



# LARGE-SCALE SPIKING NEURAL NETWORK MODELING OF PRIMATE CEREBRAL CORTEX

OSB workshop, 6 Sep 2019 | Sacha van Albada

Institute of Neuroscience and Medicine (INM-6), Jülich Research Centre



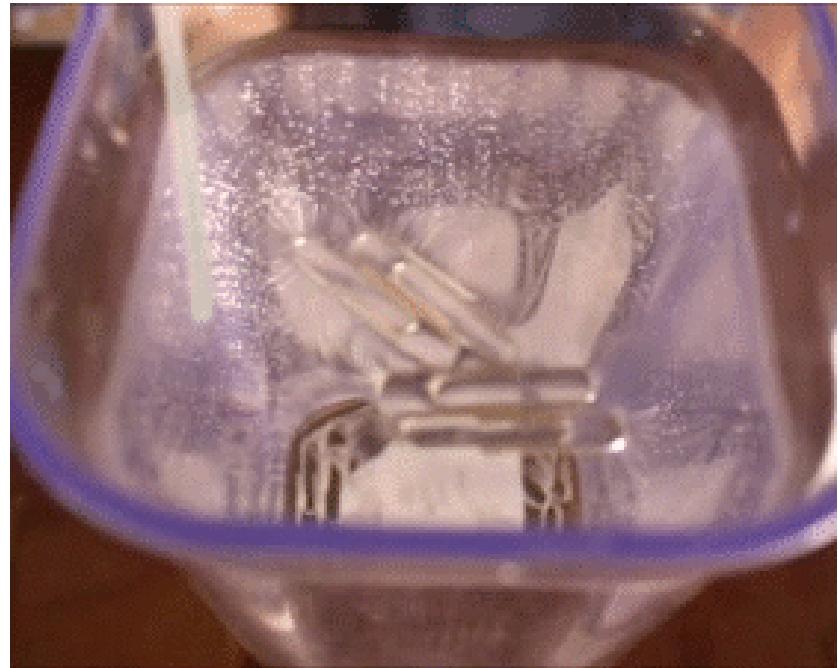
# WHY BASIC BRAIN MODELS

as a stepping stone toward understanding brain function



Explaining how a water strider stays afloat requires knowledge of a basic property of water: surface tension.

Analogously, we need a good basic model of the brain as a physical system to gain insight into its function and dysfunction.



In the wrong parameter regime (say, soapy water) we would predict that the water strider would sink.

# NEED FOR MULTI-SCALE MODELS: LINKS TO EXPERIMENT

brain-scale networks basis for various measures by forward modeling

mesoscopic measures

- local field potential (LFP)
- voltage sensitive dyes (VSD)

and macroscopic measures

- EEG, MEG
- fMRI resting-state networks

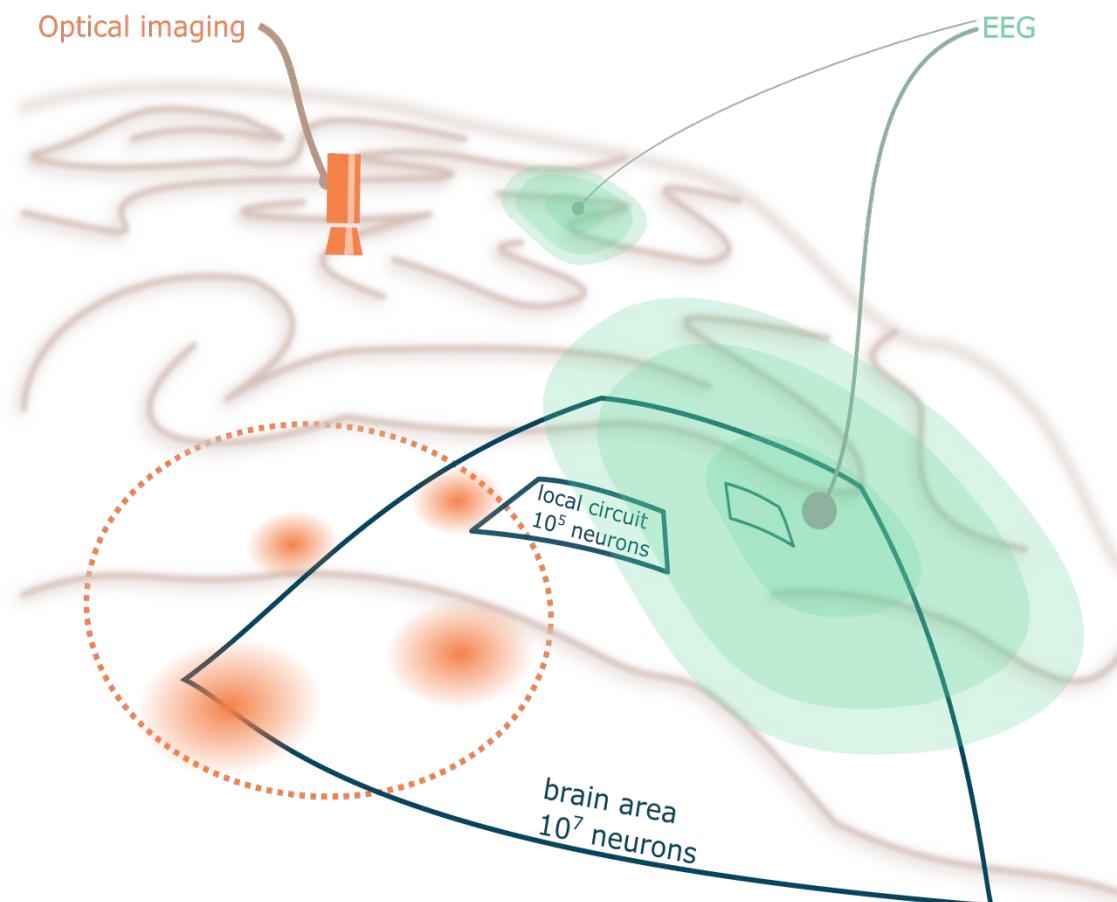
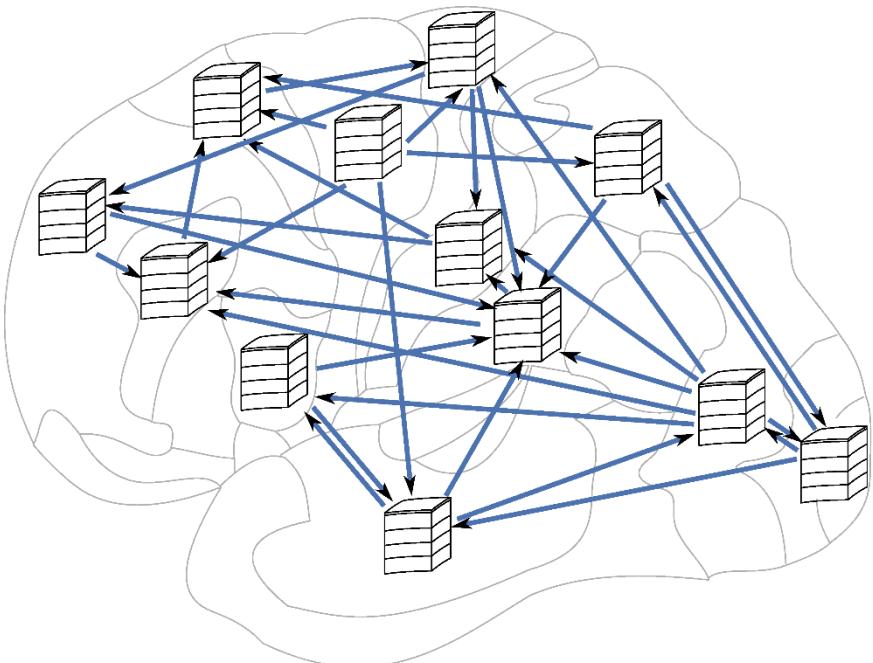
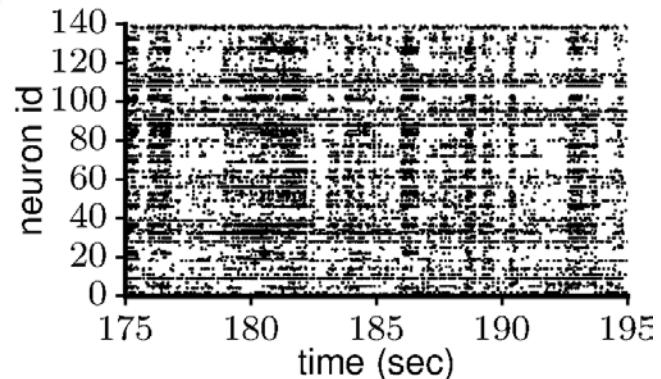


Figure by Susanne Kunkel

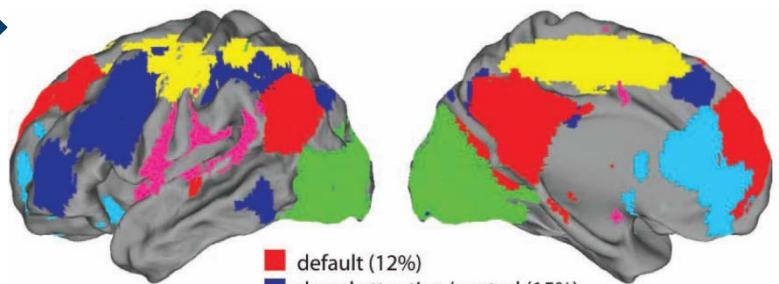
# GOAL



cortical connectivity



Chu et al. (2014) Vision Res

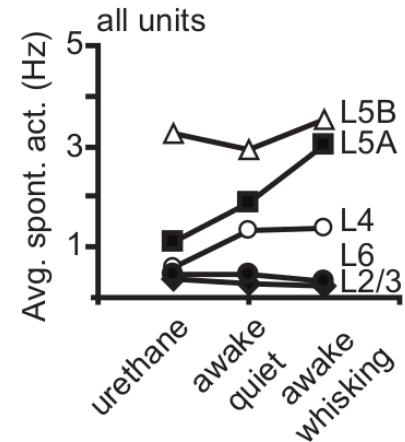
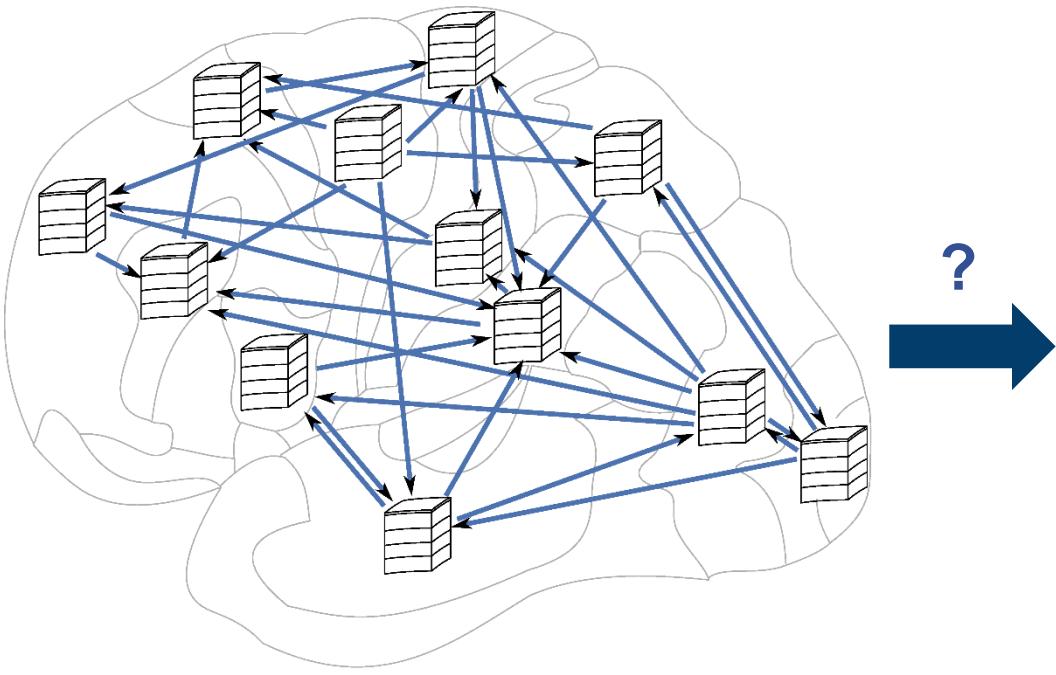


default (12%)  
dorsal attention/control (15%)  
visual (16%)  
auditory/phonology (6%)  
motor (14%)  
self-referential (10%)

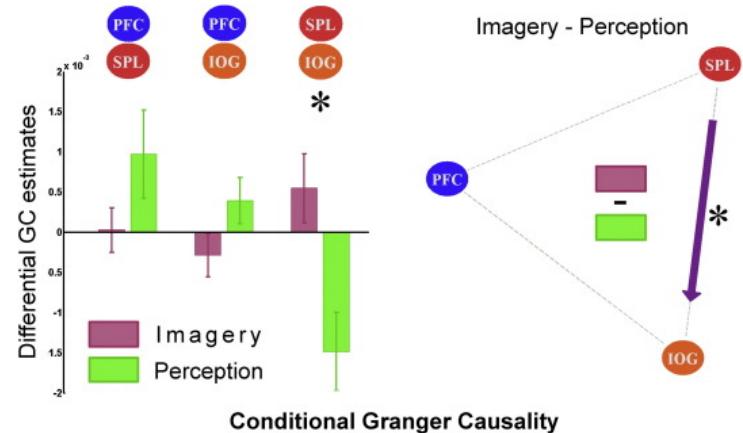
Deco and Corbetta (2011)  
*The Neuroscientist*

