

Mehmet Koyuturk

List of Publications by Year in descending order

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Version: 2024-02-01

93
papers

2,668
citations

218677

26
h-index

206112

48
g-index

101
all docs

101
docs citations

101
times ranked

3566
citing authors

#	ARTICLE	IF	CITATIONS
1	Pairwise Alignment of Protein Interaction Networks. <i>Journal of Computational Biology</i> , 2006, 13, 182-199.	1.6	232
2	Comparative analysis of algorithms for next-generation sequencing read alignment. <i>Bioinformatics</i> , 2011, 27, 2790-2796.	4.1	195
3	The KSEA App: a web-based tool for kinase activity inference from quantitative phosphoproteomics. <i>Bioinformatics</i> , 2017, 33, 3489-3491.	4.1	181
4	DA DA: Degree-Aware Algorithms for Network-Based Disease Gene Prioritization. <i>BioData Mining</i> , 2011, 4, 19.	4.0	148
5	An efficient algorithm for detecting frequent subgraphs in biological networks. <i>Bioinformatics</i> , 2004, 20, i200-i207.	4.1	141
6	An Integrative -omics Approach to Identify Functional Sub-Networks in Human Colorectal Cancer. <i>PLoS Computational Biology</i> , 2010, 6, e1000639.	3.2	140
7	Proteinâ€protein interaction networks and subnetworks in the biology of disease. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2011, 3, 357-367.	6.6	79
8	Detecting Conserved Interaction Patterns in Biological Networks. <i>Journal of Computational Biology</i> , 2006, 13, 1299-1322.	1.6	71
9	Network Signatures of Survival in Glioblastoma Multiforme. <i>PLoS Computational Biology</i> , 2013, 9, e1003237.	3.2	71
10	V<scp>avien</scp>: An Algorithm for Prioritizing Candidate Disease Genes Based on Topological Similarity of Proteins in Interaction Networks. <i>Journal of Computational Biology</i> , 2011, 18, 1561-1574.	1.6	70
11	Drug Response Prediction as a Link Prediction Problem. <i>Scientific Reports</i> , 2017, 7, 40321.	3.3	64
12	Subnetwork State Functions Define Dysregulated Subnetworks in Cancer. <i>Journal of Computational Biology</i> , 2011, 18, 263-281.	1.6	63
13	Network-Based Integration of Disparate Omic Data To Identify "Silent Players" in Cancer. <i>PLoS Computational Biology</i> , 2015, 11, e1004595.	3.2	60
14	Network biology methods integrating biological data for translational science. <i>Briefings in Bioinformatics</i> , 2012, 13, 446-459.	6.5	57
15	Assessing Significance of Connectivity and Conservation in Protein Interaction Networks. <i>Journal of Computational Biology</i> , 2007, 14, 747-764.	1.6	52
16	Gene interaction enrichment and network analysis to identify dysregulated pathways and their interactions in complex diseases. <i>BMC Systems Biology</i> , 2012, 6, 65.	3.0	47
17	Mining Electronic Health Records Data: Domestic Violence and Adverse Health Effects. <i>Journal of Family Violence</i> , 2017, 32, 79-87.	3.3	44
18	Gene, pathway and network frameworks to identify epistatic interactions of single nucleotide polymorphisms derived from GWAS data. <i>BMC Systems Biology</i> , 2012, 6, S15.	3.0	41

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19	Efficient tag detection in RFID systems. Journal of Parallel and Distributed Computing, 2009, 69, 180-196.	4.1	40
20	IDENTIFICATION OF COORDINATELY DYSREGULATED SUBNETWORKS IN COMPLEX PHENOTYPES. , 2009, , 133-144.		37
21	Robust inference of kinase activity using functional networks. Nature Communications, 2021, 12, 1177.	12.8	36
22	Generalized and Mechanistic PV Module Performance Prediction From Computer Vision and Machine Learning on Electroluminescence Images. IEEE Journal of Photovoltaics, 2020, 10, 878-887.	2.5	35
23	Visually Meaningful Histopathological Features for Automatic Grading of Prostate Cancer. IEEE Journal of Biomedical and Health Informatics, 2017, 21, 1027-1038.	6.3	33
24	Phylogenetic analysis of modularity in protein interaction networks. BMC Bioinformatics, 2009, 10, 333.	2.6	31
25	Disease gene prioritization by integrating tissue-specific molecular networks using a robust multi-network model. BMC Bioinformatics, 2016, 17, 453.	2.6	31
26	Node similarity-based graph convolution for link prediction in biological networks. Bioinformatics, 2021, 37, 4501-4508.	4.1	31
27	Nonorthogonal decomposition of binary matrices for bounded-error data compression and analysis. ACM Transactions on Mathematical Software, 2006, 32, 33-69.	2.9	30
28	CoPhosK: A method for comprehensive kinase substrate annotation using co-phosphorylation analysis. PLoS Computational Biology, 2019, 15, e1006678.	3.2	30
29	Accurate estimation of short read mapping quality for next-generation genome sequencing. Bioinformatics, 2012, 28, i349-i355.	4.1	29
30	PROXIMUS. , 2003, , .		28
31	Functional coherence in domain interaction networks. Bioinformatics, 2008, 24, i28-i34.	4.1	28
32	Algorithmic and analytical methods in network biology. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2010, 2, 277-292.	6.6	28
33	Inferring functional information from domain co-evolution. Bioinformatics, 2006, 22, 40-49.	4.1	26
34	SYSTEMS BIOLOGY ANALYSES OF GENE EXPRESSION AND GENOME WIDE ASSOCIATION STUDY DATA IN OBSTRUCTIVE SLEEP APNEA. , 2010, , 14-25.		25
35	Discovery of common sequences absent in the human reference genome using pooled samples from next generation sequencing. BMC Genomics, 2014, 15, 685.	2.8	24
36	Iterative-improvement-based declustering heuristics for multi-disk databases. Information Systems, 2005, 30, 47-70.	3.6	22

