# **Development of model-based publication for scientific communication.**

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# Problem

Currently, both paper and digital publication lack model comparison tools, model lineage inspection tools, model verification tools, and replication of results is greatly complicated. Consequently, peer review is only phenomenological, models can not be progressively improved, and science cannot advance.

How can different models be compared?

How can emergent properties of a model be quantitatively distinguished from those for which a model is tuned?

How do publications add to scientific knowledge, by their descriptive narrative or their computational extensions?

### Purkinje Cell Model Macro Evolution History 1992: Rapp et al, passive mode 1992: Cable properties and synapses, Rapp ea 1994: Active model, current injection, syns, DeSchutter ea 1994: EDS et al, change of Rm, added active channels, added spines & synapses 1994: Conduction mech, spiking probability, Schutter ea 2001: Japanese group (reused some channels in a 1997: Jaeger ea. 2001: Same channels in a different model, Japanese grp hange of Ih, change of synaptic 2002: Modulation by background input, Santamaria ea 2006: Achard et al, parameter changes after a 2005: Paired pulse responses, Santamaria ea parameter search

2007: work in progress, parameter changes fo

2007: work in progress, combine with data obtained

evolutionary comparative studie

Possible future changes: Santamaria et al 2006, Tanaka et al 2007 It is very difficult to track this evolution by just reading the paper What is the relationship with Coop & Reeke JCNS 2000, 2002

2006: Conduction mech, spiking probability, Solinas ea

2007: Pattern learning, Steuber ea

# Solution

We are developing a new set of computational tools to support the evaluation, understanding, sharing, and publication of computational models of the nervous system. This is intended to lay the ground work for making models, rather than, as at present, the written description of models, the base for scientific publication in neuroscience. The Publication System is designed to be platform independent as it adheres to the CBI federated software architecture [2].

### Purkinje Cell Model Micro Evolution

Morphology compartmentalization Changes to Rm Insertion of active conductances Updates of maximal channel conductances

Exploration of parameter space

Cerebellar Purkinje cell [1] One of the first "Community Models".

## Coupled equations: 25,471

Morphological compartments: 1600 Spines (2 compartments each): 1,474 ODEs: 16,039 Soma voltage gates: 13

### Main dendrite:

Compartments: 9 Voltage gates/compartment: 14 mooth dendrites

Compartments: 105 Voltage gates/compartment: 10 Spiny dendrites

Compartments: 1485 Voltage gates/compartment: 10

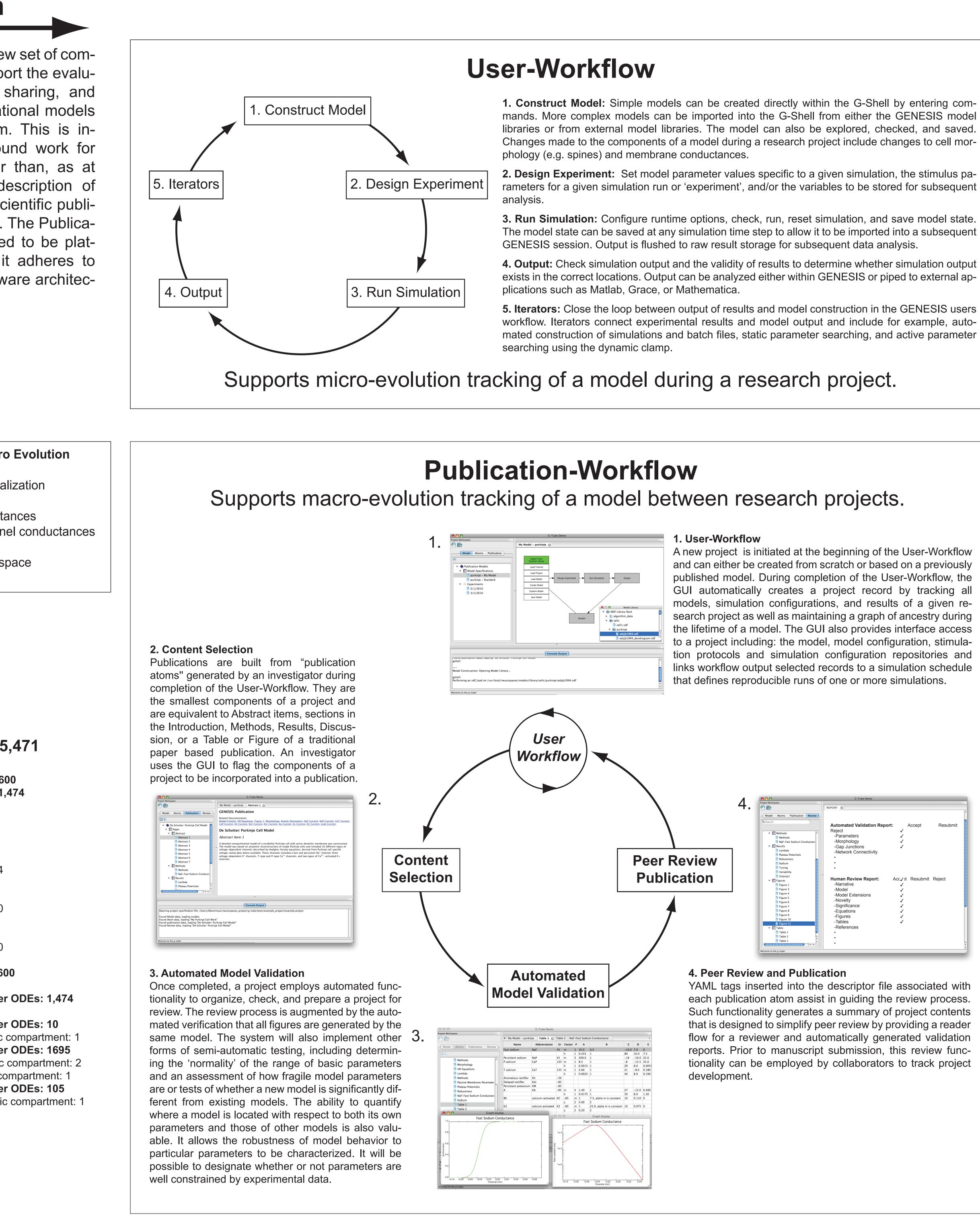
[Ca] Exponential decay eqns: 1,600 Voltage gates/compartment: 1 Ligand-gated channels, 2nd order ODEs: 1,474 Parallel fibers/spine: 2