multi-scale resting-state dynamics

# GOAL



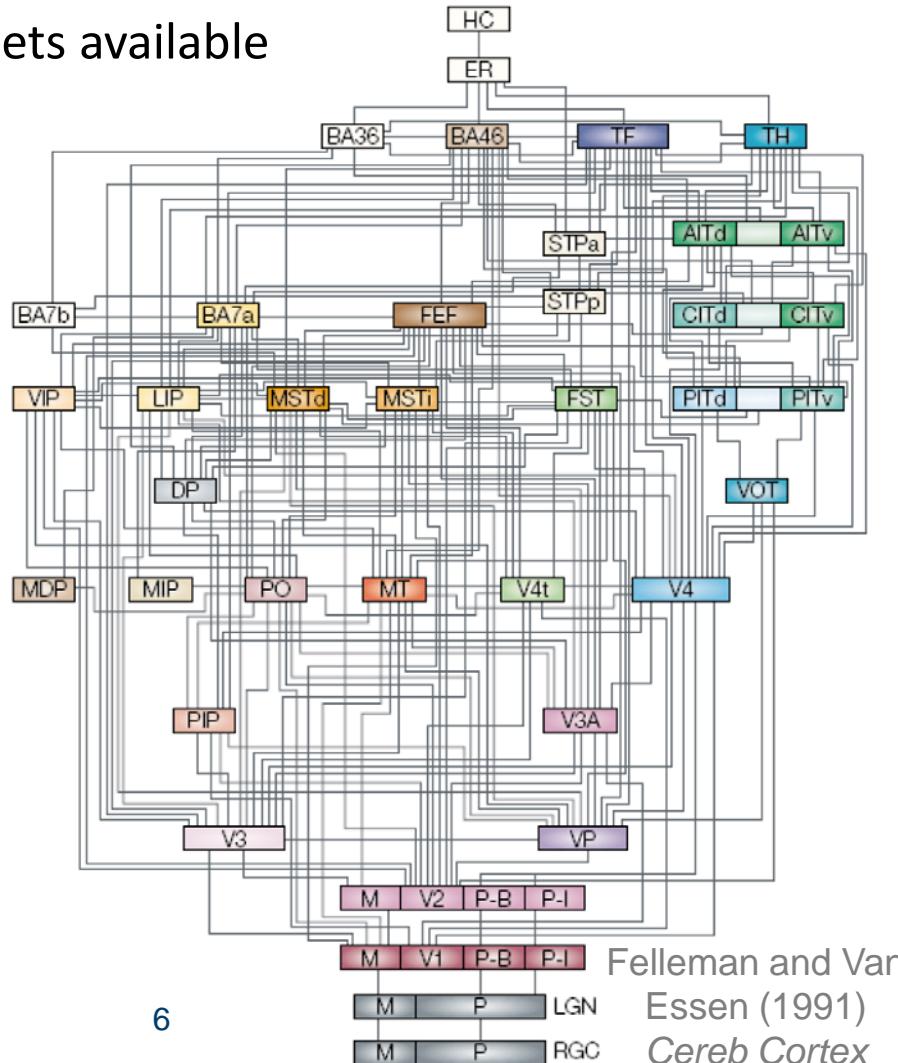
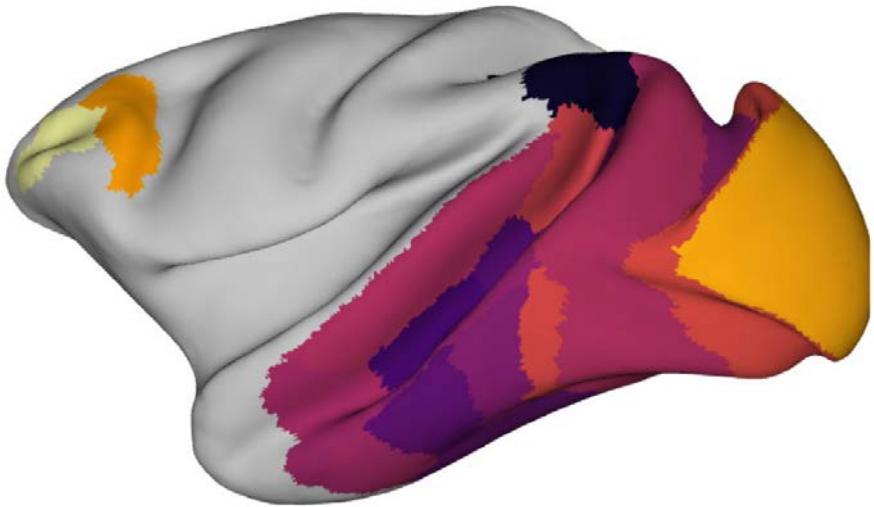
De Kock & Sakmann (2009) *PNAS*  
cell-type specific spike rates



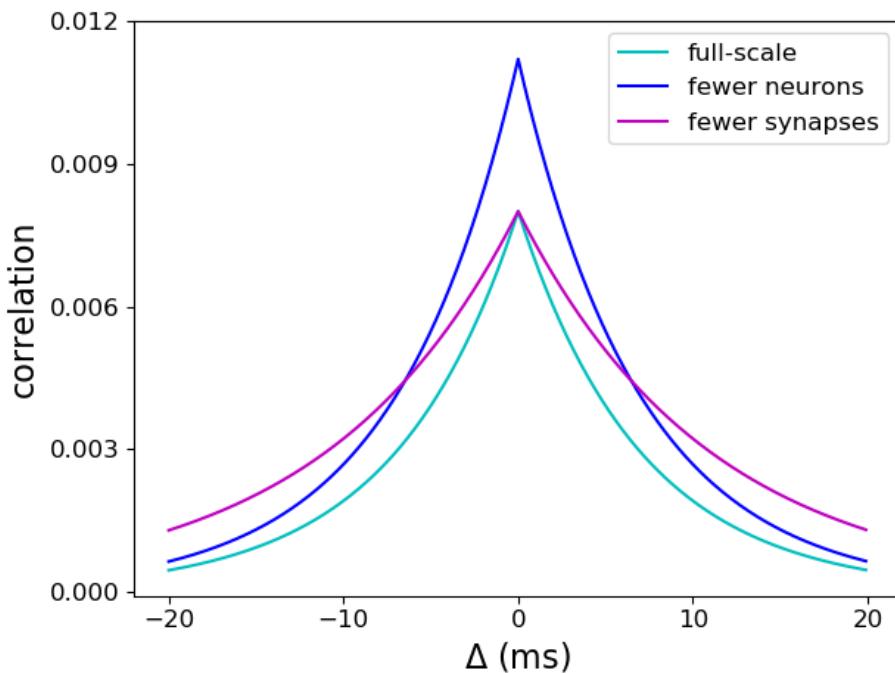
Dentico et al. (2014) *NeuroImage*  
inter-area propagation

# MULTI-AREA MODEL OF MACAQUE VISION-RELATED CORTEX

- rich anatomical and physiological data sets available
- stepping stone to human
- regularities of organization



# IRREDUCIBILITY OF NETWORK MODELS

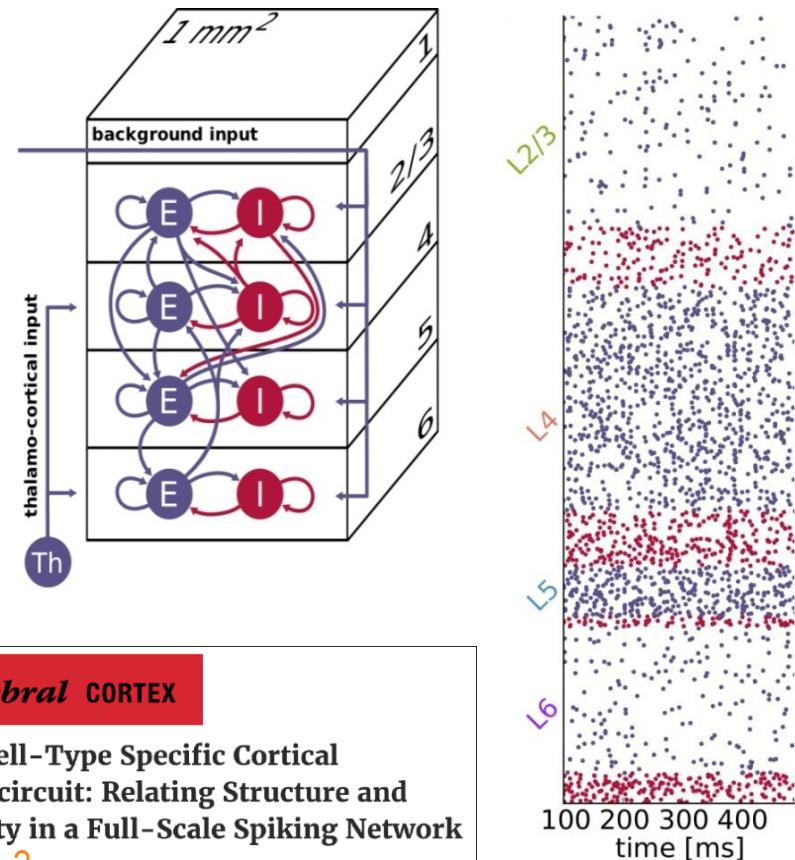


- downscaling changes dynamics
  - reducing number of neurons increases correlations
  - reducing number of synapses changes correlation shapes

van Albada SJ, Helias M, Diesmann M (2015) *PLOS CB*

# MINIMAL LAYERED CORTICAL NETWORK MODEL

- 1 mm<sup>2</sup> cortical surface
- excitatory (E) and inhibitory (I) populations of point neurons in each layer
- layer- and type-specific connection probability
- integrates knowledge of > 50 experimental papers



available as a part of NEST and PyNN, and at  
[www.opensourcebrain.org](http://www.opensourcebrain.org) Gleeson et al.  
(2019) *Neuron*

reproduced with Brian and NetPyNE/NEURON  
Shimoura et al. (2018) *ReScience*  
[https://github.com/ceciliaromaro/PD\\_in\\_NetPyNE](https://github.com/ceciliaromaro/PD_in_NetPyNE)  
ported to SpiNNaker

van Albada et al. (2018) *Front Neurosci*

## Cerebral CORTEX

The Cell-Type Specific Cortical Microcircuit: Relating Structure and Activity in a Full-Scale Spiking Network Model 

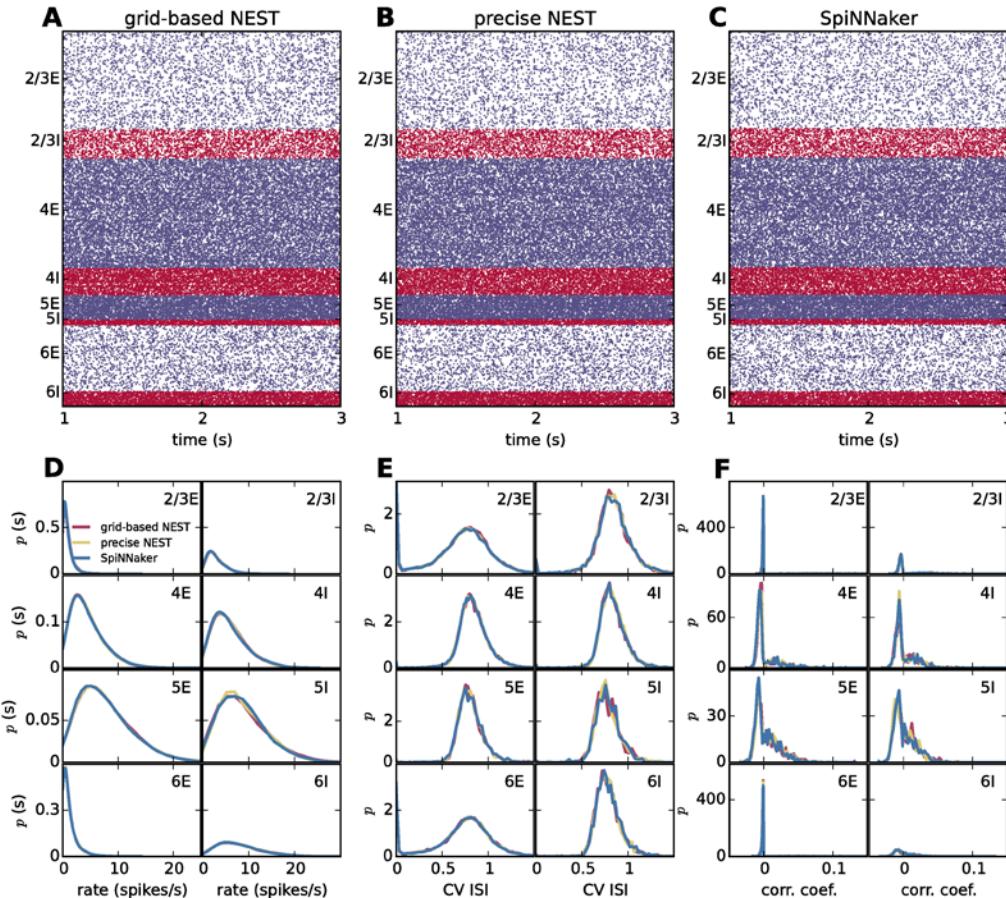
Tobias C. Potjans , Markus Diesmann

Cerebral Cortex, Volume 24, Issue 3, 1 March 2014, Pages 785–806,  
<https://doi.org/10.1093/cercor/bhs358>



# MICROCIRCUIT PORTED TO SPINNAKER

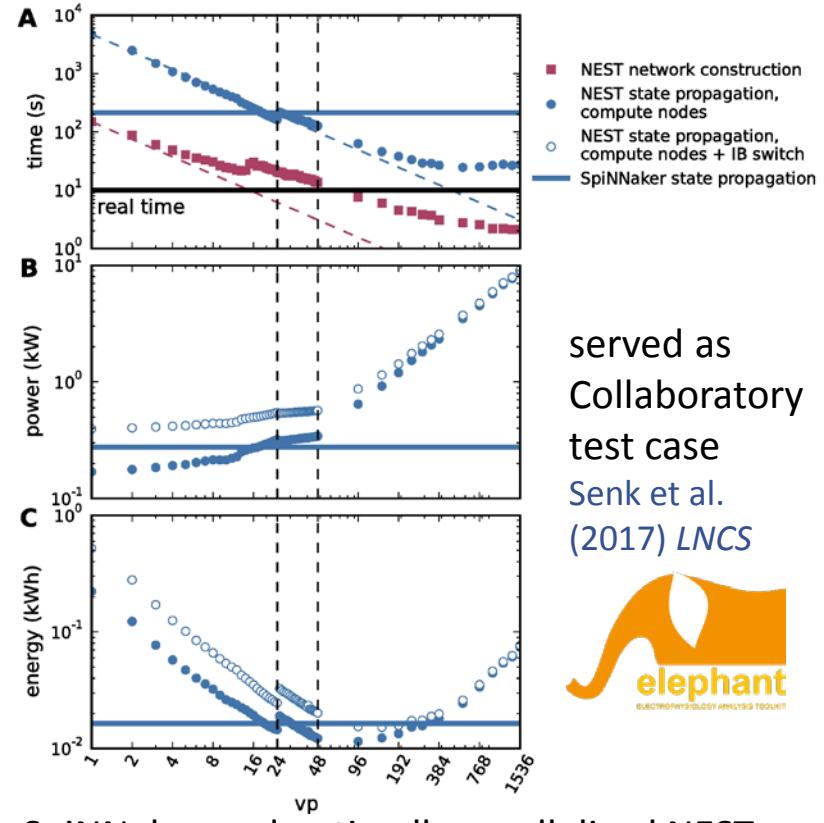
first full-density simulation of cortical microcircuit on SpiNNaker (6 boards)



van Albada, Rowley, Senk, Hopkins, Schmidt, Stokes, Lester, Diesmann, Furber (2018) *Front Neurosci*

