

Tijana Milenkovic

List of Publications by Year in descending order

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Version: 2024-02-01

79
papers

3,171
citations

236925

25
h-index

155660

55
g-index

81
all docs

81
docs citations

81
times ranked

3416
citing authors

#	ARTICLE	IF	CITATIONS
1	Evidence for Network Evolution in an <i>Arabidopsis</i> Interactome Map. <i>Science</i> , 2011, 333, 601-607.	12.6	838
2	Topological network alignment uncovers biological function and phylogeny. <i>Journal of the Royal Society Interface</i> , 2010, 7, 1341-1354.	3.4	281
3	Uncovering Biological Network Function via Graphlet Degree Signatures. <i>Cancer Informatics</i> , 2008, 6, CIN.S680.	1.9	200
4	MAGNA: Maximizing Accuracy in Global Network Alignment. <i>Bioinformatics</i> , 2014, 30, 2931-2940.	4.1	154
5	Optimal Network Alignment with Graphlet Degree Vectors. <i>Cancer Informatics</i> , 2010, 9, CIN.S4744.	1.9	149
6	Characterization of the proteasome interaction network using a QTAX-based tag-team strategy and protein interaction network analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 13333-13338.	7.1	129
7	Uncovering biological network function via graphlet degree signatures. <i>Cancer Informatics</i> , 2008, 6, 257-73.	1.9	96
8	Systems-level cancer gene identification from protein interaction network topology applied to melanogenesis-related functional genomics data. <i>Journal of the Royal Society Interface</i> , 2010, 7, 423-437.	3.4	95
9	GraphCrunch: A tool for large network analyses. <i>BMC Bioinformatics</i> , 2008, 9, 70.	2.6	93
10	Dominating Biological Networks. <i>PLoS ONE</i> , 2011, 6, e23016.	2.5	85
11	Dynamic networks reveal key players in aging. <i>Bioinformatics</i> , 2014, 30, 1721-1729.	4.1	80
12	Survey of local and global biological network alignment: the need to reconcile the two sides of the same coin. <i>Briefings in Bioinformatics</i> , 2018, 19, bbw132.	6.5	69
13	The post-genomic era of biological network alignment. <i>Eurasip Journal on Bioinformatics and Systems Biology</i> , 2015, 2015, 3.	1.4	60
14	Local versus global biological network alignment. <i>Bioinformatics</i> , 2016, 32, 3155-3164.	4.1	56
15	Characterization of Cell Cycle Specific Protein Interaction Networks of the Yeast 26S Proteasome Complex by the QTAX Strategy. <i>Journal of Proteome Research</i> , 2010, 9, 2016-2029.	3.7	51
16	Proper evaluation of alignment-free network comparison methods. <i>Bioinformatics</i> , 2015, 31, 2697-2704.	4.1	46
17	Global Network Alignment in the Context of Aging. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2015, 12, 40-52.	3.0	46
18	Revealing Missing Parts of the Interactome via Link Prediction. <i>PLoS ONE</i> , 2014, 9, e90073.	2.5	42

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19	Simultaneous Optimization of both Node and Edge Conservation in Network Alignment via WAVE. Lecture Notes in Computer Science, 2015, , 16-39.	1.3	39
20	Multiple network alignment via multiMAGNA++. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 1-1.	3.0	36
21	Optimized Null Model for Protein Structure Networks. PLoS ONE, 2009, 4, e5967.	2.5	34
22	Protein interaction network topology uncovers melanogenesis regulatory network components within functional genomics datasets. BMC Systems Biology, 2010, 4, 84.	3.0	32
23	Modeling multi-scale data via a network of networks. Bioinformatics, 2022, 38, 2544-2553.	4.1	30
24	From homogeneous to heterogeneous network alignment via colored graphlets. Scientific Reports, 2018, 8, 12524.	3.3	28
25	On the Interplay Between Individualsâ€™ Evolving Interaction Patterns and Traits in Dynamic Multiplex Social Networks. IEEE Transactions on Network Science and Engineering, 2016, 3, 32-43.	6.4	25
26	Genome-wide profiling of 24Âhr diel rhythmicity in the water flea, Daphnia pulex: network analysis reveals rhythmic gene expression and enhances functional gene annotation. BMC Genomics, 2016, 17, 653.	2.8	22
27	GRAFENE: Graphlet-based alignment-free network approach integrates 3D structural and sequence (residue order) data to improve protein structural comparison. Scientific Reports, 2017, 7, 14890.	3.3	21
28	Complementarity of network and sequence information in homologous proteins. Journal of Integrative Bioinformatics, 2010, 7, 275-289.	1.5	20
29	Temporal network alignment via GoT-WAVE. Bioinformatics, 2019, 35, 3527-3529.	4.1	19
30	Global Network Alignment In The Context Of Aging. , 2013, , .		18
31	Fair evaluation of global network aligners. Algorithms for Molecular Biology, 2015, 10, 19.	1.2	18
32	GREAT: GRaphlet Edge-based network AlignmenT. , 2015, , .		18
33	L-HetNetAligner: A novel algorithm for Local Alignment of Heterogeneous Biological Networks. Scientific Reports, 2020, 10, 3901.	3.3	18
34	Complementarity of network and sequence information in homologous proteins. Journal of Integrative Bioinformatics, 2010, 7, .	1.5	17
35	Aligning dynamic networks with DynaWAVE. Bioinformatics, 2018, 34, 1795-1798.	4.1	15
36	An integrative approach to modeling biological networks. Journal of Integrative Bioinformatics, 2010, 7, .	1.5	14

