

Giri Narasimhan

List of Publications by Year in descending order

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Version: 2024-02-01

149
papers

3,491
citations

218662

26
h-index

189881

50
g-index

169
all docs

169
docs citations

169
times ranked

3715
citing authors

#	ARTICLE	IF	CITATIONS
1	Dynamics of <i>Pseudomonas aeruginosa</i> genome evolution. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 3100-3105.	7.1	492
2	Metagenomics, Metatranscriptomics, and Metabolomics Approaches for Microbiome Analysis. Evolutionary Bioinformatics, 2016, 12s1, EBO.S36436.	1.2	227
3	So you think you can PLS-DA?. BMC Bioinformatics, 2020, 21, 2.	2.6	184
4	Alginate production affects <i>Pseudomonas aeruginosa</i> biofilm development and architecture, but is not essential for biofilm formation. Journal of Medical Microbiology, 2004, 53, 679-690.	1.8	154
5	Current concepts in the pathogenesis and treatment of chronic suppurative otitis media. Journal of Medical Microbiology, 2015, 64, 1103-1116.	1.8	151
6	Fast Greedy Algorithms for Constructing Sparse Geometric Spanners. SIAM Journal on Computing, 2002, 31, 1479-1500.	1.0	111
7	The Regulatory Repertoire of <i>Pseudomonas aeruginosa</i> AmpC β -Lactamase Regulator AmpR Includes Virulence Genes. PLoS ONE, 2012, 7, e34067.	2.5	108
8	Distinct transcriptional profiles characterize oral epithelium-microbiota interactions. Cellular Microbiology, 2005, 7, 811-823.	2.1	94
9	New sparseness results on graph spanners. , 1992, , .		72
10	Mutation-induced changes in the receptor-binding interface of the SARS-CoV-2 Delta variant B.1.617.2 and implications for immune evasion. Biochemical and Biophysical Research Communications, 2021, 574, 14-19.	2.1	70
11	Mining Protein Sequences for Motifs. Journal of Computational Biology, 2002, 9, 707-720.	1.6	67
12	A Fast Algorithm for Constructing Sparse Euclidean Spanners. International Journal of Computational Geometry and Applications, 1997, 07, 297-315.	0.5	65
13	NEW SPARSENESS RESULTS ON GRAPH SPANNERS. International Journal of Computational Geometry and Applications, 1995, 05, 125-144.	0.5	64
14	Approximating the Stretch Factor of Euclidean Graphs. SIAM Journal on Computing, 2000, 30, 978-989.	1.0	64
15	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. Nucleic Acids Research, 2014, 42, 979-998.	14.5	62
16	Dynamic interaction network inference from longitudinal microbiome data. Microbiome, 2019, 7, 54.	11.1	59
17	Microbial "social networks". BMC Genomics, 2015, 16, S6.	2.8	52
18	Optimally sparse spanners in 3-dimensional Euclidean space. , 1993, , .		51

