LARGE-SCALE MODEL DEVELOPMENT FROM THE NEST PERSPECTIVE

17 July 2018
CNS*2018 workshop “Developing, standardising and sharing large scale cortical network models”
Seattle, USA

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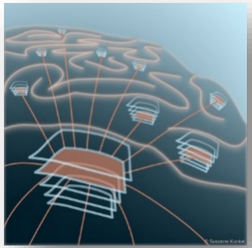
JARA Brain Institute I (INM-10)
Jülich Research Centre

www.csn.fz-juelich.de
www.nest-initiative.org



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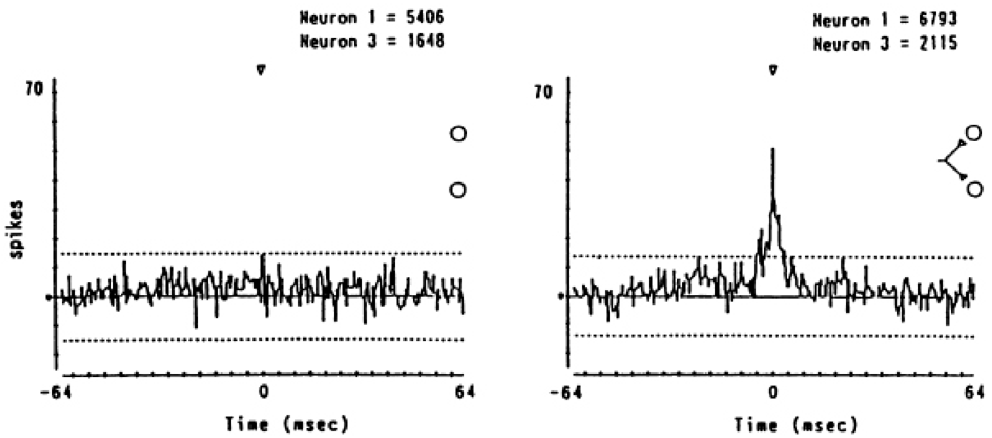
NEED FOR LARGE-SCALE MODELS: IRREDUCIBILITY



Sakurai (1999) *Neurosci Biobehav Rev*

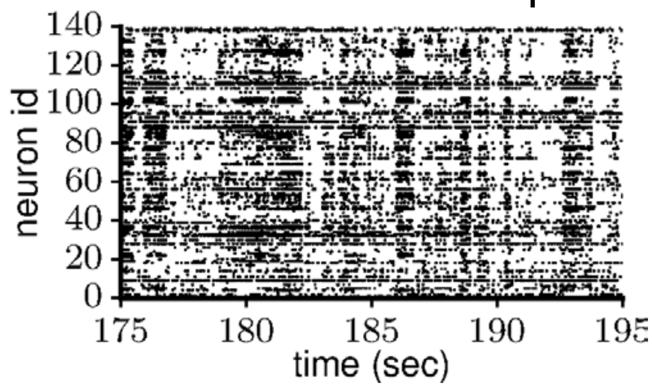
- two simultaneously recorded neurons in CA1 of a rat performing an auditory or visual discrimination task
- task-related correlation only for visual task

- downscaling can preserve certain dynamical properties, but never all; e.g.,
  - reducing number of neurons tends to increase correlations
  - simultaneously preserving mean activities and correlations is only possible over a limited range of network sizes
- testing goodness of approximation requires full-scale simulations

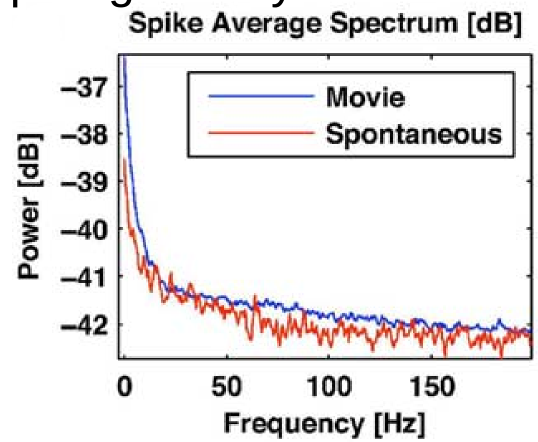
  van Albada SJ, Helias M, Diesmann M (2015) *PLOS CB*

NEED FOR MULTI-SCALE MODELS: LOCAL AND GLOBAL DYNAMICS

low frequencies in spiking activity

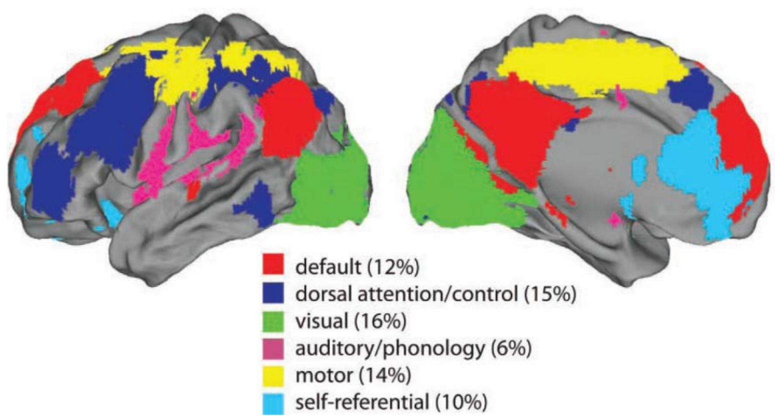


Chu et al. (2014) *Vision Res*



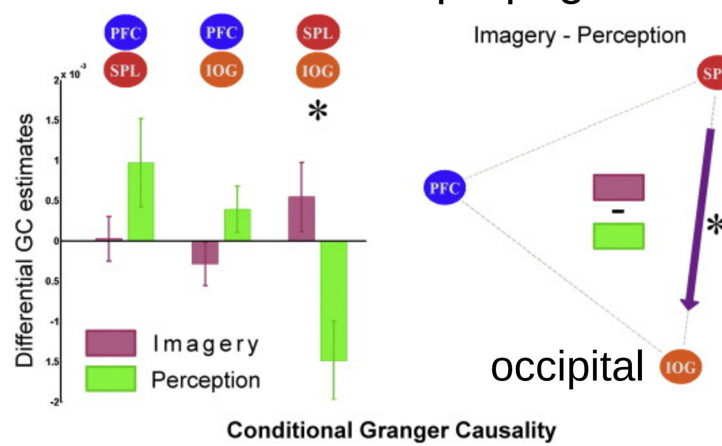
Belitski et al. (2008) *J Neurosci*

resting-state networks



Deco and Corbetta (2011) *The Neuroscientist*

inter-area propagation



parietal

occipital

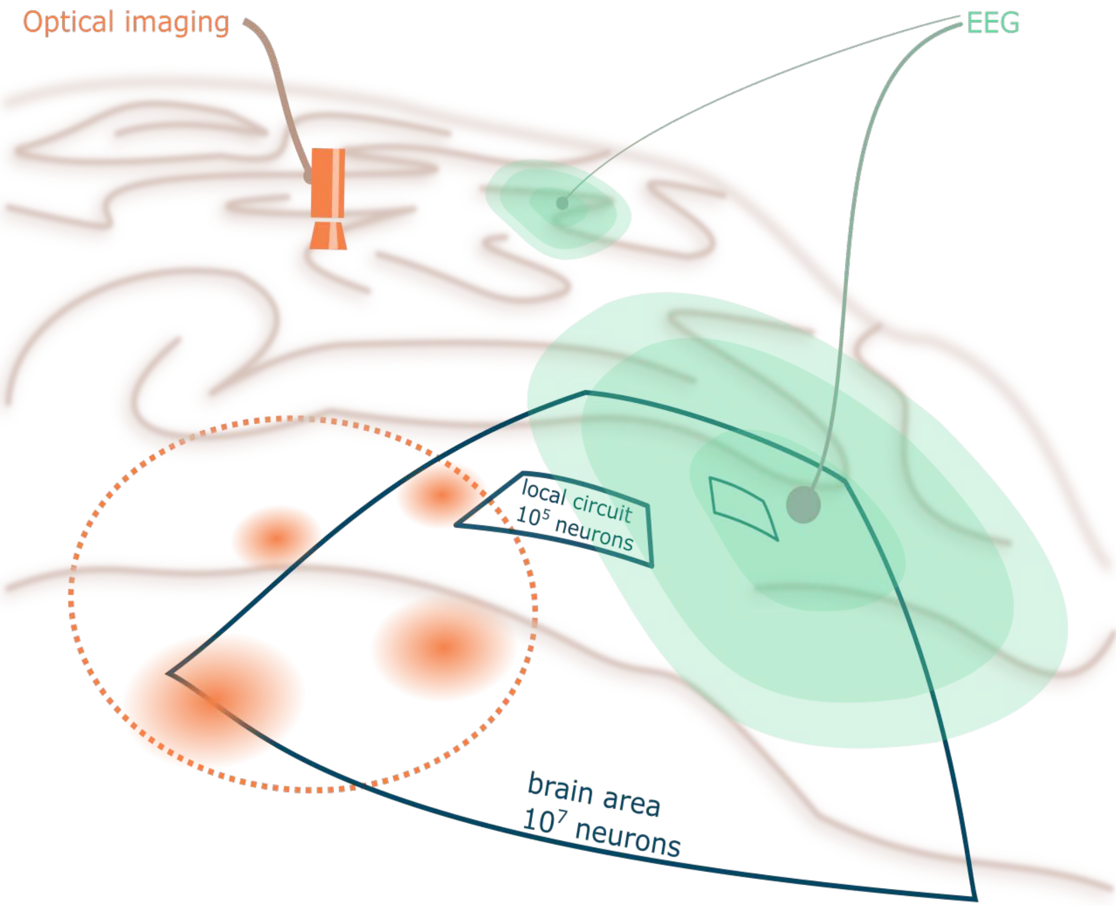
Dentico et al. (2014) *NeuroImage*

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)

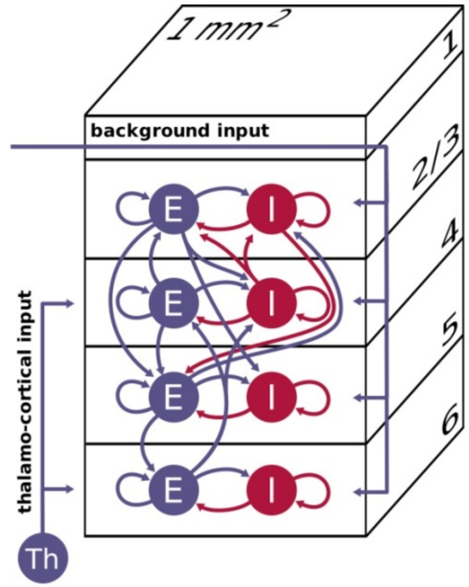
and macroscopic measures
- EEG, MEG
- fMRI resting-state networks



S Kunkel

MINIMAL LAYERED CORTICAL NETWORK MODEL

- 1 mm^3
- 300 million synapses, 80,000 neurons
- 2 populations of neurons per layer:
  - E: excitatory
  - I: inhibitory
- E and I identical neuronal dynamics
- laterally homogeneous connectivity
- layer- and type-specific connection probability



Cerebral CORTEX

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

Tobias C. Potjans, Markus Diesmann

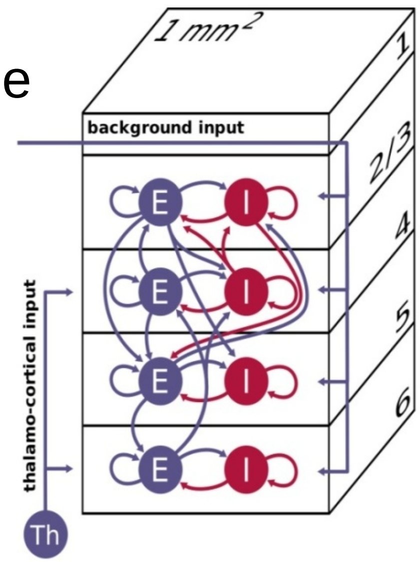
Cerebral Cortex, Volume 24, Issue 3, 1 March 2014, Pages 785–806, https://doi.org/10.1093/cercor/bhs358

