

Andrei Yu Zinovyev

List of Publications by Year in descending order

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127
papers

7,756
citations

87888

38
h-index

64796

79
g-index

156
all docs

156
docs citations

156
times ranked

11266
citing authors

#	ARTICLE	IF	CITATIONS
1	Fibroblast Heterogeneity and Immunosuppressive Environment in Human Breast Cancer. <i>Cancer Cell</i> , 2018, 33, 463-479.e10.	16.8	1,074
2	Creation and analysis of biochemical constraint-based models using the COBRA Toolbox v.3.0. <i>Nature Protocols</i> , 2019, 14, 639-702.	12.0	833
3	Single-Cell Analysis Reveals Fibroblast Clusters Linked to Immunotherapy Resistance in Cancer. <i>Cancer Discovery</i> , 2020, 10, 1330-1351.	9.4	424
4	Codon adaptation index as a measure of dominating codon bias. <i>Bioinformatics</i> , 2003, 19, 2005-2015.	4.1	274
5	The Virtual Metabolic Human database: integrating human and gut microbiome metabolism with nutrition and disease. <i>Nucleic Acids Research</i> , 2019, 47, D614-D624.	14.5	257
6	Control-free calling of copy number alterations in deep-sequencing data using GC-content normalization. <i>Bioinformatics</i> , 2011, 27, 268-269.	4.1	249
7	Single-cell trajectories reconstruction, exploration and mapping of omics data with STREAM. <i>Nature Communications</i> , 2019, 10, 1903.	12.8	198
8	Classification of microarray data using gene networks. <i>BMC Bioinformatics</i> , 2007, 8, 35.	2.6	191
9	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, 1235-1245.	6.4	181
10	Mathematical Modelling of Cell-Fate Decision in Response to Death Receptor Engagement. <i>PLoS Computational Biology</i> , 2010, 6, e1000702.	3.2	179
11	The Oncogenic EWS-FLI1 Protein Binds In Vivo GGAA Microsatellite Sequences with Potential Transcriptional Activation Function. <i>PLoS ONE</i> , 2009, 4, e4932.	2.5	160
12	Mathematical Modelling of Molecular Pathways Enabling Tumour Cell Invasion and Migration. <i>PLoS Computational Biology</i> , 2015, 11, e1004571.	3.2	130
13	Atlas of Cancer Signalling Network: a systems biology resource for integrative analysis of cancer data with Google Maps. <i>Oncogenesis</i> , 2015, 4, e160-e160.	4.9	129
14	Constructive methods of invariant manifolds for kinetic problems. <i>Physics Reports</i> , 2004, 396, 197-403.	25.6	128
15	MaBoSS 2.0: an environment for stochastic Boolean modeling. <i>Bioinformatics</i> , 2017, 33, 2226-2228.	4.1	118
16	Concomitant Notch activation and p53 deletion trigger epithelial-to-mesenchymal transition and metastasis in mouse gut. <i>Nature Communications</i> , 2014, 5, 5005.	12.8	114
17	A comprehensive modular map of molecular interactions in RB/E2F pathway. <i>Molecular Systems Biology</i> , 2008, 4, 173.	7.2	113
18	PRINCIPAL MANIFOLDS AND GRAPHS IN PRACTICE: FROM MOLECULAR BIOLOGY TO DYNAMICAL SYSTEMS. <i>International Journal of Neural Systems</i> , 2010, 20, 219-232.	5.2	102

