

Fabio Vandin

List of Publications by Year in descending order

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Version: 2024-02-01

52
papers

15,013
citations

393982

19
h-index

288905

40
g-index

54
all docs

54
docs citations

54
times ranked

26239
citing authors

#	ARTICLE	IF	CITATIONS
1	The Impact of Global Structural Information in Graph Neural Networks Applications. <i>Data</i> , 2022, 7, 10.	1.2	2
2	MCRapper: Monte-Carlo Rademacher Averages for Poset Families and Approximate Pattern Mining. <i>ACM Transactions on Knowledge Discovery From Data</i> , 2022, 16, 1-29.	2.5	3
3	SPRISS: approximating frequent <i>k</i> -mers by sampling reads, and applications. <i>Bioinformatics</i> , 2022, 38, 3343-3350.	1.8	2
4	Comparison of microbiome samples: methods and computational challenges. <i>Briefings in Bioinformatics</i> , 2021, 22, 88-95.	3.2	17
5	Attention-Based Deep Learning Framework for Human Activity Recognition With User Adaptation. <i>IEEE Sensors Journal</i> , 2021, 21, 13474-13483.	2.4	30
6	CASPITA: Mining Statistically Significant Paths in Time Series Data from an Unknown Network. , 2021, , .		2
7	Fast Approximation of Frequent <i>k</i> -Mers and Applications to Metagenomics. <i>Journal of Computational Biology</i> , 2020, 27, 534-549.	0.8	5
8	Identifying Drug Sensitivity Subnetworks with NETPHIX. <i>IScience</i> , 2020, 23, 101619.	1.9	5
9	Efficient mining of the most significant patterns with permutation testing. <i>Data Mining and Knowledge Discovery</i> , 2020, 34, 1201-1234.	2.4	15
10	Mining Sequential Patterns with VC-Dimension and Rademacher Complexity. <i>Algorithms</i> , 2020, 13, 123.	1.2	8
11	MCRapper: Monte-Carlo Rademacher Averages for Poset Families and Approximate Pattern Mining. , 2020, , .		7
12	gRosSo: Mining Statistically Robust Patterns from a Sequence of Datasets. , 2020, , .		1
13	Enriched power of disease-concordant twin-case-only design in detecting interactions in genome-wide association studies. <i>European Journal of Human Genetics</i> , 2019, 27, 631-636.	1.4	4
14	SPuManTE. , 2019, , .		19
15	Hypothesis Testing and Statistically-sound Pattern Mining. , 2019, , .		16
16	NoMAS: A Computational Approach to Find Mutated Subnetworks Associated With Survival in Genome-Wide Cancer Studies. <i>Frontiers in Genetics</i> , 2019, 10, 265.	1.1	8
17	CoExpresso: assess the quantitative behavior of protein complexes in human cells. <i>BMC Bioinformatics</i> , 2019, 20, 17.	1.2	9
18	Efficient algorithms to discover alterations with complementary functional association in cancer. <i>PLoS Computational Biology</i> , 2019, 15, e1006802.	1.5	9

