

Laxmi Parida

List of Publications by Year in descending order

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Version: 2024-02-01

94
papers

2,908
citations

279798

23
h-index

214800

47
g-index

120
all docs

120
docs citations

120
times ranked

4907
citing authors

#	ARTICLE	IF	CITATIONS
1	Utilizing stability criteria in choosing feature selection methods yields reproducible results in microbiome data. <i>Biometrics</i> , 2022, 78, 1155-1167.	1.4	4
2	Integrative molecular and clinical profiling of acral melanoma links focal amplification of 22q11.21 to metastasis. <i>Nature Communications</i> , 2022, 13, 898.	12.8	19
3	The Lipogenic Regulator SREBP2 Induces Transferrin in Circulating Melanoma Cells and Suppresses Ferroptosis. <i>Cancer Discovery</i> , 2021, 11, 678-695.	9.4	114
4	Re-purposing software for functional characterization of the microbiome. <i>Microbiome</i> , 2021, 9, 4.	11.1	7
5	Monitoring the microbiome for food safety and quality using deep shotgun sequencing. <i>Npj Science of Food</i> , 2021, 5, 3.	5.5	22
6	Functional profiling of COVID-19 respiratory tract microbiomes. <i>Scientific Reports</i> , 2021, 11, 6433.	3.3	24
7	Multiple Loci Selection with Multi-Way Epistasis in Coalescence with Recombination. <i>Algorithms</i> , 2021, 14, 136.	2.1	0
8	EMPress Enables Tree-Guided, Interactive, and Exploratory Analyses of Multi-omic Data Sets. <i>MSystems</i> , 2021, 6, .	3.8	36
9	Challenges in benchmarking metagenomic profilers. <i>Nature Methods</i> , 2021, 18, 618-626.	19.0	63
10	SARS-CoV-2 detection status associates with bacterial community composition in patients and the hospital environment. <i>Microbiome</i> , 2021, 9, 132.	11.1	37
11	Longitudinal Single-Cell Dynamics of Chromatin Accessibility and Mitochondrial Mutations in Chronic Lymphocytic Leukemia Mirror Disease History. <i>Cancer Discovery</i> , 2021, 11, 3048-3063.	9.4	31
12	Parallel Genomic Alterations of Antigen and Payload Targets Mediate Polyclonal Acquired Clinical Resistance to Sacituzumab Govitecan in Triple-Negative Breast Cancer. <i>Cancer Discovery</i> , 2021, 11, 2436-2445.	9.4	69
13	K-Mer Analyses Reveal Different Evolutionary Histories of Alpha, Beta, and Gamma Papillomaviruses. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9657.	4.1	7
14	Efficient computation of Faith's phylogenetic diversity with applications in characterizing microbiomes. <i>Genome Research</i> , 2021, 31, 2131-2137.	5.5	16
15	A common methodological phylogenomics framework for intra-patient heteroplasmies to infer SARS-CoV-2 sublineages and tumor clones. <i>BMC Genomics</i> , 2021, 22, 518.	2.8	4
16	Paralog knockout profiling identifies DUSP4 and DUSP6 as a digenic dependence in MAPK pathway-driven cancers. <i>Nature Genetics</i> , 2021, 53, 1664-1672.	21.4	61
17	Human Skin, Oral, and Gut Microbiomes Predict Chronological Age. <i>MSystems</i> , 2020, 5, .	3.8	80
18	Emergence of Drift Variants That May Affect COVID-19 Vaccine Development and Antibody Treatment. <i>Pathogens</i> , 2020, 9, 324.	2.8	184

