If you have your PC and want to follow along, download slides:

http://mybinder.org/repo/msarvestani/cni-jc

Allen Brain Observatory Dataset

Madineh Sedigh-Sarvestani

CNI JC @ Upenn

Oct 2016

[Most slides are from Allen Institute's Marina Garrett, or the Observatory website [observatory.brain-map.org/]

Observatory Team @ Allen

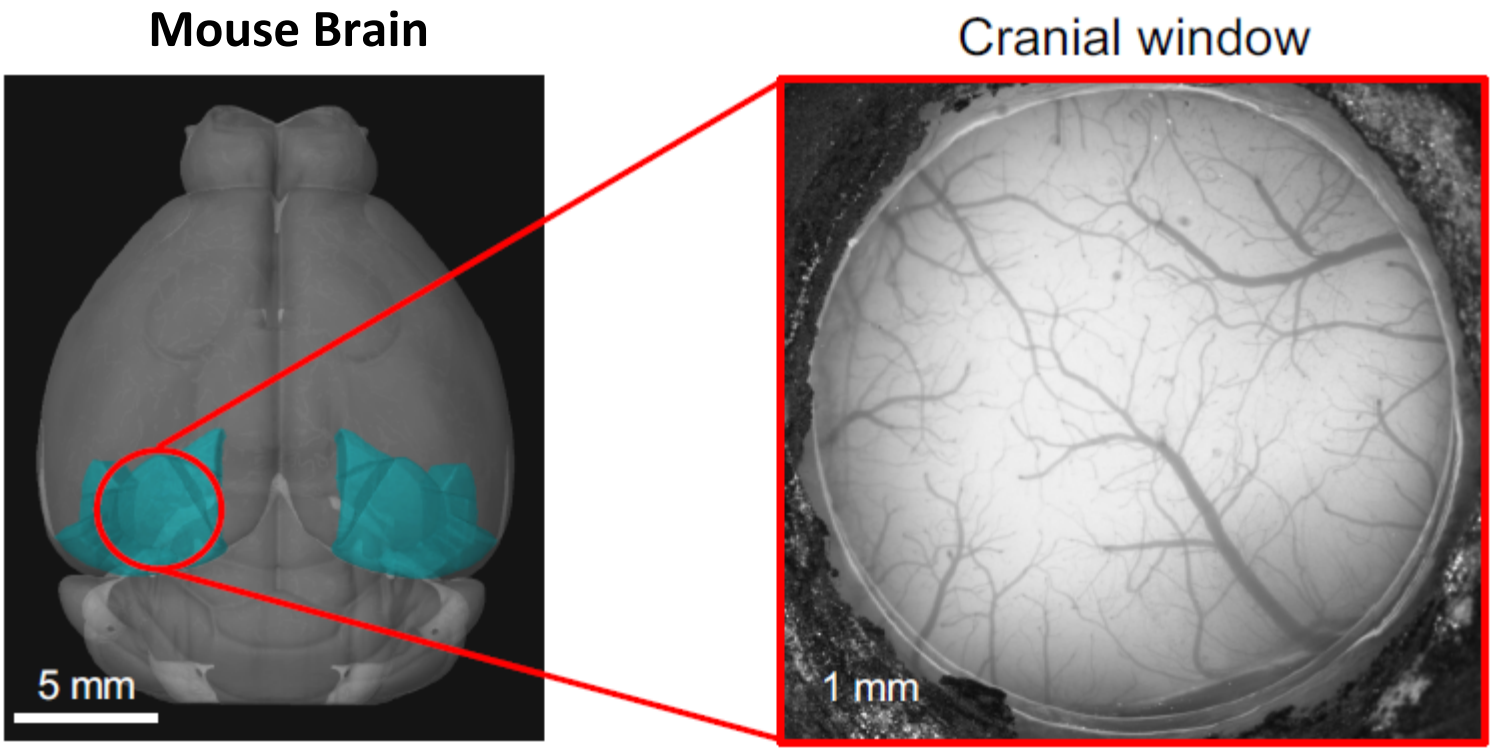
Saskia de Vries

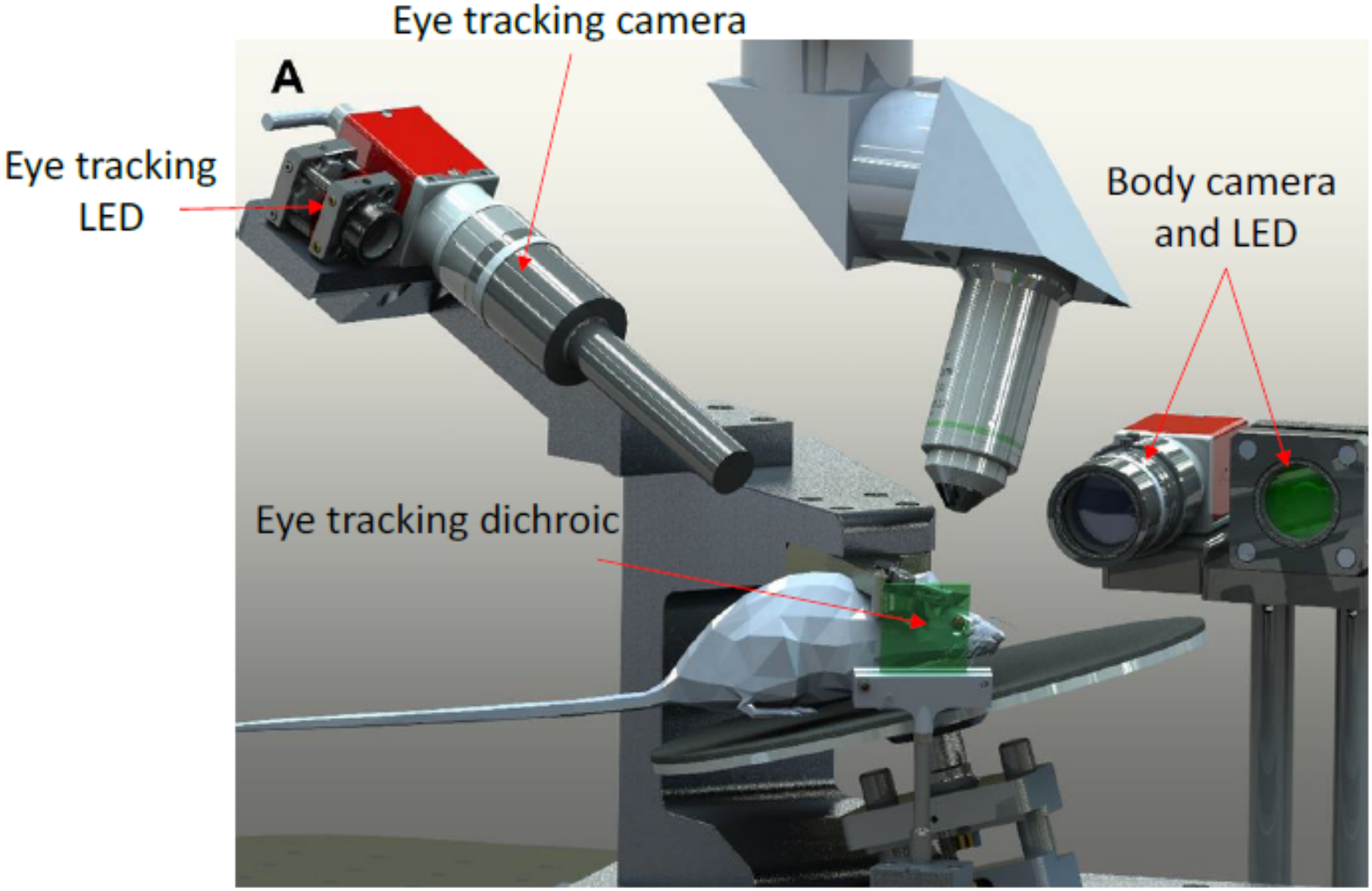
Marina Garrett

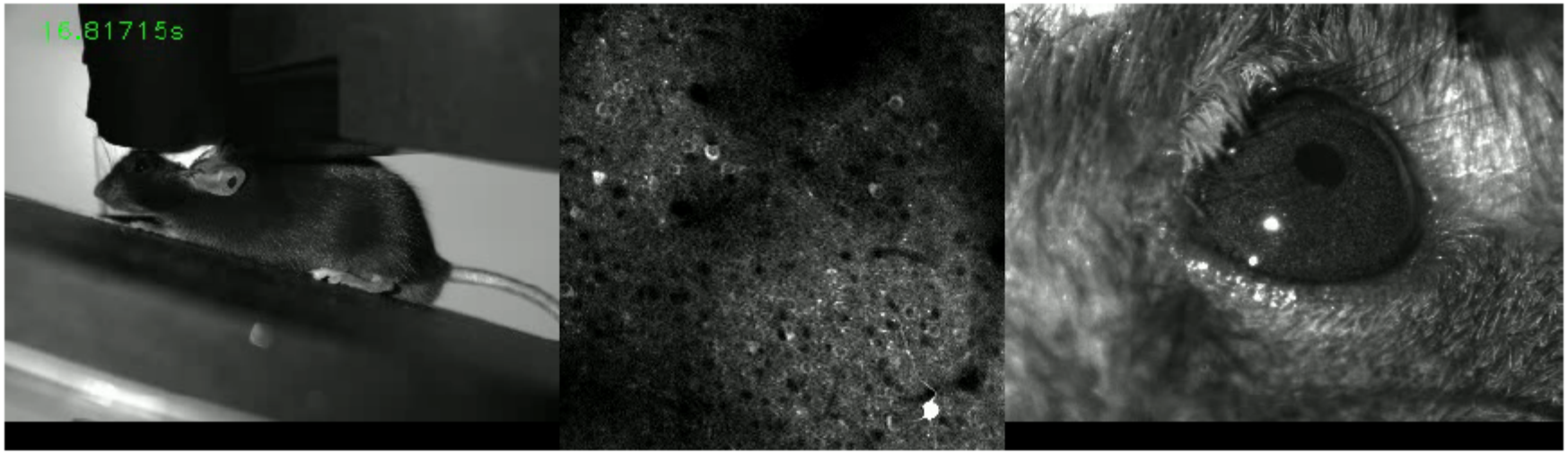
Michael Buice

+ many others

A ‘Window’ into the Brain




A
Eye tracking camera
Eye tracking LED
Body camera and LED
Eye tracking dichroic



One experiment session - AL – Cux2 – Layer 2/3

Awake, head-fixed mice, looking at visual stimuli.

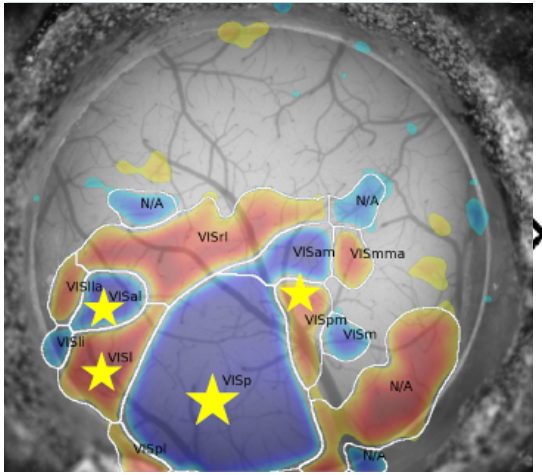
2P calcium fluorescence responses of hundreds of neurons.

+ running speed
Eye video
Mouse behavior

Genetic tools (Cre-lines x GCamp) are used to make specific cell types glow. Observatory dataset uses mice from 4 cre-lines (all exc). 7 more (exc/inh) planned for release.

