

Denis Thieffry

List of Publications by Year in descending order

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Version: 2024-02-01

117
papers

8,521
citations

44069

48
h-index

51608

86
g-index

154
all docs

154
docs citations

154
times ranked

8665
citing authors

#	ARTICLE	IF	CITATIONS
1	Dynamical analysis of a generic Boolean model for the control of the mammalian cell cycle. <i>Bioinformatics</i> , 2006, 22, e124-e131.	4.1	570
2	From specific gene regulation to genomic networks: a global analysis of transcriptional regulation in <i>Escherichia coli</i> . <i>BioEssays</i> , 1998, 20, 433-440.	2.5	421
3	Dynamical behaviour of biological regulatory networks. Biological role of feedback loops and practical use of the concept of the loop-characteristic state. <i>Bulletin of Mathematical Biology</i> , 1995, 57, 247-276.	1.9	410
4	RSAT 2015: Regulatory Sequence Analysis Tools. <i>Nucleic Acids Research</i> , 2015, 43, W50-W56.	14.5	263
5	Modeling ERBB receptor-regulated G1/S transition to find novel targets for de novo trastuzumab resistance. <i>BMC Systems Biology</i> , 2009, 3, 1.	3.0	242
6	Logical Modeling and Dynamical Analysis of Cellular Networks. <i>Frontiers in Genetics</i> , 2016, 7, 94.	2.3	216
7	RSAT 2011: regulatory sequence analysis tools. <i>Nucleic Acids Research</i> , 2011, 39, W86-W91.	14.5	213
8	A Logical Analysis of the <i>Drosophila</i> Gap-gene System. <i>Journal of Theoretical Biology</i> , 2001, 211, 115-141.	1.7	204
9	RSAT peak-motifs: motif analysis in full-size ChIP-seq datasets. <i>Nucleic Acids Research</i> , 2012, 40, e31-e31.	14.5	203
10	C/EBP β poises B cells for rapid reprogramming into induced pluripotent stem cells. <i>Nature</i> , 2014, 506, 235-239.	27.8	201
11	Logical modelling of regulatory networks with GINsim 2.3. <i>BioSystems</i> , 2009, 97, 134-139.	2.0	188
12	RSAT 2018: regulatory sequence analysis tools 20th anniversary. <i>Nucleic Acids Research</i> , 2018, 46, W209-W214.	14.5	186
13	Mathematical Modelling of Cell-Fate Decision in Response to Death Receptor Engagement. <i>PLoS Computational Biology</i> , 2010, 6, e1000702.	3.2	179
14	<sc>SBML</sc> Level 3: an extensible format for the exchange and reuse of biological models. <i>Molecular Systems Biology</i> , 2020, 16, e9110.	7.2	178
15	RegulonDB: a database on transcriptional regulation in <i>Escherichia coli</i> . <i>Nucleic Acids Research</i> , 1998, 26, 55-59.	14.5	176
16	Diversity and Plasticity of Th Cell Types Predicted from Regulatory Network Modelling. <i>PLoS Computational Biology</i> , 2010, 6, e1000912.	3.2	167
17	Integrative Modelling of the Influence of MAPK Network on Cancer Cell Fate Decision. <i>PLoS Computational Biology</i> , 2013, 9, e1003286.	3.2	167
18	GINsim: A software suite for the qualitative modelling, simulation and analysis of regulatory networks. <i>BioSystems</i> , 2006, 84, 91-100.	2.0	165

