Andrei Yu Zinovyev

List of Publications by Year
in descending order

127 papers	7,756 citations	87723 38 h-index	64668 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. Cancer Cell, 2018, 33, 463-479.e10.	7.7	1,074
2	Creation and analysis of biochemical constraint-based models using the COBRA Toolbox v.3.0. Nature Protocols, 2019, 14, 639-702.	5.5	833
3	Single-Cell Analysis Reveals Fibroblast Clusters Linked to Immunotherapy Resistance in Cancer. Cancer Discovery, 2020, 10, 1330-1351.	7.7	424
4	Codon adaptation index as a measure of dominating codon bias. Bioinformatics, 2003, 19, 2005-2015.	1.8	274
5	The Virtual Metabolic Human database: integrating human and gut microbiome metabolism with nutrition and disease. Nucleic Acids Research, 2019, 47, D614-D624.	6.5	257
6	Control-free calling of copy number alterations in deep-sequencing data using GC-content normalization. Bioinformatics, 2011, 27, 268-269.	1.8	249
7	Single-cell trajectories reconstruction, exploration and mapping of omics data with STREAM. Nature Communications, 2019, 10, 1903.	5.8	198
8	Classification of microarray data using gene networks. BMC Bioinformatics, 2007, 8, 35.	1.2	191
9	Independent Component Analysis Uncovers the Landscape of the Bladder Tumor Transcriptome and Reveals Insights into Luminal and Basal Subtypes. Cell Reports, 2014, 9, 1235-1245.	2.9	181
10	Mathematical Modelling of Cell-Fate Decision in Response to Death Receptor Engagement. PLoS Computational Biology, 2010, 6, e1000702.	1.5	179
11	The Oncogenic EWS-FLI1 Protein Binds In Vivo GGAA Microsatellite Sequences with Potential Transcriptional Activation Function. PLoS ONE, 2009, 4, e4932.	1.1	160
12	Mathematical Modelling of Molecular Pathways Enabling Tumour Cell Invasion and Migration. PLoS Computational Biology, 2015, 11, e1004571.	1.5	130
13	Atlas of Cancer Signalling Network: a systems biology resource for integrative analysis of cancer data with Google Maps. Oncogenesis, 2015, 4, e160-e160.	2.1	129
14	Constructive methods of invariant manifolds for kinetic problems. Physics Reports, 2004, 396, 197-403.	10.3	128
15	MaBoSS 2.0: an environment for stochastic Boolean modeling. Bioinformatics, 2017, 33, 2226-2228.	1.8	118
16	Concomitant Notch activation and p53 deletion trigger epithelial-to-mesenchymal transition and metastasis in mouse gut. Nature Communications, 2014, 5, 5005.	5.8	114
17	A comprehensive modular map of molecular interactions in RB/E2F pathway. Molecular Systems Biology, 2008, 4, 173.	3.2	113
18	PRINCIPAL MANIFOLDS AND GRAPHS IN PRACTICE: FROM MOLECULAR BIOLOGY TO DYNAMICAL SYSTEMS. International Journal of Neural Systems, 2010, 20, 219-232.	3.2	102

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19	Kinetic signatures of microRNA modes of action. Rna, 2012, 18, 1635-1655.	1.6	99
20	BiNoM: a Cytoscape plugin for manipulating and analyzing biological networks. Bioinformatics, 2008, 24, 876-877.	1.8	97
21	A Modeling Approach to Explain Mutually Exclusive and Co-Occurring Genetic Alterations in Bladder Tumorigenesis. Cancer Research, 2015, 75, 4042-4052.	0.4	96
22	Transcriptional Programs Define Intratumoral Heterogeneity of Ewing Sarcoma at Single-Cell Resolution. Cell Reports, 2020, 30, 1767-1779.e6.	2.9	96
23	Robust simplifications of multiscale biochemical networks. BMC Systems Biology, 2008, 2, 86.	3.0	90
24	PhysiBoSS: a multi-scale agent-based modelling framework integrating physical dimension and cell signalling. Bioinformatics, 2019, 35, 1188-1196.	1.8	88
25	Systems medicine disease maps: community-driven comprehensive representation of disease mechanisms. Npj Systems Biology and Applications, 2018, 4, 21.	1.4	84
26	Reduction of dynamical biochemical reactions networks in computational biology. Frontiers in Genetics, 2012, 3, 131.	1.1	78
27	Codon Bias Signatures, Organization of Microorganisms in Codon Space, and Lifestyle. Molecular Biology and Evolution, 2005, 22, 547-561.	3.5	73
