

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	Supervised Prediction of Aging-Related Genes From a Context-Specific Protein Interaction Subnetwork. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, 19, 2484-2498.	3.0	6
2	<scp>CHARMING</scp>: Harmonizing synonymous codon usage to replicate a desired codon usage pattern. <i>Protein Science</i> , 2022, 31, 221-231.	7.6	8
3	Modeling multi-scale data via a network of networks. <i>Bioinformatics</i> , 2022, 38, 2544-2553.	4.1	30
4	Multi-layer sequential network analysis improves protein <scp>3D</scp> structural classification. <i>Proteins: Structure, Function and Bioinformatics</i> , 2022, 90, 1721-1731.	2.6	2
5	Data-driven biological network alignment that uses topological, sequence, and functional information. <i>BMC Bioinformatics</i> , 2021, 22, 34.	2.6	3
6	Heterogeneous Network Approach to Predict Individuals' Mental Health. <i>ACM Transactions on Knowledge Discovery From Data</i> , 2021, 15, 1-26.	3.5	5
7	Improved supervised prediction of aging-related genes via weighted dynamic network analysis. <i>BMC Bioinformatics</i> , 2021, 22, 520.	2.6	6
8	Network-based protein structural classification. <i>Royal Society Open Science</i> , 2020, 7, 191461.	2.4	9
9	Inference of a Dynamic Aging-related Biological Subnetwork via Network Propagation. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, PP, 1-1.	3.0	4
10	Analysis of computational codon usage models and their association with translationally slow codons. <i>PLoS ONE</i> , 2020, 15, e0232003.	2.5	9
11	Pairwise Versus Multiple Global Network Alignment. <i>IEEE Access</i> , 2020, 8, 41961-41974.	4.2	7
12	L-HetNetAligner: A novel algorithm for Local Alignment of Heterogeneous Biological Networks. <i>Scientific Reports</i> , 2020, 10, 3901.	3.3	18
13	Network analysis of synonymous codon usage. <i>Bioinformatics</i> , 2020, 36, 4876-4884.	4.1	6
14	Data-driven network alignment. <i>PLoS ONE</i> , 2020, 15, e0234978.	2.5	11
15	The power of dynamic social networks to predict individuals' mental health. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2020, 25, 635-646.	0.7	1
16	Pairwise Versus Multiple Global Network Alignment. , 2020, , .		1
17	Analysis of computational codon usage models and their association with translationally slow codons. , 2020, 15, e0232003.		0
18	Analysis of computational codon usage models and their association with translationally slow codons. , 2020, 15, e0232003.		0

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19	Analysis of computational codon usage models and their association with translationally slow codons. , 2020, 15, e0232003.		0
20	Analysis of computational codon usage models and their association with translationally slow codons. , 2020, 15, e0232003.		0
21	Data-driven network alignment. , 2020, 15, e0234978.		0
22	Data-driven network alignment. , 2020, 15, e0234978.		0
23	Data-driven network alignment. , 2020, 15, e0234978.		0
24	Data-driven network alignment. , 2020, 15, e0234978.		0
25	Temporal network alignment via GoT-WAVE. Bioinformatics, 2019, 35, 3527-3529.	4.1	19
26	Supervised prediction of aging-related genes from a context-specific protein interaction subnetwork. , 2019, , .		4
27	The power of dynamic social networks to predict individualsâ€™ mental health. , 2019, , .		3
28	Survey of local and global biological network alignment: the need to reconcile the two sides of the same coin. Briefings in Bioinformatics, 2018, 19, bbw132.	6.5	69
29	Aligning dynamic networks with DynaWAVE. Bioinformatics, 2018, 34, 1795-1798.	4.1	15
30	Great Lakes Bioinformatics Conference (GLBIO) 2015 Special Section Editorial. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 1229-1230.	3.0	0
31	Network analysis of the NetHealth data: exploring co-evolution of individualsâ€™ social network positions and physical activities. Applied Network Science, 2018, 3, 45.	1.5	10
32	Multiple network alignment via multiMAGNA++. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 1-1.	3.0	36
33	ClueNet: Clustering a temporal network based on topological similarity rather than denseness. PLoS ONE, 2018, 13, e0195993.	2.5	12
34	From homogeneous to heterogeneous network alignment via colored graphlets. Scientific Reports, 2018, 8, 12524.	3.3	28
35	Aligning Dynamic Networks with DynaWAVE. , 2018, , .		0
36	Improving Identification of Key Players in Aging via Network De-Noising and Core Inference. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 1056-1069.	3.0	5