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19	Dynamical behaviour of biological regulatory networks—II. Immunity control in bacteriophage lambda. <i>Bulletin of Mathematical Biology</i> , 1995, 57, 277-297.	1.9	157
20	Transcription Factors Drive Tet2-Mediated Enhancer Demethylation to Reprogram Cell Fate. <i>Cell Stem Cell</i> , 2018, 23, 727-741.e9.	11.1	156
21	Graphic requirements for multistability and attractive cycles in a Boolean dynamical framework. <i>Advances in Applied Mathematics</i> , 2008, 41, 335-350.	0.7	145
22	SBML qualitative models: a model representation format and infrastructure to foster interactions between qualitative modelling formalisms and tools. <i>BMC Systems Biology</i> , 2013, 7, 135.	3.0	145
23	Functional organisation of Escherichia coli transcriptional regulatory network. <i>Journal of Molecular Biology</i> , 2008, 381, 238-247.	4.2	143
24	Logical Modelling of Gene Regulatory Networks with GINsim. <i>Methods in Molecular Biology</i> , 2012, 804, 463-479.	0.9	134
25	miR-9 Controls the Timing of Neurogenesis through the Direct Inhibition of Antagonistic Factors. <i>Developmental Cell</i> , 2012, 22, 1052-1064.	7.0	133
26	Logical modeling of lymphoid and myeloid cell specification and transdifferentiation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 5792-5799.	7.1	125
27	Discovery of Drug Synergies in Gastric Cancer Cells Predicted by Logical Modeling. <i>PLoS Computational Biology</i> , 2015, 11, e1004426.	3.2	118
28	Dynamically consistent reduction of logical regulatory graphs. <i>Theoretical Computer Science</i> , 2011, 412, 2207-2218.	0.9	117
29	Dynamical roles of biological regulatory circuits. <i>Briefings in Bioinformatics</i> , 2007, 8, 220-225.	6.5	103
30	Cooperative development of logical modelling standards and tools with CoLoMoTo. <i>Bioinformatics</i> , 2015, 31, 1154-1159.	4.1	98
31	RSAT matrix-clustering: dynamic exploration and redundancy reduction of transcription factor binding motif collections. <i>Nucleic Acids Research</i> , 2017, 45, e119-e119.	14.5	96
32	C/EBP β Activates Pre-existing and De Novo Macrophage Enhancers during Induced Pre-B Cell Transdifferentiation and Myelopoiesis. <i>Stem Cell Reports</i> , 2015, 5, 232-247.	4.8	95
33	Segmenting the fly embryo. <i>Journal of Theoretical Biology</i> , 2003, 224, 517-537.	1.7	94
34	C/EBP β creates elite cells for iPSC reprogramming by upregulating Klf4 and increasing the levels of Lsd1 and Brd4. <i>Nature Cell Biology</i> , 2016, 18, 371-381.	10.3	94
35	A complete workflow for the analysis of full-size ChIP-seq (and similar) data sets using peak-motifs. <i>Nature Protocols</i> , 2012, 7, 1551-1568.	12.0	92
36	Benchmarking joint multi-omics dimensionality reduction approaches for the study of cancer. <i>Nature Communications</i> , 2021, 12, 124.	12.8	89