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19	Improved Algorithms for Constructing Fault-Tolerant Spanners. <i>Algorithmica</i> , 2002, 32, 144-156.	1.3	48
20	Resource-constrained geometric network optimization. , 1998, , .		44
21	Structural and Functional Characterization of <i>Pseudomonas aeruginosa</i> Global Regulator AmpR. <i>Journal of Bacteriology</i> , 2014, 196, 3890-3902.	2.2	44
22	Transcriptional Response of Mucoicid <i>Pseudomonas aeruginosa</i> to Human Respiratory Mucus. <i>MBio</i> , 2012, 3, e00410-12.	4.1	41
23	The gut microbiome and neuropsychiatric disorders: implications for attention deficit hyperactivity disorder (ADHD). <i>Journal of Medical Microbiology</i> , 2020, 69, 14-24.	1.8	40
24	Potential Autoimmunity Resulting from Molecular Mimicry between SARS-CoV-2 Spike and Human Proteins. <i>Viruses</i> , 2022, 14, 1415.	3.3	39
25	Rational Design of Thermally Stable Proteins: Relevance to Bionanotechnology. <i>Journal of Nanoscience and Nanotechnology</i> , 2005, 5, 1759-1767.	0.9	37
26	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.	6.3	37
27	Influence of irrigated agriculture on soil microbial diversity. <i>Applied Soil Ecology</i> , 2008, 40, 146-154.	4.3	36
28	LR-visibility in polygons. <i>Computational Geometry: Theory and Applications</i> , 1997, 7, 37-57.	0.5	35
29	Efficient algorithms for constructing fault-tolerant geometric spanners. , 1998, , .		34
30	Approximating geometric bottleneck shortest paths. <i>Computational Geometry: Theory and Applications</i> , 2004, 29, 233-249.	0.5	31
31	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.	1.6	23
32	Approximate distance oracles for geometric spanners. <i>ACM Transactions on Algorithms</i> , 2008, 4, 1-34.	1.0	22
33	An ecoinformatics 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.	1.6	20
34	Better primer design for metagenomics applications by increasing taxonomic distinguishability. <i>BMC Proceedings</i> , 2013, 7, S4.	1.6	19
35	Dynamic Bayesian Networks for Integrating Multi-omics Time Series Microbiome Data. <i>MSystems</i> , 2021, 6, .	3.8	19
36	Optimal Algorithms for Two-Guard Walkability of Simple Polygons. <i>Lecture Notes in Computer Science</i> , 2001, , 438-449.	1.3	18

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37	Improved Greedy Algorithms for Constructing Sparse Geometric Spanners. Lecture Notes in Computer Science, 2000, , 314-328.	1.3	17
38	Degenerate primer design via clustering. , 0, , .		15
39	ESTIMATING SUPPORT FOR PROTEIN-PROTEIN INTERACTION DATA WITH APPLICATIONS TO FUNCTION PREDICTION. , 2008, , .		15
40	Approaches to analyse dynamic microbial communities such as those seen in cystic fibrosis lung. Human Genomics, 2009, 3, 246.	2.9	14
41	Degenerate primer design via clustering. Proceedings, 2003, 2, 75-83.	0.1	14
42	Gene expression patterns in transgenic mouse models of hypertrophic cardiomyopathy caused by mutations in myosin regulatory light chain. Archives of Biochemistry and Biophysics, 2016, 601, 121-132.	3.0	13
43	Inferring directional relationships in microbial communities using signed Bayesian networks. BMC Genomics, 2020, 21, 663.	2.8	13
44	A note on the Hamiltonian Circuit Problem on directed path graphs. Information Processing Letters, 1989, 32, 167-170.	0.6	12
45	A Generalization of maximal independent sets. Discrete Applied Mathematics, 2001, 109, 223-235.	0.9	12
46	Geometric Minimum Spanning Trees via Well-Separated Pair Decompositions. Journal of Experimental Algorithmics, 2001, 6, 6.	1.0	11
47	Fast Pruning of Geometric Spanners. Lecture Notes in Computer Science, 2005, , 508-520.	1.3	11
48	Distance-preserving approximations of polygonal paths. Computational Geometry: Theory and Applications, 2007, 36, 183-196.	0.5	11
49	Inferring Relationships in Microbiomes from Signed Bayesian Networks. , 2018, , .		11
50	Stability number and chromatic number of tolerance graphs. Discrete Applied Mathematics, 1992, 36, 47-56.	0.9	10
51	Sliding MinPD: building evolutionary networks of serial samples via an automated recombination detection approach. Bioinformatics, 2007, 23, 2993-3000.	4.1	10
52	Combination of 16S rRNA variable regions provides a detailed analysis of bacterial community dynamics in the lungs of cystic fibrosis patients. Human Genomics, 2010, 4, 147.	2.9	10
53	ATria: a novel centrality algorithm applied to biological networks. BMC Bioinformatics, 2017, 18, 239.	2.6	10
54	Causal effects in microbiomes using interventional calculus. Scientific Reports, 2021, 11, 5724.	3.3	10

