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A new strategy for assessing sensitivities in biochemical models

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Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences, 2008, 366, 3619-31.

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#	Paper	IF	Citations
35	Preface. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2008 , 366, 3437-44	3	1
34	A systems biology framework for modeling metabolic enzyme inhibition of Mycobacterium tuberculosis. <i>BMC Systems Biology</i> , 2009 , 3, 92	3.5	31
33	Towards a unifying, systems biology understanding of large-scale cellular death and destruction caused by poorly liganded iron: Parkinson α , Huntington α , Alzheimer α , prions, bactericides, chemical toxicology and others as examples. <i>Archives of Toxicology</i> , 2010 , 84, 825-89	5.8	292
32	Biochemical network-based drug-target prediction. <i>Current Opinion in Biotechnology</i> , 2010 , 21, 511-6	11.4	55
31	SensSB: a software toolbox for the development and sensitivity analysis of systems biology models. <i>Bioinformatics</i> , 2010 , 26, 1675-6	7.2	42
30	Modeling synergistic drug inhibition of Mycobacterium tuberculosis growth in murine macrophages. <i>Molecular BioSystems</i> , 2011 , 7, 2622-36		11
29	Identification of Critical Molecular Components in a Multiscale Cancer Model Based on the Integration of Monte Carlo, Resampling, and ANOVA. <i>Frontiers in Physiology</i> , 2011 , 2, 35	4.6	20
28	Modular metabolic control analysis of large responses in branched systems--application to aspartate metabolism. <i>FEBS Journal</i> , 2011 , 278, 2565-78	5.7	2
27	Mathematical modeling and sensitivity analysis of the integrated TNF-mediated apoptotic pathway for identifying key regulators. <i>Computers in Biology and Medicine</i> , 2011 , 41, 512-28	7	11
26	Modeling and analysis of biopathways dynamics. <i>Journal of Bioinformatics and Computational Biology</i> , 2012 , 10, 1231001	1	8
25	Conclusions via unique predictions obtained despite unidentifiability--new definitions and a general method. <i>FEBS Journal</i> , 2012 , 279, 3513-27	5.7	41
24	Biochemical fluctuations, optimisation and the linear noise approximation. <i>BMC Systems Biology</i> , 2012 , 6, 86	3.5	19
23	Condor-COPASI: high-throughput computing for biochemical networks. <i>BMC Systems Biology</i> , 2012 , 6, 91	3.5	37
22	Novel global sensitivity analysis methodology accounting for the crucial role of the distribution of input parameters: application to systems biology models. <i>International Journal of Robust and Nonlinear Control</i> , 2012 , 22, 1082-1102	3.6	33
21	Dynamics and feedback loops in the transforming growth factor β signaling pathway. <i>Biophysical Chemistry</i> , 2012 , 162, 22-34	3.5	25
20	Approaches and tools for modeling signaling pathways and calcium dynamics in neurons. <i>Journal of Neuroscience Methods</i> , 2013 , 220, 131-40	3	28
19	Model of tryptophan metabolism, readily scalable using tissue-specific gene expression data. <i>Journal of Biological Chemistry</i> , 2013 , 288, 34555-66	5.4	35

18	Molecular mechanisms underlying neuronal synaptic plasticity: systems biology meets computational neuroscience in the wilds of synaptic plasticity. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2013 , 5, 717-31	6.6	9
17	A computational model of liver iron metabolism. <i>PLoS Computational Biology</i> , 2013 , 9, e1003299	5	21
16	Prediction stability in a data-based, mechanistic model of σ regulation during sporulation in <i>Bacillus subtilis</i> . <i>Scientific Reports</i> , 2013 , 3, 2755	4.9	3
15	What can we learn from global sensitivity analysis of biochemical systems?. <i>PLoS ONE</i> , 2013 , 8, e79244	3.7	28
14	Different cancer cell lines resistant to the same drug exhibit differences in folate pathway dynamics. 2014 ,		
13	New types of experimental data shape the use of enzyme kinetics for dynamic network modeling. <i>FEBS Journal</i> , 2014 , 281, 549-71	5.7	29
12	Global sensitivity analysis of a mathematical model of acute inflammation identifies nonlinear dependence of cumulative tissue damage on host interleukin-6 responses. <i>Journal of Theoretical Biology</i> , 2014 , 358, 132-48	2.3	19
11	Sobol Sensitivity Analysis: A Tool to Guide the Development and Evaluation of Systems Pharmacology Models. <i>CPT: Pharmacometrics and Systems Pharmacology</i> , 2015 , 4, 69-79	4.5	155
10	Computational Modeling. 2016 , 9-29		
9	Ordinary Differential Equations (ODEs) Based Modeling. 2016 , 63-78		3
8	Targeting glycolysis in the malaria parasite <i>Plasmodium falciparum</i> . <i>FEBS Journal</i> , 2016 , 283, 634-46	5.7	28
7	Biosensing <i>Vibrio cholerae</i> with Genetically Engineered <i>Escherichia coli</i> . <i>ACS Synthetic Biology</i> , 2016 , 5, 1275-1283	5.7	29
6	Prediction Uncertainty Estimation Despite Unidentifiability: An Overview of Recent Developments. <i>Studies in Mechanobiology, Tissue Engineering and Biomaterials</i> , 2016 , 449-466	0.5	7
5	Search for a Minimal Set of Parameters by Assessing the Total Optimization Potential for a Dynamic Model of a Biochemical Network. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017 , 14, 978-985	3	5
4	A new conceptual framework for the therapy by optimized multidimensional pulses of therapeutic activity. The case of multiple myeloma model. <i>Journal of Theoretical Biology</i> , 2018 , 454, 292-309	2.3	
3	Computational Modeling Reveals Frequency Modulation of Calcium-cAMP/PKA Pathway in Dendritic Spines. <i>Biophysical Journal</i> , 2019 , 117, 1963-1980	2.9	15
2	Computational modeling reveals frequency modulation of calcium-cAMP/PKA pathway in dendritic spines.		6
1	Model-driven Assessment of the Effects of Brain-derived Neurotrophic Factor Deficiency on Glutamate and Gamma-Aminobutyric Acid: Implications for Understanding Schizophrenia Pathophysiology. <i>Clinical Psychopharmacology and Neuroscience</i> , 2017 , 15, 115-125	3.4	5