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11 Sep 2019



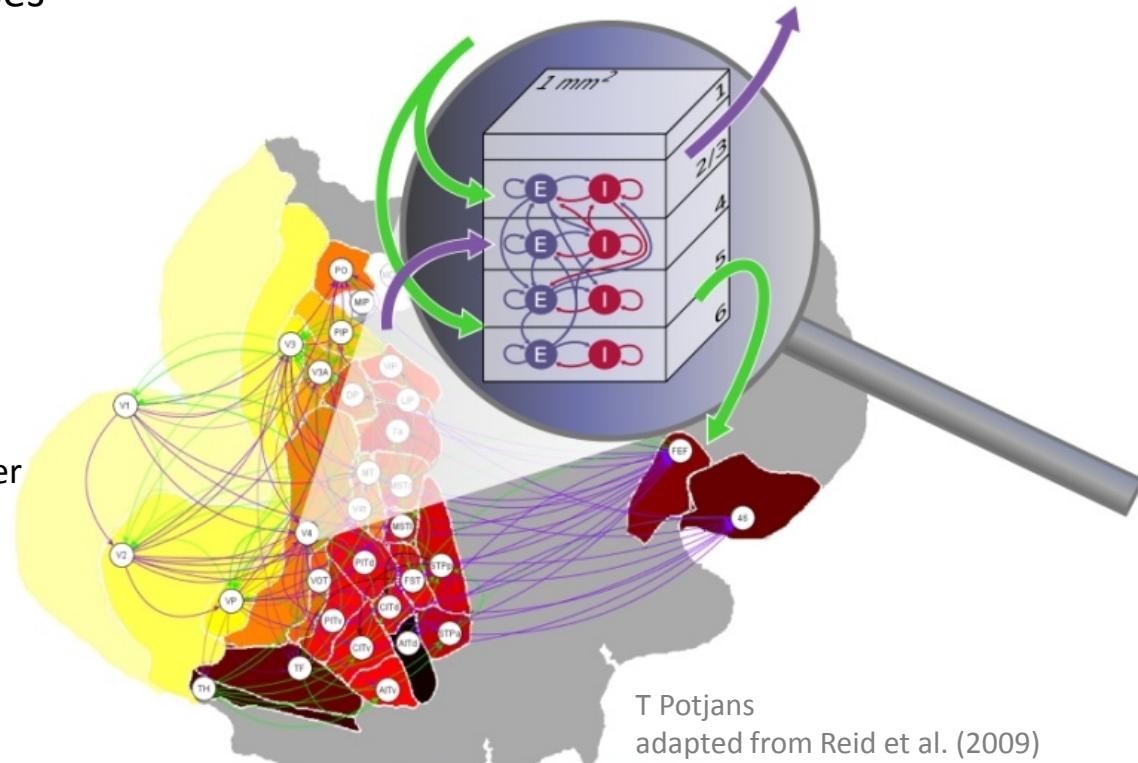
SpiNNaker and optimally parallelized NEST have comparable total energy consumption during run phase



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# MULTI-AREA MODEL OF MACAQUE VISUAL CORTEX

- 800 million neurons in one hemisphere
- 32 areas in Felleman & Van Essen parcellation
- representing each area by a  $1 \text{ mm}^2$  microcircuit
- $4 \cdot 10^6$  neurons and  $2.4 \cdot 10^{10}$  synapses
- simulated using NEST on Jülich supercomputers
  - $\sim 10^3$  MPI processes, multi-threaded
  - a few minutes for 1 s of simulation
  - largest version we ran:  $2 \cdot 10^7$  neurons
  - simulating all 800 million neurons would approximately fill an entire supercomputer

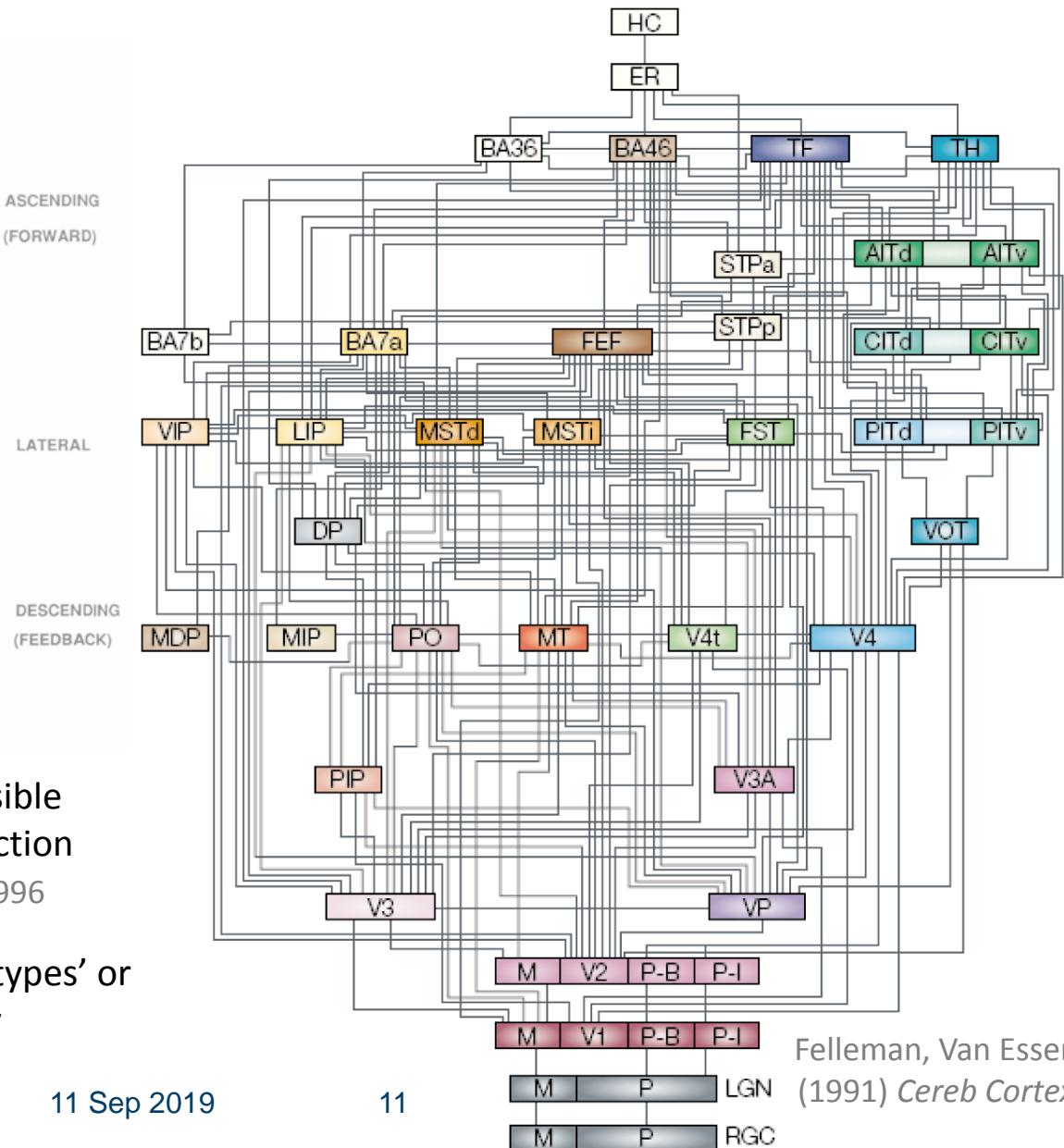
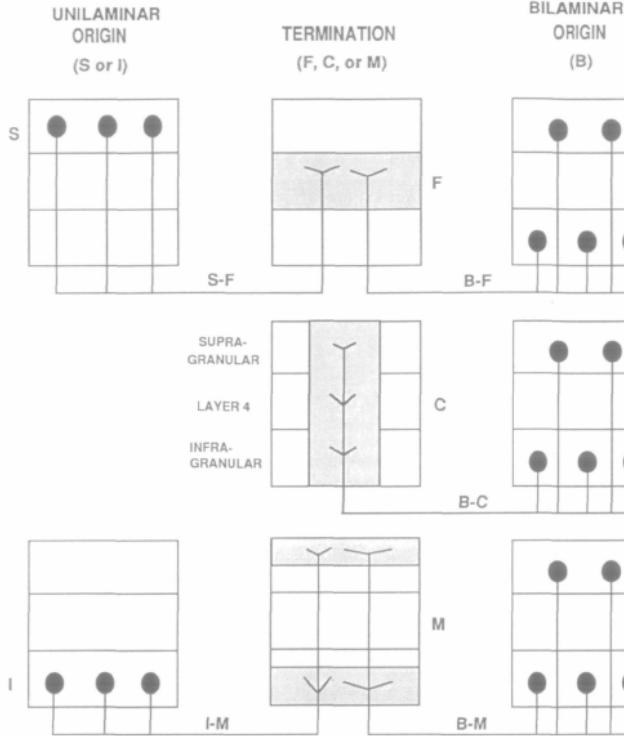


Schmidt M, Bakker R, Shen K, Bezgin G,  
Diesmann M, van Albada SJ (2018) *PLOS CB*

Member of the Helmholtz Association

T Potjans  
adapted from Reid et al. (2009)

# HIERARCHY OF VISUAL CORTICAL AREAS

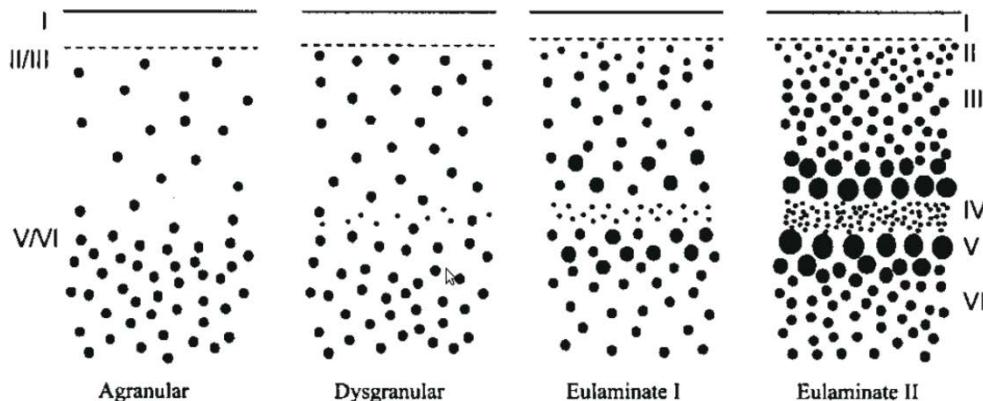


- this is only one of thousands of possible orderings fitting the pairwise connection patterns equally well Hilgetag et al., 1996
- alternatively, can use 'architectural types' or neuron densities to define hierarchy

# CORTICAL AREAS ARE NOT ALL THE SAME

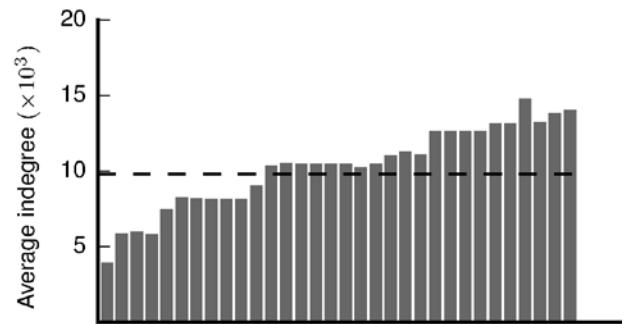
- architectural types
  - neuron densities and layer 4 thickness decrease up the hierarchy
  - total cortical thickness increases up the hierarchy

examples of architectural types



Dombrowski et al. (2001) *Cereb Cortex*

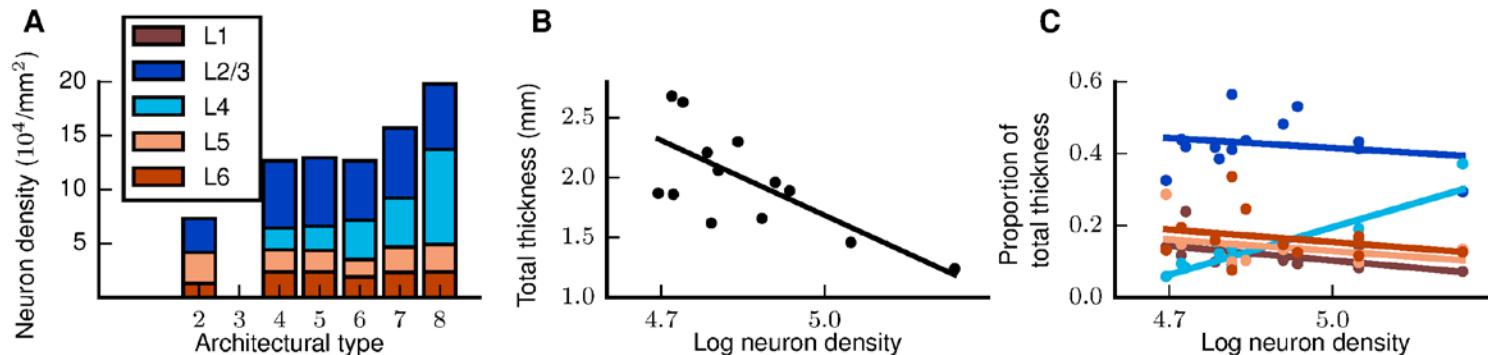
- synapse density remains roughly constant  
→ higher areas receive more synapses per neuron



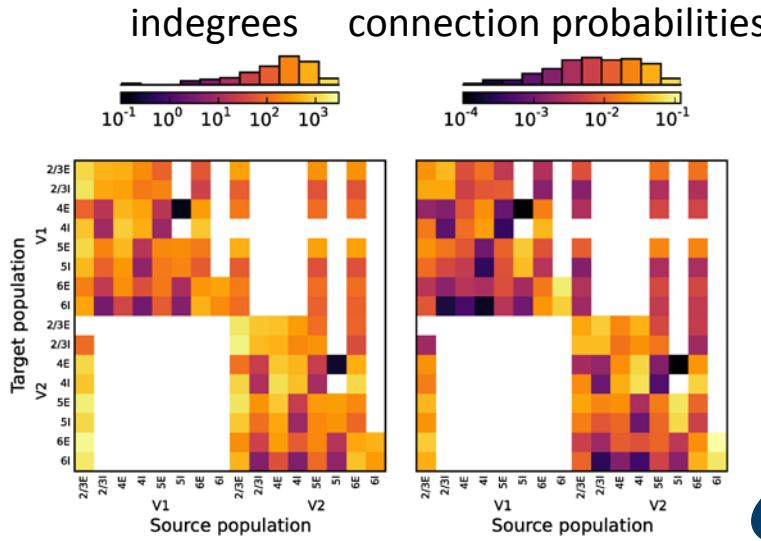
# DETERMINATION OF POPULATION SIZES

- total cortical thicknesses and overall neuron densities for 14 areas
- estimated for remaining areas based on architectural types
- reduction in L4 thickness toward higher areas based on micrographs from the literature