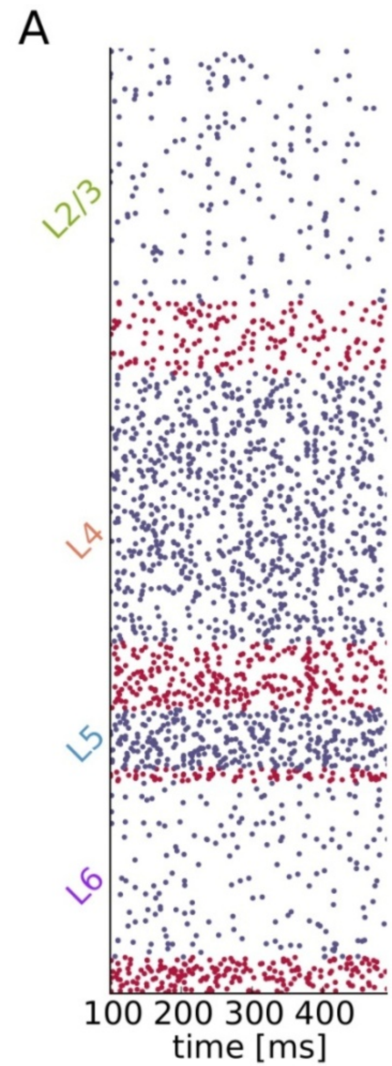
MINIMAL LAYERED CORTICAL NETWORK MODEL

integrates knowledge of more than 50 experimental papers

taking into account layer and neuron-type specific connectivity is sufficient to reproduce experimentally observed:

- asynchronous irregular spiking
- higher rate of inhibitory neurons
- correct distribution of spike rates across layers





made available as a part of NEST and PyNN, and at www.opensourcebrain.org

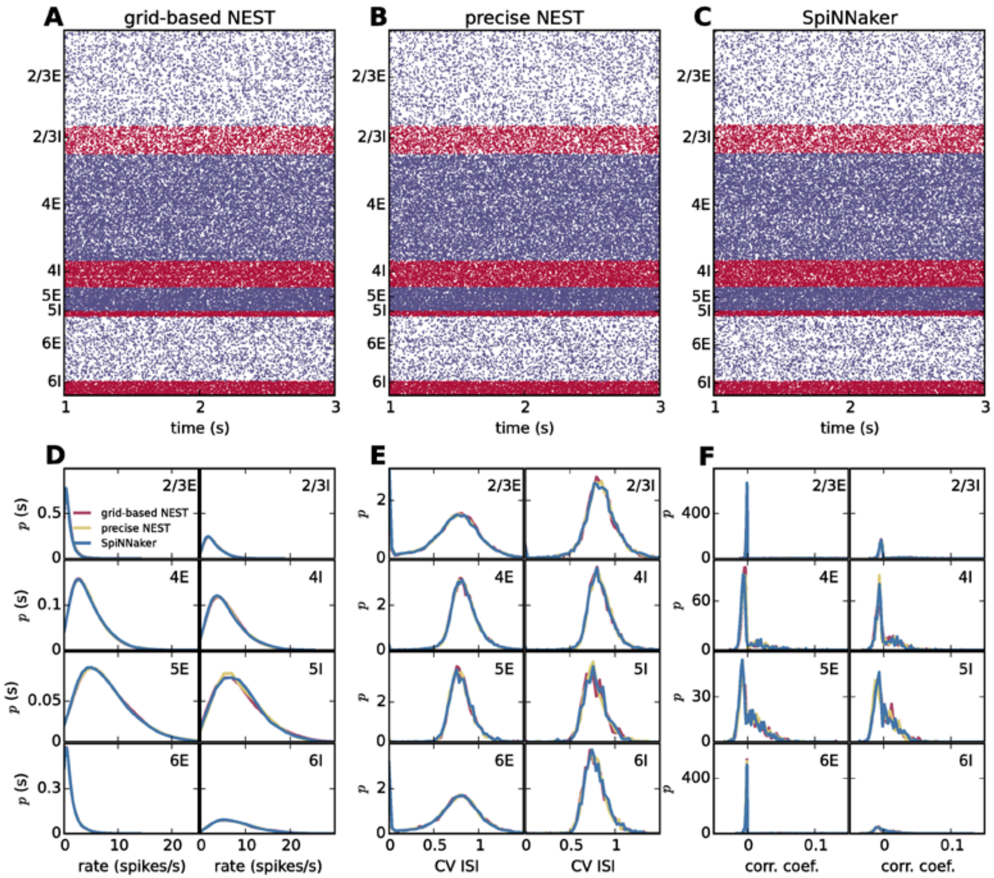
Gleeson P, Cantarelli M, Marin B, . . . van Albada SJ, van Geit W, R Silver RA. Open Source Brain: a collaborative resource for visualizing, analyzing, simulating and developing standardized models of neurons and circuits (submitted)

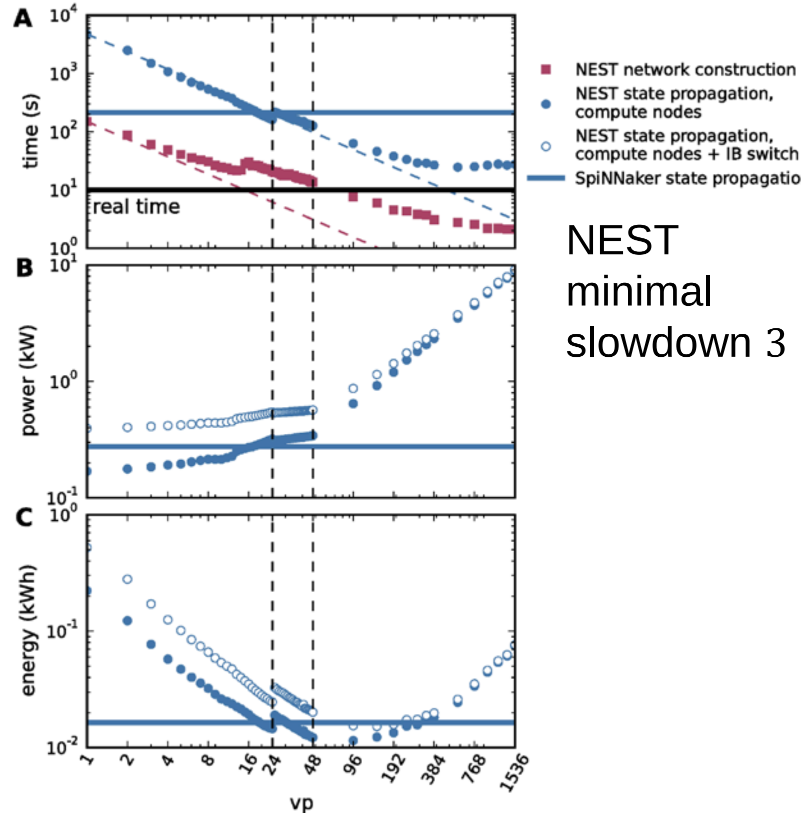
reproduced with Brian

Shimoura RO, Kamiji NL, Pena RFO, Cordeiro VL, Ceballos CC, Romaro C, Roque AC (2018) *ReScience*

MICROCIRCUIT PORTED TO SPINNAKER

largest SpiNNaker simulation to date; 6 SpiNNaker boards; 20 × slowdown to accommodate fast dynamics (0.1 ms time steps) and high input spike rates





