Multiscale approach to explore the relationships between connectivity and function in whole brain simulations

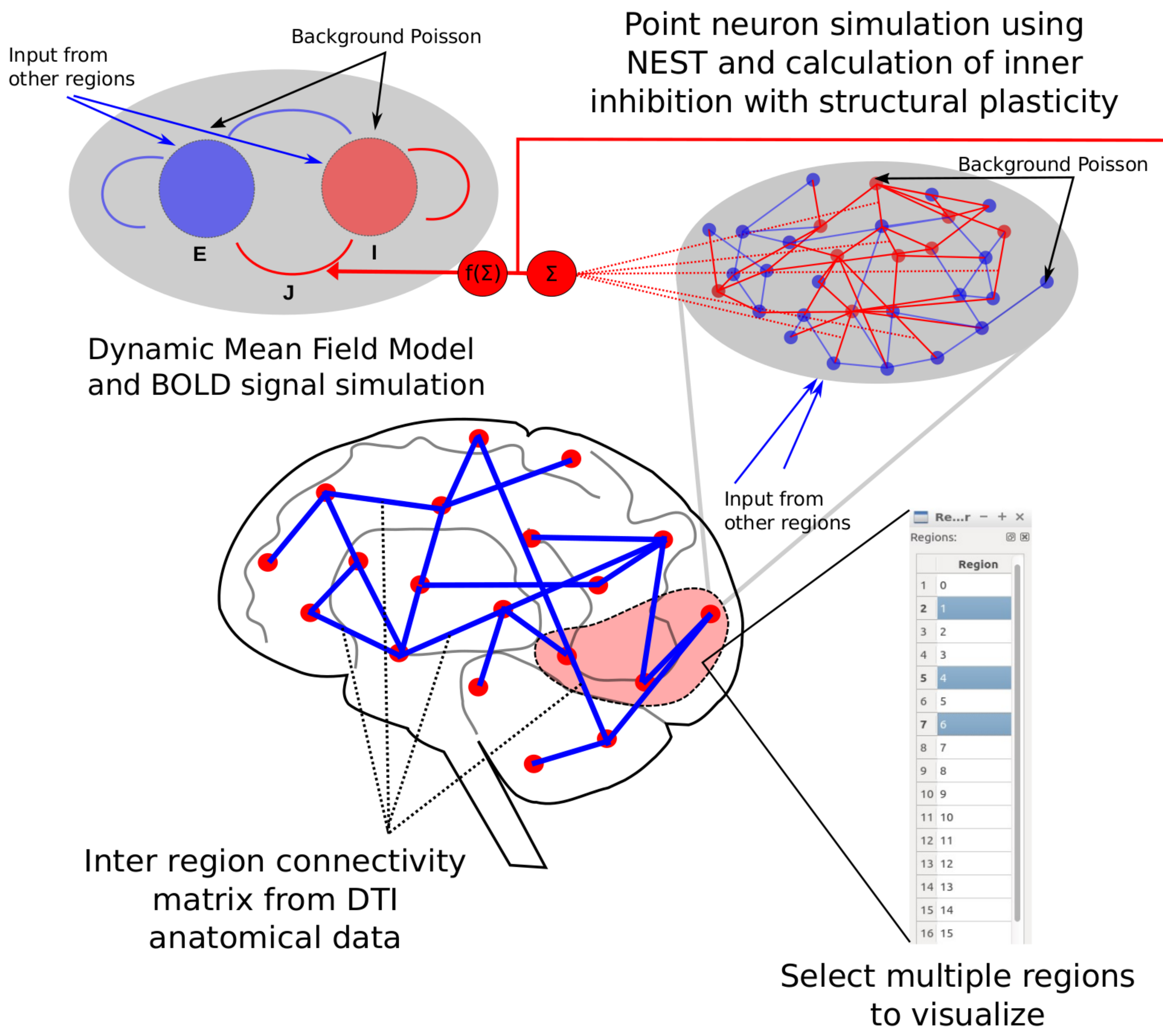
S. Diaz[1], C. Nowke[2], A. Peyser[1], B. Weyers[2], B. Hentschel[2], A. Morrison[1,3], T. W. Kuhlen[2]

1. Simulation Laboratory Neuroscience -- Bernstein Facility for Simulation and Database Technology. Institute for Advanced Simulation, Jülich Forschungszentrum, Jülich, Germany
2. Visual Computing Institute, RWTH Aachen University, Jülich Aachen Research Alliance - High-Performance Computing, Aachen, Germany
3. Institute of Cognitive Neuroscience, Faculty of Psychology, Ruhr-University Bochum, Bochum, Germany

Motivation

- **We want to better understand the relationship between connectivity and function in the brain at different scales.**
- To achieve this, in this work we use point-neuron network simulations to complement connectivity information for whole brain simulations based on a dynamic neuron mass model.
- The results of subsequent simulations will be compared with experimental data in order to find and optimize correlations between function and structure.