28	Invariant grids for reaction kinetics. Physica A: Statistical Mechanics and Its Applications, 2004, 333, 106-154.	1.2	70
29	The CoLoMoTo Interactive Notebook: Accessible and Reproducible Computational Analyses for Qualitative Biological Networks. Frontiers in Physiology, 2018, 9, 680.	1.3	67
30	Interpreting pathways to discover cancer driver genes with Moonlight. Nature Communications, 2020, 11, 69.	5.8	66
31	Identification of microRNA clusters cooperatively acting on epithelial to mesenchymal transition in triple negative breast cancer. Nucleic Acids Research, 2019, 47, 2205-2215.	6.5	65
32	Independent Component Analysis for Unraveling the Complexity of Cancer Omics Datasets. International Journal of Molecular Sciences, 2019, 20, 4414.	1.8	62
33	Applications of single-cell and bulk RNA sequencing in onco-immunology. European Journal of Cancer, 2021, 149, 193-210.	1.3	62
34	Asymptotology of chemical reaction networks. Chemical Engineering Science, 2010, 65, 2310-2324.	1.9	58
35	The second European interdisciplinary Ewing sarcoma research summit - A joint effort to deconstructing the multiple layers of a complex disease. Oncotarget, 2016, 7, 8613-8624.	0.8	55
36	NaviCell: a web-based environment for navigation, curation and maintenance of large molecular interaction maps. BMC Systems Biology, 2013, 7, 100.	3.0	52

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37	Elastic Principal Graphs and Manifolds and their Practical Applications. Computing (Vienna/New York), 2005, 75, 359-379.	3.2	50
38	BiNoM 2.0, a Cytoscape plugin for accessing and analyzing pathways using standard systems biology formats. BMC Systems Biology, 2013, 7, 18.	3.0	50
39	Determining the optimal number of independent components for reproducible transcriptomic data analysis. BMC Genomics, 2017, 18, 712.	1.2	50
40	Classification of gene signatures for their information value and functional redundancy. Npj Systems Biology and Applications, 2018, 4, 2.	1.4	50
41	Community-driven roadmap for integrated disease maps. Briefings in Bioinformatics, 2019, 20, 659-670.	3.2	48
42	Systems biology of Ewing sarcoma: a network model of EWS-FLI1 effect on proliferation and apoptosis. Nucleic Acids Research, 2013, 41, 8853-8871.	6.5	45
43	Robust and Scalable Learning of Complex Intrinsic Dataset Geometry via ElPiGraph. Entropy, 2020, 22, 296.	1.1	45
44	ROMA: Representation and Quantification of Module Activity from Target Expression Data. Frontiers in Genetics, 2016, 7, 18.	1.1	44
45	A multiscale signalling network map of innate immune response in cancer reveals cell heterogeneity signatures. Nature Communications, 2019, 10, 4808.	5.8	44
46	Scikit-Dimension: A Python Package for Intrinsic Dimension Estimation. Entropy, 2021, 23, 1368.	1.1	40
47	Drug-Driven Synthetic Lethality: Bypassing Tumor Cell Genetics with a Combination of AsiDNA and PARP Inhibitors. Clinical Cancer Research, 2017, 23, 1001-1011.	3.2	39
48	Dynamical modeling of microRNA action on the protein translation process. BMC Systems Biology, 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. Mutagenesis, 2015, 30, 191-204.	1.0	37
50	How much non-coding DNA do eukaryotes require?. Journal of Theoretical Biology, 2008, 252, 587-592.	0.8	36
51	NaviCell Web Service for network-based data visualization. Nucleic Acids Research, 2015, 43, W560-W565.	6.5	32
52	Topological grammars for data approximation. Applied Mathematics Letters, 2007, 20, 382-386.	1.5	30
53	Network-based approaches for drug response prediction and targeted therapy development in cancer. Biochemical and Biophysical Research Communications, 2015, 464, 386-391.	1.0	29
54	OCSANA: optimal combinations of interventions from network analysis. Bioinformatics, 2013, 29, 1571-1573.	1.8	28

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55	Blind source separation methods for deconvolution of complex signals in cancer biology. Biochemical and Biophysical Research Communications, 2013, 430, 1182-1187.	1.0	27
