Thuc Duy Le

List of Publications by Year
in descending order

69 papers	1,898 citations	411340 20 h-index	340414 39 g-index
83 all docs	83 docs citations	83 times ranked	2354 citing authors

#	Article	IF	Citations
1	Toward Unique and Unbiased Causal Effect Estimation From Data With Hidden Variables. IEEE Transactions on Neural Networks and Learning Systems, 2023, 34, 6108-6120.	7.2	5
2	Time to infer miRNA sponge modules. Wiley Interdisciplinary Reviews RNA, 2022, 13, e1686.	3.2	13
3	Identifying preeclampsia-associated genes using a control theory method. Briefings in Functional Genomics, 2022, 21, 296-309.	1.3	3
4	Sufficient dimension reduction for average causal effect estimation. Data Mining and Knowledge Discovery, 2022, 36, 1174-1196.	2.4	6
5	How do the existing fairness metrics and unfairness mitigation algorithms contribute to ethical learning analytics?. British Journal of Educational Technology, 2022, 53, 822-843.	3.9	17
6	A pseudotemporal causality approach to identifying miRNA–mRNA interactions during biological processes. Bioinformatics, 2021, 37, 807-814.	1.8	3
7	GraphDTA: predicting drug–target binding affinity with graph neural networks. Bioinformatics, 2021, 37, 1140-1147.	1.8	343
8	Computational methods for cancer driver discovery: A survey. Theranostics, 2021, 11, 5553-5568.	4.6	19
9	NIBNA: a network-based node importance approach for identifying breast cancer drivers. Bioinformatics, 2021, 37, 2521-2528.	1.8	6
10	A general framework for causal classification. International Journal of Data Science and Analytics, 2021, 11, 127-139.	2.4	5
11	miRSM: an R package to infer and analyse miRNA sponge modules in heterogeneous data. RNA Biology, 2021, 18, 2308-2320.	1.5	5
12	<i>pDriver</i>: a novel method for unravelling personalized coding and miRNA cancer drivers. Bioinformatics, 2021, 37, 3285-3292.	1.8	8
13	Uncovering the roles of microRNAs/lncRNAs in characterising breast cancer subtypes and prognosis. BMC Bioinformatics, 2021, 22, 300.	1.2	6
14	PAN: Personalized Annotation-Based Networks for the Prediction of Breast Cancer Relapse. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 2841-2847.	1.9	4
15	Exploring cell-specific miRNA regulation with single-cell miRNA-mRNA co-sequencing data. BMC Bioinformatics, 2021, 22, 578.	1.2	7
16	Multi-Source Causal Feature Selection. IEEE Transactions on Pattern Analysis and Machine Intelligence, 2020, 42, 2240-2256.	9.7	66
17	A novel single-cell based method for breast cancer prognosis. PLoS Computational Biology, 2020, 16, e1008133.	1.5	16
18	Efficient polygenic risk scores for biobank scale data by exploiting phenotypes from inferred relatives. Nature Communications, 2020, 11, 3074.	5.8	24

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19	Multi-Group Transfer Learning on Multiple Latent Spaces for Text Classification. IEEE Access, 2020, 8, 64120-64130.	2.6	4
20	Accurate data-driven prediction does not mean high reproducibility. Nature Machine Intelligence, 2020, 2, 13-15.	8.3	35
21	LMSM: AÂmodular approach for identifying lncRNA related miRNA sponge modules in breast cancer. PLoS Computational Biology, 2020, 16, e1007851.	1.5	17
22	<i>DriverGroup</i>: a novel method for identifying driver gene groups. Bioinformatics, 2020, 36, i583-i591.	1.8	5
23	Gene selection for optimal prediction of cell position in tissues from single-cell transcriptomics data. Life Science Alliance, 2020, 3, e202000867.	1.3	20
24	MrPC: Causal Structure Learning in Distributed Systems. Communications in Computer and Information Science, 2020, , 87-94.	0.4	0
25	LMSM: A modular approach for identifying lncRNA related miRNA sponge modules in breast cancer. , 2020, 16, e1007851.		0
26	LMSM: A modular approach for identifying lncRNA related miRNA sponge modules in breast cancer. , 2020, 16, e1007851.		0
27	LMSM: A modular approach for identifying lncRNA related miRNA sponge modules in breast cancer. , 2020, 16, e1007851.		0
28	LMSM: A modular approach for identifying lncRNA related miRNA sponge modules in breast cancer. , 2020, 16, e1007851.		0
29	Extensive transcriptional responses are co-ordinated by microRNAs as revealed by Exonâ€"Intron Split Analysis (EISA). Nucleic Acids Research, 2019, 47, 8606-8619.	6.5	9
30	miRspongeR: an R/Bioconductor package for the identification and analysis of miRNA sponge interaction networks and modules. BMC Bioinformatics, 2019, 20, 235.	1.2	40
31	Identifying miRNA-mRNA regulatory relationships in breast cancer with invariant causal prediction. BMC Bioinformatics, 2019, 20, 143.	1.2	23
32	Identifying miRNA synergism using multiple-intervention causal inference. BMC Bioinformatics, 2019, 20, 613.	1.2	14
33	Discovering context specific causal relationships. Intelligent Data Analysis, 2019, 23, 917-931.	0.4	0
34	CBNA: A control theory based method for identifying coding and non-coding cancer drivers. PLoS Computational Biology, 2019, 15, e1007538.	1.5	22
35	Data-driven discovery of causal interactions. International Journal of Data Science and Analytics, 2019, 8, 285-297.	2.4	2
36	Inferring and analyzing module-specific lncRNAâ€"mRNA causal regulatory networks in human cancer. Briefings in Bioinformatics, 2019, 20, 1403-1419.	3.2	33

