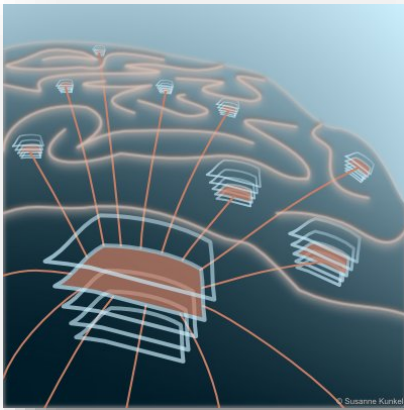




Necessity and feasibility of brain-scale simulation at cellular and synaptic resolution

April 24-29 2016
Workshop on High-Performance Computing,
Stochastic Modeling and Databases in Neuroscience
NeuroMat
São Paulo, Brazil

Markus Diesmann
Institute of Neuroscience and Medicine (INM-6)
Institute for Advanced Simulation (IAS-6)
Jülich Research Centre

Team

modeling



Maximilian Schmidt



Sacha J van Albada

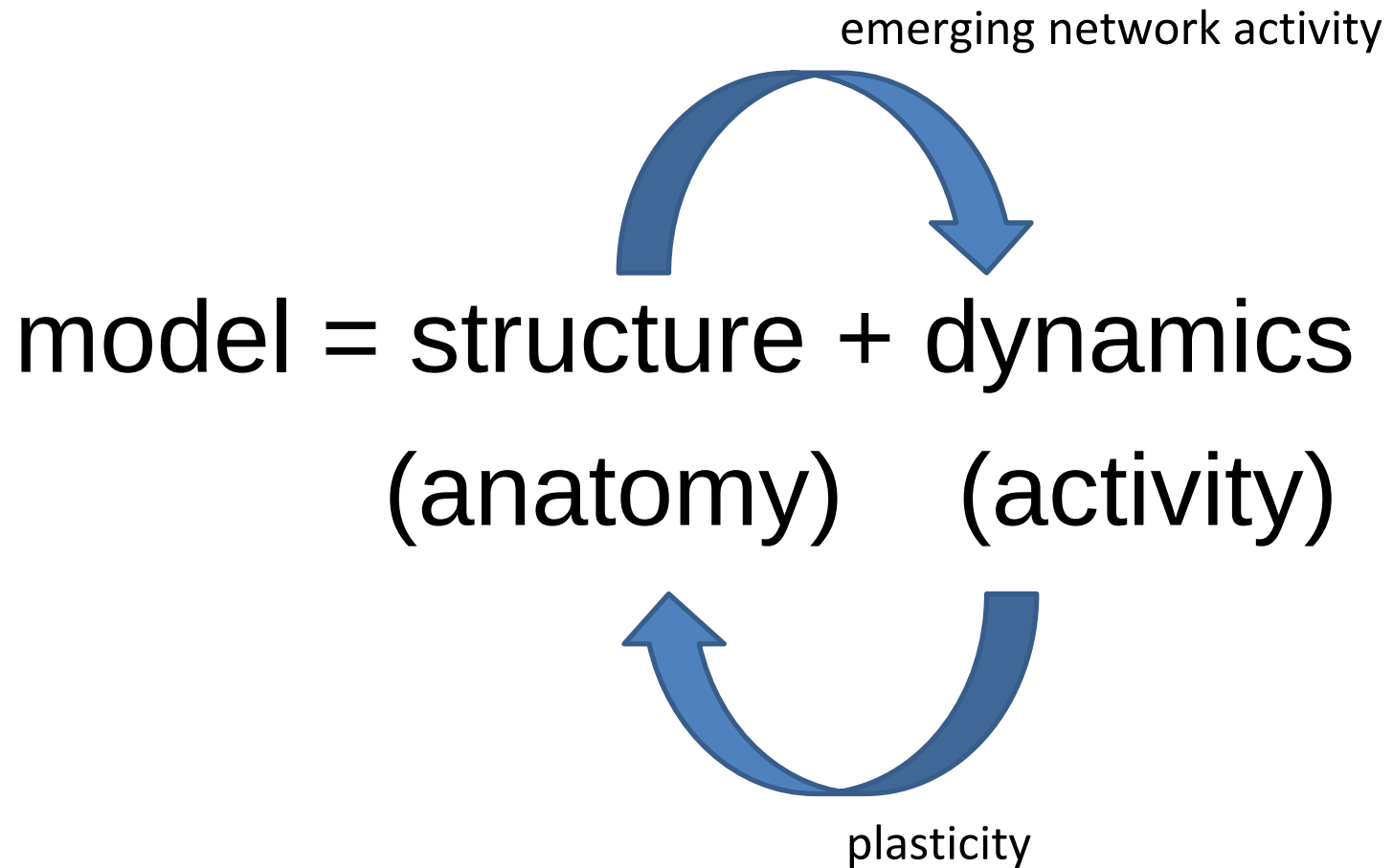
reproducibility



Sonja Gruen

others mentioned on the way

Model components in neuroscience



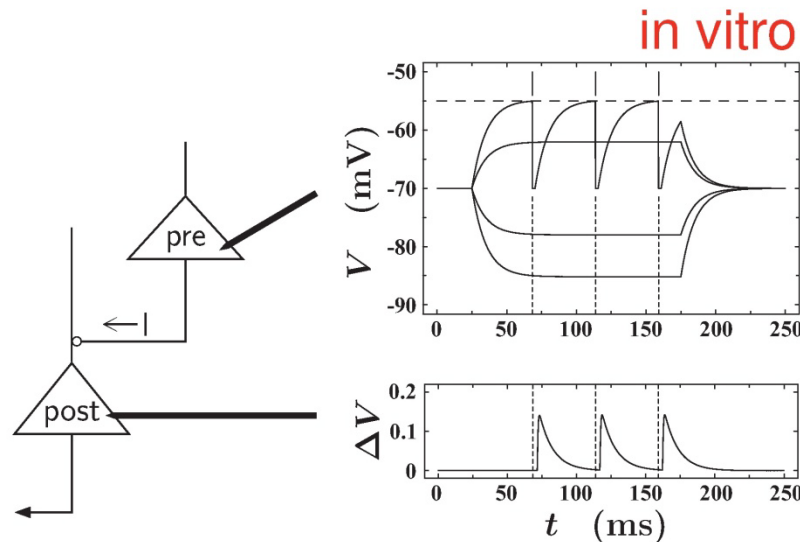
Top-down and bottom-up

the computer analogy:

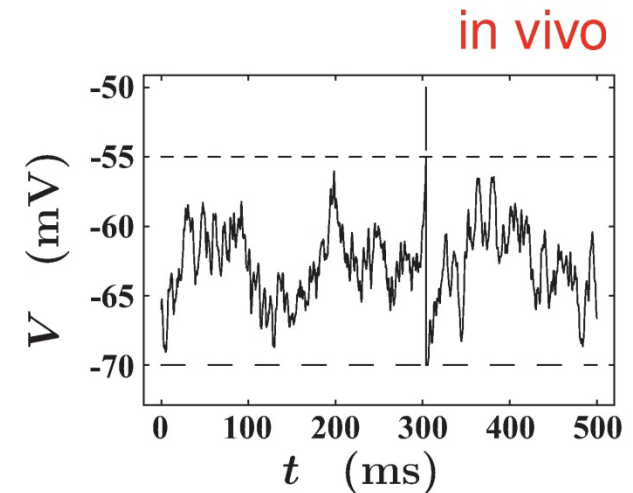
system	computer	brain	
top	multiplication	maze navigation	system-level behavior
	↓	↓	
	logical algorithm	TD-learning	system-level theory
	↕	↕ ?	
	electrical circuit	neuronal network	
	↑	↑	
	transistor	I&F neuron model	
	↑	↑	
bottom	electrons	spikes	(bio)physics

comparison between levels: compatibility and consistency

Interactions between neurons



- current injection into pre-synaptic neuron causes excursions of membrane potential
- supra-threshold value causes spike transmitted to post-synaptic neuron
- post-synaptic neuron responds with small excursion of potential after delay
- inhibitory neurons (20%) cause negative excursion



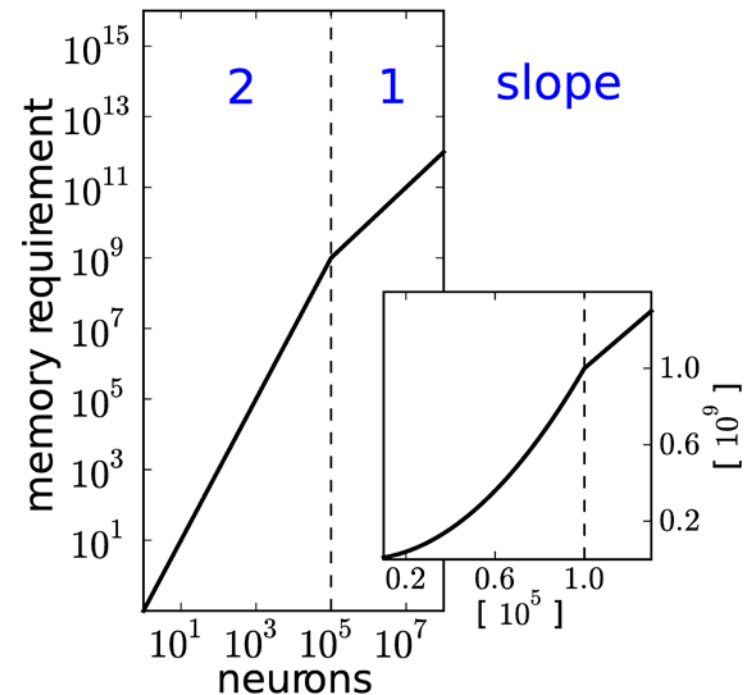
- each neuron receives input from 10,000 other neurons
- causing large fluctuations of membrane potential
- emission rate of 1 to 10 spikes per second

Realistic local cortical networks

- connectivity $c = 0.1$
- synapses per neuron = 10^4
- ⇒ minimal network size = 10^5

- network $N = 10^5$
 - considered **elementary unit**
 - corresponding to 1 mm^3

- total number of synapses = $(cN) \cdot N$ ⇒ possible

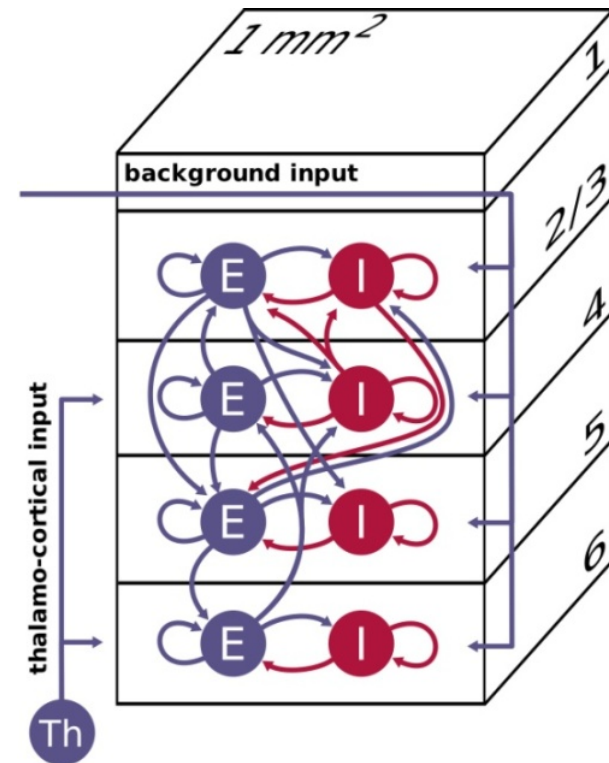


Morrison A, Mehring C, Geisel T, Aertsen A, Diesmann M (2005) Neural Comput 17(8):1776-1801

Morrison A, Straube S, Plesser HE, Diesmann M (2007) Neural Comput 19(1):47-79

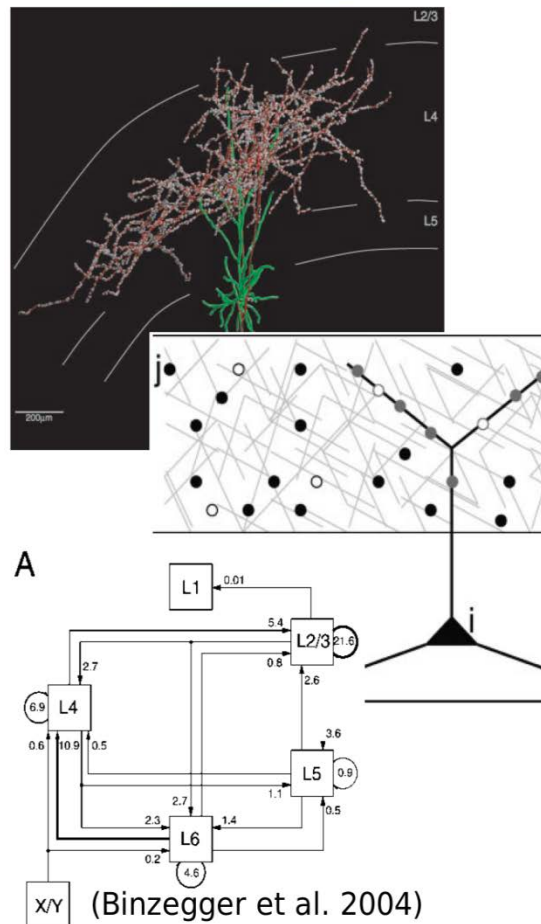
Minimal layered cortical network model

- 1 mm^3
- 1 billion synapses, 100,000 neurons
- 2 populations of neurons per layer:
 - E: Excitatory
 - I: Inhibitory
- E and I identical neuronal dynamics
- laterally homogeneous connectivity
- layer- and type-specific C_{ij}^{xy}

