

Andrei Yu Zinovyev

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/6949495/andrei-yu-zinovyev-publications-by-year.pdf>

Version: 2024-04-25

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

133
papers

4,787
citations

36
h-index

67
g-index

156
ext. papers

6,547
ext. citations

6.5
avg, IF

5.55
L-index

#	Paper	IF	Citations
133	Modeling Progression of Single Cell Populations Through the Cell Cycle as a Sequence of Switches.. <i>Frontiers in Molecular Biosciences</i> , 2021 , 8, 793912	5.6	0
132	WebMaBoSS: A Web Interface for Simulating Boolean Models Stochastically. <i>Frontiers in Molecular Biosciences</i> , 2021 , 8, 754444	5.6	0
131	Scikit-Dimension: A Python Package for Intrinsic Dimension Estimation. <i>Entropy</i> , 2021 , 23,	2.8	5
130	Meta-Analysis of Esophageal Cancer Transcriptomes Using Independent Component Analysis. <i>Frontiers in Genetics</i> , 2021 , 12, 683632	4.5	0
129	The multilayer community structure of medulloblastoma. <i>IScience</i> , 2021 , 24, 102365	6.1	0
128	Applications of single-cell and bulk RNA sequencing in onco-immunology. <i>European Journal of Cancer</i> , 2021 , 149, 193-210	7.5	11
127	Atlas of Cancer Signaling Network: A Resource of Multi-Scale Biological Maps to Study Disease Mechanisms 2021 , 490-506		
126	. <i>IEEE Transactions on Geoscience and Remote Sensing</i> , 2021 , 1-15	8.1	0
125	LNetReduce: Tool for Reducing Linear Dynamic Networks with Separated Timescales. <i>Lecture Notes in Computer Science</i> , 2021 , 238-244	0.9	
124	Adaptation through the lens of single-cell multi-omics data: Comment on "Dynamic and thermodynamic models of adaptation" by A.N. Gorban et al. <i>Physics of Life Reviews</i> , 2021 , 38, 132-134	2.1	1
123	Systems Biology Analysis for Ewing Sarcoma. <i>Methods in Molecular Biology</i> , 2021 , 2226, 303-333	1.4	2
122	Single-Cell Analysis Reveals Fibroblast Clusters Linked to Immunotherapy Resistance in Cancer. <i>Cancer Discovery</i> , 2020 , 10, 1330-1351	24.4	140
121	Exact solving and sensitivity analysis of stochastic continuous time Boolean models. <i>BMC Bioinformatics</i> , 2020 , 21, 241	3.6	0
120	Robust and Scalable Learning of Complex Intrinsic Dataset Geometry via ELPiGraph. <i>Entropy</i> , 2020 , 22,	2.8	16
119	Collective intelligence defines biological functions in Wikipedia as communities in the hidden protein connection network. <i>PLoS Computational Biology</i> , 2020 , 16, e1007652	5	1
118	Synthesis and Simulation of Ensembles of Boolean Networks for Cell Fate Decision. <i>Lecture Notes in Computer Science</i> , 2020 , 193-209	0.9	4
117	Transcriptional Programs Define Intratumoral Heterogeneity of Ewing Sarcoma at Single-Cell Resolution. <i>Cell Reports</i> , 2020 , 30, 1767-1779.e6	10.6	39

