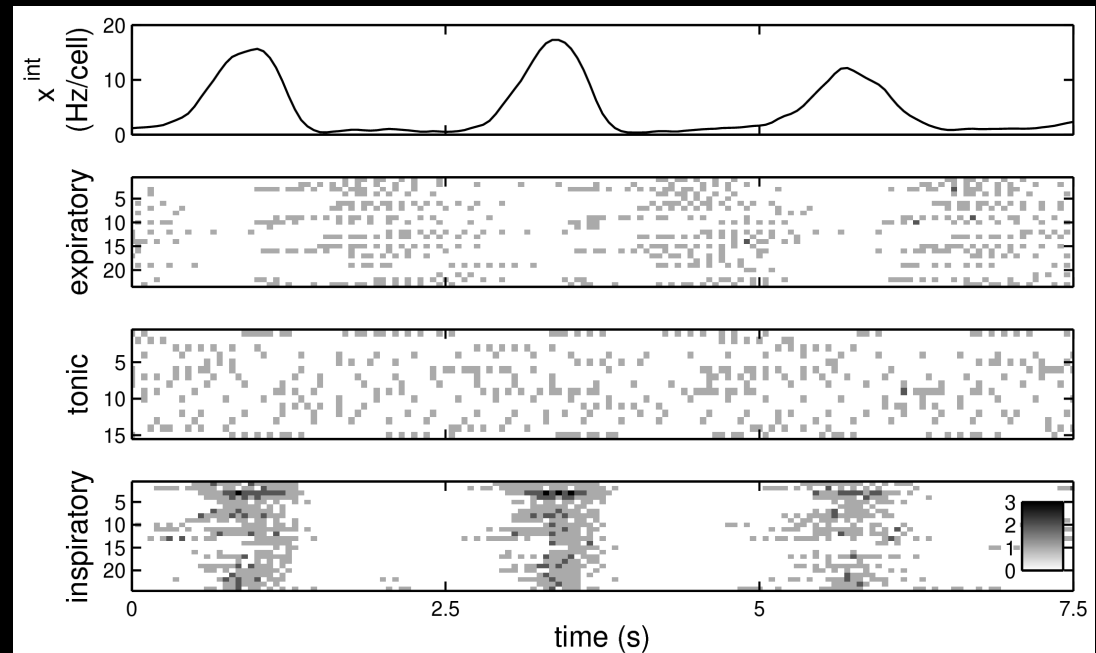
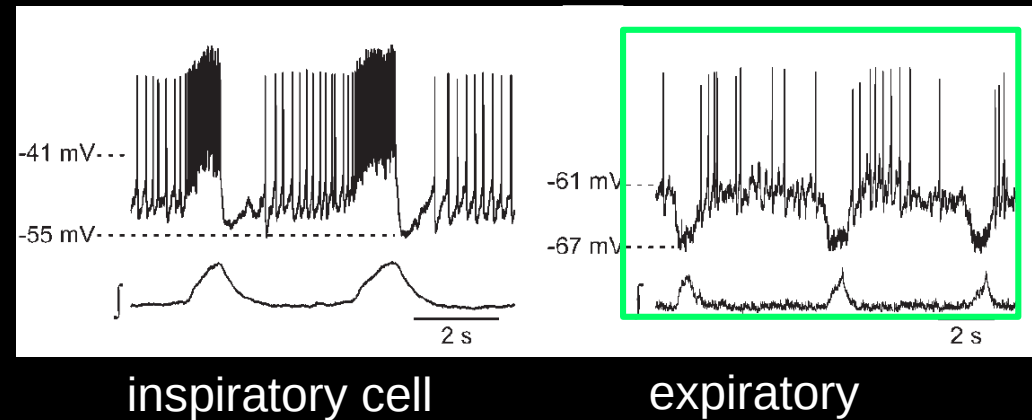
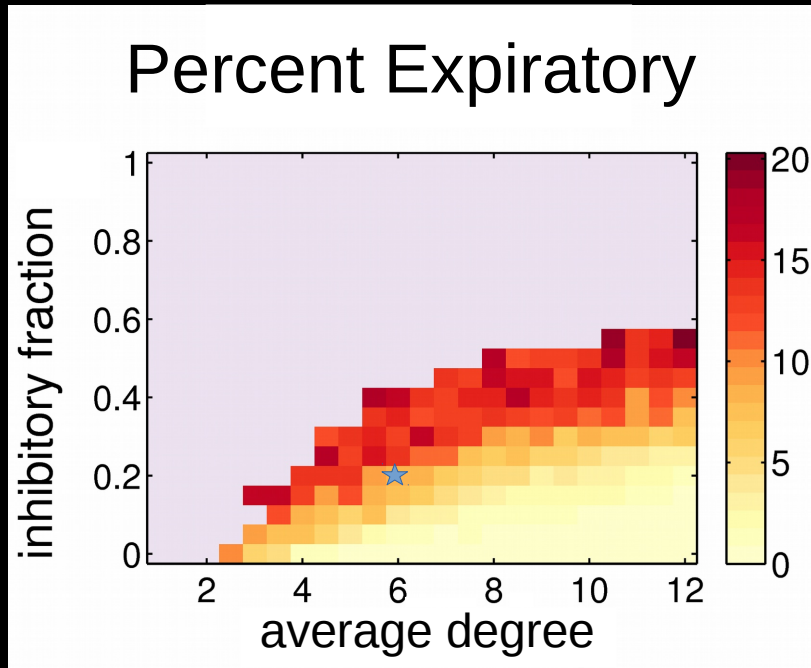


