

# 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	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
2	BIODICA: a computational environment for Independent Component Analysis of omics data. Bioinformatics, 2022, 38, 2963-2964.	4.1	4
3	Hubness reduction improves clustering and trajectory inference in single-cell transcriptomic data. Bioinformatics, 2022, 38, 1045-1051.	4.1	2
4	Atlas of Cancer Signaling Network: A Resource of Multi-Scale Biological Maps to Study Disease Mechanisms. , 2021, , 490-506.		0
5	The multilayer community structure of medulloblastoma. IScience, 2021, 24, 102365.	4.1	4
6	Applications of single-cell and bulk RNA sequencing in onco-immunology. European Journal of Cancer, 2021, 149, 193-210.	2.8	62
7	Clinical trajectories estimated from bulk tumoral molecular profiles using elastic principal trees. , 2021, , .		0
8	Adaptation through the lens of single-cell multi-omics data. Physics of Life Reviews, 2021, 38, 132-134.	2.8	2
9	Systems Biology Analysis for Ewing Sarcoma. Methods in Molecular Biology, 2021, 2226, 303-333.	0.9	2
10	Scikit-Dimension: A Python Package for Intrinsic Dimension Estimation. Entropy, 2021, 23, 1368.	2.2	40
11	Meta-Analysis of Esophageal Cancer Transcriptomes Using Independent Component Analysis. Frontiers in Genetics, 2021, 12, 683632.	2.3	2
12	WebMaBoSS: A Web Interface for Simulating Boolean Models Stochastically. Frontiers in Molecular Biosciences, 2021, 8, 754444.	3.5	3
13	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
14	cd2sbgtml: bidirectional conversion between CellDesigner and SBGN formats. Bioinformatics, 2020, 36, 2620-2622.	4.1	9
15	Interpreting pathways to discover cancer driver genes with Moonlight. Nature Communications, 2020, 11, 69.	12.8	66
16	Trajectories, bifurcations, and pseudo-time in large clinical datasets: applications to myocardial infarction and diabetes data. GigaScience, 2020, 9, .	6.4	20
17	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.	3.7	9
18	Minimum Spanning vs. Principal Trees for Structured Approximations of Multi-Dimensional Datasets. Entropy, 2020, 22, 1274.	2.2	3

#	ARTICLE	IF	CITATIONS
19	Local intrinsic dimensionality estimators based on concentration of measure. , 2020, , .		2
20	Single-Cell Analysis Reveals Fibroblast Clusters Linked to Immunotherapy Resistance in Cancer. Cancer Discovery, 2020, 10, 1330-1351.	9.4	424
21	Exact solving and sensitivity analysis of stochastic continuous time Boolean models. BMC Bioinformatics, 2020, 21, 241.	2.6	1
22	Robust and Scalable Learning of Complex Intrinsic Dataset Geometry via ElPiGraph. Entropy, 2020, 22, 296.	2.2	45
23	Collective intelligence defines biological functions in Wikipedia as communities in the hidden protein connection network. PLoS Computational Biology, 2020, 16, e1007652.	3.2	2
24	Comprehensive Map of the Regulated Cell Death Signaling Network: A Powerful Analytical Tool for Studying Diseases. Cancers, 2020, 12, 990.	3.7	5
25	Synthesis and Simulation of Ensembles of Boolean Networks for Cell Fate Decision. Lecture Notes in Computer Science, 2020, , 193-209.	1.3	12
26	Transcriptional Programs Define Intratumoral Heterogeneity of Ewing Sarcoma at Single-Cell Resolution. Cell Reports, 2020, 30, 1767-1779.e6.	6.4	96
27	Title is missing!. , 2020, 16, e1007652.		0
28	Title is missing!. , 2020, 16, e1007652.		0
29	Title is missing!. , 2020, 16, e1007652.		0
30	Title is missing!. , 2020, 16, e1007652.		0
31	A multiscale signalling network map of innate immune response in cancer reveals cell heterogeneity signatures. Nature Communications, 2019, 10, 4808.	12.8	44
32	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.	1.5	22
33	Independent Component Analysis for Unraveling the Complexity of Cancer Omics Datasets. International Journal of Molecular Sciences, 2019, 20, 4414.	4.1	62
34	ETS Proteins Bind with Glucocorticoid Receptors: Relevance for Treatment of Ewing Sarcoma. Cell Reports, 2019, 29, 104-117.e4.	6.4	16
35	Identification of microRNA clusters cooperatively acting on epithelial to mesenchymal transition in triple negative breast cancer. Nucleic Acids Research, 2019, 47, 2205-2215.	14.5	65
36	Molecular Inverse Comorbidity between Alzheimer's Disease and Lung Cancer: New Insights from Matrix Factorization. International Journal of Molecular Sciences, 2019, 20, 3114.	4.1	11