} Hilgetag et al. (2016)  
*NeuroImage*

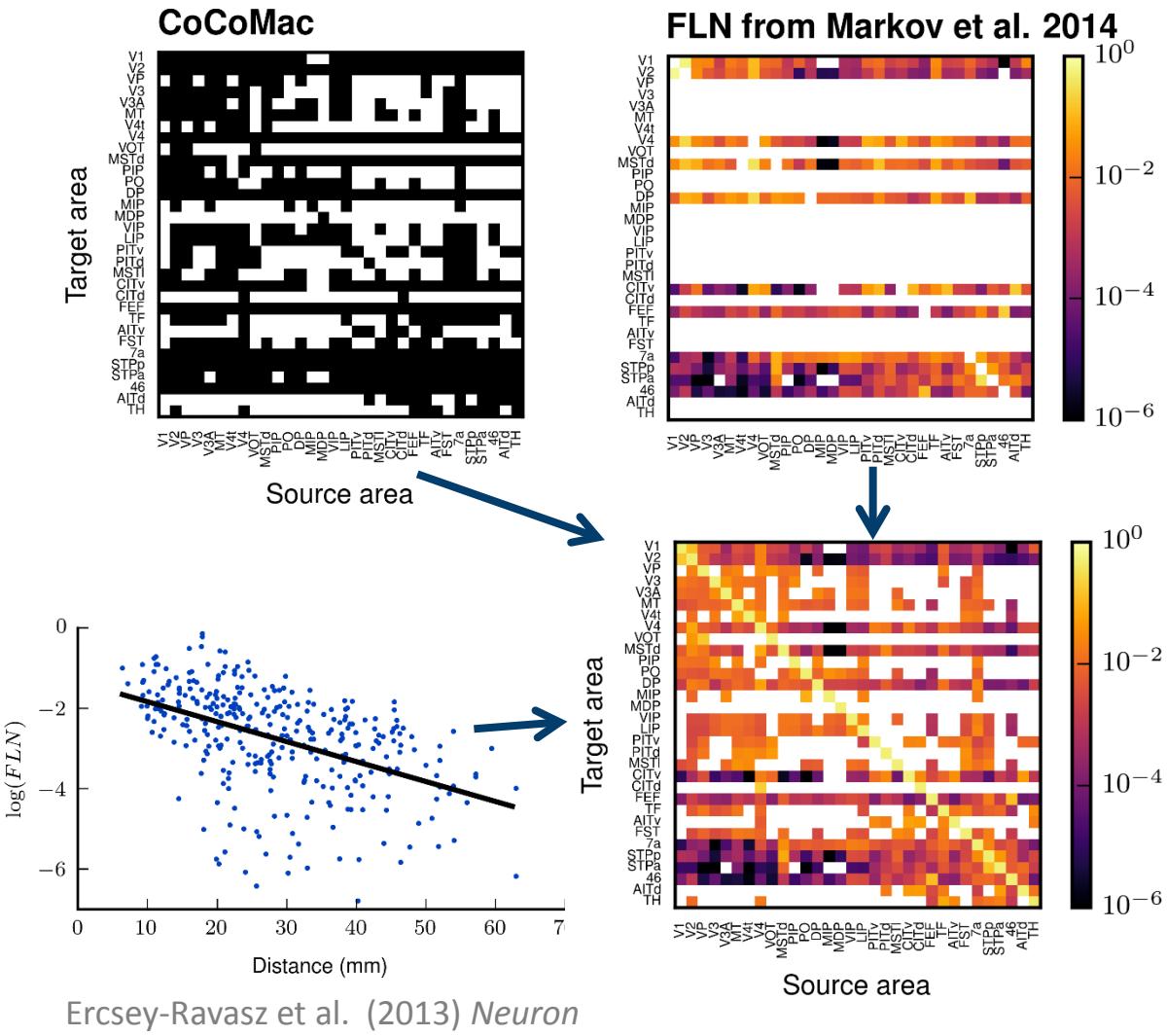


- knowing population sizes is important for simulations
- enables translating between different measures of connectivity

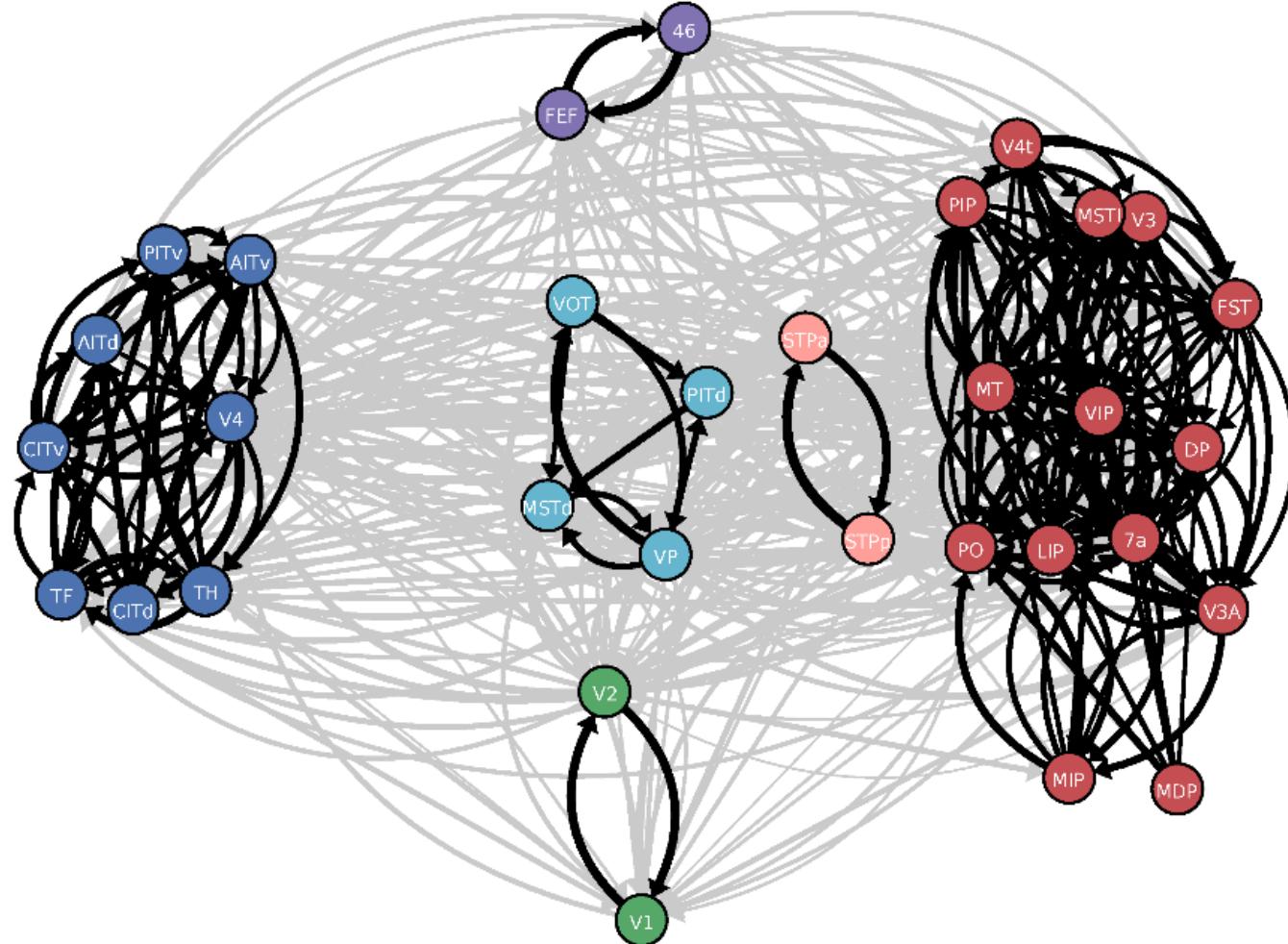


# CONNECTIVITY MAP FROM TRACING DATA

- partly binary, partly quantitative data
- connection probability decays with distance also for inter-area connections
- use this decay to estimate missing data based on distance between areas
- roughly 2/3 of area pairs are connected
- more important: connection density, spanning  $\sim 6$  orders of magnitude

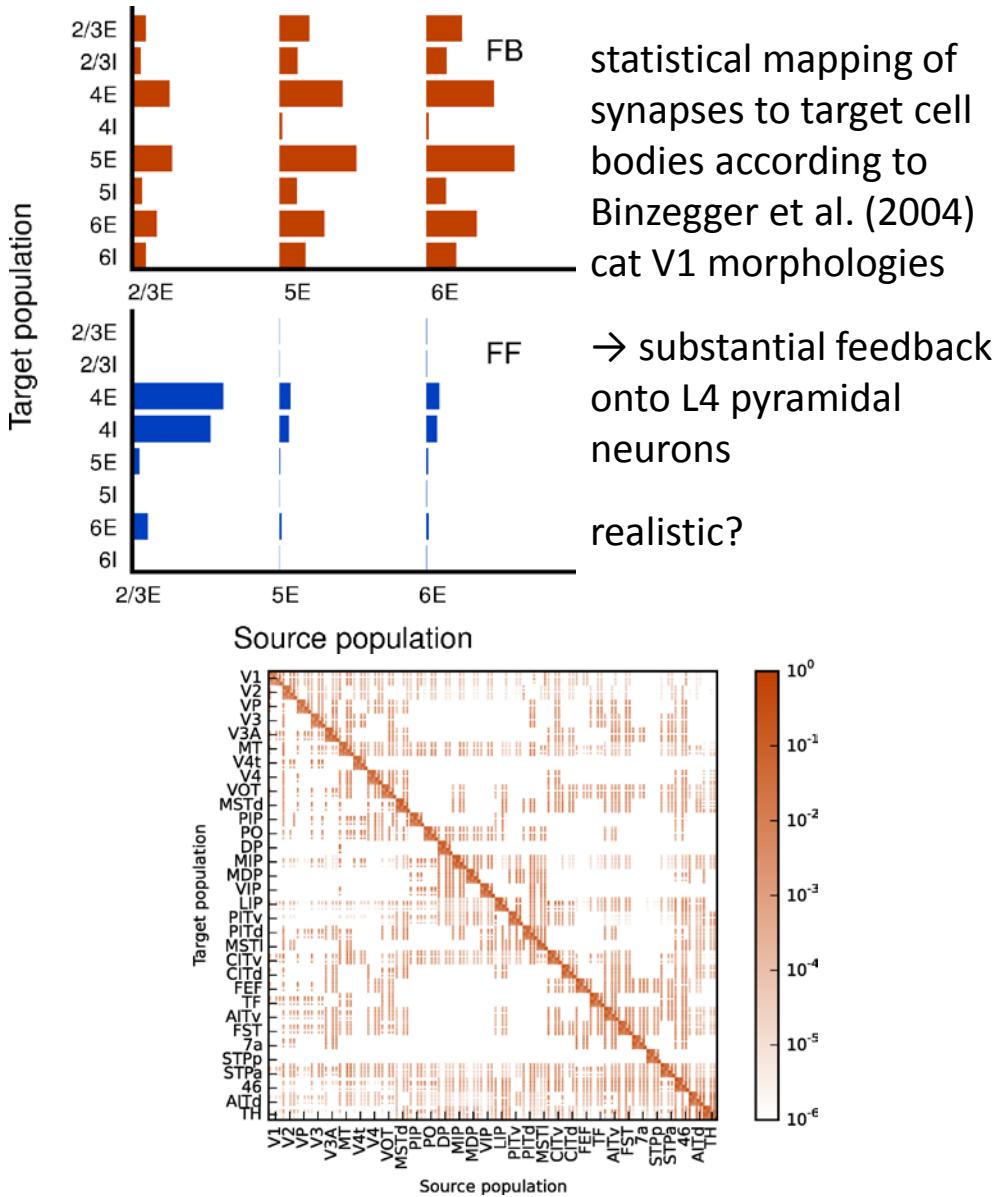
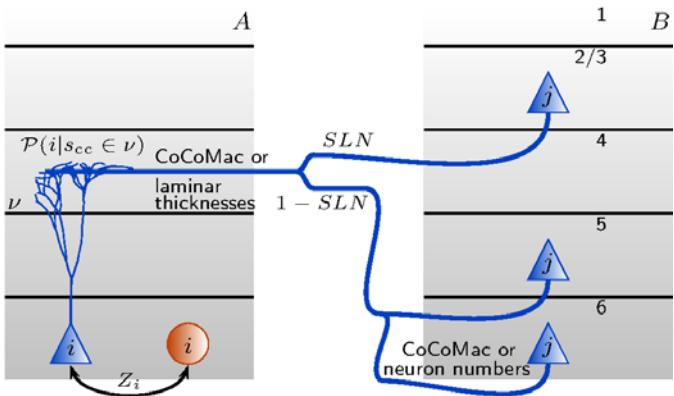
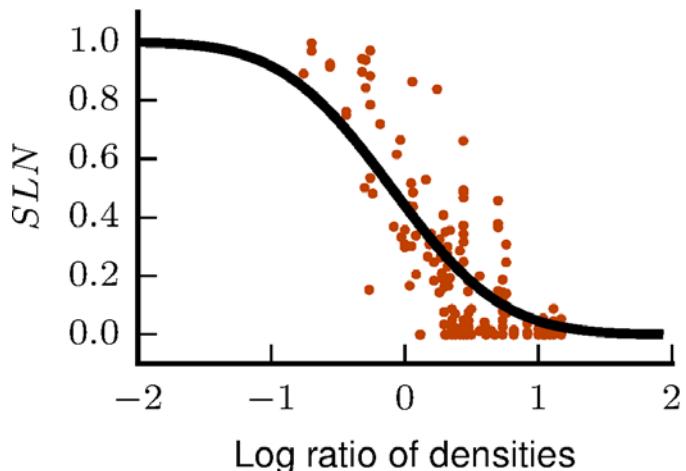


# PLAUSIBILITY CHECK



structural connectivity exhibits functionally relevant community structure

# LAMINAR PATTERNS

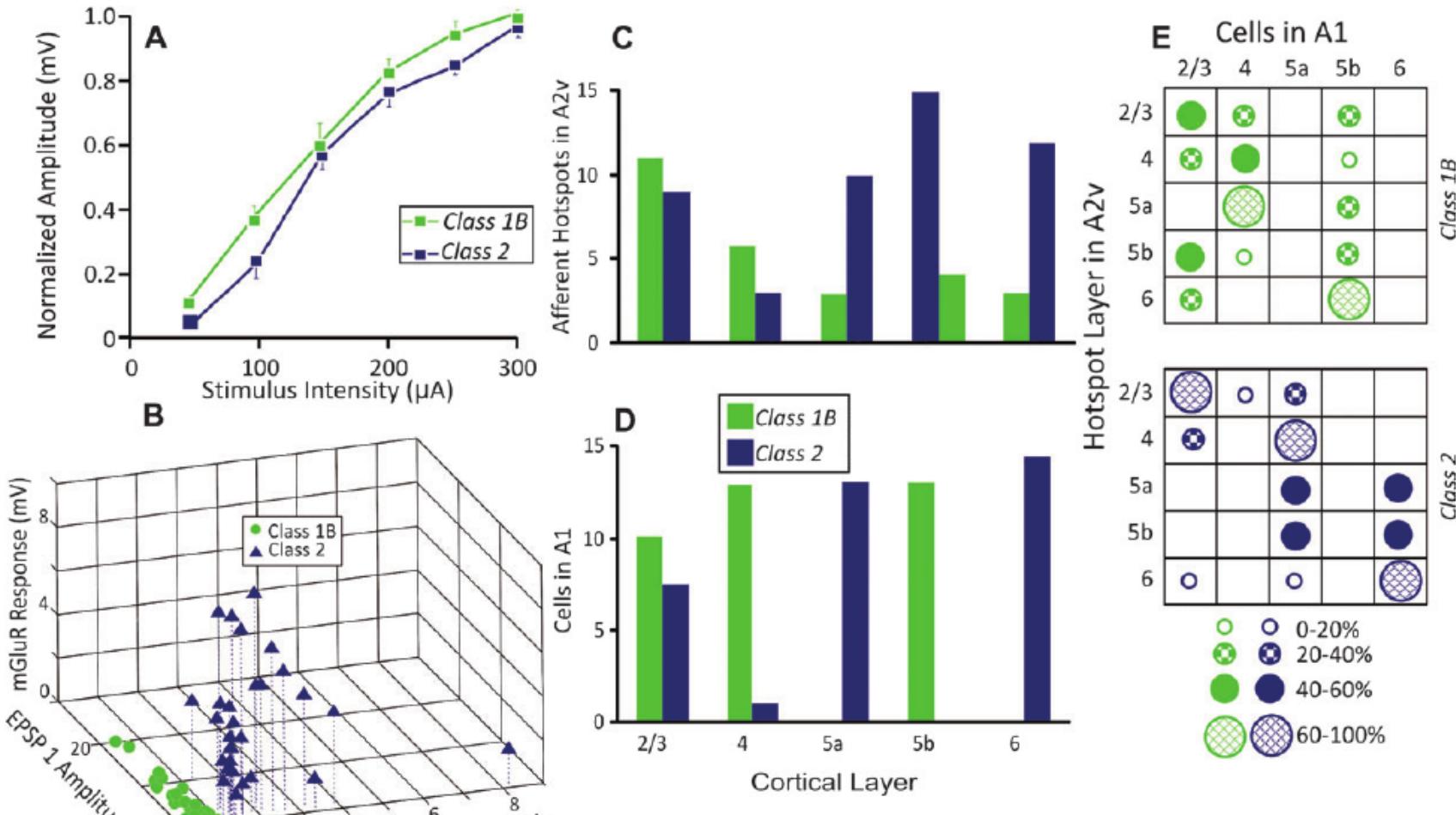


Schmidt M, Bakker R, Hilgetag CC, Diesmann M, van Albada SJ (2018) *Brain Struct Func*

