Dagmar Waltemath

List of Publications by Year in descending order

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DACMAD WALTEMATH

#	Article	IF	CITATIONS
1	Controlled vocabularies and semantics in systems biology. Molecular Systems Biology, 2011, 7, 543.	7.2	246
2	Reproducible computational biology experiments with SED-ML - The Simulation Experiment Description Markup Language. BMC Systems Biology, 2011, 5, 198.	3.0	211
3	<scp>SBML</scp> Level 3: an extensible format for the exchange and reuse of biological models. Molecular Systems Biology, 2020, 16, e9110.	7.2	178
4	Minimum Information About a Simulation Experiment (MIASE). PLoS Computational Biology, 2011, 7, e1001122.	3.2	133
5	COMBINE archive and OMEX format: one file to share all information to reproduce a modeling project. BMC Bioinformatics, 2014, 15, 369.	2.6	114
6	The Systems Biology Markup Language (SBML): Language Specification for Level 3 Version 2 Core Release 2. Journal of Integrative Bioinformatics, 2019, 16, .	1.5	78
7	Promoting Coordinated Development of Community-Based Information Standards for Modeling in Biology: The COMBINE Initiative. Frontiers in Bioengineering and Biotechnology, 2015, 3, 19.	4.1	72
8	The Systems Biology Markup Language (SBML): Language Specification for Level 3 Version 2 Core. Journal of Integrative Bioinformatics, 2018, 15, .	1.5	57
9	Harmonizing semantic annotations for computational models in biology. Briefings in Bioinformatics, 2019, 20, 540-550.	6.5	52
10	Toward Community Standards and Software for Whole-Cell Modeling. IEEE Transactions on Biomedical Engineering, 2016, 63, 2007-2014.	4.2	51
11	How Modeling Standards, Software, and Initiatives Support Reproducibility in Systems Biology and Systems Medicine. IEEE Transactions on Biomedical Engineering, 2016, 63, 1999-2006.	4.2	43
12	Combining computational models, semantic annotations and simulation experiments in a graph database. Database: the Journal of Biological Databases and Curation, 2015, 2015, .	3.0	42
13	A call for virtual experiments: Accelerating the scientific process. Progress in Biophysics and Molecular Biology, 2015, 117, 99-106.	2.9	31
14	The JWS online simulation database. Bioinformatics, 2017, 33, 1589-1590.	4.1	28
15	Simulation Experiment Description Markup Language (SED-ML) Level 1 Version 3 (L1V3). Journal of Integrative Bioinformatics, 2018, 15, .	1.5	27
16	Initiatives, Concepts, and Implementation Practices of FAIR (Findable, Accessible, Interoperable, and) Tj ETQq0 0 Research Protocols, 2021, 10, e22505.	0 rgBT /0 1.0	verlock 10 Tf 25
17	Ranked retrieval of Computational Biology models. BMC Bioinformatics, 2010, 11, 423.	2.6	24
	An algorithm to detect and communicate the differences in computational models describing		_

18 An algorithm to detect and communicate the differences in computational models describing biological systems. Bioinformatics, 2016, 32, 563-570.

4.1 23

DAGMAR WALTEMATH

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19	Improving the reuse of computational models through version control. Bioinformatics, 2013, 29, 742-748.	4.1	21
20	Meeting report from the fourth meeting of the Computational Modeling in Biology Network (COMBINE). Standards in Genomic Sciences, 2014, 9, 1285-1301.	1.5	21
21	STON: exploring biological pathways using the SBGN standard and graph databases. BMC Bioinformatics, 2016, 17, 494.	2.6	19
22	The first 10 years of the international coordination network for standards in systems and synthetic biology (COMBINE). Journal of Integrative Bioinformatics, 2020, 17, .	1.5	18
23	Notions of similarity for systems biology models. Briefings in Bioinformatics, 2018, 19, bbw090.	6.5	17
24	COMODI: an ontology to characterise differences in versions of computational models in biology. Journal of Biomedical Semantics, 2016, 7, 46.	1.6	15
25	Approaches and Criteria for Provenance in Biomedical Data Sets and Workflows: Protocol for a Scoping Review. JMIR Research Protocols, 2021, 10, e31750.	1.0	15
26	Specifications of Standards in Systems and Synthetic Biology. Journal of Integrative Bioinformatics, 2015, 12, 258.	1.5	14
27	Annotation-based feature extraction from sets of SBML models. Journal of Biomedical Semantics, 2015, 6, 20.	1.6	13
28	The Systems Biology Markup Language (SBML): Language Specification for Level 3 Version 1 Core. Journal of Integrative Bioinformatics, 2018, 15, .	1.5	13
29	Specifications of Standards in Systems and Synthetic Biology: Status and Developments in 2016. Journal of Integrative Bioinformatics, 2016, 13, 1-7.	1.5	12
30	Specifications of Standards in Systems and Synthetic Biology. Journal of Integrative Bioinformatics, 2015, 12, 1-3.	1.5	11
31	Simulation Experiment Description Markup Language (SED-ML) Level 1 Version 2. Journal of Integrative Bioinformatics, 2015, 12, 119-212.	1.5	10
32	A fully featured COMBINE archive of a simulation study on syncytial mitotic cycles in Drosophila embryos. F1000Research, 2016, 5, 2421.	1.6	10
33	Specifications of standards in systems and synthetic biology: status and developments in 2020. Journal of Integrative Bioinformatics, 2020, 17, .	1.5	10
34	Addressing <i>barriers in comprehensiveness, accessibility, reusability, interoperability and reproducibility of computational models in systems biology</i> . Briefings in Bioinformatics, 2022, 23, .	6.5	10
35	Towards standardization guidelines for <i>in silico</i> approaches in personalized medicine. Journal of Integrative Bioinformatics, 2020, 17, .	1.5	9
36	Open modeling and exchange (OMEX) metadata specification version 1.0. Journal of Integrative Bioinformatics, 2020, 17, .	1.5	9

