



The Neurospaces Project Browser in the GENESIS 3 Software Federation: Design and Targets

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The Neurospaces project develops essential stand-alone software components of a neuroscience simulator following the CBI simulator architecture. All the code developed for this project is modular, free of charge and open source (GPL). The Neurospaces project is hosted at sourceforge. More information can be found at the Neurospaces website <http://www.neurospaces.org/>.

Problem Statement

The processes underlying the publication and dissemination of knowledge have always been influenced by the toolset that supports scientific activity. Ancient publications were told as stories with strong narrative components. The invention of typography in the period of the Renaissance allowed for faster replication of the reports of scientific discovery. The increase of scientific knowledge made it necessary to formalize the structure of a scientific publication and to implement processes of quality assurance. Today scientific papers are structured using sections such as 'introduction', 'problem statement', 'methods' and 'conclusion'. The quality of a paper is assured using a process called peer review, that allows peer scientists to judge, qualify and improve papers written by their peers. Recent technological advances continue to accelerate scientific reporting. Besides the emergence of databases of archives of traditional paper publications, the internet also gives access to supplementary materials and to databases with raw experimental data.

As an example, the Human Brain Map database (HBMDb) maintained and curated at the UT Health Science Center at San Antonio stores brain coordinates of peer-reviewed fMRI studies with the experimental protocol to obtain them. In addition to focused searches, the database allows to join the results of selected publications for meta-analysis. A central property of the brain coordinates stored in the HBMDb is that they are fixed over time, a property that they share with data stored by most other scientific databases.

This is in sharp contrast to the evolution of computational models used for biological research. As an example, the Purkinje cell model originally published in 1994, has now evolved for almost 15 years. The many small modifications to this model have been made by different researchers, such that at present, many parallel versions of this model coexist. No one can explain the detailed relationships between the different development branches of this model, because no tools exist to track the development of a computational model, neither during a research project, nor between research projects.

Example: Purkinje Cell Model Evolution

History

- 1992: Rapp et al, passive model (no transmembrane currents)
- 1994: EDS et al, change of Rm, added currents, added spines & synapses
- 2006: Solinas et al, change of Ih, change of synaptic conductance strength
- 2006: Achard et al, parameter changes after a parameter search
- 2008: work in progress, parameter changes for evolutionary comparative studies
- 2008: work in progress, combine with data obtained from EM microscopy

Erik De Schutter and James M. Bower (1994). An Active Membrane Model of the Cerebellar Purkinje Cell: I. Simulation of Current Clamp in Slice

Properties

- 1992: Cable properties and synapses, Rapp ea
- 1994: Active model, current injection, syns, De Schutter ea
- 1994: Conduction mech, spiking probability, De Schutter ea
- 1997: Dendro-somatic current, Jaeger ea.
- 2002: Modulation by background input, Santamaria ea
- 2005: Paired pulse responses, Santamaria ea
- 2006: Conduction mech, spiking probability, Solinas ea
- 2007: Pattern learning, Steuber ea

Principle of Solution

The technical core of the CBI architecture separates the definition of a model definition from the definition of how a simulation is controlled. This fundamental separation allows a software system to track the changes to both independently.

We have started building a web-enabled database infrastructure, tailored to the needs of computational model publication. The Neurospaces project browser – a software component of the GENESIS 3 software federation – acts as a simulation definition and exploration frame for model behavior, and guides the definition of relationships between biological questions and a simulation. These relationships form the core of a research project, but can also be used for tutorial purposes and as an educational resource.

Screenshots

Login screen & main portal screen
Based on the Webmin framework, the interface runs over any standard web browser.

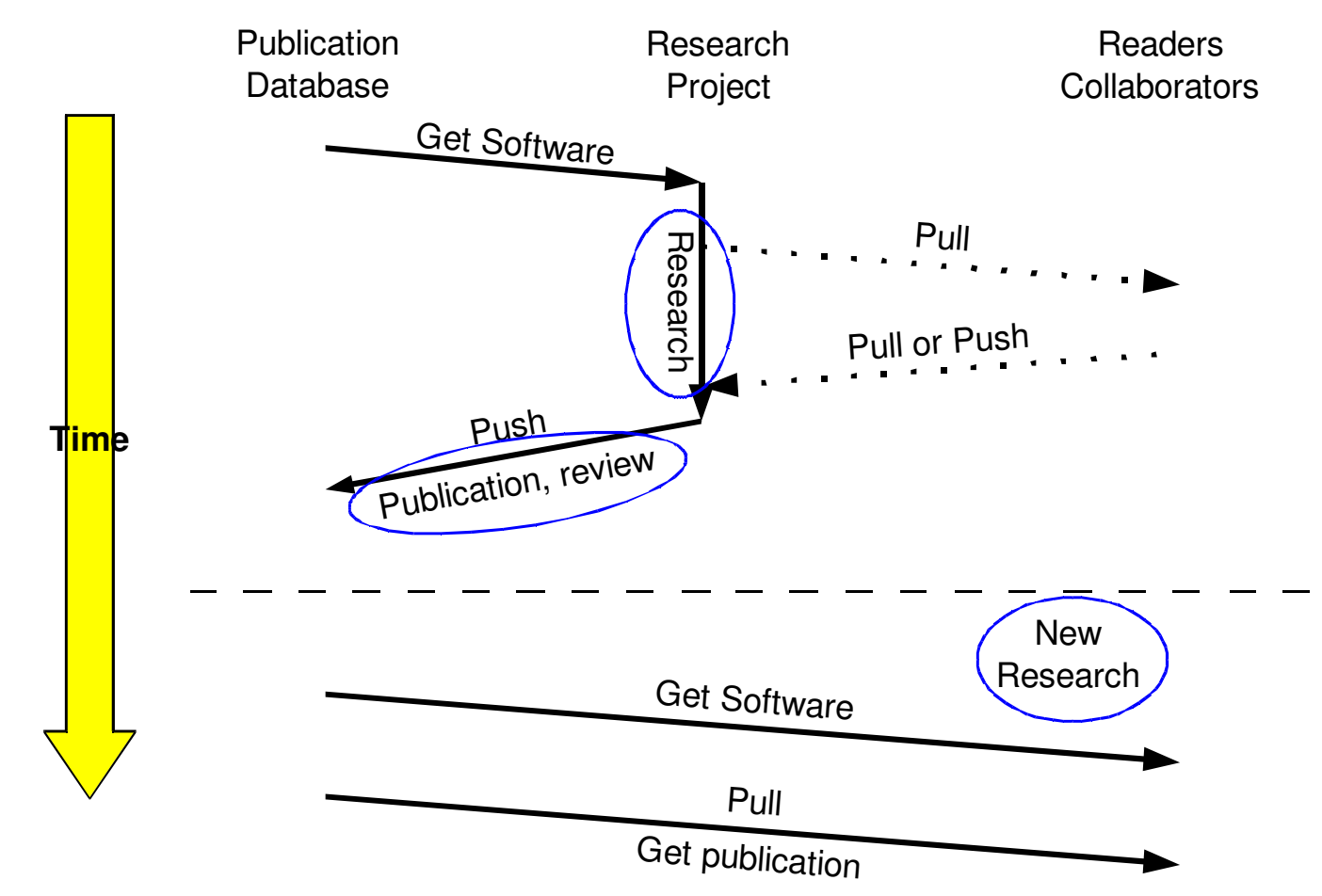
Project overview
allows to create new projects (not shown) and gives an overview of all projects available on the current laptop or PC.

