

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	UPMaBoSS: A Novel Framework for Dynamic Cell Population Modeling. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, 800152.	3.5	6
2	RSAT 2022: regulatory sequence analysis tools. <i>Nucleic Acids Research</i> , 2022, 50, W670-W676.	14.5	40
3	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
4	The Minimum Information about a Molecular Interaction CAusal STatement (MI2CAST). <i>Bioinformatics</i> , 2021, 36, 5712-5718.	4.1	14
5	<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
6	Benchmarking joint multi-omics dimensionality reduction approaches for the study of cancer. <i>Nature Communications</i> , 2021, 12, 124.	12.8	89
7	Evaluating the Reproducibility of Single-Cell Gene Regulatory Network Inference Algorithms. <i>Frontiers in Genetics</i> , 2021, 12, 617282.	2.3	21
8	Interplay between SMAD2 and STAT5A is a critical determinant of IL-17A/IL-17F differential expression. <i>Molecular Biomedicine</i> , 2021, 2, 9.	4.4	6
9	Logical modelling of <i>in vitro</i> differentiation of human monocytes into dendritic cells unravels novel transcriptional regulatory interactions. <i>Interface Focus</i> , 2021, 11, 20200061.	3.0	6
10	TFregulomeR reveals transcription factors' context-specific features and functions. <i>Nucleic Acids Research</i> , 2020, 48, e10-e10.	14.5	27
11	The activation trajectory of plasmacytoid dendritic cells <i>in vivo</i> during a viral infection. <i>Nature Immunology</i> , 2020, 21, 983-997.	14.5	58
12	Dynamical Boolean Modeling of Immunogenic Cell Death. <i>Frontiers in Physiology</i> , 2020, 11, 590479.	2.8	13
13	Deciphering and modelling the TGF- β 2 signalling interplays specifying the dorsal-ventral axis of the sea urchin embryo. <i>Development (Cambridge)</i> , 2020, 148, .	2.5	4
14	IL-12 Signaling Contributes to the Reprogramming of Neonatal CD8+ T Cells. <i>Frontiers in Immunology</i> , 2020, 11, 1089.	4.8	5
15	<i>SBML</i> Level 3: an extensible format for the exchange and reuse of biological models. <i>Molecular Systems Biology</i> , 2020, 16, e9110.	7.2	178
16	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
17	Logical modeling of cell fate specification—Application to T cell commitment. <i>Current Topics in Developmental Biology</i> , 2020, 139, 205-238.	2.2	7
18	A Quantitative Multivariate Model of Human Dendritic Cell-T Helper Cell Communication. <i>Cell</i> , 2019, 179, 432-447.e21.	28.9	23

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19	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
20	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
21	Contribution of ROS and metabolic status to neonatal and adult CD8+ T cell activation. <i>PLoS ONE</i> , 2019, 14, e0226388.	2.5	21
22	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
23	Contribution of ROS and metabolic status to neonatal and adult CD8+ T cell activation. , 2019, 14, e0226388.		0
24	Contribution of ROS and metabolic status to neonatal and adult CD8+ T cell activation. , 2019, 14, e0226388.		0
25	Contribution of ROS and metabolic status to neonatal and adult CD8+ T cell activation. , 2019, 14, e0226388.		0
26	Contribution of ROS and metabolic status to neonatal and adult CD8+ T cell activation. , 2019, 14, e0226388.		0
27	RSAT 2018: regulatory sequence analysis tools 20th anniversary. <i>Nucleic Acids Research</i> , 2018, 46, W209-W214.	14.5	186
28	Transcription Factors Drive Tet2-Mediated Enhancer Demethylation to Reprogram Cell Fate. <i>Cell Stem Cell</i> , 2018, 23, 727-741.e9.	11.1	156
29	Logical Modeling and Analysis of Cellular Regulatory Networks With GINsim 3.0. <i>Frontiers in Physiology</i> , 2018, 9, 646.	2.8	75
30	The CoLoMoTo Interactive Notebook: Accessible and Reproducible Computational Analyses for Qualitative Biological Networks. <i>Frontiers in Physiology</i> , 2018, 9, 680.	2.8	67
31	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
32	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
33	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
34	A Transcription Factor Pulse Can Prime Chromatin for Heritable Transcriptional Memory. <i>Molecular and Cellular Biology</i> , 2017, 37, .	2.3	12
35	Abstract 2848: Identifying and targeting competing endogenous RNA (ceRNAs) networks to inhibit lung metastasis in triple negative breast cancer. , 2017, , .		0
36	Logical Modeling and Dynamical Analysis of Cellular Networks. <i>Frontiers in Genetics</i> , 2016, 7, 94.	2.3	216