Ligand-gated channels, 2nd order ODEs: 10 Basket cell axon/main dendritic compartment: 7 Ligand-gated channels, 2nd order ODEs: 1695 Stellate axons/smooth dendritic compartment: 2 Stellate axons/spiny dendritic compartment: 1

Ligand-gated channels, 2nd order ODEs: 105 Climbing fibers/smooth dendtiric compartment: 1

### Acknowledgements

Research supported by NIH grants 2 RO1 NS049288-5 and 3 R01 NS049288-06S1 to UTHSCSA. HC is partially supported by the CREA Financing program (CREA/07/027) of the K.U.Leuven.

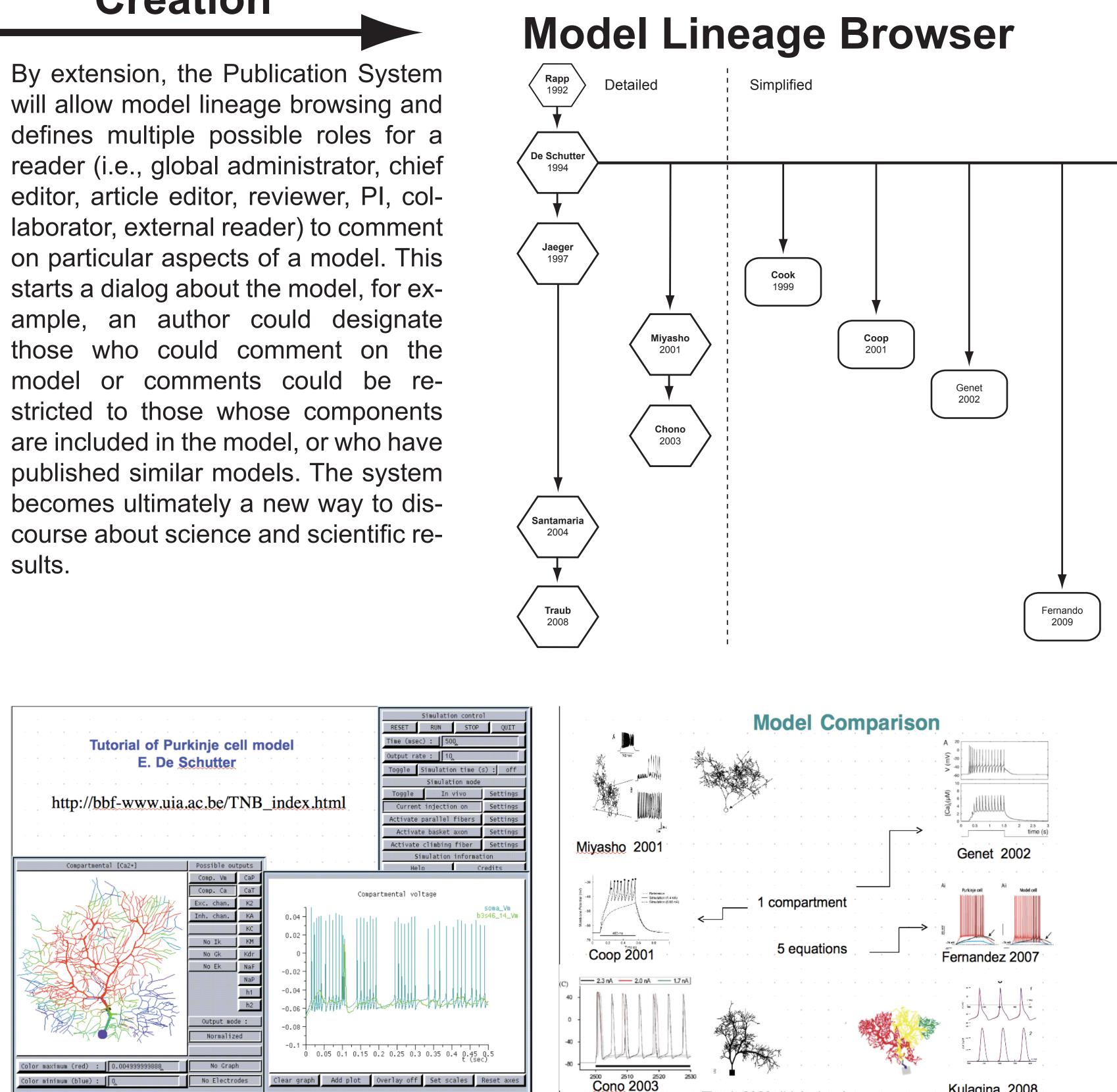


The Publication Workflow organizes model evolution to enable full lineage browsing.



# Creation

sults.



Through the user-workflow, each individual research project becomes a tutorial of model exploration. The tutorials can then be used for convenient comparisons across research projects between models that were constructed for different targets, such as performance optimization, functional (phenomenological) correctness and anatomical and morphological completeness.

The reader roles supported by the publication system enables new ways for collaborations and provides a valuable resource the construction of reports and presentations.