56	NetNorM: Capturing cancer-relevant information in somatic exome mutation data with gene networks for cancer stratification and prognosis. PLoS Computational Biology, 2017, 13, e1005573.	1.5	27
57	Synthetic Lethality between Gene Defects Affecting a Single Non-essential Molecular Pathway with Reversible Steps. PLoS Computational Biology, 2013, 9, e1003016.	1.5	26
58	Mathematical Modeling of microRNAâ€"Mediated Mechanisms of Translation Repression. Advances in Experimental Medicine and Biology, 2013, 774, 189-224.	0.8	25
59	Inferring hidden causal relations between pathway members using reduced Google matrix of directed biological networks. PLoS ONE, 2018, 13, e0190812.	1.1	25
60	Assessing reproducibility of matrix factorization methods in independent transcriptomes. Bioinformatics, 2019, 35, 4307-4313.	1.8	23
61	Deconvolution of transcriptomes and miRNomes by independent component analysis provides insights into biological processes and clinical outcomes of melanoma patients. BMC Medical Genomics, 2019, 12, 132.	0.7	22
62	Codon usage trajectories and 7-cluster structure of 143 complete bacterial genomic sequences. Physica A: Statistical Mechanics and Its Applications, 2005, 353, 365-387.	1.2	20
63	Trajectories, bifurcations, and pseudo-time in large clinical datasets: applications to myocardial infarction and diabetes data. GigaScience, 2020, 9, .	3.3	20
64	Predicting genetic interactions from Boolean models of biological networks. Integrative Biology (United Kingdom), 2015, 7, 921-929.	0.6	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-Î⁰B signaling pathways. BMC Systems Biology, 2013, 7, 13.	3.0	17
68	Data complexity measured by principal graphs. Computers and Mathematics With Applications, 2013, 65, 1471-1482.	1.4	17
69	DeDaL: Cytoscape 3 app for producing and morphing data-driven and structure-driven network layouts. BMC Systems Biology, 2015, 9, 46.	3.0	17
70	ETS Proteins Bind with Glucocorticoid Receptors: Relevance for Treatment of Ewing Sarcoma. Cell Reports, 2019, 29, 104-117.e4.	2.9	16
71	Application of Atlas of Cancer Signalling Network in preclinical studies. Briefings in Bioinformatics, 2019, 20, 701-716.	3.2	16
72	A review of computational approaches detecting microRNAs involved in cancer. Frontiers in Bioscience - Landmark, 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. Briefings in Bioinformatics, 2019, 20, 1238-1249.	3.2	15
74	Signalling maps in cancer research: construction and data analysis. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	1.4	13
75	Prediction of Mutations to Control Pathways Enabling Tumor Cell Invasion with the CoLoMoTo Interactive Notebook (Tutorial). Frontiers in Physiology, 2018, 9, 787.	1.3	13
76	Lizard Brain: Tackling Locally Low-Dimensional Yet Globally Complex Organization of Multi-Dimensional Datasets. Frontiers in Neurorobotics, 2019, 13, 110.	1.6	13
77	Self-Organizing Approach for Automated Gene Identification. Open Systems and Information Dynamics, 2003, 10, 321-333.	0.5	12
78	Detection of miRNA regulatory effect on triple negative breast cancer transcriptome. BMC Genomics, 2015, 16, S4.	1.2	12
79	NaviCom: a web application to create interactive molecular network portraits using multi-level omics data. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	1.4	12
80	Synthesis and Simulation of Ensembles of Boolean Networks for Cell Fate Decision. Lecture Notes in Computer Science, 2020, , 193-209.	1.0	12
81	Molecular Inverse Comorbidity between Alzheimer's Disease and Lung Cancer: New Insights from Matrix Factorization. International Journal of Molecular Sciences, 2019, 20, 3114.	1.8	11
82	Logical versus kinetic modeling of biological networks: applications in cancer research. Current Opinion in Chemical Engineering, 2018, 21, 22-31.	3.8	10
83	Metabolic and signalling network maps integration: application to cross-talk studies and omics data analysis in cancer. BMC Bioinformatics, 2019, 20, 140.	1.2	10