A Rich Dataset

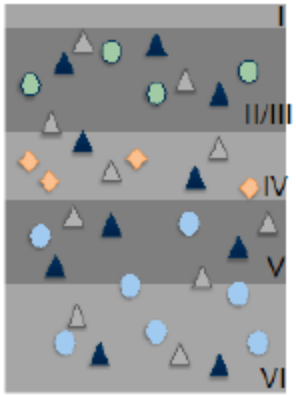
Cortical Visual Areas



4 Visual areas

×

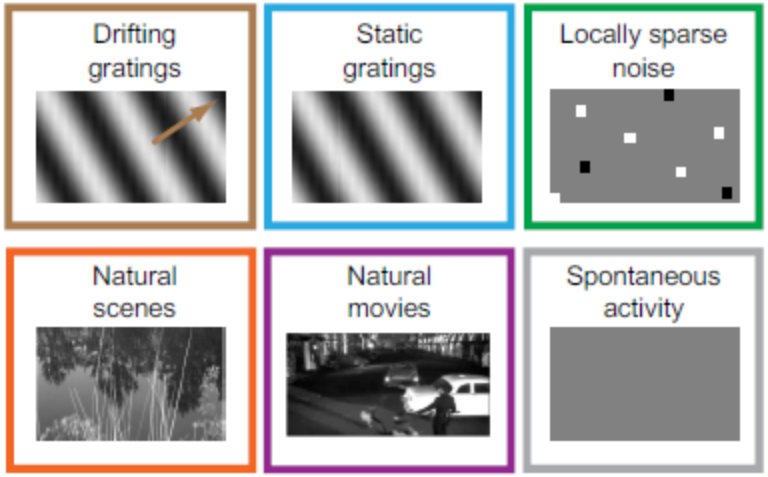
Cortical Layers
Cre Lines



4 cre-lines

×

Visual Stimuli

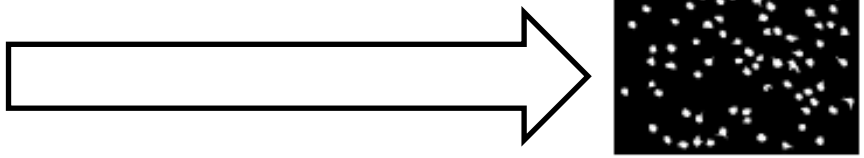


Hypothesis-free

A Rich, Standardized, Dataset

Quality control throws out bad data

2P Data Generation



- Motion correction
- Segmentation (find cells)
- Registration (match cells)
- Fluorescence extraction
- Background subtraction
- Data pre-processing (temporal alignment, etc)
- Compute df/f
- Compute stimulus-specific response features

All raw (pre-processed) data also available.

Pre-calculated Response Features

- Stimuli, shown in three 1 hour sessions

- Receptive field
- Response reliability for each stimulus type
- Orientation/direction selectivity
- Preferred: tf, sf, orientation, natural image frame
- Modulating by running

You can access some of the data (meta-data and extracted features) from the web. The rest (raw, post-processed, features) are accessible through a python package.

Accessing the Data (Web)

- Web: observatory.brain-map.org

Accessing the Data (Python)

- AllenSDK python package (toolbox) for downloading raw and processed data

- Start with this example jupyter notebook

A Jupyter/Python notebook is just a web app that lets you interactively run python code, and look at the output.

http://jupyter.org/

Accessing the Data (Python)

- Run the notebook interactively (binder)

http://mybinder.org/repo/msarvestani/cni-jc

Data Format

- Neurodata Without Borders (NWB).
  - HDF5 file
  - Includes stimulus data and metadata
- Used for CRCNS ephys data sets:
  - https://crcns.org/
- This paper has code snippets for reading;writing NWB data into matlab or python

What to do with all this data?

You could:

1) benchmark various motion correction/ spike-extraction algorithms

2) Validate previous work on bigger dataset

3) Test new theories (running?)

