

# First connectomics challenge in neuronal cultures

## Crowdsourcing network reconstruction

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Connectome Workbench 2015

## Neuronal cultures

Model system to study the interplay between activity and connectivity in neuronal systems

Mostly random network structure - dynamics leads to complex effective networks

You can easily manipulate the topology, for example by modifying the growth substrate (spatial embedding)

Develop and test network inference methods (causality) in neuroscience

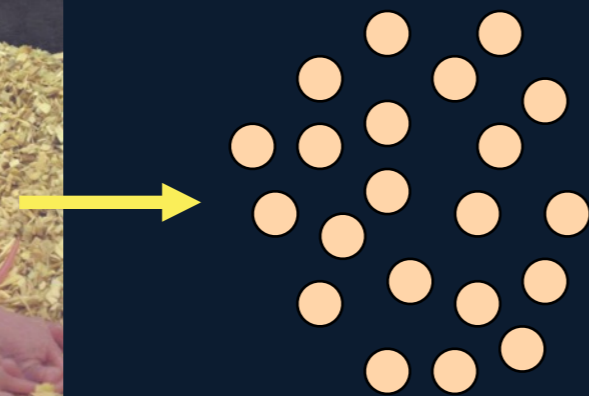
**First connectomics challenge in neuronal cultures**



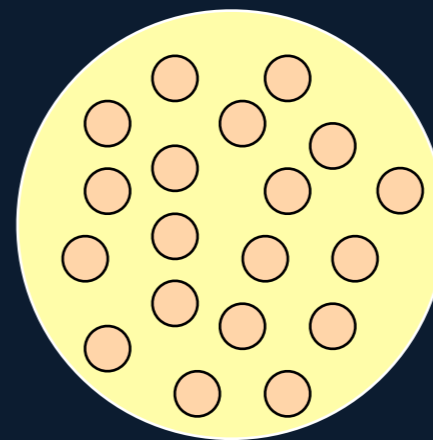
# Neuronal cultures



cortex / hippocampus  
17-19 days embryo or  
0-1 days postnatal

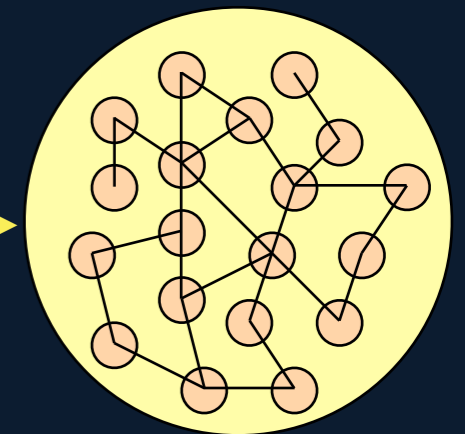


neuron dissociation



plating  
(day 0)

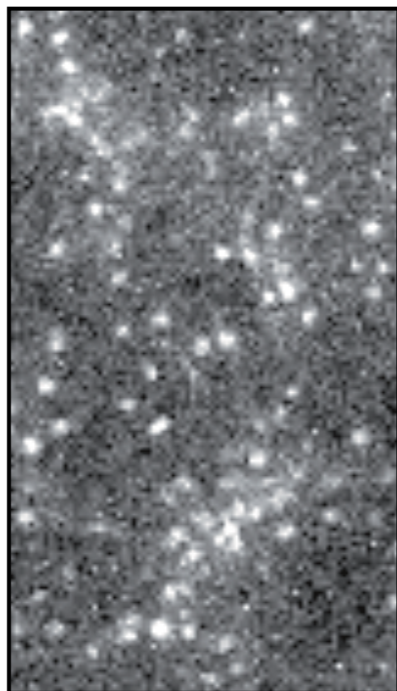
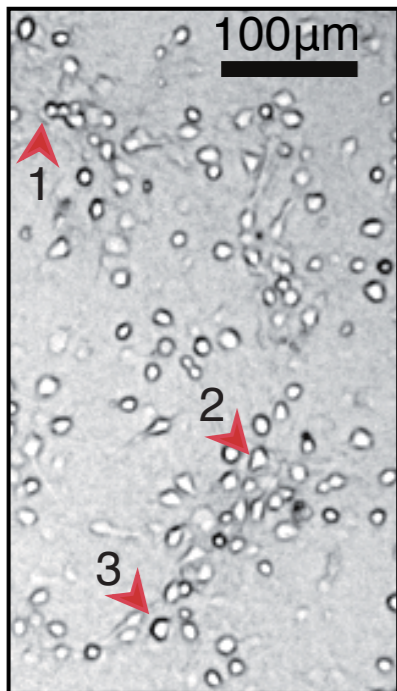
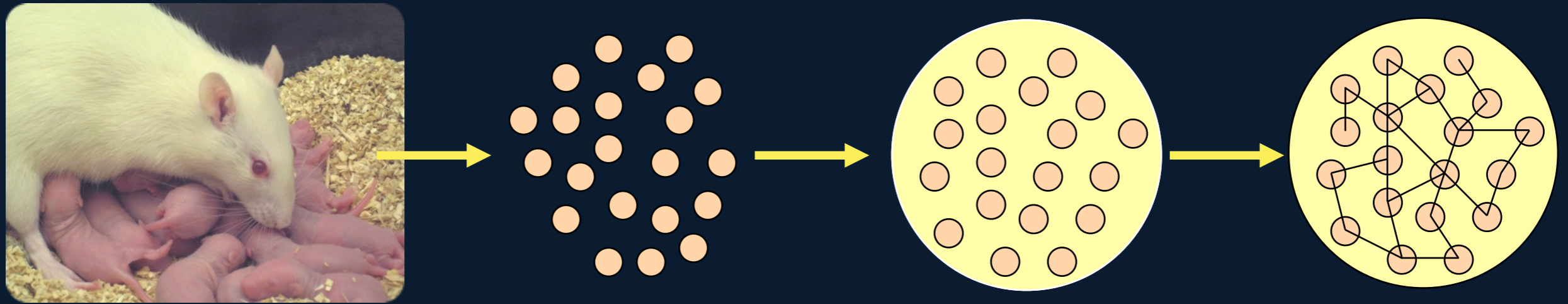
individual  
firings



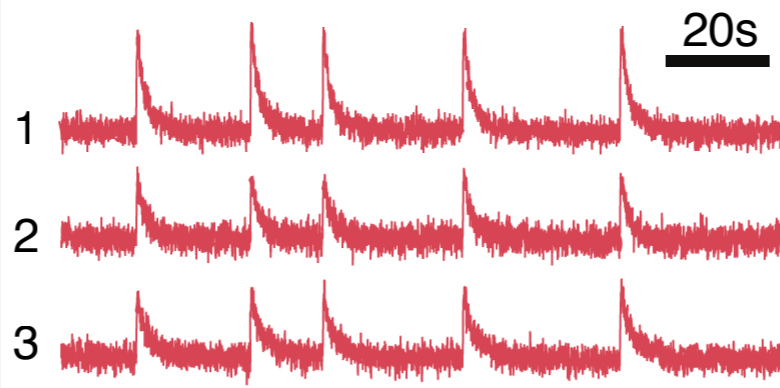
mature culture  
(day 14)

collective  
firings

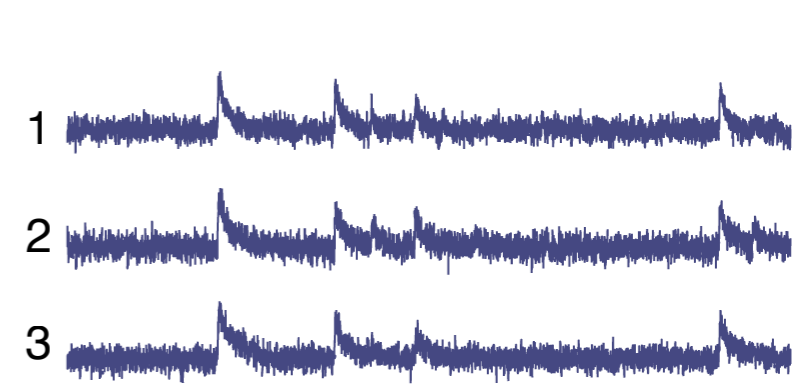
# Neuronal cultures



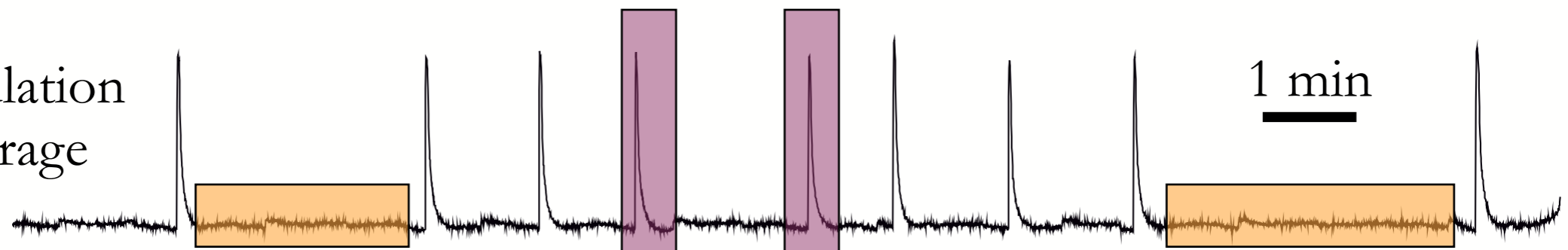
excitation only

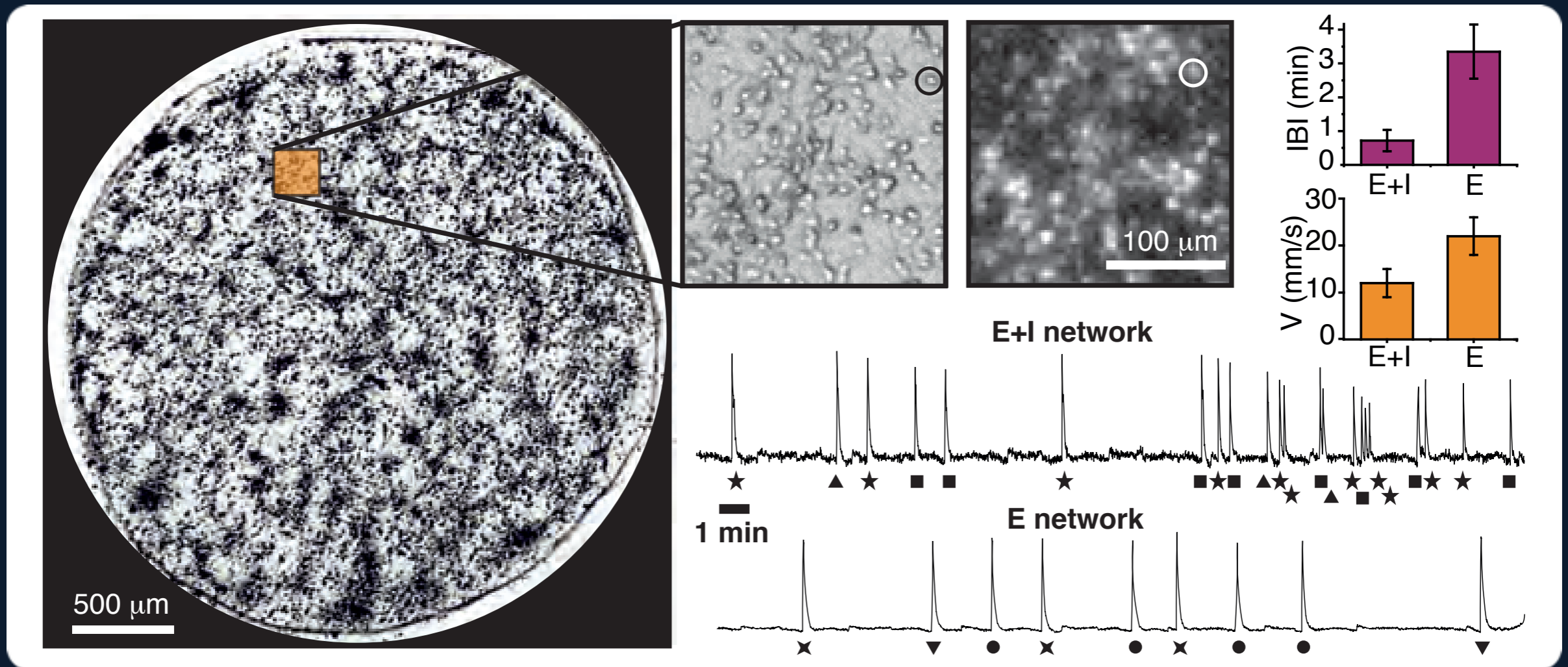


excitation and inhibition



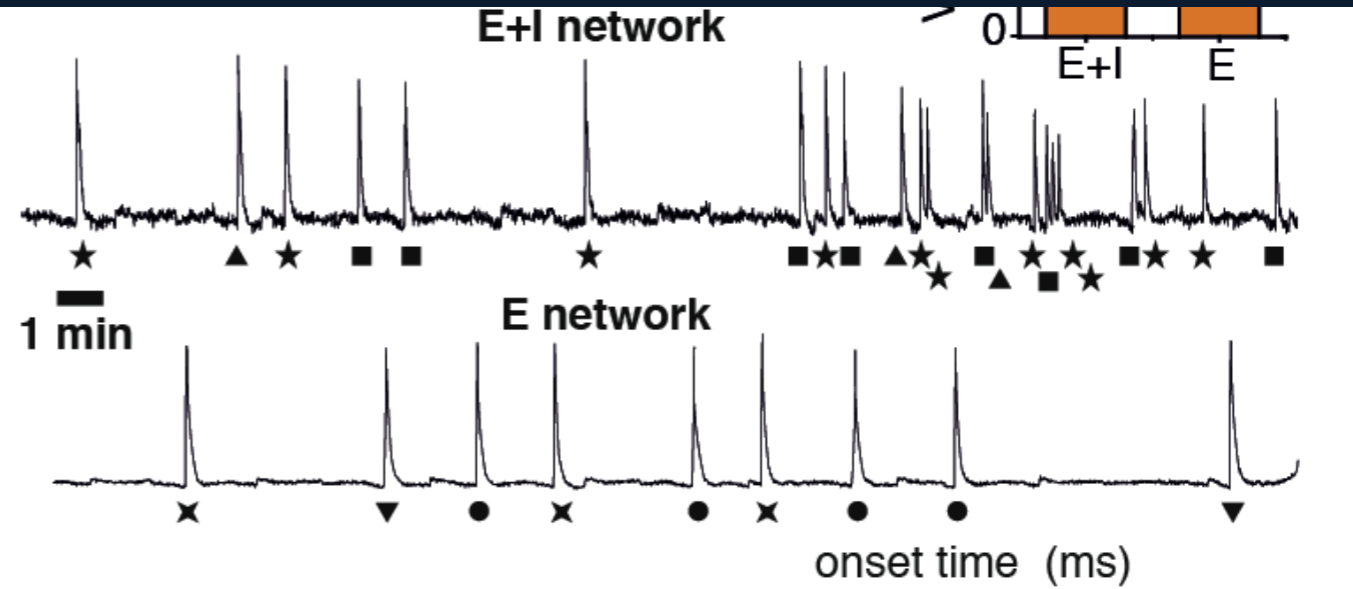
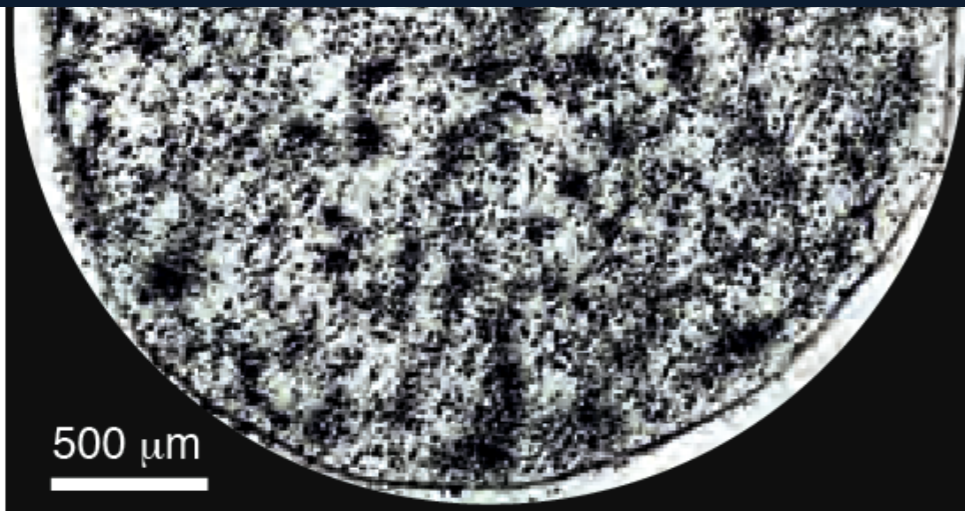
population average