Integrated morphology & model analyzer
allows to inspect all model parameters and generates tables for morphological characteristics.
Top: the main screen that gives access to all morphologies included in the project.
Bottom left: integration with the Neurospaces studio for inspection of direct models and derived model parameters.
Bottom right: Generated table of morphology characteristics with free text caption.

Simulation and Output Browser
Gives access to all configuration files each defining a single simulation, and its inputs and outputs. The browser allows to run the simulations, and shows results such as membrane potential traces.
The systems shows different versions of the same model.
Hyperlinks to related pages are configured by the researcher(s).

Narrative Components
Simulation projects can be summarized in narrative components. Common narrative components are 'Introduction', 'Problem Statement', 'Methods', 'Results' and 'Conclusions'.
Each narrative component consists of a free text message with figures.

Workflow & Dataflow



Better integration of the GUI with file distribution technology will allow to distribute research project files seamlessly.

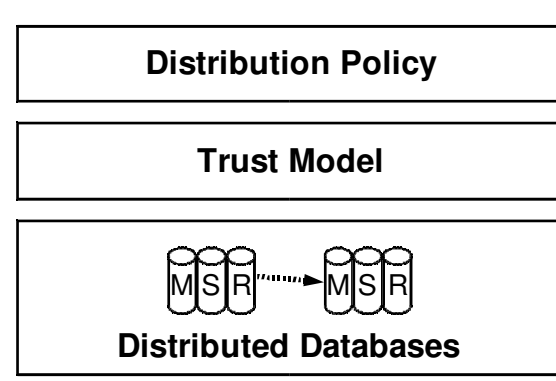
Users will push and pull files over the internet and replicate parts of a central or distributed database over the internet.

During the research project, the software tracks the differences between versions of model files and simulation control files.

Two Use Cases

Use Case A

- Single central database for pulling.
- Data comes from a well known DB.
- Replication of part of the public DB.

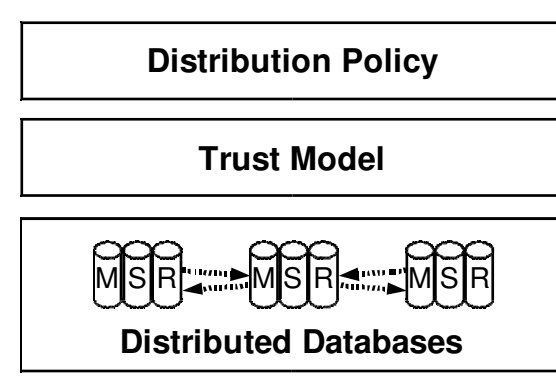


Example use cases

The proposed system has many use cases. Single users can use the system to run simulations on multiple computers (eg. a cluster and a laptop) in a manageable way.

Use Case B

- Collaboration between 3 research grps
- Many databases, push and pull
- E-signatures of trustees
- Freq. branch and merge of data



Group collaborations are facilitated by replication of parts of the database.

The trust model still needs to be implemented.

Conclusion:

The Neurospaces project browser is a web-enabled database infrastructure, tailored to the needs of computational model sharing. The system is 50% complete, and useful for testing, and to explore experimental features and workflows. The Neurospaces project browser is used for four different modeling projects. In the future, annotation of model definition and simulation control scripts will be implemented using recent advances in cryptographic signing. Such annotation can be used as a framework for quality assurance. We expect that these technologies will have a significant impact on scientific communication, publication and collaboration.

Future Work Includes

- Implementing Trust models
- Cryptographic signatures
- Interfacing to Annotation Libraries
- Possibly Automatic Benchmarking

Acknowledgements

- Mando Rodriguez: Genesis 2 coding
- Michael Edwards: Testing & Packaging
- Ja-Lyoung Joe: YAML interfaces
- Dave Beeman: General Feedback