84	Network analysis of gene lists for finding reproducible prognostic breast cancer gene signatures. Bioinformation, 2012, 8, 773-776.	0.2	10
85	Invariant Grids: Method of Complexity Reduction in Reaction Networks. Complexus, 2004, 2, 110-127.	0.7	9
86	From a Biological Hypothesis to the Construction of a Mathematical Model. Methods in Molecular Biology, 2013, 1021, 107-125.	0.4	9
87	The inconvenience of data of convenience: computational research beyond post-mortem analyses. Nature Methods, 2017, 14, 937-938.	9.0	9
88	cd2sbgnml: bidirectional conversion between CellDesigner and SBGN formats. Bioinformatics, 2020, 36, 2620-2622.	1.8	9
89	Modelling of Immune Checkpoint Network Explains Synergistic Effects of Combined Immune Checkpoint Inhibitor Therapy and the Impact of Cytokines in Patient Response. Cancers, 2020, 12, 3600.	1.7	9
90	Overcoming Complexity of Biological Systems: from Data Analysis to Mathematical Modeling. Mathematical Modelling of Natural Phenomena, 2015, 10, 186-205.	0.9	8

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91	Antagonism Pattern Detection between MicroRNA and Target Expression in Ewing's Sarcoma. PLoS ONE, 2012, 7, e41770.	1.1	7
92	Practical Use of BiNoM: A Biological Network Manager Software. Methods in Molecular Biology, 2013, 1021, 127-146.	0.4	7
93	Piece-wise quadratic approximations of arbitrary error functions for fast and robust machine learning. Neural Networks, 2016, 84, 28-38.	3.3	7
94	Cell Death and Life in Cancer: Mathematical Modeling of Cell Fate Decisions. Advances in Experimental Medicine and Biology, 2012, 736, 261-274.	0.8	6
95	Network biology elucidates metastatic colon cancer mechanisms. Cell Cycle, 2015, 14, 2189-2190.	1.3	6
96	Geometrical Complexity of Data Approximators. Lecture Notes in Computer Science, 2013, , 500-509.	1.0	6
97	Comprehensive Map of the Regulated Cell Death Signaling Network: A Powerful Analytical Tool for Studying Diseases. Cancers, 2020, 12, 990.	1.7	5
98	The Mystery of Two Straight Lines in Bacterial Genome Statistics. Bulletin of Mathematical Biology, 2007, 69, 2429-2442.	0.9	4
99	The multilayer community structure of medulloblastoma. IScience, 2021, 24, 102365.	1.9	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.	0.7	4
101	BIODICA: a computational environment for Independent Component Analysis of omics data. Bioinformatics, 2022, 38, 2963-2964.	1.8	4
102	IDENTIFICATION OF SHORTENED 3′ UNTRANSLATED REGIONS FROM EXPRESSION ARRAYS. Journal of Bioinformatics and Computational Biology, 2012, 10, 1241001.	0.3	3
103	Minimum Spanning vs. Principal Trees for Structured Approximations of Multi-Dimensional Datasets. Entropy, 2020, 22, 1274.	1.1	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.	2.7	3
105	WebMaBoSS: A Web Interface for Simulating Boolean Models Stochastically. Frontiers in Molecular Biosciences, 2021, 8, 754444.	1.6	3
106	Modeling Progression of Single Cell Populations Through the Cell Cycle as a Sequence of Switches. Frontiers in Molecular Biosciences, 2021, 8, 793912.	1.6	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.	1.0	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.	1.5	2
112	Adaptation through the lens of single-cell multi-omics data. Physics of Life Reviews, 2021, 38, 132-134.	1.5	2
113	Systems Biology Analysis for Ewing Sarcoma. Methods in Molecular Biology, 2021, 2226, 303-333.	0.4	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.	1.1	2
116	Basic, simple and extendable kinetic model of protein synthesis. Mathematical Biosciences and Engineering, 2019, 16, 6602-6622.	1.0	2
117	Hubness reduction improves clustering and trajectory inference in single-cell transcriptomic data. Bioinformatics, 2022, 38, 1045-1051.	1.8	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.	0.9	1
120	Exact solving and sensitivity analysis of stochastic continuous time Boolean models. BMC Bioinformatics, 2020, 21, 241.	1.2	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