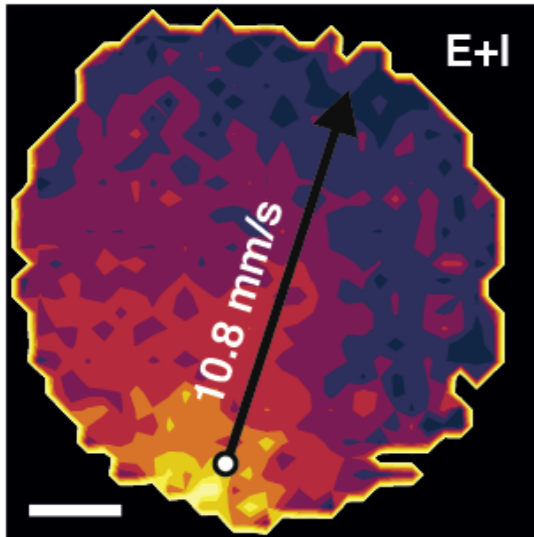


Each burst is in fact a propagating front of activity. And can only originate in specific locations of the culture (nucleation sites)

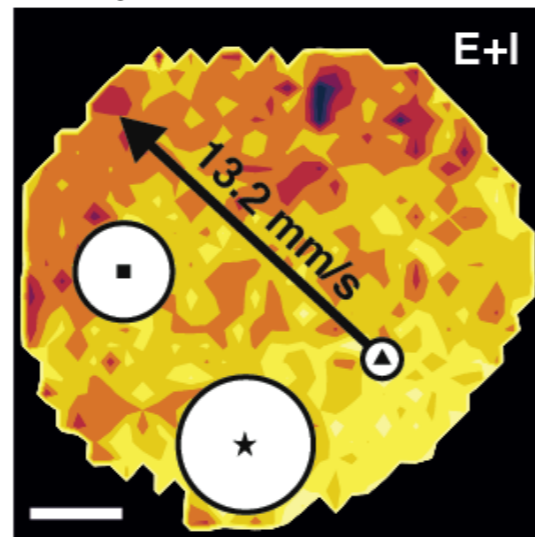
# Dynamics in young cultures



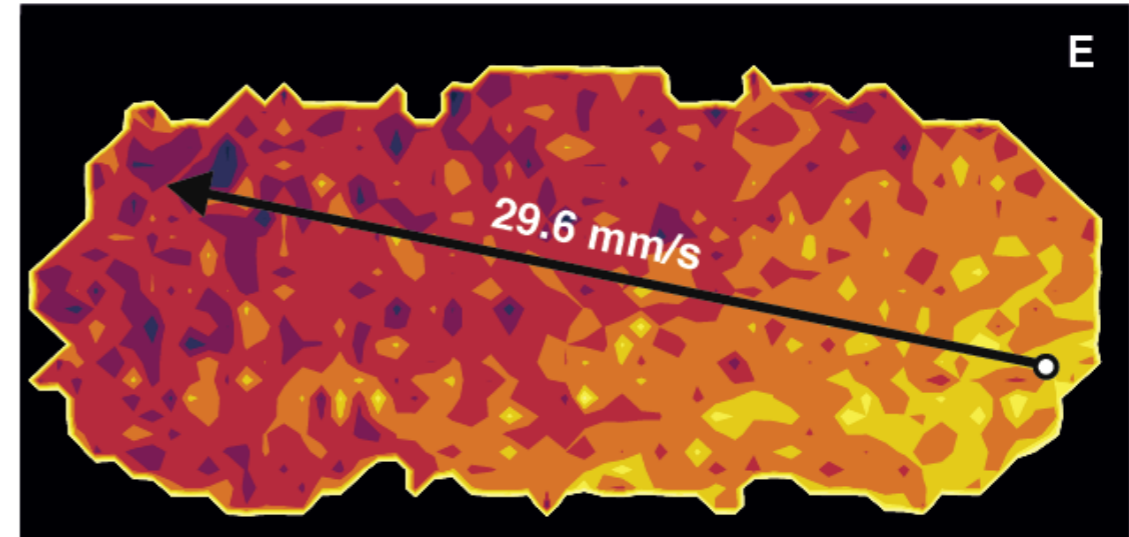
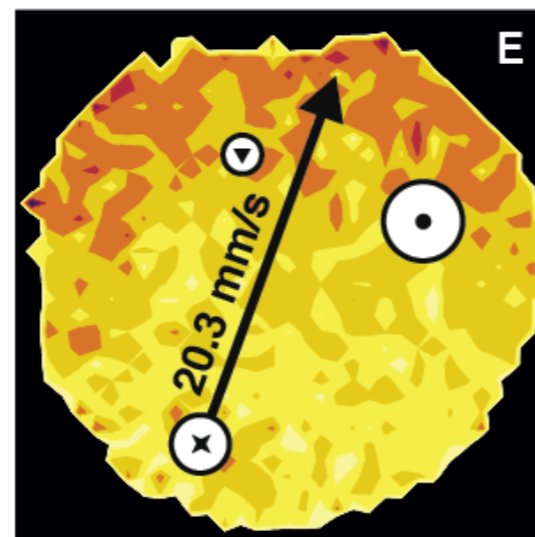
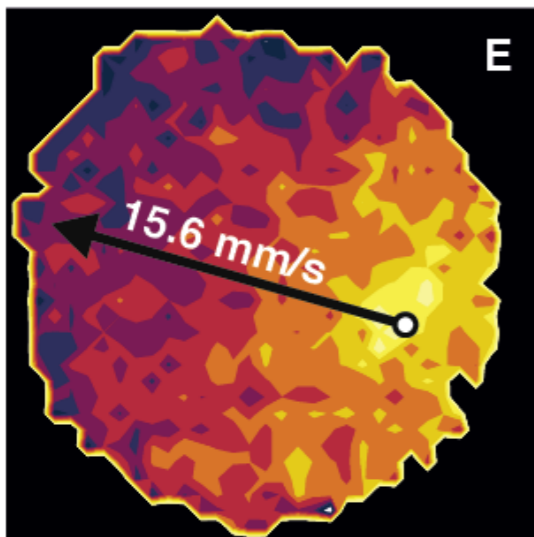
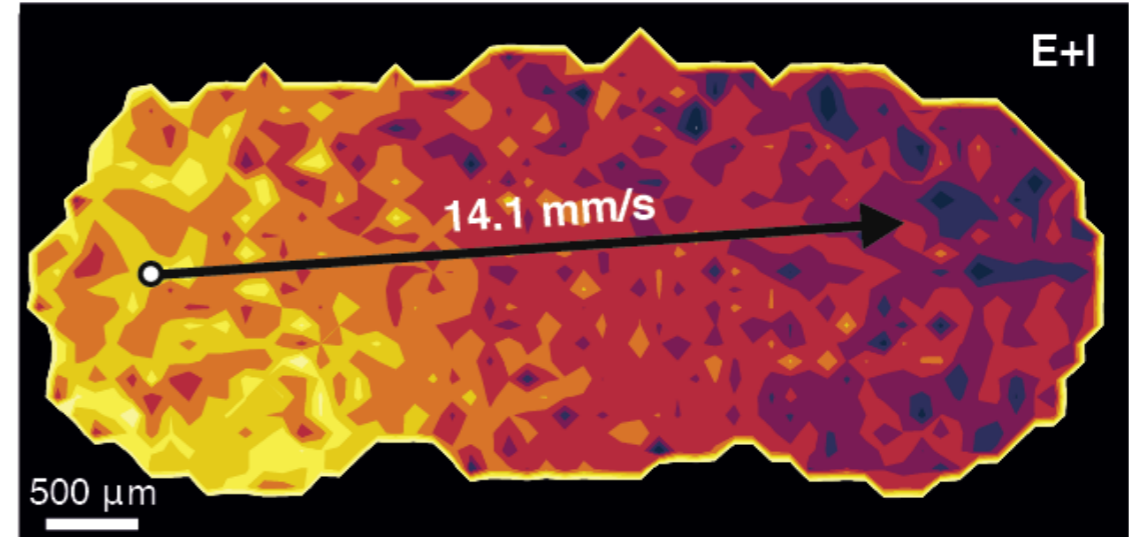
$\phi = 3 \text{ mm}$ , DIV 6



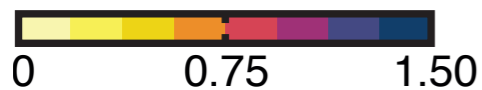
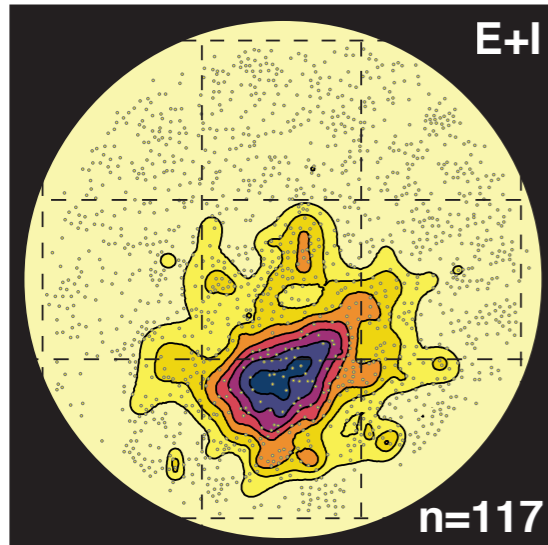
$\phi = 3 \text{ mm}$ , DIV 10



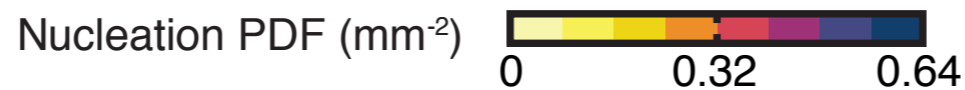
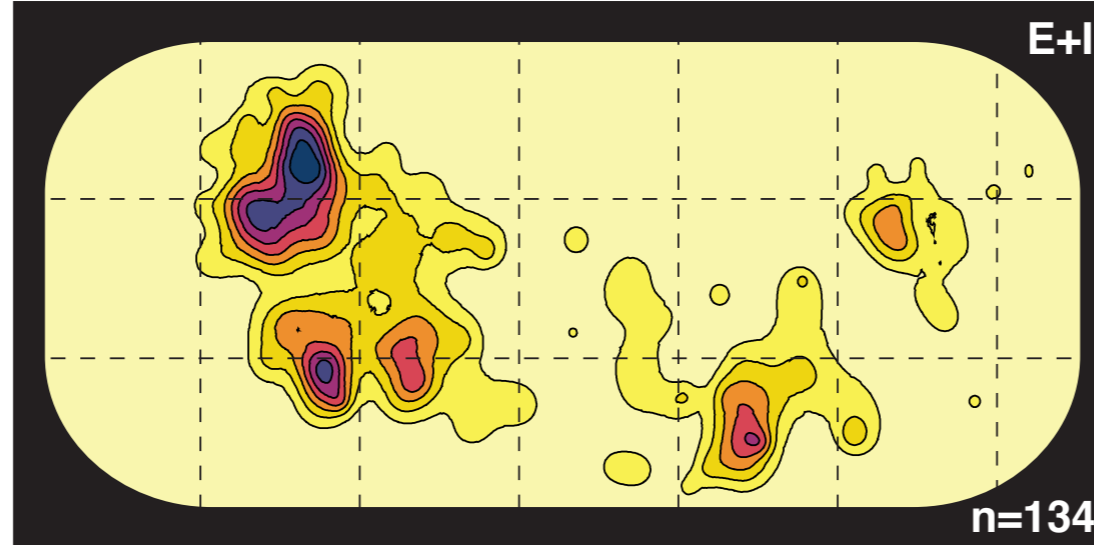
$6 \times 3 \text{ mm}^2$ , DIV 15



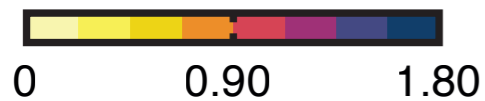
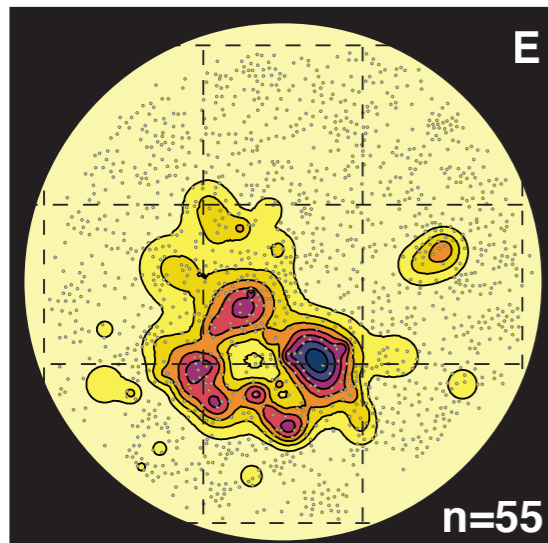
$\varphi = 3$  mm, DIV 9



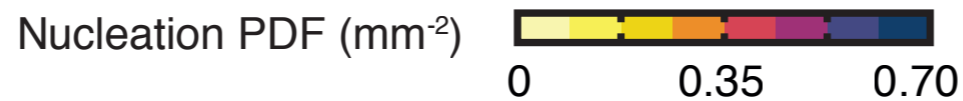
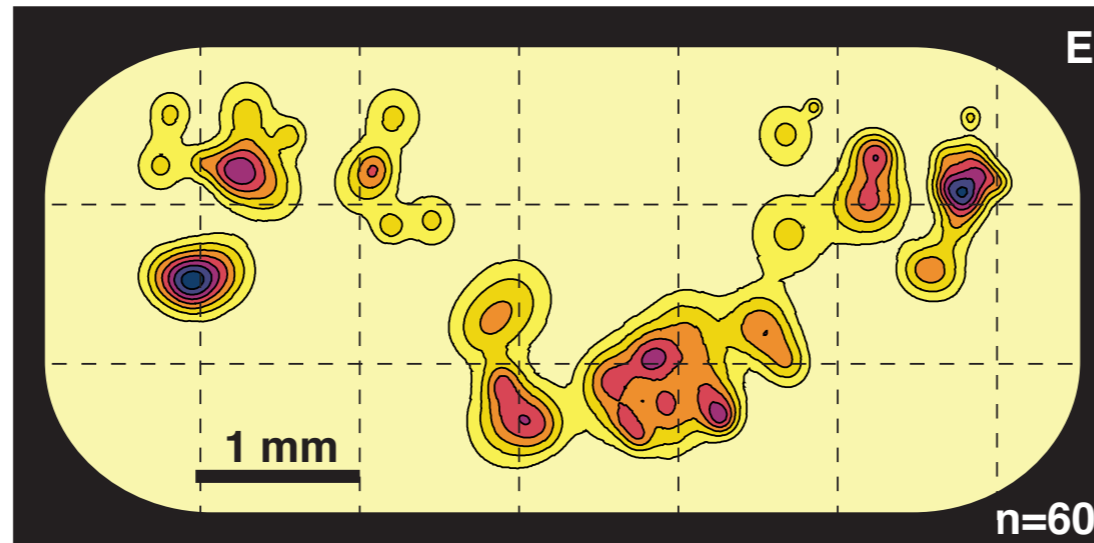
6x3 mm<sup>2</sup>, DIV 9



