

Giri Narasimhan

List of Publications by Year in Descending Order

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

135
papers

2,303
citations

26
h-index

45
g-index

169
ext. papers

2,908
ext. citations

2.9
avg, IF

4.81
L-index

#	Paper	IF	Citations
135	Guest Editors Introduction to the Special Section on Bioinformatics Research and Applications. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022 , 19, 207-208	3	
134	Causal effects in microbiomes using interventional calculus. <i>Scientific Reports</i> , 2021 , 11, 5724	4.9	4
133	Dynamic Bayesian Networks for Integrating Multi-omics Time Series Microbiome Data. <i>MSystems</i> , 2021 , 6,	7.6	10
132	Effect of metronidazole on vaginal microbiota associated with asymptomatic bacterial vaginosis. <i>Access Microbiology</i> , 2021 , 3, 000226	1	0
131	Causal Inference Methods and their Challenges: The Case of 311 Data 2021 ,		2
130	Mutation-induced changes in the receptor-binding interface of the SARS-CoV-2 Delta variant B.1.617.2 and implications for immune evasion. <i>Biochemical and Biophysical Research Communications</i> , 2021 , 574, 14-19	3.4	23
129	So you think you can PLS-DA?. <i>BMC Bioinformatics</i> , 2020 , 21, 2	3.6	44
128	Effects of Various Alpha-1 Antitrypsin Supplement Dosages on the Lung Microbiome and Metabolome. <i>Lecture Notes in Computer Science</i> , 2020 , 90-101	0.9	
127	The gut microbiome and neuropsychiatric disorders: implications for attention deficit hyperactivity disorder (ADHD). <i>Journal of Medical Microbiology</i> , 2020 , 69, 14-24	3.2	19
126	Inferring directional relationships in microbial communities using signed Bayesian networks. <i>BMC Genomics</i> , 2020 , 21, 663	4.5	5
125	MATria: a unified centrality algorithm. <i>BMC Bioinformatics</i> , 2019 , 20, 278	3.6	1
124	Dynamic interaction network inference from longitudinal microbiome data. <i>Microbiome</i> , 2019 , 7, 54	16.6	29
123	Large scale microbiome profiling in the cloud. <i>Bioinformatics</i> , 2019 , 35, i13-i22	7.2	3
122	Bioinformatics Approach to Assess the Biogeographical Patterns of Soil Communities: The Utility for Soil Provenance. <i>Journal of Forensic Sciences</i> , 2018 , 63, 1033-1042	1.8	14
121	Constructing lightweight and flexible pipelines using Plugin-Based Microbiome Analysis (PluMA). <i>Bioinformatics</i> , 2018 , 34, 2881-2888	7.2	1
120	So you think you can PLS-DA? 2018 ,		3
119	Inferring Relationships in Microbiomes from Signed Bayesian Networks 2018 ,		7

118	Can SLE classification rules be effectively applied to diagnose unclear SLE cases?. <i>Lupus</i> , 2017 , 26, 150-162	6.26	4
117	ATria: a novel centrality algorithm applied to biological networks. <i>BMC Bioinformatics</i> , 2017 , 18, 239	3.6	7
116	Metagenomics, Metatranscriptomics, and Metabolomics Approaches for Microbiome Analysis. <i>Evolutionary Bioinformatics</i> , 2016 , 12, 5-16	1.9	140
115	Gene expression patterns in transgenic mouse models of hypertrophic cardiomyopathy caused by mutations in myosin regulatory light chain. <i>Archives of Biochemistry and Biophysics</i> , 2016 , 601, 121-32	4.1	6
114	Planar Geometric Spanners 2016 , 1570-1574		
113	Microbiome Analysis: State of the Art and Future Trends 2016 , 401-424		3
112	GPUDePiCt: A Parallel Implementation of a Clustering Algorithm for Computing Degenerate Primers on Graphics Processing Units. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2015 , 12, 445-54	3	4
111	Automatic Construction of 3-D Building Model From Airborne LIDAR Data Through 2-D Snake Algorithm. <i>IEEE Transactions on Geoscience and Remote Sensing</i> , 2015 , 53, 3-14	8.1	28
110	Microbial "social networks". <i>BMC Genomics</i> , 2015 , 16 Suppl 11, S6	4.5	26
109	Computational Methods in Epigenetics 2015 , 153-180		
108	Current concepts in the pathogenesis and treatment of chronic suppurative otitis media. <i>Journal of Medical Microbiology</i> , 2015 , 64, 1103-1116	3.2	96
107	Structural and Functional characterization of <i>Pseudomonas aeruginosa</i> global regulator AmpR. <i>Journal of Bacteriology</i> , 2014 , 196, 3890-902	3.5	26
106	Deep sequencing analyses expands the <i>Pseudomonas aeruginosa</i> AmpR regulon to include small RNA-mediated regulation of iron acquisition, heat shock and oxidative stress response. <i>Nucleic Acids Research</i> , 2014 , 42, 979-98	20.1	45
105	Better primer design for metagenomics applications by increasing taxonomic distinguishability. <i>BMC Proceedings</i> , 2013 , 7, S4	2.3	11
104	Comment on On the Uniqueness of Stable Marriage Matchings [Economic Letters 69(1):18, 2000]. <i>Economics Letters</i> , 2013 , 121, 468	1.3	1
103	Transcriptional response of mucoid <i>Pseudomonas aeruginosa</i> to human respiratory mucus. <i>MBio</i> , 2013 , 3, e00410-12	7.8	30
102	The regulatory repertoire of <i>Pseudomonas aeruginosa</i> AmpC β -lactamase regulator AmpR includes virulence genes. <i>PLoS ONE</i> , 2012 , 7, e34067	3.7	82
101	Gene Function Prediction and Functional Network: The Role of Gene Ontology. <i>Intelligent Systems Reference Library</i> , 2012 , 123-162	0.8	1