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37	Single-cell trajectories reconstruction, exploration and mapping of omics data with STREAM. Nature Communications, 2019, 10, 1903.	12.8	198
38	Metabolic and signalling network maps integration: application to cross-talk studies and omics data analysis in cancer. BMC Bioinformatics, 2019, 20, 140.	2.6	10
39	Assessing reproducibility of matrix factorization methods in independent transcriptomes. Bioinformatics, 2019, 35, 4307-4313.	4.1	23
40	Creation and analysis of biochemical constraint-based models using the COBRA Toolbox v.3.0. Nature Protocols, 2019, 14, 639-702.	12.0	833
41	Estimating the effective dimension of large biological datasets using Fisher separability analysis. , 2019, , .		18
42	The Virtual Metabolic Human database: integrating human and gut microbiome metabolism with nutrition and disease. Nucleic Acids Research, 2019, 47, D614-D624.	14.5	257
43	PhysiBoSS: a multi-scale agent-based modelling framework integrating physical dimension and cell signalling. Bioinformatics, 2019, 35, 1188-1196.	4.1	88
44	Community-driven roadmap for integrated disease maps. Briefings in Bioinformatics, 2019, 20, 659-670.	6.5	48
45	Conceptual and computational framework for logical modelling of biological networks deregulated in diseases. Briefings in Bioinformatics, 2019, 20, 1238-1249.	6.5	15
46	Application of Atlas of Cancer Signalling Network in preclinical studies. Briefings in Bioinformatics, 2019, 20, 701-716.	6.5	16
47	Lizard Brain: Tackling Locally Low-Dimensional Yet Globally Complex Organization of Multi-Dimensional Datasets. Frontiers in Neuroinformatics, 2019, 13, 110.	2.8	13
48	Basic, simple and extendable kinetic model of protein synthesis. Mathematical Biosciences and Engineering, 2019, 16, 6602-6622.	1.9	2
49	Logical versus kinetic modeling of biological networks: applications in cancer research. Current Opinion in Chemical Engineering, 2018, 21, 22-31.	7.8	10
50	Classification of gene signatures for their information value and functional redundancy. Npj Systems Biology and Applications, 2018, 4, 2.	3.0	50
51	Fibroblast Heterogeneity and Immunosuppressive Environment in Human Breast Cancer. Cancer Cell, 2018, 33, 463-479.e10.	16.8	1,074
52	Data analysis with arbitrary error measures approximated by piece-wise quadratic PQSQ functions. , 2018, , .		2
53	Signalling maps in cancer research: construction and data analysis. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	3.0	13
54	The CoLoMoTo Interactive Notebook: Accessible and Reproducible Computational Analyses for Qualitative Biological Networks. Frontiers in Physiology, 2018, 9, 680.	2.8	67

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55	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
56	Systems medicine disease maps: community-driven comprehensive representation of disease mechanisms. <i>Npj Systems Biology and Applications</i> , 2018, 4, 21.	3.0	84
57	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.	1.3	2
58	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
59	The inconvenience of data of convenience: computational research beyond post-mortem analyses. <i>Nature Methods</i> , 2017, 14, 937-938.	19.0	9
60	MaBoSS 2.0: an environment for stochastic Boolean modeling. <i>Bioinformatics</i> , 2017, 33, 2226-2228.	4.1	118
61	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
62	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
63	A review of computational approaches detecting microRNAs involved in cancer. <i>Frontiers in Bioscience - Landmark</i> , 2017, 22, 1774-1791.	3.0	15
64	Determining the optimal number of independent components for reproducible transcriptomic data analysis. <i>BMC Genomics</i> , 2017, 18, 712.	2.8	50
65	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
66	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
67	ROMA: Representation and Quantification of Module Activity from Target Expression Data. <i>Frontiers in Genetics</i> , 2016, 7, 18.	2.3	44
68	Piece-wise quadratic approximations of arbitrary error functions for fast and robust machine learning. <i>Neural Networks</i> , 2016, 84, 28-38.	5.9	7
69	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.	1.8	4
70	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
71	Detection of miRNA regulatory effect on triple negative breast cancer transcriptome. <i>BMC Genomics</i> , 2015, 16, S4.	2.8	12
72	Predicting genetic interactions from Boolean models of biological networks. <i>Integrative Biology (United Kingdom)</i> , 2015, 7, 921-929.	1.3	18