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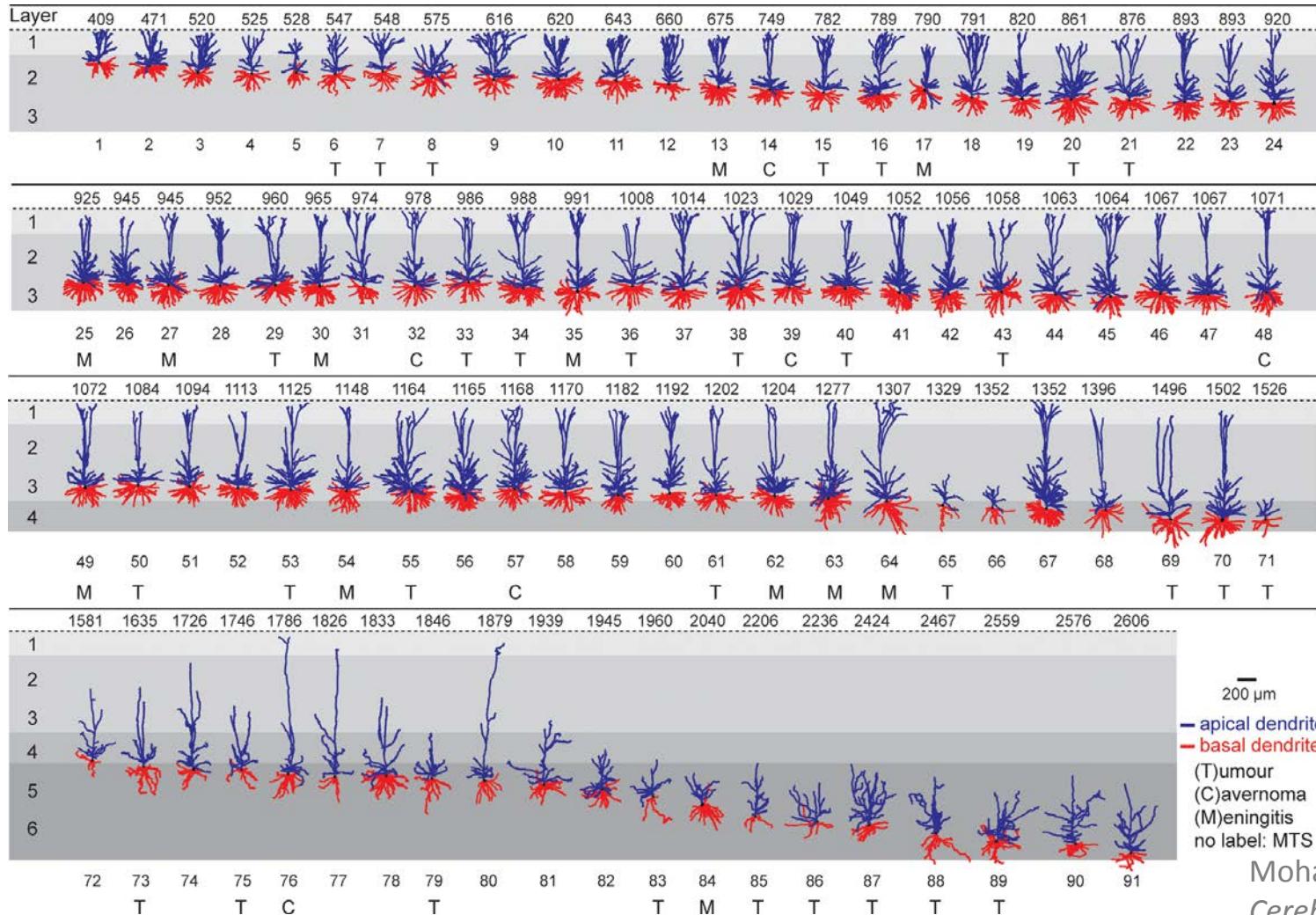
16

# FEEDBACK ONTO L4 NEURONS IN MOUSE



Covic & Sherman (2011) *Cereb Cortex*  
Glutamate uncaging in mouse auditory cortex

# HUMAN NEURON MORPHOLOGIES

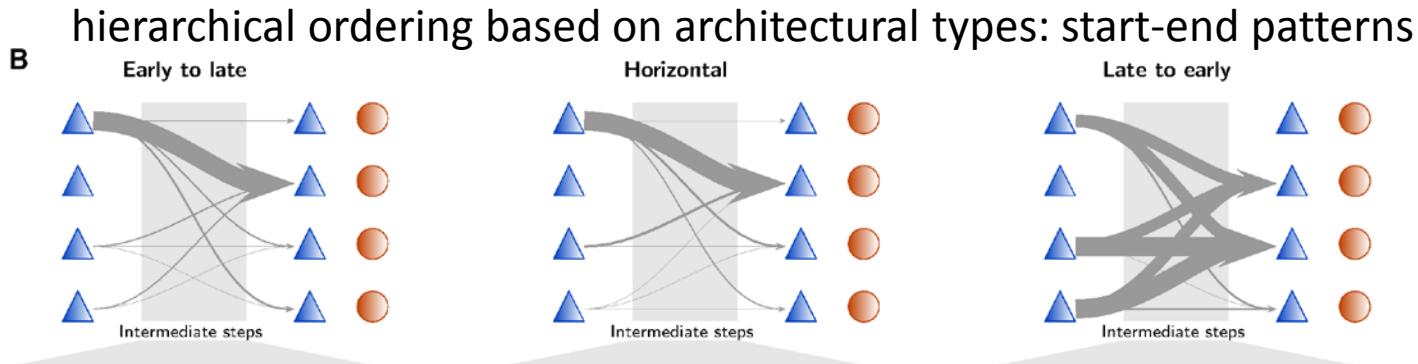
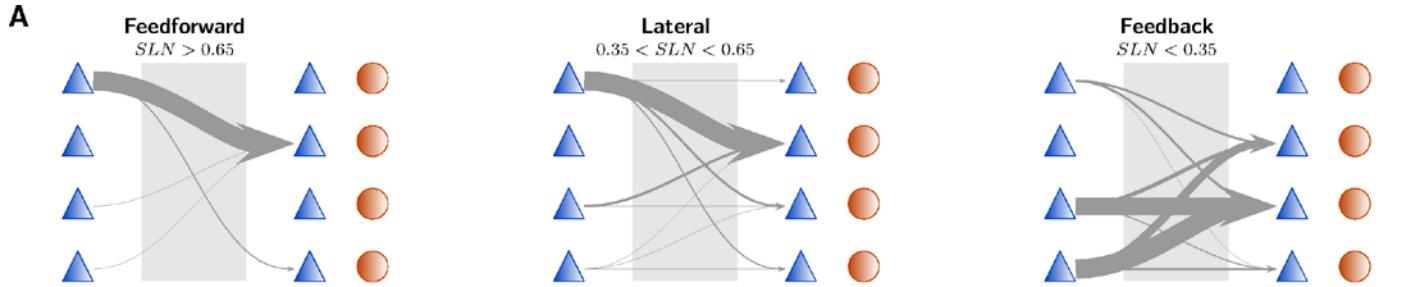


Mohan et al. (2015)  
*Cereb Cortex*

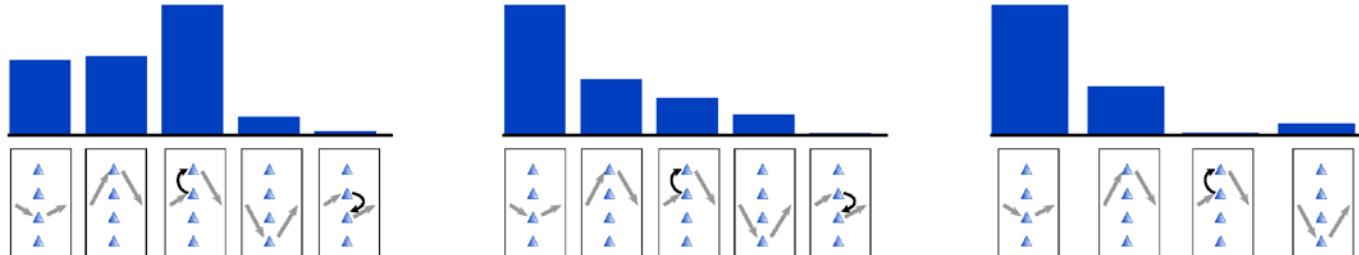


# LAYER-SPECIFIC STRONGEST PATHS

hierarchical ordering based on laminar source patterns: direct connections

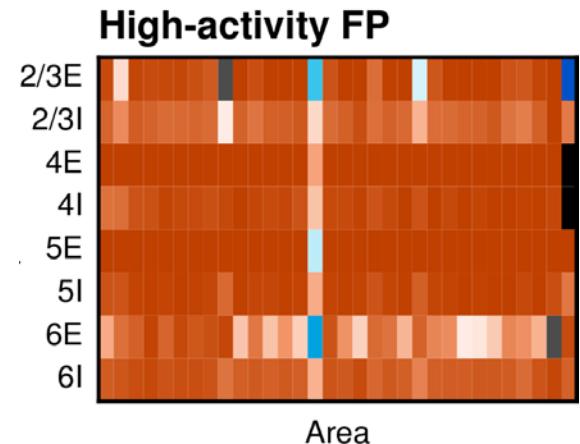
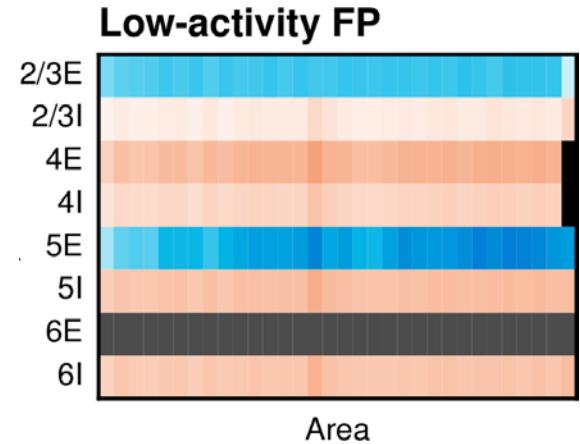
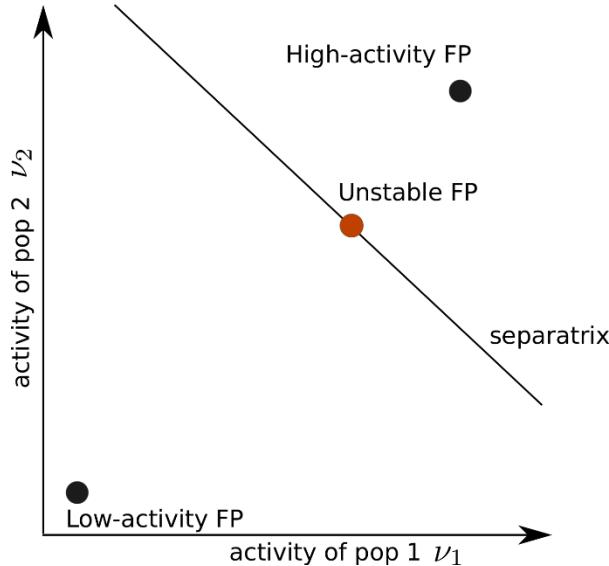
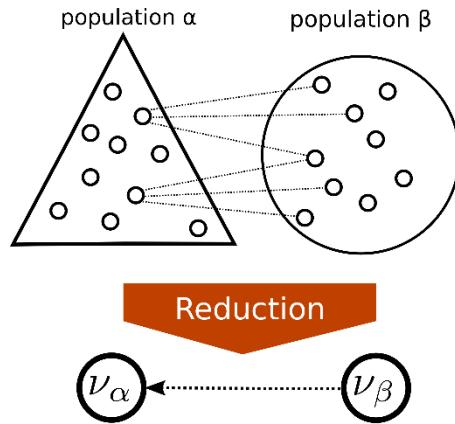


**c** laminar patterns in intermediate areas (when present)



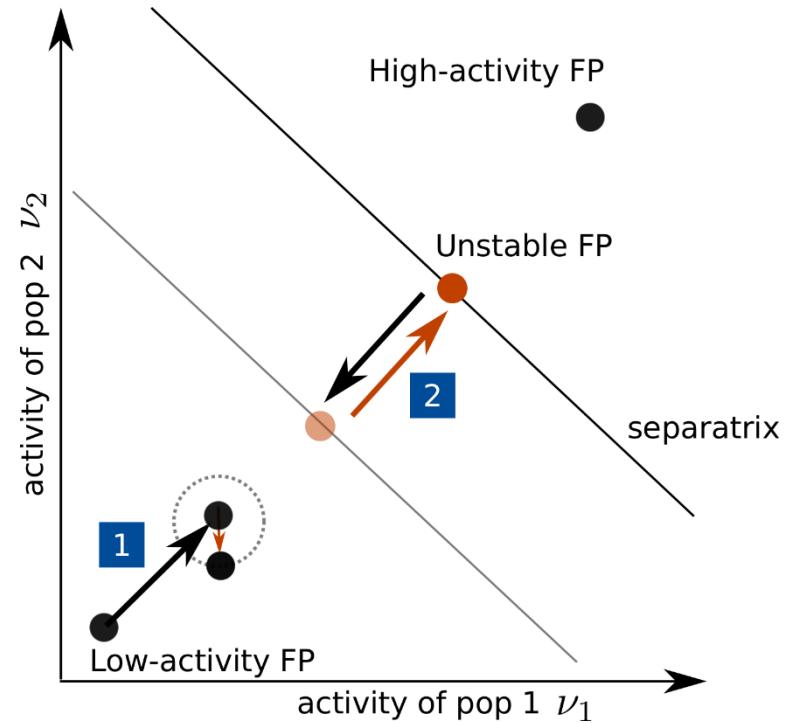
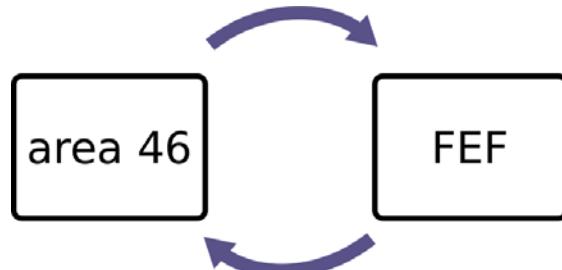
# BISTABLE GROUND STATE