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55	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.	4.1	10
56	ON HAMILTONIAN TRIANGULATIONS IN SIMPLE POLYGONS. <i>International Journal of Computational Geometry and Applications</i> , 1999, 09, 261-275.	0.5	9
57	Serial NetEvolve: a flexible utility for generating serially-sampled sequences along a tree or recombinant network. <i>Bioinformatics</i> , 2006, 22, 2313-2314.	4.1	9
58	Large scale microbiome profiling in the cloud. <i>Bioinformatics</i> , 2019, 35, i13-i22.	4.1	9
59	Optimal linear-time algorithm for the shortest illuminating line segment in a polygon. , 1994, , .		8
60	Geometric searching and link distance. , 1991, , 261-272.		7
61	Region-Restricted Clustering for Geographic Data Mining. <i>Lecture Notes in Computer Science</i> , 2006, , 399-410.	1.3	7
62	Detection of DNA-Binding Helix-Turn-Helix Motifs in Proteins Using the Pattern Dictionary Method. <i>Methods in Enzymology</i> , 2003, 370, 250-264.	1.0	6
63	Clustering genes using gene expression and text literature data. , 2005, , 329-40.		6
64	On the Effectiveness of Constraints Sets in Clustering Genes. , 2007, , .		6
65	Weighted Consensus Clustering for Identifying Functional Modules in Protein-Protein Interaction Networks. , 2009, , .		6
66	So you think you can PLS-DA?. , 2018, , .		6
67	Effect of metronidazole on vaginal microbiota associated with asymptomatic bacterial vaginosis. <i>Access Microbiology</i> , 2021, 3, 000226.	0.5	6
68	Prior exposure to microcystin alters host gut resistome and is associated with dysregulated immune homeostasis in translatable mouse models. <i>Scientific Reports</i> , 2022, 12, .	3.3	6
69	Graph-theoretic techniques in D-optimal design problems. <i>Journal of Statistical Planning and Inference</i> , 2002, 102, 377-387.	0.6	5
70	Microarray Data Analysis Using Neural Network Classifiers and Gene Selection Methods. , 2005, , 207-222.		5
71	A Graph Reduction Method for 2D Snake Problems. , 2007, , .		5
72	Constructing lightweight and flexible pipelines using Plugin-Based Microbiome Analysis (PluMA). <i>Bioinformatics</i> , 2018, 34, 2881-2888.	4.1	5