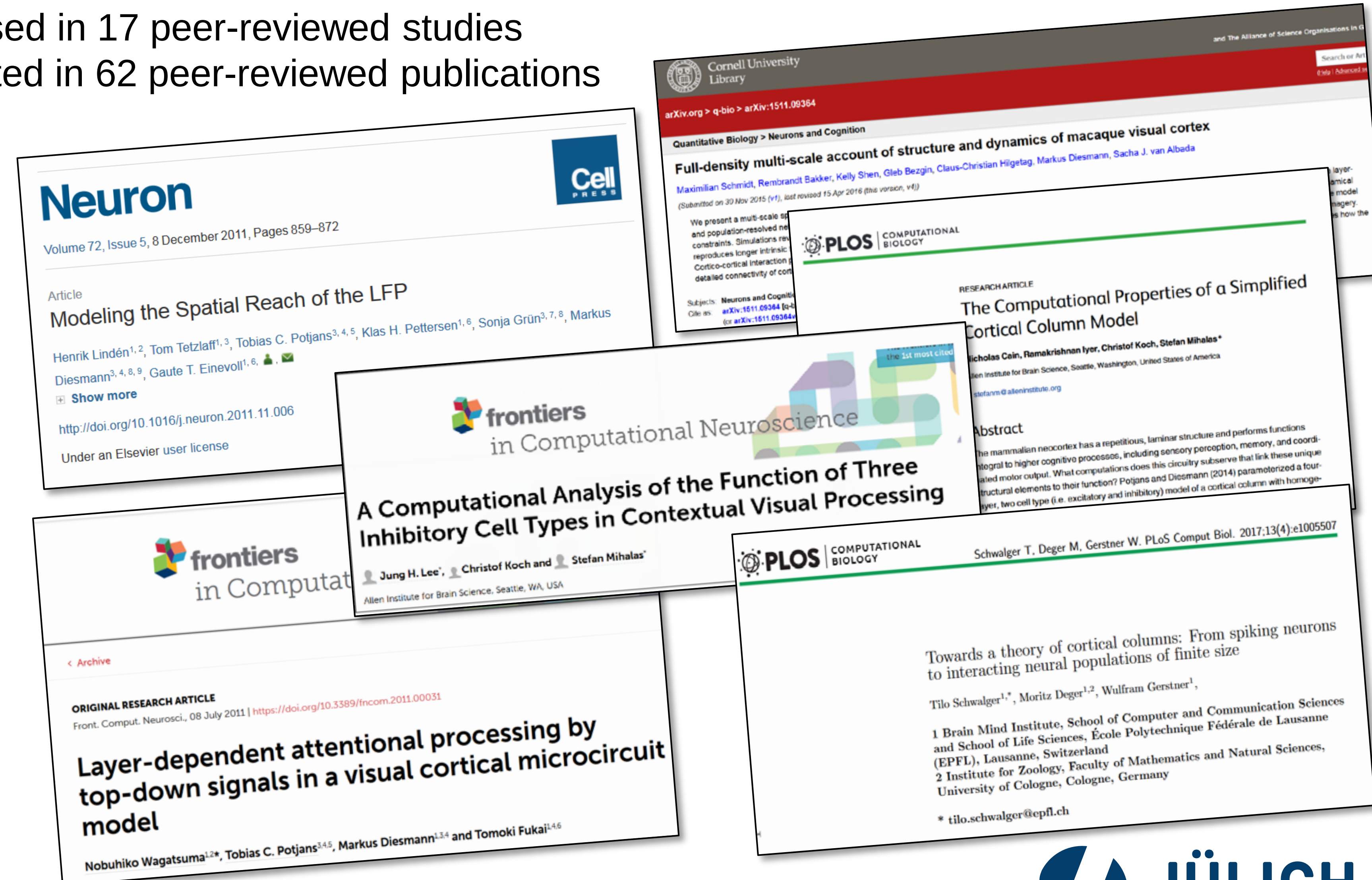
NEST minimal slowdown 3 ×

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

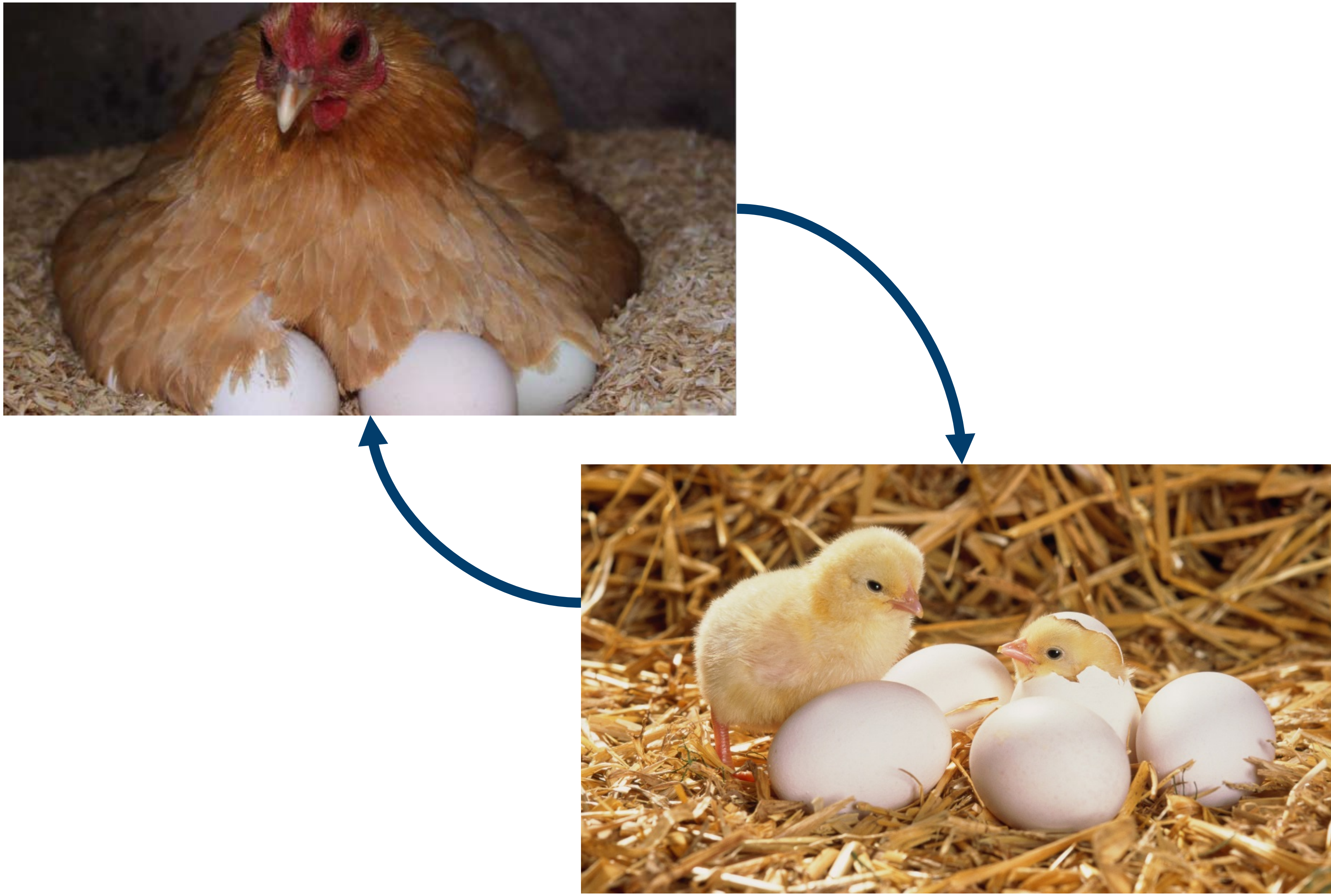
van Albada, Rowley, Senk, Hopkins, Schmidt, Stokes, Lester, Diesmann, Furber (2018) *Front Neurosci*

BUILDING BLOCK FOR FURTHER STUDIES

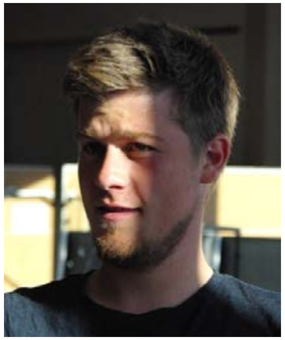
- used in 17 peer-reviewed studies
- cited in 62 peer-reviewed publications




THIS RACE
could be interesting
VERY DEMOTIVATIONAL.com

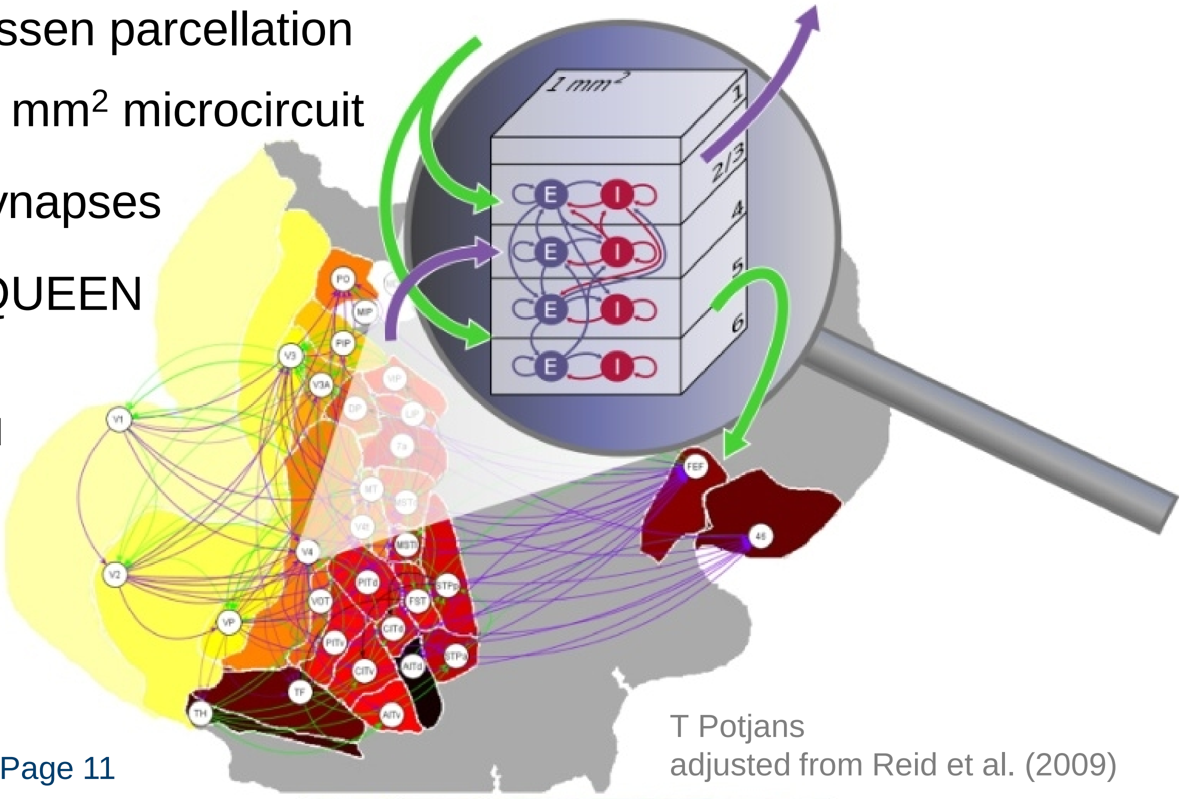


MULTI-AREA MODEL OF MACAQUE VISUAL CORTEX



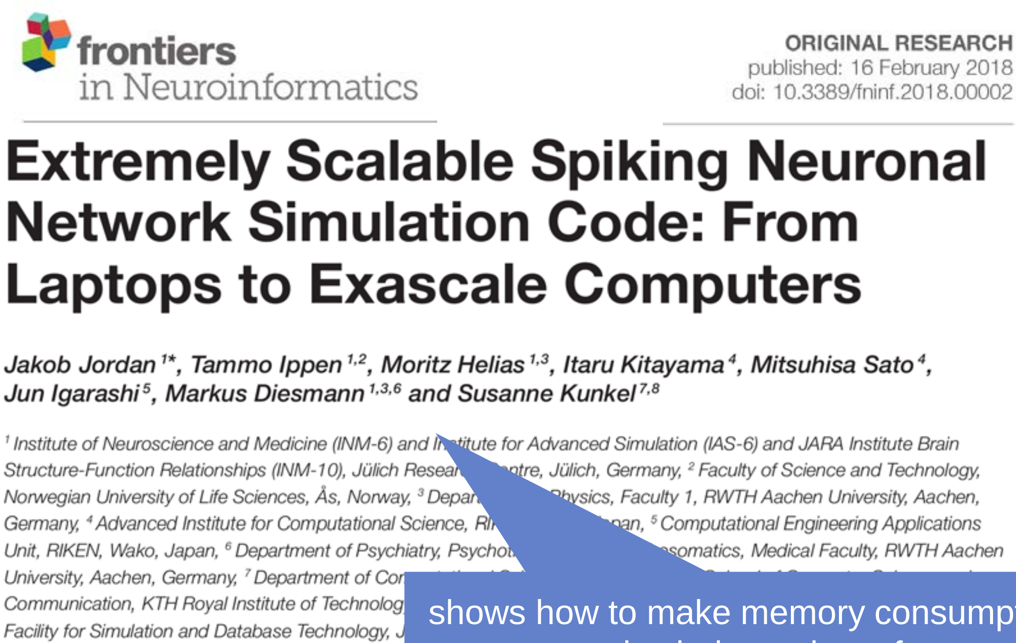
Maximilian Schmidt

- rich anatomical and physiological data sets available
- relatively close to human
- 800 million neurons in one hemisphere
- 32 areas in Felleman & Van Essen parcellation
- representing each area by a 1 mm^2 microcircuit
- $4 \cdot 10^6$ neurons and $2.4 \cdot 10^{10}$ synapses
- simulated using NEST on JUQUEEN and JURECA supercomputers
  - $\sim 10^3$ MPI processes, multi-threaded
  - a few minutes for 1 s of simulation



T Potjans
adjusted from Reid et al. (2009)

SIMULATION TECHNOLOGY FOR EXASCALE



frontiers in Neuroinformatics

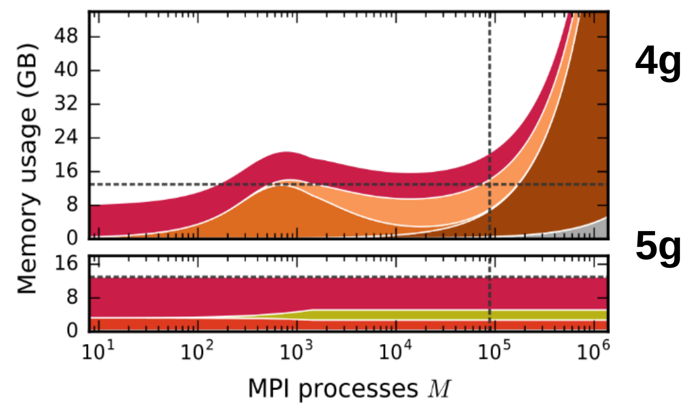
ORIGINAL RESEARCH
published: 16 February 2018
doi: 10.3389/fninf.2018.00002

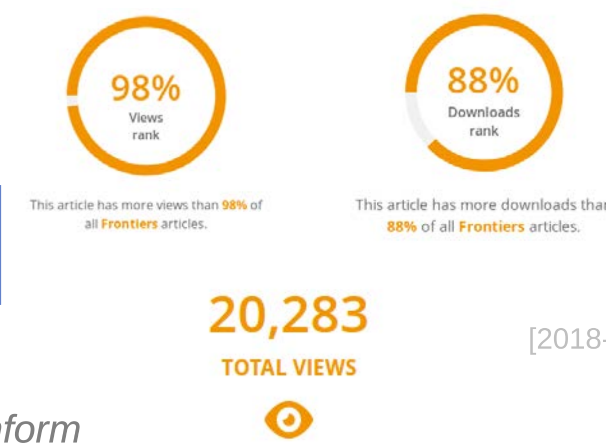
Extremely Scalable Spiking Neuronal Network Simulation Code: From Laptops to Exascale Computers

Jakob Jordan[1], Tammo Ippen[1,2], Moritz Helias[1,3], Itaru Kitayama[4], Mitsuhisa Sato[4], Jun Igarashi[5], Markus Diesmann[1,3,6] and Susanne Kunkel[7,8]*