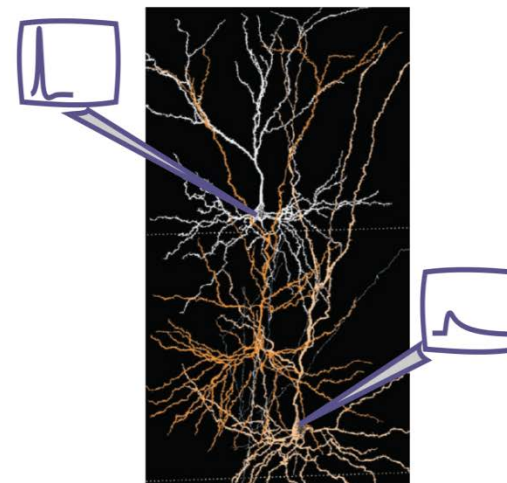


Anatomical data sets

in vivo anatomy



in vitro physiology



Type of connection^a Connectivity ratio

L5 pyramid to L5 pyramid	1:11 (15:163)
L2/3 pyramid to L2/3 pyramid	1:4 (65:247)
	1:10 (8:81)
L4 excitatory to L4 excitatory	1:5.7 (4:23)
L3 pyramid to L5 pyramid	1:1.8 (16:29)
[Postsynaptic apical dendrite]	
	1:1 (2:2)
L5 pyramid to L3 pyramid	1:29
L4 excitatory to L3 pyramid	1:3.6 (7:25)
(Presynaptic spiny stellates) (<i>n</i> = 4)	1:10 (7:70)
L5 pyramid to L5 interneuron	1:10.4 (7:73)
L5 interneuron to L5 pyramid	1:8 (9:73)

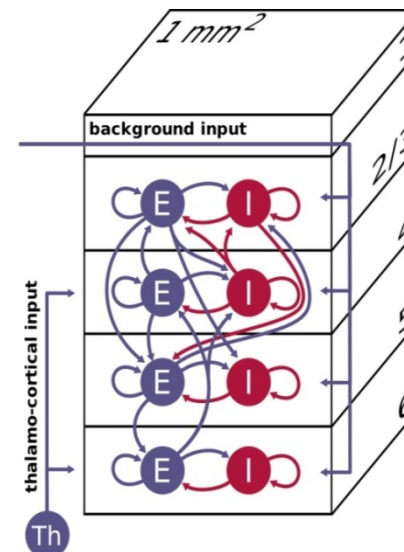
(Thomson et al. 2002)

Local cortical microcircuit

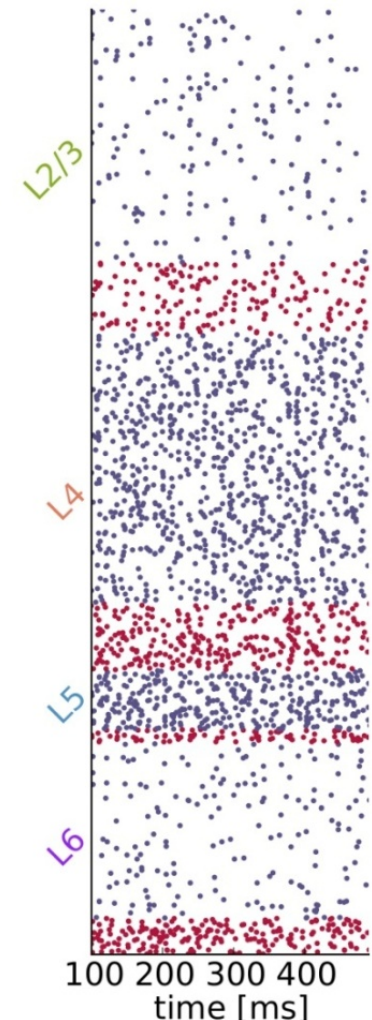
taking into account layer and neuron-type specific connectivity is sufficient to reproduce experimentally observed:

- asynchronous-irregular spiking of neurons
- higher spike rate of inhibitory neurons
- correct distribution of spike rates across layers
- integrates knowledge of more than 50 experimental papers

Potjans TC & Diesmann M (2014) The cell-type specific connectivity of the local cortical network explains prominent features of neuronal activity. *Cerebral Cortex* 24 (3): 785-806

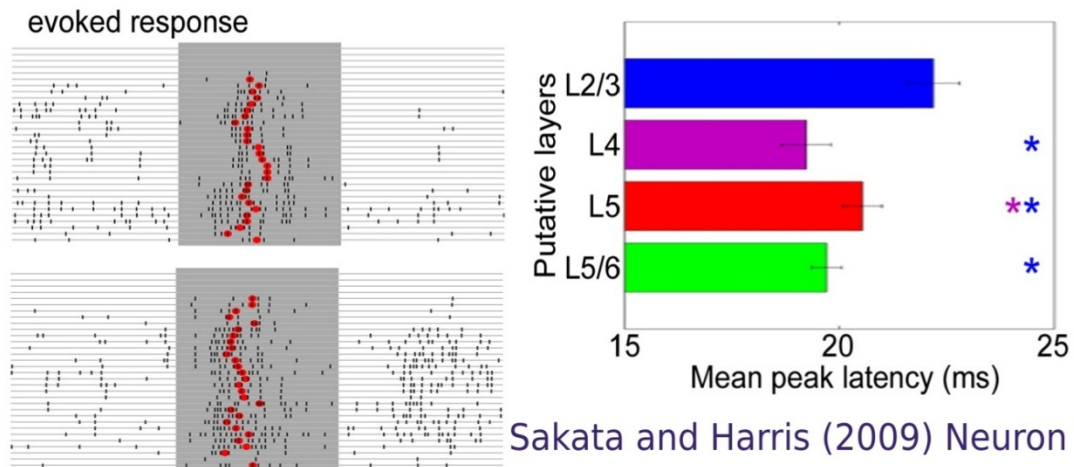
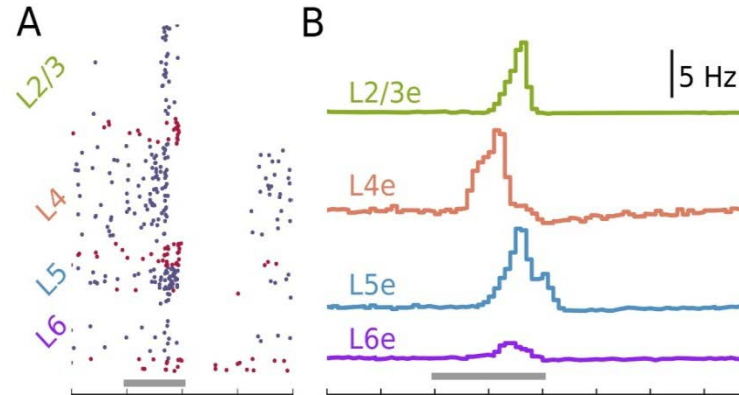


10^5 neurons
 10^9 synapses



available at: www.opensourcebrain.org

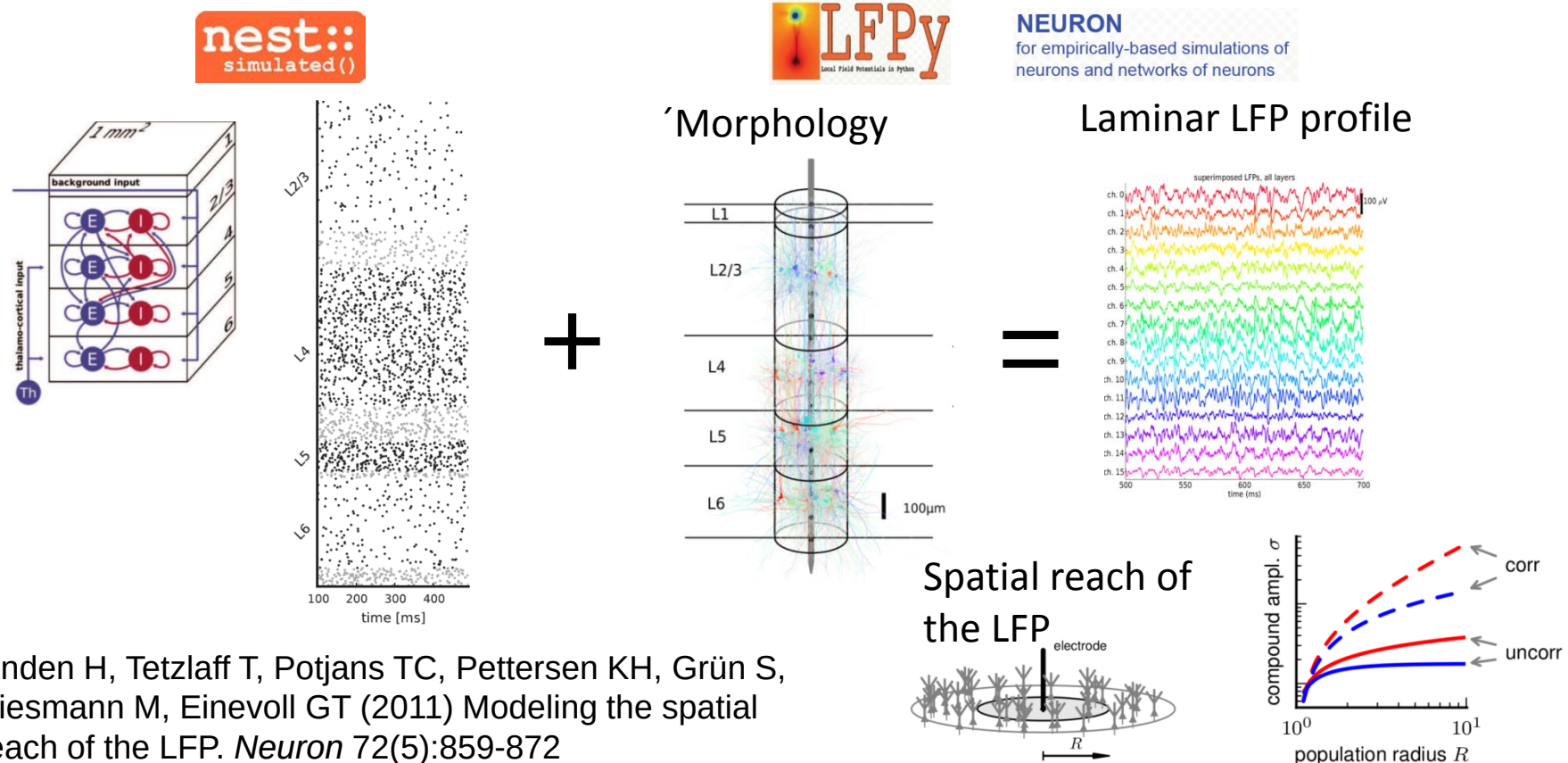
Response to transient inputs



Sakata and Harris (2009) Neuron

Building block for mesoscopic studies

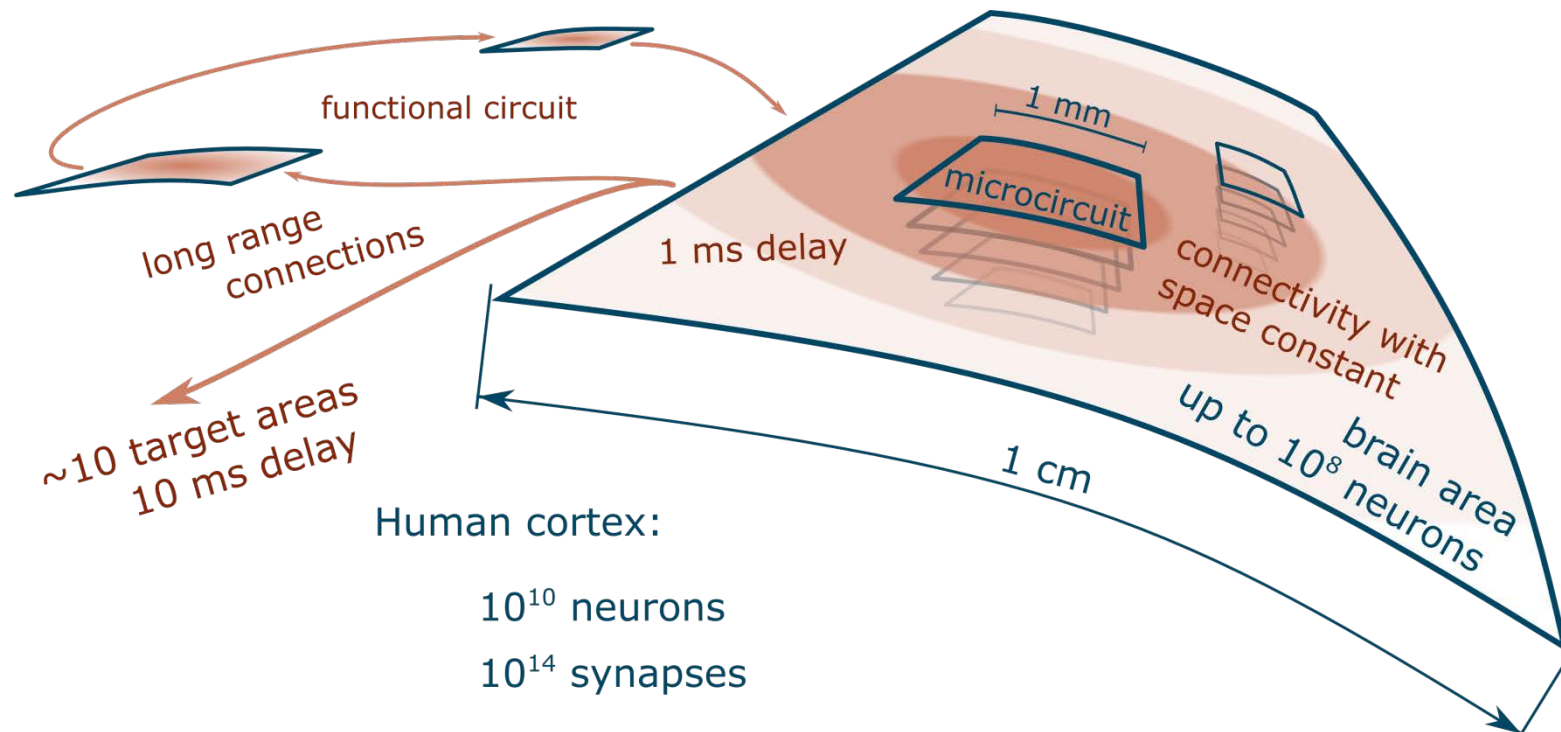
- collaboration with Gaute Einevoll (UMB, Norway)