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37	An optimization framework for unsupervised identification of rare copy number variation from SNP array data. <i>Genome Biology</i> , 2009, 10, R119.	9.6	22
38	Phosphoproteomics Profiling of Nonsmall Cell Lung Cancer Cells Treated with a Novel Phosphatase Activator. <i>Proteomics</i> , 2017, 17, 1700214.	2.2	21
39	Weighted Matrix Ordering and Parallel Banded Preconditioners for Iterative Linear System Solvers. <i>SIAM Journal of Scientific Computing</i> , 2010, 32, 1201-1216.	2.8	19
40	Efficient Processing of Network Proximity Queries via Chebyshev Acceleration. , 2016, , .		18
41	Functional annotation of regulatory pathways. <i>Bioinformatics</i> , 2007, 23, i377-i386.	4.1	17
42	PHALANX. , 2008, , .		17
43	MOBAS: identification of disease-associated protein subnetworks using modularity-based scoring. <i>Eurasip Journal on Bioinformatics and Systems Biology</i> , 2015, 2015, 7.	1.4	17
44	Prioritizing tests of epistasis through hierarchical representation of genomic redundancies. <i>Nucleic Acids Research</i> , 2017, 45, e131-e131.	14.5	15
45	Efficiently Enumerating All Connected Induced Subgraphs of a Large Molecular Network. <i>Lecture Notes in Computer Science</i> , 2014, , 171-182.	1.3	15
46	Functional characterization and topological modularity of molecular interaction networks. <i>BMC Bioinformatics</i> , 2010, 11, S35.	2.6	13
47	Using Protein Interaction Networks to Understand Complex Diseases. <i>Computer</i> , 2012, 45, 31-38.	1.1	13
48	Circulating microbial content in myeloid malignancy patients is associated with disease subtypes and patient outcomes. <i>Nature Communications</i> , 2022, 13, 1038.	12.8	13
49	Link Prediction in Large Networks by Comparing the Global View of Nodes in the Network. , 2015, , .		11
50	Emotion -and area-driven topic shift analysis in social media discussions. , 2016, , .		10
51	Whole-exome sequencing enhances prognostic classification of myeloid malignancies. <i>Journal of Biomedical Informatics</i> , 2015, 58, 104-113.	4.3	9
52	Interplay between traumatic brain injury and intimate partner violence: data driven analysis utilizing electronic health records. <i>BMC Women's Health</i> , 2020, 20, 269.	2.0	9
53	DB2: a probabilistic approach for accurate detection of tandem duplication breakpoints using paired-end reads. <i>BMC Genomics</i> , 2014, 15, 175.	2.8	7
54	Linearity of network proximity measures: implications for set-based queries and significance testing. <i>Bioinformatics</i> , 2017, 33, 1354-1361.	4.1	7

