Resource Summary Report

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CVODE

RRID:SCR_014696
Type: Tool

Proper Citation

CVODE (RRID:SCR_014696)

Resource Information

URL: http://computation.llnl.gov/projects/sundials/cvode

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Description: Solver for stiff and nonstiff ordinary differential equation (ODE) systems (initial value problem), given in explicit form y' = f(t,y), based on Adams and BDF methods. It is one of the programs that makes up the Suite of Nonlinear and Differential/Algebraic Equation Solvers (SUNDIALS).

Synonyms: SUNDIALS CVODE

Resource Type: data processing software, data analysis software, software application, software resource

Keywords: data analysis software, solver, equation solver, ordinary differential equation, differential equation, stiff, nonstiff

Funding:

Availability: Available as part of the SUNDIALS software package

Resource Name: CVODE

Resource ID: SCR_014696

Record Creation Time: 20220129T080321+0000

Record Last Update: 20250420T014719+0000

Ratings and Alerts

No rating or validation information has been found for CVODE.

No alerts have been found for CVODE.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 54 mentions in open access literature.

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

Mate-Kole EM, et al. (2024) Mathematical complexities in radionuclide metabolic modelling: a review of ordinary differential equation kinetics solvers in biokinetic modelling. Journal of radiological protection : official journal of the Society for Radiological Protection, 44(2).

Kutumova EO, et al. (2024) Physiologically based pharmacokinetic model for predicting the biodistribution of albumin nanoparticles after induction and recovery from acute lung injury. Heliyon, 10(10), e30962.

Yip HYK, et al. (2024) Integrative modeling uncovers p21-driven drug resistance and prioritizes therapies for PIK3CA-mutant breast cancer. NPJ precision oncology, 8(1), 20.

Mahardika T NQ, et al. (2024) Evaluation of cardiac pro-arrhythmic risks using the artificial neural network with ToR-ORd in silico model output. Frontiers in physiology, 15, 1374355.

Birgiolas J, et al. (2023) NeuroML-DB: Sharing and characterizing data-driven neuroscience models described in NeuroML. PLoS computational biology, 19(3), e1010941.

Whittaker DG, et al. (2022) Ion channel model reduction using manifold boundaries. Journal of the Royal Society, Interface, 19(193), 20220193.

Britton OJ, et al. (2022) A population of in silico models identifies the interplay between Nav 1.8 conductance and potassium currents as key in regulating human dorsal root ganglion neuron excitability. F1000Research, 11, 104.

Miller C, et al. (2022) Multiscale modelling of desquamation in the interfollicular epidermis. PLoS computational biology, 18(8), e1010368.

Ataullakhanov FI, et al. (2022) Significance of two transmembrane ion gradients for human erythrocyte volume stabilization. PloS one, 17(12), e0272675.

Hendrix M, et al. (2021) cellmlmanip and chaste_codegen: automatic CellML to C++ code generation with fixes for singularities and automatically generated Jacobians. Wellcome open research, 6, 261.

Marques CST, et al. (2021) Reduced Reaction Mechanisms for Ethanol under Ultra-lean Conditions in Internal Combustion Engines. ACS omega, 6(1), 206.

Yang B, et al. (2021) Reverse engineering gene regulatory network based on complex-valued ordinary differential equation model. BMC bioinformatics, 22(Suppl 3), 448.

Morii Y, et al. (2020) Optimization of one-parameter family of integration formulae for solving stiff chemical-kinetic ODEs. Scientific reports, 10(1), 21330.

Tötsch N, et al. (2020) Bayesian Data Integration Questions Classic Study on Protease Self-Digest Kinetics. ACS omega, 5(25), 15162.

Kopa? D, et al. (2020) First-Principles-Based Multiscale Modelling of Nonoxidative Butane Dehydrogenation on Cr2O3(0001). ACS catalysis, 10(24), 14732.

Gupta S, et al. (2020) Parallel Tempering with Lasso for model reduction in systems biology. PLoS computational biology, 16(3), e1007669.

Salazar-Cavazos E, et al. (2020) Multisite EGFR phosphorylation is regulated by adaptor protein abundances and dimer lifetimes. Molecular biology of the cell, 31(7), 695.

Heldt FS, et al. (2020) A Single Light-Responsive Sizer Can Control Multiple-Fission Cycles in Chlamydomonas. Current biology : CB, 30(4), 634.

Dubinkina V, et al. (2019) Multistability and regime shifts in microbial communities explained by competition for essential nutrients. eLife, 8.

Fabbri A, et al. (2019) Required GK1 to Suppress Automaticity of iPSC-CMs Depends Strongly on IK1 Model Structure. Biophysical journal, 117(12), 2303.