E

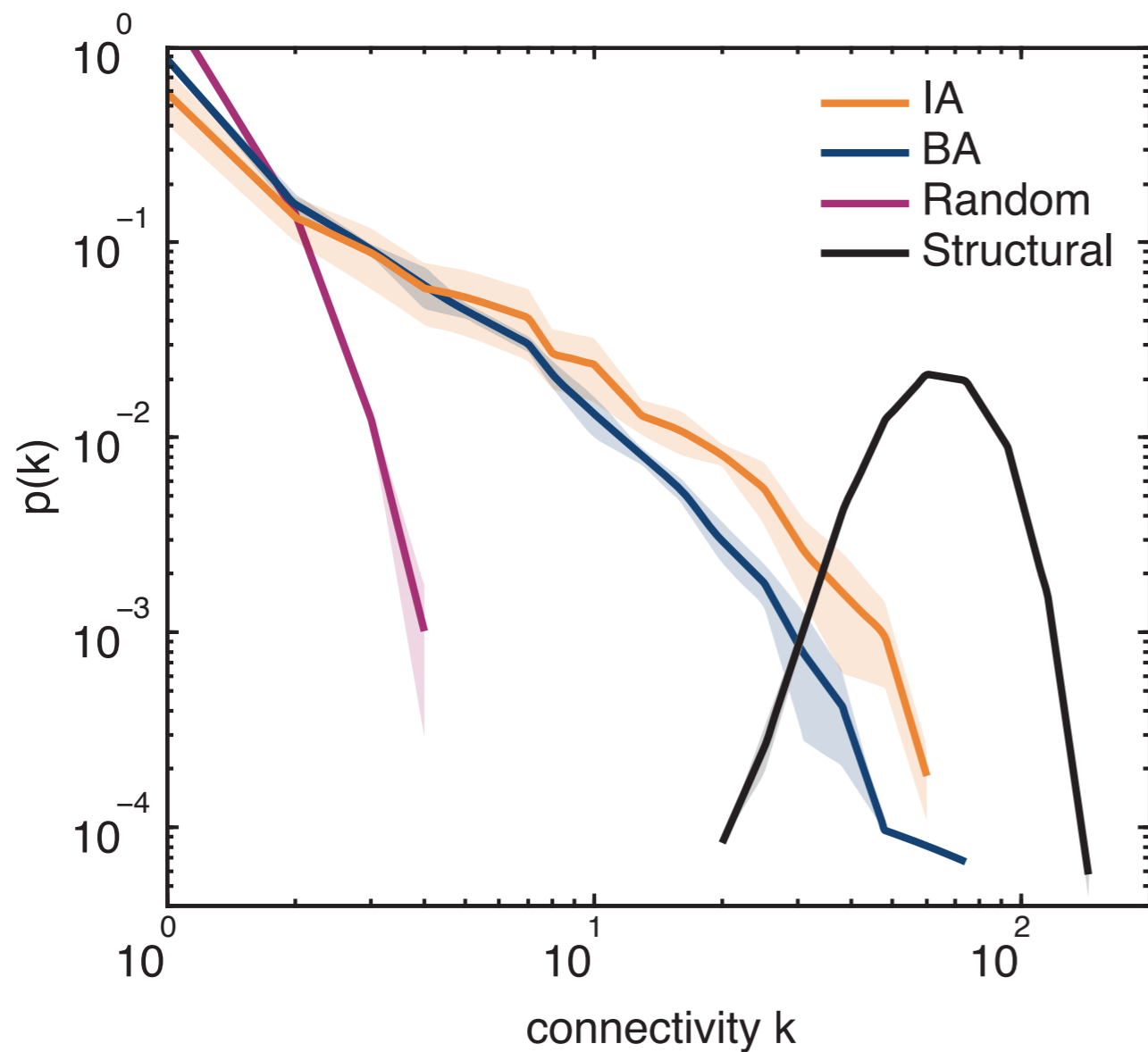


E



Bursts only originate in specific regions

Only a part of the network is capable of burst generation



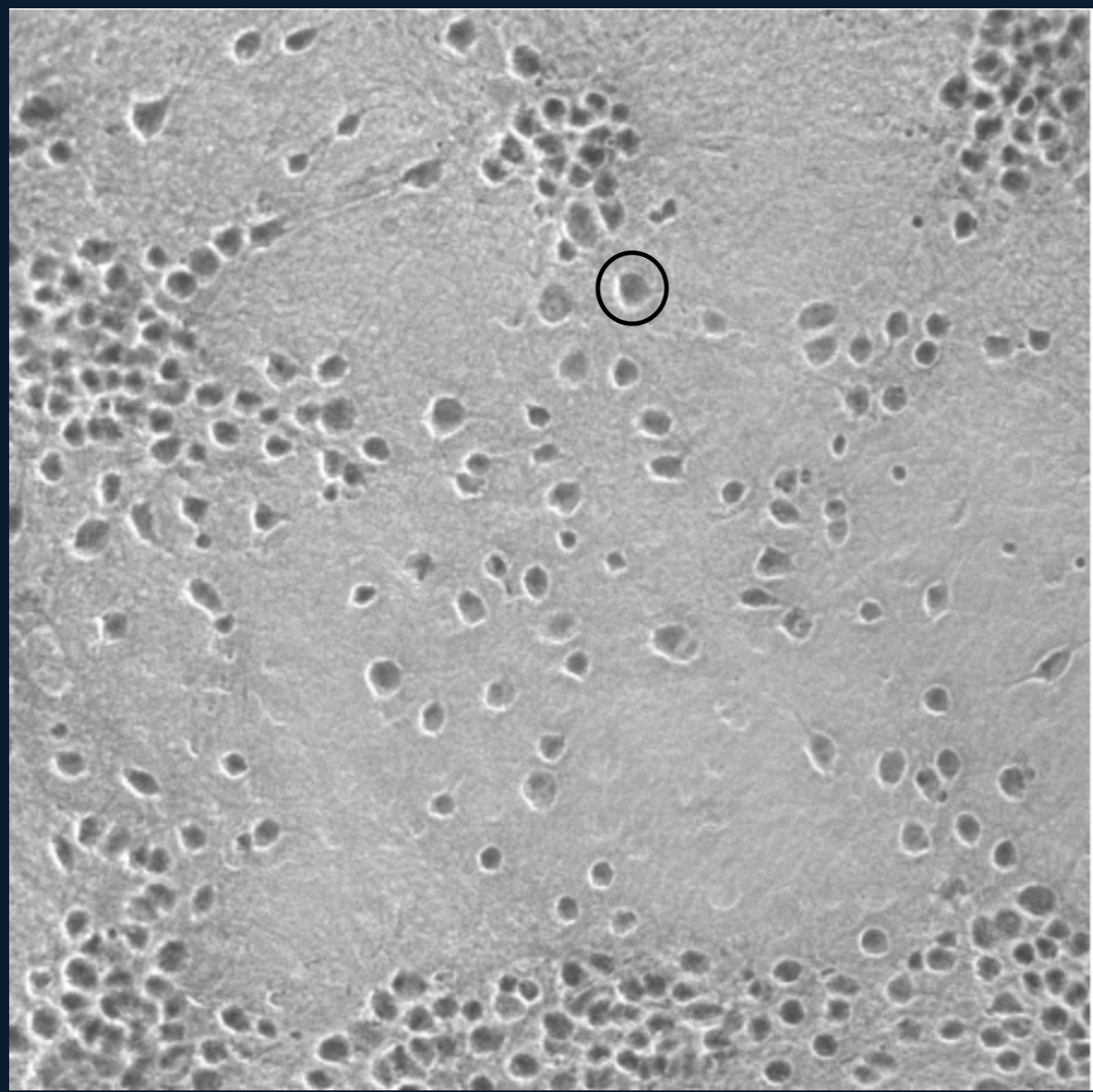
Characterize the structure of the effective network responsible of burst initiation

‘trivial’ structural connectivity gives rise to effective networks with broad-degree distributions

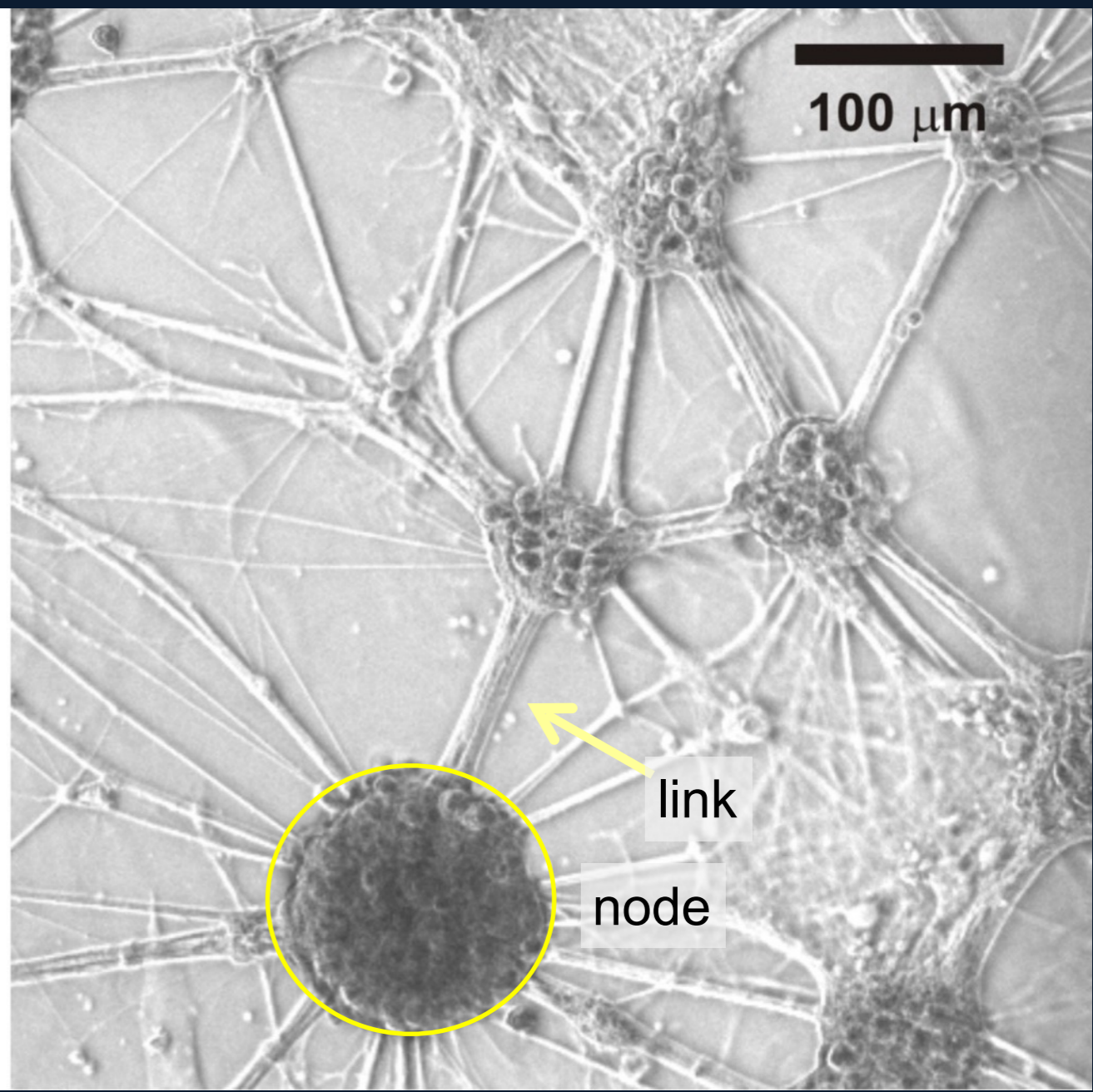


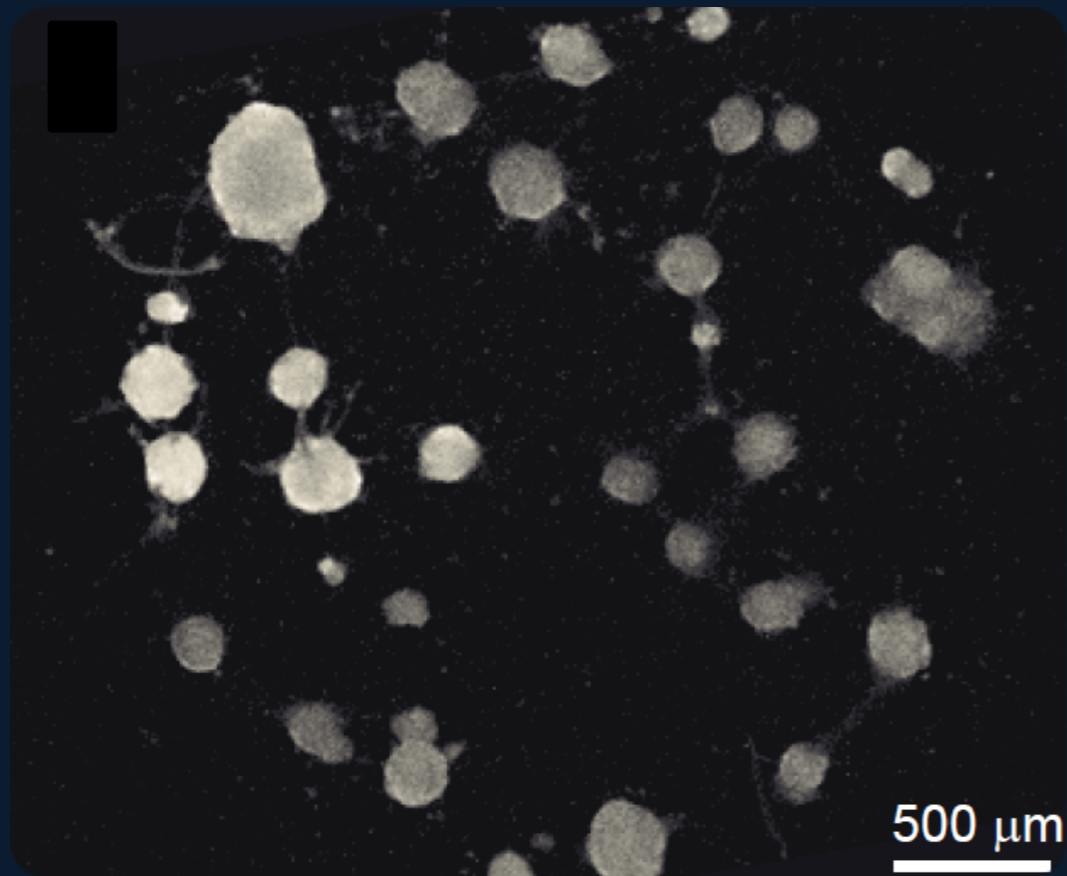


Homogeneous (coated substrate)