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19	Kinetic signatures of microRNA modes of action. <i>Rna</i> , 2012, 18, 1635-1655.	3.5	99
20	BiNoM: a Cytoscape plugin for manipulating and analyzing biological networks. <i>Bioinformatics</i> , 2008, 24, 876-877.	4.1	97
21	A Modeling Approach to Explain Mutually Exclusive and Co-Occurring Genetic Alterations in Bladder Tumorigenesis. <i>Cancer Research</i> , 2015, 75, 4042-4052.	0.9	96
22	Transcriptional Programs Define Intratumoral Heterogeneity of Ewing Sarcoma at Single-Cell Resolution. <i>Cell Reports</i> , 2020, 30, 1767-1779.e6.	6.4	96
23	Robust simplifications of multiscale biochemical networks. <i>BMC Systems Biology</i> , 2008, 2, 86.	3.0	90
24	PhysiBoSS: a multi-scale agent-based modelling framework integrating physical dimension and cell signalling. <i>Bioinformatics</i> , 2019, 35, 1188-1196.	4.1	88
25	Systems medicine disease maps: community-driven comprehensive representation of disease mechanisms. <i>Npj Systems Biology and Applications</i> , 2018, 4, 21.	3.0	84
26	Reduction of dynamical biochemical reactions networks in computational biology. <i>Frontiers in Genetics</i> , 2012, 3, 131.	2.3	78
27	Codon Bias Signatures, Organization of Microorganisms in Codon Space, and Lifestyle. <i>Molecular Biology and Evolution</i> , 2005, 22, 547-561.	8.9	73
28	Invariant grids for reaction kinetics. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2004, 333, 106-154.	2.6	70
29	The CoLoMoTo Interactive Notebook: Accessible and Reproducible Computational Analyses for Qualitative Biological Networks. <i>Frontiers in Physiology</i> , 2018, 9, 680.	2.8	67
30	Interpreting pathways to discover cancer driver genes with Moonlight. <i>Nature Communications</i> , 2020, 11, 69.	12.8	66
31	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.	14.5	65
32	Independent Component Analysis for Unraveling the Complexity of Cancer Omics Datasets. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4414.	4.1	62
33	Applications of single-cell and bulk RNA sequencing in onco-immunology. <i>European Journal of Cancer</i> , 2021, 149, 193-210.	2.8	62
34	Asymptotology of chemical reaction networks. <i>Chemical Engineering Science</i> , 2010, 65, 2310-2324.	3.8	58
35	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, 8613-8624.	1.8	55
36	NaviCell: a web-based environment for navigation, curation and maintenance of large molecular interaction maps. <i>BMC Systems Biology</i> , 2013, 7, 100.	3.0	52

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37	Elastic Principal Graphs and Manifolds and their Practical Applications. <i>Computing (Vienna/New York)</i> , 2005, 75, 359-379.	4.8	50
38	BiNoM 2.0, a Cytoscape plugin for accessing and analyzing pathways using standard systems biology formats. <i>BMC Systems Biology</i> , 2013, 7, 18.	3.0	50
39	Determining the optimal number of independent components for reproducible transcriptomic data analysis. <i>BMC Genomics</i> , 2017, 18, 712.	2.8	50
40	Classification of gene signatures for their information value and functional redundancy. <i>Npj Systems Biology and Applications</i> , 2018, 4, 2.	3.0	50
41	Community-driven roadmap for integrated disease maps. <i>Briefings in Bioinformatics</i> , 2019, 20, 659-670.	6.5	48
42	Systems biology of Ewing sarcoma: a network model of EWS-FLI1 effect on proliferation and apoptosis. <i>Nucleic Acids Research</i> , 2013, 41, 8853-8871.	14.5	45
43	Robust and Scalable Learning of Complex Intrinsic Dataset Geometry via ELPIGraph. <i>Entropy</i> , 2020, 22, 296.	2.2	45
44	ROMA: Representation and Quantification of Module Activity from Target Expression Data. <i>Frontiers in Genetics</i> , 2016, 7, 18.	2.3	44
45	A multiscale signalling network map of innate immune response in cancer reveals cell heterogeneity signatures. <i>Nature Communications</i> , 2019, 10, 4808.	12.8	44
46	Scikit-Dimension: A Python Package for Intrinsic Dimension Estimation. <i>Entropy</i> , 2021, 23, 1368.	2.2	40
47	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.	7.0	39
48	Dynamical modeling of microRNA action on the protein translation process. <i>BMC Systems Biology</i> , 2010, 4, 13.	3.0	37
49	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
50	How much non-coding DNA do eukaryotes require?. <i>Journal of Theoretical Biology</i> , 2008, 252, 587-592.	1.7	36
51	NaviCell Web Service for network-based data visualization. <i>Nucleic Acids Research</i> , 2015, 43, W560-W565.	14.5	32
52	Topological grammars for data approximation. <i>Applied Mathematics Letters</i> , 2007, 20, 382-386.	2.7	30
53	Network-based approaches for drug response prediction and targeted therapy development in cancer. <i>Biochemical and Biophysical Research Communications</i> , 2015, 464, 386-391.	2.1	29
54	OCSANA: optimal combinations of interventions from network analysis. <i>Bioinformatics</i> , 2013, 29, 1571-1573.	4.1	28