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19	Hierarchically Labeled Database Indexing Allows Scalable Characterization of Microbiomes. <i>IScience</i> , 2020, 23, 100988.	4.1	7
20	A Topological Data Analysis Approach on Predicting Phenotypes from Gene Expression Data. <i>Lecture Notes in Computer Science</i> , 2020, , 178-187.	1.3	11
21	Variant analysis of SARS-CoV-2 genomes. <i>Bulletin of the World Health Organization</i> , 2020, 98, 495-504.	3.3	451
22	Simultaneous Phasing of Multiple Polyploids. <i>Lecture Notes in Computer Science</i> , 2020, , 50-68.	1.3	0
23	Transcriptome characterization and differentially expressed genes under flooding and drought stress in the biomass grasses <i>Phalaris arundinacea</i> and <i>Dactylis glomerata</i> . <i>Annals of Botany</i> , 2019, 124, 717-730.	2.9	7
24	Dark-matter matters: Discriminating subtle blood cancers using the darkest DNA. <i>PLoS Computational Biology</i> , 2019, 15, e1007332.	3.2	7
25	Liquid versus tissue biopsy for detecting acquired resistance and tumor heterogeneity in gastrointestinal cancers. <i>Nature Medicine</i> , 2019, 25, 1415-1421.	30.7	359
26	Haplotype assembly of autotetraploid potato using integer linear programming. <i>Bioinformatics</i> , 2019, 35, 3279-3286.	4.1	10
27	Signal enrichment with strain-level resolution in metagenomes using topological data analysis. <i>BMC Genomics</i> , 2019, 20, 194.	2.8	2
28	Food authentication from shotgun sequencing reads with an application on high protein powders. <i>Npj Science of Food</i> , 2019, 3, 24.	5.5	31
29	Linear Time Algorithms to Construct Populations Fitting Multiple Constraint Distributions at Genomic Scales. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 1132-1142.	3.0	4
30	A Quantitative and Qualitative Characterization of k-mer Based Alignment-Free Phylogeny Construction. <i>Lecture Notes in Computer Science</i> , 2019, , 19-31.	1.3	1
31	Enhancing Next-Generation Sequencing-Guided Cancer Care Through Cognitive Computing. <i>Oncologist</i> , 2018, 23, 179-185.	3.7	78
32	Evaluating Clinical Genome Sequence Analysis by Watson for Genomics. <i>Frontiers in Medicine</i> , 2018, 5, 305.	2.6	15
33	Efficient algorithms for polyploid haplotype phasing. <i>BMC Genomics</i> , 2018, 19, 110.	2.8	25
34	Application of Genome Wide Association and Genomic Prediction for Improvement of Cacao Productivity and Resistance to Black and Frosty Pod Diseases. <i>Frontiers in Plant Science</i> , 2017, 8, 1905.	3.6	50
35	Scalable Algorithms at Genomic Resolution to fit LD Distributions. , 2016, , .		1
36	Sampling ARG of multiple populations under complex configurations of subdivision and admixture. <i>Bioinformatics</i> , 2016, 32, 1048-1056.	4.1	4

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37	Watson for Genomics: Moving Personalized Medicine Forward. Trends in Cancer, 2016, 2, 392-395.	7.4	23
38	Characterizing redescrptions using persistent homology to isolate genetic pathways contributing to pathogenesis. BMC Systems Biology, 2016, 10, 10.	3.0	6
39	Variable-Selection Emerges on Top in Empirical Comparison of Whole-Genome Complex-Trait Prediction Methods. PLoS ONE, 2015, 10, e0138903.	2.5	15
40	SimBA: simulation algorithm to fit extant-population distributions. BMC Bioinformatics, 2015, 16, 82.	2.6	3
41	Topological Signatures for Population Admixture. Lecture Notes in Computer Science, 2015, , 261-275.	1.3	3
42	Effect of sampling on the extent and accuracy of the inferred genetic history of recombining genome. Computational Biology and Chemistry, 2014, 50, 68-74.	2.3	0
43	Irredundant tandem motifs. Theoretical Computer Science, 2014, 525, 89-102.	0.9	14
44	Comparative exomics of Phalariscultivars under salt stress. BMC Genomics, 2014, 15, S18.	2.8	13
45	Using Random Graphs in Population Genomics. Lecture Notes in Computer Science, 2013, , 340-341.	1.3	0
46	iXora: exact haplotype inferencing and trait association. BMC Genetics, 2013, 14, 48.	2.7	23
47	Sum of parts is greater than the whole: inference of common genetic history of populations. BMC Genomics, 2013, 14, S10.	2.8	5
48	IPED: Inheritance Path-based Pedigree Reconstruction Algorithm Using Genotype Data. Journal of Computational Biology, 2013, 20, 780-791.	1.6	13
49	Efficient in silico Chromosomal Representation of Populations via Indexing Ancestral Genomes. Algorithms, 2013, 6, 430-441.	2.1	5
50	Genetic History of Populations: Limits to Inference. Computational Biology, 2013, , 309-323.	0.2	0
51	Recombination Gives a New Insight in the Effective Population Size and the History of the Old World Human Populations. Molecular Biology and Evolution, 2012, 29, 25-30.	8.9	31
52	Discovering Patterns in Gene Order. Methods in Molecular Biology, 2012, 855, 431-455.	0.9	0
53	Nonredundant Representation of Ancestral Recombinations Graphs. Methods in Molecular Biology, 2012, 856, 315-332.	0.9	3
54	ARG-based genome-wide analysis of cacao cultivars. BMC Bioinformatics, 2012, 13, S17.	2.6	8

