Applying Techila PC-Grid in Computational Neuroscience Research

Computational Neuroscience Laboratory
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Computational Neuroscience Lab

www.cs.tut.fi/sgn/cns/

The lab was founded in 2003 and is located in the Department of Signal Processing at Tampere University of Technology (TUT), Finland.

One of the sub-units of the large Computational Systems Biology Research Group at TUT.

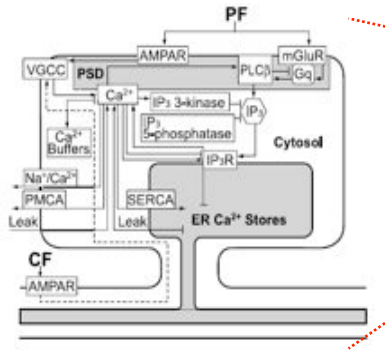
Lab members

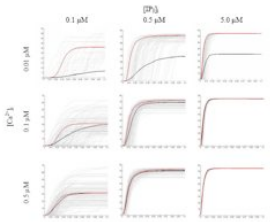
- PI: Dr. Marja-Leena Linne, Academy Research Fellow
- 3 postdoctoral researchers, 6 PhD students, 1 graduate student

Research in the CNS Lab

The development of computational *methods* and *models* to understand the function of neuronal systems on different levels.

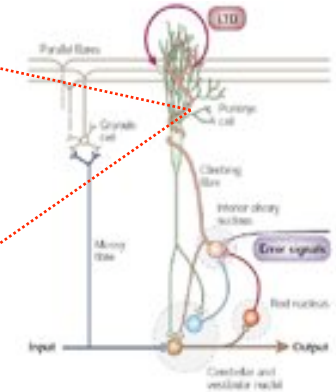
Molecular level

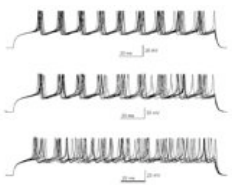




Katri Hituri

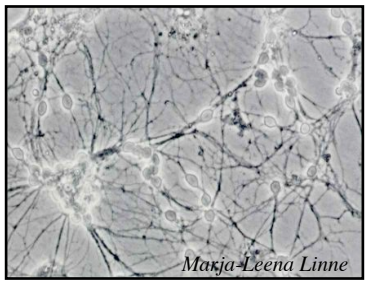
Single neuron level



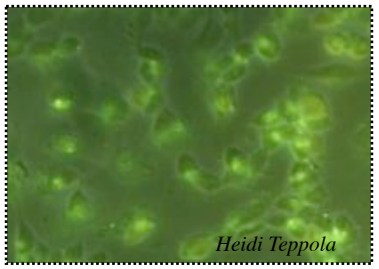


Antti Saarinen

Biological neural network level



Marja-Leena Linne



Heidi Teppola

Role of Techila PC-Grid in Research

Accurate statistics from Monte-Carlo simulations

• stochastic simulation of large signal transduction network models, single neuron models, and biological neural network models

Reliable parameter estimation in a reasonable time

• distributed sequental Monte-Carlo estimation

Data analysis of high-throughput measurements

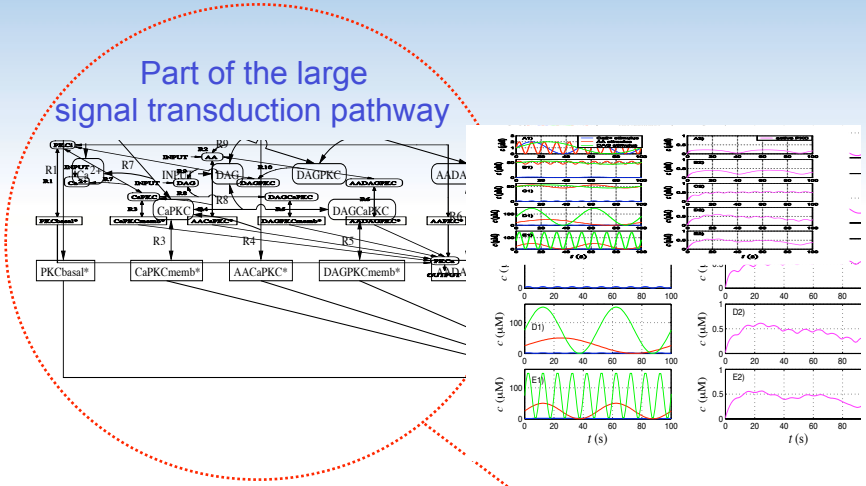
• distributed Bayesian analysis for microelectrode array data

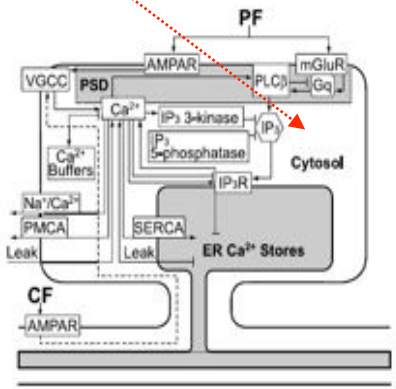
Solving these computationally intensive problems on a desktop computer is practically impossible.

Example:
Simulation of large signal transduction network

- How does a network process and store information in cells?
- Previously only small parts of the network could be simulated stochastically because the full simulation would have lasted 7 years.
- Using the PC-grid the full simulation was carried out in six days.
- Results were reliable and accurate when compared to the previous approximations.

Part of the large signal transduction pathway





Dendritic spine

Future Work

- Techila PC-grid will play an essential role especially in the development of novel data analysis methods and models for large biological neural networks.
- The amount of computational testing of biological hypotheses will increase due to easy access to powerful computing resources.