4) Use it for teaching

Observatory Data *Not* Good for:

- High temporal resolution (Calcium imaging)
  - Imaging frame rate is 30 Hz
- For now: anything requiring precise spatial position on retina
  - Eye movement (1/4 RF width) not controlled for, until future release

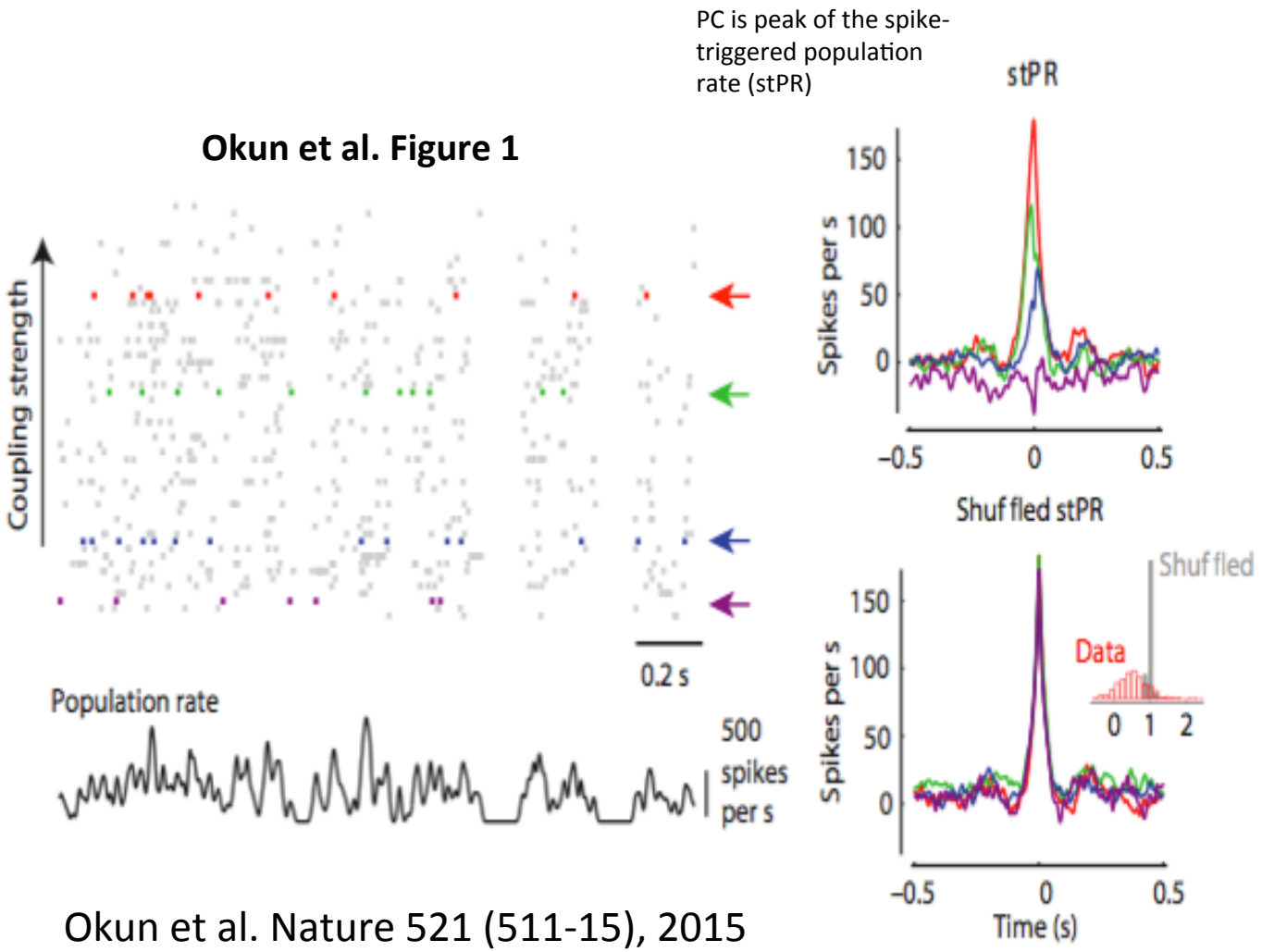
Observatory Data Good for:

- Response variability with: areas, cre-lines, layers, running, pupil diameter (extract)
- Modeling signal and noise variability with brain state (Scholvinck 2015+)
- Encoding with correlations (Pillow 2008+)
  - Also as a function of tuning similarity (sign-rule?)
- Decoding with correlations
  - Does shuffling trials reduce performance?