#	ARTICLE	IF	CITATIONS
19	Differentially mutated subnetworks discovery. <i>Algorithms for Molecular Biology</i> , 2019, 14, 10.	0.3	7
20	Permutation Strategies for Mining Significant Sequential Patterns. , 2019, , .		14
21	Principles of Systems Biology, No. 31. <i>Cell Systems</i> , 2018, 7, 133-135.	2.9	0
22	Efficient Mining of the Most Significant Patterns with Permutation Testing. , 2018, , .		15
23	Efficient detection of differentially methylated regions using DiMmeR. <i>Bioinformatics</i> , 2017, 33, 549-551.	1.8	9
24	Diseaseâ€Concordant Twins Empower Genetic Association Studies. <i>Annals of Human Genetics</i> , 2017, 81, 20-26.	0.3	46
25	De novo pathway-based biomarker identification. <i>Nucleic Acids Research</i> , 2017, 45, e151-e151.	6.5	48
26	HIT'nDRIVE: patient-specific multidriver gene prioritization for precision oncology. <i>Genome Research</i> , 2017, 27, 1573-1588.	2.4	78
27	Clustering uncertain graphs. <i>Proceedings of the VLDB Endowment</i> , 2017, 11, 472-484.	2.1	30
28	Computational Methods for Characterizing Cancer Mutational Heterogeneity. <i>Frontiers in Genetics</i> , 2017, 8, 83.	1.1	27
29	Differentially Methylated Genomic Regions in Birthâ€Weight Discordant Twin Pairs. <i>Annals of Human Genetics</i> , 2016, 80, 81-87.	0.3	19
30	Illumina - A comprehensive Java-based API for statistical Illumina Infinium HumanMethylation450 and Infinium MethylationEPIC BeadChip data processing. <i>Journal of Integrative Bioinformatics</i> , 2016, 13, 24-32.	1.0	2
31	Reply: Co-occurrence of MYC amplification and TP53 mutations in human cancer. <i>Nature Genetics</i> , 2016, 48, 106-108.	9.4	2
32	On the Sample Complexity of Cancer Pathways Identification. <i>Journal of Computational Biology</i> , 2016, 23, 30-41.	0.8	6
33	CoMEt: a statistical approach to identify combinations of mutually exclusive alterations in cancer. <i>Genome Biology</i> , 2015, 16, 160.	3.8	182
34	Simultaneous Inference of Cancer Pathways and Tumor Progression from Cross-Sectional Mutation Data. <i>Journal of Computational Biology</i> , 2015, 22, 510-527.	0.8	28
35	Accurate Computation of Survival Statistics in Genome-Wide Studies. <i>PLoS Computational Biology</i> , 2015, 11, e1004071.	1.5	24
36	Pan-cancer network analysis identifies combinations of rare somatic mutations across pathways and protein complexes. <i>Nature Genetics</i> , 2015, 47, 106-114.	9.4	830

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37	Integrated Genomic Characterization of Papillary Thyroid Carcinoma. <i>Cell</i> , 2014, 159, 676-690.	13.5	2,318
38	Identifying driver mutations in sequenced cancer genomes: computational approaches to enable precision medicine. <i>Genome Medicine</i> , 2014, 6, 5.	3.6	186
39	Mutational landscape and significance across 12 major cancer types. <i>Nature</i> , 2013, 502, 333-339.	13.7	3,695
40	<scp>Ballast</scp>: A Ball-based Algorithm for Structural Motifs. <i>Journal of Computational Biology</i> , 2013, 20, 137-151.	0.8	4
41	Genomic and Epigenomic Landscapes of Adult De Novo Acute Myeloid Leukemia. <i>New England Journal of Medicine</i> , 2013, 368, 2059-2074.	13.9	4,139
42	Identifying significant mutations in large cohorts of cancer genomes. , 2013, , .		0
43	Workshop: Algorithms for discovery of mutated pathways in cancer. , 2012, , .		0
44	The mutational landscape of lethal castration-resistant prostate cancer. <i>Nature</i> , 2012, 487, 239-243.	13.7	2,128
45	De novo discovery of mutated driver pathways in cancer. <i>Genome Research</i> , 2012, 22, 375-385.	2.4	391
46	Algorithms and Genome Sequencing: Identifying Driver Pathways in Cancer. <i>Computer</i> , 2012, 45, 39-46.	1.2	10
47	Discovery of mutated subnetworks associated with clinical data in cancer. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2012, , 55-66.	0.7	60
48	DISCOVERY OF MUTATED SUBNETWORKS ASSOCIATED WITH CLINICAL DATA IN CANCER. , 2011, , .		59
49	Algorithms for Detecting Significantly Mutated Pathways in Cancer. <i>Journal of Computational Biology</i> , 2011, 18, 507-522.	0.8	434
50	MADMX: A Strategy for Maximal Dense Motif Extraction. <i>Journal of Computational Biology</i> , 2011, 18, 535-545.	0.8	14
51	Mining top-K frequent itemsets through progressive sampling. <i>Data Mining and Knowledge Discovery</i> , 2010, 21, 310-326.	2.4	33
52	Efficient Incremental Mining of Top-K Frequent Closed Itemsets. , 2007, , 275-280.		13