116	cd2sbgmml: bidirectional conversion between CellDesigner and SBGN formats. <i>Bioinformatics</i> , 2020 , 36, 2620-2622	7.2	7
115	Interpreting pathways to discover cancer driver genes with Moonlight. <i>Nature Communications</i> , 2020 , 11, 69	17.4	23
114	Trajectories, bifurcations, and pseudo-time in large clinical datasets: applications to myocardial infarction and diabetes data. <i>GigaScience</i> , 2020 , 9,	7.6	7
113	Modelling of Immune Checkpoint Network Explains Synergistic Effects of Combined Immune Checkpoint Inhibitor Therapy and the Impact of Cytokines in Patient Response. <i>Cancers</i> , 2020 , 12,	6.6	4
112	Minimum Spanning vs. Principal Trees for Structured Approximations of Multi-Dimensional Datasets. <i>Entropy</i> , 2020 , 22,	2.8	2
111	Collective intelligence defines biological functions in Wikipedia as communities in the hidden protein connection network 2020 , 16, e1007652		
110	Collective intelligence defines biological functions in Wikipedia as communities in the hidden protein connection network 2020 , 16, e1007652		
109	Collective intelligence defines biological functions in Wikipedia as communities in the hidden protein connection network 2020 , 16, e1007652		
108	Collective intelligence defines biological functions in Wikipedia as communities in the hidden protein connection network 2020 , 16, e1007652		
107	Deconvolution of transcriptomes and miRNomes by independent component analysis provides insights into biological processes and clinical outcomes of melanoma patients. <i>BMC Medical Genomics</i> , 2019 , 12, 132	3.7	13
106	Independent Component Analysis for Unraveling the Complexity of Cancer Omics Datasets. <i>International Journal of Molecular Sciences</i> , 2019 , 20,	6.3	32
105	ETS Proteins Bind with Glucocorticoid Receptors: Relevance for Treatment of Ewing Sarcoma. <i>Cell Reports</i> , 2019 , 29, 104-117.e4	10.6	7
104	Identification of microRNA clusters cooperatively acting on epithelial to mesenchymal transition in triple negative breast cancer. <i>Nucleic Acids Research</i> , 2019 , 47, 2205-2215	20.1	44
103	Molecular Inverse Comorbidity between Alzheimer's Disease and Lung Cancer: New Insights from Matrix Factorization. <i>International Journal of Molecular Sciences</i> , 2019 , 20,	6.3	6
102	Single-cell trajectories reconstruction, exploration and mapping of omics data with STREAM. <i>Nature Communications</i> , 2019 , 10, 1903	17.4	97
101	Metabolic and signalling network maps integration: application to cross-talk studies and omics data analysis in cancer. <i>BMC Bioinformatics</i> , 2019 , 20, 140	3.6	4
100	Assessing reproducibility of matrix factorization methods in independent transcriptomes. <i>Bioinformatics</i> , 2019 , 35, 4307-4313	7.2	14
99	Lizard Brain: Tackling Locally Low-Dimensional Yet Globally Complex Organization of Multi-Dimensional Datasets. <i>Frontiers in Neurobotics</i> , 2019 , 13, 110	3.4	8

98	A multiscale signalling network map of innate immune response in cancer reveals cell heterogeneity signatures. <i>Nature Communications</i> , 2019 , 10, 4808	17.4	23
97	Basic, simple and extendable kinetic model of protein synthesis. <i>Mathematical Biosciences and Engineering</i> , 2019 , 16, 6602-6622	2.1	1
96	Creation and analysis of biochemical constraint-based models using the COBRA Toolbox v.3.0. <i>Nature Protocols</i> , 2019 , 14, 639-702	18.8	385
95	Estimating the effective dimension of large biological datasets using Fisher separability analysis 2019 ,		10
94	The Virtual Metabolic Human database: integrating human and gut microbiome metabolism with nutrition and disease. <i>Nucleic Acids Research</i> , 2019 , 47, D614-D624	20.1	132
93	PhysiBoSS: a multi-scale agent-based modelling framework integrating physical dimension and cell signalling. <i>Bioinformatics</i> , 2019 , 35, 1188-1196	7.2	44
92	Community-driven roadmap for integrated disease maps. <i>Briefings in Bioinformatics</i> , 2019 , 20, 659-670	13.4	30
91	Conceptual and computational framework for logical modelling of biological networks deregulated in diseases. <i>Briefings in Bioinformatics</i> , 2019 , 20, 1238-1249	13.4	9
90	Application of Atlas of Cancer Signalling Network in preclinical studies. <i>Briefings in Bioinformatics</i> , 2019 , 20, 701-716	13.4	7
89	Logical versus kinetic modeling of biological networks: applications in cancer research. <i>Current Opinion in Chemical Engineering</i> , 2018 , 21, 22-31	5.4	5
88	Classification of gene signatures for their information value and functional redundancy. <i>Npj Systems Biology and Applications</i> , 2018 , 4, 2	5	34
87	Fibroblast Heterogeneity and Immunosuppressive Environment in Human Breast Cancer. <i>Cancer Cell</i> , 2018 , 33, 463-479.e10	24.3	579
86	The CoLoMoTo Interactive Notebook: Accessible and Reproducible Computational Analyses for Qualitative Biological Networks. <i>Frontiers in Physiology</i> , 2018 , 9, 680	4.6	29
85	Prediction of Mutations to Control Pathways Enabling Tumor Cell Invasion with the CoLoMoTo Interactive Notebook (Tutorial). <i>Frontiers in Physiology</i> , 2018 , 9, 787	4.6	6
84	Systems medicine disease maps: community-driven comprehensive representation of disease mechanisms. <i>Npj Systems Biology and Applications</i> , 2018 , 4, 21	5	47
83	Application of Independent Component Analysis to Tumor Transcriptomes Reveals Specific and Reproducible Immune-Related Signals. <i>Lecture Notes in Computer Science</i> , 2018 , 501-513	0.9	2
82	Inferring hidden causal relations between pathway members using reduced Google matrix of directed biological networks. <i>PLoS ONE</i> , 2018 , 13, e0190812	3.7	19
81	Data analysis with arbitrary error measures approximated by piece-wise quadratic PQSQ functions 2018 ,		2

