Davide Chicco

List of Publications by Year
in descending order

42 papers	7,010 citations	394421 19 h-index	345221 36 g-index
46 all docs	46 docs citations	46 times ranked	7543 citing authors

#	Article	IF	Citations
1	The advantages of the Matthews correlation coefficient (MCC) over F1 score and accuracy in binary classification evaluation. BMC Genomics, 2020, 21, 6.	2.8	2,549
2	The coefficient of determination R-squared is more informative than SMAPE, MAE, MAPE, MSE and RMSE in regression analysis evaluation. PeerJ Computer Science, 2021, 7, e623.	4.5	1,095
3	Bioconda: sustainable and comprehensive software distribution for the life sciences. Nature Methods, 2018, 15, 475-476.	19.0	714
4	Ten quick tips for machine learning in computational biology. BioData Mining, 2017, 10, 35.	4.0	588
5	The Matthews correlation coefficient (MCC) is more reliable than balanced accuracy, bookmaker informedness, and markedness in two-class confusion matrix evaluation. BioData Mining, 2021, 14, 13.	4.0	364
6	Machine learning can predict survival of patients with heart failure from serum creatinine and ejection fraction alone. BMC Medical Informatics and Decision Making, 2020, 20, 16.	3.0	282
7	Siamese Neural Networks: An Overview. Methods in Molecular Biology, 2021, 2190, 73-94.	0.9	275
8	Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen. Nature Communications, 2019, 10, 2674.	12.8	240
9	The Matthews Correlation Coefficient (MCC) is More Informative Than Cohen's Kappa and Brier Score in Binary Classification Assessment. IEEE Access, 2021, 9, 78368-78381.	4.2	147
10	Deep autoencoder neural networks for gene ontology annotation predictions. , 2014, , .		105
11	Machine learning vs. conventional statistical models for predicting heart failure readmission and mortality. ESC Heart Failure, 2021, 8, 106-115.	3.1	82
12	Supervised deep learning embeddings for the prediction of cervical cancer diagnosis. PeerJ Computer Science, 2018, 4, e154.	4.5	55
13	Computational prediction of diagnosis and feature selection on mesothelioma patient health records. PLoS ONE, 2019, 14, e0208737.	2.5	48
14	The Benefits of the Matthews Correlation Coefficient (MCC) Over the Diagnostic Odds Ratio (DOR) in Binary Classification Assessment. IEEE Access, 2021, 9, 47112-47124.	4.2	48
15	Stratification of amyotrophic lateral sclerosis patients: a crowdsourcing approach. Scientific Reports, 2019, 9, 690.	3.3	46
16	Machine Learning Compared With Conventional Statistical Models for Predicting Myocardial Infarction Readmission and Mortality: A Systematic Review. Canadian Journal of Cardiology, 2021, 37, 1207-1214.	1.7	29
17	An Ensemble Learning Approach for Enhanced Classification of Patients With Hepatitis and Cirrhosis. IEEE Access, 2021, 9, 24485-24498.	4.2	28
18	Probabilistic Latent Semantic Analysis for prediction of Gene Ontology annotations. , 2012, , .		25

#	ARTICLE	IF	CITATIONS
19	Computational algorithms to predict Gene Ontology annotations. BMC Bioinformatics, 2015, 16, S4.	2.6	24
20	Survival prediction of patients with sepsis from age, sex, and septic episode number alone. Scientific Reports, 2020, 10, 17156.	3.3	24
21	Software Suite for Gene and Protein Annotation Prediction and Similarity Search. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 837-843.	3.0	22
22	Latent Dirichlet Allocation based on Gibbs Sampling for gene function prediction. , 2014, , .		20
23	Ontology-Based Prediction and Prioritization of Gene Functional Annotations. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2016, 13, 248-260.	3.0	18
24	Enhanced probabilistic latent semantic analysis with weighting schemes to predict genomic annotations. , 2013, , .		15
25	geoCancerPrognosticDatasetsRetriever: a bioinformatics tool to easily identify cancer prognostic datasets on Gene Expression Omnibus (GEO). Bioinformatics, 2022, 38, 1761-1763.	4.1	14
26	A discrete optimization approach for SVD best truncation choice based on ROC curves. , 2013, , .		13
27	Data analytics and clinical feature ranking of medical records of patients with sepsis. BioData Mining, 2021, 14, 12.	4.0	13
28	An Invitation to Greater Use of Matthews Correlation Coefficient in Robotics and Artificial Intelligence. Frontiers in Robotics and AI, 2022, 9, 876814.	3.2	13
29	geneExpressionFromGEO: An R Package to Facilitate Data Reading from Gene Expression Omnibus (GEO). Methods in Molecular Biology, 2022, 2401, 187-194.	0.9	10
30	Computational intelligence identifies alkaline phosphatase (ALP), alpha-fetoprotein (AFP), and hemoglobin levels as most predictive survival factors for hepatocellular carcinoma. Health Informatics Journal, 2021, 27, 146045822098420.	2.1	9
31	An Enhanced Random Forests Approach to Predict Heart Failure From Small Imbalanced Gene Expression Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 2759-2765.	3.0	9
32	A Machine Learning Analysis of Health Records of Patients With Chronic Kidney Disease at Risk of Cardiovascular Disease. IEEE Access, 2021, 9, 165132-165144.	4.2	9
33	Editorial: Artificial Intelligence Bioinformatics: Development and Application of Tools for Omics and Inter-Omics Studies. Frontiers in Genetics, 2020, 11, 309.	2.3	8
34	Genomic Annotation Prediction Based on Integrated Information. Lecture Notes in Computer Science, 2012, , 238-252.	1.3	7
35	Arterial disease computational prediction and health record feature ranking among patients diagnosed with inflammatory bowel disease. IEEE Access, 2021, , 1-1.	4.2	6
36	Extended Spearman and Kendall Coefficients for Gene Annotation List Correlation. Lecture Notes in Computer Science, 2015, , 19-32.	1.3	6

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37	Brief Survey on Machine Learning in Epistasis. Methods in Molecular Biology, 2021, 2212, 169-179.	0.9	5
38	Weighting Scheme Methods for Enhanced Genomic Annotation Prediction. Lecture Notes in Computer Science, 2014, , 76-89.	1.3	5
39	Semantically improved genome-wide prediction of Gene Ontology annotations. , 2011, , .		4
40	Novelty Indicator for Enhanced Prioritization of Predicted Gene Ontology Annotations. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 954-965.	3.0	3
41	Validation Pipeline for Computational Prediction of Genomics Annotations. Lecture Notes in Computer Science, 2016, , 233-244.	1.3	2
42	Biological and Medical Ontologies: Protein Ontology (PRO). , 2019, , 832-837.		0