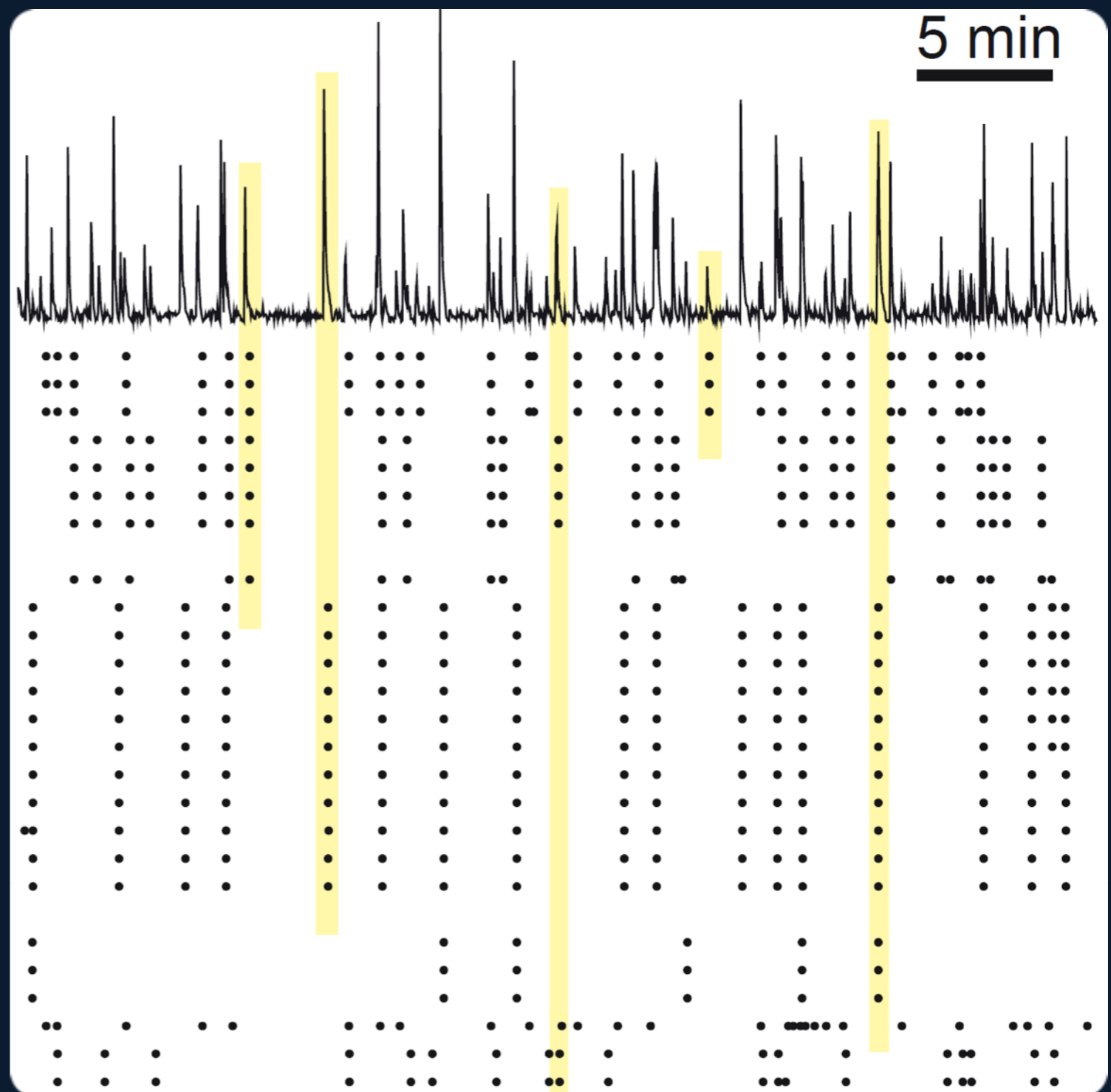
Clustered (uncoated)

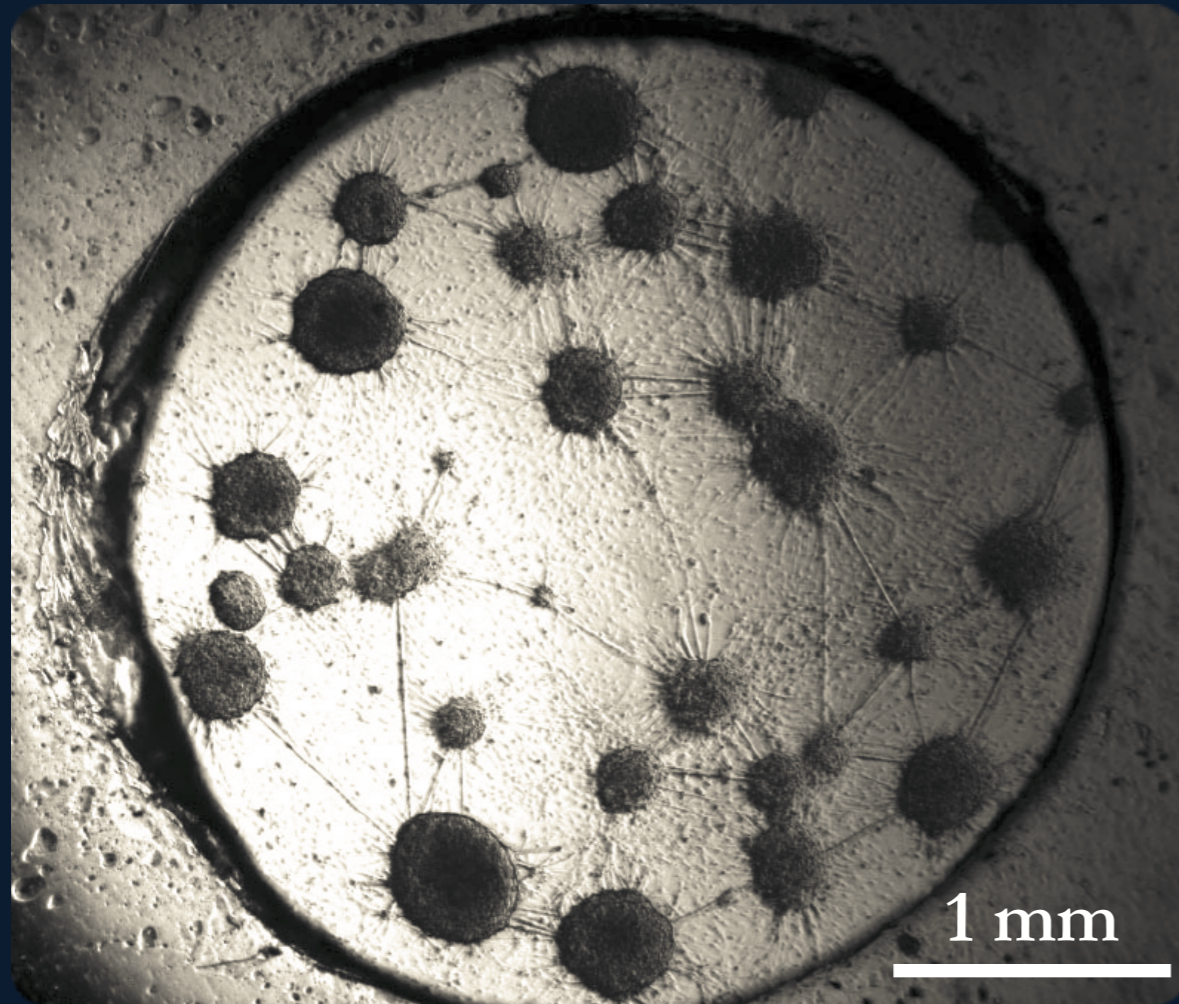




Each cluster acts as a single unit

Modular firing patterns

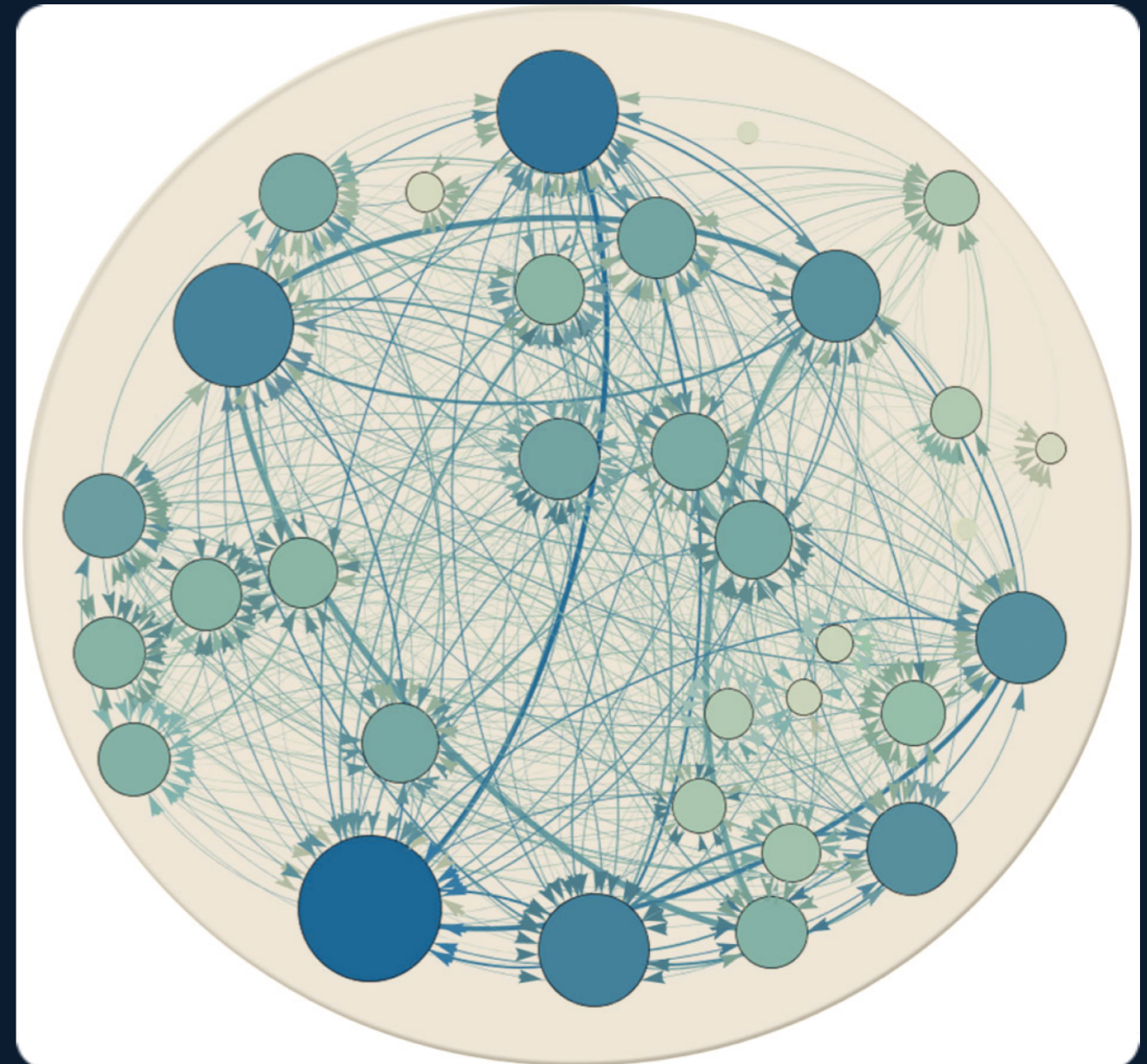




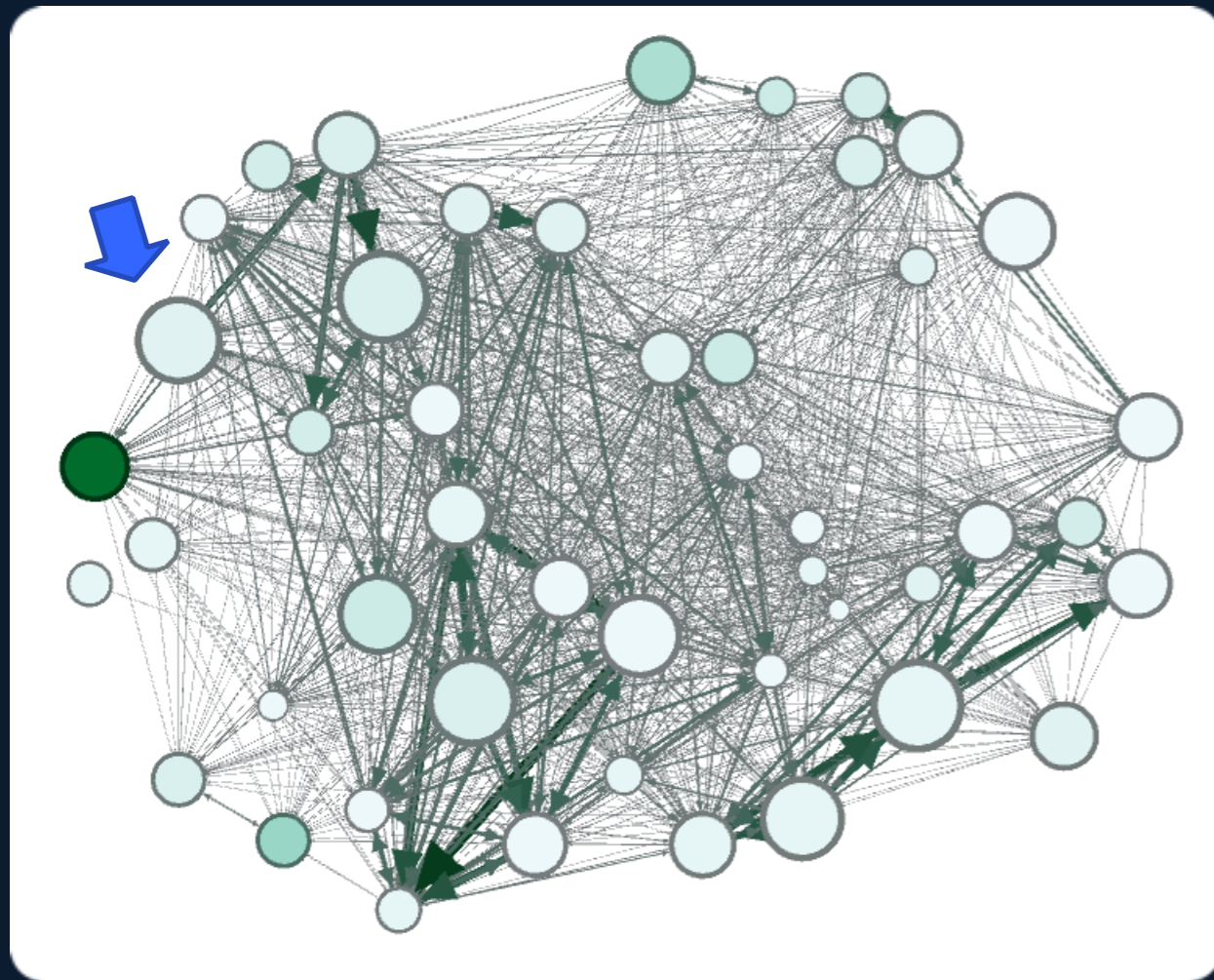
‘structural’ network

Assortative mixing  
Rich club structure

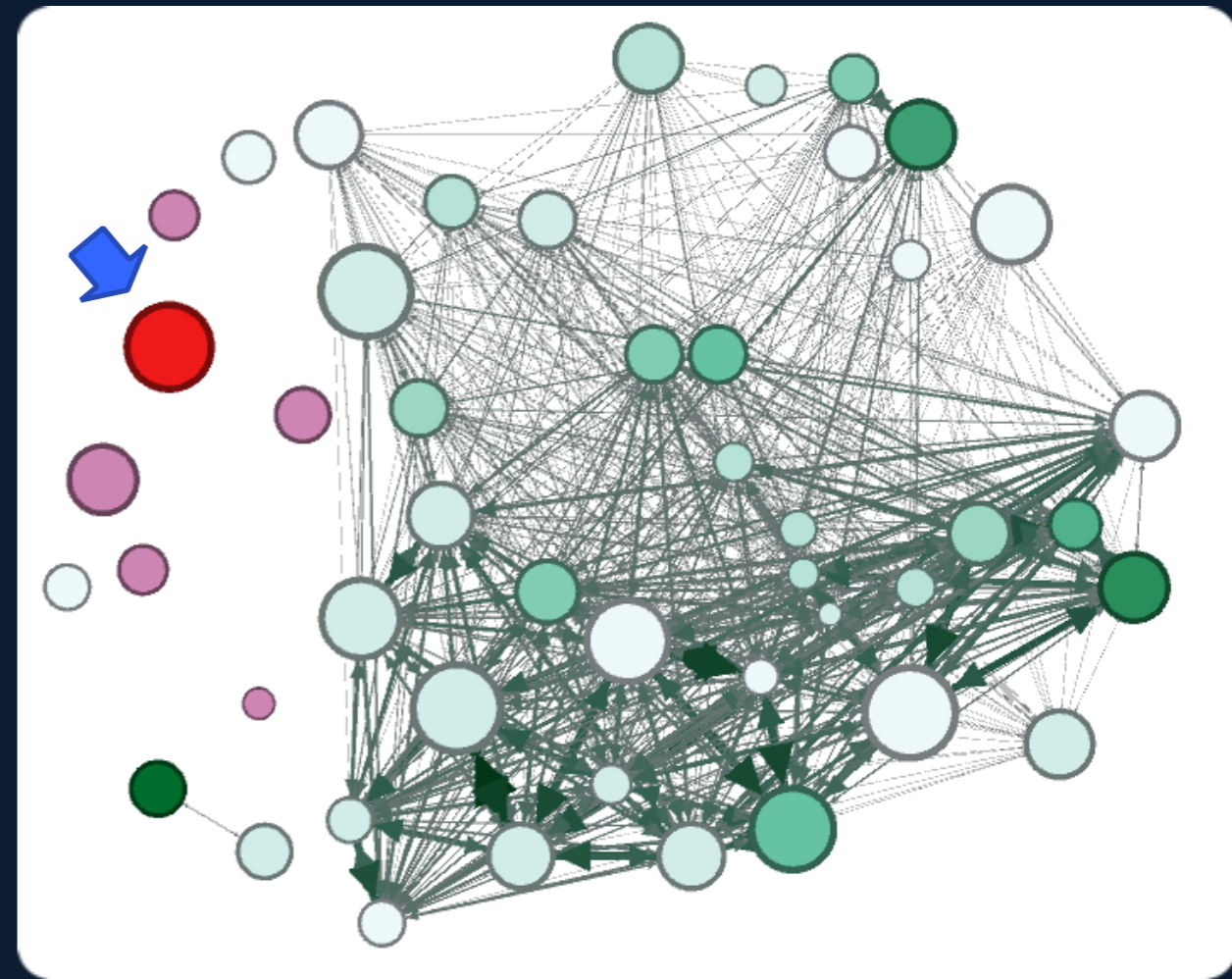
effective network  
(from causal inference)



before



after



Evolution of the effective network after node removal (laser ablation)