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73	Fast and user-friendly non-linear principal manifold learning by method of elastic maps. , 2015, , .		18
74	NaviCell Web Service for network-based data visualization. Nucleic Acids Research, 2015, 43, W560-W565.	14.5	32
75	The shortest path is not the one you know: application of biological network resources in precision oncology research. Mutagenesis, 2015, 30, 191-204.	2.6	37
76	Atlas of Cancer Signalling Network: a systems biology resource for integrative analysis of cancer data with Google Maps. Oncogenesis, 2015, 4, e160-e160.	4.9	129
77	Network-based approaches for drug response prediction and targeted therapy development in cancer. Biochemical and Biophysical Research Communications, 2015, 464, 386-391.	2.1	29
78	Network biology elucidates metastatic colon cancer mechanisms. Cell Cycle, 2015, 14, 2189-2190.	2.6	6
79	DeDaL: Cytoscape 3 app for producing and morphing data-driven and structure-driven network layouts. BMC Systems Biology, 2015, 9, 46.	3.0	17
80	A Modeling Approach to Explain Mutually Exclusive and Co-Occurring Genetic Alterations in Bladder Tumorigenesis. Cancer Research, 2015, 75, 4042-4052.	0.9	96
81	Mathematical Modelling of Molecular Pathways Enabling Tumour Cell Invasion and Migration. PLoS Computational Biology, 2015, 11, e1004571.	3.2	130
82	Concomitant Notch activation and p53 deletion trigger epithelial-to-mesenchymal transition and metastasis in mouse gut. Nature Communications, 2014, 5, 5005.	12.8	114
83	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.	6.4	181
84	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
85	Model composition through model reduction: a combined model of CD95 and NF- $\kappa$ B signaling pathways. BMC Systems Biology, 2013, 7, 13.	3.0	17
86	OCSANA: optimal combinations of interventions from network analysis. Bioinformatics, 2013, 29, 1571-1573.	4.1	28
87	NaviCell: a web-based environment for navigation, curation and maintenance of large molecular interaction maps. BMC Systems Biology, 2013, 7, 100.	3.0	52
88	Blind source separation methods for deconvolution of complex signals in cancer biology. Biochemical and Biophysical Research Communications, 2013, 430, 1182-1187.	2.1	27
89	Mathematical Modeling of microRNA-Mediated Mechanisms of Translation Repression. Advances in Experimental Medicine and Biology, 2013, 774, 189-224.	1.6	25
90	Data complexity measured by principal graphs. Computers and Mathematics With Applications, 2013, 65, 1471-1482.	2.7	17