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37	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
38	Formal derivation of qualitative dynamical models from biochemical networks. <i>BioSystems</i> , 2016, 149, 70-112.	2.0	16
39	Boolean Dynamics of Compound Regulatory circuits. , 2016, , 43-53.		6
40	Histone Chaperone SSRP1 is Essential for Wnt Signaling Pathway Activity During Osteoblast Differentiation. <i>Stem Cells</i> , 2016, 34, 1369-1376.	3.2	32
41	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
42	Qualitative Dynamical Modelling Can Formally Explain Mesoderm Specification and Predict Novel Developmental Phenotypes. <i>PLoS Computational Biology</i> , 2016, 12, e1005073.	3.2	10
43	SBML Level 3 package: Qualitative Models, Version 1, Release 1. <i>Journal of Integrative Bioinformatics</i> , 2015, 12, 691-730.	1.5	15
44	RSAT 2015: Regulatory Sequence Analysis Tools. <i>Nucleic Acids Research</i> , 2015, 43, W50-W56.	14.5	263
45	Cooperative development of logical modelling standards and tools with CoLoMoTo. <i>Bioinformatics</i> , 2015, 31, 1154-1159.	4.1	98
46	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
47	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
48	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
49	Discovery of Drug Synergies in Gastric Cancer Cells Predicted by Logical Modeling. <i>PLoS Computational Biology</i> , 2015, 11, e1004426.	3.2	118
50	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
51	Derivation of Qualitative Dynamical Models from Biochemical Networks. <i>Lecture Notes in Computer Science</i> , 2015, , 195-207.	1.3	2
52	C/EBP β poises B cells for rapid reprogramming into induced pluripotent stem cells. <i>Nature</i> , 2014, 506, 235-239.	27.8	201
53	Model Checking Logical Regulatory Networks. <i>IFAC Postprint Volumes IPPV / International Federation of Automatic Control</i> , 2014, 47, 170-175.	0.4	4
54	Model Checking to Assess T-Helper Cell Plasticity. <i>Frontiers in Bioengineering and Biotechnology</i> , 2014, 2, 86.	4.1	82

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55	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
56	Transcriptional and epigenetic signatures of zygotic genome activation during early drosophila embryogenesis. <i>BMC Genomics</i> , 2013, 14, 226.	2.8	13
57	On Circuit Functionality in Boolean Networks. <i>Bulletin of Mathematical Biology</i> , 2013, 75, 906-919.	1.9	27
58	Dynamical modeling and analysis of large cellular regulatory networks. <i>Chaos</i> , 2013, 23, 025114.	2.5	62
59	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
60	Logical modelling of Drosophila signalling pathways. <i>Molecular BioSystems</i> , 2013, 9, 2248.	2.9	27
61	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
62	Integrative Modelling of the Influence of MAPK Network on Cancer Cell Fate Decision. <i>PLoS Computational Biology</i> , 2013, 9, e1003286.	3.2	167
63	Cell Cycle Modeling Using Logical Rules. , 2013, , 278-282.		0
64	RSAT peak-motifs: Efficient prediction of transcription factor motifs and binding sites from genome-wide sequencing peak sets. <i>EMBnet Journal</i> , 2013, 19, 28.	0.6	0
65	RSAT peak-motifs: motif analysis in full-size ChIP-seq datasets. <i>Nucleic Acids Research</i> , 2012, 40, e31-e31.	14.5	203
66	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
67	Logical Modelling of Gene Regulatory Networks with GINsim. <i>Methods in Molecular Biology</i> , 2012, 804, 463-479.	0.9	134
68	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
69	Bacterial Molecular Networks: Bridging the Gap Between Functional Genomics and Dynamical Modelling. <i>Methods in Molecular Biology</i> , 2012, 804, 1-11.	0.9	4
70	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
71	RSAT peak-motifs: fast extraction of transcription factor binding motifs from full-size ChIP-seq datasets. <i>EMBnet Journal</i> , 2012, 17, 20.	0.6	0
72	RSAT 2011: regulatory sequence analysis tools. <i>Nucleic Acids Research</i> , 2011, 39, W86-W91.	14.5	213