Linden H, Tetzlaff T, Potjans TC, Pettersen KH, Grün S, Diesmann M, Einevoll GT (2011) Modeling the spatial reach of the LFP. *Neuron* 72(5):859-872

Critique of local network model

a **network of networks** with at least three levels of organization:



- neurons in local microcircuit models are missing 50% of synapses
- e.g., power spectrum shows discrepancies, slow oscillations missing
- solution by taking brain-scale anatomy into account

Meso- and macro-scale measures

brain-scale networks basis for:

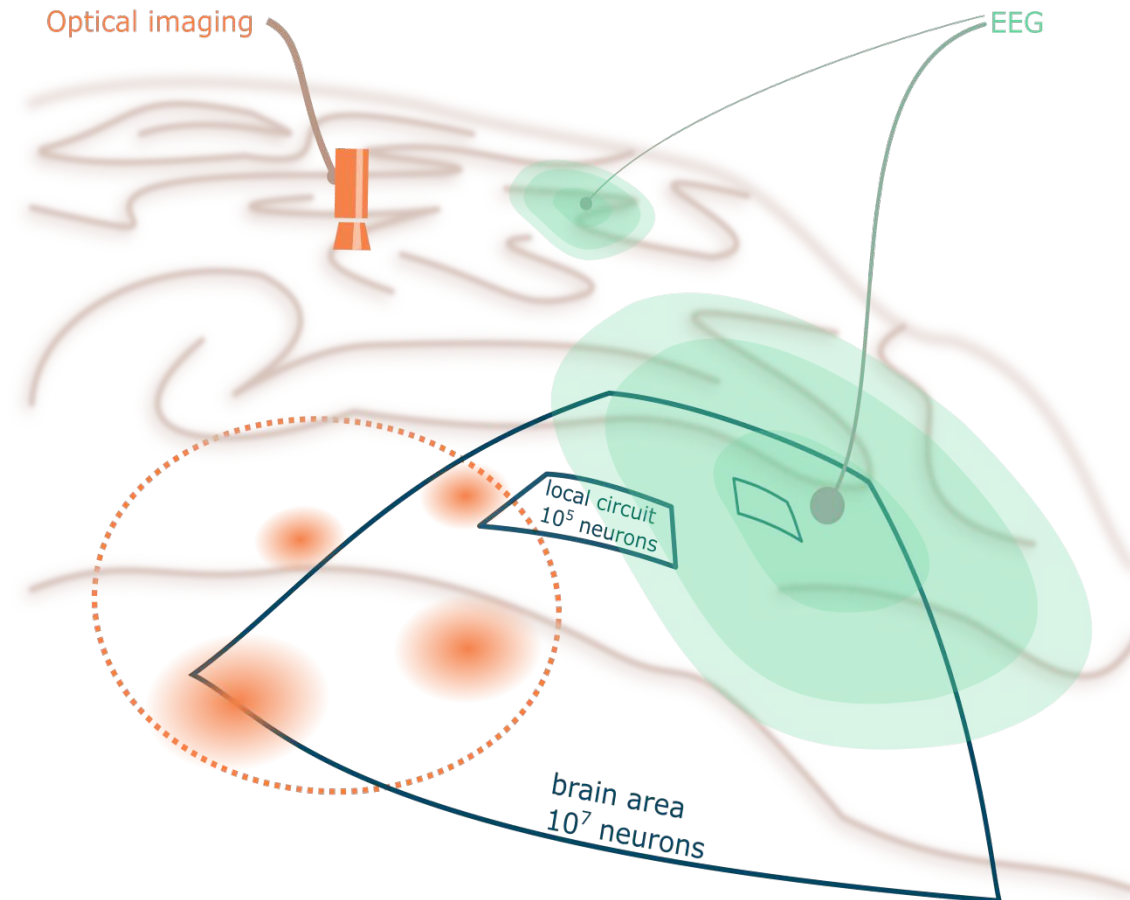
- further measures by forward modeling
- comparison with mean-field models

mesoscopic measures

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

and macroscopic measures

- EEG, MEG
- fMRI resting state networks



Feasibility and necessity

- Can we do simulations at the brain scale?
- Do we need to simulate full scale (at cellular resolution)?



Supercomputers ready for use as discovery machines for neuroscience

Moritz Helias^{1,2*}, Susanne Kunkel^{1,3,4}, Gen Masumoto⁵, Jun Igarashi⁶, Jochen Martin Eppler¹, Shin Ishii⁷, Tomoki Fukai⁶, Abigail Morrison^{1,3,4,8} and Markus Diesmann^{1,2,4,9}

¹ Institute of Neuroscience and Medicine (INM-6), Computational and Systems Neuroscience, Jülich Research Centre, Jülich, Germany

² RIKEN Brain Science Institute, Wako, Japan

³ Simulation Laboratory Neuroscience – Bernstein Facility for Simulation and Database Technology, Institute for Advanced Simulation, Jülich Aachen Research Alliance, Jülich Research Centre, Jülich, Germany

⁴ Bernstein Center Freiburg, Albert-Ludwig University of Freiburg, Freiburg, Germany

makes supercomputers
accessible for neuroscience

provides the evidence that neuroscience
can exploit petascale systems



Spiking network simulation code for petascale computers

Susanne Kunkel^{1,2*}, Maximilian Schmidt³, Jochen M. Eppler³, Hans E. Plesser^{3,4}, Gen Masumoto⁵, Jun Igarashi^{6,7}, Shin Ishii⁸, Tomoki Fukai⁷, Abigail Morrison^{1,3,9}, Markus Diesmann^{3,7,10} and Moritz Helias^{2,3}

¹ Simulation Laboratory Neuroscience – Bernstein Facility for Simulation and Database Technology, Institute for Advanced Simulation, Jülich Aachen Research Alliance, Jülich Research Centre, Jülich, Germany

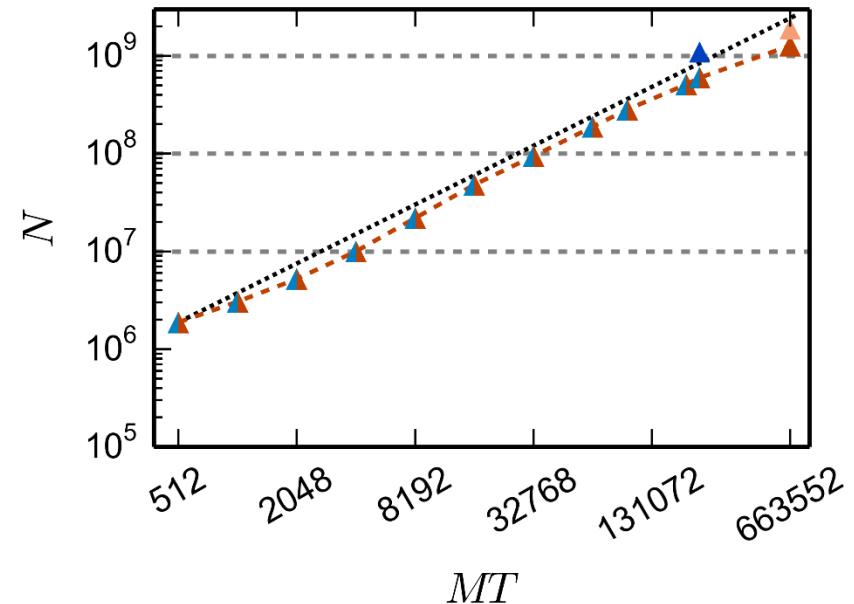
² Programming Environment Research Team, RIKEN Advanced Institute for Computational Science, Kobe, Japan

³ Institute of Neuroscience and Medicine (INM-6), Institute for Advanced Simulation (IAS-6), Jülich Research Centre and JARA, Jülich, Germany

⁴ Department of Mathematical Sciences and Technology, Norwegian University of Life Sciences, Aas, Norway

NEST – Maximum network size

- using 663,552 cores of K
- using 229,376 cores of JUQUEEN
- worst case: random network
- exc-exc STDP



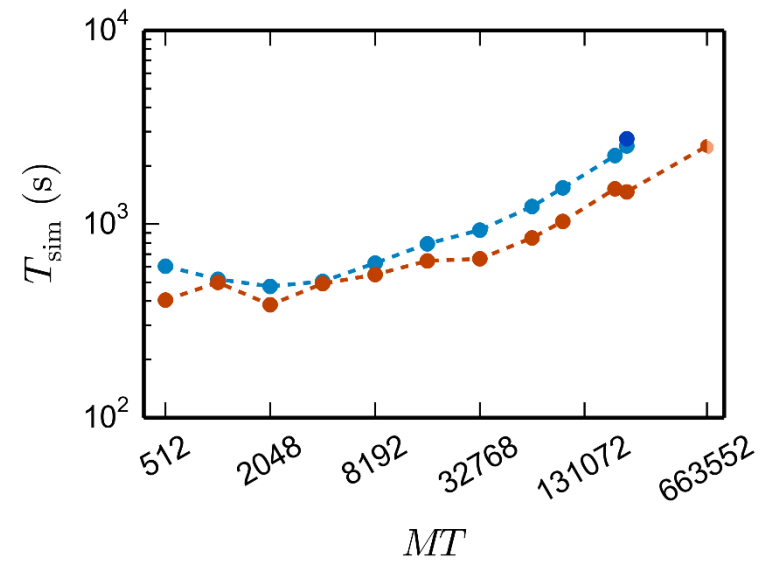
- largest general network simulation performed to date:
 - 1.86x10⁹ neurons, 6000 synapses per neuron
 - 1.08x10⁹ neurons, 6000 synapses per neuron



NEST simulation software

NEST – Scaling of run time

- runtime for 1 second biological time:
- between 6 and 42 min on K computer
- between 8 and 41 min on JUQUEEN
- wiring: between 3 and 15 min

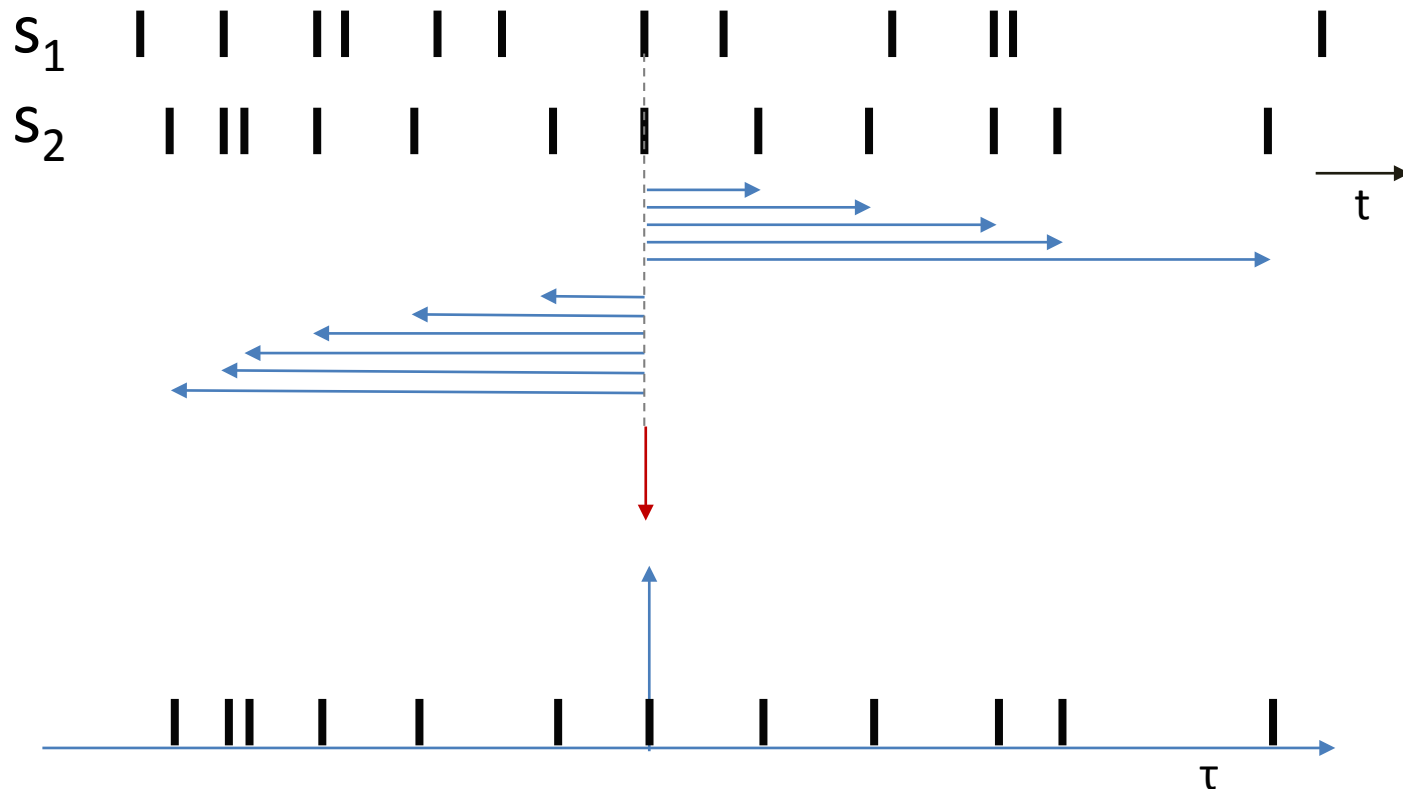


- still not fast enough for studies of plasticity
- need to increase multi-threading