Indirect access to the network structure (from the dynamics)

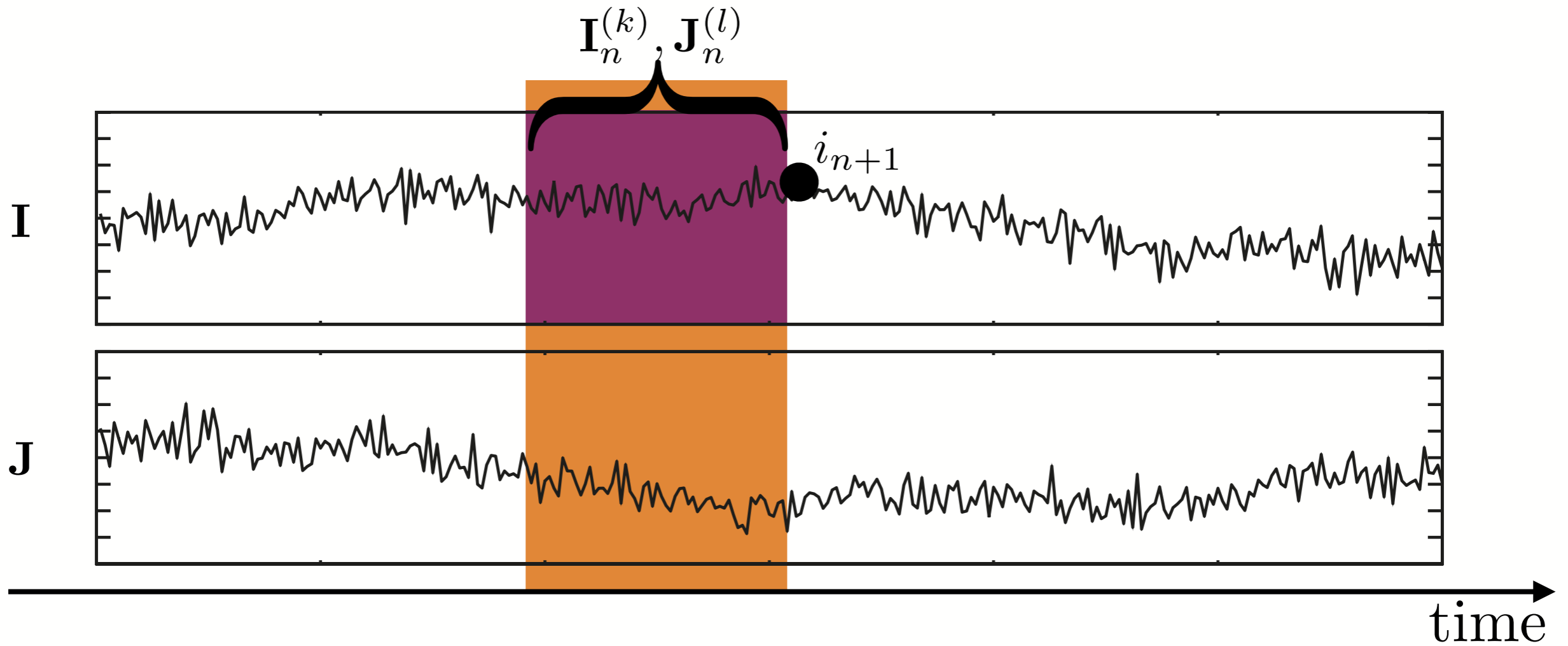
Identify causal interactions in time series

- Correlation
- Mutual information
- Granger causality
- Transfer entropy

Given sets of interdependent variables  $X$  and  $Y$ , it is said that “ $Y$  G-causes  $X$ ” if, in an appropriate statistical sense,  $Y$  assists in predicting the future of  $X$  beyond the degree to which  $X$  already predicts its own future.



Barnett, PRL 2009



Schreiber, PRL 2000

$$T_{J \rightarrow I} = \sum p(i_{n+1}, i_n^{(k)}, j_n^{(l)}) \log \frac{p(i_{n+1} | i_n^{(k)}, j_n^{(l)})}{p(i_{n+1} | i_n^{(k)})}$$

$$\text{GTE}_{J \rightarrow I} = \sum P(i_n, i_{n-1}^{(k)}, j_{n-1+S}^{(k)} | g_n < \tilde{g}) \log \frac{P(i_n | i_{n-1}^{(k)}, j_{n-1+S}^{(k)}, g_n < \tilde{g})}{P(i_n | i_{n-1}^{(k)}, g_n < \tilde{g})}$$

Developed to deal with the singularities of culture dynamics

Fluorescence imaging

Bursting dynamics

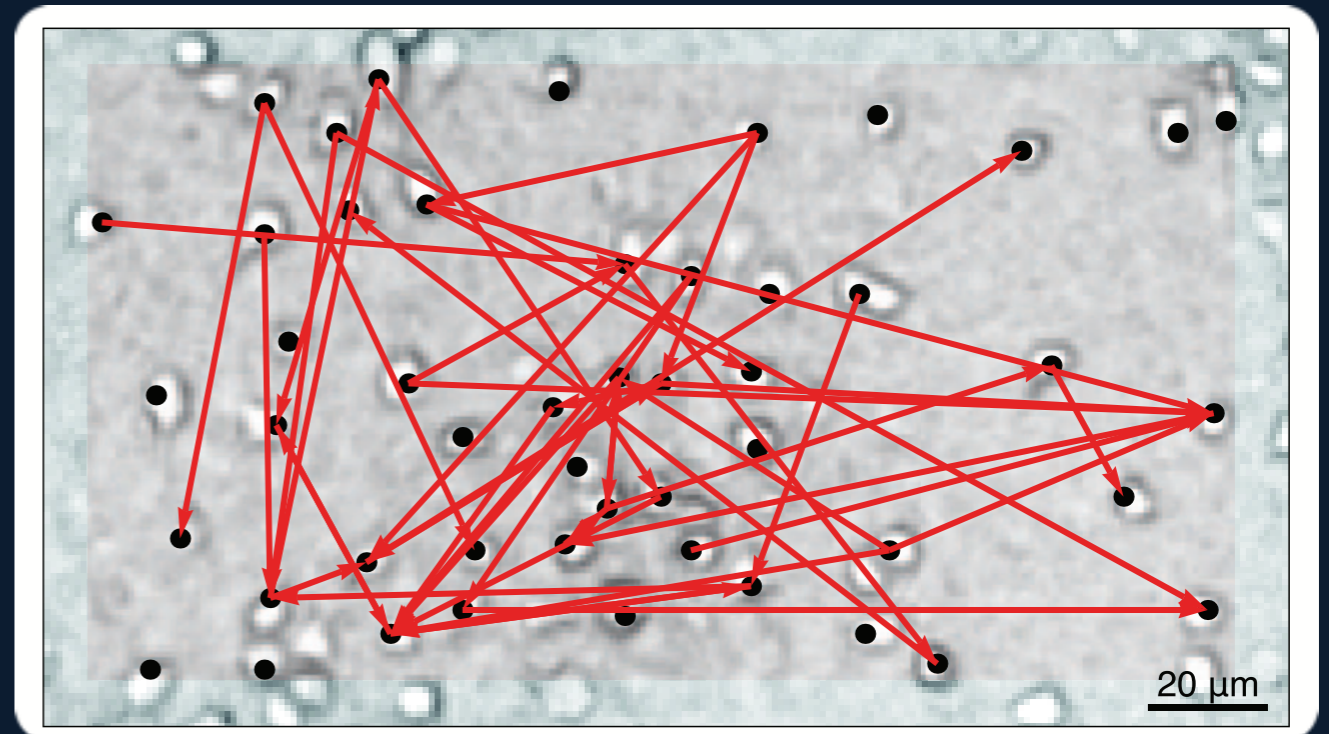
Low acquisition speeds

Low signal to noise ratio

Light scattering

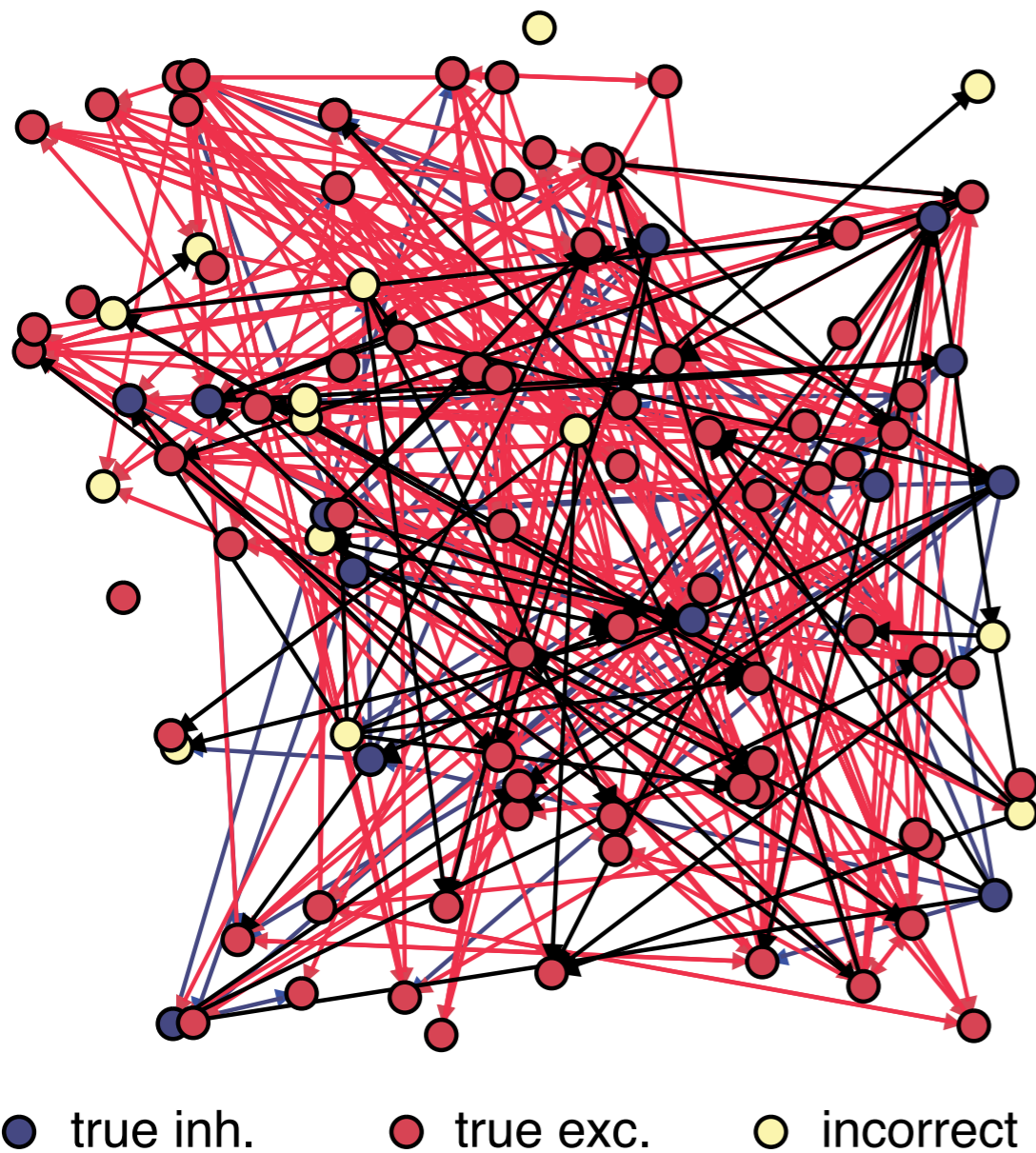
Purely excitatory networks

From the causal interactions, obtain the underlying network



Stetter et al, PLOS Comput Biol 2012

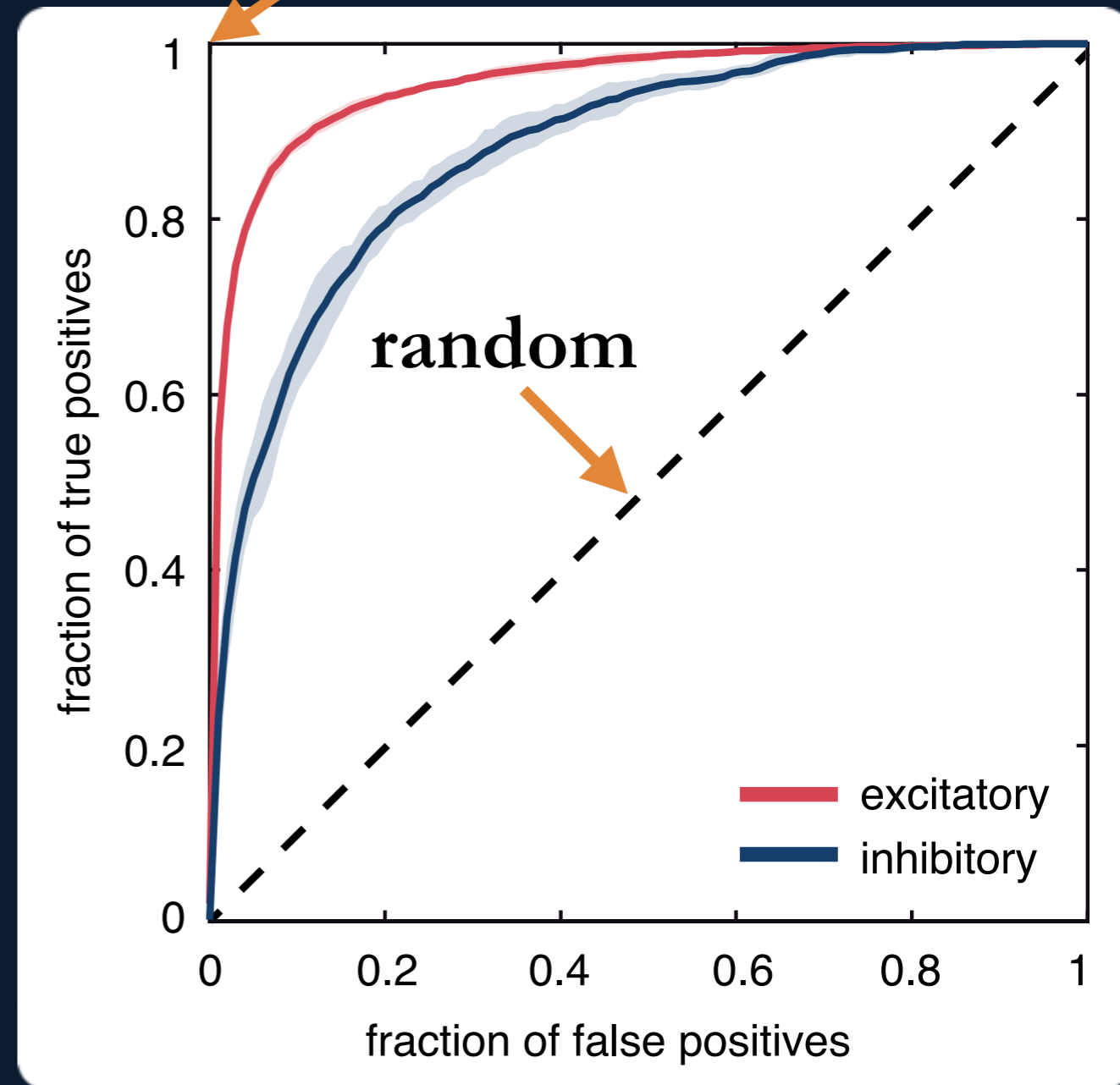
Extended to deal with inhibition



Also possible to infer neuronal type (excitatory/inhibitory)