[1] Institute of Neuroscience and Medicine (INM-6) and In[...]titute for Advanced Simulation (IAS-6) and JARA Institute Brain Structure-Function Relationships (INM-10), Jülich Resear[...]ntre, Jülich, Germany, [2] Faculty of Science and Technology, Norwegian University of Life Sciences, Ås, Norway, [3] Depar[...]hysics, Faculty 1, RWTH Aachen University, Aachen, Germany, [4] Advanced Institute for Computational Science, RI[...]pan, [5] Computational Engineering Applications Unit, RIKEN, Wako, Japan, [6] Department of Psychiatry, Psycho[...]somatics, Medical Faculty, RWTH Aachen University, Aachen, Germany, [7] Department of Co[...] Communication, KTH Royal Institute of Technolog[...] Facility for Simulation and Database Technology, J[...]

shows how to make memory consumption of compute nodes independent of network size





[2018-07-16]

parallel network construction Ippen et al. (2017) *Front Neuroinform*

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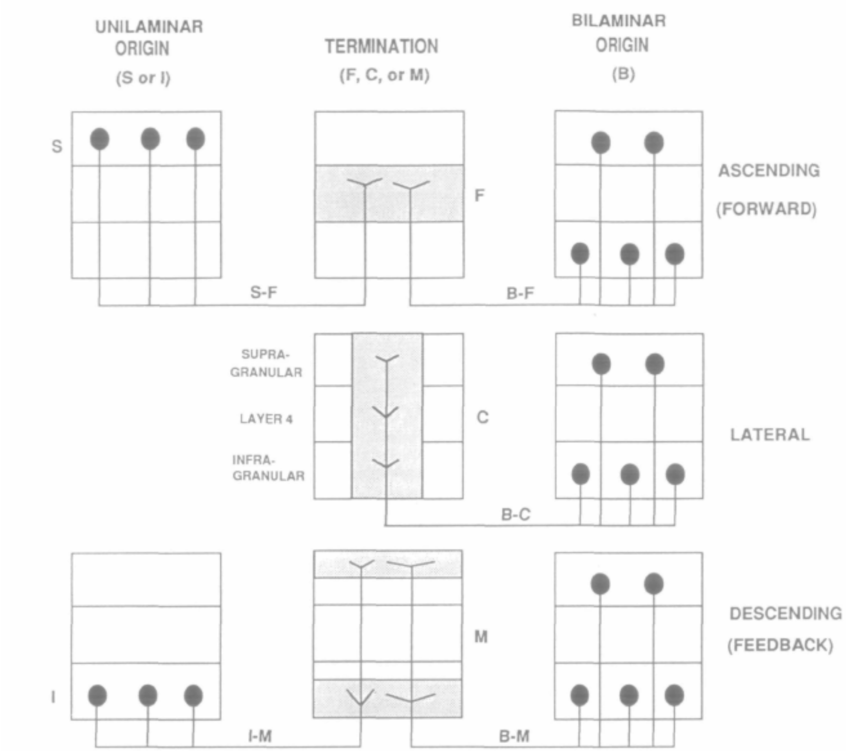
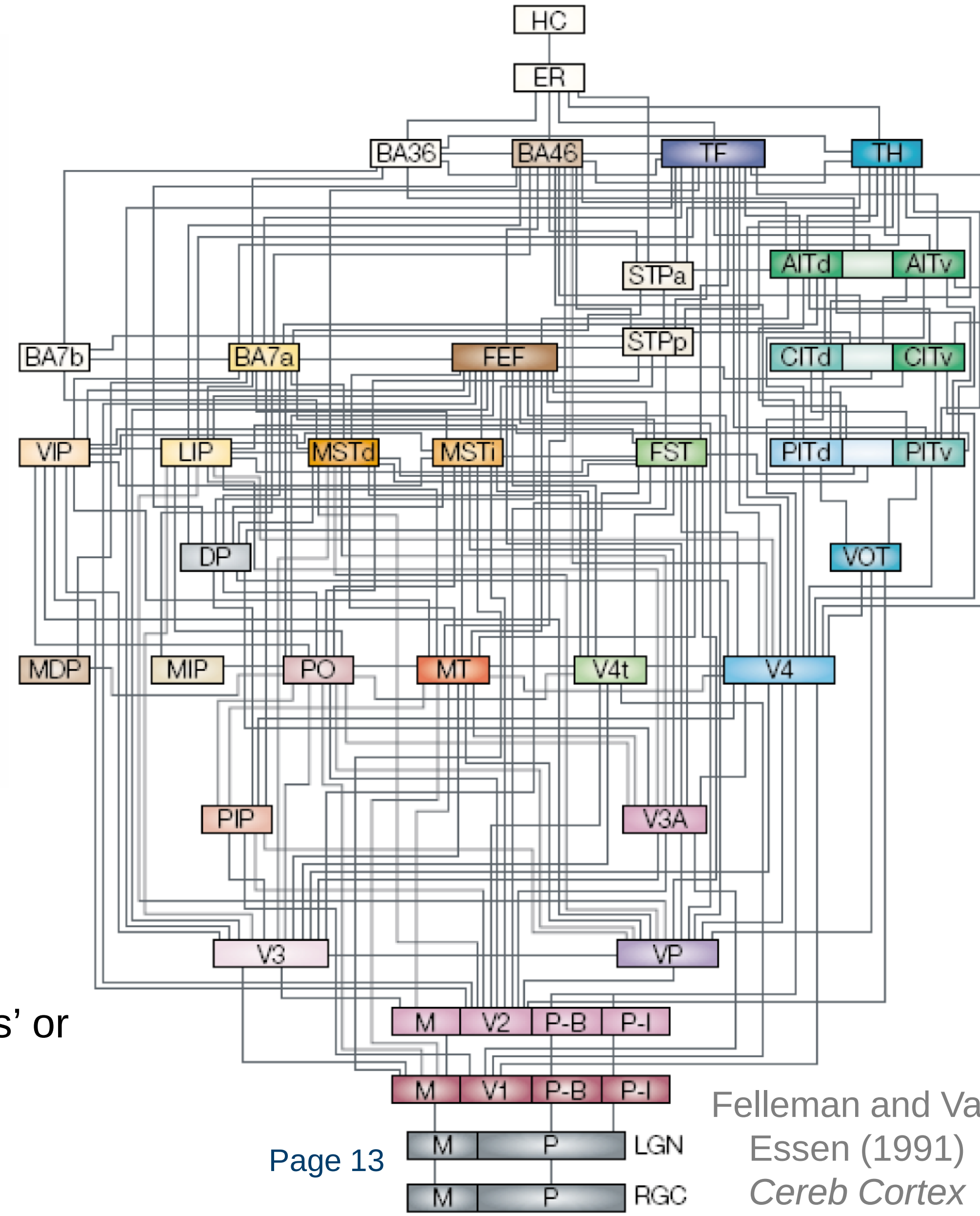
HIERARCHY OF VISUAL CORTICAL AREAS





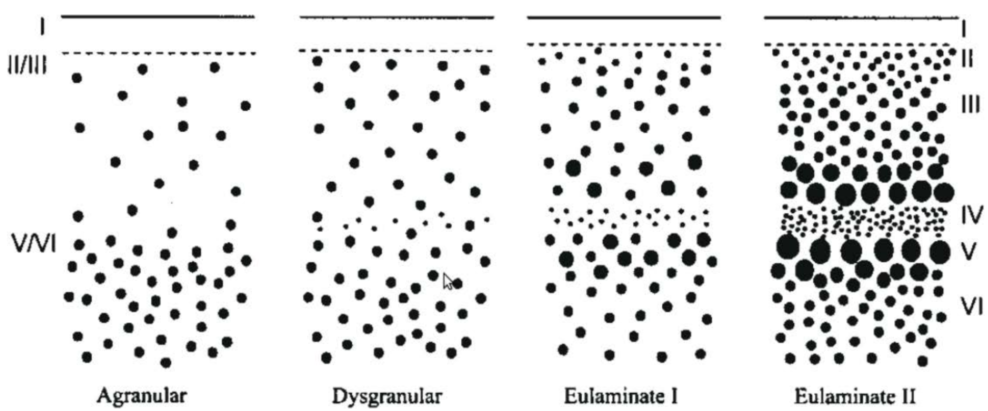
Felleman and Van Essen (1991) *Cereb Cortex*

- 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

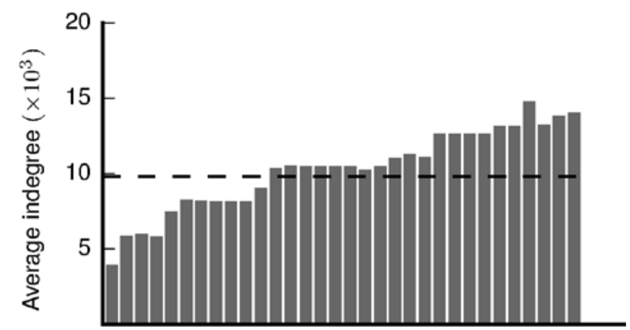
CORTICAL AREAS ARE NOT ALL THE SAME

- 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*



high neuron density → low neuron density

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

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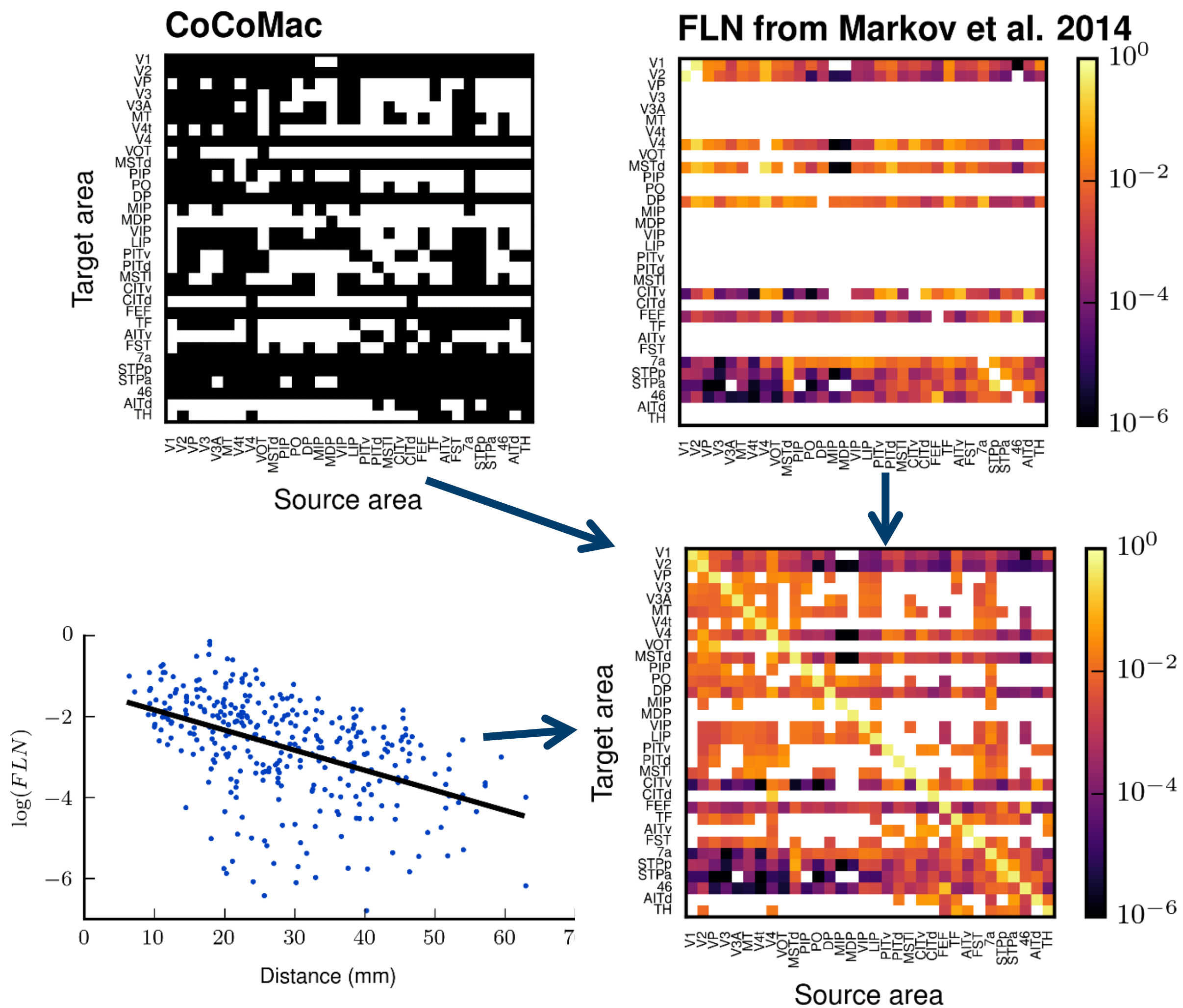
CONNECTIVITY MAP FROM TRACING DATA