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55	Recombination networks as genetic markers in a human variation study of the Old World. <i>Human Genetics</i> , 2012, 131, 601-613.	3.8	7
56	Population Differentiation of Southern Indian Male Lineages Correlates with Agricultural Expansions Predating the Caste System. <i>PLoS ONE</i> , 2012, 7, e50269.	2.5	40
57	Evaluation of Methods for De Novo Genome Assembly from High-Throughput Sequencing Reads Reveals Dependencies That Affect the Quality of the Results. <i>PLoS ONE</i> , 2011, 6, e24182.	2.5	29
58	A minimal descriptor of an ancestral recombinations graph. <i>BMC Bioinformatics</i> , 2011, 12, S6.	2.6	7
59	IRiS: Construction of ARG networks at genomic scales. <i>Bioinformatics</i> , 2011, 27, 2448-2450.	4.1	14
60	APBC 2010. The Eighth Asia Pacific Bioinformatics Conference Bangalore, India, 18-21 January 2010. <i>BMC Bioinformatics</i> , 2010, 11, 11.	2.6	0
61	Ancestral Recombinations Graph: A Reconstructability Perspective Using Random-Graphs Framework. <i>Journal of Computational Biology</i> , 2010, 17, 1345-1370.	1.6	14
62	A New Method to Reconstruct Recombination Events at a Genomic Scale. <i>PLoS Computational Biology</i> , 2010, 6, e1001010.	3.2	14
63	Graph Model of Coalescence with Recombinations. , 2010, , 85-100.		4
64	Combinatorics in Recombinational Population Genomics. <i>Lecture Notes in Computer Science</i> , 2010, , 126-127.	1.3	0
65	Minimizing recombinations in consensus networks for phylogeographic studies. <i>BMC Bioinformatics</i> , 2009, 10, S72.	2.6	12
66	Detection of subtle variations as consensus motifs. <i>Theoretical Computer Science</i> , 2008, 395, 158-170.	0.9	13
67	Estimating the Ancestral Recombinations Graph (ARG) as Compatible Networks of SNP Patterns. <i>Journal of Computational Biology</i> , 2008, 15, 1133-1153.	1.6	27
68	Discovering Topological Motifs Using a Compact Notation. <i>Journal of Computational Biology</i> , 2007, 14, 300-323.	1.6	22
69	Gapped Permutation Pattern Discovery for Gene Order Comparisons. <i>Journal of Computational Biology</i> , 2007, 14, 45-55.	1.6	5
70	Statistical Significance of Large Gene Clusters. <i>Journal of Computational Biology</i> , 2007, 14, 1145-1159.	1.6	4
71	SUBTLE MOTIF DISCOVERY FOR DETECTION OF DNA REGULATORY SITES. , 2007, , .		7
72	Using PQ Structures for Genomic Rearrangement Phylogeny. <i>Journal of Computational Biology</i> , 2006, 13, 1685-1700.	1.6	6

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73	Gapped Permutation Patterns for Comparative Genomics. Lecture Notes in Computer Science, 2006, , 376-387.	1.3	8
74	Bridging Lossy and Lossless Compression by Motif Pattern Discovery. Electronic Notes in Discrete Mathematics, 2005, 21, 219-225.	0.4	5
75	An inexact-suffix-tree-based algorithm for detecting extensible patterns. Theoretical Computer Science, 2005, 335, 3-14.	0.9	13
76	Malware phylogeny generation using permutations of code. Journal in Computer Virology, 2005, 1, 13-23.	1.9	155
77	Conservative extraction of over-represented extensible motifs. Bioinformatics, 2005, 21, i9-i18.	4.1	20
78	Gene Proximity Analysis across Whole Genomes via PQ Trees1. Journal of Computational Biology, 2005, 12, 1289-1306.	1.6	30
79	Using PQ Trees for Comparative Genomics. Lecture Notes in Computer Science, 2005, , 128-143.	1.3	17
80	Combinatorial Pattern Discovery Approach for the Folding Trajectory Analysis of a $\hat{1}^2$ -Hairpin. PLoS Computational Biology, 2005, 1, e8.	3.2	4
81	Incremental Paradigms of Motif Discovery. Journal of Computational Biology, 2004, 11, 15-25.	1.6	58
82	Permutation Pattern Discovery in Biosequences. Journal of Computational Biology, 2004, 11, 1050-1060.	1.6	26
83	The web server of IBM's Bioinformatics and Pattern Discovery group. Nucleic Acids Research, 2003, 31, 3645-3650.	14.5	4
84	In Silico Pattern-Based Analysis of the Human Cytomegalovirus Genome. Journal of Virology, 2003, 77, 4326-4344.	3.4	54
85	Dictionary-driven protein annotation. Nucleic Acids Research, 2002, 30, 3901-3916.	14.5	24
86	The Emergence of Pattern Discovery Techniques in Computational Biology. Metabolic Engineering, 2000, 2, 159-177.	7.0	71
87	Partitioning single-molecule maps into multiple populations: algorithms and probabilistic analysis. Discrete Applied Mathematics, 2000, 104, 203-227.	0.9	4
88	Some Results on Flexible-Pattern Discovery. Lecture Notes in Computer Science, 2000, , 33-45.	1.3	6
89	An Approximation Algorithm for Alignment of Multiple Sequences using Motif Discovery. Journal of Combinatorial Optimization, 1999, 3, 247-275.	1.3	16
90	Dictionary building via unsupervised hierarchical motif discovery in the sequence space of natural proteins. , 1999, 37, 264-277.		45

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91	A Uniform Framework for Ordered Restriction Map Problems. Journal of Computational Biology, 1998, 5, 725-739.	1.6	2
92	Computational methods for evaluating swept object boundaries. Visual Computer, 1994, 10, 266-276.	3.5	16
93	A computational technique for general shape deformations for use in font design. Computers and Graphics, 1993, 17, 349-356.	2.5	1
94	A closed form solution to the problem of tangential circles, lines, points with extension to 3D. Computers and Graphics, 1991, 15, 49-55.	2.5	1