Feasibility and necessity

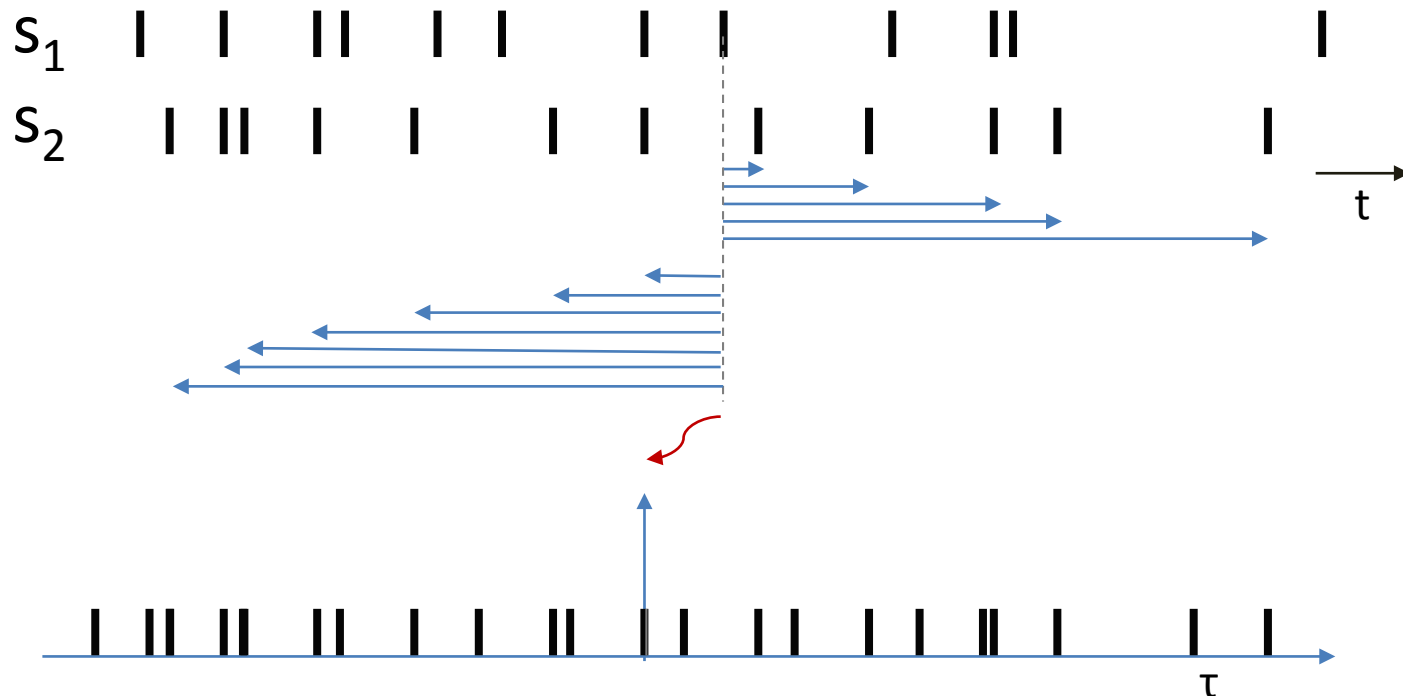
- Can we do simulations at the brain scale? ✓
- Do we need to simulate full scale (at cellular resolution)?

Measure of neural interaction: Cross-Correlation



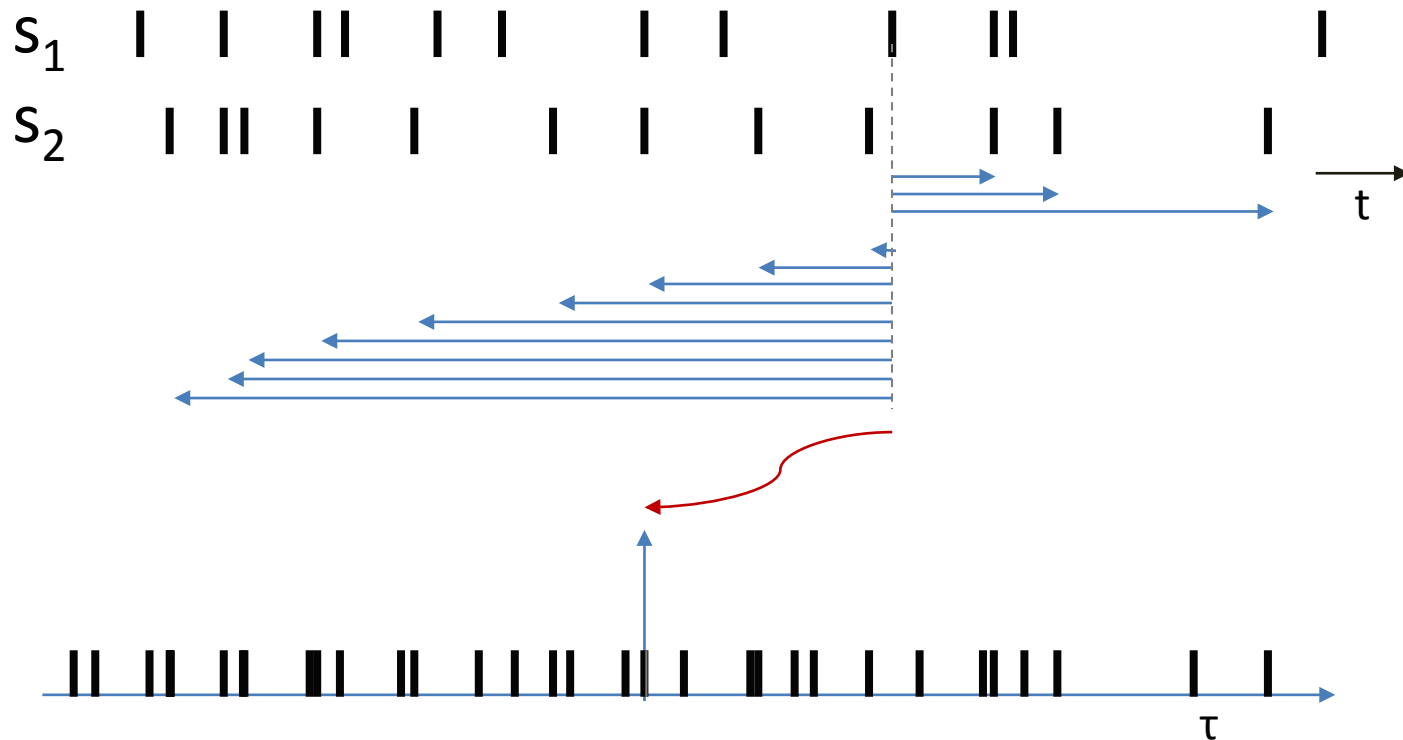
The cross-correlation represents the probability of finding any spike in train s_2 as a function of time before or after a spike in train s_1 : $\rho(\tau) = \int s_1(t)s_2(t - \tau)dt$

Cross-Correlation



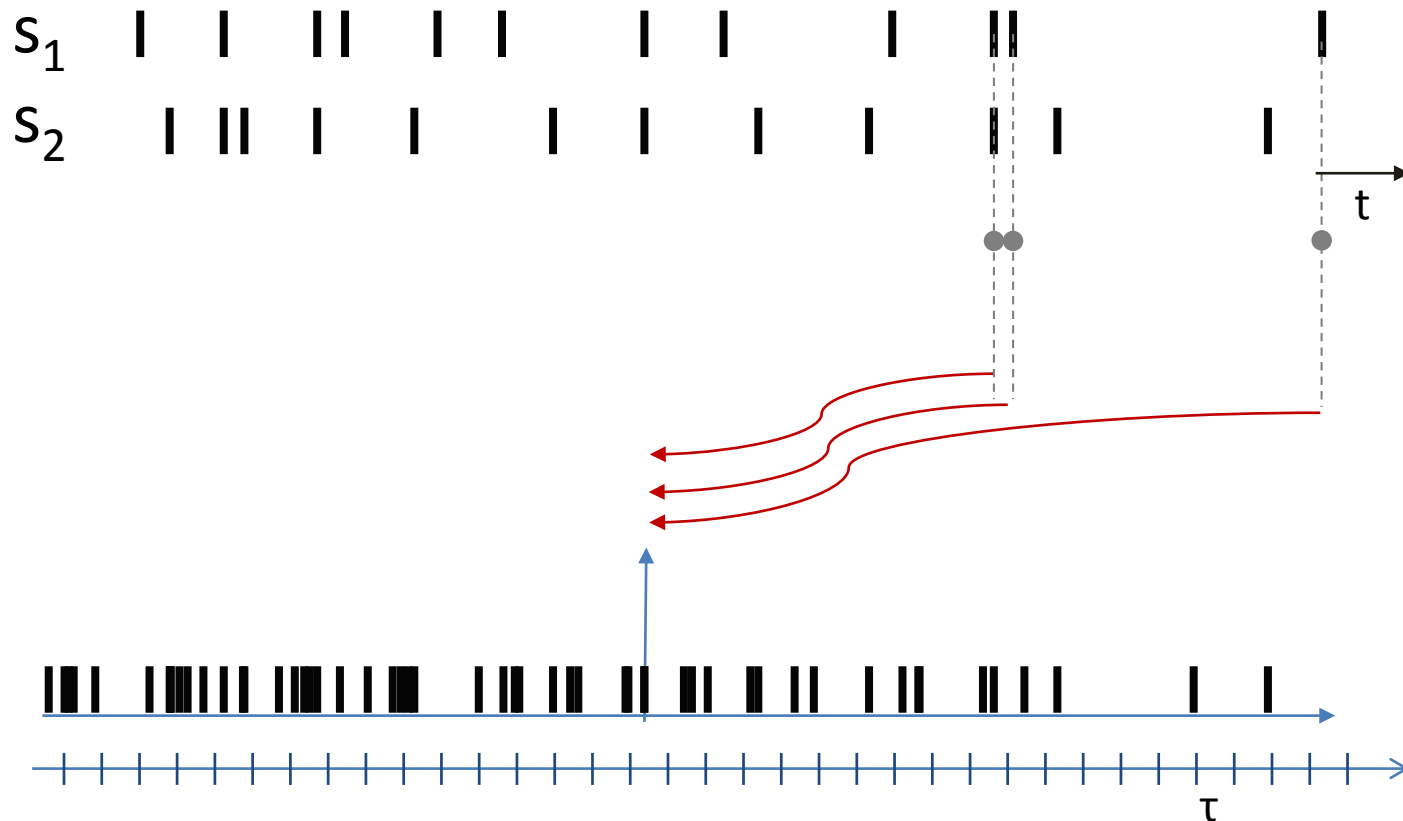
The cross-correlation represents the probability of finding any spike in train s_2 as a function of time before or after a spike in train s_1 : $\rho(\tau) = \int s_1(t)s_2(t - \tau)dt$

Cross-Correlation



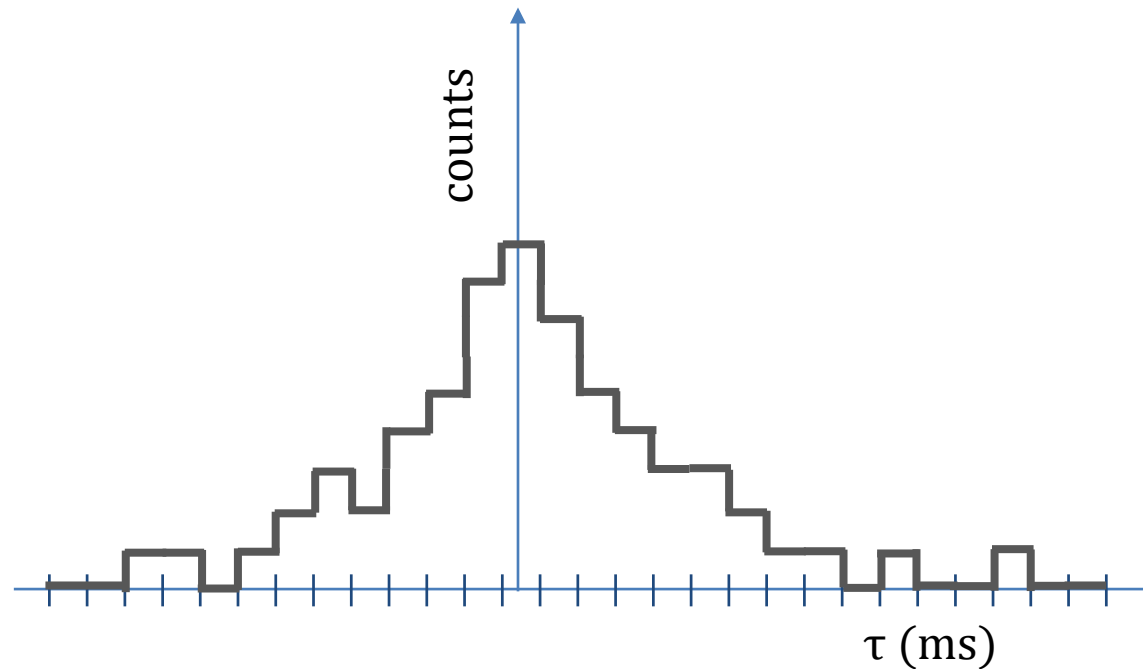
The cross-correlation represents the probability of finding any spike in train s_2 as a function of time before or after a spike in train s_1 : $\rho(\tau) = \int s_1(t)s_2(t - \tau)dt$