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55	Blind source separation methods for deconvolution of complex signals in cancer biology. <i>Biochemical and Biophysical Research Communications</i> , 2013, 430, 1182-1187.	2.1	27
56	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.	3.2	27
57	Synthetic Lethality between Gene Defects Affecting a Single Non-essential Molecular Pathway with Reversible Steps. <i>PLoS Computational Biology</i> , 2013, 9, e1003016.	3.2	26
58	Mathematical Modeling of microRNA-Mediated Mechanisms of Translation Repression. <i>Advances in Experimental Medicine and Biology</i> , 2013, 774, 189-224.	1.6	25
59	Inferring hidden causal relations between pathway members using reduced Google matrix of directed biological networks. <i>PLoS ONE</i> , 2018, 13, e0190812.	2.5	25
60	Assessing reproducibility of matrix factorization methods in independent transcriptomes. <i>Bioinformatics</i> , 2019, 35, 4307-4313.	4.1	23
61	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.	1.5	22
62	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.	2.6	20
63	Trajectories, bifurcations, and pseudo-time in large clinical datasets: applications to myocardial infarction and diabetes data. <i>GigaScience</i> , 2020, 9, .	6.4	20
64	Predicting genetic interactions from Boolean models of biological networks. <i>Integrative Biology (United Kingdom)</i> , 2015, 7, 921-929.	1.3	18
65	Fast and user-friendly non-linear principal manifold learning by method of elastic maps. , 2015, , .		18
66	Estimating the effective dimension of large biological datasets using Fisher separability analysis. , 2019, , .		18
67	Model composition through model reduction: a combined model of CD95 and NF- κ B signaling pathways. <i>BMC Systems Biology</i> , 2013, 7, 13.	3.0	17
68	Data complexity measured by principal graphs. <i>Computers and Mathematics With Applications</i> , 2013, 65, 1471-1482.	2.7	17
69	DeDaL: Cytoscape 3 app for producing and morphing data-driven and structure-driven network layouts. <i>BMC Systems Biology</i> , 2015, 9, 46.	3.0	17
70	ETS Proteins Bind with Glucocorticoid Receptors: Relevance for Treatment of Ewing Sarcoma. <i>Cell Reports</i> , 2019, 29, 104-117.e4.	6.4	16
71	Application of Atlas of Cancer Signalling Network in preclinical studies. <i>Briefings in Bioinformatics</i> , 2019, 20, 701-716.	6.5	16
72	A review of computational approaches detecting microRNAs involved in cancer. <i>Frontiers in Bioscience - Landmark</i> , 2017, 22, 1774-1791.	3.0	15