80	Signalling maps in cancer research: construction and data analysis. <i>Database: the Journal of Biological Databases and Curation</i> , 2018 , 2018,	5	8
79	The inconvenience of data of convenience: computational research beyond post-mortem analyses. <i>Nature Methods</i> , 2017 , 14, 937-938	21.6	8
78	Determining the optimal number of independent components for reproducible transcriptomic data analysis. <i>BMC Genomics</i> , 2017 , 18, 712	4.5	32
77	MaBoSS 2.0: an environment for stochastic Boolean modeling. <i>Bioinformatics</i> , 2017 , 33, 2226-2228	7.2	59
76	NaviCom: a web application to create interactive molecular network portraits using multi-level omics data. <i>Database: the Journal of Biological Databases and Curation</i> , 2017 , 2017,	5	9
75	Drug-Driven Synthetic Lethality: Bypassing Tumor Cell Genetics with a Combination of AsiDNA and PARP Inhibitors. <i>Clinical Cancer Research</i> , 2017 , 23, 1001-1011	12.9	30
74	A review of computational approaches detecting microRNAs involved in cancer. <i>Frontiers in Bioscience - Landmark</i> , 2017 , 22, 1774-1791	2.8	10
73	NetNorM: Capturing cancer-relevant information in somatic exome mutation data with gene networks for cancer stratification and prognosis. <i>PLoS Computational Biology</i> , 2017 , 13, e1005573	5	16
72	Piece-wise quadratic approximations of arbitrary error functions for fast and robust machine learning. <i>Neural Networks</i> , 2016 , 84, 28-38	9.1	7
71	Calculating Biological Module Enrichment or Depletion and Visualizing Data on Large-scale Molecular Maps with ACSNMiner and RNavicell Packages. <i>R Journal</i> , 2016 , 8, 293	3.3	2
70	The second European interdisciplinary Ewing sarcoma research summit--A joint effort to deconstructing the multiple layers of a complex disease. <i>Oncotarget</i> , 2016 , 7, 8613-24	3.3	38
69	ROMA: Representation and Quantification of Module Activity from Target Expression Data. <i>Frontiers in Genetics</i> , 2016 , 7, 18	4.5	25
68	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	2.8	23
67	Atlas of Cancer Signalling Network: a systems biology resource for integrative analysis of cancer data with Google Maps. <i>Oncogenesis</i> , 2015 , 4, e160	6.6	90
66	Network-based approaches for drug response prediction and targeted therapy development in cancer. <i>Biochemical and Biophysical Research Communications</i> , 2015 , 464, 386-91	3.4	23
65	DeDaL: Cytoscape 3 app for producing and morphing data-driven and structure-driven network layouts. <i>BMC Systems Biology</i> , 2015 , 9, 46	3.5	16
64	A Modeling Approach to Explain Mutually Exclusive and Co-Occurring Genetic Alterations in Bladder Tumorigenesis. <i>Cancer Research</i> , 2015 , 75, 4042-52	10.1	58
63	Overcoming Complexity of Biological Systems: from Data Analysis to Mathematical Modeling. <i>Mathematical Modelling of Natural Phenomena</i> , 2015 , 10, 186-205	3	7