- 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 ~6 orders of magnitude



Ercsey-Ravasz et al. (2013) *Neuron*

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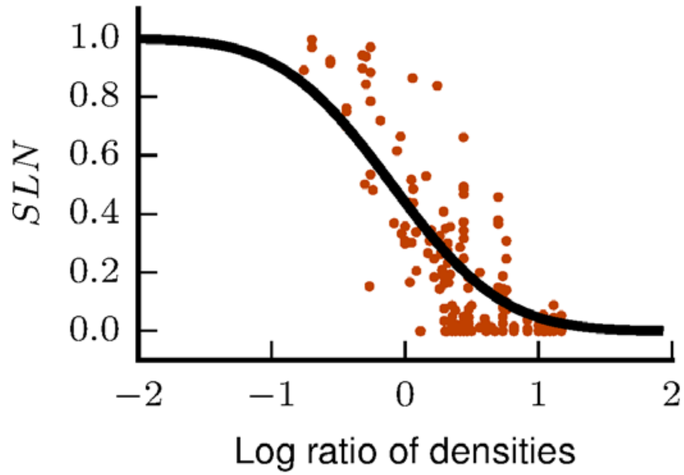
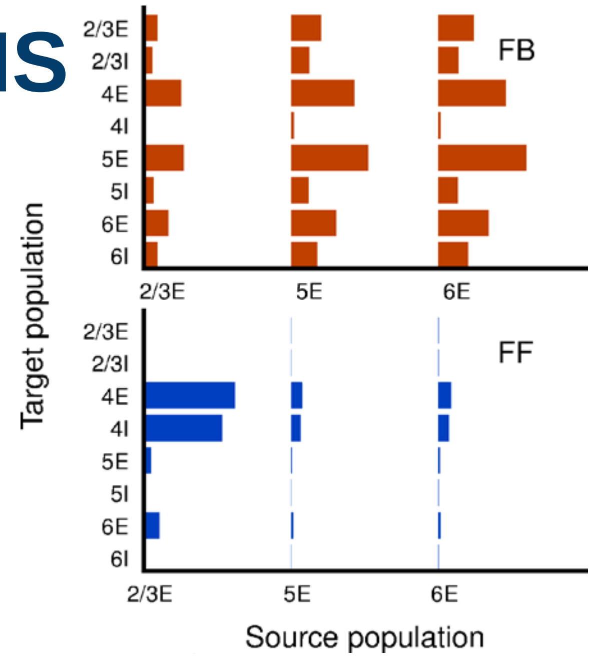
LAMINAR PATTERNS

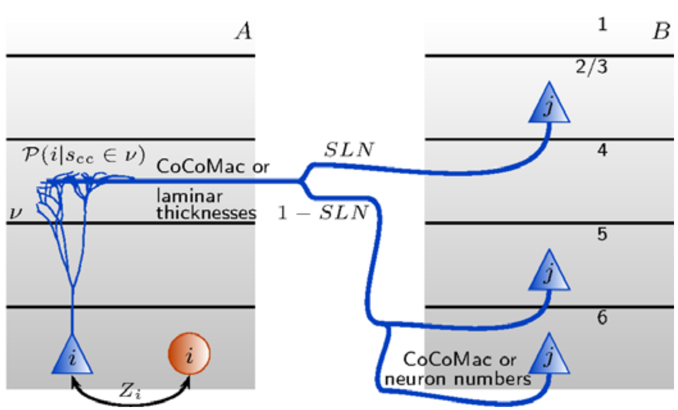


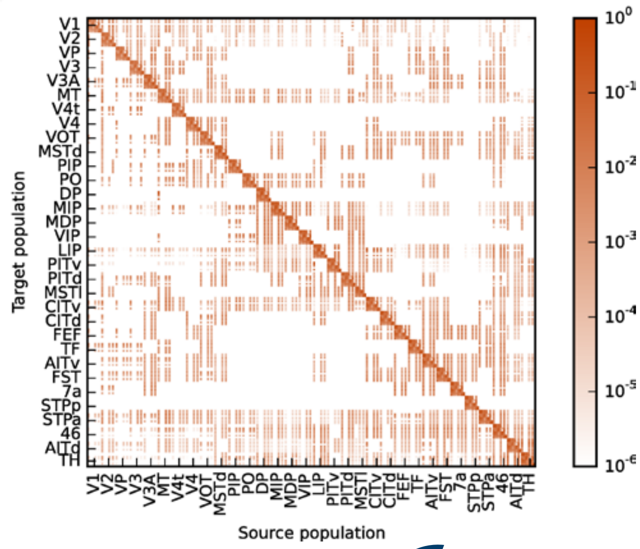


statistical mapping of synapses to target cell bodies according to Binzegger et al. (2004) cat V1 morphologies

→ predicts substantial feedback onto L4 pyramidal neurons

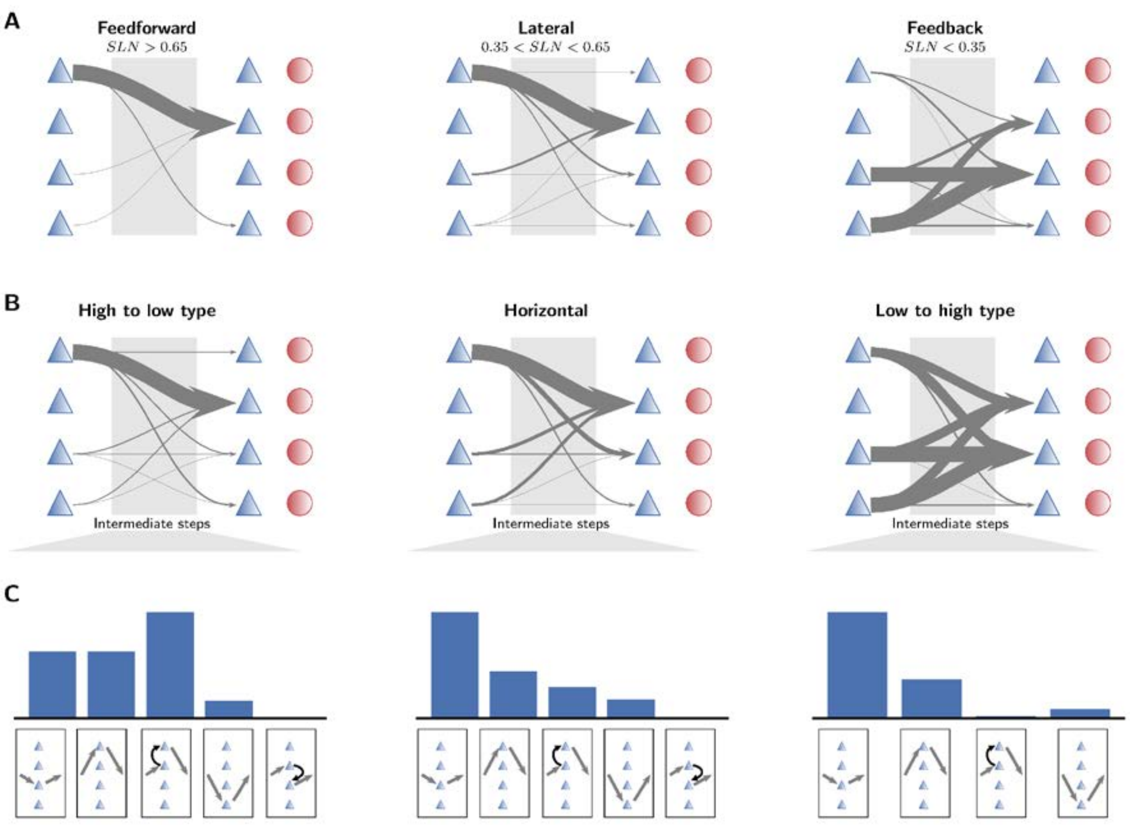
SLN = fraction of supragranular labeled neurons

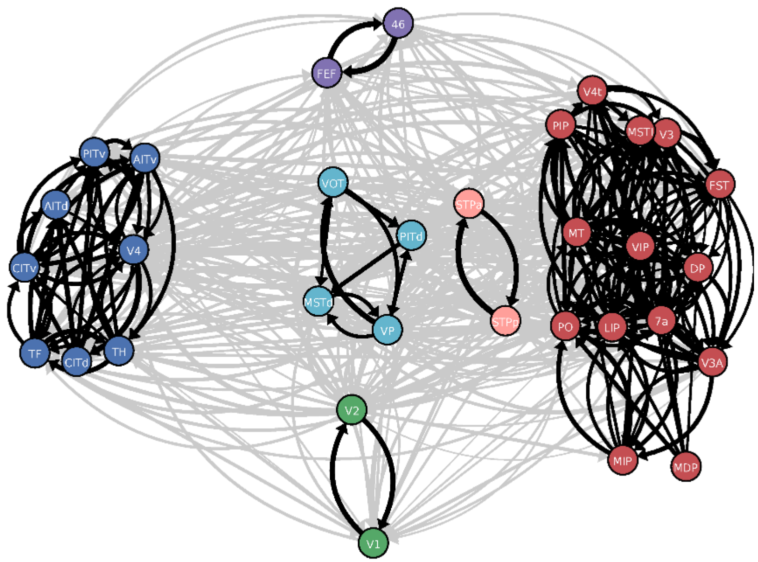




CONNECTIVITY ANALYSIS

data integration enables novel characterization of laminar pathways





structural connectivity reveals functionally relevant community structure

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

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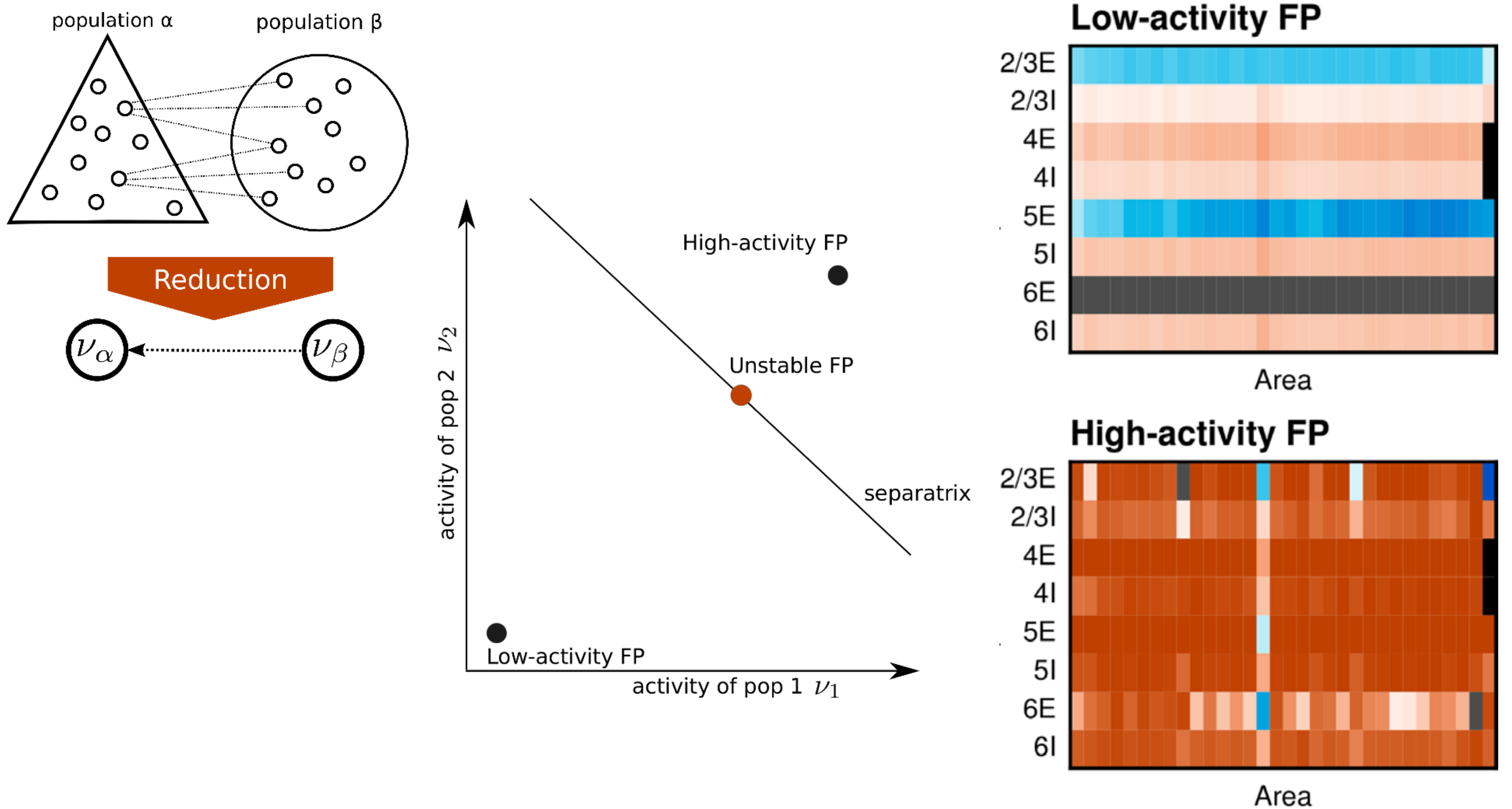
BISTABLE GROUND STATE

