NEOSIM : Modelling large networks of spiking neurons

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Introduction

NEOSIM is a new simulation framework addressed at building large scale and detailed models of the nervous system. Its essence is a set of interfaces and protocols that enable a plug and play architecture for incorporating existing simulation modules such as NEURON and GENESIS as well as future visualisation and data analysis modules. From the start it has been designed to exploit parallel and distributed computers to reduce simulation run times to managable levels, without the additional modelling effort required for earlier publicly-available parallel simulation tools.

The problems

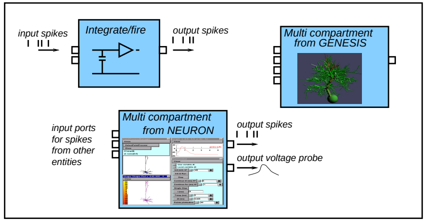
- Building useful models of the nervous system is difficult as there are many interacting levels (from ion channels to network behaviour). The wide variety / constantly changing modelling requirements mean that a single simulation program will not be sufficient.
- Realistic network models of small parts of nervous system have enormous memory and CPU requirements. Software tools are required to support "Biology as reverse engineering" (cf CAD tools for VLSI).
- Issues: memory for storing huge numbers of *connections*.
- Issues: CPU time for numerically evaluating electrical and chemical behaviour of single cells.
- Parallel supercomputers / networks of workstations provide sufficient power to construct detailed models of small areas of brain - but at a significant cost in model development time.

The NEOSIM approach

- At the heart : model constructed from entities which communicate using discrete time stamped events (e.g. action potential spikes).
- NEOSIM provides a "parallel discrete event simulation" kernel which manages the entities and the communication of events. Entities are partitioned between processors by the kernel.
- "entities" are plug in modules which can be existing simulation tools such as NEURON and GENESIS, or can be user provided to allow for new types of model.
- A NEOSIM model composed of entities can run on parallel machines without requiring additional modelling effort, so scaling up models to more realistic "brain-like" levels of complexity becomes practical.

Single cell model descriptions

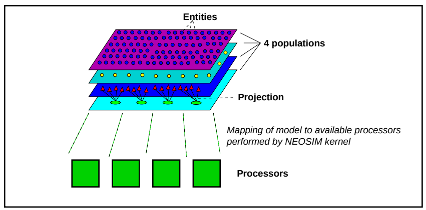
- Compartmental models
- Simplified integrate/fire models
- User coded C++ or Java models



Example single cell models.

Network model descriptions

- Construct *Populations* of similar cells
- Add *Projections* between populations
- Some connection styles provided (e.g. connect to proportion of cells within a given radius)
- In general, the connection strategy will be highly model specific, so can also be user defined function based on the source and destination neuron models (e.g. "make synapse where axon is within x microns of dendrite").



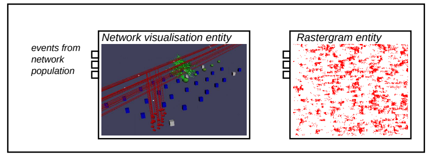
Large networks are specified as populations of similar entities connected using projecttions between populations.

Example large scale models

- Cerebellar cortex, O(250,000) granule cells, O(10) purkinje cells, with Eric De Schutter
- CA3 hippocampal model, O(100000) threshold pyramidal cells, 10% connectivity, with Chip Levy

Results

- Parallel kernel running on networks of workstations.
- NEURON module for compartmental models described using hoc and NMODL.
- GENESIS module including the fast numerical solver from GENESIS.
- Prototype visualisation module based on Java3D.



Example visualisation modules.

Conclusion

- Reuses existing models
- Allows incorporation of new methods for single cell models.
- Allows incorporation of new methods for network models.
- Supports integration of cells and networks which grow.
- Aim: publicly available software tools for supporting development of models which more closely approach realistic complexity.

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