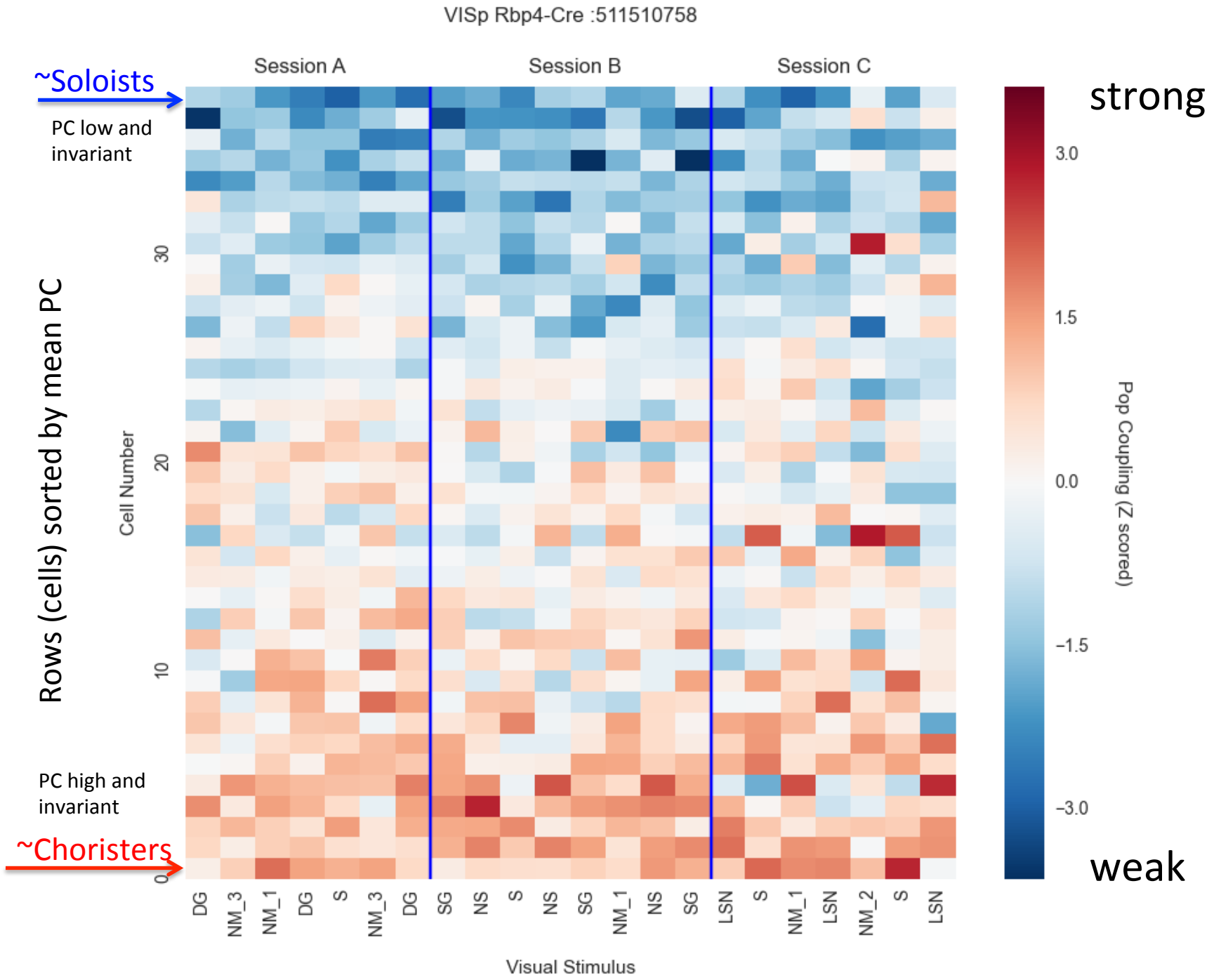
Population Coupling: an invariant neuronal property?

Pop coupling: correlation between each cell's activity and total population activity.

