Resource Summary Report

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PyDSTool

RRID:SCR_014771
Type: Tool

Proper Citation

PyDSTool (RRID:SCR_014771)

Resource Information

URL: http://www.ni.gsu.edu/~rclewley/PyDSTool/FrontPage.html

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Description: Integrated simulation and analysis environment for dynamic systems models of physical systems. It supports symbolic math, optimization, phase plane analysis, continuation and bifurcation analysis, data analysis, and other tools for modeling. It is written in Python with some underlying C and Fortran legacy code.

Resource Type: software resource, software application, simulation software, standalone software

Defining Citation: DOI:10.1371/journal.pcbi.1002628

Keywords: integrated software, integrated analysis, model, simulation software, physical system, python

Funding:

Availability: Open source, Available for download, Acknowledgement requested

Resource Name: PyDSTool

Resource ID: SCR_014771

License: BSD License

Record Creation Time: 20220129T080322+0000

Record Last Update: 20250514T061656+0000

Ratings and Alerts

No rating or validation information has been found for PyDSTool.

No alerts have been found for PyDSTool.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 16 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Garcia GC, et al. (2023) Mitochondrial morphology governs ATP production rate. The Journal of general physiology, 155(9).

Nordick B, et al. (2022) Nonmodular oscillator and switch based on RNA decay drive regeneration of multimodal gene expression. Nucleic acids research, 50(7), 3693.

Martinez-Corral R, et al. (2018) Self-Amplifying Pulsatile Protein Dynamics without Positive Feedback. Cell systems, 7(4), 453.

Perez-Carrasco R, et al. (2018) Combining a Toggle Switch and a Repressilator within the AC-DC Circuit Generates Distinct Dynamical Behaviors. Cell systems, 6(4), 521.

Bocci F, et al. (2018) A mechanism-based computational model to capture the interconnections among epithelial-mesenchymal transition, cancer stem cells and Notch-Jagged signaling. Oncotarget, 9(52), 29906.

Mönke G, et al. (2017) Excitability in the p53 network mediates robust signaling with tunable activation thresholds in single cells. Scientific reports, 7, 46571.

Ryl T, et al. (2017) Cell-Cycle Position of Single MYC-Driven Cancer Cells Dictates Their Susceptibility to a Chemotherapeutic Drug. Cell systems, 5(3), 237.

Bocci F, et al. (2017) Numb prevents a complete epithelial-mesenchymal transition by modulating Notch signalling. Journal of the Royal Society, Interface, 14(136).

Boareto M, et al. (2016) Notch-Jagged signalling can give rise to clusters of cells exhibiting a hybrid epithelial/mesenchymal phenotype. Journal of the Royal Society, Interface, 13(118).

Berger SD, et al. (2015) Modeling the Influence of Ion Channels on Neuron Dynamics in Drosophila. Frontiers in computational neuroscience, 9, 139.

Jolly MK, et al. (2015) Coupling the modules of EMT and stemness: A tunable 'stemness window' model. Oncotarget, 6(28), 25161.

Hong T, et al. (2015) An Ovol2-Zeb1 Mutual Inhibitory Circuit Governs Bidirectional and Multi-step Transition between Epithelial and Mesenchymal States. PLoS computational biology, 11(11), e1004569.

Wojcik J, et al. (2014) Key bifurcations of bursting polyrhythms in 3-cell central pattern generators. PloS one, 9(4), e92918.

Marin B, et al. (2013) High prevalence of multistability of rest states and bursting in a database of a model neuron. PLoS computational biology, 9(3), e1002930.

Hong T, et al. (2012) A simple theoretical framework for understanding heterogeneous differentiation of CD4+ T cells. BMC systems biology, 6, 66.

Hong T, et al. (2011) A mathematical model for the reciprocal differentiation of T helper 17 cells and induced regulatory T cells. PLoS computational biology, 7(7), e1002122.