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37	ClueNet: Clustering a temporal network based on topological similarity rather than denseness. PLoS ONE, 2018, 13, e0195993.	2.5	12
38	SCOUT: simultaneous time segmentation and community detection in dynamic networks. Scientific Reports, 2016, 6, 37557.	3.3	11
39	Data-driven network alignment. PLoS ONE, 2020, 15, e0234978.	2.5	11
40	Network analysis of the NetHealth data: exploring co-evolution of individuals' social network positions and physical activities. Applied Network Science, 2018, 3, 45.	1.5	10
41	Systematic Dynamic and Heterogeneous Analysis of Rich Social Network Data. Studies in Computational Intelligence, 2014, , 25-37.	0.9	10
42	Network-based protein structural classification. Royal Society Open Science, 2020, 7, 191461.	2.4	9
43	Analysis of computational codon usage models and their association with translationally slow codons. PLoS ONE, 2020, 15, e0232003.	2.5	9
44	<scp>CHARMING</scp>: Harmonizing synonymous codon usage to replicate a desired codon usage pattern. Protein Science, 2022, 31, 221-231.	7.6	8
45	An integrative approach to modeling biological networks. Journal of Integrative Bioinformatics, 2010, 7, .	1.5	8
46	Topological network alignment uncovers biological function and phylogeny. Nature Precedings, 2009, , .	0.1	7
47	Pairwise Versus Multiple Global Network Alignment. IEEE Access, 2020, 8, 41961-41974.	4.2	7
48	Network analysis of synonymous codon usage. Bioinformatics, 2020, 36, 4876-4884.	4.1	6
49	Supervised Prediction of Aging-Related Genes From a Context-Specific Protein Interaction Subnetwork. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 2484-2498.	3.0	6
50	Improved supervised prediction of aging-related genes via weighted dynamic network analysis. BMC Bioinformatics, 2021, 22, 520.	2.6	6
51	Networks' characteristics are important for systems biology. Network Science, 2014, 2, 139-161.	1.0	5
52	Improving Identification of Key Players in Aging via Network De-Noiseing and Core Inference. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 1056-1069.	3.0	5
53	Heterogeneous Network Approach to Predict Individuals' Mental Health. ACM Transactions on Knowledge Discovery From Data, 2021, 15, 1-26.	3.5	5
54	Topological Characteristics of Molecular Networks. , 2012, , 15-48.		5

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55	Computational Methods for Analyzing and Modeling Biological Networks. Chapman & Hall/CRC Data Mining and Knowledge Discovery Series, 2009, , 397-427.	0.2	5
56	Network Analysis Improves Interpretation of Affective Physiological Data. , 2013, , .		4
57	Supervised prediction of aging-related genes from a context-specific protein interaction subnetwork. , 2019, , .		4
58	Inference of a Dynamic Aging-related Biological Subnetwork via Network Propagation. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, PP, 1-1.	3.0	4
59	Improving identification of key players in aging via network de-noising. , 2014, , .		3
60	Data-driven biological network alignment that uses topological, sequence, and functional information. BMC Bioinformatics, 2021, 22, 34.	2.6	3
61	The power of dynamic social networks to predict individuals' mental health. , 2019, , .		3
62	Using Global Network Alignment In The Context Of Aging. , 2013, , .		2
63	Fair evaluation of global network aligners. , 2015, , .		2
64	Multi-layer sequential network analysis improves protein 3D structural classification. Proteins: Structure, Function and Bioinformatics, 2022, 90, 1721-1731.	2.6	2
65	Dynamic networks reveal key players in aging. , 2013, , .		1
66	Fair evaluation of global network aligners. , 2015, , .		1
67	Rebuttal to the Letter to the Editor in response to the paper: proper evaluation of alignment-free network comparison methods. Bioinformatics, 2017, 33, 1107-1109.	4.1	1
68	The power of dynamic social networks to predict individuals' mental health. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2020, 25, 635-646.	0.7	1
69	Pairwise Versus Multiple Global Network Alignment. , 2020, , .		1
70	Great Lakes Bioinformatics Conference (GLBIO) 2015 Special Section Editorial. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 1229-1230.	3.0	0
71	Aligning Dynamic Networks with DynaWAVE. , 2018, , .		0
72	Analysis of computational codon usage models and their association with translationally slow codons. , 2020, 15, e0232003.		0

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73	Analysis of computational codon usage models and their association with translationally slow codons. , 2020, 15, e0232003.		0
74	Analysis of computational codon usage models and their association with translationally slow codons. , 2020, 15, e0232003.		0
75	Analysis of computational codon usage models and their association with translationally slow codons. , 2020, 15, e0232003.		0
76	Data-driven network alignment. , 2020, 15, e0234978.		0
77	Data-driven network alignment. , 2020, 15, e0234978.		0
78	Data-driven network alignment. , 2020, 15, e0234978.		0
79	Data-driven network alignment. , 2020, 15, e0234978.		0