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Virtual Cell at the National Resource for Cell Analysis and Modeling

RRID:SCR_007421 Type: Tool

Proper Citation

Virtual Cell at the National Resource for Cell Analysis and Modeling (RRID:SCR_007421)

Resource Information

URL: http://vcell.org/

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Description: V-Cell is a remote user modeling and simulation environment utilizing Java"s Remote Method Invocation (RMI). The biologically oriented user interface allows experimentalists to create models, define cellular geometry, specify simulations and analyze the simulation results. The results are run and stored on a remote server and can be reviewed in the software and/or exported in a variety of popular formats. The design of the biological to mathematical mapping allows for separate use of biological and math components, and includes automatic mathematical simplification using pseudo-steady approximations and mass conservation relationships. This allows for direct specification of mathematical problems, performing simulations and analysis on those systems. The stand alone mathematics user interface is also a powerful tool for modeling reaction-diffusion systems. A transparent general purpose solver is used to translate the initial biological description into a set of concise mathematical problems. The solver is transparent to the average user, but is accessible to the theorist as the Math Editor component. The software is composed of three main components: 1. The modeling framework represents the physiological models of the Virtual Cell and allows for persistence and database support. 2. The mathematics framework transparently solves an important class of mathematical problems encountered in the cellular modeling. 3. The WWW accessible graphical user interface provides access to the technology mentioned above. The user interface has been developed using Java 2 Applets.

Abbreviations: V-Cell, VCell

Synonyms: VCell - The Virtual Cell, Virtual Cell

Resource Type: software resource, simulation software, software application

Keywords: cell modeling, model cell, virtual cell, virtual cell, FASEB list

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Alternate IDs: nif-0000-00529

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Ratings and Alerts

No rating or validation information has been found for Virtual Cell at the National Resource for Cell Analysis and Modeling.

No alerts have been found for Virtual Cell at the National Resource for Cell Analysis and Modeling.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 69 mentions in open access literature.

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

Zhou X, et al. (2024) A noncanonical GTPase signaling mechanism controls exit from mitosis in budding yeast. bioRxiv : the preprint server for biology.

Norman CA, et al. (2023) The release of inhibition model reproduces kinetics and plasticity of neurotransmitter release in central synapses. Research square.

Loconte V, et al. (2023) Soft X-ray tomograms provide a structural basis for whole-cell modeling. FASEB journal : official publication of the Federation of American Societies for Experimental Biology, 37(1), e22681.

Danielsson BE, et al. (2023) Nuclear lamina strain states revealed by intermolecular force biosensor. Nature communications, 14(1), 3867.

Mendes P, et al. (2023) Reproducibility and FAIR Principles: The Case of a Segment Polarity Network Model. ArXiv.

Ruiter FAA, et al. (2023) Optimization of Media Change Intervals through Hydrogels Using Mathematical Models. Biomacromolecules, 24(2), 604.

Karagöz Z, et al. (2023) Computational evidence for multi-layer crosstalk between the cadherin-11 and PDGFR pathways. Scientific reports, 13(1), 15804.

Mendes P, et al. (2023) Reproducibility and FAIR principles: the case of a segment polarity network model. Frontiers in cell and developmental biology, 11, 1201673.

Sinner EK, et al. (2022) Purification and characterization of sequential cobalamin-dependent radical SAM methylases ThnK and TokK in carbapenem ?-lactam antibiotic biosynthesis. Methods in enzymology, 669, 29.

Nosbisch JL, et al. (2022) A kinetic model of phospholipase C-?1 linking structure-based insights to dynamics of enzyme autoinhibition and activation. The Journal of biological chemistry, 298(5), 101886.

Liu F, et al. (2022) Hybrid modelling of biological systems: current progress and future prospects. Briefings in bioinformatics, 23(3).

Paes D, et al. (2022) Computational investigation of the dynamic control of cAMP signaling by PDE4 isoform types. Biophysical journal, 121(14), 2693.

Schmitt O, et al. (2022) Reaction-diffusion models in weighted and directed connectomes. PLoS computational biology, 18(10), e1010507.

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

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Karagöz Z, et al. (2021) Towards understanding the messengers of extracellular space: Computational models of outside-in integrin reaction networks. Computational and structural biotechnology journal, 19, 303.

Kenner B, et al. (2021) Artificial Intelligence and Early Detection of Pancreatic Cancer: 2020 Summative Review. Pancreas, 50(3), 251.

Dale R, et al. (2021) Overcoming the Challenges to Enhancing Experimental Plant Biology With Computational Modeling. Frontiers in plant science, 12, 687652.

Afzal N, et al. (2021) Effect of crista morphology on mitochondrial ATP output: A computational study. Current research in physiology, 4, 163.

Yang L, et al. (2021) High-Throughput Methods in the Discovery and Study of Biomaterials and Materiobiology. Chemical reviews, 121(8), 4561.