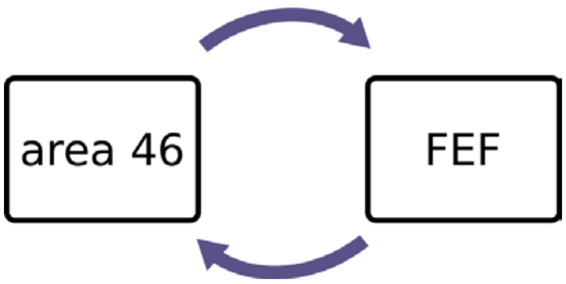
- low rates of excitatory neurons in infragranular layers
- increasing external drive leads to high-activity state with excessive rates

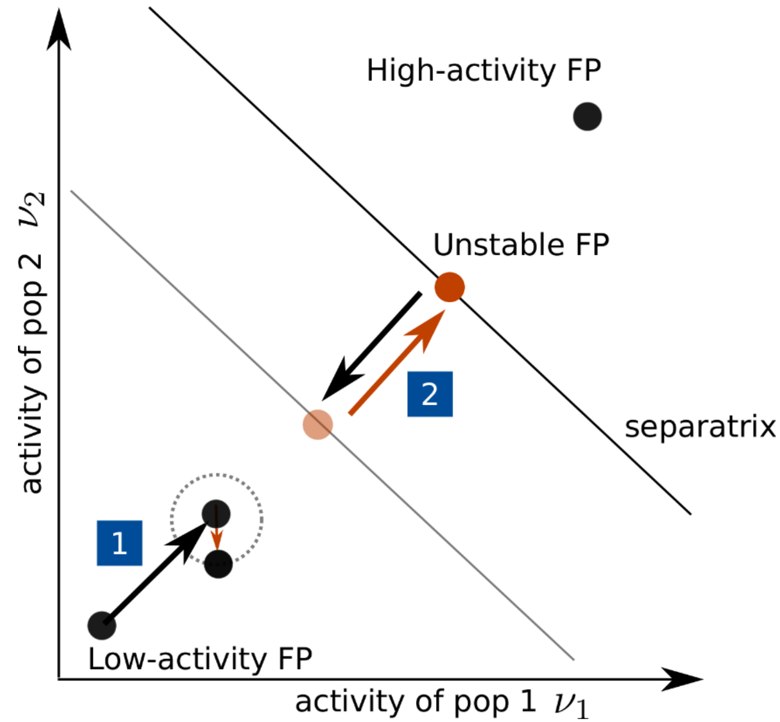


STABILIZATION USING MEAN-FIELD THEORY

1) increase in external drive shifts both low-activity fixed point and separatrix
2) compensation by change in connectivity shifts back separatrix

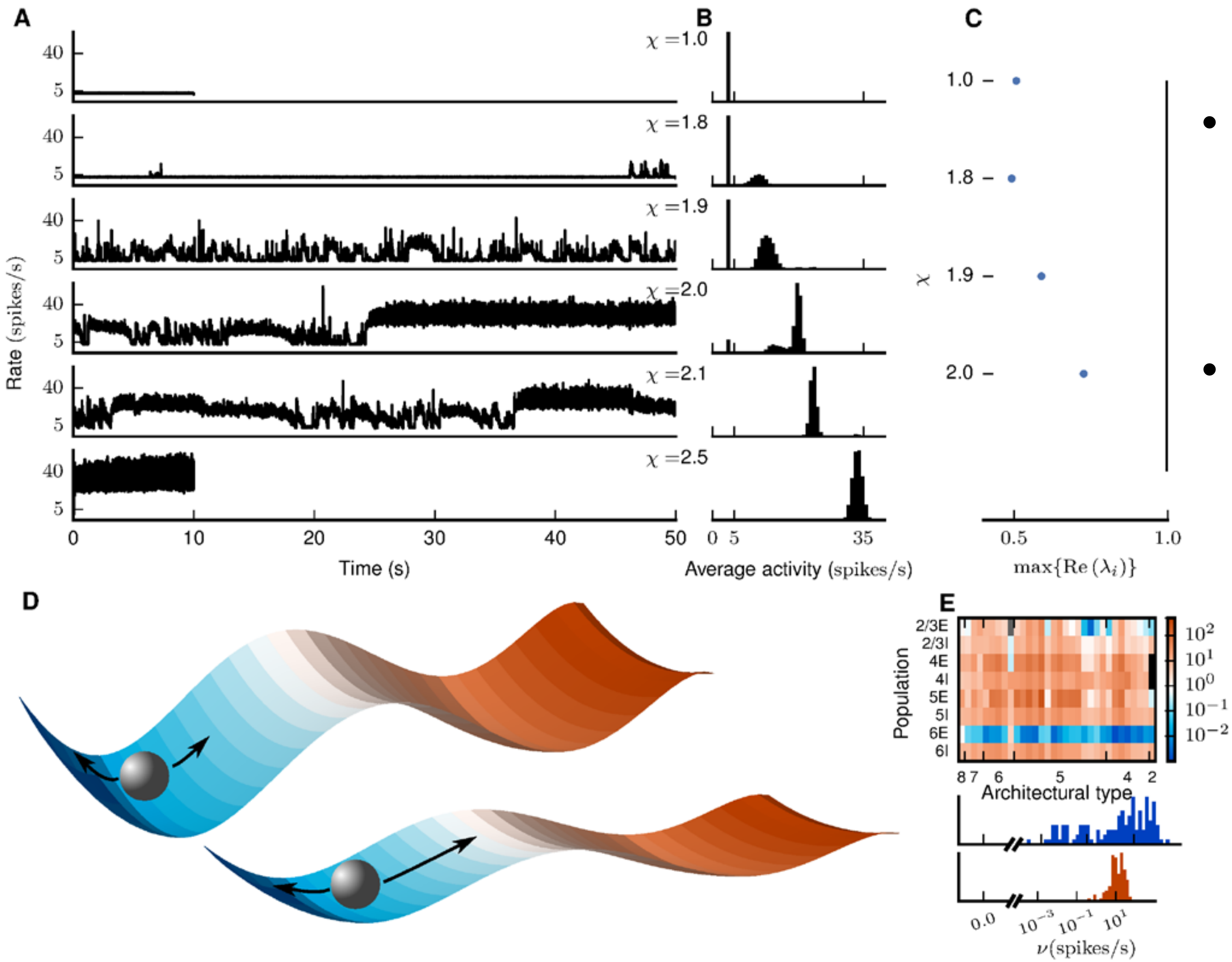
- yields reasonable rates in all populations
- reduced connectivity in frontal loop





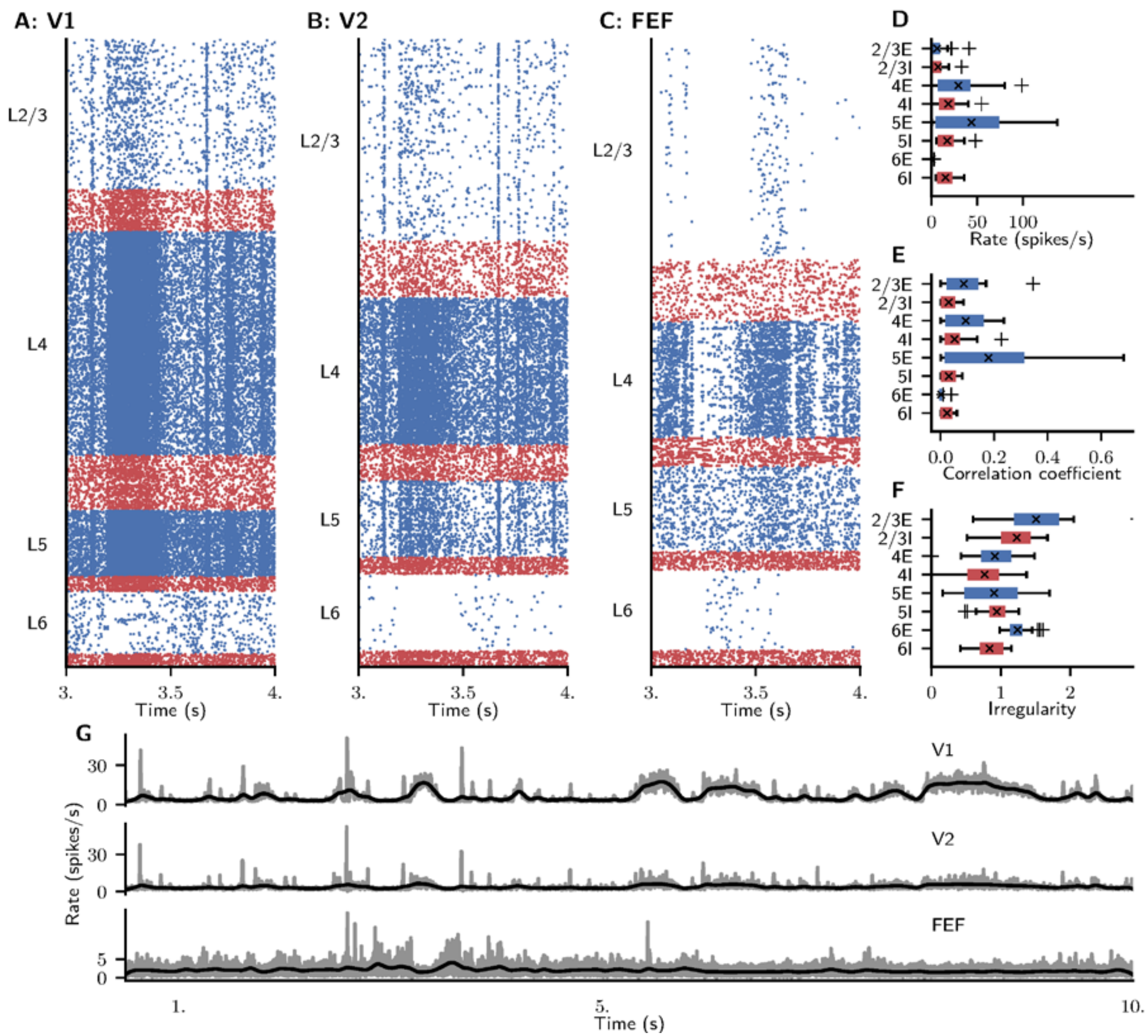
Schuecker J, Schmidt M, van Albada SJ, Diesmann M, Helias M (2017) *PLOS CB*

