

Rajat K De

List of Publications by Year in descending order

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Version: 2024-02-01

65
papers

845
citations

623734

14
h-index

526287

27
g-index

68
all docs

68
docs citations

68
times ranked

1108
citing authors

#	ARTICLE	IF	CITATIONS
1	Immunoinformatics: an integrated scenario. <i>Immunology</i> , 2010, 131, 153-168.	4.4	116
2	Feature analysis: Neural network and fuzzy set theoretic approaches. <i>Pattern Recognition</i> , 1997, 30, 1579-1590.	8.1	90
3	Obesity: An Immunometabolic Perspective. <i>Frontiers in Endocrinology</i> , 2016, 7, 157.	3.5	77
4	Unsupervised feature selection using a neuro-fuzzy approach. <i>Pattern Recognition Letters</i> , 1998, 19, 997-1006.	4.2	75
5	Divisive Correlation Clustering Algorithm (DCCA) for grouping of genes: detecting varying patterns in expression profiles. <i>Bioinformatics</i> , 2008, 24, 1359-1366.	4.1	56
6	Comparing methods for metabolic network analysis and an application to metabolic engineering. <i>Gene</i> , 2013, 521, 1-14.	2.2	47
7	Estimating gene expression from DNA methylation and copy number variation: A deep learning regression model for multi-omics integration. <i>Genomics</i> , 2020, 112, 2833-2841.	2.9	36
8	Wnt signal transduction pathways: modules, development and evolution. <i>BMC Systems Biology</i> , 2016, 10, 44.	3.0	23
9	Selection of genes mediating certain cancers, using a neuro-fuzzy approach. <i>Neurocomputing</i> , 2014, 133, 122-140.	5.9	22
10	Catestatin improves insulin sensitivity by attenuating endoplasmic reticulum stress: In vivo and in silico validation. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 464-481.	4.1	21
11	Average correlation clustering algorithm (ACCA) for grouping of co-regulated genes with similar pattern of variation in their expression values. <i>Journal of Biomedical Informatics</i> , 2010, 43, 560-568.	4.3	20
12	Analyzing methods for path mining with applications in metabolomics. <i>Gene</i> , 2014, 534, 125-138.	2.2	18
13	Metabolic pathway engineering: Perspectives and applications. <i>Computer Methods and Programs in Biomedicine</i> , 2020, 192, 105436.	4.7	18
14	Unsupervised feature extraction using neuro-fuzzy approach. <i>Fuzzy Sets and Systems</i> , 2002, 126, 277-291.	2.7	14
15	Fuzzy Correlated Association Mining: Selecting altered associations among the genes, and some possible marker genes mediating certain cancers. <i>Applied Soft Computing Journal</i> , 2016, 38, 587-605.	7.2	13
16	An algorithm for modularization of MAPK and calcium signaling pathways: Comparative analysis among different species. <i>Journal of Biomedical Informatics</i> , 2007, 40, 726-749.	4.3	12
17	Incorporation of enzyme concentrations into FBA and identification of optimal metabolic pathways. <i>BMC Systems Biology</i> , 2008, 2, 65.	3.0	12
18	PyPredT6: A python-based prediction tool for identification of Type VI effector proteins. <i>Journal of Bioinformatics and Computational Biology</i> , 2019, 17, 1950019.	0.8	11

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19	Interval based fuzzy systems for identification of important genes from microarray gene expression data: Application to carcinogenic development. <i>Journal of Biomedical Informatics</i> , 2009, 42, 1022-1028.	4.3	10
20	Linguistic recognition system for identification of some possible genes mediating the development of lung adenocarcinoma. <i>Information Fusion</i> , 2009, 10, 260-269.	19.1	10
21	OCDD: an obesity and co-morbid disease database. <i>BioData Mining</i> , 2017, 10, 33.	4.0	10
22	Exploring the Altered Dynamics of Mammalian Central Carbon Metabolic Pathway in Cancer Cells: A Classical Control Theoretic Approach. <i>PLoS ONE</i> , 2015, 10, e0137728.	2.5	10
23	Deciphering the cause of evolutionary variance within intrinsically disordered regions in human proteins. <i>Journal of Biomolecular Structure and Dynamics</i> , 2017, 35, 233-249.	3.5	9
24	Gradient Descent Optimization in Gene Regulatory Pathways. <i>PLoS ONE</i> , 2010, 5, e12475.	2.5	8
25	Computational neuroscience and neuroinformatics: Recent progress and resources. <i>Journal of Biosciences</i> , 2018, 43, 1037-1054.	1.1	8
26	CNV-CH: A Convex Hull Based Segmentation Approach to Detect Copy Number Variations (CNV) Using Next-Generation Sequencing Data. <i>PLoS ONE</i> , 2015, 10, e0135895.	2.5	8
27	CASSL: A cell-type annotation method for single cell transcriptomics data using semi-supervised learning. <i>Applied Intelligence</i> , 2023, 53, 1287-1305.	5.3	7
28	MODELING THE OPTIMAL CENTRAL CARBON METABOLIC PATHWAYS UNDER FEEDBACK INHIBITION USING FLUX BALANCE ANALYSIS. <i>Journal of Bioinformatics and Computational Biology</i> , 2012, 10, 1250019.	0.8	6
29	Identification of certain cancer-mediating genes using Gaussian fuzzy cluster validity index. <i>Journal of Biosciences</i> , 2015, 40, 741-754.	1.1	6
30	An integrated pathway system modeling of <i>Saccharomyces cerevisiae</i> HOG pathway: a Petri net based approach. <i>Molecular Biology Reports</i> , 2013, 40, 1103-1125.	2.3	5
31	Disease Co-Morbidity and the Human Wnt Signaling Pathway: A Network-Wise Study. <i>OMICS A Journal of Integrative Biology</i> , 2013, 17, 318-337.	2.0	5
32	A Model for Distributed Processing and Analyses of NGS Data under Map-Reduce Paradigm. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 827-840.	3.0	5
33	Comparative Analysis of Cluster Validity Indices in Identifying Some Possible Genes Mediating Certain Cancers. <i>Molecular Informatics</i> , 2013, 32, 347-354.	2.5	4
34	A fuzzy logic controller based approach to model the switching mechanism of the mammalian central carbon metabolic pathway in normal and cancer cells. <i>Molecular BioSystems</i> , 2016, 12, 2490-2505.	2.9	4
35	Structural disorder: a tool for housekeeping proteins performing tissue-specific interactions. <i>Journal of Biomolecular Structure and Dynamics</i> , 2016, 34, 1930-1945.	3.5	4
36	GenSeg and MR-GenSeg: A Novel Segmentation Algorithm and its Parallel MapReduce Based Approach for Identifying Genomic Regions With Copy Number Variations. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, 19, 443-454.	3.0	4

