Resource Summary Report

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General Neural Simulation System

RRID:SCR_006316
Type: Tool

Proper Citation

General Neural Simulation System (RRID:SCR_006316)

Resource Information

URL: http://genesis-sim.org/

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Description: General purpose simulation platform developed to support the simulation of neural systems ranging from subcellular components and biochemical reactions to complex models of single neurons, simulations of large networks, and systems-level models. As such, GENESIS, and its version for parallel and networked computers (PGENESIS) was the first broad scale modeling system in computational biology to encourage modelers to develop and share model features and components. User contributed GENESIS models and simulations are available. You may to contribute a model or simulation. Educational tutorials for instruction in both neurobiology and computational methods have been developed. These tutorials and GENESIS are now being widely used in graduate and undergraduate instruction. These uses include full semester courses in computational neuroscience or neural modeling, short intensive courses or workshops, an option for a course project, and short units on computational neuroscience within courses on artificial neural nets. They also have a repository of user-contributed tutorials and materials for use in neuroscience education. If you have course descriptions, syllabi, exercises, tutorials, or short HOWTO documents, please upload them to Education.

Abbreviations: GENESIS

Synonyms: GENESIS, GENESIS Simulator, GEneral NEural SImulation System

Resource Type: data set, simulation software, training material, software resource, source code, software application, software library, software toolkit, narrative resource, data or information resource

Keywords: electrophysiology, computer, in silico, model, modeling, simulation, neural system, network, neurobiology, computational neuroscience, neural modeling, subcellular, biochemical reaction, neuron, channel, cell, FASEB list

Availability: The community can contribute to this resource

Resource Name: General Neural Simulation System

Resource ID: SCR_006316

Alternate IDs: nif-0000-00091

Alternate URLs: http://www.nitrc.org/projects/genesis http://genesis-sim.org/GENESIS/

Record Creation Time: 20220129T080235+0000

Record Last Update: 20260728T043231+0000

Ratings and Alerts

No rating or validation information has been found for General Neural Simulation System.

No alerts have been found for General Neural Simulation System.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 434 mentions in open access literature.

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

Esmaeili M, et al. (2026) Distinct regulatory elements of SLC6A14 expression contribute to modification of cystic fibrosis phenotypes. Human genetics, 145(1), 8.

Chen X, et al. (2025) Old vs. New Local Ancestry Inference in HCHS/SOL: A Comparative Study. bioRxiv : the preprint server for biology.

Viart NM, et al. (2025) Breast tumors from ATM pathogenic variant carriers display a specific genome-wide DNA methylation profile. Breast cancer research : BCR, 27(1), 36.

Hernangomez-Laderas A, et al. (2025) Saliva as a potential diagnostic medium: DNA methylation biomarkers for disorders beyond the oral cavity. NPJ genomic medicine, 10(1), 49.

Yang S, et al. (2025) Macroscopic bubble generation promoted by nanobubble seeds as a traceless anti-fluctuation strategy for water splitting. Nature communications, 16(1), 5732.

Jawinski P, et al. (2025) Genome-wide analysis of brain age identifies 59 associated loci and unveils relationships with mental and physical health. Nature aging, 5(10), 2086.

Vujkovic M, et al. (2025) Germline Variants Influence Chronic Liver Disease Progression through Distinct Pathways. medRxiv : the preprint server for health sciences.

Rao H, et al. (2025) Advancements in genetic research by the Hispanic Community Health Study/Study of Latinos: A 10-year retrospective review. HGG advances, 6(1), 100376.

Goda K, et al. (2025) Gene-environment interactions contribute to blood pressure variation across global populations. medRxiv : the preprint server for health sciences.

Lee MK, et al. (2025) Genome scan reveals several loci associated with torus palatinus. Orthodontics & craniofacial research, 28(1), 159.

Griswold AJ, et al. (2025) Generalizability of tau and amyloid plasma biomarkers in Alzheimer's disease cohorts of diverse genetic ancestries. Alzheimer's & dementia : the journal of the Alzheimer's Association, 21(3), e14367.

Evans LM, et al. (2025) A simple approach for multiple observations improves power to detect genetic effects and genomic prediction accuracy. medRxiv : the preprint server for health sciences.

Gagnon M, et al. (2025) Rare variants and founder effect in the Beauce region of Quebec. Communications biology, 8(1), 1184.

Kumar P, et al. (2025) Genetic structuring and estimation of reproductive adults in Onchocerca volvulus: A genome-wide analysis across hosts and regions. PLoS neglected tropical diseases, 19(7), e0013221.

Venkataraman A, et al. (2025) A genome-wide association study of methamphetamine use among people with HIV. BMC medical genomics, 18(1), 46.

Hubers N, et al. (2025) Polygenic Scores for Dizygotic Twinning: Insights into the Genetic Architecture of Female Fertility. medRxiv : the preprint server for health sciences.

Zhu J, et al. (2025) Development of a 101.6K liquid-phased probe for GWAS and genomic selection in pine wilt disease-resistance breeding in Masson pine. The plant genome, 18(1), e70005.

Mack JA, et al. (2025) Genetic Variants Associated With Preeclampsia and Maternal Serum sFLT1 Levels. Hypertension (Dallas, Tex. : 1979), 82(5), 839.

, et al. (2025) Trans-ancestry genome-wide study of depression identifies 697 associations implicating cell types and pharmacotherapies. Cell, 188(3), 640.

Wilson AC, et al. (2025) Novel risk loci encompassing genes influencing STAT3, GPCR, and oxidative stress signaling are associated with co-morbid GERD and COPD. PLoS genetics, 21(2), e1011531.