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73	IEM: AN ALGORITHM FOR ITERATIVE ENHANCEMENT OF MOTIFS USING COMPARATIVE GENOMICS DATA. , 2007, , .		5
74	Identification of Cacao TIR-NBS-LRR Resistance Gene Homologues and Their Use as Genetic Markers. Journal of the American Society for Horticultural Science, 2006, 131, 806-813.	1.0	5
75	MinPD: distance-based phylogenetic analysis and recombination detection of serially-sampled HIV quasispecies. Proceedings, 2004, , 110-9.	0.0	5
76	Enhancement of protein thermal stability: toward the design of robust proteins for bionanotechnological applications. , 2006, , 117-139.		4
77	Region-restricted clustering for geographic data mining. Computational Geometry: Theory and Applications, 2009, 42, 231-240.	0.5	4
78	On the dilation spectrum of paths, cycles, and trees. Computational Geometry: Theory and Applications, 2009, 42, 923-933.	0.5	4
79	CloG: A pipeline for closing gaps in a draft assembly using short reads. , 2011, , .		4
80	GPUDePiCt: A Parallel Implementation of a Clustering Algorithm for Computing Degenerate Primers on Graphics Processing Units. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 445-454.	3.0	4
81	Can SLE classification rules be effectively applied to diagnose unclear SLE cases?. Lupus, 2017, 26, 150-162.	1.6	4
82	Causal Inference Methods and their Challenges: The Case of 311 Data. , 2021, , .		4
83	Geometric Spanners. , 2008, , 360-364.		4
84	Distance-Preserving Approximations of Polygonal Paths. Lecture Notes in Computer Science, 2003, , 217-228.	1.3	4
85	IEM: an algorithm for iterative enhancement of motifs using comparative genomics data. Computational Systems Bioinformatics / Life Sciences Society Computational Systems Bioinformatics Conference, 2007, 6, 227-35.	0.4	4
86	Information capacity of binary weights associative memories. Neurocomputing, 1998, 19, 35-58.	5.9	3
87	Optimally computing a shortest weakly visible line segment inside a simple polygon. Computational Geometry: Theory and Applications, 2002, 23, 1-29.	0.5	3
88	CyberBridges A Model Collaboration Infrastructure for e-Science. , 2007, , .		3
89	Serial evolutionary networks of within-patient HIV-1 sequences reveal patterns of evolution of X4 strains. BMC Systems Biology, 2009, 3, 62.	3.0	3
90	MATria: a unified centrality algorithm. BMC Bioinformatics, 2019, 20, 278.	2.6	3

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91	Gene Function Prediction and Functional Network: The Role of Gene Ontology. Intelligent Systems Reference Library, 2012, , 123-162.	1.2	3
92	Approximating Minimum Manhattan Networks. Lecture Notes in Computer Science, 1999, , 28-38.	1.3	2
93	BALANCED PARTITION OF MINIMUM SPANNING TREES. International Journal of Computational Geometry and Applications, 2003, 13, 303-316.	0.5	2
94	Clustering Using Adaptive Self-organizing Maps (ASOM) and Applications. Lecture Notes in Computer Science, 2005, , 944-951.	1.3	2
95	SBLAST: Structural Basic Local Alignment Searching Tools using Geometric Hashing. , 2007, , .		2
96	The role of internal node sequences and the molecular clock in the analysis of serially-sampled data. International Journal of Bioinformatics Research and Applications, 2008, 4, 107.	0.2	2
97	Applications of Geometric Spanner Networks. , 2008, , 40-43.		2
98	Geometric Spanners. , 2016, , 846-852.		2
99	A Knowledge-Driven Method to Evaluate Multi-source Clustering. Lecture Notes in Computer Science, 2005, , 196-202.	1.3	1
100	Comment on "On the Uniqueness of Stable Marriage Matchings" [Economic Letters 69(1):1-8, 2000]. Economics Letters, 2013, 121, 468.	1.9	1
101	ATria: A novel centrality algorithm applied to biological networks. , 2015, , .		1
102	On hamiltonian triangulations in simple polygons (Extended Abstract). Lecture Notes in Computer Science, 1997, , 321-330.	1.3	1
103	Balanced Partition of Minimum Spanning Trees. Lecture Notes in Computer Science, 2002, , 26-35.	1.3	1
104	AN APPLICATION OF ASSOCIATION RULE MINING TO HLA-A*0201 EPITOPE PREDICTION. , 2005, , .		1
105	Pooling Evidence to Identify Cell Cycle-Regulated Genes. Lecture Notes in Computer Science, 2006, , 694-701.	1.3	1
106	Mining the Database of Transcription Binding Sites. , 2006, , .		0
107	Discovering Sequence-Structure Patterns in Proteins with Variable Secondary Structure. Lecture Notes in Computer Science, 2006, , 702-709.	1.3	0
108	The Dumbbell Theorem. , 0, , 196-218.		0