Multiscale single region models



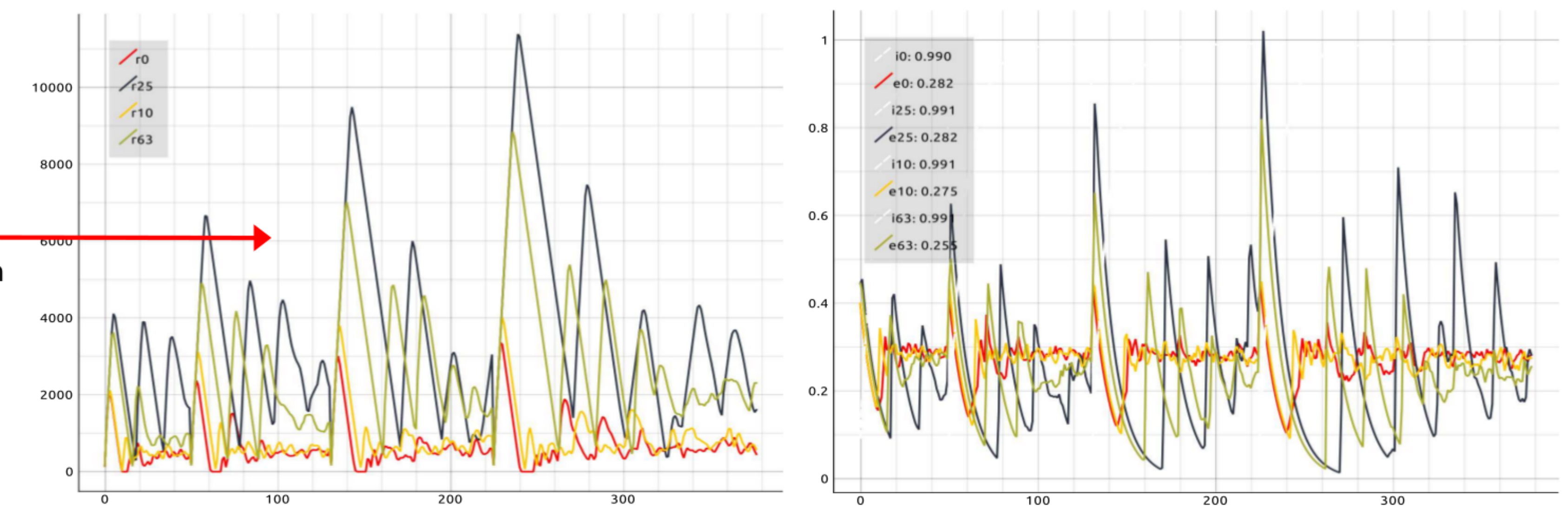
Multiscale approach

- We simulate a whole brain parcellated into 68 regions based on [1]
- Each region is modeled as a dynamic neuron mass [2], and in parallel, as small 200 point-neuron populations in NEST [3].
- Structural plasticity in NEST [4] is then used to calculate the inner inhibitory connectivity required to match experimentally observed firing rates inside each region.
- The point-neuron network self-generates the inner inhibitory connectivity using simple homeostatic rules.
- With the resulting connectivity data from the NEST simulations and experimentally obtained DTI inter-region connectivity, simulations of the whole brain producing results comparable to experimental fMRI data are performed.

Interactive steering and visualization

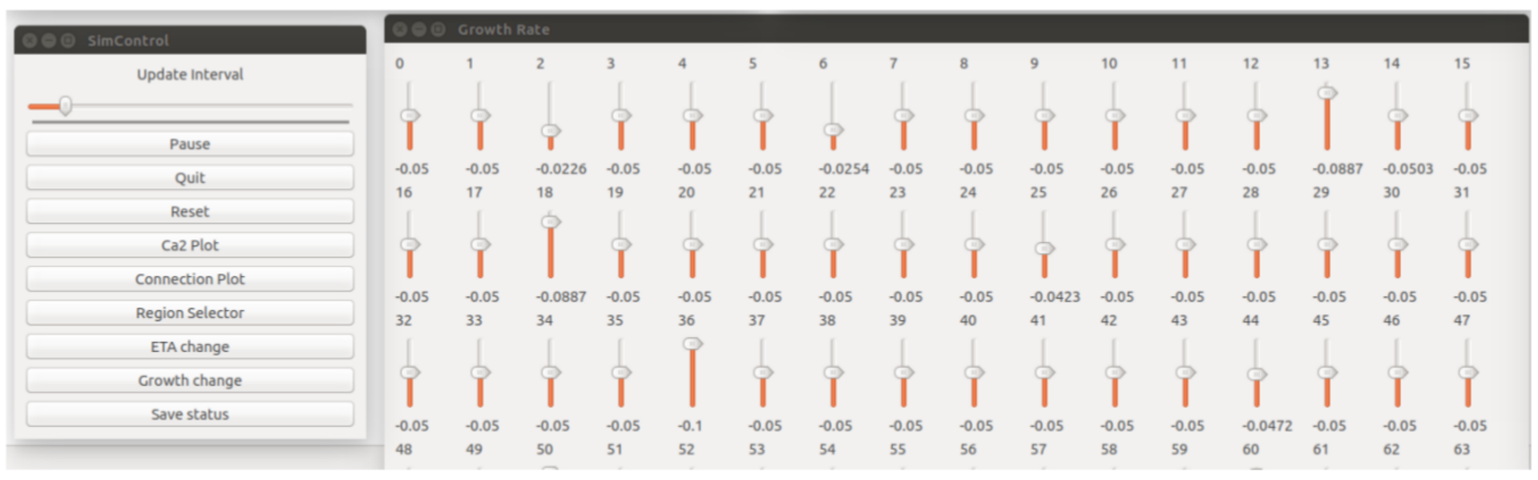
- We use an interactive tool based on the NETT framework developed for visualization and steering of the structural plasticity algorithm to bring all regions to their ideal firing activity.
- The user can see the evolution of the firing rate and the creation/ deletion of connections, modify parameters and visualize the impact of the modifications while the simulation progresses.
- This steering tool can be used interactively on supercomputers for larger number of regions or neurons per region.