EMERGENCE OF META-STABLE NETWORK DYNAMICS



- well-known phenomenon of dynamical slowing near instability
- confirms metastability previously found in less detailed simulation studies Deco et al. 2009 *PNAS*, Cabral et al. 2011 *NeuroImage*; Deco and Jirsa 2012 *J Neurosci*; Cabral et al. 2014 *Prog Neurobiol*

GROUND STATE WITH MULTIPLE TIME SCALES



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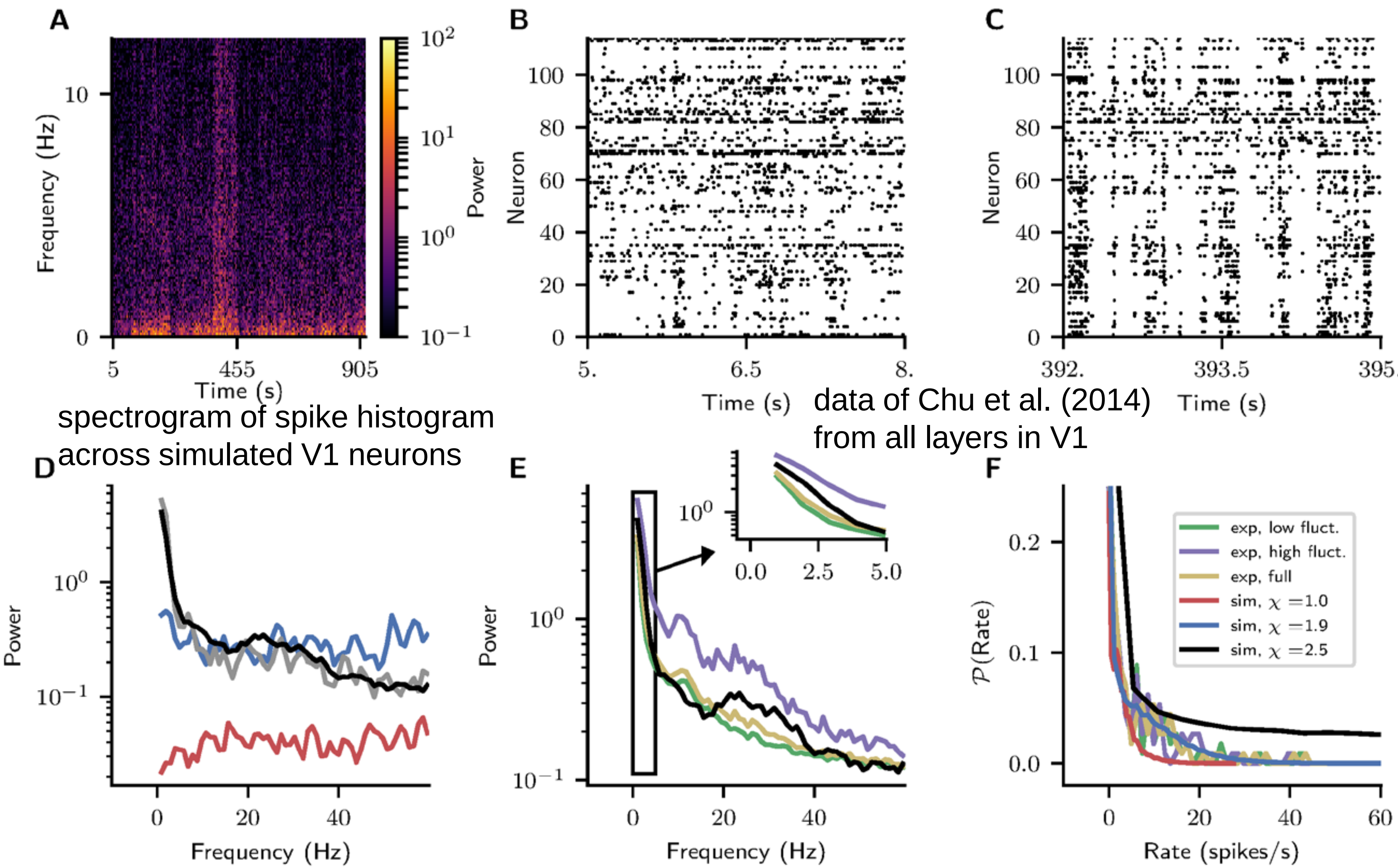
V1 SPIKING STATISTICS



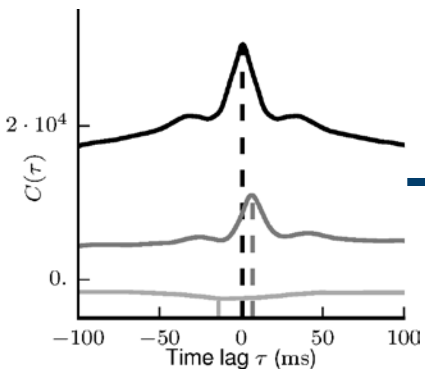
spectrogram of spike histogram across simulated V1 neurons

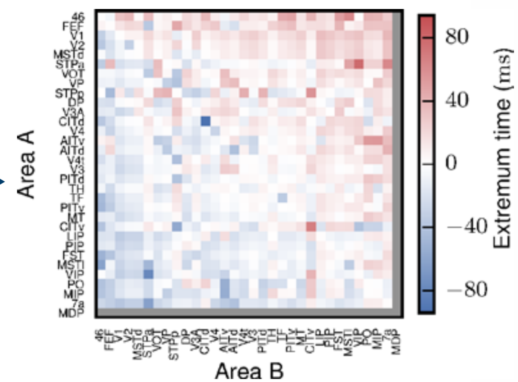
data of Chu et al. (2014) from all layers in V1

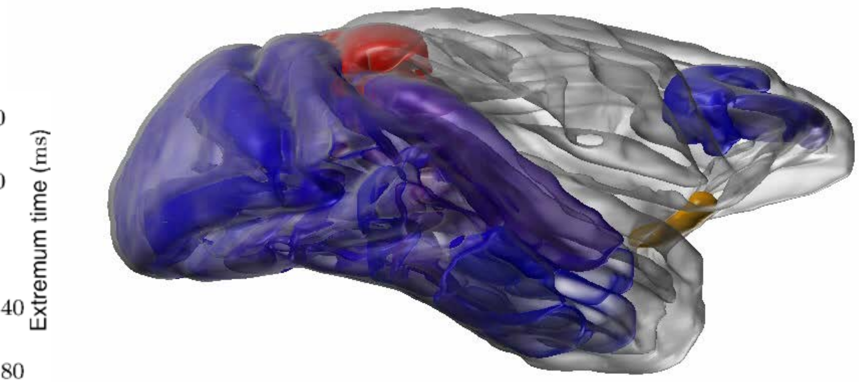
simulations with weak (red), medium (black/gray), and strong (blue) cortico-cortical interactions

comparison of power spectra and rate distributions between simulation and experiment

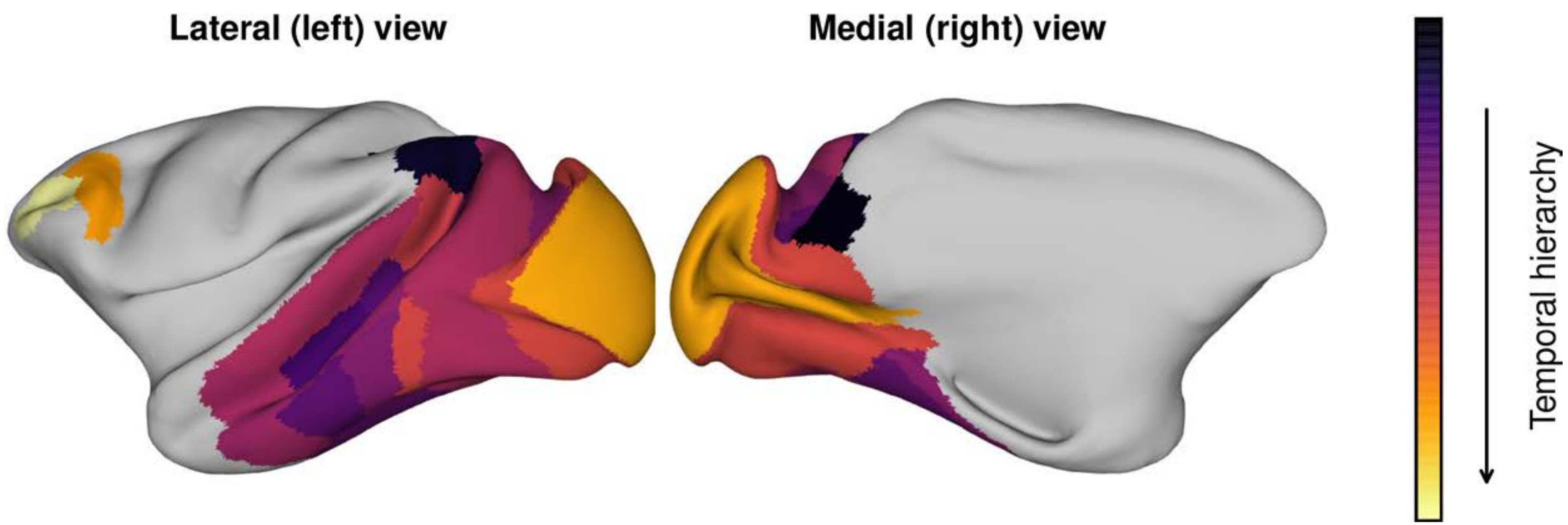
TEMPORAL HIERARCHY







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



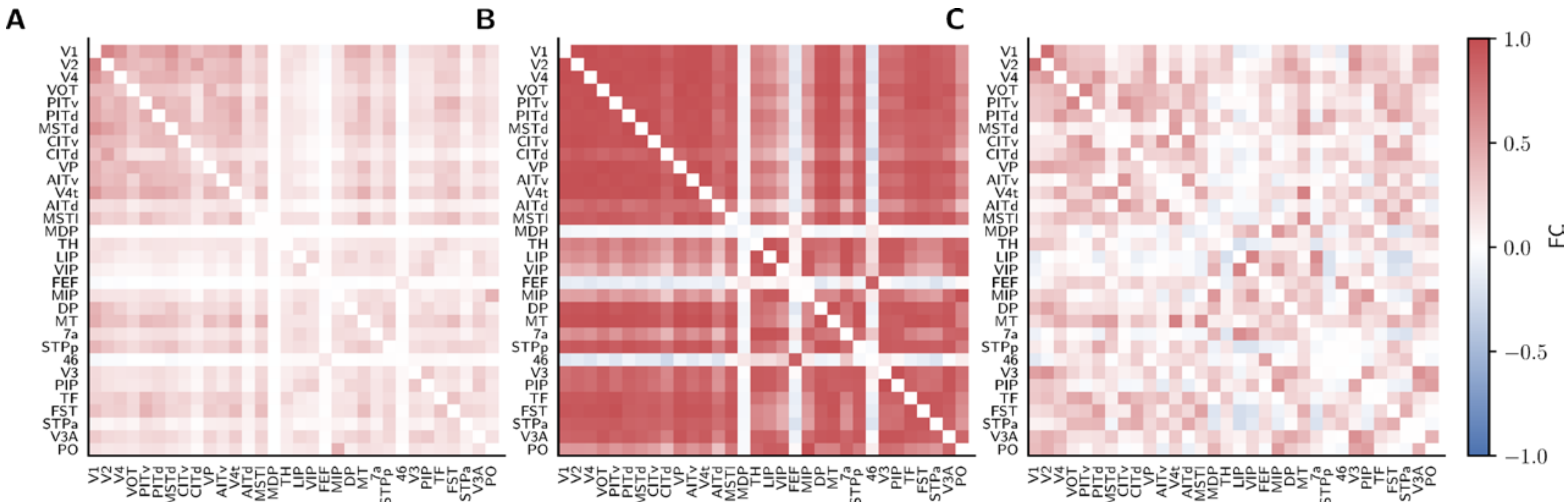
FUNCTIONAL CONNECTIVITY

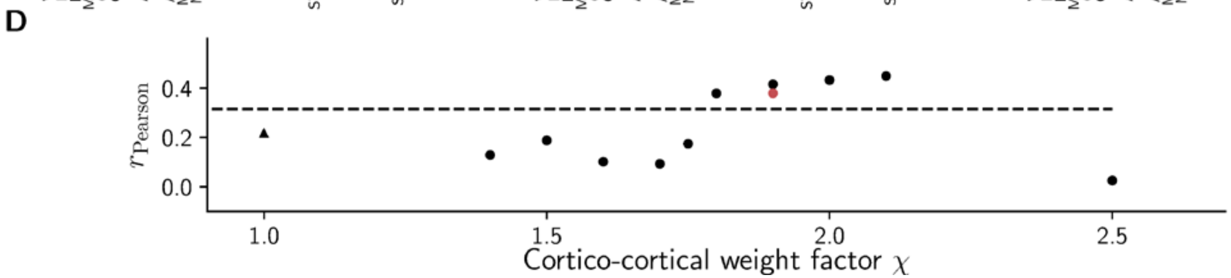
inter-area interactions in metastable state resemble experimental resting-state fMRI