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73	Dynamically consistent reduction of logical regulatory graphs. Theoretical Computer Science, 2011, 412, 2207-2218.	0.9	117
74	Diversity and Plasticity of Th Cell Types Predicted from Regulatory Network Modelling. PLoS Computational Biology, 2010, 6, e1000912.	3.2	167
75	Mathematical Modelling of Cell-Fate Decision in Response to Death Receptor Engagement. PLoS Computational Biology, 2010, 6, e1000702.	3.2	179
76	Reduction of logical models of regulatory networks yields insight into dynamical properties. , 2010, , .		0
77	CoCAS: a ChIP-on-chip analysis suite. Bioinformatics, 2009, 25, 954-955.	4.1	25
78	Modeling ERBB receptor-regulated G1/S transition to find novel targets for de novo trastuzumab resistance. BMC Systems Biology, 2009, 3, 1.	3.0	242
79	Logical modelling of regulatory networks with GINsim 2.3. BioSystems, 2009, 97, 134-139.	2.0	188
80	Logical modelling of cell cycle control in eukaryotes: a comparative study. Molecular BioSystems, 2009, 5, 1569.	2.9	60
81	Modular logical modelling of the budding yeast cell cycle. Molecular BioSystems, 2009, 5, 1787.	2.9	58
82	Petri net modelling of biological regulatory networks. Journal of Discrete Algorithms, 2008, 6, 165-177.	0.7	61
83	Graphic requirements for multistability and attractive cycles in a Boolean dynamical framework. Advances in Applied Mathematics, 2008, 41, 335-350.	0.7	145
84	Functional organisation of Escherichia coli transcriptional regulatory network. Journal of Molecular Biology, 2008, 381, 238-247.	4.2	143
85	Logical modelling of the role of the Hh pathway in the patterning of the <i>Drosophila</i> wing disc. Bioinformatics, 2008, 24, i234-i240.	4.1	41
86	Segmenting the fly embryo: logical analysis of the role of the Segment Polarity cross-regulatory module. International Journal of Developmental Biology, 2008, 52, 1059-1075.	0.6	85
87	Metagenome Annotation Using a Distributed Grid of Undergraduate Students. PLoS Biology, 2008, 6, e296.	5.6	19
88	Dynamical modeling of syncytial mitotic cycles in <i>Drosophila</i> embryos. Molecular Systems Biology, 2007, 3, 131.	7.2	41
89	Decision Diagrams for the Representation and Analysis of Logical Models of Genetic Networks. Lecture Notes in Computer Science, 2007, , 233-247.	1.3	77
90	Dynamical roles of biological regulatory circuits. Briefings in Bioinformatics, 2007, 8, 220-225.	6.5	103

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91	Graphing genes, cells and embryos. <i>BioEssays</i> , 2007, 29, 1059-1061.	2.5	0
92	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
93	GINsim: A software suite for the qualitative modelling, simulation and analysis of regulatory networks. <i>BioSystems</i> , 2006, 84, 91-100.	2.0	165
94	Dynamical modeling of biological regulatory networks. <i>BioSystems</i> , 2006, 84, 77-80.	2.0	16
95	Dynamical Analysis of the Regulatory Network Defining the Dorsal-Ventral Boundary of the <i>Drosophila</i> Wing Imaginal Disc. <i>Genetics</i> , 2006, 174, 1625-1634.	2.9	23
96	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
97	Course 10 Modeling, analysis, and simulation of genetic regulatory networks: From differential equations to logical models. <i>Les Houches Summer School Proceedings</i> , 2005, , 325-354.	0.2	0
98	Epigenomics: Large scale analysis of chromatin modifications and transcription factors/genome interactions. <i>BioEssays</i> , 2005, 27, 1203-1205.	2.5	0
99	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
100	Segmenting the fly embryo:. <i>Journal of Theoretical Biology</i> , 2003, 224, 517-537.	1.7	94
101	Dynamical modelling of pattern formation during embryonic development. <i>Current Opinion in Genetics and Development</i> , 2003, 13, 326-330.	3.3	18
102	Qualitative modelling and simulation of developmental regulatory networks. , 2003, , 109-134.		5
103	Modélisation, analyse et simulation des réseaux génétiques. <i>Medecine/Sciences</i> , 2002, 18, 492-502.	0.2	2
104	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
105	A Logical Analysis of the <i>Drosophila</i> Gap-gene System. <i>Journal of Theoretical Biology</i> , 2001, 211, 115-141.	1.7	204
106	Rationalizing early embryogenesis in the 1930s: Albert Dalcq on gradients and fields. , 2001, 34, 149-181.		7
107	The modularity of biological regulatory networks. <i>BioSystems</i> , 1999, 50, 49-59.	2.0	74
108	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

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109	Forty years under the central dogma. Trends in Biochemical Sciences, 1998, 23, 312-316.	7.5	59
110	RegulonDB: a database on transcriptional regulation in Escherichia coli. Nucleic Acids Research, 1998, 26, 55-59.	14.5	176
111	Jean Brachet's alternative scheme for protein synthesis. Trends in Biochemical Sciences, 1996, 21, 114-117.	7.5	14
112	Syntactic recognition of regulatory regions in Escherichia coli. Bioinformatics, 1996, 12, 415-422.	4.1	8
113	Jean Brachet's alternative scheme for protein synthesis. Trends in Biochemical Sciences, 1996, 21, 114-117.	7.5	1
114	Dynamical behaviour of biological regulatory networksâ€™II. Immunity control in bacteriophage lambda. Bulletin of Mathematical Biology, 1995, 57, 277-297.	1.9	157
115	Dynamical behaviour of biological regulatory networksâ€™I. Biological role of feedback loops and practical use of the concept of the loop-characteristic state. Bulletin of Mathematical Biology, 1995, 57, 247-276.	1.9	410
116	Positive or Negative Regulatory Circuit Inference from Multilevel Dynamics. , 0, , 263-270.		9
117	A Quantitative Multivariate Model of Human Dendritic Cell-T Helper Cell Communication. SSRN Electronic Journal, 0, , .	0.4	1