100	CloG: A pipeline for closing gaps in a draft assembly using short reads 2011 ,		3
99	Combination of 16S rRNA variable regions provides a detailed analysis of bacterial community dynamics in the lungs of cystic fibrosis patients. <i>Human Genomics</i> , 2010 , 4, 147-69	6.8	6
98	Serial evolutionary networks of within-patient HIV-1 sequences reveal patterns of evolution of X4 strains. <i>BMC Systems Biology</i> , 2009 , 3, 62	3.5	3
97	Region-restricted clustering for geographic data mining. <i>Computational Geometry: Theory and Applications</i> , 2009 , 42, 231-240	0.4	1
96	On the dilation spectrum of paths, cycles, and trees. <i>Computational Geometry: Theory and Applications</i> , 2009 , 42, 923-933	0.4	2
95	Weighted Consensus Clustering for Identifying Functional Modules in Protein-Protein Interaction Networks 2009 ,		4
94	Approaches to analyse dynamic microbial communities such as those seen in cystic fibrosis lung. <i>Human Genomics</i> , 2009 , 3, 246-56	6.8	10
93	Influence of irrigated agriculture on soil microbial diversity. <i>Applied Soil Ecology</i> , 2008 , 40, 146-154	5	26
92	Dynamics of <i>Pseudomonas aeruginosa</i> genome evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 3100-5	11.5	367
91	Approximate distance oracles for geometric spanners. <i>ACM Transactions on Algorithms</i> , 2008 , 4, 1-34	1.2	11
90	The role of internal node sequences and the molecular clock in the analysis of serially-sampled data. <i>International Journal of Bioinformatics Research and Applications</i> , 2008 , 4, 107-21	0.9	1
89	ESTIMATING SUPPORT FOR PROTEIN-PROTEIN INTERACTION DATA WITH APPLICATIONS TO FUNCTION PREDICTION 2008 ,		6
88	Distance-preserving approximations of polygonal paths. <i>Computational Geometry: Theory and Applications</i> , 2007 , 36, 183-196	0.4	10
87	A Graph Reduction Method for 2D Snake Problems 2007 ,		4
86	On the Effectiveness of Constraints Sets in Clustering Genes 2007 ,		2
85	SBLAST: Structural Basic Local Alignment Searching Tools using Geometric Hashing 2007 ,		1
84	Sliding MinPD: building evolutionary networks of serial samples via an automated recombination detection approach. <i>Bioinformatics</i> , 2007 , 23, 2993-3000	7.2	6
83	IEM: AN ALGORITHM FOR ITERATIVE ENHANCEMENT OF MOTIFS USING COMPARATIVE GENOMICS DATA 2007 ,		3