How good are the reconstructions? **perfect**

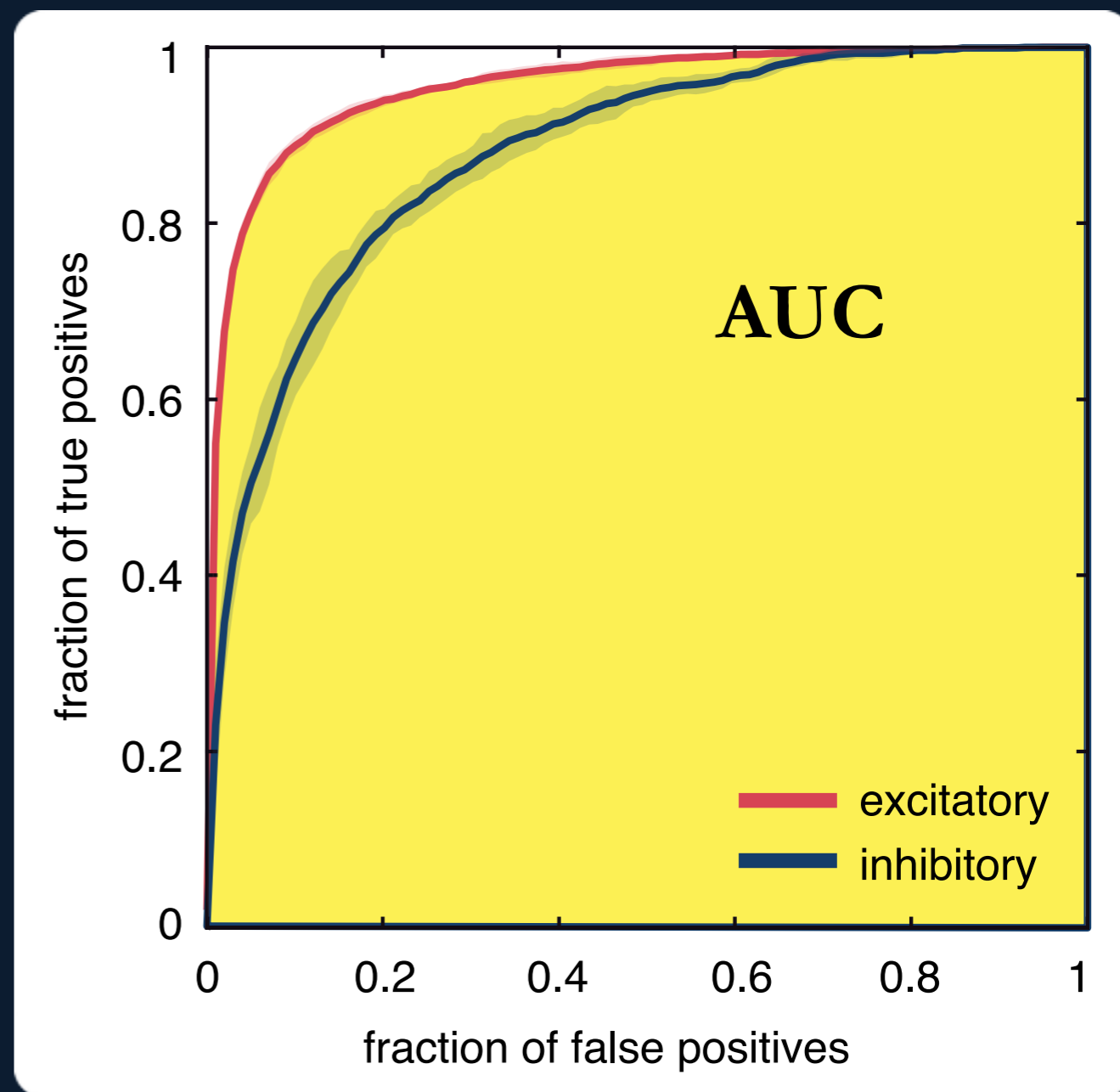


How good are the reconstructions?

AUC  $\sim$  0.89

Still room for improvement!  
A lot actually...

Also, do not trust any single  
method (for causal inference)





Spend many years, (or many PhDs) improving the techniques

Or rather outsource it



## Challenges in Machine Learning (collaborative competitions)

Challenges to stimulate research across different fields

Launch the first (of a series) of online challenges in connectomics

Infer the network structure of neuronal cultures based solely on simulated calcium fluorescence imaging data

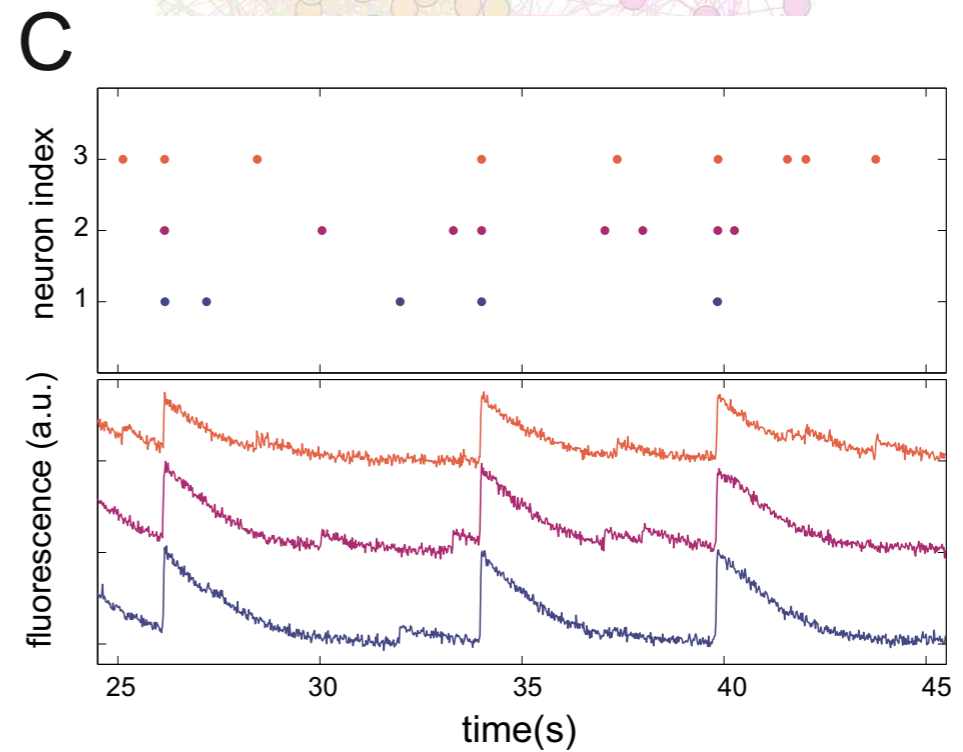
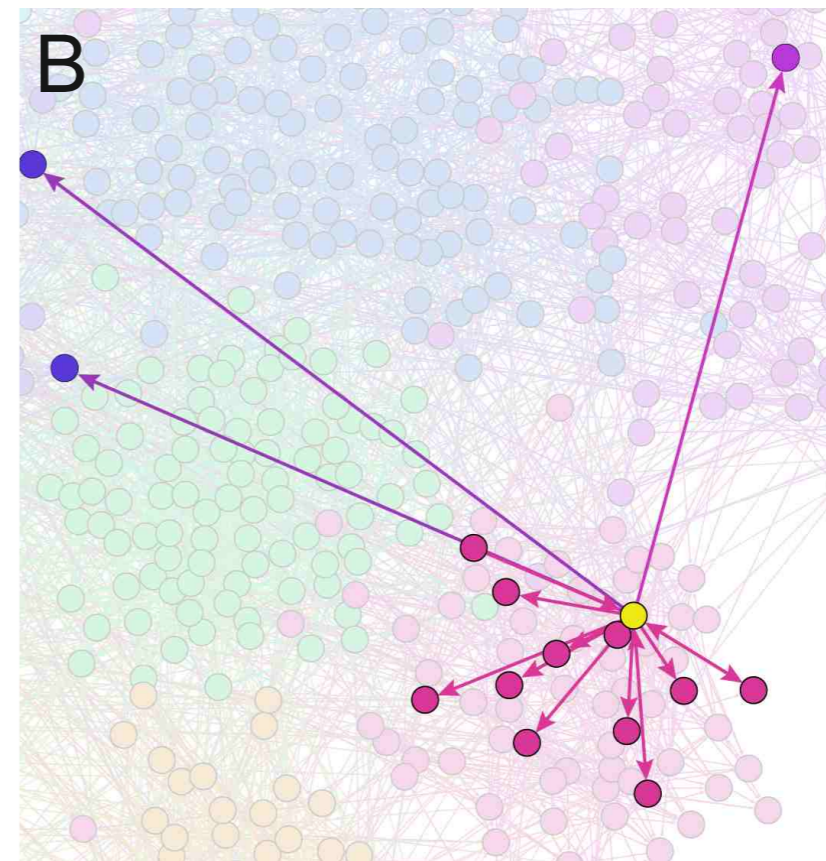
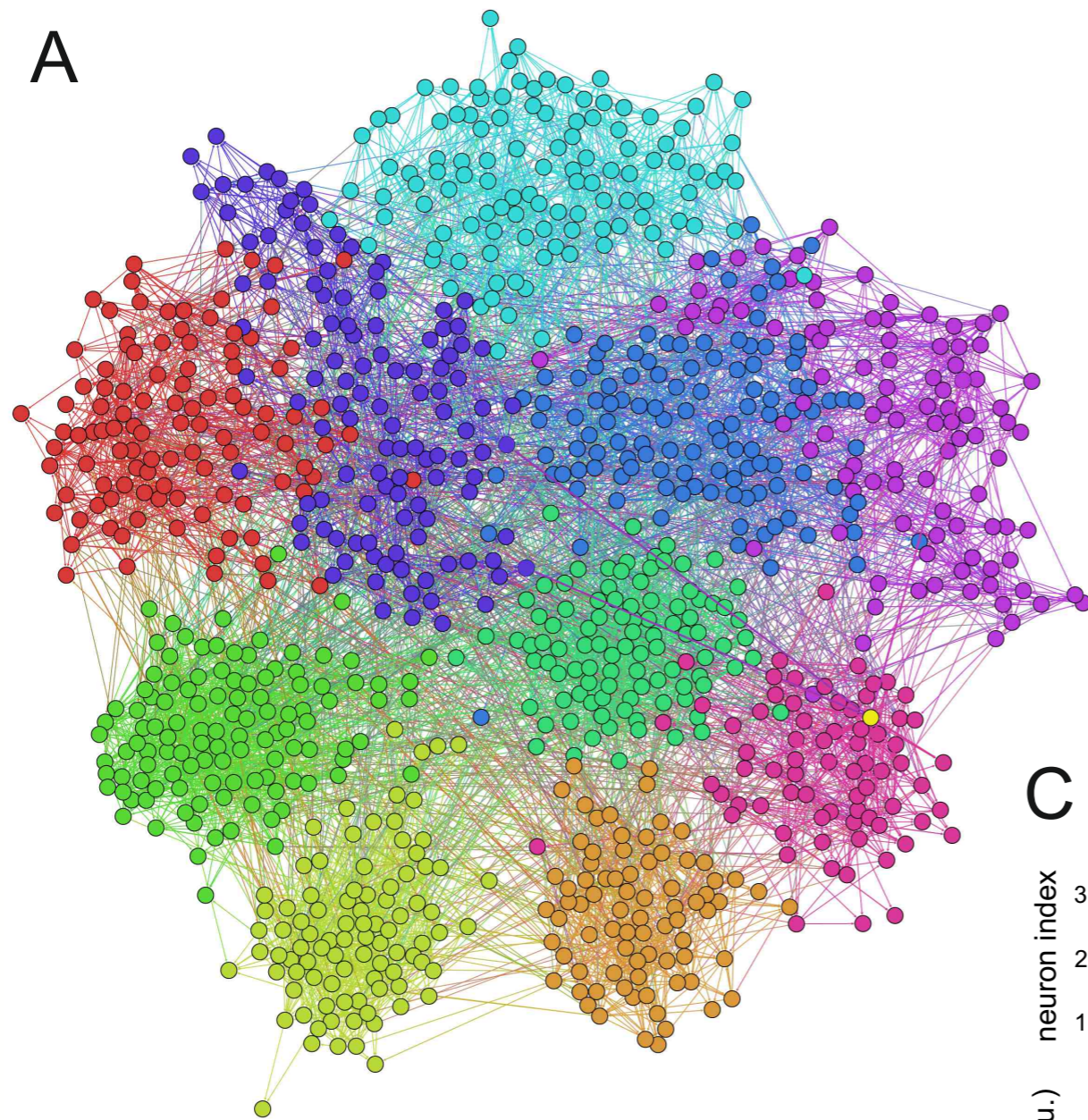
Provided:

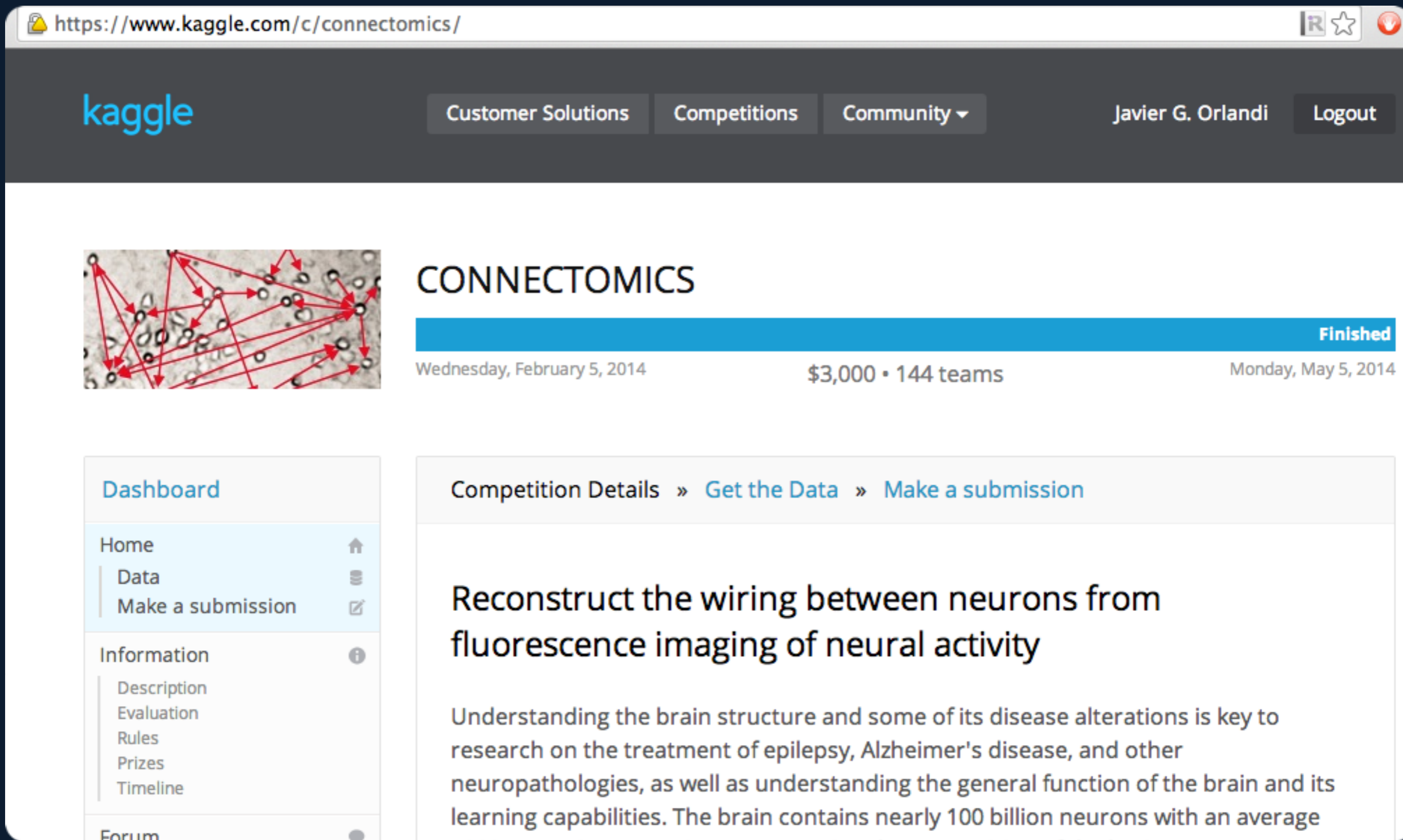
Fluorescence traces of 1000 neurons

Neuronal positions

10 sample datasets with known-truth topology with different conditions (signal to noise ratio, framerate, ...)