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91	Practical Use of BiNoM: A Biological Network Manager Software. <i>Methods in Molecular Biology</i> , 2013, 1021, 127-146.	0.9	7
92	From a Biological Hypothesis to the Construction of a Mathematical Model. <i>Methods in Molecular Biology</i> , 2013, 1021, 107-125.	0.9	9
93	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
94	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
95	How Cell Decides Between Life and Death: Mathematical Modeling of Epigenetic Landscapes of Cellular Fates. <i>Springer Proceedings in Mathematics</i> , 2013, , 191-204.	0.5	2
96	Geometrical Complexity of Data Approximators. <i>Lecture Notes in Computer Science</i> , 2013, , 500-509.	1.3	6
97	IDENTIFICATION OF SHORTENED 3' UNTRANSLATED REGIONS FROM EXPRESSION ARRAYS. <i>Journal of Bioinformatics and Computational Biology</i> , 2012, 10, 1241001.	0.8	3
98	Analysis of the Growth Control Network Specific for Human Lung Adenocarcinoma Cells. <i>Mathematical Modelling of Natural Phenomena</i> , 2012, 7, 337-368.	2.4	1
99	Understanding Different Types of Cell Death Using Systems Biology. , 2012, , 125-143.		2
100	Antagonism Pattern Detection between MicroRNA and Target Expression in Ewing's Sarcoma. <i>PLoS ONE</i> , 2012, 7, e41770.	2.5	7
101	Reduction of dynamical biochemical reactions networks in computational biology. <i>Frontiers in Genetics</i> , 2012, 3, 131.	2.3	78
102	Kinetic signatures of microRNA modes of action. <i>Rna</i> , 2012, 18, 1635-1655.	3.5	99
103	Cell Death and Life in Cancer: Mathematical Modeling of Cell Fate Decisions. <i>Advances in Experimental Medicine and Biology</i> , 2012, 736, 261-274.	1.6	6
104	Network analysis of gene lists for finding reproducible prognostic breast cancer gene signatures. <i>Bioinformatics</i> , 2012, 8, 773-776.	0.5	10
105	Abstract A13: A signaling pathway rationale for the design of combination therapies for cancer. , 2012, , .		0
106	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
107	Dynamical modeling of microRNA action on the protein translation process. <i>BMC Systems Biology</i> , 2010, 4, 13.	3.0	37
108	Asymptotology of chemical reaction networks. <i>Chemical Engineering Science</i> , 2010, 65, 2310-2324.	3.8	58

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109	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
110	Mathematical Modelling of Cell-Fate Decision in Response to Death Receptor Engagement. <i>PLoS Computational Biology</i> , 2010, 6, e1000702.	3.2	179
111	The Oncogenic EWS-FLI1 Protein Binds In Vivo GCAA Microsatellite Sequences with Potential Transcriptional Activation Function. <i>PLoS ONE</i> , 2009, 4, e4932.	2.5	160
112	How much non-coding DNA do eukaryotes require?. <i>Journal of Theoretical Biology</i> , 2008, 252, 587-592.	1.7	36
113	Robust simplifications of multiscale biochemical networks. <i>BMC Systems Biology</i> , 2008, 2, 86.	3.0	90
114	A comprehensive modular map of molecular interactions in RB/E2F pathway. <i>Molecular Systems Biology</i> , 2008, 4, 173.	7.2	113
115	BiNoM: a Cytoscape plugin for manipulating and analyzing biological networks. <i>Bioinformatics</i> , 2008, 24, 876-877.	4.1	97
116	Branching Principal Components: Elastic Graphs, Topological Grammars and Metro Maps. <i>Neural Networks (IJCNN)</i> , International Joint Conference on, 2007, , .	0.0	1
117	Classification of microarray data using gene networks. <i>BMC Bioinformatics</i> , 2007, 8, 35.	2.6	191
118	The Mystery of Two Straight Lines in Bacterial Genome Statistics. <i>Bulletin of Mathematical Biology</i> , 2007, 69, 2429-2442.	1.9	4
119	Topological grammars for data approximation. <i>Applied Mathematics Letters</i> , 2007, 20, 382-386.	2.7	30
120	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
121	Elastic Principal Graphs and Manifolds and their Practical Applications. <i>Computing (Vienna/New York)</i> , 2005, 75, 359-379.	4.8	50
122	Codon Bias Signatures, Organization of Microorganisms in Codon Space, and Lifestyle. <i>Molecular Biology and Evolution</i> , 2005, 22, 547-561.	8.9	73
123	Invariant Grids: Method of Complexity Reduction in Reaction Networks. <i>Complexus</i> , 2004, 2, 110-127.	0.6	9
124	Constructive methods of invariant manifolds for kinetic problems. <i>Physics Reports</i> , 2004, 396, 197-403.	25.6	128
125	Invariant grids for reaction kinetics. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2004, 333, 106-154.	2.6	70
126	Self-Organizing Approach for Automated Gene Identification. <i>Open Systems and Information Dynamics</i> , 2003, 10, 321-333.	1.2	12



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127	Codon adaptation index as a measure of dominating codon bias. Bioinformatics, 2003, 19, 2005-2015.	4.1	274