- low rates of excitatory neurons in infragranular layers
- increasing external drive leads to high-activity state with excessive rates



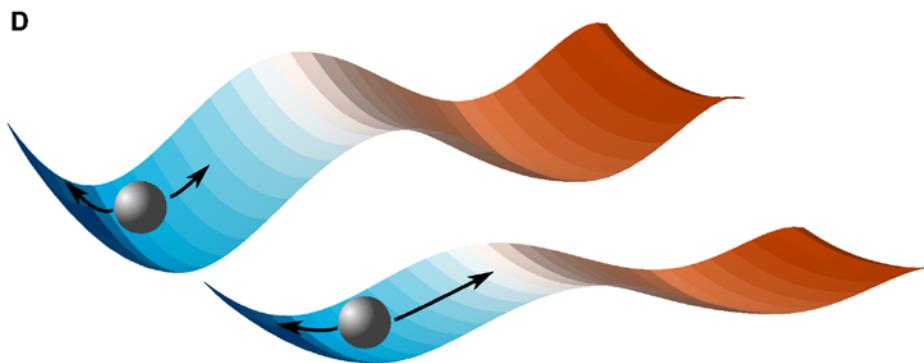
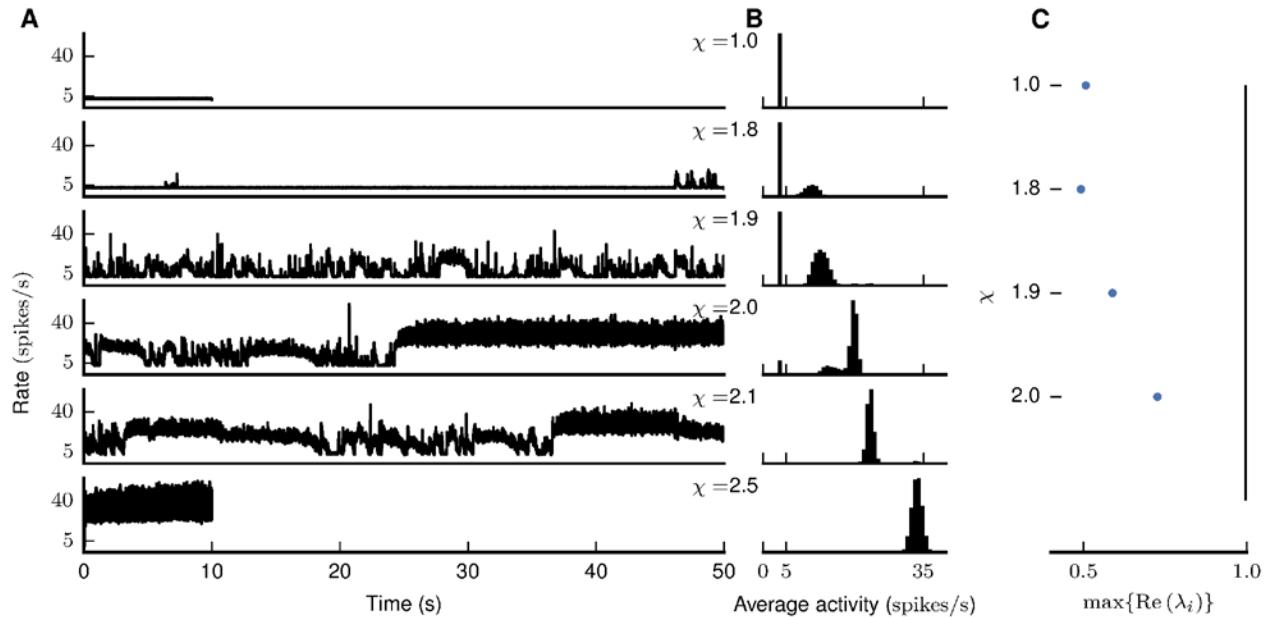
# STABILIZATION USING MEAN-FIELD THEORY

- 1) increase in external drive shifts both low-activity fixed point and separatrix
  - 2) compensation by change in connectivity shifts back separatrix
- yields reasonable rates in all populations
  - reduced connectivity in frontal loop



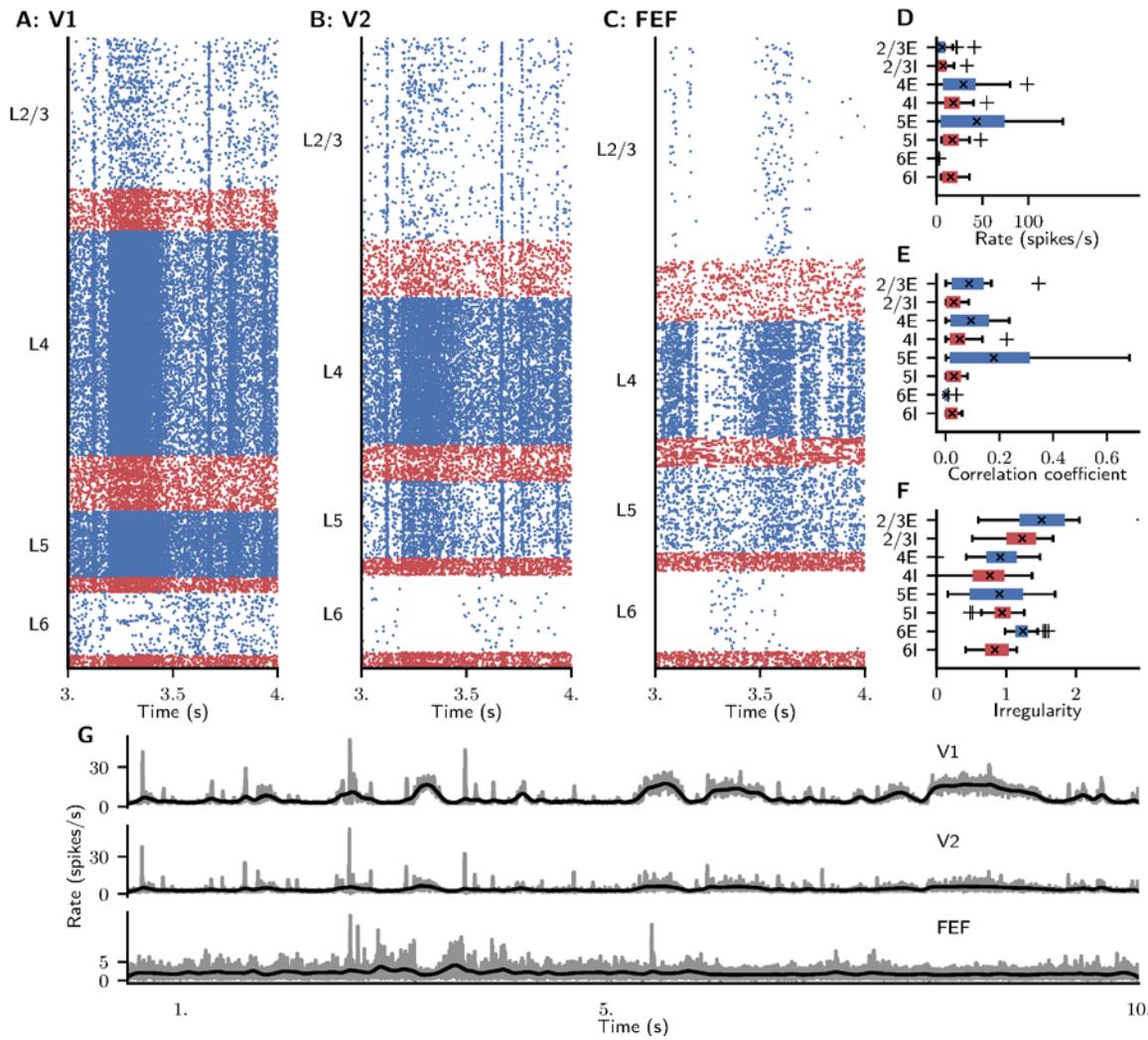
Schuecker J, Schmidt M, van Albada SJ,  
Diesmann M, Helias M (2017) *PLOS CB*

# INTER-AREA INTERACTIONS CAUSE SLOW FLUCTUATIONS

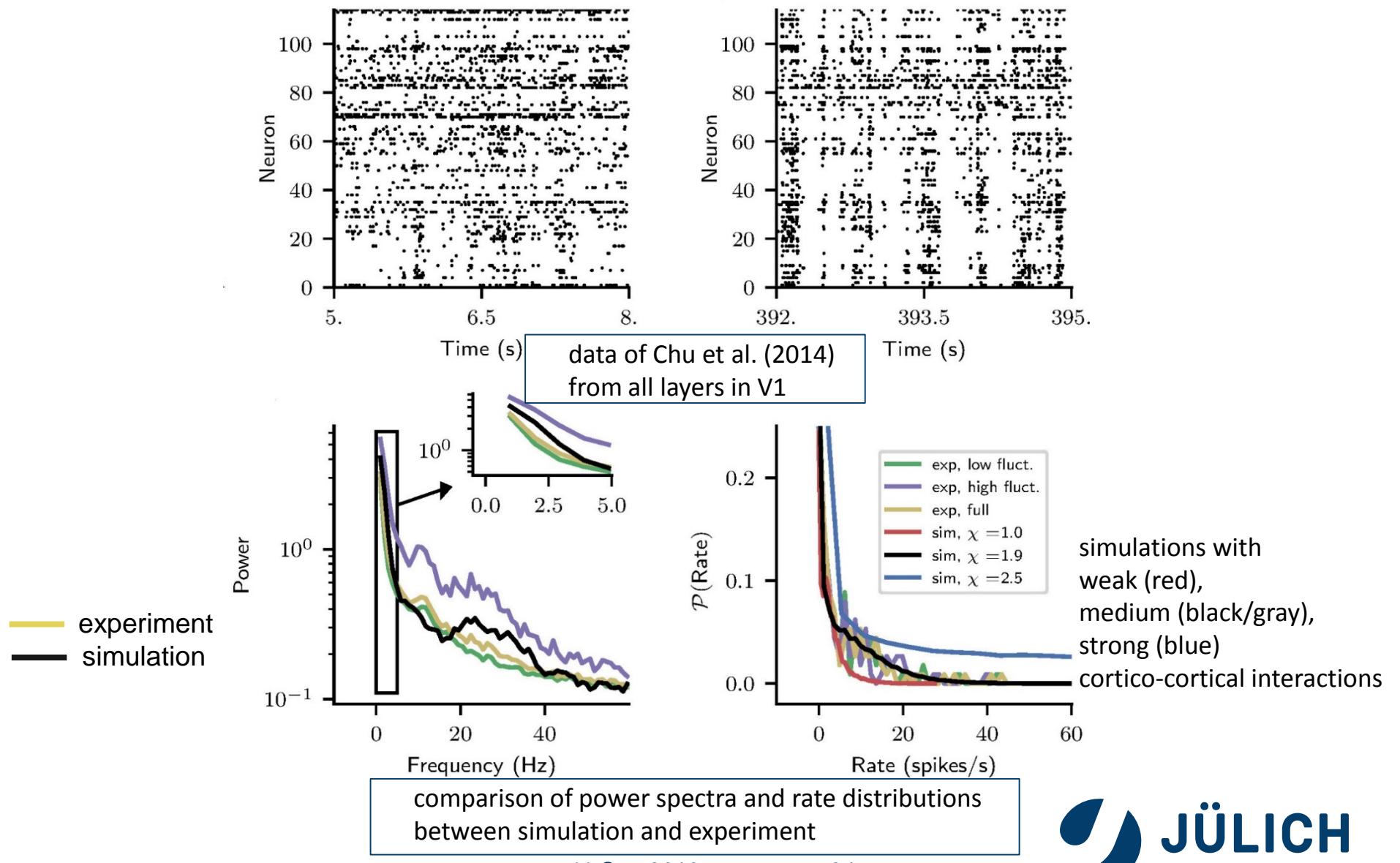


dynamical slowing near instability

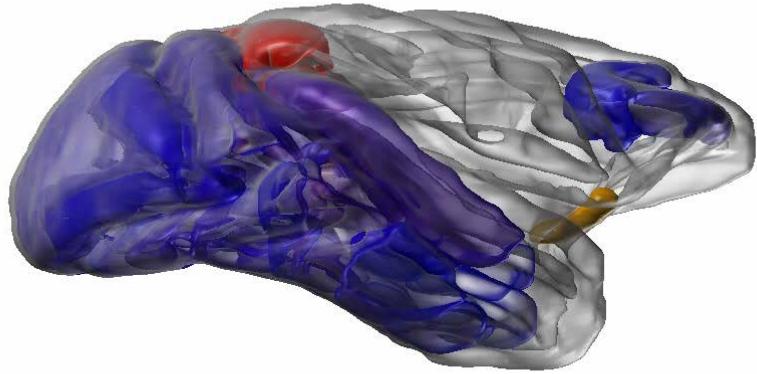
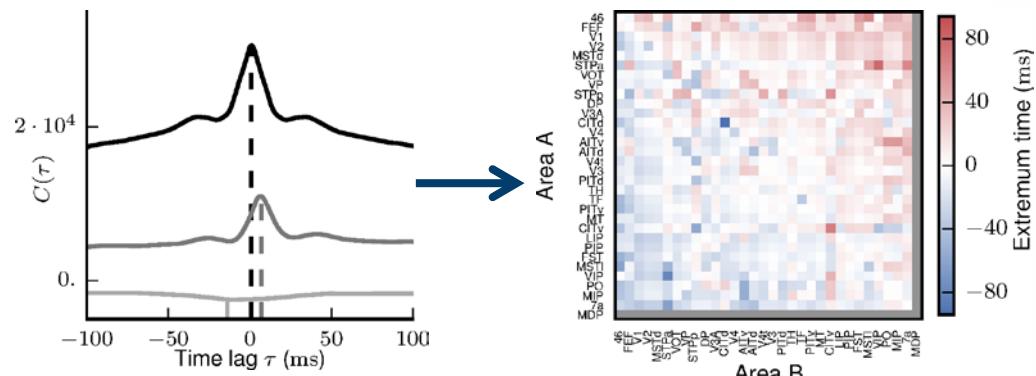
# GROUND STATE WITH MULTIPLE TIME SCALES



