

Yu-Da Lin

List of Publications by Year in descending order

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Version: 2024-02-01

64
papers

780
citations

430843

18
h-index

580810

25
g-index

65
all docs

65
docs citations

65
times ranked

509
citing authors

#	ARTICLE	IF	CITATIONS
1	Evaluation of Breast Cancer Susceptibility Using Improved Genetic Algorithms to Generate Genotype SNP Barcodes. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013, 10, 361-371.	3.0	50
2	CMDR based differential evolution identifies the epistatic interaction in genome-wide association studies. <i>Bioinformatics</i> , 2017, 33, 2354-2362.	4.1	47
3	An Improved PSO Algorithm for Generating Protective SNP Barcodes in Breast Cancer. <i>PLoS ONE</i> , 2012, 7, e37018.	2.5	45
4	A Systematic Geneâ€“Gene and Geneâ€“Environment Interaction Analysis of DNA Repair Genes <i><i>XRCC1</i></i> , <i><i>XRCC2</i></i> , <i><i>XRCC3</i></i> , <i><i>XRCC4</i></i> , and Oral Cancer Risk. <i>OMICS A Journal of Integrative Biology</i> , 2015, 19, 238-247.	2.0	37
5	Single nucleotide polymorphism barcoding to evaluate oral cancer risk using odds ratioâ€“based genetic algorithms. <i>Kaohsiung Journal of Medical Sciences</i> , 2012, 28, 362-368.	1.9	34
6	Particle swarm optimization algorithm for analyzing SNPâ€“SNP interaction of renin-angiotensin system genes against hypertension. <i>Molecular Biology Reports</i> , 2013, 40, 4227-4233.	2.3	32
7	Multiobjective multifactor dimensionality reduction to detect SNPâ€“SNP interactions. <i>Bioinformatics</i> , 2018, 34, 2228-2236.	4.1	31
8	MDR-ER: Balancing Functions for Adjusting the Ratio in Risk Classes and Classification Errors for Imbalanced Cases and Controls Using Multifactor-Dimensionality Reduction. <i>PLoS ONE</i> , 2013, 8, e79387.	2.5	30
9	Breast cancer-associated high-order SNP-SNP interaction of CXCL12/CXCR4-related genes by an improved multifactor dimensionality reduction (MDR-ER). <i>Oncology Reports</i> , 2016, 36, 1739-1747.	2.6	28
10	Identifying the Association Rules between Clinicopathologic Factors and Higher Survival Performance in Operation-Centric Oral Cancer Patients Using the Apriori Algorithm. <i>BioMed Research International</i> , 2013, 2013, 1-7.	1.9	23
11	An efficiency analysis of high-order combinations of geneâ€“gene interactions using multifactor-dimensionality reduction. <i>BMC Genomics</i> , 2015, 16, 489.	2.8	23
12	A comparative analysis of chaotic particle swarm optimizations for detecting single nucleotide polymorphism barcodes. <i>Artificial Intelligence in Medicine</i> , 2016, 73, 23-33.	6.5	23
13	Identifying Risk Stratification Associated With a Cancer for Overall Survival by Deep Learning-Based CoxPH. <i>IEEE Access</i> , 2019, 7, 67708-67717.	4.2	22
14	Identifying association model for single-nucleotide polymorphisms of ORAI1 gene for breast cancer. <i>Cancer Cell International</i> , 2014, 14, 29.	4.1	20
15	Identification of SNP barcode biomarkers for genes associated with facial emotion perception using particle swarm optimization algorithm. <i>Annals of General Psychiatry</i> , 2014, 13, 15.	2.7	20
16	Preventive SNPâ€“SNP interactions in the mitochondrial displacement loop (D-loop) from chronic dialysis patients. <i>Mitochondrion</i> , 2013, 13, 698-704.	3.4	19
17	Genetic algorithm-generated SNP barcodes of the mitochondrial D-loop for chronic dialysis susceptibility. <i>Mitochondrial DNA</i> , 2014, 25, 231-237.	0.6	19
18	Applications of Deep Learning and Fuzzy Systems to Detect Cancer Mortality in Next-Generation Genomic Data. <i>IEEE Transactions on Fuzzy Systems</i> , 2021, , 1-1.	9.8	19