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73	Conceptual and computational framework for logical modelling of biological networks deregulated in diseases. <i>Briefings in Bioinformatics</i> , 2019, 20, 1238-1249.	6.5	15
74	Signalling maps in cancer research: construction and data analysis. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	3.0	13
75	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
76	Lizard Brain: Tackling Locally Low-Dimensional Yet Globally Complex Organization of Multi-Dimensional Datasets. <i>Frontiers in Neurorobotics</i> , 2019, 13, 110.	2.8	13
77	Self-Organizing Approach for Automated Gene Identification. <i>Open Systems and Information Dynamics</i> , 2003, 10, 321-333.	1.2	12
78	Detection of miRNA regulatory effect on triple negative breast cancer transcriptome. <i>BMC Genomics</i> , 2015, 16, S4.	2.8	12
79	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, .	3.0	12
80	Synthesis and Simulation of Ensembles of Boolean Networks for Cell Fate Decision. <i>Lecture Notes in Computer Science</i> , 2020, , 193-209.	1.3	12
81	Molecular Inverse Comorbidity between Alzheimer's Disease and Lung Cancer: New Insights from Matrix Factorization. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3114.	4.1	11
82	Logical versus kinetic modeling of biological networks: applications in cancer research. <i>Current Opinion in Chemical Engineering</i> , 2018, 21, 22-31.	7.8	10
83	Metabolic and signalling network maps integration: application to cross-talk studies and omics data analysis in cancer. <i>BMC Bioinformatics</i> , 2019, 20, 140.	2.6	10
84	Network analysis of gene lists for finding reproducible prognostic breast cancer gene signatures. <i>Bioinformatics</i> , 2012, 8, 773-776.	0.5	10
85	Invariant Grids: Method of Complexity Reduction in Reaction Networks. <i>Complexus</i> , 2004, 2, 110-127.	0.6	9
86	From a Biological Hypothesis to the Construction of a Mathematical Model. <i>Methods in Molecular Biology</i> , 2013, 1021, 107-125.	0.9	9
87	The inconvenience of data of convenience: computational research beyond post-mortem analyses. <i>Nature Methods</i> , 2017, 14, 937-938.	19.0	9
88	cd2sbgmml: bidirectional conversion between CellDesigner and SBGN formats. <i>Bioinformatics</i> , 2020, 36, 2620-2622.	4.1	9
89	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, 3600.	3.7	9
90	Overcoming Complexity of Biological Systems: from Data Analysis to Mathematical Modeling. <i>Mathematical Modelling of Natural Phenomena</i> , 2015, 10, 186-205.	2.4	8

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91	Antagonism Pattern Detection between MicroRNA and Target Expression in Ewing's Sarcoma. PLoS ONE, 2012, 7, e41770.	2.5	7
92	Practical Use of BiNoM: A Biological Network Manager Software. Methods in Molecular Biology, 2013, 1021, 127-146.	0.9	7
93	Piece-wise quadratic approximations of arbitrary error functions for fast and robust machine learning. Neural Networks, 2016, 84, 28-38.	5.9	7
94	Cell Death and Life in Cancer: Mathematical Modeling of Cell Fate Decisions. Advances in Experimental Medicine and Biology, 2012, 736, 261-274.	1.6	6
95	Network biology elucidates metastatic colon cancer mechanisms. Cell Cycle, 2015, 14, 2189-2190.	2.6	6
96	Geometrical Complexity of Data Approximators. Lecture Notes in Computer Science, 2013, , 500-509.	1.3	6
97	Comprehensive Map of the Regulated Cell Death Signaling Network: A Powerful Analytical Tool for Studying Diseases. Cancers, 2020, 12, 990.	3.7	5
98	The Mystery of Two Straight Lines in Bacterial Genome Statistics. Bulletin of Mathematical Biology, 2007, 69, 2429-2442.	1.9	4
99	The multilayer community structure of medulloblastoma. IScience, 2021, 24, 102365.	4.1	4
100	Calculating Biological Module Enrichment or Depletion and Visualizing Data on Large-scale Molecular Maps with ACSNMiner and RNavicell Packages. R Journal, 2016, 8, 293.	1.8	4
101	BIODICA: a computational environment for Independent Component Analysis of omics data. Bioinformatics, 2022, 38, 2963-2964.	4.1	4
102	IDENTIFICATION OF SHORTENED 3' UNTRANSLATED REGIONS FROM EXPRESSION ARRAYS. Journal of Bioinformatics and Computational Biology, 2012, 10, 1241001.	0.8	3
103	Minimum Spanning vs. Principal Trees for Structured Approximations of Multi-Dimensional Datasets. Entropy, 2020, 22, 1274.	2.2	3
104	Coloring Panchromatic Nighttime Satellite Images: Comparing the Performance of Several Machine Learning Methods. IEEE Transactions on Geoscience and Remote Sensing, 2022, 60, 1-15.	6.3	3
105	WebMaBoSS: A Web Interface for Simulating Boolean Models Stochastically. Frontiers in Molecular Biosciences, 2021, 8, 754444.	3.5	3
106	Modeling Progression of Single Cell Populations Through the Cell Cycle as a Sequence of Switches. Frontiers in Molecular Biosciences, 2021, 8, 793912.	3.5	3
107	Understanding Different Types of Cell Death Using Systems Biology. , 2012, , 125-143.		2
108	Data analysis with arbitrary error measures approximated by piece-wise quadratic PQSQ functions. , 2018, , .		2

