

Bastian Pfeifer

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/974298/publications.pdf>

Version: 2024-02-01

12
papers

1,158
citations

1684188

5
h-index

1474206

9
g-index

17
all docs

17
docs citations

17
times ranked

2460
citing authors

#	ARTICLE	IF	CITATIONS
1	Robust Random Forest-Based All-Relevant Feature Ranks for Trustworthy AI. <i>Studies in Health Technology and Informatics</i> , 2022, , .	0.3	7
2	A hierarchical clustering and data fusion approach for disease subtype discovery. <i>Journal of Biomedical Informatics</i> , 2021, 113, 103636.	4.3	13
3	Towards multi-modal causability with Graph Neural Networks enabling information fusion for explainable AI. <i>Information Fusion</i> , 2021, 71, 28-37.	19.1	210
4	Integrative hierarchical ensemble clustering for improved disease subtype discovery. , 2021, , .		1
5	Genome scans for selection and introgression based on <i>k</i> -nearest neighbour techniques. <i>Molecular Ecology Resources</i> , 2020, 20, 1597-1609.	4.8	13
6	Estimates of introgression as a function of pairwise distances. <i>BMC Bioinformatics</i> , 2019, 20, 207.	2.6	21
7	EHR problem list clustering for improved topic-space navigation. <i>BMC Medical Informatics and Decision Making</i> , 2019, 19, 72.	3.0	7
8	<i>BlockFeST</i> : Bayesian calculation of region-specific <i>F_{ST}</i> to detect local adaptation. <i>Bioinformatics</i> , 2018, 34, 3205-3207.	4.1	2
9	Problem List Clustering for Improved Patient-Based Disease Perception. , 2018, , .		0
10	EHR Text Categorization for Enhanced Patient-Based Document Navigation. <i>Studies in Health Technology and Informatics</i> , 2018, 248, 100-107.	0.3	0
11	WhopGenome: high-speed access to whole-genome variation and sequence data in R. <i>Bioinformatics</i> , 2015, 31, 413-415.	4.1	4
12	PopGenome: An Efficient Swiss Army Knife for Population Genomic Analyses in R. <i>Molecular Biology and Evolution</i> , 2014, 31, 1929-1936.	8.9	871