82	PlasmoTFBM: An Intelligent Queriable Database for Predicted Transcription Factor Binding Motifs in <i>Plasmodium falciparum</i> 2007 , 121-136		
81	Searching for Recombinant Donors in a Phylogenetic Network of Serial Samples 2007 , 109-120		
80	Enhancing Motif Refinement by Incorporating Comparative Genomics Data 2007 , 329-337		
79	Geometric Spanner Networks 2007 ,		173
78	IEM: an algorithm for iterative enhancement of motifs using comparative genomics data. <i>Computational Systems Bioinformatics / Life Sciences Society Computational Systems Bioinformatics Conference</i> , 2007 , 6, 227-35		4
77	Discovering Sequence-Structure Patterns in Proteins with Variable Secondary Structure. <i>Lecture Notes in Computer Science</i> , 2006 , 702-709	0.9	
76	Serial NetEvolve: a flexible utility for generating serially-sampled sequences along a tree or recombinant network. <i>Bioinformatics</i> , 2006 , 22, 2313-4	7.2	6
75	Enhancement of protein thermal stability: toward the design of robust proteins for bionanotechnological applications 2006 , 117-139		3
74	An eco-informatics tool for microbial community studies: supervised classification of Amplicon Length Heterogeneity (ALH) profiles of 16S rRNA. <i>Journal of Microbiological Methods</i> , 2006 , 65, 49-62	2.8	18
73	Identification of Cacao TIR-NBS-LRR Resistance Gene Homologues and Their Use as Genetic Markers. <i>Journal of the American Society for Horticultural Science</i> , 2006 , 131, 806-813	2.3	4
72	Pooling Evidence to Identify Cell Cycle Regulated Genes. <i>Lecture Notes in Computer Science</i> , 2006 , 694-701	0.9	
71	Reconstructing Ancestor-Descendant Lineages from Serially-Sampled Data: A Comparison Study. <i>Lecture Notes in Computer Science</i> , 2006 , 807-814	0.9	0
70	Region-Restricted Clustering for Geographic Data Mining. <i>Lecture Notes in Computer Science</i> , 2006 , 399-410	0.9	6
69	Clustering genes using gene expression and text literature data 2005 , 329-40		3
68	A Knowledge-Driven Method to Evaluate Multi-source Clustering. <i>Lecture Notes in Computer Science</i> , 2005 , 196-202	0.9	
67	Clustering Using Adaptive Self-organizing Maps (ASOM) and Applications. <i>Lecture Notes in Computer Science</i> , 2005 , 944-951	0.9	1
66	Rational design of thermally stable proteins: relevance to bionanotechnology. <i>Journal of Nanoscience and Nanotechnology</i> , 2005 , 5, 1759-67	1.3	31
65	Distinct transcriptional profiles characterize oral epithelium-microbiota interactions. <i>Cellular Microbiology</i> , 2005 , 7, 811-23	3.9	89

64	Microarray Data Analysis Using Neural Network Classifiers and Gene Selection Methods 2005 , 207-222		4
63	Fast Pruning of Geometric Spanners. <i>Lecture Notes in Computer Science</i> , 2005 , 508-520	0.9	7
62	Exact and Approximation Algorithms for Computing the Dilation Spectrum of Paths, Trees, and Cycles. <i>Lecture Notes in Computer Science</i> , 2005 , 849-858	0.9	
61	Approximating geometric bottleneck shortest paths. <i>Computational Geometry: Theory and Applications</i> , 2004 , 29, 233-249	0.4	29
60	Alginate production affects <i>Pseudomonas aeruginosa</i> biofilm development and architecture, but is not essential for biofilm formation. <i>Journal of Medical Microbiology</i> , 2004 , 53, 679-690	3.2	125
59	MinPD: distance-based phylogenetic analysis and recombination detection of serially-sampled HIV quasispecies 2004 , 110-9		5
58	BALANCED PARTITION OF MINIMUM SPANNING TREES. <i>International Journal of Computational Geometry and Applications</i> , 2003 , 13, 303-316	0.3	2
57	Detection of DNA-binding helix-turn-helix motifs in proteins using the pattern dictionary method. <i>Methods in Enzymology</i> , 2003 , 370, 250-64	1.7	4
56	Distance-Preserving Approximations of Polygonal Paths. <i>Lecture Notes in Computer Science</i> , 2003 , 217-228	0.9	4
55	Degenerate primer design via clustering 2003 , 2, 75-83		13
54	Optimally computing a shortest weakly visible line segment inside a simple polygon. <i>Computational Geometry: Theory and Applications</i> , 2002 , 23, 1-29	0.4	3
53	Graph-theoretic techniques in D-optimal design problems. <i>Journal of Statistical Planning and Inference</i> , 2002 , 102, 377-387	0.8	3
52	Improved Algorithms for Constructing Fault-Tolerant Spanners. <i>Algorithmica</i> , 2002 , 32, 144-156	0.9	33
51	Mining protein sequences for motifs. <i>Journal of Computational Biology</i> , 2002 , 9, 707-20	1.7	55
50	Fast Greedy Algorithms for Constructing Sparse Geometric Spanners. <i>SIAM Journal on Computing</i> , 2002 , 31, 1479-1500	1.1	71
49	Balanced Partition of Minimum Spanning Trees. <i>Lecture Notes in Computer Science</i> , 2002 , 26-35	0.9	1
48	Approximate Distance Oracles Revisited. <i>Lecture Notes in Computer Science</i> , 2002 , 357-368	0.9	17
47	Multiple comparisons model-based clustering and ternary pattern tree numerical display of gene response to treatment: procedure and application to the preclinical evaluation of chemopreventive agents. <i>Molecular Cancer Therapeutics</i> , 2002 , 1, 1283-92	6.1	9