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109	Application of Independent Component Analysis to Tumor Transcriptomes Reveals Specific and Reproducible Immune-Related Signals. Lecture Notes in Computer Science, 2018, , 501-513.	1.3	2
110	Local intrinsic dimensionality estimators based on concentration of measure. , 2020, , .		2
111	Collective intelligence defines biological functions in Wikipedia as communities in the hidden protein connection network. PLoS Computational Biology, 2020, 16, e1007652.	3.2	2
112	Adaptation through the lens of single-cell multi-omics data. Physics of Life Reviews, 2021, 38, 132-134.	2.8	2
113	Systems Biology Analysis for Ewing Sarcoma. Methods in Molecular Biology, 2021, 2226, 303-333.	0.9	2
114	How Cell Decides Between Life and Death: Mathematical Modeling of Epigenetic Landscapes of Cellular Fates. Springer Proceedings in Mathematics, 2013, , 191-204.	0.5	2
115	Meta-Analysis of Esophageal Cancer Transcriptomes Using Independent Component Analysis. Frontiers in Genetics, 2021, 12, 683632.	2.3	2
116	Basic, simple and extendable kinetic model of protein synthesis. Mathematical Biosciences and Engineering, 2019, 16, 6602-6622.	1.9	2
117	Hubness reduction improves clustering and trajectory inference in single-cell transcriptomic data. Bioinformatics, 2022, 38, 1045-1051.	4.1	2
118	Branching Principal Components: Elastic Graphs, Topological Grammars and Metro Maps. Neural Networks (IJCNN), International Joint Conference on, 2007, , .	0.0	1
119	Analysis of the Growth Control Network Specific for Human Lung Adenocarcinoma Cells. Mathematical Modelling of Natural Phenomena, 2012, 7, 337-368.	2.4	1
120	Exact solving and sensitivity analysis of stochastic continuous time Boolean models. BMC Bioinformatics, 2020, 21, 241.	2.6	1
121	Atlas of Cancer Signaling Network: A Resource of Multi-Scale Biological Maps to Study Disease Mechanisms. , 2021, , 490-506.		0
122	Clinical trajectories estimated from bulk tumoral molecular profiles using elastic principal trees. , 2021, , .		0
123	Abstract A13: A signaling pathway rationale for the design of combination therapies for cancer. , 2012, , .		0
124	Title is missing!. , 2020, 16, e1007652.		0
125	Title is missing!. , 2020, 16, e1007652.		0
126	Title is missing!. , 2020, 16, e1007652.		0

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127	Title is missing!. , 2020, 16, e1007652.		0