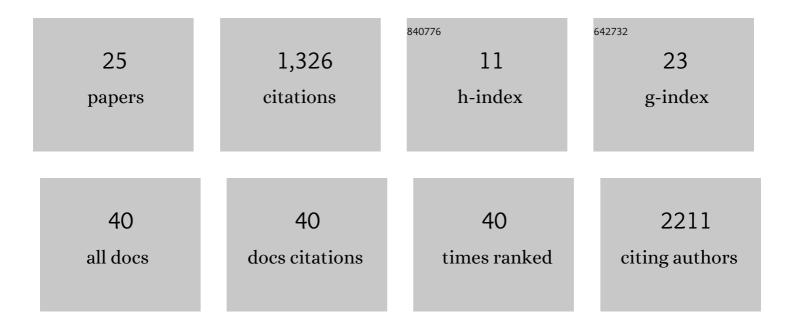
Trang T Le

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/8970447/publications.pdf Version: 2024-02-01



TRANC TIE

#	Article	IF	CITATIONS
1	Genetic Analysis of Coronary Artery Disease Using Tree-Based Automated Machine Learning Informed By Biology-Based Feature Selection. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 1379-1386.	3.0	9
2	Repetitive head impacts in a collegiate football season: Exposure and effects. International Journal of Sports Science and Coaching, 2022, 17, 285-297.	1.4	3
3	<i>treeheatr</i> : an R package for interpretable decision tree visualizations. Bioinformatics, 2021, 37, 282-284.	4.1	13
4	Theoretical properties of distance distributions and novel metrics for nearest-neighbor feature selection. PLoS ONE, 2021, 16, e0246761.	2.5	3
5	TPOT-NN: augmenting tree-based automated machine learning with neural network estimators. Genetic Programming and Evolvable Machines, 2021, 22, 207-227.	2.2	13
6	REGENS: an open source Python package for simulating realistic autosomal genotypes. Journal of Open Source Software, 2021, 6, 2743.	4.6	0
7	Pitfalls in brain age analyses. Human Brain Mapping, 2021, 42, 4092-4101.	3.6	50
8	International Changes in COVID-19 Clinical Trajectories Across 315 Hospitals and 6 Countries: Retrospective Cohort Study. Journal of Medical Internet Research, 2021, 23, e31400.	4.3	19
9	Analysis of scientific society honors reveals disparities. Cell Systems, 2021, 12, 900-906.e5.	6.2	10
10	Multinational characterization of neurological phenotypes in patients hospitalized with COVID-19. Scientific Reports, 2021, 11, 20238.	3.3	10
11	Scaling tree-based automated machine learning to biomedical big data with a feature set selector. Bioinformatics, 2020, 36, 250-256.	4.1	245
12	Nearest-neighbor Projected-Distance Regression (NPDR) for detecting network interactions with adjustments for multiple tests and confounding. Bioinformatics, 2020, 36, 2770-2777.	4.1	7
13	Expanding Polygenic Risk Scores to Include Automatic Genotype Encodings and Gene-gene Interactions. , 2020, , .		3
14	Large scale biomedical data analysis with tree-based automated machine learning. , 2020, , .		0
15	Generalization of the Fermi pseudopotential. Physica Scripta, 2019, 94, 065203.	2.5	2
16	STatistical Inference Relief (STIR) feature selection. Bioinformatics, 2019, 35, 1358-1365.	4.1	47
17	Structural and practical identifiability analysis of outbreak models. Mathematical Biosciences, 2018, 299, 1-18.	1.9	52
18	Interoception and Mental Health: A Roadmap. Biological Psychiatry: Cognitive Neuroscience and Neuroimaging, 2018, 3, 501-513.	1.5	524

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#	Article	IF	CITATIONS
19	A Nonlinear Simulation Framework Supports Adjusting for Age When Analyzing BrainAGE. Frontiers in Aging Neuroscience, 2018, 10, 317.	3.4	183
20	Identification and replication of RNA-Seq gene network modules associated with depression severity. Translational Psychiatry, 2018, 8, 180.	4.8	37
21	Effect of Ibuprofen on BrainAGE: A Randomized, Placebo-Controlled, Dose-Response ExploratoryÂStudy. Biological Psychiatry: Cognitive Neuroscience and Neuroimaging, 2018, 3, 836-843.	1.5	23
22	F128. Transcriptomics of Brain Age Gap Estimate (BrainAGE): Association Analysis of Depressed and Healthy Individuals. Biological Psychiatry, 2018, 83, S287.	1.3	1
23	Integrated machine learning pipeline for aberrant biomarker enrichment (i-mAB): characterizing clusters of differentiation within a compendium of systemic lupus erythematosus patients. AMIA Annual Symposium proceedings, 2018, 2018, 1358-1367.	0.2	4
24	Differential privacy-based evaporative cooling feature selection and classification with relief-F and random forests. Bioinformatics, 2017, 33, 2906-2913.	4.1	24
25	Effect of air travel on the spread of an avian influenza pandemic to the United States. International Journal of Critical Infrastructure Protection, 2014, 7, 27-47.	4.6	14