Participants asked to predict the structural topology of two different networks with unknown topology - ranked based on AUC performance

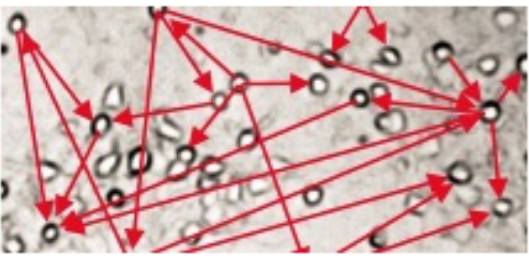




The screenshot shows the Kaggle website interface for the 'CONNECTOMICS' challenge. The browser address bar displays 'https://www.kaggle.com/c/connectomics/'. The navigation bar includes the Kaggle logo, 'Customer Solutions', 'Competitions', and 'Community' menus, along with the user name 'Javier G. Orlandi' and a 'Logout' button. The challenge title 'CONNECTOMICS' is prominently displayed, followed by a blue bar indicating the status 'Finished'. Below this, the dates 'Wednesday, February 5, 2014' and 'Monday, May 5, 2014' are shown, along with the prize amount '\$3,000' and the number of teams '144 teams'. A navigation breadcrumb trail reads 'Competition Details » Get the Data » Make a submission'. The main content area features the challenge title 'Reconstruct the wiring between neurons from fluorescence imaging of neural activity' and a descriptive paragraph: 'Understanding the brain structure and some of its disease alterations is key to research on the treatment of epilepsy, Alzheimer's disease, and other neuropathologies, as well as understanding the general function of the brain and its learning capabilities. The brain contains nearly 100 billion neurons with an average'. On the left side, a sidebar menu is visible with sections for 'Dashboard', 'Home', 'Data', 'Make a submission', 'Information', and 'Forum'. The 'Information' section is expanded, showing links for 'Description', 'Evaluation', 'Rules', 'Prizes', and 'Timeline'.

https://www.kaggle.com/c/connectomics/

kaggle Customer Solutions Competitions Community Javier G. Orlandi Logout



## CONNECTOMICS

Finished

Wednesday, February 5, 2014 \$3,000 • 144 teams Monday, May 5, 2014

Competition Details » [Get the Data](#) » [Make a submission](#)

### Reconstruct the wiring between neurons from fluorescence imaging of neural activity

Understanding the brain structure and some of its disease alterations is key to research on the treatment of epilepsy, Alzheimer's disease, and other neuropathologies, as well as understanding the general function of the brain and its learning capabilities. The brain contains nearly 100 billion neurons with an average

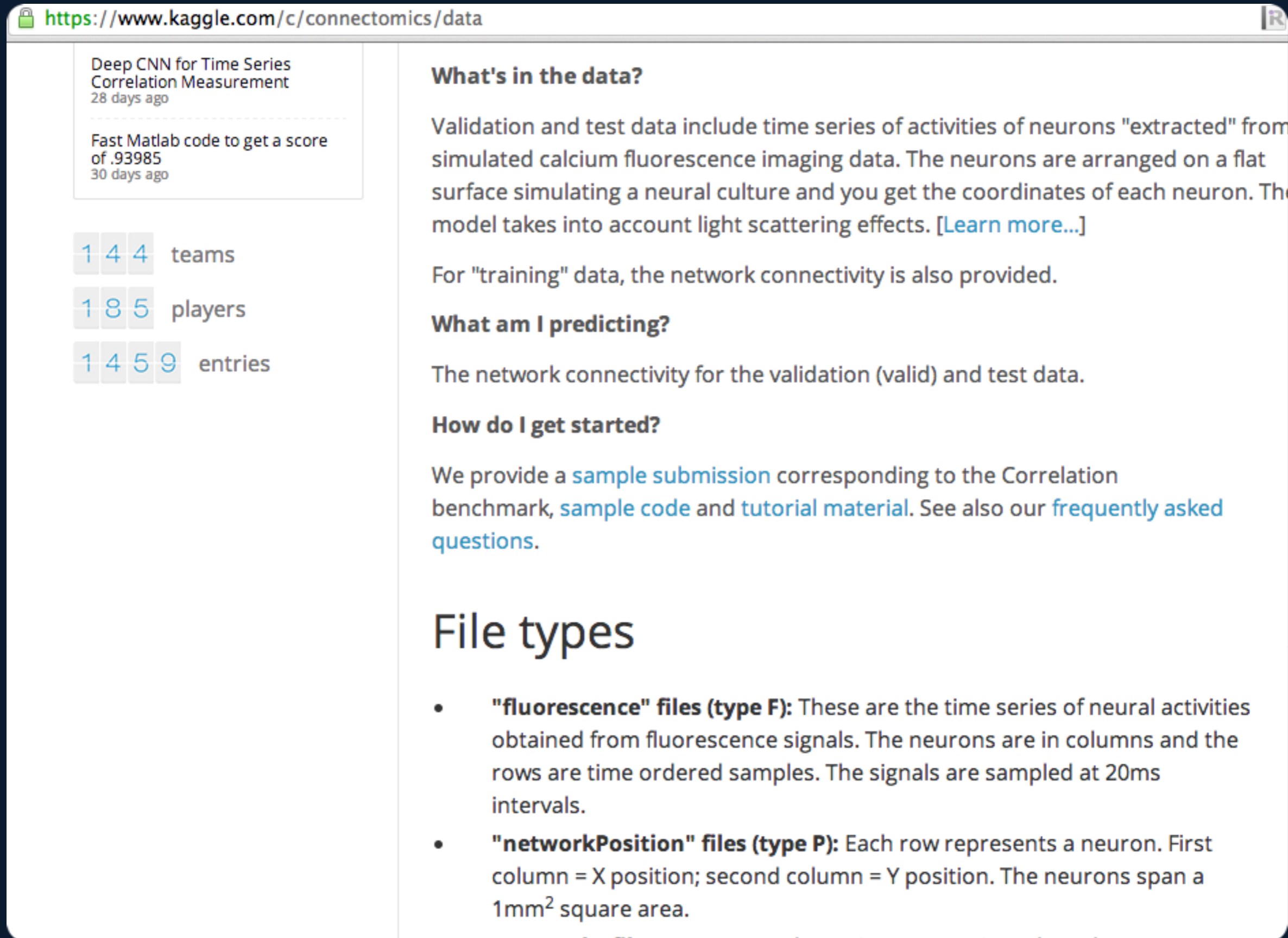
Dashboard

- Home
- Data
- Make a submission

Information

- Description
- Evaluation
- Rules
- Prizes
- Timeline

Forum



The screenshot shows a Kaggle challenge page for 'connectomics/data'. The browser address bar displays 'https://www.kaggle.com/c/connectomics/data'. On the left sidebar, there are two recent submissions: 'Deep CNN for Time Series Correlation Measurement' (28 days ago) and 'Fast Matlab code to get a score of .93985' (30 days ago). Below these are statistics: 144 teams, 185 players, and 1459 entries. The main content area has a section titled 'What's in the data?' which describes the validation and test data as time series of activities of neurons from simulated calcium fluorescence imaging data. It also mentions that network connectivity is provided for training data. Below this is a section 'What am I predicting?' stating that network connectivity for validation and test data is the target. The 'How do I get started?' section provides links to a sample submission, sample code, and tutorial material. The 'File types' section lists two types: 'fluorescence' files (type F) and 'networkPosition' files (type P).

https://www.kaggle.com/c/connectomics/data

Deep CNN for Time Series Correlation Measurement  
28 days ago

Fast Matlab code to get a score of .93985  
30 days ago

144 teams

185 players

1459 entries

## What's in the data?

Validation and test data include time series of activities of neurons "extracted" from simulated calcium fluorescence imaging data. The neurons are arranged on a flat surface simulating a neural culture and you get the coordinates of each neuron. The model takes into account light scattering effects. [[Learn more...](#)]

For "training" data, the network connectivity is also provided.

## What am I predicting?

The network connectivity for the validation (valid) and test data.

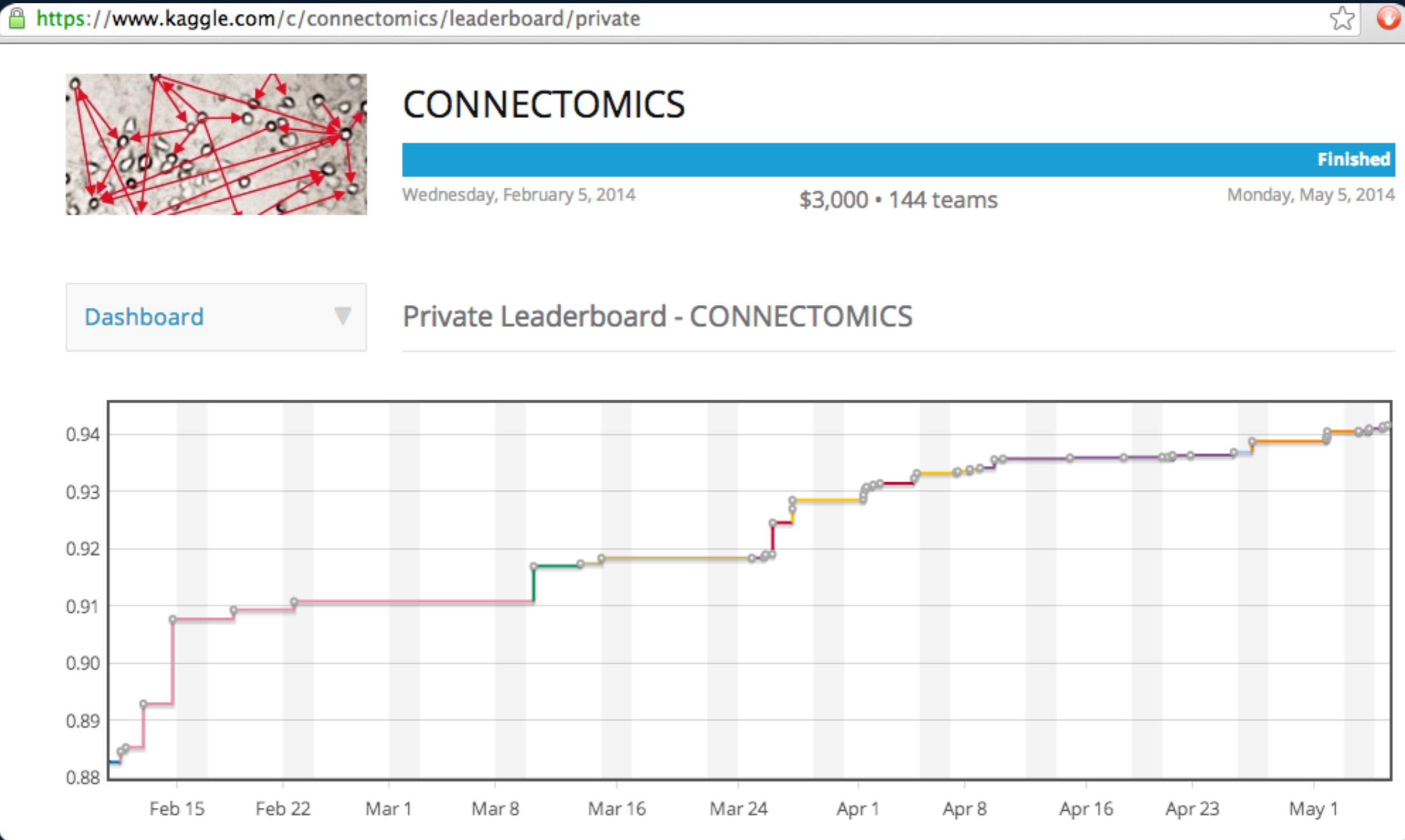
## How do I get started?

We provide a [sample submission](#) corresponding to the Correlation benchmark, [sample code](#) and [tutorial material](#). See also our [frequently asked questions](#).

## File types

- **"fluorescence" files (type F):** These are the time series of neural activities obtained from fluorescence signals. The neurons are in columns and the rows are time ordered samples. The signals are sampled at 20ms intervals.
- **"networkPosition" files (type P):** Each row represents a neuron. First column = X position; second column = Y position. The neurons span a 1mm<sup>2</sup> square area.