Cross-Correlation Histogram: Binning

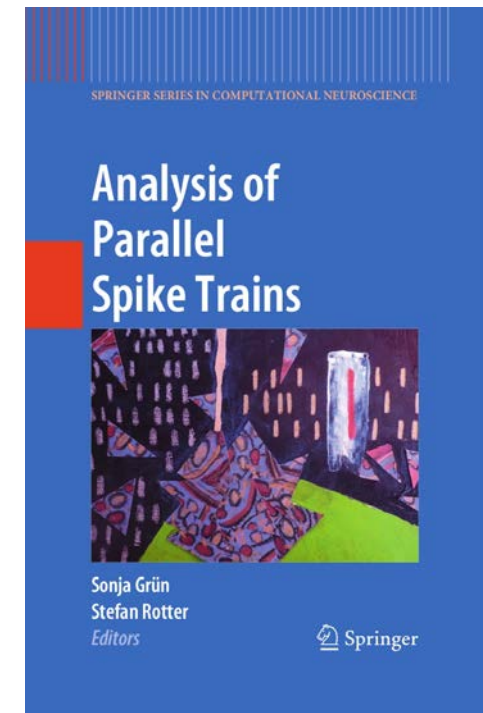


The cross-correlation histogram results by binning of the cross-correlation function

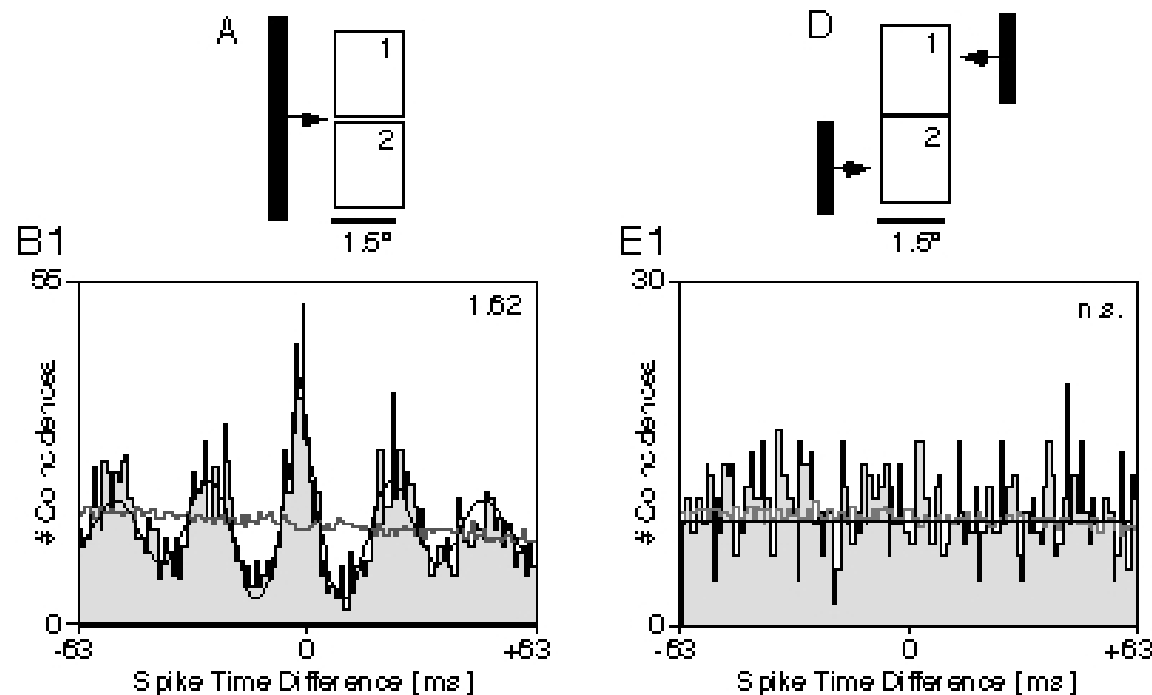
Cross-Correlation Histogram (CCH)



- number of coincidences for each time delay τ
- often task of neuroscientist: significance of correlation



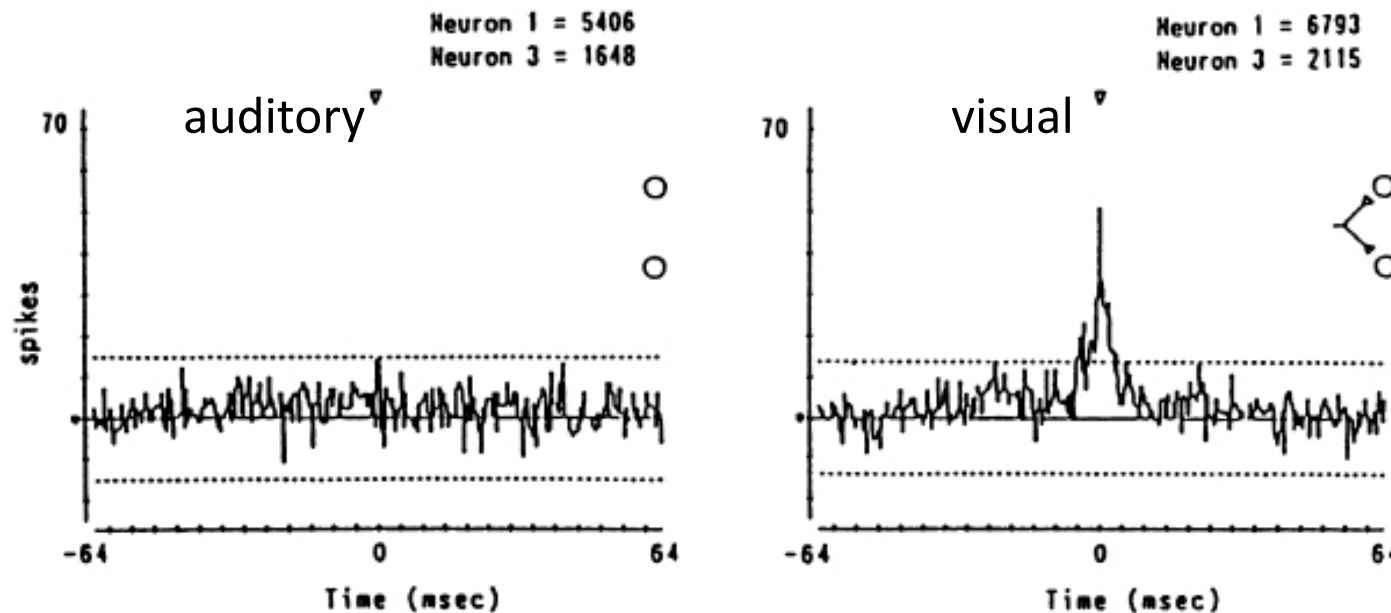
Perception Related Correlation



Freiwald et al (1995) NeuroReport 6: 2348--2352

- Simultaneous recording of two single units (stereotrodes) from different columns of visual cortex (A17) of cat
 - Long bar condition induces synchronized spike responses
 - Dual bar condition: absence of synchronization
- interpretation: Gestalt perception requires binding (by synchrony)

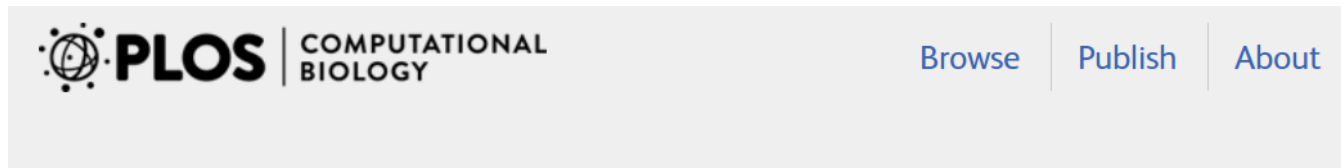
Functional Correlation



Sakurai, Y. (1999) Neuroscience & Biobehavioral Reviews 23: 785-796

- two simultaneously recorded neurons in CA1 of a rat performing an auditory or visual discrimination task
 - task related correlation only for visual task (although spike rates in same range in both tasks)
- interpretation: these two neurons belong to a cell assembly processing visual information

Networks generally not reducible



 OPEN ACCESS  PEER-REVIEWED

RESEARCH ARTICLE

Scalability of Asynchronous Networks Is Limited by One-to-One Mapping between Effective Connectivity and Correlations

Sacha Jennifer van Albada , Moritz Helias, Markus Diesmann

Published: September 1, 2015 • DOI: 10.1371/journal.pcbi.1004490

Article	Authors	Metrics	Comments	Related Content
				

- downscaling works well for first order statistics like spike rate
- severe constraints already for second order like spike correlation
- spike correlation drives mesoscopic measures like LFP and EEG

Effective connectivity and correlations

$$\left[\begin{array}{c} \text{Susceptibility} \\ S_i(\mu, \sigma) \end{array} \right] \times \left[\begin{array}{c} \text{Connectivity} \\ J_{ij} K_{ij} \end{array} \right] = \left[\begin{array}{c} \text{Effective} \\ \text{connectivity} \\ W_{ij} \end{array} \right]$$

$$\left[\begin{array}{c} \text{Correlations} \\ c_{ij} \end{array} \right] = f \left(\left[\begin{array}{c} \text{Effective} \\ \text{connectivity} \\ W_{ij} \end{array} \right] \right)$$

One-to-one under:

- fixed single-neuron parameters and delays
- stationarity
- diffusion approximation
- absence of degeneracies

Uniqueness of effective connectivity

- for single-population binary network with $d = 0$,

Correlation $\leftarrow$

Autocorrelation, determined by mean activity $\rightarrow$

Time lag $\leftarrow$

Time constant of neuronal dynamics $\rightarrow$

Number of neurons $\rightarrow$

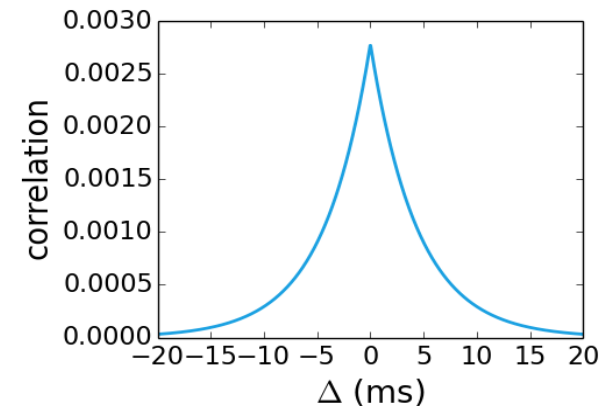
$$c(\Delta) = \frac{a}{N(1-W)} e^{\frac{W-1}{\tau}|\Delta|}$$

$\rightarrow W$ uniquely determines temporal structure

- more generally, $C_{ij}(\omega) = \sum \tilde{f} \left(W_{kl} \frac{e^{\pm i\omega d_{kl}}}{1 \mp i\omega \tau_k} \right)$

$\rightarrow$ each W_{kl} determines unique ω -dependence unless some delays are equal

- narrower set of exceptions when transfer functions are identical

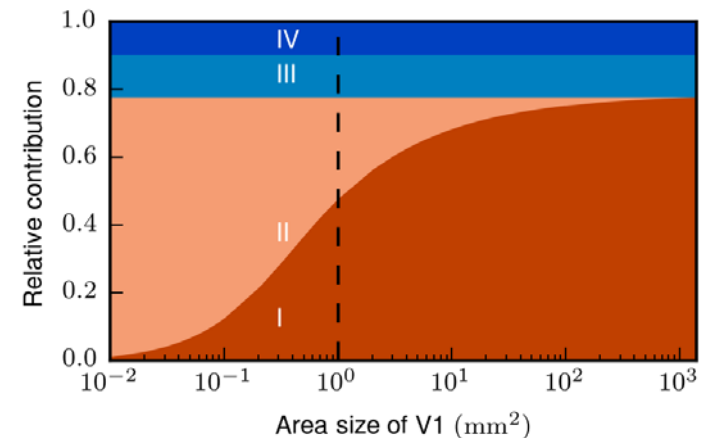
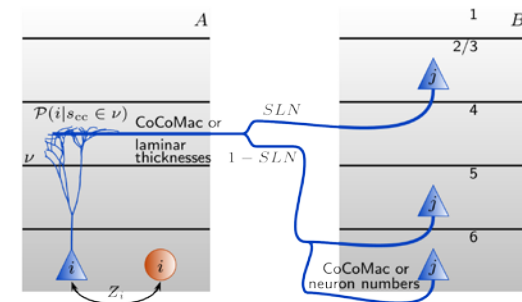
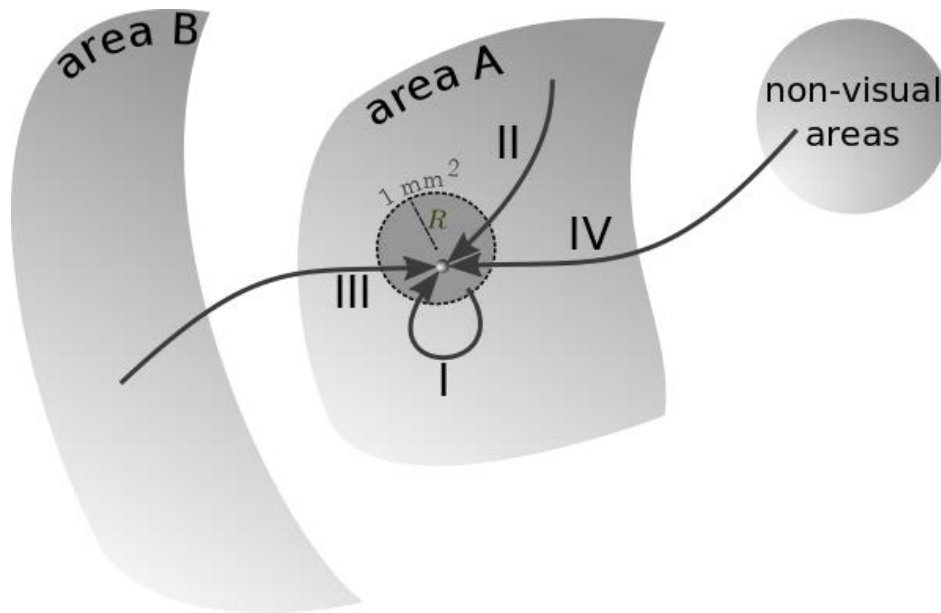


$$\begin{pmatrix} \text{Effective} \\ \text{connectivity} \\ W_{ij} \end{pmatrix} = f^{-1} \left(\begin{pmatrix} \text{Correlations} \\ C_{ij} \end{pmatrix} \right)$$