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37	A Fast PC Algorithm for High Dimensional Causal Discovery with Multi-Core PCs. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1483-1495.	1.9	58
38	Estimating heterogeneous treatment effect by balancing heterogeneity and fitness. BMC Bioinformatics, 2018, 19, 518.	1.2	3
39	miRBaseConverter: an R/Bioconductor package for converting and retrieving miRNA name, accession, sequence and family information in different versions of miRBase. BMC Bioinformatics, 2018, 19, 514.	1.2	59
40	ParallelPC: An R Package for Efficient Causal Exploration in Genomic Data. Lecture Notes in Computer Science, 2018, , 207-218.	1.0	4
41	LncmiRSRN: identification and analysis of long non-coding RNA related miRNA sponge regulatory network in human cancer. Bioinformatics, 2018, 34, 4232-4240.	1.8	73
42	Use of Haploid Model of Candida albicans to Uncover Mechanism of Action of a Novel Antifungal Agent. Frontiers in Cellular and Infection Microbiology, 2018, 8, 164.	1.8	15
43	Effective Outlier Detection based on Bayesian Network and Proximity. , 2018, , .		2
44	Computational methods for identifying miRNA sponge interactions. Briefings in Bioinformatics, 2017, 18, bbw042.	3.2	111
45	Inferring miRNA sponge co-regulation of protein-protein interactions in human breast cancer. BMC Bioinformatics, 2017, 18, 243.	1.2	20
46	CancerSubtypes: an R/Bioconductor package for molecular cancer subtype identification, validation and visualization. Bioinformatics, 2017, 33, 3131-3133.	1.8	196
47	Mining heterogeneous causal effects for personalized cancer treatment. Bioinformatics, 2017, 33, 2372-2378.	1.8	25
48	Nonparametric Sparse Matrix Decomposition for Cross-View Dimensionality Reduction. IEEE Transactions on Multimedia, 2017, 19, 1848-1859.	5.2	13
49	Identifying microRNA targets in epithelial-mesenchymal transition using joint-intervention causal inference. , 2017, , .		2
50	Identifying miRNA sponge modules using biclustering and regulatory scores. BMC Bioinformatics, 2017, 18, 44.	1.2	25
51	Discrimination detection by causal effect estimation. , 2017, , .		8
52	Identifying Cancer Subtypes from miRNA-TF-mRNA Regulatory Networks and Expression Data. PLoS ONE, 2016, 11, e0152792.	1.1	59
53	Predicting miRNA Targets by Integrating Gene Regulatory Knowledge with Expression Profiles. PLoS ONE, 2016, 11, e0152860.	1.1	15
54	Identification of miRNA-mRNA regulatory modules by exploring collective group relationships. BMC Genomics, 2016, 17, 7.	1.2	25

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55	From Observational Studies to Causal Rule Mining. ACM Transactions on Intelligent Systems and Technology, 2016, 7, 1-27.	2.9	19
56	Mining combined causes in large data sets. Knowledge-Based Systems, 2016, 92, 104-111.	4.0	14
57	A novel framework for inferring condition-specific TF and miRNA co-regulation of protein–protein interactions. Gene, 2016, 577, 55-64.	1.0	8
58	Identifying miRNA synergistic regulatory networks in heterogeneous human data via network motifs. Molecular BioSystems, 2016, 12, 454-463.	2.9	9
59	Ensemble Methods for MiRNA Target Prediction from Expression Data. PLoS ONE, 2015, 10, e0131627.	1.1	35
60	Practical Approaches to Causal Relationship Exploration. Springer Briefs in Electrical and Computer Engineering, 2015, , .	0.3	21
61	From miRNA regulation to miRNA-TF co-regulation: computational approaches and challenges. Briefings in Bioinformatics, 2015, 16, 475-496.	3.2	36
62	miRLAB: An R Based Dry Lab for Exploring miRNA-mRNA Regulatory Relationships. PLoS ONE, 2015, 10, e0145386.	1.1	33
63	Causal Rule Discovery with Cohort Studies. Springer Briefs in Electrical and Computer Engineering, 2015, , 51-66.	0.3	0
64	Inferring condition-specific miRNA activity from matched miRNA and mRNA expression data. Bioinformatics, 2014, 30, 3070-3077.	1.8	22
65	Identifying direct miRNA–mRNA causal regulatory relationships in heterogeneous data. Journal of Biomedical Informatics, 2014, 52, 438-447.	2.5	27
66	Inferring microRNA and transcription factor regulatory networks in heterogeneous data. BMC Bioinformatics, 2013, 14, 92.	1.2	35
67	Mining Causal Association Rules. , 2013, , .		32
68	Inferring microRNA–mRNA causal regulatory relationships from expression data. Bioinformatics, 2013, 29, 765-771.	1.8	75
69	Discovery of Causal Rules Using Partial Association. , 2012, , .		23