Resource Summary Report

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PottersWheel

RRID:SCR_021118
Type: Tool

Proper Citation

PottersWheel (RRID:SCR_021118)

Resource Information

URL: https://potterswheel.de/

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Description: Software MATLAB toolbox for mathematical modeling of time dependent dynamical systems that can be expressed as chemical reaction networks or ordinary differential equations. Allows to automatically calibrate model parameters by fitting model to experimental measurements.Fits model to several data sets at once (multi-experiment fitting). Accessible via graphical user interfaces, from command line and scripts,determines parameter identifiability and confidence intervals,imports and exports SBML models and supports biochemical network modeling.

Synonyms: PottersWheel mathematical modeling

Resource Type: software toolkit, software resource

Keywords: Mechanistic mathematical modeling, time dependent dynamical systems, parameter estimation, reaction network, ordinary differential equation based modeling, confidence intervals determination, parameter identifiability, biochemical network modeling, SBML models

Funding: TIKANIS GmbH ;
German Federal Ministry of Economics and Technology ;
Baden-Württemberg Ministry of Science ;
Research and the Arts ;
Germany

Availability: Free, Available for download, Freely available

Resource Name: PottersWheel

Resource ID: SCR_021118

Record Creation Time: 20220129T080353+0000

Record Last Update: 20250331T061719+0000

Ratings and Alerts

No rating or validation information has been found for PottersWheel .

No alerts have been found for PottersWheel .

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 15 mentions in open access literature.

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

Eriksson O, et al. (2022) Combining hypothesis- and data-driven neuroscience modeling in FAIR workflows. eLife, 11.

Gao X, et al. (2019) Estrogen receptors promote NSCLC progression by modulating the membrane receptor signaling network: a systems biology perspective. Journal of translational medicine, 17(1), 308.

Kolczyk K, et al. (2016) Challenges in horizontal model integration. BMC systems biology, 10, 28.

Rateitschak K, et al. (2016) Autocrine TGF-?/ZEB/microRNA-200 signal transduction drives epithelial-mesenchymal transition: Kinetic models predict minimal drug dose to inhibit metastasis. Cellular signalling, 28(8), 861.

Meng Q, et al. (2015) Reversible ubiquitination shapes NLRC5 function and modulates NF-?B activation switch. The Journal of cell biology, 211(5), 1025.

Konrath F, et al. (2014) Identification of new I?B? complexes by an iterative experimental and mathematical modeling approach. PLoS computational biology, 10(3), e1003528.

Siciliano V, et al. (2013) MiRNAs confer phenotypic robustness to gene networks by suppressing biological noise. Nature communications, 4, 2364.

Petelenz-Kurdziel E, et al. (2013) Quantitative analysis of glycerol accumulation, glycolysis and growth under hyper osmotic stress. PLoS computational biology, 9(6), e1003084.

Witt J, et al. (2012) Analysing the role of UVB-induced translational inhibition and PP2Ac deactivation in NF-?B signalling using a minimal mathematical model. PloS one, 7(7), e40274.

Rateitschak K, et al. (2012) Parameter identifiability and sensitivity analysis predict targets for enhancement of STAT1 activity in pancreatic cancer and stellate cells. PLoS computational biology, 8(12), e1002815.

Siciliano V, et al. (2011) Construction and modelling of an inducible positive feedback loop stably integrated in a mammalian cell-line. PLoS computational biology, 7(6), e1002074.

Lange F, et al. (2011) Studies on mechanisms of interferon-gamma action in pancreatic cancer using a data-driven and model-based approach. Molecular cancer, 10(1), 13.

Wangorsch G, et al. (2011) Time-resolved in silico modeling of fine-tuned cAMP signaling in platelets: feedback loops, titrated phosphorylations and pharmacological modulation. BMC systems biology, 5, 178.

Hsieh MY, et al. (2010) Spatio-temporal modeling of signaling protein recruitment to EGFR. BMC systems biology, 4, 57.

Costa MN, et al. (2009) Coupled stochastic spatial and non-spatial simulations of ErbB1 signaling pathways demonstrate the importance of spatial organization in signal transduction. PloS one, 4(7), e6316.