46	A Generalization of maximal independent sets. <i>Discrete Applied Mathematics</i> , 2001 , 109, 223-235	1	10
45	Geometric Minimum Spanning Trees via Well-Separated Pair Decompositions. <i>Journal of Experimental Algorithmics</i> , 2001 , 6, 6	1.1	3
44	Approximation Algorithms for the Bottleneck Stretch Factor Problem. <i>Lecture Notes in Computer Science</i> , 2001 , 502-513	0.9	
43	Optimal Algorithms for Two-Guard Walkability of Simple Polygons. <i>Lecture Notes in Computer Science</i> , 2001 , 438-449	0.9	13
42	Approximating the Stretch Factor of Euclidean Graphs. <i>SIAM Journal on Computing</i> , 2000 , 30, 978-989	1.1	52
41	Improved Greedy Algorithms for Constructing Sparse Geometric Spanners. <i>Lecture Notes in Computer Science</i> , 2000 , 314-328	0.9	13
40	ON HAMILTONIAN TRIANGULATIONS IN SIMPLE POLYGONS. <i>International Journal of Computational Geometry and Applications</i> , 1999 , 09, 261-275	0.3	7
39	Approximating Minimum Manhattan Networks. <i>Lecture Notes in Computer Science</i> , 1999 , 28-38	0.9	2
38	Information capacity of binary weights associative memories. <i>Neurocomputing</i> , 1998 , 19, 35-58	5.4	3
37	Efficient algorithms for constructing fault-tolerant geometric spanners 1998 ,		23
36	Resource-constrained geometric network optimization 1998 ,		38
35	A Fast Algorithm for Constructing Sparse Euclidean Spanners. <i>International Journal of Computational Geometry and Applications</i> , 1997 , 07, 297-315	0.3	46
34	LR-visibility in polygons. <i>Computational Geometry: Theory and Applications</i> , 1997 , 7, 37-57	0.4	31
33	On hamiltonian triangulations in simple polygons (Extended Abstract). <i>Lecture Notes in Computer Science</i> , 1997 , 321-330	0.9	1
32	NEW SPARSENESS RESULTS ON GRAPH SPANNERS. <i>International Journal of Computational Geometry and Applications</i> , 1995 , 05, 125-144	0.3	51
31	Optimal linear-time algorithm for the shortest illuminating line segment in a polygon 1994 ,		6
30	Finding all weakly-visible chords of a polygon in linear time. <i>Lecture Notes in Computer Science</i> , 1994 , 119-130	0.9	1
29	Optimally sparse spanners in 3-dimensional Euclidean space 1993 ,		38

28	New sparseness results on graph spanners 1992 ,		49
27	Stability number and chromatic number of tolerance graphs. <i>Discrete Applied Mathematics</i> , 1992 , 36, 47-56	1	8
26	Geometric searching and link distance 1991 , 261-272		6
25	A note on the Hamiltonian Circuit Problem on directed path graphs. <i>Information Processing Letters</i> , 1989 , 32, 167-170	0.8	9
24	Fault-Tolerant Spanners 427-442		
23	The Dumbbell Theorem 196-218		
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