correlations between simulated synaptic inputs

Balloon model applied to simulated inputs

fMRI functional connectivity averaged over six monkeys





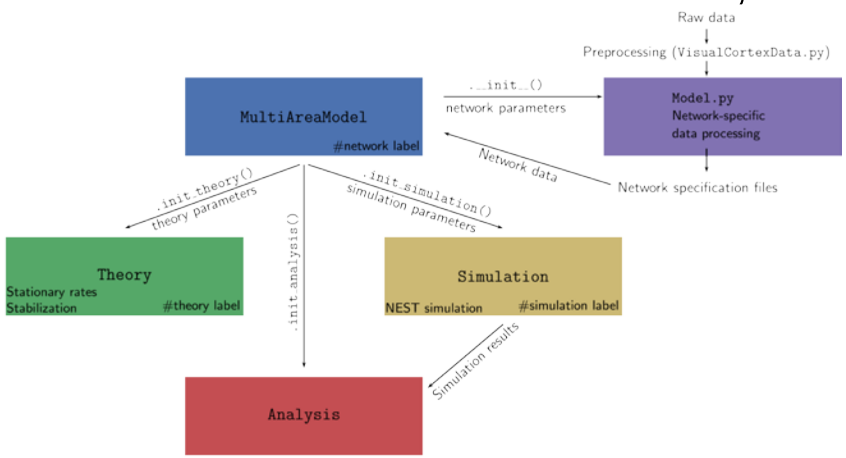
black: raw inputs

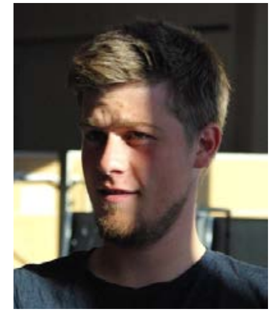
red: Balloon model applied to inputs (100 s simulation)

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

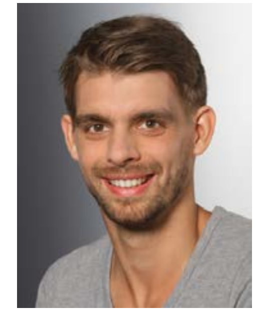
IMPLEMENTATION AND HURDLES

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





Maximilian Schmidt



Alexander van Meegen

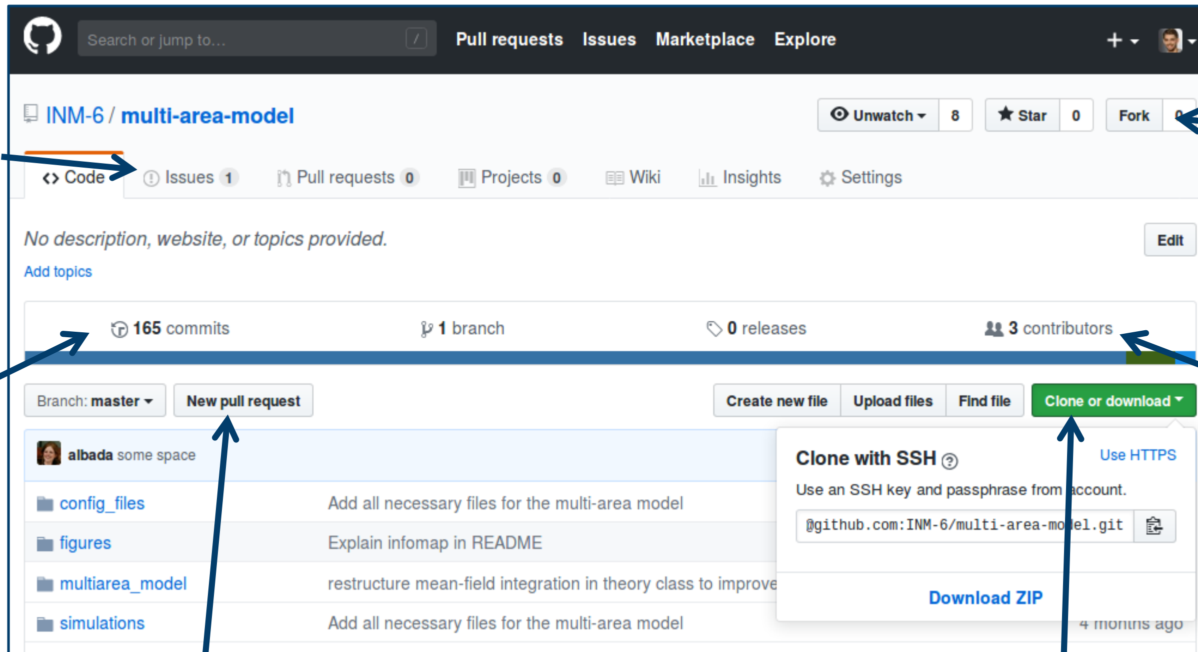
- M created private GitHub repository, added files; created README; extended documentation
- M requested permission to publish data; *not yet obtained* → start from processed data
- S & especially A reviewed code → knowledge about model transferred from M to A
- mean-field integration gave different results on different machines
    - problem with package versions? → use Conda
        - problem persisted → check OS environment, incl. GSL
            - problem persisted → create minimal reproducer
                - NEST turned out not to combine well with Conda → *under investigation*

GITHUB REPOSITORY

https://github.com/INM-6/multi-area-model

landing page

code is actively maintained, issues and solutions are tracked



fork to start building your own work on top of the model

code is alive, frequent new commits

multiple contributors, detailed knowledge beyond main author

enhance the model via pull requests

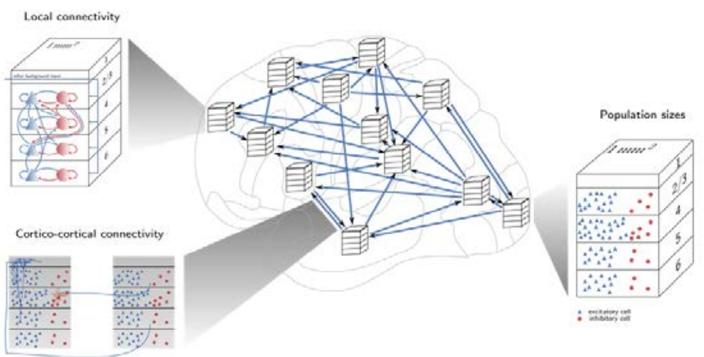
clone to get local copy of the code

EXTENSIVE README

README.md

Multi-scale spiking network model of macaque visual cortex

python 3.6 | nest | License CC BY-NC-SA 4.0



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_dicthash (https://github.com/INM-6/python-dicthash), 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/.

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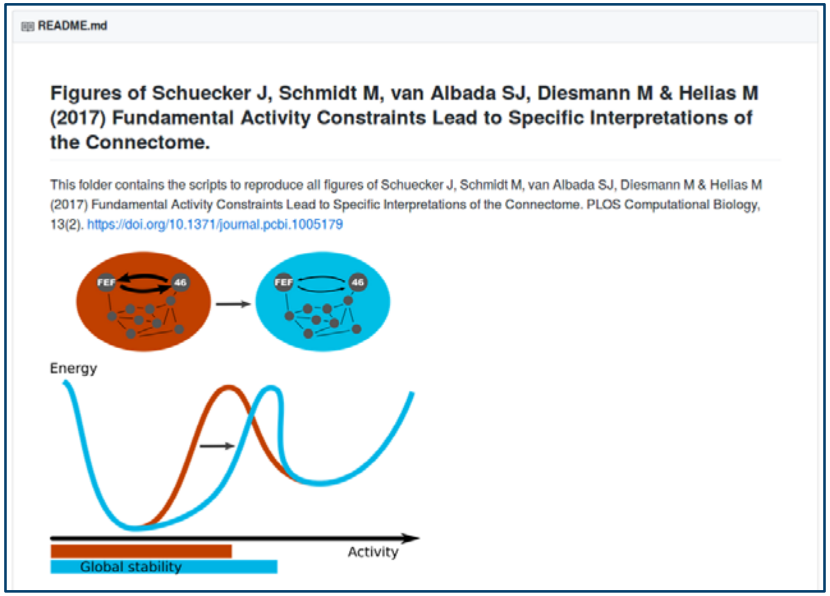
REPRODUCING FIGURES

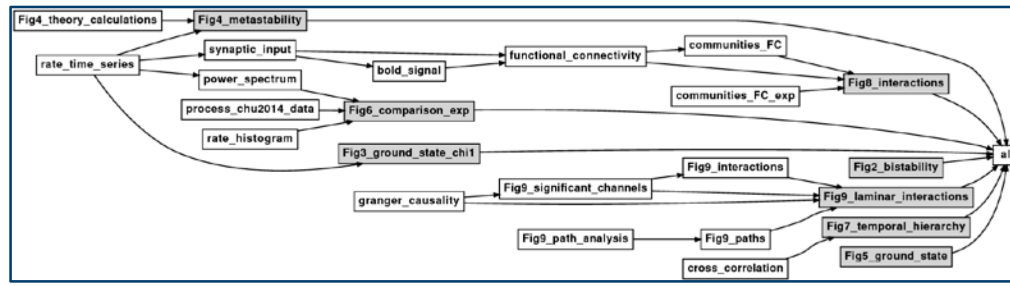

README.md

Figures of Schuecker J, Schmidt M, van Albada SJ, Diesmann M & Helias M (2017) Fundamental Activity Constraints Lead to Specific Interpretations of the Connectome.

This folder contains the scripts to reproduce all figures of 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). https://doi.org/10.1371/journal.pcbi.1005179

additional README with specific instructions for each publication

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



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

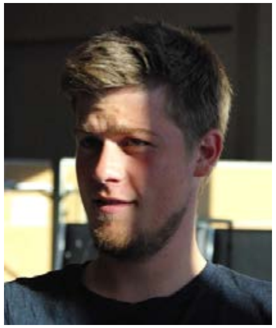
  → Sumatra; Conda
- be provenance-tracked; enable continued development

  → Sumatra; GitHub

ACKNOWLEDGMENTS

Jülich

modeling, theory



Maximilian Schmidt

testing

Alexander van Meegen

anatomical data

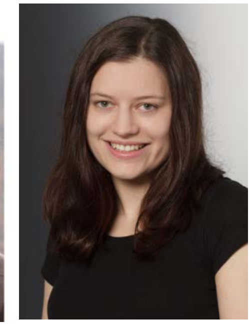
Rembrandt Bakker

Jannis Schuecker

theory

Moritz Helias

performance measurements



Johanna Senk

Markus Diesmann

fMRI data

Kelly Shen
Baycrest, Toronto

Gleb Bezgin
McGill, Montreal

anatomy

Claus Hilgetag
UKE Hamburg

Manchester (SpiNNaker)

Andrew Rowley
Michael Hopkins
Alan Stokes
Dave Lester
Steve Furber