Italo Zoppis

List of Publications by Year
in descending order

44 papers	515 citations	759233 12 h-index	713466 21 g-index
45 all docs	45 docs citations	45 times ranked	846 citing authors

#	Article	IF	Citations
1	Explainable Attentional Neural Recommendations for Personalized Social Learning. Lecture Notes in Computer Science, 2021, , 67-79.	1.3	1
2	Fighting the COVID-19 pandemic using the technology-based second-line in Italy and Lombardy: The urgent need of home-based remote monitoring systems to avoid the collapse of the hospital-centred first line. Journal of Global Health, 2020, 10, 010371.	2.7	8
3	Online Social Space Identification. A Computational Tool for Optimizing Social Recommendations. Applied Sciences (Switzerland), 2020, 10, 3024.	2.5	0
4	Attentional Neural Mechanisms for Social Recommendations in Educational Platforms. , 2020, , .		1
5	An Attention-based Architecture for EEG Classification. , 2020, , .		2
6	Kernel Machines: Introduction. , 2019, , 495-502.		3
7	Kernel Methods: Support Vector Machines. , 2019, , 503-510.		12
8	Kernel Machines: Applications. , 2019, , 511-518.		0
9	Computational Methods for Resting-State EEG of Patients With Disorders of Consciousness. Frontiers in Neuroscience, 2019, 13, 807.	2.8	17
10	A Computational Model for Promoting Targeted Communication and Supplying Social Explainable Recommendations. , 2019, , .		2
11	On the tractability of finding disjoint clubs in a network. Theoretical Computer Science, 2019, 777, 243-251.	0.9	10
12	Optimized Social Explanation for Educational Platforms. , 2019, , .		2
13	Top k 2-Clubs in a Network: A Genetic Algorithm. Lecture Notes in Computer Science, 2019, , 656-663.	1.3	0
14	Editorial of the Special Issue of the 10th Workshop on Biomedical and Bioinformatics Challenges for Computer Scienceâ€"BBC 2017. Computers, 2018, 7, 17.	3.3	0
15	Distributed Heuristics for Optimizing Cohesive Groups: A Support for Clinical Patient Engagement in Social Network Analysis. , 2018, , .		0
16	From protein-protein interactions to protein co-expression networks: a new perspective to evaluate large-scale proteomic data. Eurasip Journal on Bioinformatics and Systems Biology, 2017, 2017, 6.	1.4	81
17	Orthology Correction for Gene Tree Reconstruction: Theoretical and Experimental Results. Procedia Computer Science, 2017, 108, 1115-1124.	2.0	17
18	DIABESITY: A Study for mHealth Integrated Solutions. Lecture Notes of the Institute for Computer Sciences, Social-Informatics and Telecommunications Engineering, 2017, , 195-199.	0.3	1

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19	A Support Vector Machine Classification of Thyroid Bioptic Specimens Using MALDI-MSI Data. Advances in Bioinformatics, 2016, 2016, 1-7.	5.7	17
20	Trend of FEV1 in Cystic Fibrosis patients: A telehomecare experience. , 2016, , .		0
21	Machine learning approaches in MALDI-MSI: clinical applications. Expert Review of Proteomics, 2016, 13, 685-696.	3.0	22
22	Clique Editing to Support Case Versus Control Discrimination. Smart Innovation, Systems and Technologies, 2016, , 27-36.	0.6	6
23	Tumor size, stage and grade alterations of urinary peptidome in RCC. Journal of Translational Medicine, 2015, 13, 332.	4.4	38
24	Social media and mobile applications in chronic disease prevention and management. Frontiers in Psychology, 2015, 6, 567.	2.1	53
25	Managing chronic pathologies with a stepped mHealth-based approach in clinical psychology and medicine. Frontiers in Psychology, 2015, 06, 407.	2.1	32
26	Robust Conclusions in Mass Spectrometry Analysis. Procedia Computer Science, 2015, 51, 683-692.	2.0	0
27	Restricted and Swap Common Superstring: A Multivariate Algorithmic Perspective. Algorithmica, 2015, 72, 914-939.	1.3	1
28	Integration of mRNA Expression Profile, Copy Number Alterations, and microRNA Expression Levels in Breast Cancer to Improve Grade Definition. PLoS ONE, 2014, 9, e97681.	2.5	53
29	Urinary Signatures of Renal Cell Carcinoma Investigated by Peptidomic Approaches. PLoS ONE, 2014, 9, e106684.	2.5	30
30	Combined analysis of chromosomal instabilities and gene expression for colon cancer progression inference. Journal of Clinical Bioinformatics, 2014, 4, 2.	1.2	15
31	Availability of MudPIT data for classification of biological samples. Journal of Clinical Bioinformatics, 2013, 3, 1.	1.2	14
32	Candidate biomarkers for response to tamoxifen in breast cancer metastatic patients. , 2013, , .		1
33	The<mml:math xmlns:mml="http://www.w3.org/1998/Math/MathML" altimg="si1.gif" display="inline" overflow="scroll"><mml:mi>l</mml:mi></mml:math>-Diversity problem: Tractability and approximability. Theoretical Computer Science, 2013, 511, 159-171.	0.9	9
34	Copyâ€"Number Alterations for Tumor Progression Inference. Lecture Notes in Computer Science, 2013, , 104-109.	1.3	11
35	Mutual Information Optimization for Mass Spectra Data Alignment. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 934-939.	3.0	7
36	Poster: Characterization of distinguishing regions for Renal Cell Carcinoma discrimination. , 2012, , .		0

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37	Restricted and Swap Common Superstring: A Parameterized View. Lecture Notes in Computer Science, 2012, , 49-60.	1.3	1
38	On the Complexity of the l-diversity Problem. Lecture Notes in Computer Science, 2011, , 266-277.	1.3	3
39	Playing monotone games to understand learning behaviors. Theoretical Computer Science, 2010, 411, 2384-2405.	0.9	0
40	An application of kernel methods to gene cluster temporal meta-analysis. Computers and Operations Research, 2010, 37, 1361-1368.	4.0	8
41	Serum Biomarkers of Renal Cell Carcinoma Assessed Using a Protein Profiling Approach Based on ClinProt Technique. Urology, 2010, 75, 842-847.	1.0	27
42	A Mutual Information Approach to Data Integration for Alzheimer's Disease Patients. Lecture Notes in Computer Science, 2009, , 431-435.	1.3	1
43	Discovering Relations Among GO-Annotated Clusters by Graph Kernel Methods. , 2007, , 158-169.		9
44	Clustering Causal Relationships in Genes Expression Data. Lecture Notes in Computer Science, 2006, , 132-139.	1.3	0