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55	NETWORK MAP OF ADVERSE HEALTH EFFECTS AMONG VICTIMS OF INTIMATE PARTNER VIOLENCE. , 2017, 22, 324-335.		7
56	Co-phosphorylation networks reveal subtype-specific signaling modules in breast cancer. Bioinformatics, 2021, 37, 221-228.	4.1	7
57	Identifying stage-specific protein subnetworks for colorectal cancer. BMC Proceedings, 2012, 6, S1.	1.6	6
58	Subnetwork State Functions Define Dysregulated Subnetworks in Cancer. Lecture Notes in Computer Science, 2010, , 80-95.	1.3	6
59	Semantic indexing in structured peer-to-peer networks. Journal of Parallel and Distributed Computing, 2008, 68, 64-77.	4.1	5
60	Prioritization of genomic locus pairs for testing epistasis. , 2014, , .		5
61	Co-occurrence Patterns of Intimate Partner Violence. , 2020, , .		5
62	Identification of intimate partner violence from free text descriptions in social media. Journal of Computational Social Science, 2022, 5, 1207-1233.	2.4	5
63	Functional characterization of co-phosphorylation networks. Bioinformatics, 2022, 38, 3785-3793.	4.1	5
64	Disease Gene Prioritization Based on Topological Similarity in Protein-Protein Interaction Networks. Lecture Notes in Computer Science, 2011, , 54-68.	1.3	4
65	Suffix-Tree Based Error Correction of NGS Reads Using Multiple Manifestations of an Error. , 2013, , .		4
66	Integrated querying and version control of context-specific biological networks. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	3.0	4
67	PoCos: Population Covering Locus Sets for Risk Assessment in Complex Diseases. PLoS Computational Biology, 2016, 12, e1005195.	3.2	4
68	Data-driven identification of subtypes of intimate partner violence. Scientific Reports, 2021, 11, 6736.	3.3	3
69	Network-based approaches for extending the Wnt signalling pathway and identifying context-specific sub-networks. International Journal of Computational Biology and Drug Design, 2012, 5, 185.	0.3	2
70	Comprehensive Evaluation of Composite Gene Features in Cancer Outcome Prediction. Cancer Informatics, 2014, 13s3, CIN.S14028.	1.9	2
71	Assessing the collective disease association of multiple genomic loci. , 2015, , .		2
72	Integrated querying of disparate association and interaction data in biomedical applications. , 2015, , .		2

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73	Effects of emotion and topic area on topic shifts in social media discussions. <i>Social Network Analysis and Mining</i> , 2017, 7, 1.	2.8	2
74	Pluribusâ€”Exploring the Limits of Error Correction Using a Suffix Tree. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017, 14, 1378-1388.	3.0	2
75	Querying of Disparate Association and Interaction Data in Biomedical Applications. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 1052-1065.	3.0	2
76	Cross-population analysis for functional characterization of type II diabetes variants. <i>BMC Bioinformatics</i> , 2019, 20, 320.	2.6	2
77	Identifying health correlates of intimate partner violence against pregnant women. <i>Health Information Science and Systems</i> , 2020, 8, 36.	5.2	2
78	Fast computation of Katz index for efficient processing of link prediction queries. <i>Data Mining and Knowledge Discovery</i> , 2021, 35, 1342-1368.	3.7	2
79	CONQUEST: A Coarse-Grained Algorithm for Constructing Summaries of Distributed Discrete Datasets. <i>Algorithmica</i> , 2006, 45, 377-401.	1.3	1
80	Algorithms for detecting complementary SNPs within a region of interest that are associated with diseases. , 2012, , .		1
81	Introduction to Network Biology. , 2012, , 1-13.		1
82	Uncovering complementary sets of variants for predicting quantitative phenotypes. <i>Bioinformatics</i> , 2022, 38, 908-917.	4.1	1
83	Protein Biomarkers in Monocytes and CD4 Lymphocytes for Predicting Lithium Treatment Response of Bipolar Disorder: a Feasibility Study with Tyramine-Based Signal-Amplified Flow Cytometry.. <i>Psychopharmacology Bulletin</i> , 2022, 52, 8-35.	0.0	1
84	Consensus embedding for multiple networks: Computation and applications. <i>Network Science</i> , 0, , 1-17.	1.0	1
85	Comparative Analysis of Modularity in Biological Systems. , 2009, , .		0
86	Guest Editorial for Special Section on BLOKDD. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013, 10, 1199-1200.	3.0	0
87	Sets Visualization using their Graph Representation. , 2015, , .		0
88	Characterizing human genomic coevolution in locus-gene regulatory interactions. <i>BioData Mining</i> , 2019, 12, 8.	4.0	0
89	ANNOTATING PATHWAYS IN INTERACTION NETWORKS. , 2007, , .		0
90	Optimization Algorithms for Identification and Genotyping of Copy Number Polymorphisms in Human Populations. <i>Lecture Notes in Computer Science</i> , 2010, , 74-85.	1.3	0

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91	Identification of Modules in Protein-Protein Interaction Networks. , 2010, , 253-267.		0
92	Molecular Networks and Complex Diseases. , 2012, , 171-199.		0
93	Omics and Biomarkers Development for Intestinal Tumorigenesis. , 2015, , 365-389.		0