inspiratory cell

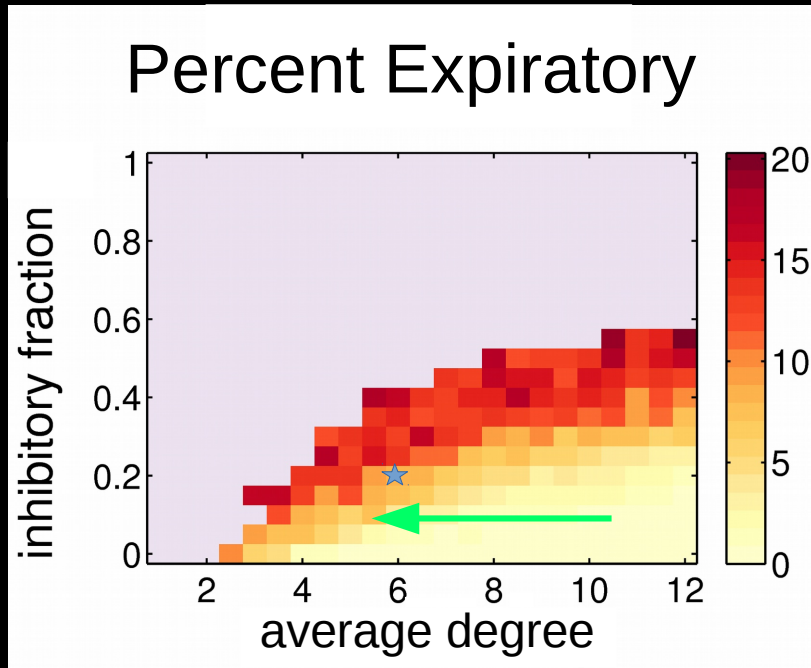
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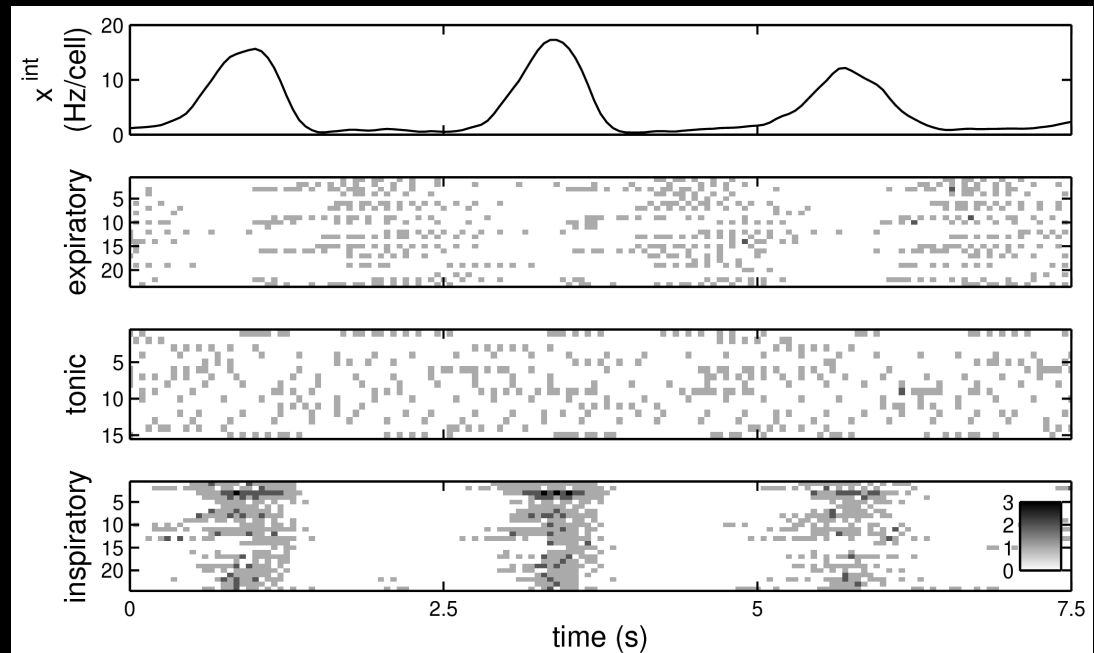
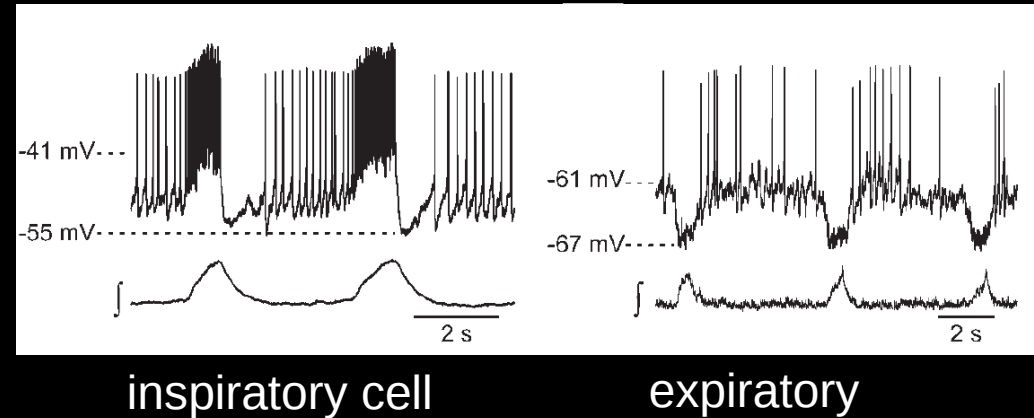
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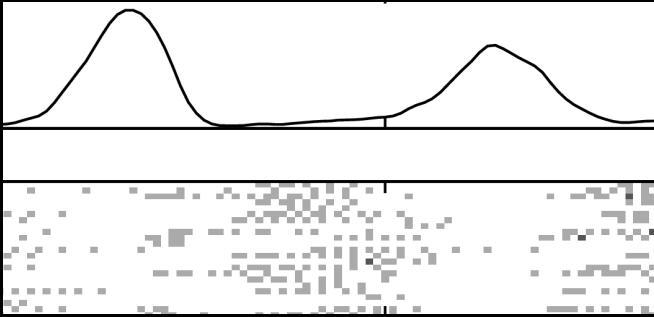