Feasibility and necessity

- Can we do simulations at the brain scale? ✓
- Do we need to simulate full scale (at cellular resolution)? ✓

Toward a self-consistent model

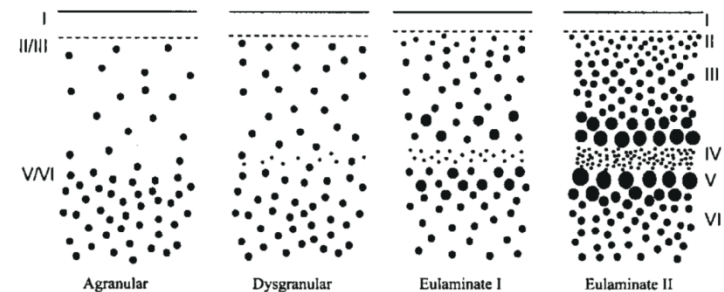
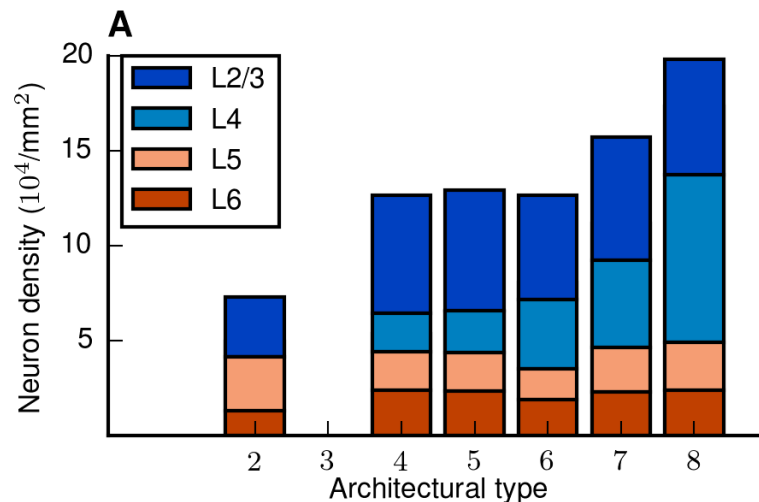


- I. Intra-areal synapses
- II. Intra-areal synapses replaced by random input
- III. Cortico-cortical synapses
- IV. External input represented by random input

- Sacha van Albada
- Maximilian Schmidt
- Rembrandt Bakker

Multi-area model of macaque visual cortex

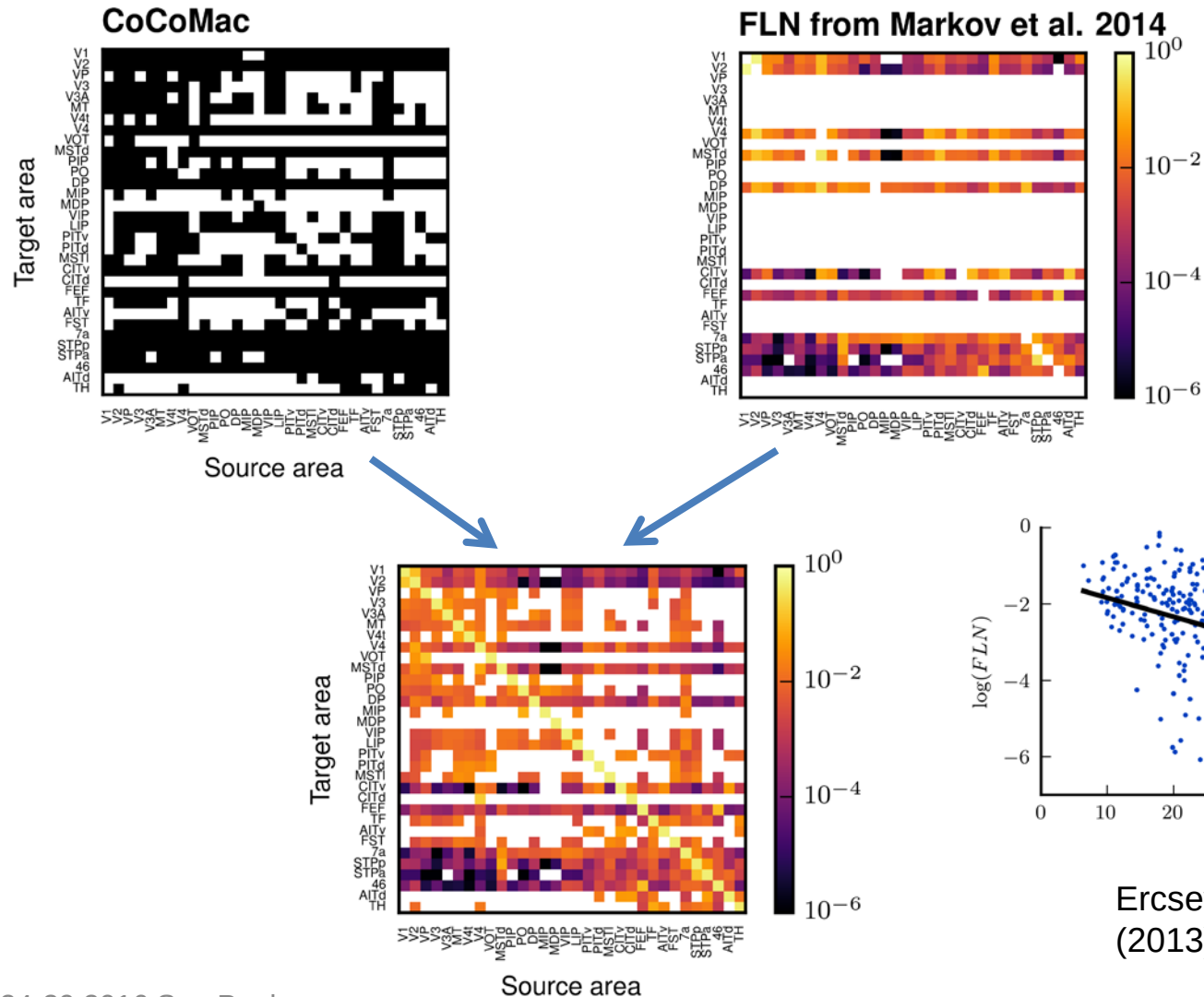
- rich anatomical data sets available (e.g CoCoMac)
- close to human
- 32 areas structured in layers comprising $8 \cdot 10^8$ neurons
- downscaled model with $4.1 \cdot 10^6$ neurons and $3.9 \cdot 10^{10}$ synapses



From Dombrowski et al. (2001), Cereb Cortex

architectural types from Hilgetag et al. (2015)
with data by Helen Barbas

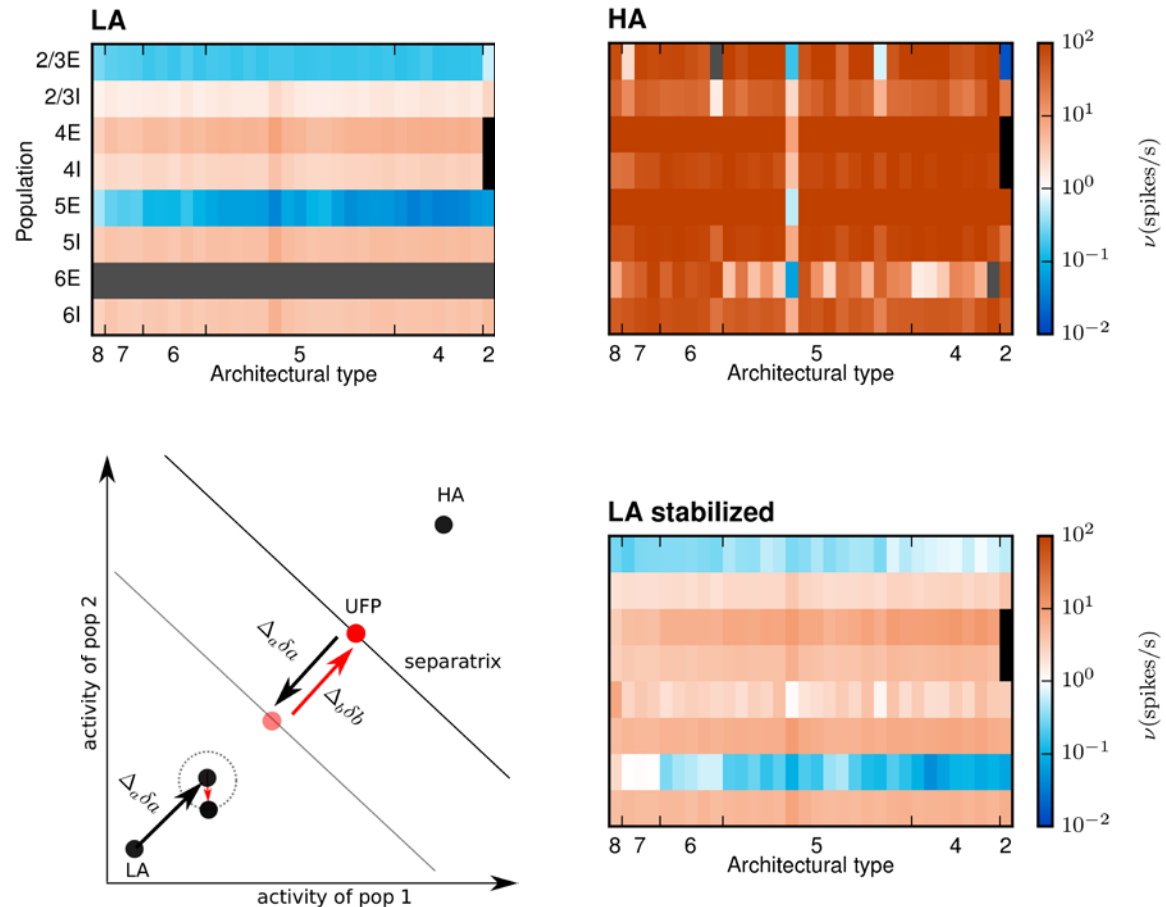
Construction of cortico-cortical connectivity



Ercsey-Ravasz et al.
(2013), Neuron

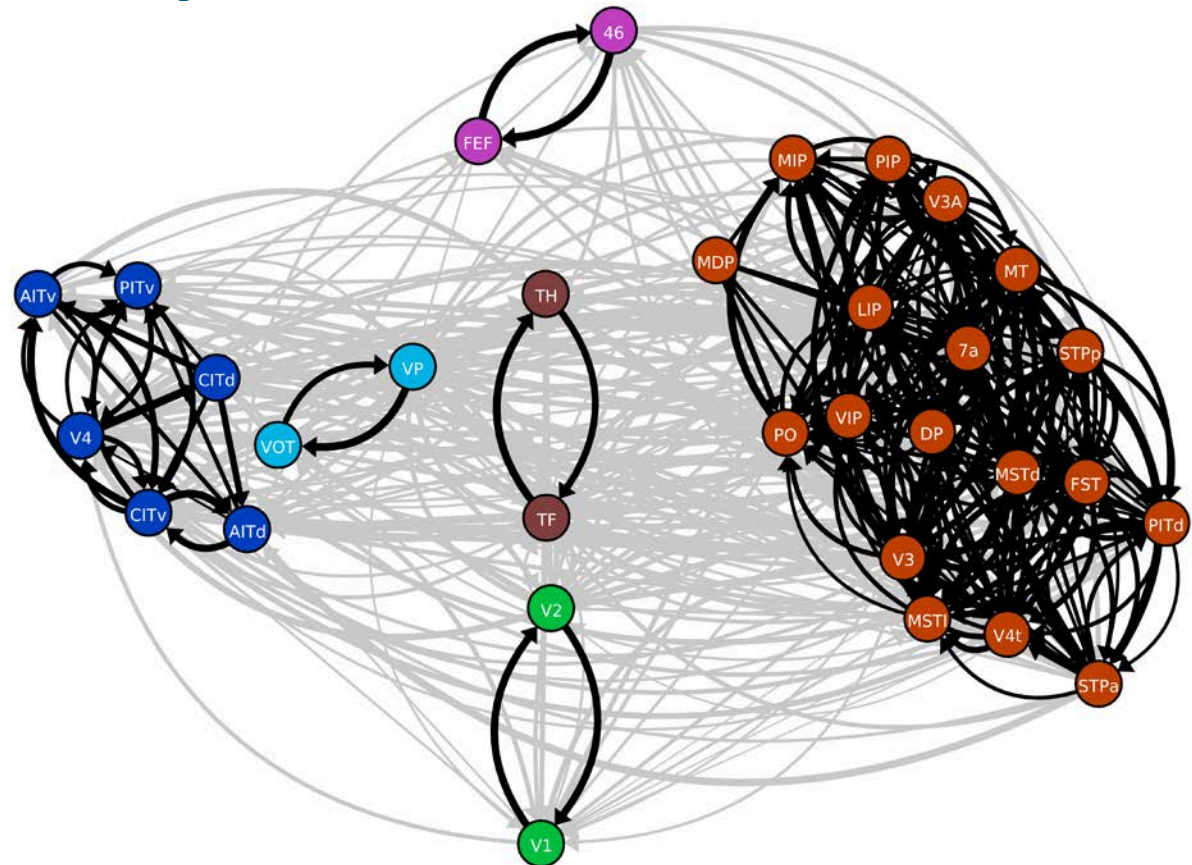
Stabilization of multi-area network

- partly quiescent low activity (LA)
- unrealistic high activity (HA)
- goal: Increase excitation while preserving global stability
- method: control location of separatrix by modifying model connectivity
- inclusion of dynamical constraints into model definition
- feedback link to structural experiments



