

# Bud Mishra

## List of Publications by Year in descending order

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86  
papers

2,139  
citations

304743

22  
h-index

265206

42  
g-index

92  
all docs

92  
docs citations

92  
times ranked

3036  
citing authors

#	ARTICLE	IF	CITATIONS
1	How signalling games explain mimicry at many levels: from viral epidemiology to human sociology. <i>Journal of the Royal Society Interface</i> , 2021, 18, 20200689.	3.4	9
2	PHENSIM: Phenotype Simulator. <i>PLoS Computational Biology</i> , 2021, 17, e1009069.	3.2	9
3	Decidability in robot manipulation planning. <i>Autonomous Robots</i> , 2021, 45, 679-692.	4.8	0
4	Distinct Classes of Complex Structural Variation Uncovered across Thousands of Cancer Genome Graphs. <i>Cell</i> , 2020, 183, 197-210.e32.	28.9	141
5	ANERGY TO SYNERGY-THE ENERGY FUELING THE RXCOVEA FRAMEWORK. <i>International Journal for Multiscale Computational Engineering</i> , 2020, 18, 329-333.	1.2	1
6	Tech and the City: Axialization, Institutionalization and Disruption. <i>Lecture Notes of the Institute for Computer Sciences, Social-Informatics and Telecommunications Engineering</i> , 2020, , 3-12.	0.3	0
7	On the Origin of Biomolecular Networks. <i>Frontiers in Genetics</i> , 2019, 10, 240.	2.3	17
8	Causal data science for financial stress testing. <i>Journal of Computational Science</i> , 2018, 26, 294-304.	2.9	7
9	Probabilistic Causal Analysis of Social Influence. , 2018, , .		3
10	Deception, identity, and security. <i>Communications of the ACM</i> , 2018, 62, 85-93.	4.5	13
11	Origin of biomolecular games: deception and molecular evolution. <i>Journal of the Royal Society Interface</i> , 2018, 15, 20180429.	3.4	20
12	Exposing the probabilistic causal structure of discrimination. <i>International Journal of Data Science and Analytics</i> , 2017, 3, 1-21.	4.1	42
13	Efficient Simulation of Financial Stress Testing Scenarios with Suppes-Bayes Causal Networks. <i>Procedia Computer Science</i> , 2017, 108, 272-284.	2.0	9
14	DNA nanomapping using CRISPR-Cas9 as a programmable nanoparticle. <i>Nature Communications</i> , 2017, 8, 1665.	12.8	27
15	Simulating Heterogeneous Tumor Cell Populations. <i>PLoS ONE</i> , 2016, 11, e0168984.	2.5	4
16	Epistatic Signaling and Minority Games, the Adversarial Dynamics in Social Technological Systems. <i>Mobile Networks and Applications</i> , 2016, 21, 161-174.	3.3	3
17	Compliance signaling games: toward modeling the deterrence of insider threats. <i>Computational and Mathematical Organization Theory</i> , 2016, 22, 318-349.	2.0	22
18	Algorithmic methods to infer the evolutionary trajectories in cancer progression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E4025-34.	7.1	80

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19	High-Speed Atomic Force Microscopy Revealing Contamination in DNA Purification Systems. Analytical Chemistry, 2016, 88, 2527-2532.	6.5	9
20	TRONCO: an R package for the inference of cancer progression models from heterogeneous genomic data. Bioinformatics, 2016, 32, 1911-1913.	4.1	39
21	Histological Image Processing Features Induce a Quantitative Characterization of Chronic Tumor Hypoxia. PLoS ONE, 2016, 11, e0153623.	2.5	7
22	Cancer megafunds with in silico and in vitro validation: accelerating cancer drug discovery via financial engineering without financial crisis. Oncotarget, 2016, 7, 57671-57678.	1.8	8
23	Identity Deception and Game Deterrence via Signaling Games. , 2016, , .		3
24	Compliance Control. , 2015, , .		11
25	CAPRI: efficient inference of cancer progression models from cross-sectional data. Bioinformatics, 2015, 31, 3016-3026.	4.1	90
26	Inferring Tree Causal Models of Cancer Progression with Probability Raising. PLoS ONE, 2014, 9, e108358.	2.5	57
27	Systems Biology of Cancer: A Challenging Expedition for Clinical and Quantitative Biologists. Frontiers in Bioengineering and Biotechnology, 2014, 2, 27.	4.1	13
28	Agent-based trace learning in a recommendation-verification system for cybersecurity. , 2014, , .		9
29	Improving Detection of Driver Genes: Power-Law Null Model of Copy Number Variation in Cancer. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2014, 11, 1260-1263.	3.0	1
30	Atomic Force Microscopic Detection Enabling Multiplexed Low-Cycle-Number Quantitative Polymerase Chain Reaction for Biomarker Assays. Analytical Chemistry, 2014, 86, 6180-6183.	6.5	9
31	Cancer hybrid automata: Model, beliefs and therapy. Information and Computation, 2014, 236, 68-86.	0.7	11
32	On Algorithmic Complexity of Biomolecular Sequence Assembly Problem. Lecture Notes in Computer Science, 2014, , 183-195.	1.3	2
33	Focus on Personalized Molecular Based Medicine. , 2013, , 319-352.		0
34	What can information-asymmetric games tell us about the context of Crick's "frozen accident"? Journal of the Royal Society Interface, 2013, 10, 20130614.	3.4	13
35	Identifying individual DNA species in a complex mixture by precisely measuring the spacing between nicking restriction enzymes with atomic force microscope. Journal of the Royal Society Interface, 2012, 9, 2341-2350.	3.4	11
36	Image Analysis and Length Estimation of Biomolecules Using AFM. IEEE Transactions on Information Technology in Biomedicine, 2012, 16, 1200-1207.	3.2	14