# V1 SPIKING STATISTICS



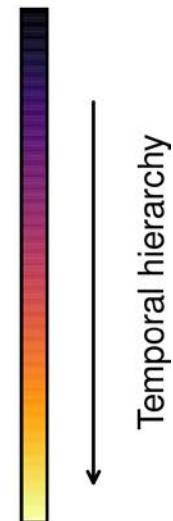
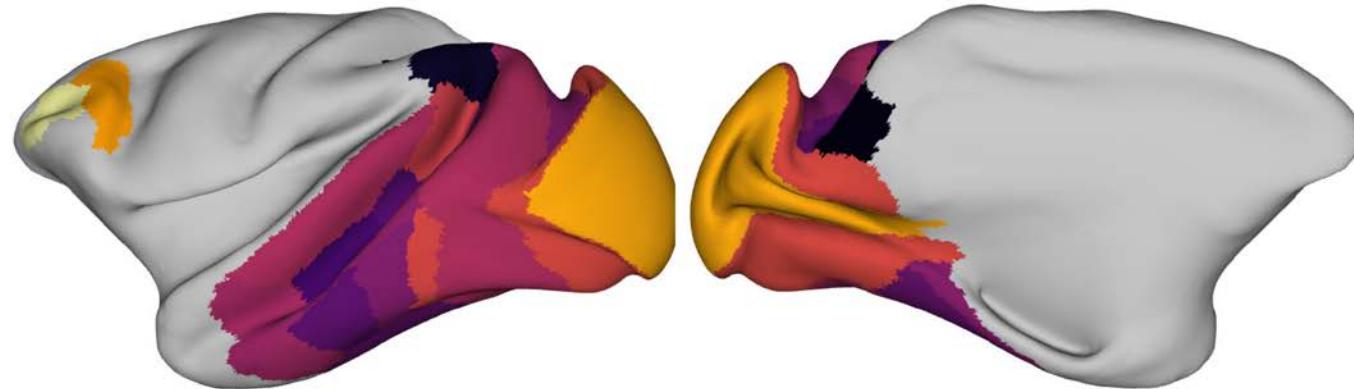
# TEMPORAL HIERARCHY



Nowke C, Schmidt M, van Albada SJ, Eppler JM,  
Bakker R, Diesmann M, Hentschel B, Kuhlen T (2013)  
*IEEE BioVis*

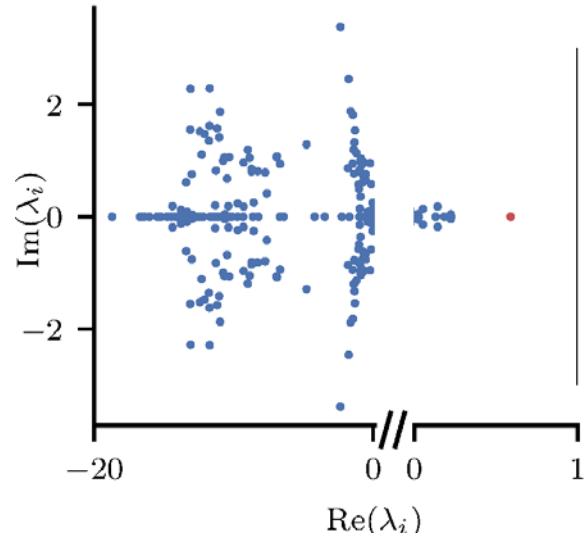
Lateral (left) view

Medial (right) view

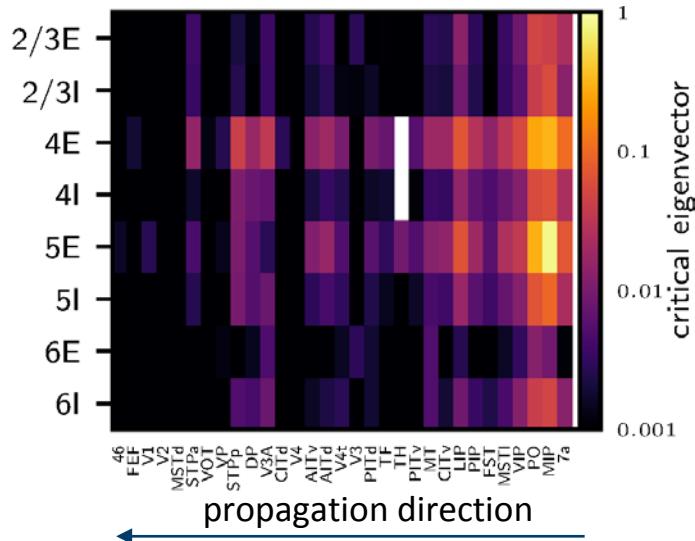


# LOCAL STABILITY IN NETWORK DETERMINES PROPAGATION DIRECTION

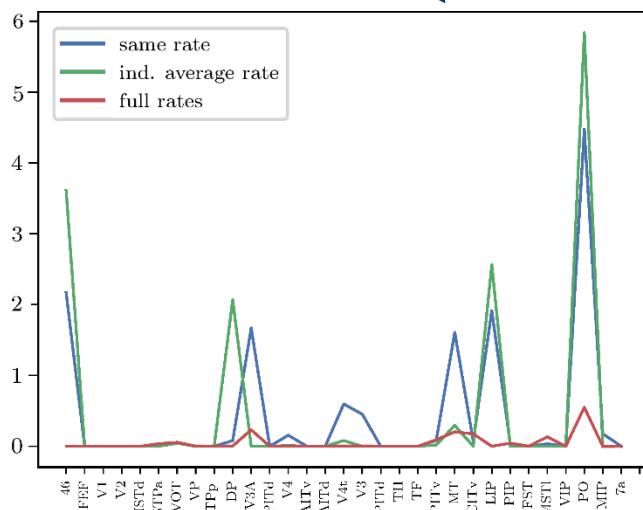
red, critical eigenvalue of effective connectivity of entire network



projection of critical eigenvector to populations and areas



propagation direction



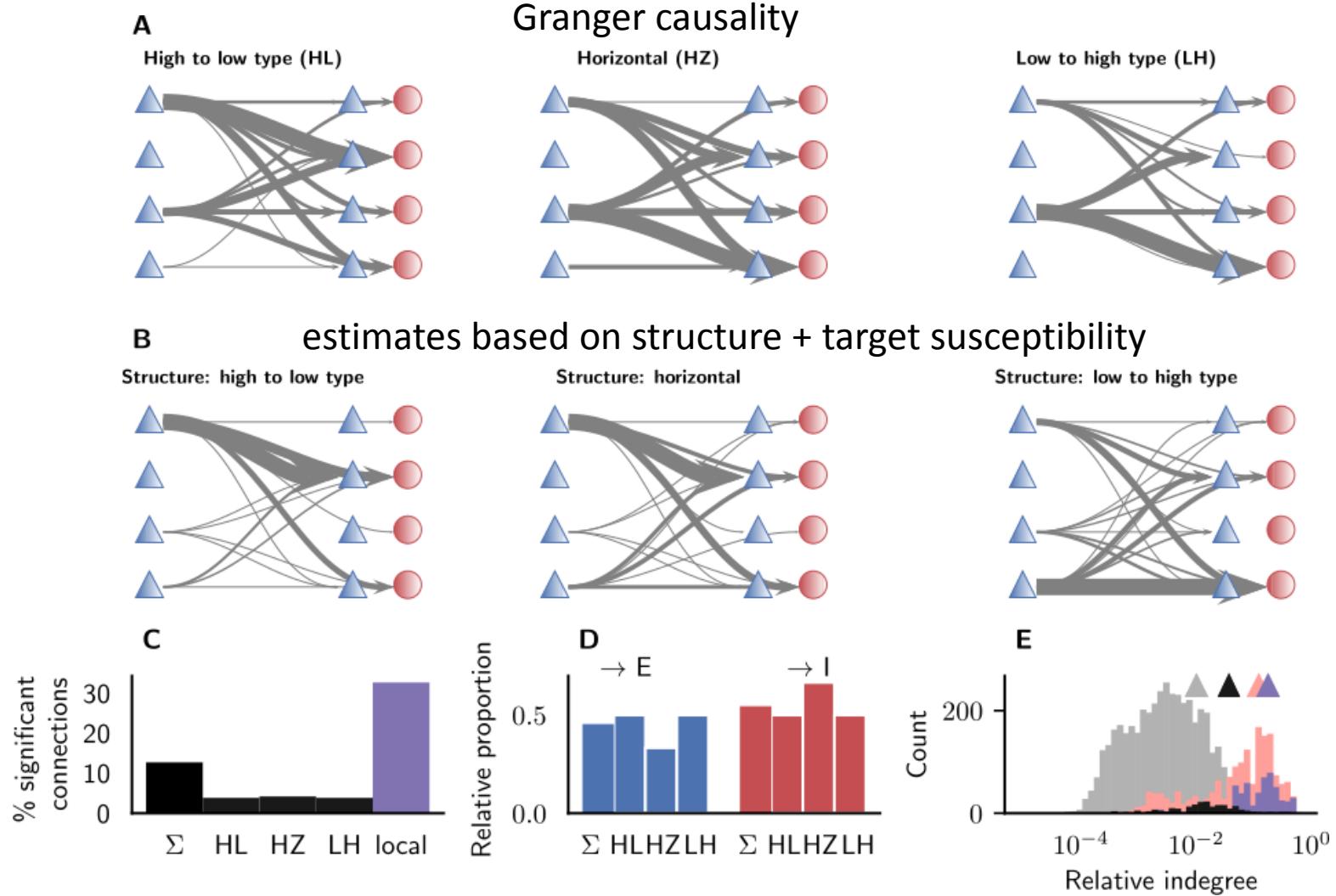
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stability of isolated areas is not correlated with temporal hierarchy



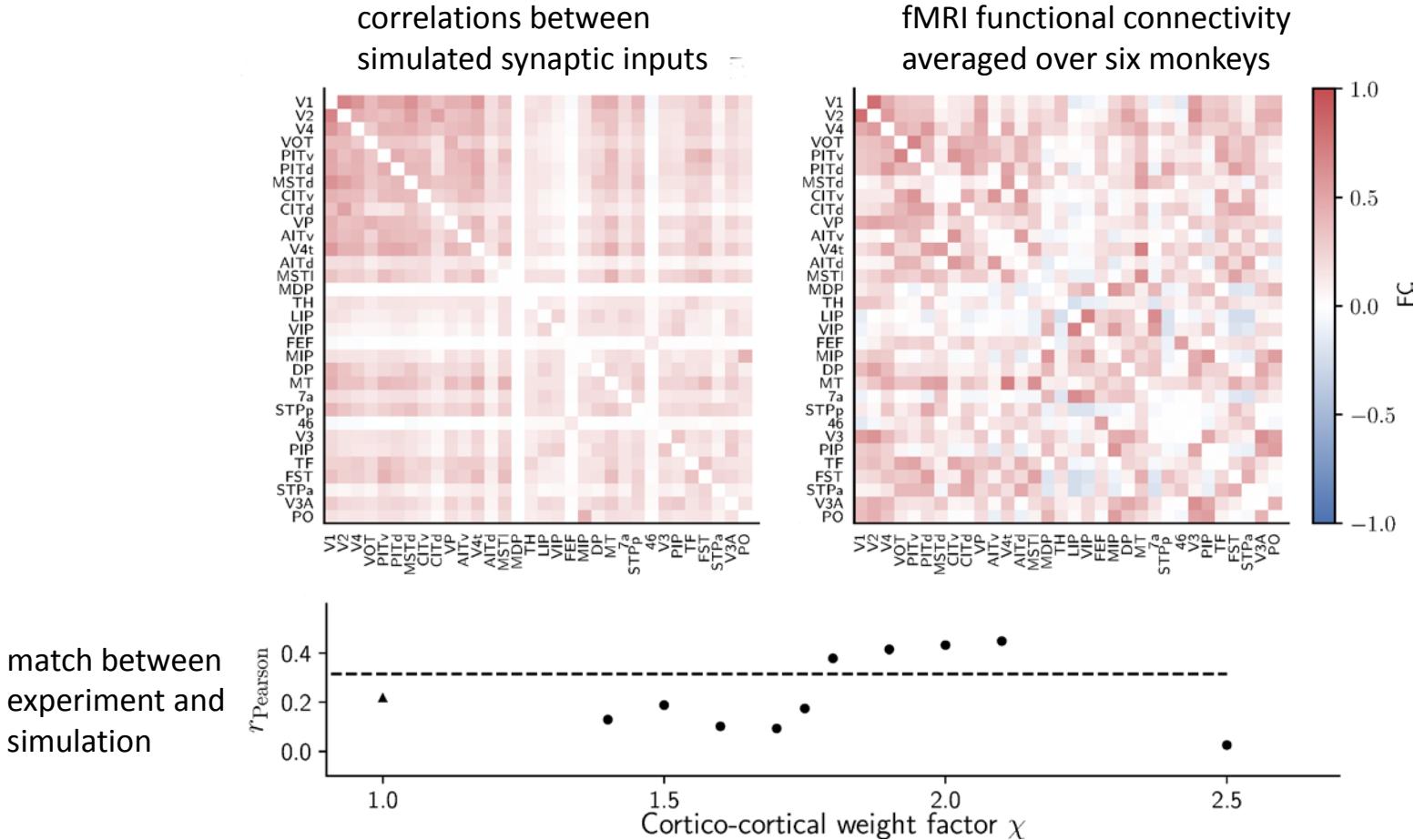
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# LAMINAR INTERACTIONS



# FUNCTIONAL CONNECTIVITY

inter-area interactions in metastable state resemble experimental resting-state fMRI



Schmidt M, Bakker R, Shen K, Bezgin G, Diesmann M, van Albada SJ (2018) *PLOS CB*

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# VISUAL AREAS EXHIBIT A HIERARCHY OF INTRINSIC TIMESCALES

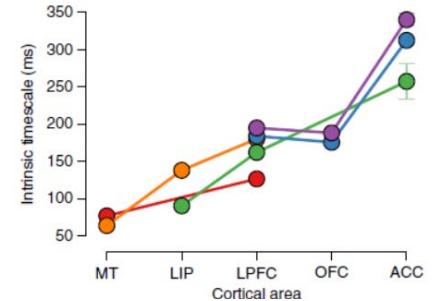
- widths of neural autocorrelation functions are smaller closer to the sensory periphery
- thought to be relevant for hierarchical processing: different temporal integration windows