DAGMAR WALTEMATH

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37	Identifying frequent patterns in biochemical reaction networks: a workflow. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	3.0	8
38	OMEX metadata specification (version 1.2). Journal of Integrative Bioinformatics, 2021, 18, .	1.5	8
39	The simulation experiment description markup language (SED-ML): language specification for level 1 version 4. Journal of Integrative Bioinformatics, 2021, 18, 20210021.	1.5	8
40	Systems Biology Markup Language (SBML) Level 2 Version 5: Structures and Facilities for Model Definitions. Journal of Integrative Bioinformatics, 2015, 12, 731-901.	1.5	7
41	SED-ML web tools: generate, modify and export standard-compliant simulation studies. Bioinformatics, 2017, 33, 1253-1254.	4.1	7
42	Specifications of Standards in Systems and Synthetic Biology: Status and Developments in 2017. Journal of Integrative Bioinformatics, 2018, 15, .	1.5	7
43	Specifications of Standards in Systems and Synthetic Biology: Status and Developments in 2019. Journal of Integrative Bioinformatics, 2019, 16, .	1.5	7
44	Reproducibility of Model-Based Results in Systems Biology. , 2013, , 301-320.		7
45	Simulation Experiment Description Markup Language (SED-ML) : Level 1 Version 1. Nature Precedings, 2011, , .	0.1	6
46	A brief history of COMBINE. , 2017, , .		6
47	Quick tips for creating effective and impactful biological pathways using the Systems Biology Graphical Notation. PLoS Computational Biology, 2018, 14, e1005740.	3.2	6
48	Information Retrieval in Life Sciences: A Programmatic Survey. , 2014, , 73-109.		6
49	Overview: Standards for Modeling in Systems Medicine. , 2021, , 345-353.		4
50	SBGN Bricks Ontology as a tool to describe recurring concepts in molecular networks. Briefings in Bioinformatics, 2021, 22, .	6.5	4
51	Opportunities of Digital Infrastructures for Disease Management—Exemplified on COVID-19-Related Change in Diagnosis Counts for Diabetes-Related Eye Diseases. Nutrients, 2022, 14, 2016.	4.1	4
52	Evolution of computational models in BioModels Database and the Physiome Model Repository. BMC Systems Biology, 2018, 12, 53.	3.0	3
53	Facilitating Study and Item Level Browsing for Clinical and Epidemiological COVID-19 Studies. Studies in Health Technology and Informatics, 2021, 281, 794-798.	0.3	3
54	Data Management in Computational Systems Biology: Exploring Standards, Tools, Databases, and Packaging Best Practices. Methods in Molecular Biology, 2019, 2049, 285-314.	0.9	3

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55	Specifications of standards in systems and synthetic biology: status and developments in 2021. Journal of Integrative Bioinformatics, 2021, 18, .	1.5	2
56	SBML Level 3 Package Proposal: Annotation. Nature Precedings, 2011, , .	0.1	1
57	SBML Level 3 Package Proposal: Annotation. Nature Precedings, 0, , .	0.1	1
58	Annotation-Based Feature Extraction from Sets of SBML Models. Lecture Notes in Computer Science, 2014, , 81-95.	1.3	1
59	Exploring the evolution of biochemical models at the network level. PLoS ONE, 2022, 17, e0265735.	2.5	0