Schuecker J, Schmidt M, van Albada SJ, Diesmann M, Helias M (2016) arXiv:1509.03162

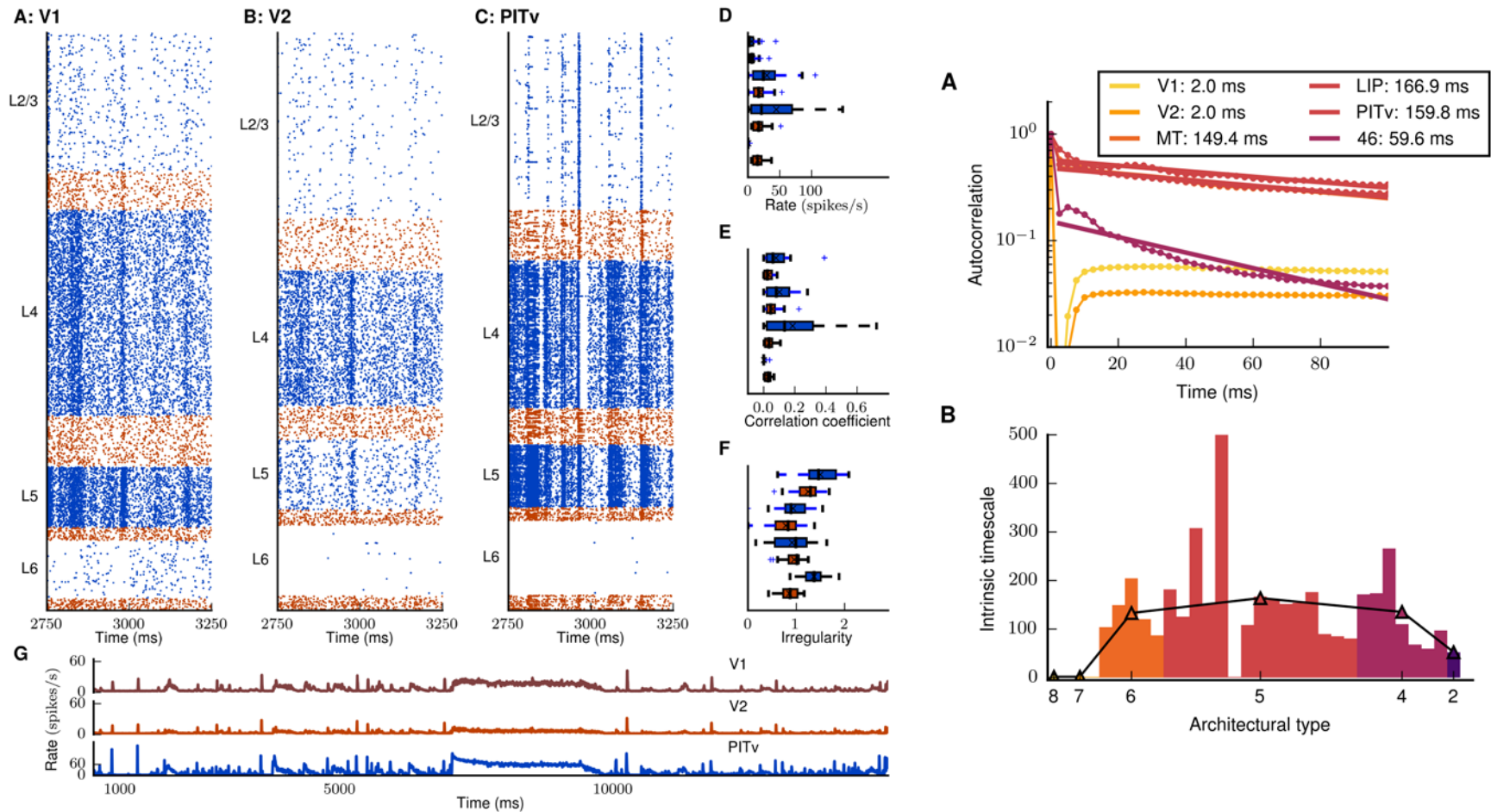
Structural connectivity reveals functionally relevant community structure



clustering by map equation method (Rosvall et al. 2010)

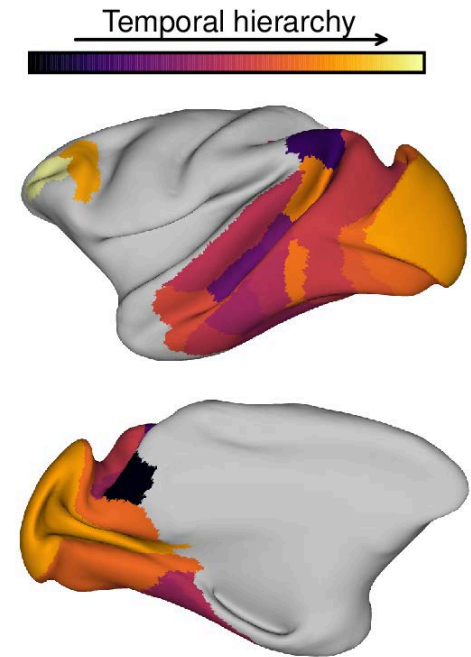
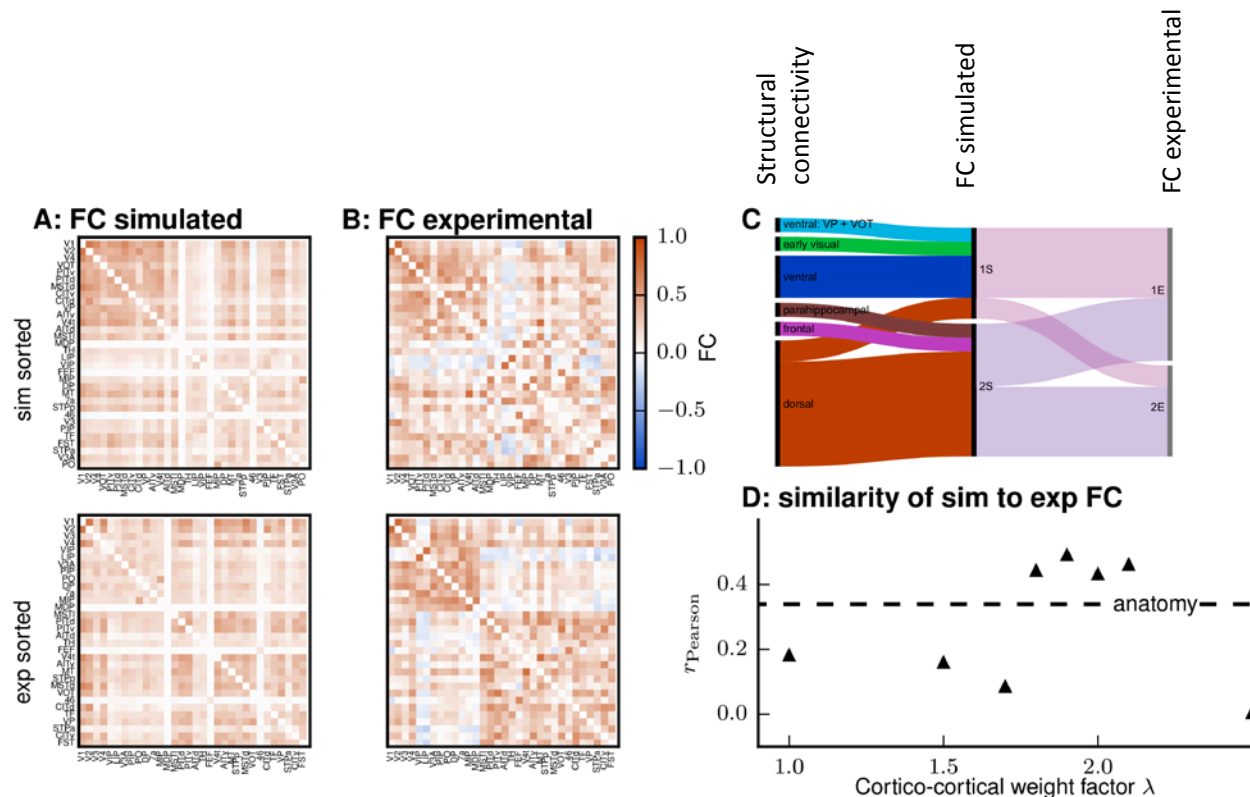
Multi-area model: Dynamical results

- stable resting state with heterogeneous laminar rate patterns and irregular firing
- cortico-cortical interactions trigger increased time scales in higher visual areas



Multi-area model: Dynamical results

- activity propagates in feedback direction
- inter-area interactions mimic experimental resting-state fMRI



FC sorted according to Louvain clustering (Blondel et al. 2008)

Schmidt M, Bakker R, Shen K, Bezgin G, Hilgetag CC, Diesmann M, van Albada SJ (2016) arXiv:1511.09364

Key Challenge

- **Reproducibility** is the ability of an entire experiment or study to be duplicated, either by the same researcher or by someone else working independently. Reproducing an experiment is called **replicating** it. Reproducibility is one of the main principles of the **scientific method**.

[From Wikipedia]

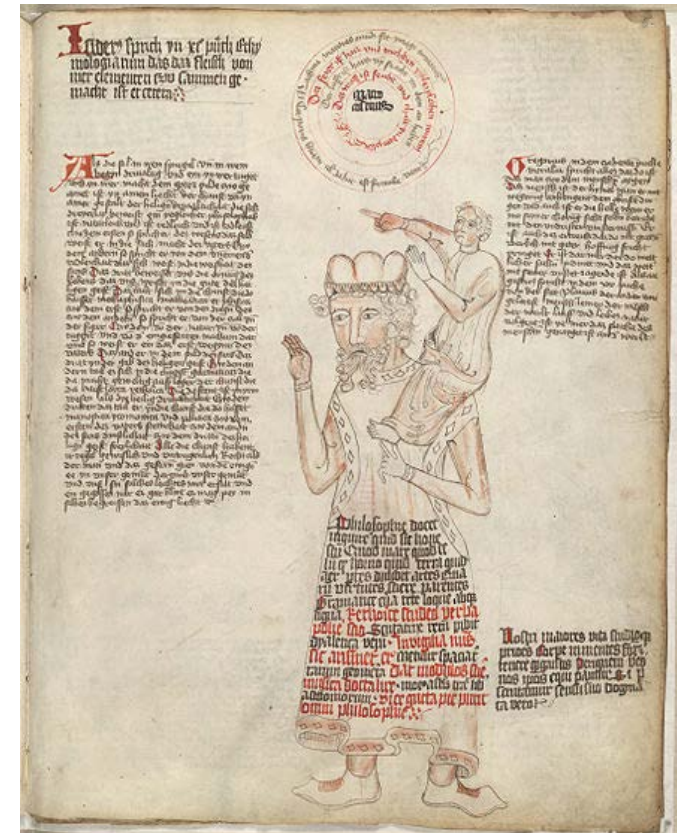
- here we are talking about the reproducibility of modeling and analysis, not experiments

Simplest example

- PhD student left the lab, now the reviews came back, and another person wants to reproduce a figure of the manuscript
 - as experience shows in most cases this does not work

Consequences of current situation

- slow down of scientific progress
- complexity barrier: without new technologies more advanced modeling and analysis impossible
→ violation of “discovering truth by building on previous discoveries”
- reduced efficiency of use of research funds



Isaac Newton: “If I have seen further, it is by standing on the shoulders of giants” [from: Wikipedia]

New journals emerge

- Scientific Data: www.nature.com/sdata/

nature.com : Publications A-Z index : Browse by subject

SCIENTIFIC DATA

Principles

Scientific Data is a new open-access, online-only journal for descriptions of scientifically valuable datasets. Our articles, known as Data Descriptors, combine traditional narrative content with curated, structured descriptions (metadata) of the published data to provide a new framework for data-sharing and -reuse that we believe will ultimately accelerate the pace of scientific discovery.