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19	Double-Bottom Chaotic Map Particle Swarm Optimization Based on Chi-Square Test to Determine Gene-Gene Interactions. <i>BioMed Research International</i> , 2014, 2014, 1-10.	1.9	18
20	Impact of risk factors on functional status in maintenance hemodialysis patients. <i>European Journal of Medical Research</i> , 2017, 22, 54.	2.2	18
21	Epistasis Analysis Using an Improved Fuzzy C-Means-Based Entropy Approach. <i>IEEE Transactions on Fuzzy Systems</i> , 2020, 28, 718-730.	9.8	18
22	High Order Gene-Gene Interactions in Eight Single Nucleotide Polymorphisms of Renin-Angiotensin System Genes for Hypertension Association Study. <i>BioMed Research International</i> , 2015, 2015, 1-11.	1.9	16
23	The Combinational Polymorphisms of <i>ORAI1</i> Gene Are Associated with Preventive Models of Breast Cancer in the Taiwanese. <i>BioMed Research International</i> , 2015, 2015, 1-7.	1.9	16
24	Genetic Algorithm Combined with a Local Search Method for Identifying Susceptibility Genes. <i>Journal of Artificial Intelligence and Soft Computing Research</i> , 2016, 6, 203-212.	4.3	15
25	Class Balanced Multifactor Dimensionality Reduction to Detect Gene-Gene Interactions. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, 17, 71-81.	3.0	14
26	Analysis of high-order SNP barcodes in mitochondrial D-loop for chronic dialysis susceptibility. <i>Journal of Biomedical Informatics</i> , 2016, 63, 112-119.	4.3	12
27	Catfish Taguchi-Based Binary Differential Evolution Algorithm for Analyzing Single Nucleotide Polymorphism Interactions in Chronic Dialysis. <i>IEEE Transactions on Nanobioscience</i> , 2018, 17, 291-299.	3.3	12
28	A Hybrid Approach for CpG Island Detection in the Human Genome. <i>PLoS ONE</i> , 2016, 11, e0144748.	2.5	11
29	Determination of the SNP-SNP Interaction between Breast Cancer Related Genes to Analyze the Disease Susceptibility. <i>International Journal of Machine Learning and Computing</i> , 2014, 4, 468-473.	0.6	11
30	Multiple-Criteria Decision Analysis-Based Multifactor Dimensionality Reduction for Detecting Gene-Gene Interactions. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2019, 23, 416-426.	6.3	10
31	Multiobjective differential evolution-based multifactor dimensionality reduction for detecting gene-gene interactions. <i>Scientific Reports</i> , 2017, 7, 12869.	3.3	8
32	Effect of Baseline Characteristics and Tumor Burden on Vaspin Expression and Progressive Disease in Operable Colorectal Cancer. <i>Diagnostics</i> , 2020, 10, 801.	2.6	7
33	Joint Analysis of SNP-SNP-Environment Interactions for Chronic Dialysis by an Improved Branch and Bound Algorithm. <i>Journal of Computational Biology</i> , 2017, 24, 1212-1225.	1.6	6
34	An improved fuzzy set-based multifactor dimensionality reduction for detecting epistasis. <i>Artificial Intelligence in Medicine</i> , 2020, 102, 101768.	6.5	6
35	Who Donates on Line? Segmentation Analysis and Marketing Strategies Based on Machine Learning for Online Charitable Donations in Taiwan. <i>IEEE Access</i> , 2021, 9, 52728-52740.	4.2	6
36	Lagrange interpolation-driven access control mechanism: Towards secure and privacy-preserving fusion of personal health records. <i>Knowledge-Based Systems</i> , 2022, 236, 107679.	7.1	6