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37	Segmenting the fly embryo: logical analysis of the role of the Segment Polarity cross-regulatory module. <i>International Journal of Developmental Biology</i> , 2008, 52, 1059-1075.	0.6	85
38	Model Checking to Assess T-Helper Cell Plasticity. <i>Frontiers in Bioengineering and Biotechnology</i> , 2014, 2, 86.	4.1	82
39	Decision Diagrams for the Representation and Analysis of Logical Models of Genetic Networks. <i>Lecture Notes in Computer Science</i> , 2007, , 233-247.	1.3	77
40	Logical Modeling and Analysis of Cellular Regulatory Networks With GINsim 3.0. <i>Frontiers in Physiology</i> , 2018, 9, 646.	2.8	75
41	The modularity of biological regulatory networks. <i>BioSystems</i> , 1999, 50, 49-59.	2.0	74
42	The CoLoMoTo Interactive Notebook: Accessible and Reproducible Computational Analyses for Qualitative Biological Networks. <i>Frontiers in Physiology</i> , 2018, 9, 680.	2.8	67
43	Dynamical modeling and analysis of large cellular regulatory networks. <i>Chaos</i> , 2013, 23, 025114.	2.5	62
44	Petri net modelling of biological regulatory networks. <i>Journal of Discrete Algorithms</i> , 2008, 6, 165-177.	0.7	61
45	Logical modelling of cell cycle control in eukaryotes: a comparative study. <i>Molecular BioSystems</i> , 2009, 5, 1569.	2.9	60
46	Forty years under the central dogma. <i>Trends in Biochemical Sciences</i> , 1998, 23, 312-316.	7.5	59
47	Modular logical modelling of the budding yeast cell cycle. <i>Molecular BioSystems</i> , 2009, 5, 1787.	2.9	58
48	The activation trajectory of plasmacytoid dendritic cells in vivo during a viral infection. <i>Nature Immunology</i> , 2020, 21, 983-997.	14.5	58
49	MethMotif: an integrative cell specific database of transcription factor binding motifs coupled with DNA methylation profiles. <i>Nucleic Acids Research</i> , 2019, 47, D145-D154.	14.5	52
50	Dynamical modeling of syncytial mitotic cycles in <i>Drosophila</i> embryos. <i>Molecular Systems Biology</i> , 2007, 3, 131.	7.2	41
51	Logical modelling of the role of the Hh pathway in the patterning of the <i>Drosophila</i> wing disc. <i>Bioinformatics</i> , 2008, 24, i234-i240.	4.1	41
52	Logical model specification aided by model-checking techniques: application to the mammalian cell cycle regulation. <i>Bioinformatics</i> , 2016, 32, i772-i780.	4.1	41
53	RSAT 2022: regulatory sequence analysis tools. <i>Nucleic Acids Research</i> , 2022, 50, W670-W676.	14.5	40
54	Qualitative Modelling of Genetic Networks: From Logical Regulatory Graphs to Standard Petri Nets. <i>Lecture Notes in Computer Science</i> , 2004, , 137-156.	1.3	39

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55	Cooperation between T cell receptor and Toll-like receptor 5 signaling for CD4 ⁺ T cell activation. <i>Science Signaling</i> , 2019, 12, .	3.6	38
56	The shortest path is not the one you know: application of biological network resources in precision oncology research. <i>Mutagenesis</i> , 2015, 30, 191-204.	2.6	37
57	Histone Chaperone SSRP1 is Essential for Wnt Signaling Pathway Activity During Osteoblast Differentiation. <i>Stem Cells</i> , 2016, 34, 1369-1376.	3.2	32
58	On Circuit Functionality in Boolean Networks. <i>Bulletin of Mathematical Biology</i> , 2013, 75, 906-919.	1.9	27
59	Logical modelling of Drosophila signalling pathways. <i>Molecular BioSystems</i> , 2013, 9, 2248.	2.9	27
60	TFregulomeR reveals transcription factors' context-specific features and functions. <i>Nucleic Acids Research</i> , 2020, 48, e10-e10.	14.5	27
61	CoCAS: a ChIP-on-chip analysis suite. <i>Bioinformatics</i> , 2009, 25, 954-955.	4.1	25
62	Setting the basis of best practices and standards for curation and annotation of logical models in biology—highlights of the [BC]2 2019 CoLoMoTo/SysMod Workshop. <i>Briefings in Bioinformatics</i> , 2021, 22, 1848-1859.	6.5	25
63	From Logical Regulatory Graphs to Standard Petri Nets: Dynamical Roles and Functionality of Feedback Circuits. <i>Lecture Notes in Computer Science</i> , 2006, , 56-72.	1.3	25
64	Syncytial apoptosis signaling network induced by the HIV-1 envelope glycoprotein complex: an overview. <i>Cell Death and Disease</i> , 2015, 6, e1846-e1846.	6.3	24
65	Dynamical Analysis of the Regulatory Network Defining the Dorsal-Ventral Boundary of the Drosophila Wing Imaginal Disc. <i>Genetics</i> , 2006, 174, 1625-1634.	2.9	23
66	A Quantitative Multivariate Model of Human Dendritic Cell-T Helper Cell Communication. <i>Cell</i> , 2019, 179, 432-447.e21.	28.9	23
67	Computational Modeling of the Main Signaling Pathways Involved in Mast Cell Activation. <i>Current Topics in Microbiology and Immunology</i> , 2014, 382, 69-93.	1.1	22
68	Contribution of ROS and metabolic status to neonatal and adult CD8 ⁺ T cell activation. <i>PLoS ONE</i> , 2019, 14, e0226388.	2.5	21
69	Evaluating the Reproducibility of Single-Cell Gene Regulatory Network Inference Algorithms. <i>Frontiers in Genetics</i> , 2021, 12, 617282.	2.3	21
70	The Systems Biology Markup Language (SBML) Level 3 Package: Qualitative Models, Version 1, Release 1. <i>Journal of Integrative Bioinformatics</i> , 2015, 12, 270.	1.5	21
71	<i>Cis</i> -acting variation is common across regulatory layers but is often buffered during embryonic development. <i>Genome Research</i> , 2021, 31, 211-224.	5.5	19
72	Metagenome Annotation Using a Distributed Grid of Undergraduate Students. <i>PLoS Biology</i> , 2008, 6, e296.	5.6	19