- ReScience: github.com/ReScience/ReScience/wiki

ReScience is a peer-reviewed journal that targets computational research and encourages the explicit replication of already published research, promoting new and open-source implementations in order to ensure that the original research is reproducible. To achieve such a goal, the whole editing chain is radically different from any other traditional scientific journal. **ReScience** lives on [github](#) where each new implementation is made available together with comments, explanations and tests. Each submission takes the form of a pull request that is publicly reviewed and tested in order to guarantee that any researcher can re-use it. If you ever replicated computational results from the literature in your research, **ReScience** is the perfect place to publish this new implementation.



Levels of reproducibility

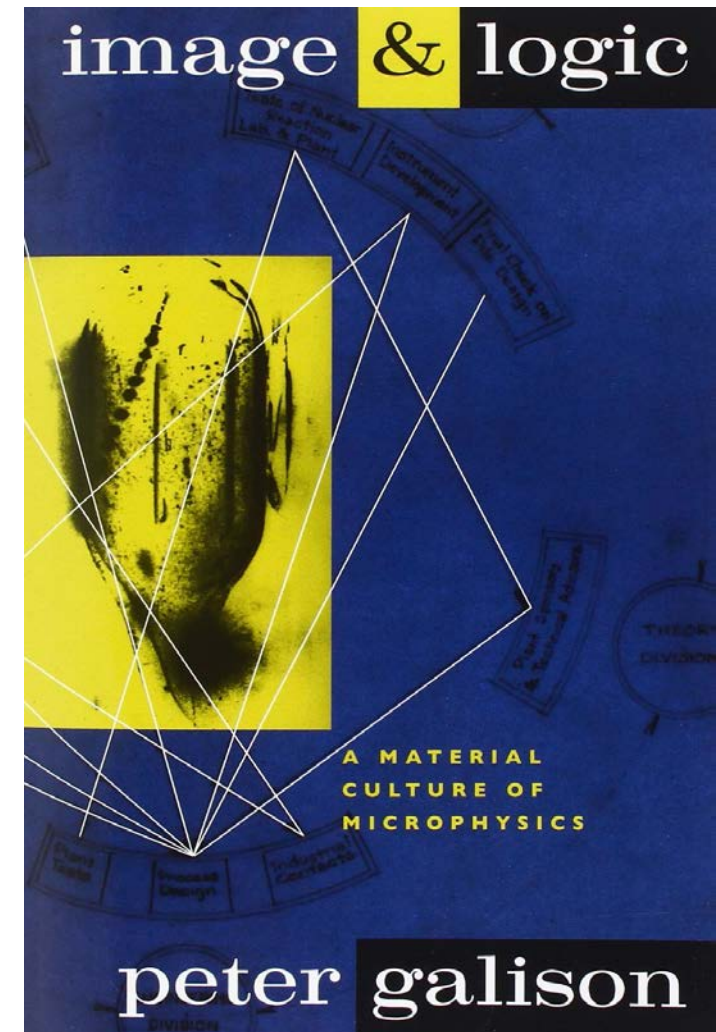
- in the weakest sense: running the same program leads to the same result
- actually wanted: reproducibility in the stronger sense, i.e. conceptual insight, control, understanding

We have been unable to compile this original implementation but we were able to run the provided Windows executable. We found some factual errors in the original article that have been corrected in this implementation.

From: [Re] Interaction between cognitive and motor cortico-basal ganglia loops during decision making: a computational study, M. Topalidou and N.P. Rougier, ReScience, volume 1, issue 1, 2015.

Collaboration: conditions and consequences

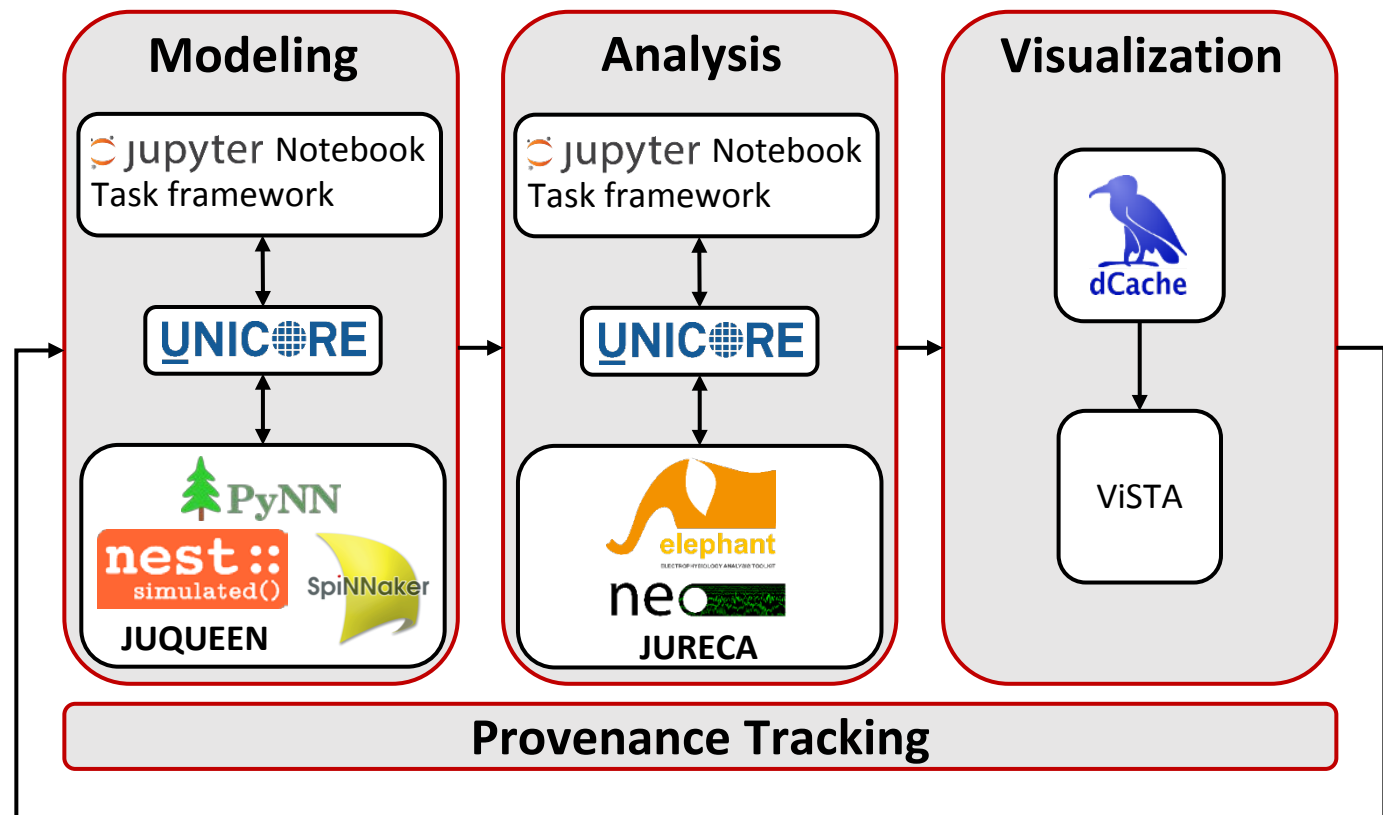
- have experience from other branches of science
- example of high energy physics (982 pages)
- accounts of the sociological and organizational problems are elucidating
- a cultural transformation was induced
- even better example may be meteorology



Infrastructure for collaborative work

- long-term support of tools
- infrastructure for collaboration of scientists
- infrastructure for data integration and model re-use
- infrastructure for provenance tracking and review
- HBP platform open since We March 30th 2016
check <https://collab.humanbrainproject.eu>

A Collaboratory



- mapping of the complete integrative loop of research

Collaboratory, example



HOME COLLABS HELP FEEDBACK



Cortical Microcircuit Simulation Collab

Navigation

ADD

Workspace

Overview

Collaboration

Overview

Use Cases SP6

Storage

Parameters Notebook

Microcircuit Task

List Jobs (HPC)

Microcircuit Notebook

Job Manager

Team

Settings

Cortical microcircuit simulation

This Collab corresponds to **use case 020** in [Use Cases SP6](#).

The Collab demonstrates interactive and collaborative research with a full scale neuronal network model. Full scale means that the model represents a particular biological circuit with neurons and synapses at their natural density. A multi-layered microcircuit model of early sensory cortex. The model (Potjans, T. C., & Diesmann, M. (2014) *Cerebral Cortex* 24(3):785-806) represents 1 mm² of cortex and contains around 100,000 spiking point-neurons connected by around 1 billion synapses in four cortical layers. Each layer contains an excitatory and an inhibitory neuron population which are interconnected with cell-type and layer specific connection probabilities derived from experimental data.

The **App Microcircuit Task** is a **Task** for a simulation of the microcircuit model.

The simulation code is a **PyNN** (<http://neuralensemble.org/PyNN/>, [Software Catalog](#)) implementation based on a [public version](#) with **NEST** (<http://www.nest-simulator.org/>, [Software Catalog](#)) as simulator backend.

It is possible to run the simulation either directly on the Collaboratory's local resources (cscs_viz) or on an HPC system via **UNICORE**. The Juelich supercomputer **JUQUEEN** can be selected. Note that access to HPC sites requires to undergo an application procedure for computing time. For getting test access to JUQUEEN please contact HBP-HPC-Platform@fz-juelich.de.

Figure 1 illustrates the possible workflows that can be realized in this Collab including interactive computing with **Jupyter Notebooks**, the **Collaboratory's Task framework** and submitting simulation jobs to an **HPC** site.

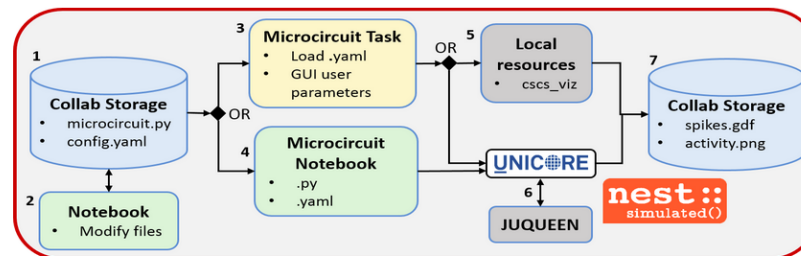
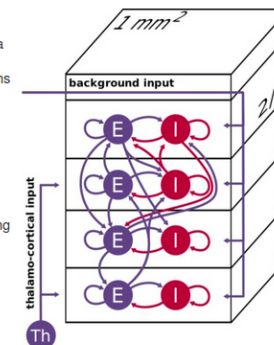


Figure 1: Workflows realized in this Collab.

Collab Walkthrough



5 members in this collab



10:16
thanks

10:23
I just added a first version of a workflow figure to Overview.

20:40
Yesterday

nice to also see your face now

10:32
I like the overview page.

14:30

Send a message

Activity

Provenance

- example “collab”
- mapping of complex workflows

Collaboratory, example

The screenshot displays the JARA|BRAIN Collaboratory web interface. The top navigation bar includes the JARA|BRAIN logo, a 'COLLABORATORY' button, and links for HOME, COLLABS, HELP, and FEEDBACK. On the right, there are user avatars, a notification bell with '61', and a share icon.

The main workspace is titled 'Cortical Microcircuit Simulation Collab'. It features a left sidebar with a 'Navigation' panel containing links like Overview, Use Cases SP6, Storage, Parameters Notebook (highlighted), Microcircuit Task, List Jobs (HPC), Microcircuit Notebook, Job Manager, Team, and Settings. The central area is a 'Parameters Notebook' showing a Python script for a simulation. The script includes comments and parameters for recording correlations, saving connections, simulator settings, and neuron populations. The right sidebar shows a 'Collaboration' panel with 5 members, a chat window with messages, and sections for Activity and Provenance.

```

# whether to record correlations
record_corr: false,
# Whether to save connections to file.
# Even if save_connections is set to True, at the moment connections are not
# saved because the output exceeds the user's default capacity on the Collaboratory.
save_connections: false}
# Simulator back-end, currently it has to be nest
simulator: nest
simulator_params:
  nest: {max_delay: 100.0, min_delay: 0.1, sim_duration: 1000.0, threads: 1, timestep: 0.1}
# Parameters for plots of spiking activity
plot_spiking_activity: true
# Fraction of recorded neurons to include in raster plot
frac_to_plot: 0.5
# Excitatory and inhibitory population
pops: {E: 0, I: 1}
# raster_t_min and raster_t_max include the time scaling factor
# if raster_t_max == 'sim_duration': plot for the whole duration of the simulation
# else: enter float
raster_t_max: sim_duration
raster_t_min: 0.0
# In-degrees for external inputs
K_ext:
  L23: {E: 1600, I: 1500}
  L4: {E: 2100, I: 1900}
  L5: {E: 2000, I: 1900}
  L6: {E: 2900, I: 2100}
# Numbers of neurons in full-scale model
N_full:
  L23: {E: 20683, I: 5834}
  L4: {E: 21915, I: 5479}
  L5: {E: 4850, I: 1065}
  L6: {E: 14395, I: 2948}
# Mean and standard deviation of initial membrane potential distribution
  
```

Human Brain Project, 2015

- research on integration with style of work of computational neuroscientist (python notebook)

Summary

- full-scale model explains prominent features of network activity
- is building block of further studies (www.opensourcebrain.org)
- need for brain-scale models
 - increase self consistency
 - compute meso- and macroscopic measures of activity
- need for full-scale models
 - irreducibility
 - verify mean-field results
- machines ready for use by neuroscience (www.nest-initiative.org)
- full-scale model of macaque visual cortex
- functional connectivity shows correspondence with fMRI
- problem of reproducibility, research and funds required to overcome

References

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