Open cortical multi-area model as research platform

In a recent perspective article [1] researchers of the European Human Brain Project (HBP) argued for the need of brain simulations to integrate the experimental data obtained on different scales. However, the article also argues that the principle of science —to advance by standing on the shoulders of giants— is challenged by a complexity barrier in brain modeling. This talk introduces, using the example of a multi-scale network model of one hemisphere of macaque vision-related cortex at cellular resolution, conceptual and technological progress in the reproducibility of modeling studies and collaborative workflows.

Our model [2] integrates data on cortical architecture and axonal tracing. The experimental data are incomplete and parameters are only known up to margins of uncertainty. Therefore we extract regularities in the data to bridge the gaps and employ mean-field theory to explore consistent configurations [3]. Simulations [4] confirm a realistic activity regime. At a sufficiently strong coupling between the areas, we find that spike patterns, the distribution of spike rates, and the power spectrum of the activity are compatible with in-vivo resting-state data. Furthermore, the matrix of correlations between the activities of areas is more similar to the experimentally measured functional connectivity of resting-state fMRI than the anatomical matrix. Thus, the model relates the single-neuron level to brain imaging data. This is achieved in a metastable state exhibiting time scales larger than any time constant of the system.

The structure to be modeled contains about 1 billion neurons, the limit of what supercomputers can simulate today but too costly for routine work. Therefore, our model represents each of the 32 areas by one microcircuit adapted to the area-specific cellular and laminar composition, reducing network size to a few million neurons. The microcircuits are based on an earlier model [5] containing roughly 100,000 neurons. This model found resonance in the community and the results were quickly reproduced. To date, 25 peer-reviewed studies use the model and 98 cite the original work. The next step is a faithful representation of the relative extents of cortical areas. Therefore, we continue to advance technology [6] for the next generation of supercomputers like Fugaku but also investigate neuromorphic computing approaches.

Progressing to the brain scale requires a new approach to model development because of the amount and heterogeneity of the data that need to be aggregated. Therefore, we adopted methods of software development such as version control, collaborative development, and code review. We noticed that the final executable model description is not sufficient for making the model reusable by colleagues. Researchers can only add new data to the model or modify assumptions if they have access to the construction process. Borrowing techniques from computer science and systems biology [7], we present a digital workflow reproducing all figures of our respective publications. The open model repository is https://inm-6.github.io/multi-area-model and a tutorial video is located at https://youtu.be/YsH3BcyZBcU.

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