62	Detection of miRNA regulatory effect on triple negative breast cancer transcriptome. <i>BMC Genomics</i> , 2015 , 16, S4	4.5	11
61	Predicting genetic interactions from Boolean models of biological networks. <i>Integrative Biology (United Kingdom)</i> , 2015 , 7, 921-9	3.7	15
60	Fast and user-friendly non-linear principal manifold learning by method of elastic maps 2015 ,		11
59	NaviCell Web Service for network-based data visualization. <i>Nucleic Acids Research</i> , 2015 , 43, W560-5	20.1	26
58	Mathematical Modelling of Molecular Pathways Enabling Tumour Cell Invasion and Migration. <i>PLoS Computational Biology</i> , 2015 , 11, e1004571	5	72
57	Concomitant Notch activation and p53 deletion trigger epithelial-to-mesenchymal transition and metastasis in mouse gut. <i>Nature Communications</i> , 2014 , 5, 5005	17.4	88
56	Independent component analysis uncovers the landscape of the bladder tumor transcriptome and reveals insights into luminal and basal subtypes. <i>Cell Reports</i> , 2014 , 9, 1235-45	10.6	131
55	BiNoM 2.0, a Cytoscape plugin for accessing and analyzing pathways using standard systems biology formats. <i>BMC Systems Biology</i> , 2013 , 7, 18	3.5	40
54	Model composition through model reduction: a combined model of CD95 and NF- κ B signaling pathways. <i>BMC Systems Biology</i> , 2013 , 7, 13	3.5	14
53	OCSANA: optimal combinations of interventions from network analysis. <i>Bioinformatics</i> , 2013 , 29, 1571-37.2		21
52	NaviCell: a web-based environment for navigation, curation and maintenance of large molecular interaction maps. <i>BMC Systems Biology</i> , 2013 , 7, 100	3.5	39
51	Blind source separation methods for deconvolution of complex signals in cancer biology. <i>Biochemical and Biophysical Research Communications</i> , 2013 , 430, 1182-7	3.4	20
50	Mathematical modeling of microRNA-mediated mechanisms of translation repression. <i>Advances in Experimental Medicine and Biology</i> , 2013 , 774, 189-224	3.6	23
49	Data complexity measured by principal graphs. <i>Computers and Mathematics With Applications</i> , 2013 , 65, 1471-1482	2.7	12
48	Practical use of BiNoM: a biological network manager software. <i>Methods in Molecular Biology</i> , 2013 , 1021, 127-46	1.4	5
47	From a biological hypothesis to the construction of a mathematical model. <i>Methods in Molecular Biology</i> , 2013 , 1021, 107-25	1.4	7
46	Systems biology of Ewing sarcoma: a network model of EWS-FLI1 effect on proliferation and apoptosis. <i>Nucleic Acids Research</i> , 2013 , 41, 8853-71	20.1	39
45	Synthetic lethality between gene defects affecting a single non-essential molecular pathway with reversible steps. <i>PLoS Computational Biology</i> , 2013 , 9, e1003016	5	19

44	How Cell Decides Between Life and Death: Mathematical Modeling of Epigenetic Landscapes of Cellular Fates. <i>Springer Proceedings in Mathematics</i> , 2013 , 191-204		1
43	Geometrical Complexity of Data Approximators. <i>Lecture Notes in Computer Science</i> , 2013 , 500-509	0.9	5
42	Understanding Different Types of Cell Death Using Systems Biology 2012 , 125-143		1
41	Antagonism pattern detection between microRNA and target expression in Ewing's sarcoma. <i>PLoS ONE</i> , 2012 , 7, e41770	3.7	7
40	Reduction of dynamical biochemical reactions networks in computational biology. <i>Frontiers in Genetics</i> , 2012 , 3, 131	4.5	59
39	Kinetic signatures of microRNA modes of action. <i>Rna</i> , 2012 , 18, 1635-55	5.8	77
38	Cell death and life in cancer: mathematical modeling of cell fate decisions. <i>Advances in Experimental Medicine and Biology</i> , 2012 , 736, 261-74	3.6	5
37	Identification of shortened 3' untranslated regions from expression arrays. <i>Journal of Bioinformatics and Computational Biology</i> , 2012 , 10, 1241001	1	3
36	Analysis of the Growth Control Network Specific for Human Lung Adenocarcinoma Cells. <i>Mathematical Modelling of Natural Phenomena</i> , 2012 , 7, 337-368	3	1
35	Network analysis of gene lists for finding reproducible prognostic breast cancer gene signatures. <i>Bioinformatics</i> , 2012 , 8, 773-6	1.1	7
34	Control-free calling of copy number alterations in deep-sequencing data using GC-content normalization. <i>Bioinformatics</i> , 2011 , 27, 268-9	7.2	190
33	Principal manifolds and graphs in practice: from molecular biology to dynamical systems. <i>International Journal of Neural Systems</i> , 2010 , 20, 219-32	6.2	84
32	Mathematical modelling of cell-fate decision in response to death receptor engagement. <i>PLoS Computational Biology</i> , 2010 , 6, e1000702	5	140
31	Dynamical modeling of microRNA action on the protein translation process. <i>BMC Systems Biology</i> , 2010 , 4, 13	3.5	30
30	Asymptotology of chemical reaction networks. <i>Chemical Engineering Science</i> , 2010 , 65, 2310-2324	4.4	44
29	The oncogenic EWS-FLI1 protein binds in vivo GGAA microsatellite sequences with potential transcriptional activation function. <i>PLoS ONE</i> , 2009 , 4, e4932	3.7	121
28	Robust simplifications of multiscale biochemical networks. <i>BMC Systems Biology</i> , 2008 , 2, 86	3.5	76
27	A comprehensive modular map of molecular interactions in RB/E2F pathway. <i>Molecular Systems Biology</i> , 2008 , 4, 173	12.2	99