#	ARTICLE	IF	CITATIONS
109	Approximating the Stretch Factor of Euclidean Graphs. , 0, , 242-254.		0
110	Geometric Analysis: The Gap Property. , 0, , 108-119.		0
111	Applications of Well-Separated Pairs. , 0, , 178-195.		0
112	The Path-Greedy Algorithm. , 0, , 318-382.		0
113	The Distance Range Hierarchy. , 0, , 385-414.		0
114	The Gap-Greedy Algorithm. , 0, , 120-138.		0
115	Enumerating Distances Using Spanners of Bounded Degree. , 0, , 139-148.		0
116	Geometric Analysis: The Leapfrog Property. , 0, , 257-317.		0
117	The Algebraic Computation-Tree Model. , 2007, , 41-60.		0
118	Approximating Shortest Paths in Spanners. , 0, , 415-426.		0
119	The Well-Separated Pair Decomposition. , 0, , 151-177.		0
120	Shortcutting Trees and Spanners with Low Spanner Diameter. , 0, , 219-241.		0
121	Cones in Higher Dimensional Space and $\hat{\Gamma}$ -Graphs. , 0, , 92-107.		0
122	Designing Approximation Algorithms with Spanners. , 0, , 443-467.		0
123	Further Results and Open Problems. , 0, , 468-482.		0
124	Algorithms and Graphs. , 0, , 18-40.		0
125	Spanners Based on the $\hat{\Gamma}$ -Graph. , 0, , 63-91.		0
126	Fault-Tolerant Spanners. , 0, , 427-442.		0

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127	A Functional Network of Yeast Genes Using Gene Ontology Information. , 2008, , .		0
128	A branch-and-bound approach to knowledge-based protein structure assembly. , 2008, , .		0
129	Guest Editors' Introduction to the Special Section on Bioinformatics Research and Applications. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2010, 7, 577-578.	3.0	0
130	Invited: Comparative microbial genomics. , 2011, , .		0
131	Designing Primers with Higher Taxonomic Distinguishability. , 2013, , .		0
132	Vector repacking algorithms for power-aware computing. , 2013, , .		0
133	A Metagenomic Approach to the Airways Microbiome of Chronic Obstructive Pulmonary Disease (COPD). , 2013, , .		0
134	Computational Methods in Epigenetics. , 2015, , 153-180.		0
135	Geometric Spanners. , 2015, , 1-8.		0
136	MATria: A unified centrality algorithm. , 2017, , .		0
137	Approximation Algorithms for the Bottleneck Stretch Factor Problem. Lecture Notes in Computer Science, 2001, , 502-513.	1.3	0
138	Exact and Approximation Algorithms for Computing the Dilation Spectrum of Paths, Trees, and Cycles. Lecture Notes in Computer Science, 2005, , 849-858.	1.3	0
139	TRAINING SET DESIGN FOR PATTERN DISCOVERY WITH APPLICATIONS TO PROTEIN MOTIF DETECTION. , 2005, , .		0
140	QUERYING A DATABASE OF REGULATORY ELEMENTS. , 2005, , .		0
141	Planar Geometric Spanners. , 2008, , 653-656.		0
142	Applications of Geometric Spanner Networks. , 2014, , 1-6.		0
143	Planar Geometric Spanners. , 2016, , 1570-1574.		0
144	Applications of Geometric Spanner Networks. , 2016, , 86-90.		0

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145	Effects of Various Alpha-1 Antitrypsin Supplement Dosages on the Lung Microbiome and Metabolome. Lecture Notes in Computer Science, 2020, , 90-101.	1.3	0
146	PlasmoTFBM: An Intelligent Queriable Database for Predicted Transcription Factor Binding Motifs in Plasmodium falciparum. , 2007, , 121-136.		0
147	Searching for Recombinant Donors in a Phylogenetic Network of Serial Samples. , 2007, , 109-120.		0
148	Enhancing Motif Refinement by Incorporating Comparative Genomics Data. , 2007, , 329-337.		0
149	Guest Editorsâ€™ Introduction to the Special Section on Bioinformatics Research and Applications. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 207-208.	3.0	0