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37	Towards Cancer Hybrid Automata. Electronic Proceedings in Theoretical Computer Science, EPTCS, 2012, 92, 137-151.	0.8	1
38	Feature-by-Feature “ Evaluating De Novo Sequence Assembly. PLoS ONE, 2012, 7, e31002.	2.5	50
39	Reevaluating Assembly Evaluations with Feature Response Curves: GAGE and Assemblathons. PLoS ONE, 2012, 7, e52210.	2.5	90
40	Discovering the Ebb and Flow of Ideas from Text Corpora. Computer, 2012, 45, 73-77.	1.1	3
41	Comparing De Novo Genome Assembly: The Long and Short of It. PLoS ONE, 2011, 6, e19175.	2.5	95
42	T<scp>otal</scp>R<scp>e</scp>C<scp>aller</scp>: improved accuracy and performance via integrated alignment and base-calling. Bioinformatics, 2011, 27, 2330-2337.	4.1	12
43	Scoring-and-unfolding trimmed tree assembler: concepts, constructs and comparisons. Bioinformatics, 2011, 27, 153-160.	4.1	26
44	Predicting malaria interactome classifications from time-course transcriptomic data along the intraerythrocytic developmental cycle. Artificial Intelligence in Medicine, 2010, 49, 167-176.	6.5	11
45	Reverse engineering dynamic temporal models of biological processes and their relationships. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 12511-12516.	7.1	23
46	SIMULTANEOUSLY SEGMENTING MULTIPLE GENE EXPRESSION TIME COURSES BY ANALYZING CLUSTER DYNAMICS. Journal of Bioinformatics and Computational Biology, 2009, 07, 339-356.	0.8	7
47	Intelligently deciphering unintelligible designs: algorithmic algebraic model checking in systems biology. Journal of the Royal Society Interface, 2009, 6, 575-597.	3.4	11
48	The apoptotic machinery as a biological complex system: analysis of its omics and evolution, identification of candidate genes for fourteen major types of cancer, and experimental validation in CML and neuroblastoma. BMC Medical Genomics, 2009, 2, 20.	1.5	20
49	Metamorphosis: the Coming Transformation of Translational Systems Biology. Queue, 2009, 7, 40-52.	1.1	1
50	Mathematical modeling of the formation of apoptosome in intrinsic pathway of apoptosis. Systems and Synthetic Biology, 2008, 2, 49-66.	1.0	13
51	Copy Number Variant Analysis of Human Embryonic Stem Cells. Stem Cells, 2008, 26, 1484-1489.	3.2	50
52	Inclusion dynamics hybrid automata. Information and Computation, 2008, 206, 1394-1424.	0.7	14
53	Systems Biology via Redescription and Ontologies (III): Protein Classification Using Malaria Parasite's Temporal Transcriptomic Profiles. , 2008, , .		3
54	Integrative Protein Function Transfer Using Factor Graphs and Heterogeneous Data Sources. , 2008, , .		6