The model publication database can be used to automate the discovery of relationships between models and otherwise hidden features, and to identify critical new research paths for modeling and experiment.

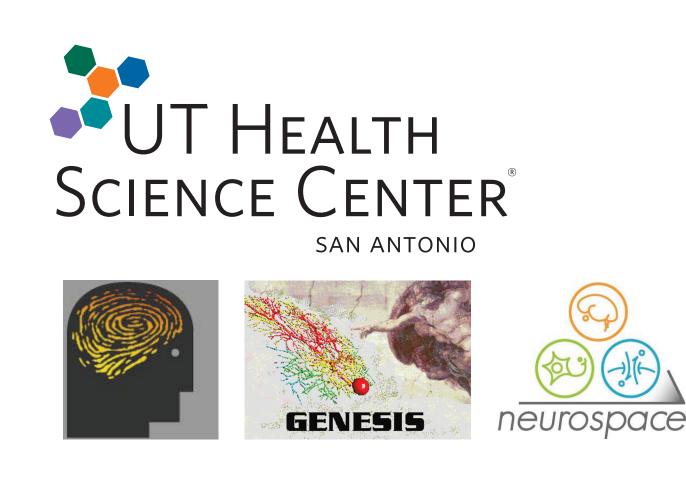
### Conclusion

Electronic model publication enables quantitative model lineage tracking and model comparison at both macro and micro levels, detailed author attribution, objective impact measures, and thus a clear path for progress in scientific knowledge and communication

### References

clamps in slice. J. Neurophysiol. 71:375-400. **10**(S1):P52.





Kulagina, 2008

<sup>1.</sup> De Schutter E and Bower JM (1994) An active membrane model of the cerebellar Purkinje cell. I. Simulation of current

<sup>2.</sup> Cornelis H, Edwards M, Coop AD and Bower JM: The CBI architecture for computational simulation of realistic neurons and circuits in the GENESIS 3 software federation. 2008, BMC Neurosci. 9(S1):P88.

<sup>3.</sup> Coop AD, Cornelis H, Rodriguez M and Bower JM: Using GENESIS 3 for single neuron modeling. 2009, BMC Neurosci