Resource Summary Report

Generated by dkNET on May 21, 2025

Multiscale Object Orientation Simulation Environment

RRID:SCR_008031
Type: Tool

Proper Citation

Multiscale Object Orientation Simulation Environment (RRID:SCR_008031)

Resource Information

URL: http://moose.sourceforge.net/

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Description: MOOSE is the Multiscale Object-Oriented Simulation Environment. It is the base and numerical core for large, detailed simulations including Computational Neuroscience and Systems Biology. MOOSE spans the range from single molecules to subcellular networks, from single cells to neuronal networks, and to still larger systems. it is backwards-compatible with GENESIS, and forward compatible with Python and XML-based model definition standards like SBML and MorphML. MOOSE is coordinating with the GENESIS-3 project towards the goals of developing educational resources for modeling. MOOSE is open source software, licensed under the LGPL (Lesser GNU Public License). It has absolutely no warranty. Sponsors: - National Center of Biological Sciences (NCBS) - National Institutes of Health (NIH) Collaboration - EU-India grid - Department of Atomic Energy Science Research Council (DAE/SRC) - Department of Biotechnology (DBT)

Synonyms: MOOSE

Resource Type: simulation software, software resource, software application

Keywords: cell, computational, molecule, network, neuronal, neuroscience, simulation, subcellular, systems biology

Funding:

Resource Name: Multiscale Object Orientation Simulation Environment

Resource ID: SCR_008031

Alternate IDs: nif-0000-10307

Alternate URLs: http://www.nitrc.org/projects/moose

Record Creation Time: 20220129T080245+0000

Record Last Update: 20250521T061217+0000

Ratings and Alerts

No rating or validation information has been found for Multiscale Object Orientation Simulation Environment.

No alerts have been found for Multiscale Object Orientation Simulation Environment.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 10 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

McDougal RA, et al. (2022) Efficient Simulation of 3D Reaction-Diffusion in Models of Neurons and Networks. Frontiers in neuroinformatics, 16, 847108.

Bhatia A, et al. (2019) Precise excitation-inhibition balance controls gain and timing in the hippocampus. eLife, 8.

Gleeson P, et al. (2019) Open Source Brain: A Collaborative Resource for Visualizing, Analyzing, Simulating, and Developing Standardized Models of Neurons and Circuits. Neuron, 103(3), 395.

McDougal RA, et al. (2013) Water-tight membranes from neuronal morphology files. Journal of neuroscience methods, 220(2), 167.

Manninen T, et al. (2010) Postsynaptic signal transduction models for long-term potentiation and depression. Frontiers in computational neuroscience, 4, 152.

Pecevski D, et al. (2009) PCSIM: A Parallel Simulation Environment for Neural Circuits Fully Integrated with Python. Frontiers in neuroinformatics, 3, 11.

King JG, et al. (2009) A Component-Based Extension Framework for Large-Scale Parallel Simulations in NEURON. Frontiers in neuroinformatics, 3, 10.

Wils S, et al. (2009) STEPS: Modeling and Simulating Complex Reaction-Diffusion Systems with Python. Frontiers in neuroinformatics, 3, 15.

Ray S, et al. (2008) PyMOOSE: Interoperable Scripting in Python for MOOSE. Frontiers in neuroinformatics, 2, 6.

Djurfeldt M, et al. (2008) Large-scale modeling - a tool for conquering the complexity of the brain. Frontiers in neuroinformatics, 2, 1.