# Challenge evolution

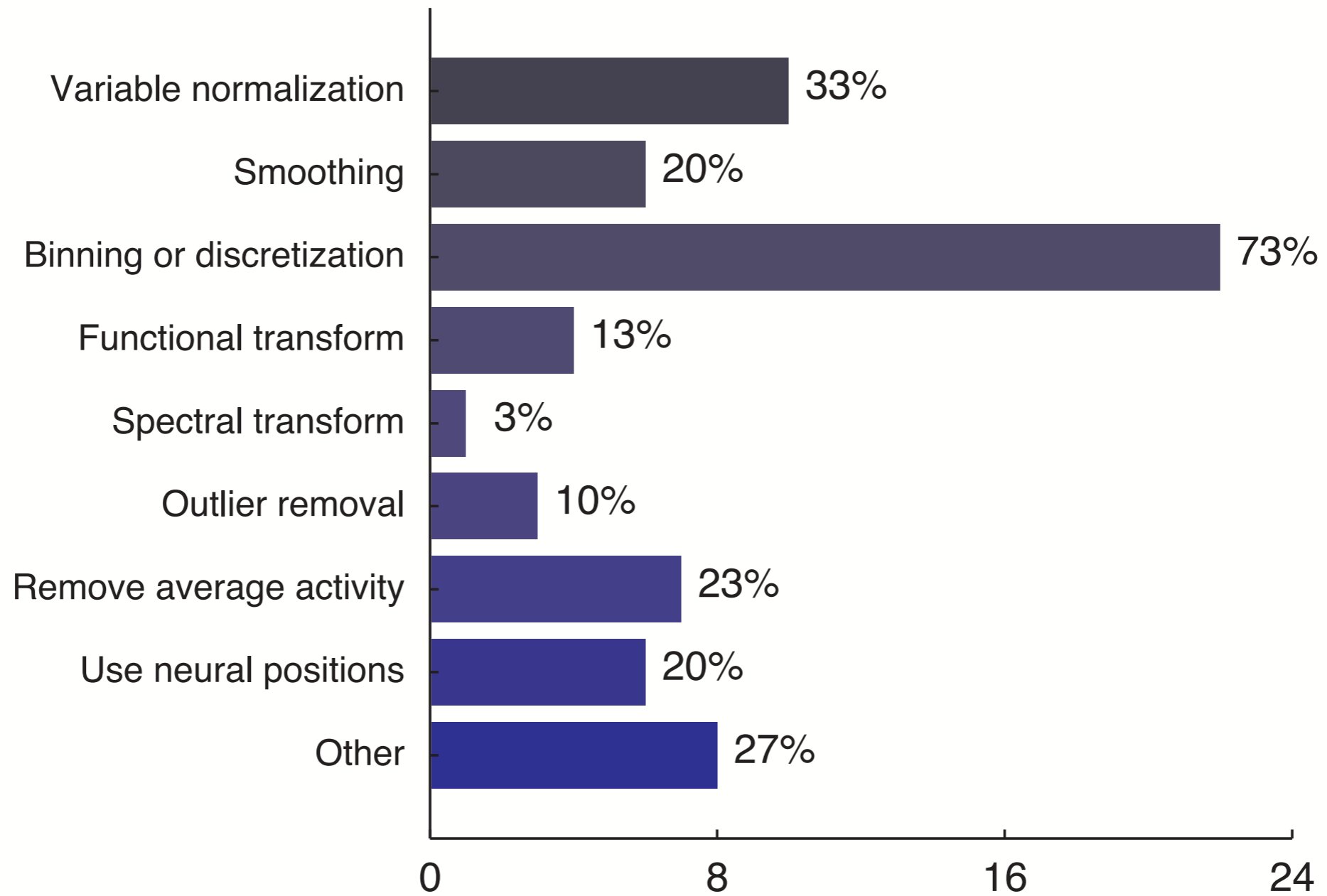


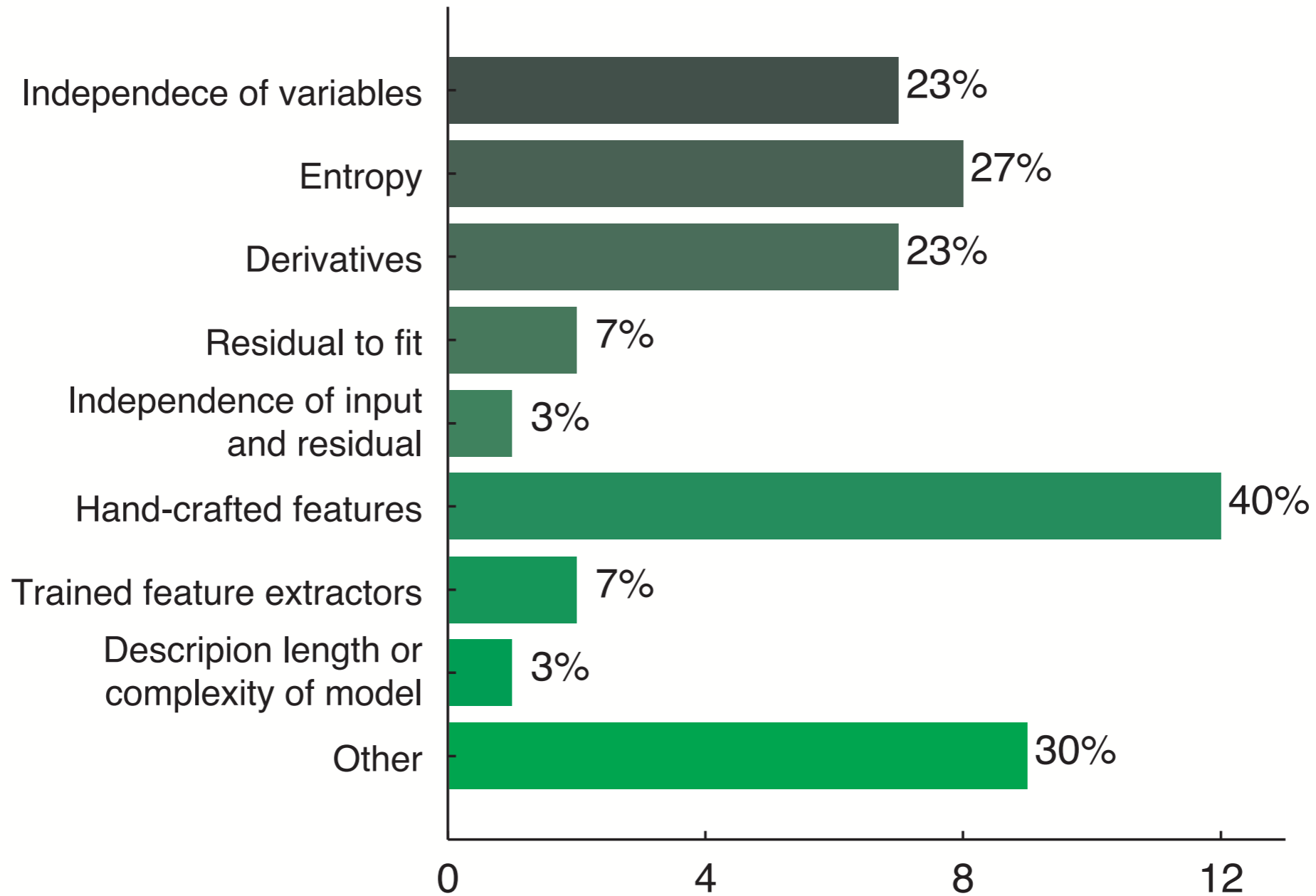
~20% performance increase over standard techniques (in 3 months)

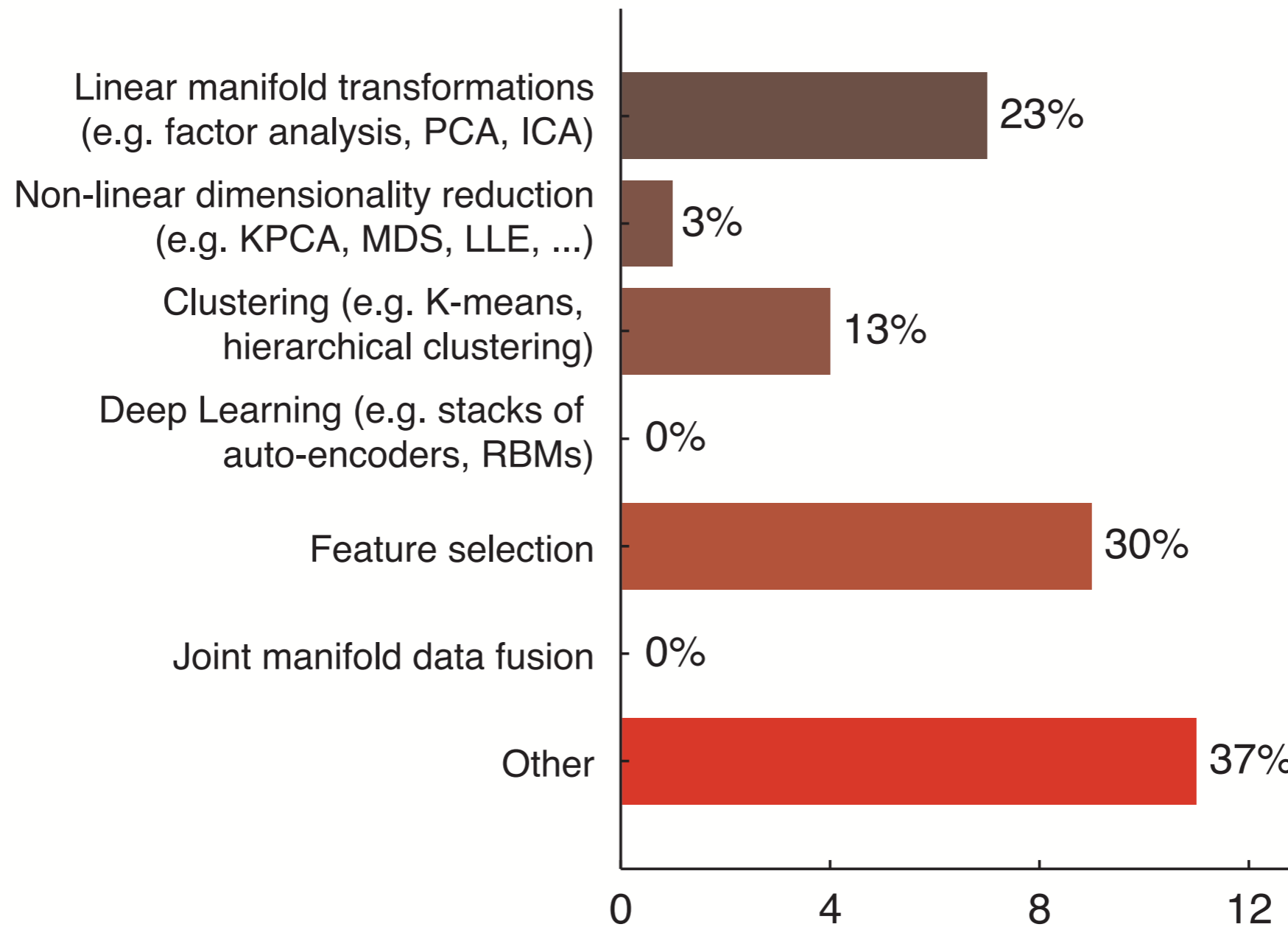


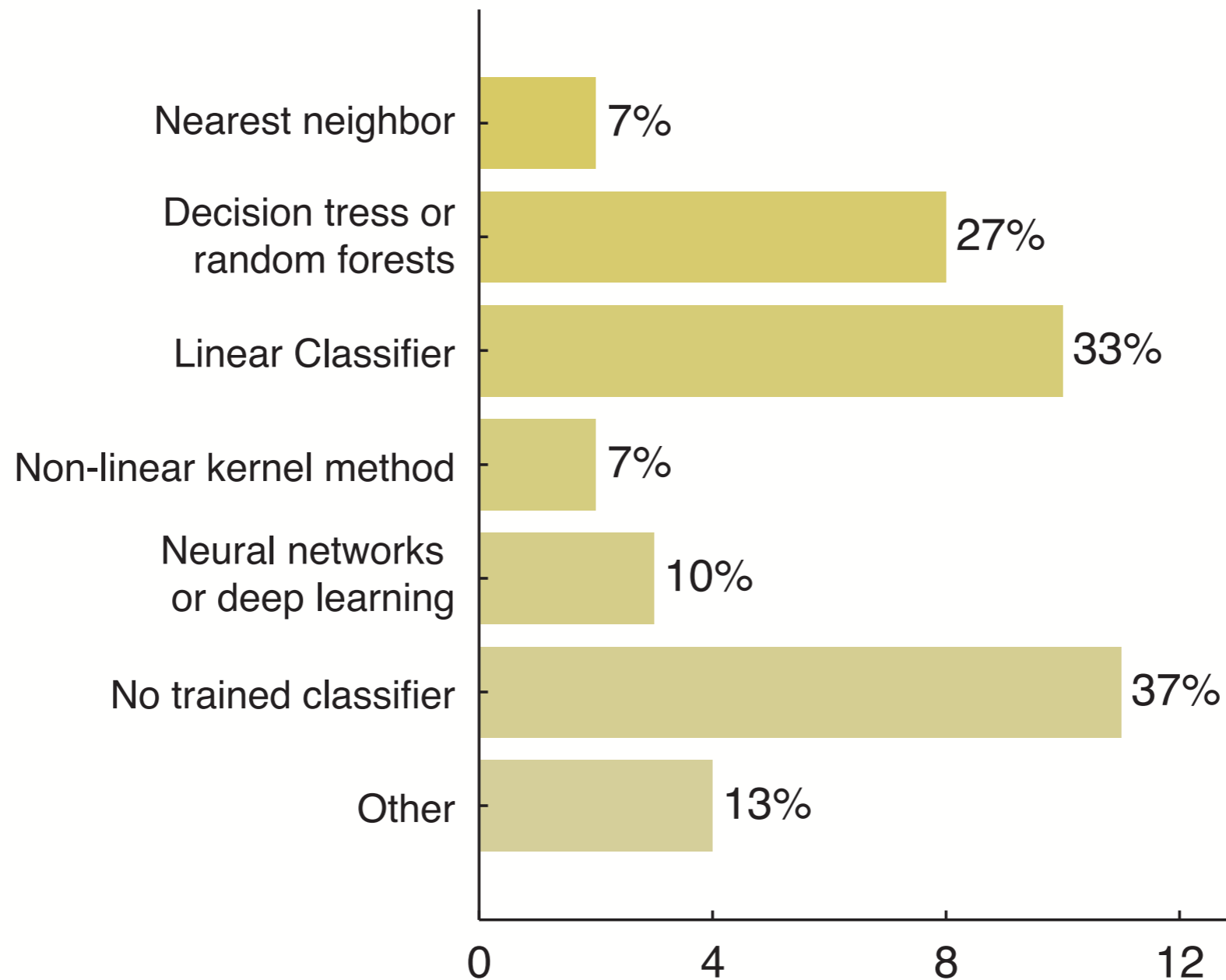
# Challenge final scores

#	Δ1w	Team Name <small>‡ model uploaded * in the money</small>	Score <small>🔍</small>	Entries	Last Submission UTC (Best – Last Submission)
1	↑6	AAAGV <small>👤 ‡ *</small>	0.94161	145	Mon, 05 May 2014 20:50:39
2	↑3	Matthias Ossadnik <small>*</small>	0.94102	71	Mon, 05 May 2014 19:27:34 (-0h)
3	↓2	Ildefons Magrans <small>‡ *</small>	0.94063	21	Sun, 04 May 2014 13:47:26 (-0.3h)
4	↓2	Lukasz 8000	0.93956	101	Mon, 05 May 2014 15:54:48 (-18.1h)
5	↓2	Lejlot & Rafal <small>👤</small>	0.93826	97	Mon, 05 May 2014 15:39:39 (-20.9h)
6	—	Sium	0.93711	28	Mon, 05 May 2014 21:45:26 (-0.2h)
7	↓3	Alexander N & vopern <small>👤</small>	0.93666	7	Sat, 03 May 2014 23:46:07
8	—	gaucho81	0.93385	43	Sun, 04 May 2014 21:48:37 (-30.2h)
9	↑8	killertom	0.93011	13	Mon, 05 May 2014 12:50:08
10	new	dhanson	0.92885	6	Mon, 05 May 2014 21:02:20
11	↓2	DJMN <small>👤</small>	0.92609	20	Mon, 05 May 2014 19:44:13
12	↓2	Gideon & Alex <small>👤</small>	0.92420	48	Mon, 05 May 2014 16:16:57 (-19.7h)
13	↓1	Sandro	0.92039	18	Mon, 05 May 2014 23:15:48 (-8.7h)
14	↑5	Selfish Gene	0.92039	20	Sun, 04 May 2014 16:38:44
15	↑7	Nitai Dean	0.91945	3	Mon, 05 May 2014 12:43:11









## **Analysis of methods used by the participants:**

Deep convolutional neural networks

State selection

Multivariate logistic regression of inferred spike trains

Inverse covariance matrix

Random forests and gradient boosting machines

Network deconvolution

...

## **Checking for robustness of the methods**

**Pool together the different approaches (wisdom of crowds)**

**Code from the winning teams is publicly available with open sources licenses (and all the data associated with the challenge) <http://www.kaggle.com/c/connectomics>**

## Neuronal cultures

Useful tool to test concepts and properties related to the connectome in a well controlled environment

## Challenges

A different approach to collaborative research

Universitat de Barcelona



Jordi  
Soriano



Sara  
Teller



Jaume  
Casademunt

Max Planck Institute for Dynamics and Self-Organization

Olav  
Stetter



Demian  
Battaglia



Theo  
Geisel



**Isabelle Guyon**, ChaLearn, California, USA

**Alexander Statnikov**, New York University, Langome Medical Center, NY, USA

**Bisakha Ray**, New York University, Langome Medical Center, NY, USA

**Mehreen Saeed**, Department of Computer Science, FAST, National University of Computer & Emerging Sciences, Lahore Campus, Pakistan