26	BiNoM: a Cytoscape plugin for manipulating and analyzing biological networks. <i>Bioinformatics</i> , 2008 , 24, 876-7	7.2	87
25	How much non-coding DNA do eukaryotes require?. <i>Journal of Theoretical Biology</i> , 2008 , 252, 587-92	2.3	29
24	Classification of microarray data using gene networks. <i>BMC Bioinformatics</i> , 2007 , 8, 35	3.6	149
23	The mystery of two straight lines in bacterial genome statistics. <i>Bulletin of Mathematical Biology</i> , 2007 , 69, 2429-42	2.1	4
22	Topological grammars for data approximation. <i>Applied Mathematics Letters</i> , 2007 , 20, 382-386	3.5	25
21	Branching Principal Components: Elastic Graphs, Topological Grammars and Metro Maps. <i>Neural Networks (IJCNN), International Joint Conference on</i> , 2007 ,		1
20	Codon usage trajectories and 7-cluster structure of 143 complete bacterial genomic sequences. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2005 , 353, 365-387	3.3	11
19	Elastic Principal Graphs and Manifolds and their Practical Applications. <i>Computing (Vienna/New York)</i> , 2005 , 75, 359-379	2.2	45
18	Codon bias signatures, organization of microorganisms in codon space, and lifestyle. <i>Molecular Biology and Evolution</i> , 2005 , 22, 547-61	8.3	63
17	Invariant Grids: Method of Complexity Reduction in Reaction Networks. <i>Complexus</i> , 2004 , 2, 110-127		7
16	Constructive methods of invariant manifolds for kinetic problems. <i>Physics Reports</i> , 2004 , 396, 197-403	27.7	112
15	Invariant grids for reaction kinetics. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2004 , 333, 106-154		62
14	Codon adaptation index as a measure of dominating codon bias. <i>Bioinformatics</i> , 2003 , 19, 2005-15	7.2	219
13	Self-Organizing Approach for Automated Gene Identification. <i>Open Systems and Information Dynamics</i> , 2003 , 10, 321-333	0.4	11
12	Computational Systems Biology of Cancer		47
11	The CoLoMoTo Interactive Notebook: Accessible and Reproducible Computational Analyses for Qualitative Biological Networks		1
10	Stabilized Independent Component Analysis outperforms other methods in finding reproducible signals in tumoral transcriptomes		1
9	Collective intelligence defines biological functions in Wikipedia as communities in the hidden protein connection network		1

8	Calculating Biological Module Enrichment or Depletion and Visualizing Data on Large-scale Molecular Maps with ACSNMiner and RNavicell R packages	2
7	Moonlight: a tool for biological interpretation and driver genes discovery	5
6	PhysiBoSS: a multi-scale agent based modelling framework integrating physical dimension and cell signalling	2
5	Metabolic and signalling network map integration: application to cross-talk studies and omics data analysis in cancer	1
4	STREAM: Single-cell Trajectories Reconstruction, Exploration And Mapping of omics data	4
3	Independent component analysis provides clinically relevant insights into the biology of melanoma patients	2
2	Hubness reduction improves clustering and trajectory inference in single-cell transcriptomic data	1
1	Modeling Progression of Single Cell Populations Through the Cell Cycle as a Sequence of Switches	1