Hasson et al. (2008) *J Neurosci*

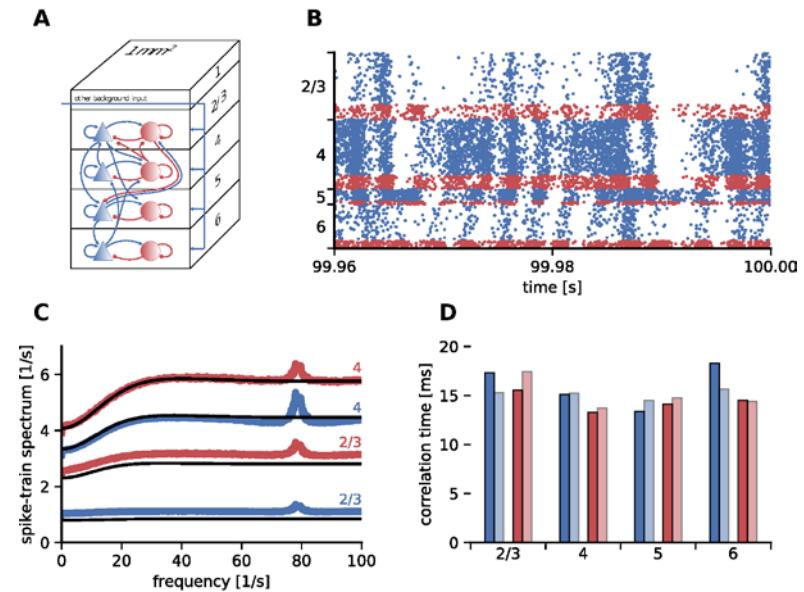
- dynamical mean-field theory enables us to predict timescales from network parameters

van Meegen & van Albada (arXiv preprint) A microscopic theory of intrinsic timescales in spiking neural networks

- allows the origin of the hierarchy of timescales to be studied

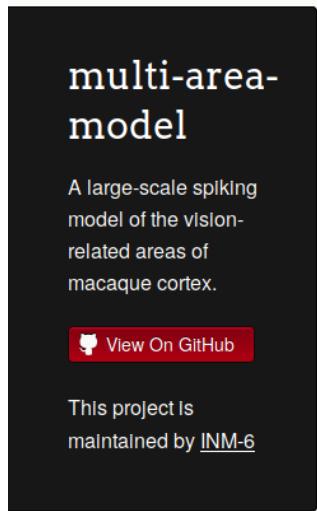


Murray et al. (2014)  
*Nat Neurosci*



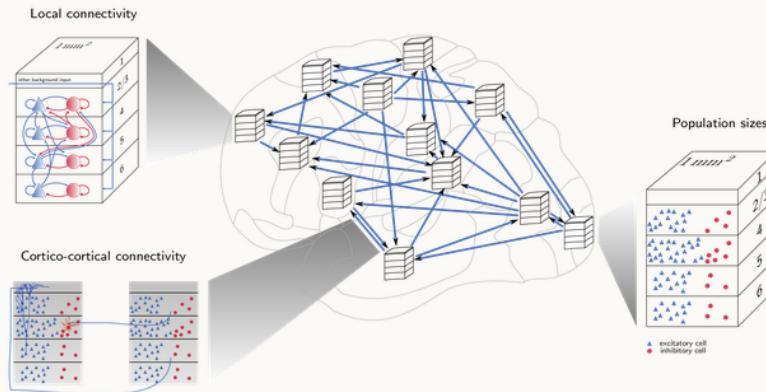
# GITHUB REPOSITORY

<https://inm-6.github.io/multi-area-model/>



## Multi-scale spiking network model of macaque visual cortex

python 3.6 nest:: license CC BY-NC-SA 4.0



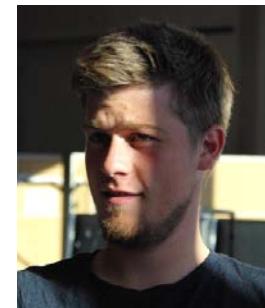
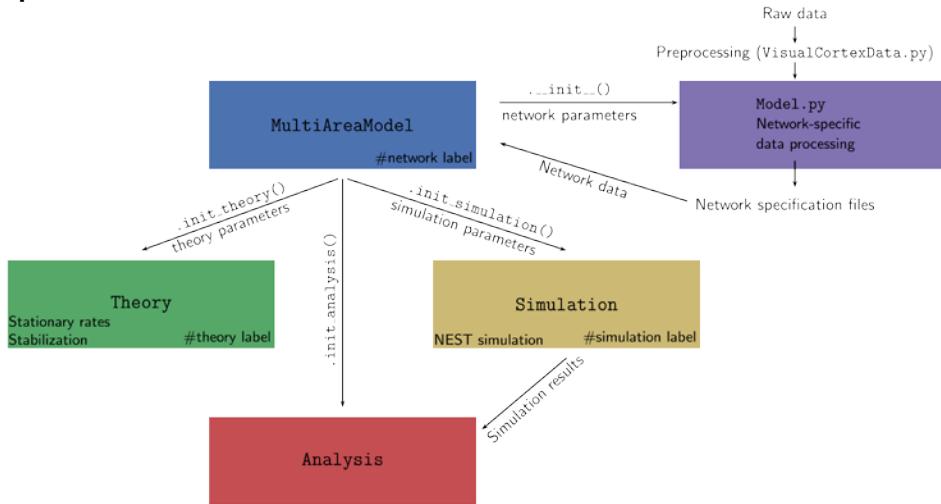
This code implements the spiking network model of macaque visual cortex developed at the Institute of Neuroscience and Medicine (INM-6), Research Center Jülich. The model has been documented in the following publications:

1. Schmidt M, Bakker R, Hilgetag CC, Diesmann M & van Albada SJ Multi-scale account of the network structure of macaque visual cortex Brain Structure and Function (2018), 223: 1409  
<https://doi.org/10.1007/s00429-017-1554-4>
2. Schuecker J, Schmidt M, van Albada SJ, Diesmann M & Helias M (2017) Fundamental Activity Constraints Lead to Specific Interpretations of the Connectome. PLOS Computational Biology, 13(2): e1005179. <https://doi.org/10.1371/journal.pcbi.1005179>
3. Schmidt M, Bakker R, Shen K, Bezgin B, Diesmann M & van Albada SJ (accepted) A multi-scale layer-resolved spiking network model of resting-state dynamics in macaque cortex. PLOS Computational Biology, 14(9): e1006359.

Hosted on [GitHub Pages](#)

# IMPLEMENTATION AND HURDLES

- M ported SLI code to PyNEST → more readable; new implementation from scratch enabled clean, modular setup



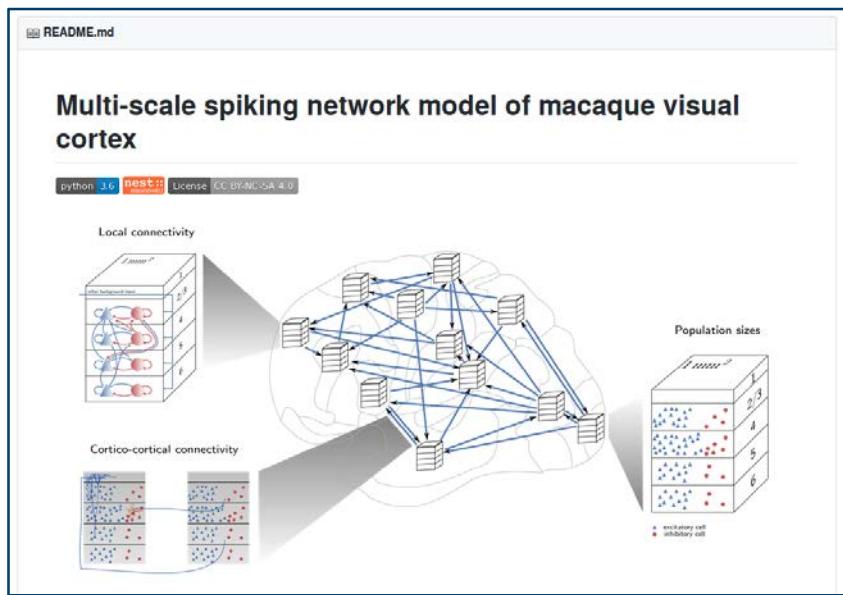
Maximilian  
Schmidt



Alexander  
van Meegen

- M created private GitHub repository, added files; created README; extended documentation
- M requested permission to publish data; *not yet obtained* → start from processed data
- S & especially A reviewed code → knowledge about model transferred from M to A
- mean-field integration gave different results on different machines
  - problem with package versions? → use Conda
  - problem solved by compiling NEST with different MPI compiler

# DOCUMENTATION



README provides all technical information needed to instantiate and run the model

## instructions for running a simulation

### Running a simulation

A simple simulation can be run in the following way:

1. Define custom parameters `custom_params = ...` `custom_simulation_params = ...`
2. Instantiate the model class together with a simulation class instance.

```
M = MultiAreaModel(custom_params, simulation=True, sim_spec=custom_simulation_params)
```

3. Start the simulation.

```
M.simulation.simulate()
```

## software requirements

### Requirements

`python_dichash` (<https://github.com/INM-6/python-dichash>), `correlation_toolbox` (<https://github.com/INM-6/correlation-toolbox>), `pandas`, `numpy`, `nested_dict`, `matplotlib` (2.1.2), `scipy`, `NEST` 2.14.0

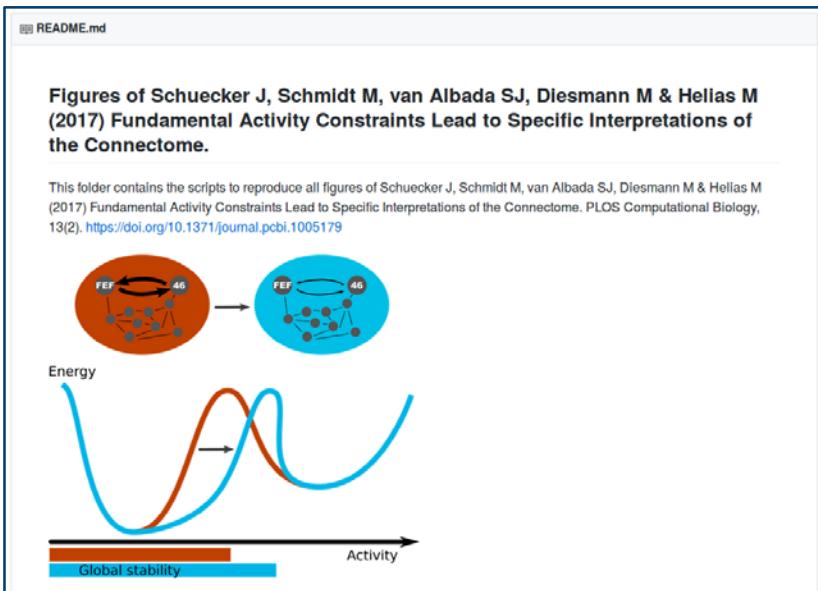
Optional: `seaborn`, `Sumatra`

To install the required packages with pip, execute:

```
pip install -r requirements.txt
```

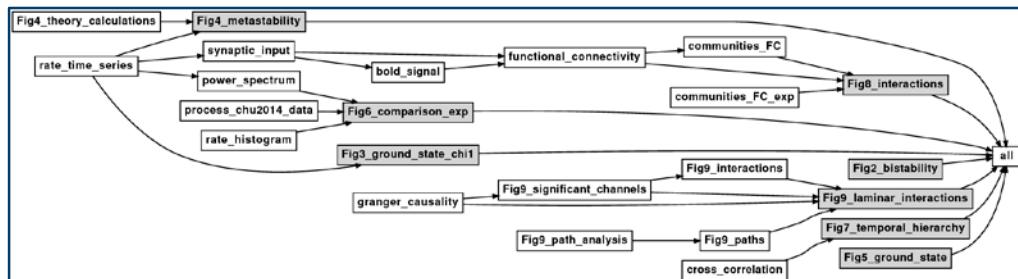
Note that NEST needs to be installed separately, see <http://www.nest-simulator.org/installation/>.

# REPRODUCING FIGURES



additional README with specific instructions for each publication

**Snakemake\*-based workflow to reproduce figures of Schmidt et al. *PLOS CB* (2018)**



code snippet from the above Snakemake file

```
rule Fig4_metastability:
    input:
        expand(os.path.join(DATA_DIR, '{simulation}', 'Analysis', 'rate_time_series_full', 'rate_time_series_full_V1.npy'),
              simulation=SIM_LABELS['Fig4']),
        expand('Fig4_theory_data/results_{cc_weights_factor}.npy',
              cc_weights_factor=[1.0, 1.8, 1.9, 2., 2.1, 2.5])
    output:
        'Fig4_metastability.eps'
    shell:
        'python3 Fig4_metastability.py'
```

\* Köster J, Rahmann S (2012) *Bioinformatics*

# EXECUTABLE WORKFLOW

open-source material should:

- be correct
  - testing by main developer(s) and others  
great opportunity for knowledge transfer
- enable testing dependence on underlying data
  - include raw data; obtain permission early
- trace entire workflow from model construction to execution and visualization
  - include figure scripts; Snakemake removes manual steps
- be easy to understand and use
  - readable code; modularity; documentation; open-source packages
- fully specify package versions
  - Sumatra; Conda
- be provenance-tracked; enable continued development
  - Sumatra; GitHub, OSB!

# CONCLUSIONS

- multi-scale point-neuron model of macaque visual cortex
  - model code available from <https://inm-6.github.io/multi-area-model>
  - candidate for porting to OSB!
- provides updated connectivity map incl. population sizes
  - predicts non-negligible feedback onto L4 neurons
- just below instability:
  - reproduces V1 spiking statistics
  - functional connectivity shows correspondence with fMRI
- stronger cortico-cortical connections onto inhibitory than to excitatory neurons enable stable inter-area propagation
- propagation mainly in feedback direction

# OUTLOOK

- expand multi-area model with motor areas



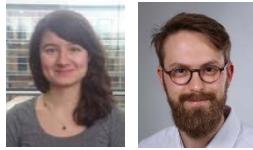
- explain hierarchy of intrinsic time scales



- distinguish inhibitory cell types



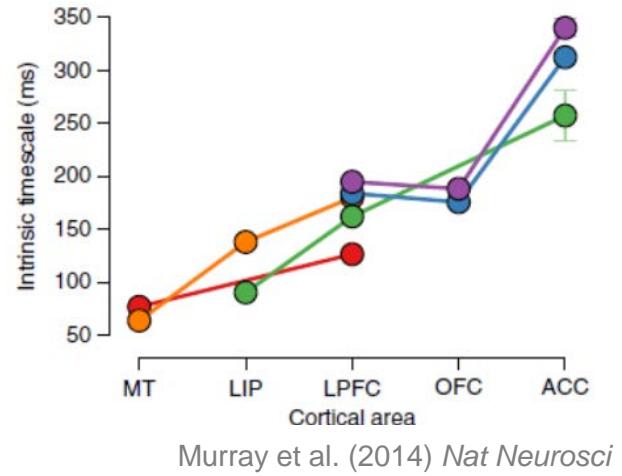
- model visual attention



- build in functional properties using learning-to-learn framework



- model human cortex



Murray et al. (2014) *Nat Neurosci*

# ACKNOWLEDGMENTS

## Jülich

modeling,  
theory



Maximilian  
Schmidt  
(now Tokyo)

testing



anatomical  
data



theory



Jannis  
Schuecker  
(now Bonn)



Moritz  
Helias



Markus  
Diesmann

fMRI data



Kelly  
Shen  
Baycrest,  
Toronto



Gleb  
Bezgin  
McGill,  
Montreal

anatomy



Claus  
Hilgetag  
UKE  
Hamburg

## visualization



Christian  
Nowke  
RWTH Aachen University



Bernd  
Hentschel  
Kuhlen



Human Brain Project

grant JINB33 for compute time on  
the Jülich supercomputers