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37	Application of Fuzzy-Based Support Vector Regression to Forecast of International Airport Freight Volumes. <i>Mathematics</i> , 2022, 10, 2399.	2.2	6
38	SNP-SNP Interaction Using Gauss Chaotic Map Particle Swarm Optimization to Detect Susceptibility to Breast Cancer. , 2014, , .		5
39	Effect of Money Supply, Population, and Rent on Real Estate: A Clustering Analysis in Taiwan. <i>Mathematics</i> , 2022, 10, 1155.	2.2	5
40	A CpGCluster-Teaching-Based Learning-Based Optimization for Prediction of CpG Islands in the Human Genome. <i>Journal of Computational Biology</i> , 2018, 25, 158-169.	1.6	4
41	Machine Learning Data Imputation and Prediction of Foraging Group Size in a Kleptoparasitic Spider. <i>Mathematics</i> , 2021, 9, 415.	2.2	4
42	SNP barcodes generated using particle swarm optimization to detect susceptibility to breast cancer. <i>Natural Science</i> , 2013, 05, 359-367.	0.4	4
43	tRNAfeature: An algorithm for tRNA features to identify tRNA genes in DNA sequences. <i>Journal of Theoretical Biology</i> , 2016, 404, 251-261.	1.7	3
44	Detecting SNP-SNP Interactions in Imbalanced Case-Control Study. <i>IEEE Access</i> , 2019, 7, 143036-143045.	4.2	3
45	Fuzzy Logic System Application for Detecting SNP-SNP Interaction. <i>IEEE Access</i> , 2020, 8, 49951-49960.	4.2	3
46	Multiobjective optimization-driven primer design mechanism: towards user-specified parameters of PCR primer. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	3
47	Effective hybrid approach for protein structure prediction in a two-dimensional Hydrophobic-Polar model. <i>Computers in Biology and Medicine</i> , 2019, 113, 103397.	7.0	2
48	An improved GA for identifying susceptibility genes in the presence of epistasis. , 2015, , .		1
49	High-performance computing for protein fold prediction. , 2017, , .		1
50	Improved Classification Method for Detecting Potential Interactions Between Genes. <i>Advances in Intelligent Systems and Computing</i> , 2019, , 394-403.	0.6	1
51	Identification of Kidney Clear Cell Carcinoma Mortality Risk-Associated Gene Mutation by Using a Random Survival Forest Approach. , 2020, , .		1
52	A Clustering-based Feature Selection for Automatic Labeling in Human Activity Recognition. , 2022, , .		1
53	A Clustering-Based Gauss Chaotic Mapping Particle Swarm Optimization for Auto Labeling in Human Activity Recognition. , 2021, , .		1
54	An Improved Natural PCR-RFLP Primer Design Method. , 2011, , .		0

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55	PCR-RFLP Primer Design Using Particle Swarm Optimization Combined with Chaotic Logistic Map. , 2012, , .		0
56	Taguchi-enhanced binary differential evolution algorithm. , 2017, , .		0
57	Improved Multifactor Dimensionality Reduction for Epistasis Detection. , 2018, , .		0
58	An Improved Multi-factor Dimensionality Reduction Approach to Identify Gene-Gene Interactions. Advances in Intelligent Systems and Computing, 2019, , 109-114.	0.6	0
59	Improved Multiobjective Multifactor Dimensionality Reduction using Fuzzy Theory. , 2019, , .		0
60	MOAI: a multi-outcome interaction identification approach reveals an interaction between vaspin and carcinoembryonic antigen on colorectal cancer prognosis. Briefings in Bioinformatics, 2022, 23, .	6.5	0
61	SNP Barcode for Breast Cancer Prediction using Catfish Particle Swarm Optimization. , 2012, , .		0
62	New Evaluation Measures for Multifactor Dimensionality Reduction in SNP-SNP Interaction Analysis. , 2020, , .		0
63	Fuzzy-based multiobjective multifactor dimensionality reduction for epistasis analysis. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, PP, 1-1.	3.0	0
64	Analyze influence factors in customerâ€™s insurance transaction by decision tree model. , 2021, , .		0