Multiple regions view



Changes in Inhibitory Connections guided by the structural plasticity algorithm

Evolution of the average firing rate in each region

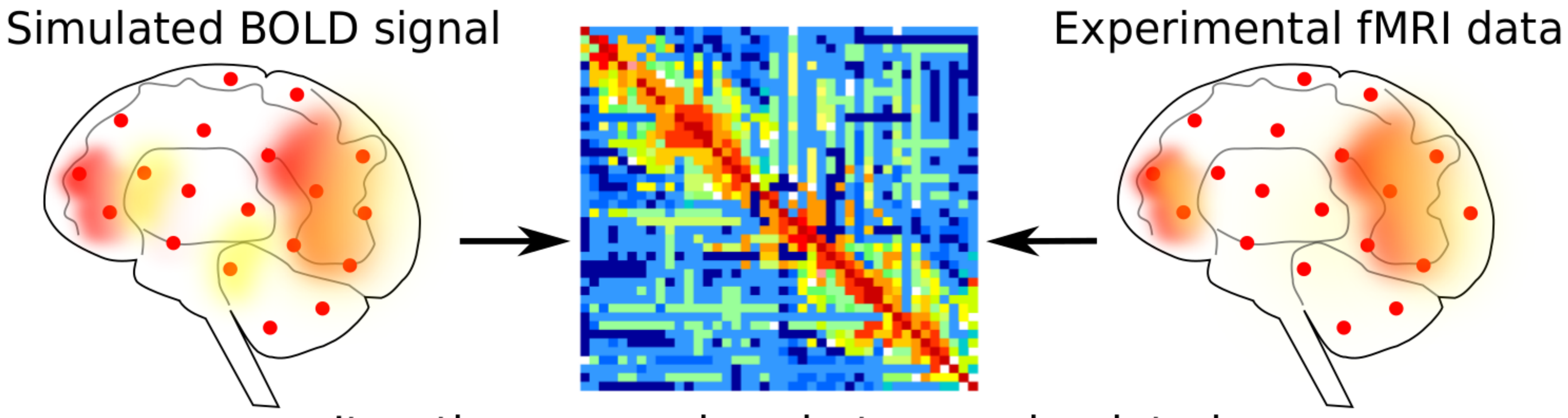


Change multiple parameters and store status

Discussion

- Fitting and parameter space exploration:
  - is around 10 times faster than iterative fitting algorithms
  - is more robust since it progressively achieves global stability
  - aids a better understanding of the parameter space
- **Our multiscale approach enables a new method to explore the impact of connectivity in function at different scales.**

How does the underlying *structural* connectivity affect our ability to predict experimental *functional* data with our simulations?



Iterative comparison between simulated and experimental BOLD signals

Acknowledgments

The Excellence Initiative of the German federal and state governments, JARA-HPC and the CRCNS grant. This project has received funding from the European Union's Horizon 2020 research and innovation programme under grant agreement No 720270 (HBP SGA1).

References

[1] Deco, Gustavo, et al. "How local excitation–inhibition ratio impacts the whole brain dynamics." The Journal of Neuroscience 34.23 (2014): 7886-7898.
[2] Deco, Gustavo, et al. "Resting-state functional connectivity emerges from structurally and dynamically shaped slow linear fluctuations." The Journal of Neuroscience 33.27 (2013): 11239-11252.
[3] Bos, Hannah et al.. (2015). NEST 2.10.0. Zenodo. 10.5281/zenodo.44222.
[4] Diaz-Pier, Sandra, et al. "Automatic Generation of Connectivity for Large-Scale Neuronal Network Models through Structural Plasticity." Front Neuroanat (2016).

Mitglieder Helmholtz-Gemeinschaft

Presenters:
Alexander Peyser, Forschungszentrum Jülich, WP 7.6
Benjamin Weyers, RWTH Aachen University, WP 7.3