

Davide Chicco

List of Publications by Year in descending order

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Version: 2024-02-01

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	geneExpressionFromGEO: An R Package to Facilitate Data Reading from Gene Expression Omnibus (GEO). <i>Methods in Molecular Biology</i> , 2022, 2401, 187-194.	0.9	10
2	geoCancerPrognosticDatasetsRetriever: a bioinformatics tool to easily identify cancer prognostic datasets on Gene Expression Omnibus (GEO). <i>Bioinformatics</i> , 2022, 38, 1761-1763.	4.1	14
3	An Invitation to Greater Use of Matthews Correlation Coefficient in Robotics and Artificial Intelligence. <i>Frontiers in Robotics and AI</i> , 2022, 9, 876814.	3.2	13
4	Machine learning vs. conventional statistical models for predicting heart failure readmission and mortality. <i>ESC Heart Failure</i> , 2021, 8, 106-115.	3.1	82
5	Brief Survey on Machine Learning in Epistasis. <i>Methods in Molecular Biology</i> , 2021, 2212, 169-179.	0.9	5
6	The Matthews Correlation Coefficient (MCC) is More Informative Than Cohen's Kappa and Brier Score in Binary Classification Assessment. <i>IEEE Access</i> , 2021, 9, 78368-78381.	4.2	147
7	The Benefits of the Matthews Correlation Coefficient (MCC) Over the Diagnostic Odds Ratio (DOR) in Binary Classification Assessment. <i>IEEE Access</i> , 2021, 9, 47112-47124.	4.2	48
8	Computational intelligence identifies alkaline phosphatase (ALP), alpha-fetoprotein (AFP), and hemoglobin levels as most predictive survival factors for hepatocellular carcinoma. <i>Health Informatics Journal</i> , 2021, 27, 146045822098420.	2.1	9
9	An Ensemble Learning Approach for Enhanced Classification of Patients With Hepatitis and Cirrhosis. <i>IEEE Access</i> , 2021, 9, 24485-24498.	4.2	28
10	The Matthews correlation coefficient (MCC) is more reliable than balanced accuracy, bookmaker informedness, and markedness in two-class confusion matrix evaluation. <i>BioData Mining</i> , 2021, 14, 13.	4.0	364
11	Data analytics and clinical feature ranking of medical records of patients with sepsis. <i>BioData Mining</i> , 2021, 14, 12.	4.0	13
12	The coefficient of determination R-squared is more informative than SMAPE, MAE, MAPE, MSE and RMSE in regression analysis evaluation. <i>PeerJ Computer Science</i> , 2021, 7, e623.	4.5	1,095
13	Machine Learning Compared With Conventional Statistical Models for Predicting Myocardial Infarction Readmission and Mortality: A Systematic Review. <i>Canadian Journal of Cardiology</i> , 2021, 37, 1207-1214.	1.7	29
14	Arterial disease computational prediction and health record feature ranking among patients diagnosed with inflammatory bowel disease. <i>IEEE Access</i> , 2021, , 1-1.	4.2	6
15	Siamese Neural Networks: An Overview. <i>Methods in Molecular Biology</i> , 2021, 2190, 73-94.	0.9	275
16	An Enhanced Random Forests Approach to Predict Heart Failure From Small Imbalanced Gene Expression Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 2759-2765.	3.0	9
17	A Machine Learning Analysis of Health Records of Patients With Chronic Kidney Disease at Risk of Cardiovascular Disease. <i>IEEE Access</i> , 2021, 9, 165132-165144.	4.2	9
18	The advantages of the Matthews correlation coefficient (MCC) over F1 score and accuracy in binary classification evaluation. <i>BMC Genomics</i> , 2020, 21, 6.	2.8	2,549

#	ARTICLE	IF	CITATIONS
19	Survival prediction of patients with sepsis from age, sex, and septic episode number alone. Scientific Reports, 2020, 10, 17156.	3.3	24
20	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
21	Editorial: Artificial Intelligence Bioinformatics: Development and Application of Tools for Omics and Inter-Omics Studies. Frontiers in Genetics, 2020, 11, 309.	2.3	8
22	Biological and Medical Ontologies: Protein Ontology (PRO). , 2019, , 832-837.		0
23	Stratification of amyotrophic lateral sclerosis patients: a crowdsourcing approach. Scientific Reports, 2019, 9, 690.	3.3	46
24	Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen. Nature Communications, 2019, 10, 2674.	12.8	240
25	Computational prediction of diagnosis and feature selection on mesothelioma patient health records. PLoS ONE, 2019, 14, e0208737.	2.5	48
26	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
27	Bioconda: sustainable and comprehensive software distribution for the life sciences. Nature Methods, 2018, 15, 475-476.	19.0	714
28	Supervised deep learning embeddings for the prediction of cervical cancer diagnosis. PeerJ Computer Science, 2018, 4, e154.	4.5	55
29	Ten quick tips for machine learning in computational biology. BioData Mining, 2017, 10, 35.	4.0	588
30	Ontology-Based Prediction and Prioritization of Gene Functional Annotations. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2016, 13, 248-260.	3.0	18
31	Validation Pipeline for Computational Prediction of Genomics Annotations. Lecture Notes in Computer Science, 2016, , 233-244.	1.3	2
32	Computational algorithms to predict Gene Ontology annotations. BMC Bioinformatics, 2015, 16, S4.	2.6	24
33	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
34	Extended Spearman and Kendall Coefficients for Gene Annotation List Correlation. Lecture Notes in Computer Science, 2015, , 19-32.	1.3	6
35	Deep autoencoder neural networks for gene ontology annotation predictions. , 2014, , .		105
36	Latent Dirichlet Allocation based on Gibbs Sampling for gene function prediction. , 2014, , .		20

#	ARTICLE	IF	CITATIONS
37	Weighting Scheme Methods for Enhanced Genomic Annotation Prediction. Lecture Notes in Computer Science, 2014, , 76-89.	1.3	5
38	A discrete optimization approach for SVD best truncation choice based on ROC curves. , 2013, , .		13
39	Enhanced probabilistic latent semantic analysis with weighting schemes to predict genomic annotations. , 2013, , .		15
40	Probabilistic Latent Semantic Analysis for prediction of Gene Ontology annotations. , 2012, , .		25
41	Genomic Annotation Prediction Based on Integrated Information. Lecture Notes in Computer Science, 2012, , 238-252.	1.3	7
42	Semantically improved genome-wide prediction of Gene Ontology annotations. , 2011, , .		4