PC is peak of the spike-triggered population rate (stPR)



Okun et al. Nature 521 (511-15), 2015


VISp Rbp4-Cre :511510758
Session A
Session B
Session C
~Soloists
PC low and invariant
Rows (cells) sorted by mean PC
PC high and invariant
~Choristers
Cell Number
0
10
20
30
DG
NM_3
NM_1
DG
S
NM_3
DG
SG
NS
S
NS
SG
NM_1
NS
SG
LSN
S
NM_1
LSN
NM_2
S
LSN
Visual Stimulus
strong
3.0
1.5
0.0
−1.5
−3.0
weak
Pop Coupling (Z scored)

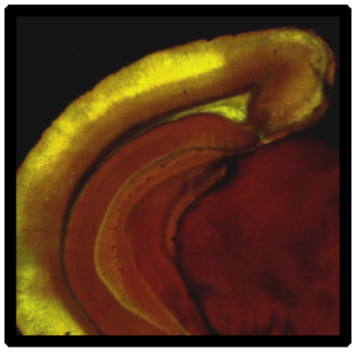
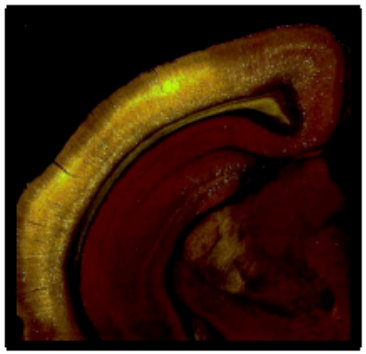
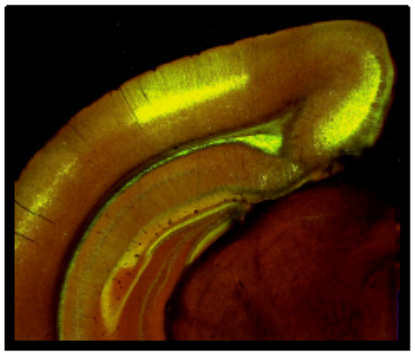
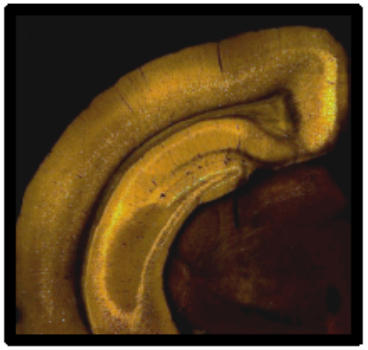
Slides and Jupyter notebook:

https://github.com/msarvestani/CNI-JC

Much More info on Observatory:

http://observatory.brain-map.org/

Cre-lines

Cux2-CreERT2	Rorb-IRES2-Cre	Scnn1a-Tg3-Cre	Rbp4-Cre
			
Layer 2/3 and 4	Layer 4	Layer 4	Layer 5

Cross with reporter lines that express the genetically encoded calcium indicator GCaMP6 in Cre positive cells

Upcoming Data Dumps

area	V1				LM				AL				PM				AM?				RL?			
layer	2/3	4	5	6	2/3	4	5	6	2/3	4	5	6	2/3	4	5	6	2/3	4	5	6	2/3	4	5	6
Cux2	8	6			6	6			6	6			8	6			6	6			6	6		
Emx1-S	6	6	6																					
Emx1-F	6	6	6		6	6	6		6	6	6		6	6	6		6	6	6		6	6	6	
Scnn1a		6																						
Nr5a1		6				6				6				6				6				6		
Rorb		6				6				6				6				6				6		
EXC			6				6				6				6				6				6	
EXC			6				6				6				6				6				6	
Rbp4			6				6				6				6				6				6	
Ntsr1				6				6				6				6				6				6
Pvalb	6	6	6		6	6	6		6	6	6		6	6	6		6	6	6		6	6	6	
SST	6	6	6		6	6	6		6	6	6		6	6	6		6	6	6		6	6	6	

Green = June 2016
Yellow = October 2016
Orange = 2017

GCaMPf6f (Chen 2013)

Using the genetically encoded calcium indicator GCaMP6f to measure neural activity