

Jonathan Cooper

List of Publications by Year in descending order

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Version: 2024-02-01

47
papers

2,547
citations

279798

23
h-index

276875

41
g-index

54
all docs

54
docs citations

54
times ranked

2746
citing authors

#	ARTICLE	IF	CITATIONS
1	CMakeCatchTemplate: A C++ template project. <i>Journal of Open Research Software</i> , 2021, 9, 17.	5.9	0
2	chaste codegen: automatic CellML to C++ code generation with fixes for singularities and automatically generated Jacobians. <i>Wellcome Open Research</i> , 2021, 6, 261.	1.8	1
3	CellML 2.0. <i>Journal of Integrative Bioinformatics</i> , 2020, 17, .	1.5	24
4	Chaste: Cancer, Heart and Soft Tissue Environment. <i>Journal of Open Source Software</i> , 2020, 5, 1848.	4.6	58
5	Use of Bayesian Inference for Parameter Recovery in DC and AC Voltammetry. <i>ChemElectroChem</i> , 2018, 5, 917-935.	3.4	26
6	Simulation Experiment Description Markup Language (SED-ML) Level 1 Version 3 (L1V3). <i>Journal of Integrative Bioinformatics</i> , 2018, 15, .	1.5	27
7	Reproducible model development in the cardiac electrophysiology Web Lab. <i>Progress in Biophysics and Molecular Biology</i> , 2018, 139, 3-14.	2.9	21
8	Inference-based assessment of parameter identifiability in nonlinear biological models. <i>Journal of the Royal Society Interface</i> , 2018, 15, 20180318.	3.4	18
9	Comparing two sequential Monte Carlo samplers for exact and approximate Bayesian inference on biological models. <i>Journal of the Royal Society Interface</i> , 2017, 14, 20170340.	3.4	20
10	Where next for the reproducibility agenda in computational biology?. <i>BMC Systems Biology</i> , 2016, 10, 52.	3.0	23
11	The Cardiac Electrophysiology Web Lab. <i>Biophysical Journal</i> , 2016, 110, 292-300.	0.5	49
12	Hodgkin-Huxley revisited: reparametrization and identifiability analysis of the classic action potential model with approximate Bayesian methods. <i>Royal Society Open Science</i> , 2015, 2, 150499.	2.4	22
13	Simulation Experiment Description Markup Language (SED-ML) Level 1 Version 2. <i>Journal of Integrative Bioinformatics</i> , 2015, 12, 119-212.	1.5	10
14	Promoting Coordinated Development of Community-Based Information Standards for Modeling in Biology: The COMBINE Initiative. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 19.	4.1	72
15	Ten Simple Rules for a Successful Cross-Disciplinary Collaboration. <i>PLoS Computational Biology</i> , 2015, 11, e1004214.	3.2	46
16	An integrated approach to quantitative modelling in angiogenesis research. <i>Journal of the Royal Society Interface</i> , 2015, 12, 20150546.	3.4	23
17	A call for virtual experiments: Accelerating the scientific process. <i>Progress in Biophysics and Molecular Biology</i> , 2015, 117, 99-106.	2.9	31
18	Simulation Experiment Description Markup Language (SED-ML) Level 1 Version 2. <i>Journal of Integrative Bioinformatics</i> , 2015, 12, 262.	1.5	8

#	ARTICLE	IF	CITATIONS
19	Ten Simple Rules for Effective Computational Research. <i>PLoS Computational Biology</i> , 2014, 10, e1003506.	3.2	47
20	Chaste. <i>International Journal of High Performance Computing Applications</i> , 2014, 28, 13-32.	3.7	6
21	COMBINE archive and OMEX format: one file to share all information to reproduce a modeling project. <i>BMC Bioinformatics</i> , 2014, 15, 369.	2.6	114
22	Cellular cardiac electrophysiology modeling with Chaste and CellML. <i>Frontiers in Physiology</i> , 2014, 5, 511.	2.8	27
23	Connecting Models to Data in Multiscale Multicellular Tissue Simulations. <i>Procedia Computer Science</i> , 2013, 18, 712-721.	2.0	9
24	Computational assessment of drug-induced effects on the electrocardiogram: from ion channel to body surface potentials. <i>British Journal of Pharmacology</i> , 2013, 168, 718-733.	5.4	98
25	Chaste: An Open Source C++ Library for Computational Physiology and Biology. <i>PLoS Computational Biology</i> , 2013, 9, e1002970.	3.2	375
26	TumorML: Concept and requirements of an in silico cancer modelling markup language. , 2011, 2011, 441-4.		7
27	Functional Curation: Potential Future Directions for SED-ML. <i>Nature Precedings</i> , 2011, , .	0.1	0
28	Considerations for the use of cellular electrophysiology models within cardiac tissue simulations. <i>Progress in Biophysics and Molecular Biology</i> , 2011, 107, 74-80.	2.9	28
29	High-throughput functional curation of cellular electrophysiology models. <i>Progress in Biophysics and Molecular Biology</i> , 2011, 107, 11-20.	2.9	46
30	Simulation of multiple ion channel block provides improved early prediction of compounds' clinical torsadogenic risk. <i>Cardiovascular Research</i> , 2011, 91, 53-61.	3.8	282
31	Minimum Information About a Simulation Experiment (MIASE). <i>PLoS Computational Biology</i> , 2011, 7, e1001122.	3.2	133
32	The Virtual Physiological Human Toolkit. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2010, 368, 3925-3936.	3.4	18
33	A numerical guide to the solution of the bidomain equations of cardiac electrophysiology. <i>Progress in Biophysics and Molecular Biology</i> , 2010, 102, 136-155.	2.9	71
34	An overview of the CellML API and its implementation. <i>BMC Bioinformatics</i> , 2010, 11, 178.	2.6	67
35	Toward a VPH/Physiome Toolkit. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2010, 2, 134-147.	6.6	24
36	A Posteriori Error Analysis for the Use of Lookup Tables in Cardiac Electrophysiology Simulations. <i>SIAM Journal of Scientific Computing</i> , 2010, 32, 2167-2189.	2.8	1

#	ARTICLE	IF	CITATIONS
37	A computational study of discrete mechanical tissue models. <i>Physical Biology</i> , 2009, 6, 036001.	1.8	99
38	Chaste: A test-driven approach to software development for biological modelling. <i>Computer Physics Communications</i> , 2009, 180, 2452-2471.	7.5	207
39	An integrative computational model for intestinal tissue renewal. <i>Cell Proliferation</i> , 2009, 42, 617-636.	5.3	142
40	C haste : incorporating a novel multi-scale spatial and temporal algorithm into a large-scale open source library. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2009, 367, 1907-1930.	3.4	36
41	A model-driven approach to automatic conversion of physical units. <i>Software - Practice and Experience</i> , 2008, 38, 337-359.	3.6	16
42	CellML and associated tools and techniques. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2008, 366, 3017-3043.	3.4	121
43	Chaste: using agile programming techniques to develop computational biology software. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2008, 366, 3111-3136.	3.4	61
44	Experience report. , 2007, , .		0
45	Experience report. <i>ACM SIGPLAN Notices</i> , 2007, 42, 247-250.	0.2	2
46	On the application of partial evaluation to the optimisation of cardiac electrophysiological simulations. , 2006, , .		23
47	cellmlmanip and chaste_codegen: automatic CellML to C++ code generation with fixes for singularities and automatically generated Jacobians. <i>Wellcome Open Research</i> , 0, 6, 261.	1.8	2