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73	Dynamical modelling of pattern formation during embryonic development. <i>Current Opinion in Genetics and Development</i> , 2003, 13, 326-330.	3.3	18
74	Computational Verification of Large Logical Models – Application to the Prediction of T Cell Response to Checkpoint Inhibitors. <i>Frontiers in Physiology</i> , 2020, 11, 558606.	2.8	18
75	Alternative Epigenetic States Understood in Terms of Specific Regulatory Structures. <i>Annals of the New York Academy of Sciences</i> , 2002, 981, 135-153.	3.8	17
76	Dynamical modeling of biological regulatory networks. <i>BioSystems</i> , 2006, 84, 77-80.	2.0	16
77	Formal derivation of qualitative dynamical models from biochemical networks. <i>BioSystems</i> , 2016, 149, 70-112.	2.0	16
78	SBML Level 3 package: Qualitative Models, Version 1, Release 1. <i>Journal of Integrative Bioinformatics</i> , 2015, 12, 691-730.	1.5	15
79	Jean Brachet's alternative scheme for protein synthesis. <i>Trends in Biochemical Sciences</i> , 1996, 21, 114-117.	7.5	14
80	The Minimum Information about a Molecular Interaction CAusal Statement (MI2CAST). <i>Bioinformatics</i> , 2021, 36, 5712-5718.	4.1	14
81	Transcriptional and epigenetic signatures of zygotic genome activation during early drosophila embryogenesis. <i>BMC Genomics</i> , 2013, 14, 226.	2.8	13
82	Prediction of Mutations to Control Pathways Enabling Tumor Cell Invasion with the CoLoMoTo Interactive Notebook (Tutorial). <i>Frontiers in Physiology</i> , 2018, 9, 787.	2.8	13
83	Dynamical Boolean Modeling of Immunogenic Cell Death. <i>Frontiers in Physiology</i> , 2020, 11, 590479.	2.8	13
84	A Transcription Factor Pulse Can Prime Chromatin for Heritable Transcriptional Memory. <i>Molecular and Cellular Biology</i> , 2017, 37, .	2.3	12
85	Proteomic Analysis of the SH2Domain-containing Leukocyte Protein of 76 kDa (SLP76) Interactome. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 2874-2889.	3.8	11
86	Automatic Inference of Regulatory and Dynamical Properties from Incomplete Gene Interaction and Expression Data. <i>Lecture Notes in Computer Science</i> , 2012, , 25-30.	1.3	10
87	Qualitative Dynamical Modelling Can Formally Explain Mesoderm Specification and Predict Novel Developmental Phenotypes. <i>PLoS Computational Biology</i> , 2016, 12, e1005073.	3.2	10
88	RSAT variation-tools: An accessible and flexible framework to predict the impact of regulatory variants on transcription factor binding. <i>Computational and Structural Biotechnology Journal</i> , 2019, 17, 1415-1428.	4.1	9
89	Positive or Negative Regulatory Circuit Inference from Multilevel Dynamics. , 0, , 263-270.		9
90	Syntactic recognition of regulatory regions in Escherichia coli. <i>Bioinformatics</i> , 1996, 12, 415-422.	4.1	8