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37	Rebuttal to the Letter to the Editor in response to the paper: proper evaluation of alignment-free network comparison methods. <i>Bioinformatics</i> , 2017, 33, 1107-1109.	4.1	1
38	GRAFENE: Graphlet-based alignment-free network approach integrates 3D structural and sequence (residue order) data to improve protein structural comparison. <i>Scientific Reports</i> , 2017, 7, 14890.	3.3	21
39	Local versus global biological network alignment. <i>Bioinformatics</i> , 2016, 32, 3155-3164.	4.1	56
40	Genome-wide profiling of 24-hour diel rhythmicity in the water flea, <i>Daphnia pulex</i> : network analysis reveals rhythmic gene expression and enhances functional gene annotation. <i>BMC Genomics</i> , 2016, 17, 653.	2.8	22
41	SCOUT: simultaneous time segmentation and community detection in dynamic networks. <i>Scientific Reports</i> , 2016, 6, 37557.	3.3	11
42	On the Interplay Between Individuals' Evolving Interaction Patterns and Traits in Dynamic Multiplex Social Networks. <i>IEEE Transactions on Network Science and Engineering</i> , 2016, 3, 32-43.	6.4	25
43	Fair evaluation of global network aligners. <i>Algorithms for Molecular Biology</i> , 2015, 10, 19.	1.2	18
44	Fair evaluation of global network aligners. , 2015, , .		1
45	GREAT: GRaphlet Edge-based network Alignment. , 2015, , .		18
46	Fair evaluation of global network aligners. , 2015, , .		2
47	Proper evaluation of alignment-free network comparison methods. <i>Bioinformatics</i> , 2015, 31, 2697-2704.	4.1	46
48	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
49	The post-genomic era of biological network alignment. <i>Eurasip Journal on Bioinformatics and Systems Biology</i> , 2015, 2015, 3.	1.4	60
50	Simultaneous Optimization of both Node and Edge Conservation in Network Alignment via WAVE. <i>Lecture Notes in Computer Science</i> , 2015, , 16-39.	1.3	39
51	Revealing Missing Parts of the Interactome via Link Prediction. <i>PLoS ONE</i> , 2014, 9, e90073.	2.5	42
52	Improving identification of key players in aging via network de-noising. , 2014, , .		3
53	Networks' characteristics are important for systems biology. <i>Network Science</i> , 2014, 2, 139-161.	1.0	5
54	MAGNA: Maximizing Accuracy in Global Network Alignment. <i>Bioinformatics</i> , 2014, 30, 2931-2940.	4.1	154

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55	Dynamic networks reveal key players in aging. <i>Bioinformatics</i> , 2014, 30, 1721-1729.	4.1	80
56	Systematic Dynamic and Heterogeneous Analysis of Rich Social Network Data. <i>Studies in Computational Intelligence</i> , 2014, , 25-37.	0.9	10
57	Network Analysis Improves Interpretation of Affective Physiological Data. , 2013, , .		4
58	Global Network Alignment In The Context Of Aging. , 2013, , .		18
59	Dynamic networks reveal key players in aging. , 2013, , .		1
60	Using Global Network Alignment In The Context Of Aging. , 2013, , .		2
61	Topological Characteristics of Molecular Networks. , 2012, , 15-48.		5
62	Evidence for Network Evolution in an <i>Arabidopsis</i> Interactome Map. <i>Science</i> , 2011, 333, 601-607.	12.6	838
63	Dominating Biological Networks. <i>PLoS ONE</i> , 2011, 6, e23016.	2.5	85
64	Protein interaction network topology uncovers melanogenesis regulatory network components within functional genomics datasets. <i>BMC Systems Biology</i> , 2010, 4, 84.	3.0	32
65	Complementarity of network and sequence information in homologous proteins. <i>Journal of Integrative Bioinformatics</i> , 2010, 7, 275-289.	1.5	20
66	Optimal Network Alignment with Graphlet Degree Vectors. <i>Cancer Informatics</i> , 2010, 9, CIN.S4744.	1.9	149
67	An integrative approach to modeling biological networks. <i>Journal of Integrative Bioinformatics</i> , 2010, 7, .	1.5	14
68	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
69	Topological network alignment uncovers biological function and phylogeny. <i>Journal of the Royal Society Interface</i> , 2010, 7, 1341-1354.	3.4	281
70	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
71	An integrative approach to modeling biological networks. <i>Journal of Integrative Bioinformatics</i> , 2010, 7, .	1.5	8
72	Complementarity of network and sequence information in homologous proteins. <i>Journal of Integrative Bioinformatics</i> , 2010, 7, .	1.5	17

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73	Optimized Null Model for Protein Structure Networks. PLoS ONE, 2009, 4, e5967.	2.5	34
74	Topological network alignment uncovers biological function and phylogeny. Nature Precedings, 2009, , .	0.1	7
75	Computational Methods for Analyzing and Modeling Biological Networks. Chapman & Hall/CRC Data Mining and Knowledge Discovery Series, 2009, , 397-427.	0.2	5
76	GraphCrunch: A tool for large network analyses. BMC Bioinformatics, 2008, 9, 70.	2.6	93
77	Characterization of the proteasome interaction network using a QTAX-based tag-team strategy and protein interaction network analysis. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 13333-13338.	7.1	129
78	Uncovering Biological Network Function via Graphlet Degree Signatures. Cancer Informatics, 2008, 6, CIN.S680.	1.9	200
79	Uncovering biological network function via graphlet degree signatures. Cancer Informatics, 2008, 6, 257-73.	1.9	96