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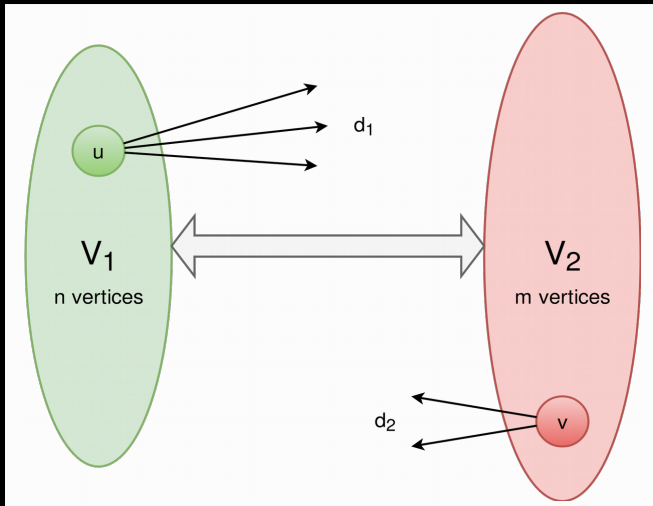
Sparse graph:
some cells randomly
driven into expiratory phase





- Neuronal network dynamics

- Choose graph class with measurable parameters

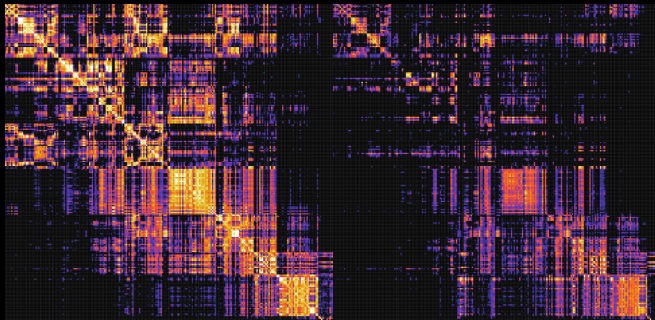


- Random graph theory

- Rich mathematical area
- Spectra, expansion, & dynamics

- Mesoscopic network inference

- Methods tailored to new datasets



More acknowledgements







Jason Griffith



Drew Tabke

Thank you
for listening!

