

Gianvito Pio

List of Publications by Year in descending order

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Version: 2024-02-01

32
papers

611
citations

643344

15
h-index

685536

24
g-index

35
all docs

35
docs citations

35
times ranked

762
citing authors

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

| # | 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 |