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55	Atomic force microscope observation of branching in single transcript molecules derived from human cardiac muscle. <i>Nanotechnology</i> , 2008, 19, 384021.	2.6	1
56	Modeling and simulation of e-mail social networks: A new stochastic agent-based approach. , 2008, , .		8
57	A New Approach to the Estimation of Inter-Variable Correlation. <i>Communications in Statistics - Theory and Methods</i> , 2008, 37, 2315-2330.	1.0	0
58	From Bytes to Bedside: Data Integration and Computational Biology for Translational Cancer Research. <i>PLoS Computational Biology</i> , 2007, 3, e12.	3.2	52
59	Single molecule transcription profiling with AFM. <i>Nanotechnology</i> , 2007, 18, 044032.	2.6	17
60	Systems biology via redescription and ontologies (I): finding phase changes with applications to malaria temporal data. <i>Systems and Synthetic Biology</i> , 2007, 1, 197-205.	1.0	4
61	Algebraic Systems Biology: Theses and Hypotheses. <i>Lecture Notes in Computer Science</i> , 2007, , 1-14.	1.3	2
62	Algorithmic Algebraic Model Checking IV: Characterization of Metabolic Networks. <i>Lecture Notes in Computer Science</i> , 2007, , 170-184.	1.3	6
63	Translating Time-Course Gene Expression Profiles into Semi-algebraic Hybrid Automata Via Dimensionality Reduction. <i>Lecture Notes in Computer Science</i> , 2007, , 51-65.	1.3	3
64	Simpathica: A Computational Systems Biology Tool Within the Valis Bioinformatics Environment. , 2006, , 79-102.		5
65	Mapping Tumor-Suppressor Genes with Multipoint Statistics from Copy-Number Variation Data. <i>American Journal of Human Genetics</i> , 2006, 79, 13-22.	6.2	8
66	Algorithmic Algebraic Model Checking III: Approximate Methods. <i>Electronic Notes in Theoretical Computer Science</i> , 2006, 149, 61-77.	0.9	7
67	Interpreter of maladies: redescription mining applied to biomedical data analysis. <i>Pharmacogenomics</i> , 2006, 7, 503-509.	1.3	6
68	ALIGNING SEQUENCES WITH NON-AFFINE GAP PENALTY: PLAINS ALGORITHM, A PRACTICAL IMPLEMENTATION, AND ITS BIOLOGICAL APPLICATIONS IN COMPARATIVE GENOMICS. , 2005, , .		0
69	Quantifying the mechanisms for segmental duplications in mammalian genomes by statistical analysis and modeling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 4051-4056.	7.1	45
70	A versatile statistical analysis algorithm to detect genome copy number variation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 16292-16297.	7.1	53
71	Distribution of short paired duplications in mammalian genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 10349-10354.	7.1	23
72	Model Building and Model Checking for Biochemical Processes. <i>Cell Biochemistry and Biophysics</i> , 2003, 38, 271-286.	1.8	77

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73	A Sense of Life: Computational and Experimental Investigations with Models of Biochemical and Evolutionary Processes. OMICS A Journal of Integrative Biology, 2003, 7, 253-268.	2.0	4
74	Shrinkage-based similarity metric for cluster analysis of microarray data. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 9668-9673.	7.1	36
75	A Nearly Linear-Time General Algorithm for Genome-Wide Bi-allele Haplotype Phasing. Lecture Notes in Computer Science, 2003, , 204-215.	1.3	1
76	GENETICS: Wild by Nature. Science, 2002, 296, 1407-1408.	12.6	6
77	XS-systems: eXtended S-Systems and Algebraic Differential Automata for Modeling Cellular Behavior. Lecture Notes in Computer Science, 2002, , 431-442.	1.3	10
78	False Positives in Genomic Map Assembly and Sequence Validation. Lecture Notes in Computer Science, 2001, , 27-40.	1.3	18
79	Partitioning single-molecule maps into multiple populations: algorithms and probabilistic analysis. Discrete Applied Mathematics, 2000, 104, 203-227.	0.9	4
80	A shotgun optical map of the entire Plasmodium falciparum genome. Nature Genetics, 1999, 23, 309-313.	21.4	78
81	Optical PCR: Genomic analysis by long-range PCR and optical mapping. Mammalian Genome, 1999, 10, 1005-1009.	2.2	13
82	Optical mapping and its potential for large-scale sequencing projects. Trends in Biotechnology, 1999, 17, 297-302.	9.3	181
83	Whole-Genome Shotgun Optical Mapping of Deinococcus radiodurans. Science, 1999, 285, 1558-1562.	12.6	184
84	Optical Mapping of <i>Plasmodium falciparum</i> Chromosome 2. Genome Research, 1999, 9, 175-181.	5.5	30
85	Partitioning K clones. , 1998, , .		3
86	Genomics via Optical Mapping II: Ordered Restriction Maps. Journal of Computational Biology, 1997, 4, 91-118.	1.6	77