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91	Rationalizing early embryogenesis in the 1930s: Albert Dalcq on gradients and fields. , 2001, 34, 149-181.		7
92	Logical modeling of cell fate specification Application to T cell commitment. Current Topics in Developmental Biology, 2020, 139, 205-238.	2.2	7
93	Boolean Dynamics of Compound Regulatory circuits. , 2016, , 43-53.		6
94	Interplay between SMAD2 and STAT5A is a critical determinant of IL-17A/IL-17F differential expression. Molecular Biomedicine, 2021, 2, 9.	4.4	6
95	Logical modelling of <i>in vitro</i> differentiation of human monocytes into dendritic cells unravels novel transcriptional regulatory interactions. Interface Focus, 2021, 11, 20200061.	3.0	6
96	UPMaBoSS: A Novel Framework for Dynamic Cell Population Modeling. Frontiers in Molecular Biosciences, 2022, 9, 800152.	3.5	6
97	IL-12 Signaling Contributes to the Reprogramming of Neonatal CD8+ T Cells. Frontiers in Immunology, 2020, 11, 1089.	4.8	5
98	Qualitative modelling and simulation of developmental regulatory networks. , 2003, , 109-134.		5
99	Bacterial Molecular Networks: Bridging the Gap Between Functional Genomics and Dynamical Modelling. Methods in Molecular Biology, 2012, 804, 1-11.	0.9	4
100	Model Checking Logical Regulatory Networks. IFAC Postprint Volumes IPPV / International Federation of Automatic Control, 2014, 47, 170-175.	0.4	4
101	Deciphering and modelling the TGF- β^2 signalling interplays specifying the dorsal-ventral axis of the sea urchin embryo. Development (Cambridge), 2020, 148, .	2.5	4
102	Modélisation, analyse et simulation des réseaux génétiques. Medecine/Sciences, 2002, 18, 492-502.	0.2	2
103	Derivation of Qualitative Dynamical Models from Biochemical Networks. Lecture Notes in Computer Science, 2015, , 195-207.	1.3	2
104	Jean Brachet's alternative scheme for protein synthesis. Trends in Biochemical Sciences, 1996, 21, 114-117.	7.5	1
105	A Quantitative Multivariate Model of Human Dendritic Cell-T Helper Cell Communication. SSRN Electronic Journal, 0, , .	0.4	1
106	Course 10 Modeling, analysis, and simulation of genetic regulatory networks: From differential equations to logical models. Les Houches Summer School Proceedings, 2005, , 325-354.	0.2	0
107	Epigenomics: Large scale analysis of chromatin modifications and transcription factors/genome interactions. BioEssays, 2005, 27, 1203-1205.	2.5	0
108	Graphing genes, cells and embryos. BioEssays, 2007, 29, 1059-1061.	2.5	0

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109	Reduction of logical models of regulatory networks yields insight into dynamical properties. , 2010, , .		0
110	RSAT peak-motifs: fast extraction of transcription factor binding motifs from full-size ChIP-seq datasets. EMBnet Journal, 2012, 17, 20.	0.6	0
111	Cell Cycle Modeling Using Logical Rules. , 2013, , 278-282.		0
112	RSAT peak-motifs: Efficient prediction of transcription factor motifs and binding sites from genome-wide sequencing peak sets. EMBnet Journal, 2013, 19, 28.	0.6	0
113	Abstract 2848: Identifying and targeting competing endogenous RNA (ceRNAs) networks to inhibit lung metastasis in triple negative breast cancer. , 2017, , .		0
114	Contribution of ROS and metabolic status to neonatal and adult CD8+ T cell activation. , 2019, 14, e0226388.		0
115	Contribution of ROS and metabolic status to neonatal and adult CD8+ T cell activation. , 2019, 14, e0226388.		0
116	Contribution of ROS and metabolic status to neonatal and adult CD8+ T cell activation. , 2019, 14, e0226388.		0
117	Contribution of ROS and metabolic status to neonatal and adult CD8+ T cell activation. , 2019, 14, e0226388.		0