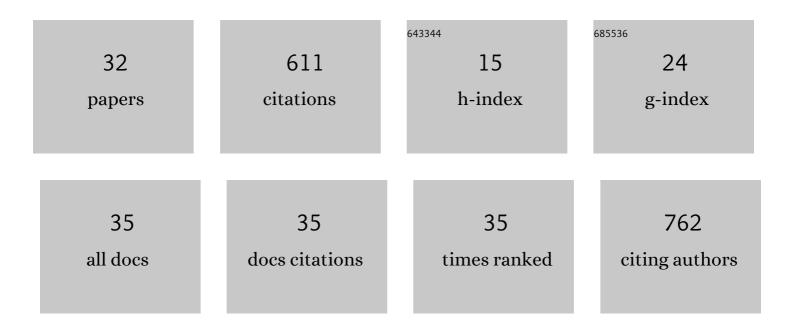
## Gianvito Pio

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/8387767/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	PRILJ: an efficient two-step method based on embedding and clustering for the identification of regularities in legal case judgments. Artificial Intelligence and Law, 2022, 30, 359-390.	3.0	10
2	Integrating genome-scale metabolic modelling and transfer learning for human gene regulatory network reconstruction. Bioinformatics, 2022, 38, 487-493.	1.8	26
3	LP-ROBIN: Link prediction in dynamic networks exploiting incremental node embedding. Information Sciences, 2022, 606, 702-721.	4.0	10
4	Relational tree ensembles and feature rankings. Knowledge-Based Systems, 2022, 251, 109254.	4.0	2
5	Statistical and Machine Learning Techniques in Human Microbiome Studies: Contemporary Challenges and Solutions. Frontiers in Microbiology, 2021, 12, 635781.	1.5	51
6	Big Data analytics for knowledge transfer among organisms while reconstructing Gene Regulatory Networks. EMBnet Journal, 2021, 26, e956.	0.2	0
7	LP-HCLUS: a novel tool for the prediction of relationships between ncRNAs and human diseases. EMBnet Journal, 2021, 26, e955.	0.2	О
8	BROCCOLI: overlapping and outlier-robust biclustering through proximal stochastic gradient descent. Data Mining and Knowledge Discovery, 2021, 35, 2542-2576.	2.4	10
9	Spatially-Aware Autoencoders for Detecting Contextual Anomalies in Geo-Distributed Data. Lecture Notes in Computer Science, 2021, , 461-471.	1.0	9
10	Exploiting transfer learning for the reconstruction of the human gene regulatory network. Bioinformatics, 2020, 36, 1553-1561.	1.8	44
11	Exploiting causality in gene network reconstruction based on graph embedding. Machine Learning, 2020, 109, 1231-1279.	3.4	25
12	ECHAD: Embedding-Based Change Detection From Multivariate Time Series in Smart Grids. IEEE Access, 2020, 8, 156053-156066.	2.6	36
13	Multi-task learning for the simultaneous reconstruction of the human and mouse gene regulatory networks. Scientific Reports, 2020, 10, 22295.	1.6	22
14	Prediction of new associations between ncRNAs and diseases exploiting multi-type hierarchical clustering. BMC Bioinformatics, 2020, 21, 70.	1.2	25
15	DENCAST: distributed density-based clustering for multi-target regression. Journal of Big Data, 2019, 6,	6.9	40
16	Ensemble Learning for Multi-Type Classification in Heterogeneous Networks. IEEE Transactions on Knowledge and Data Engineering, 2018, 30, 2326-2339.	4.0	26
17	Multi-type clustering and classification from heterogeneous networks. Information Sciences, 2018, 425, 107-126.	4.0	37
18	ldentifying IncRNA-Disease Relationships via Heterogeneous Clustering. Lecture Notes in Computer Science, 2018, , 35-48.	1.0	9

**GIANVITO PIO** 

#	Article	IF	CITATIONS
19	Positive Unlabeled Link Prediction via Transfer Learning for Gene Network Reconstruction. Lecture Notes in Computer Science, 2018, , 13-23.	1.0	6
20	LOCANDA: Exploiting Causality in the Reconstruction of Gene Regulatory Networks. Lecture Notes in Computer Science, 2017, , 283-297.	1.0	1
21	ComiRNet: a web-based system for the analysis of miRNA-gene regulatory networks. BMC Bioinformatics, 2015, 16, S7.	1.2	43
22	Semi-Supervised Multi-View Learning for Gene Network Reconstruction. PLoS ONE, 2015, 10, e0144031.	1.1	32
23	Non-negative Matrix Tri-Factorization for co-clustering: An analysis of the block matrix. Information Sciences, 2015, 301, 13-26.	4.0	48
24	Discovering Novelty Patterns from the Ancient Christian Inscriptions of Rome. Journal on Computing and Cultural Heritage, 2015, 7, 1-21.	1.2	1
25	Hierarchical Multidimensional Classification of Web Documents with MultiWebClass. Lecture Notes in Computer Science, 2015, , 236-250.	1.0	5
26	Integrating microRNA target predictions for the discovery of gene regulatory networks: a semi-supervised ensemble learning approach. BMC Bioinformatics, 2014, 15, S4.	1.2	45
27	Network Reconstruction for the Identification of miRNA:mRNA Interaction Networks. Lecture Notes in Computer Science, 2014, , 508-511.	1.0	1
28	A Novel Biclustering Algorithm for the Discovery of Meaningful Biological Correlations between microRNAs and their Target Genes. BMC Bioinformatics, 2013, 14, S8.	1.2	38
29	Fast Fuzzy Inference in Octave. International Journal of Computational Intelligence Systems, 2013, 6, 307-317.	1.6	0
30	Semi- supervised ensemble learning to boost miRNA target predictions EMBnet Journal, 2013, 19, 74.	0.2	0
31	A novel biclustering algorithm for the discovery of meaningful biological correlations between miRNAs and mRNAs. EMBnet Journal, 2012, 18, 43.	0.2	2
32	The integration of microRNA target data by biclustering techniques opens new roads for signaling networks analysis. EMBnet Journal, 2012, 18, 142.	0.2	1