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37	Neuro-fuzzy Methodology for Selecting Genes Mediating Lung Cancer. Lecture Notes in Computer Science, 2011, , 388-393.	1.3	4
38	A connectionist model for selection of cases. Information Sciences, 2001, 132, 179-194.	6.9	3
39	Development of a fuzzy entropy based method for detecting altered gene-gene interactions in carcinogenic state. Journal of Intelligent and Fuzzy Systems, 2014, 26, 2731-2746.	1.4	3
40	Succinate aggravates NAFLD progression to liver cancer on the onset of obesity: An <i>in silico</i> model. Journal of Bioinformatics and Computational Biology, 2018, 16, 1850008.	0.8	3
41	A control theoretic three timescale model for analyzing energy management in mammalian cancer cells. Computational and Structural Biotechnology Journal, 2021, 19, 477-508.	4.1	3
42	Epidemiological challenges in pandemic coronavirus disease (COVID-19): Role of artificial intelligence. Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery, 2022, 12, .	6.8	3
43	Modularized study of human calcium signalling pathway. Journal of Biosciences, 2007, 32, 1009-1017.	1.1	2
44	Detecting breakdown points in metabolic networks. Computational Biology and Chemistry, 2011, 35, 371-380.	2.3	2
45	SAGPAR: Structural Grammar-based automated pathway reconstruction. Interdisciplinary Sciences, Computational Life Sciences, 2012, 4, 116-127.	3.6	2
46	Evolutionary growth of certain metabolic pathways involved in the functioning of GAD and INS genes in Type 1 Diabetes Mellitus: Their architecture and stability. Computers in Biology and Medicine, 2015, 61, 19-35.	7.0	2
47	A novel locally guided genome reassembling technique using an artificial ant system. Applied Intelligence, 2015, 43, 397-411.	5.3	2
48	Feature Selection and Fuzzy Rule Mining for Epileptic Patients from Clinical EEG Data. Lecture Notes in Computer Science, 2017, , 87-95.	1.3	2
49	Slow update stochastic simulation algorithms for modeling complex biochemical networks. BioSystems, 2017, 162, 135-146.	2.0	2
50	Block Search Stochastic Simulation Algorithm (BISSA): A Fast Stochastic Simulation Algorithm for Modeling Large Biochemical Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 2111-2123.	3.0	2
51	A Model of an Integrated Immune System Pathway in Homo sapiens and Its Interaction with Superantigen Producing Expression Regulatory Pathway in Staphylococcus aureus: Comparing Behavior of Pathogen Perturbed and Unperturbed Pathway. PLoS ONE, 2013, 8, e80918.	2.5	2
52	Cluster Quality based Non-Reductional (CQNR) oversampling technique and effector protein predictor based on 3D structure (EPP3D) of proteins. Computers in Biology and Medicine, 2019, 112, 103374.	7.0	1
53	Gaussian Fuzzy Index (GFI) for Cluster Validation: Identification of High Quality Biologically Enriched Clusters of Genes and Selection of Some Possible Genes Mediating Lung Cancer. Lecture Notes in Computer Science, 2013, , 680-687.	1.3	1
54	Developmental Trend Derived from Modules of Wnt Signaling Pathways. Lecture Notes in Computer Science, 2011, , 400-405.	1.3	1

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55	A novel noise handling method to improve clustering of gene expression patterns. BMC Bioinformatics, 2011, 12, .	2.6	0
56	Modeling host-pathogen interactions: <i>H. sapiens</i> as a host and <i>C. difficile</i> as a pathogen. Journal of Molecular Recognition, 2012, 25, 474-485.	2.1	0
57	Simulating an Infection Growth Model in Certain Healthy Metabolic Pathways of Homo sapiens for Highlighting Their Role in Type I Diabetes mellitus Using Fire-Spread Strategy, Feedbacks and Sensitivities. PLoS ONE, 2013, 8, e69724.	2.5	0
58	Second order optimization for the inference of gene regulatory pathways. Statistical Applications in Genetics and Molecular Biology, 2014, 13, 19-33.	0.6	0
59	Concepts of relative sample outlier (RSO) and weighted sample similarity (WSS) for improving performance of clustering genes: co-function and co-regulation. International Journal of Data Mining and Bioinformatics, 2015, 11, 314.	0.1	0
60	A module tree of Wnt signal transduction pathways. , 2015, , .		0
61	ASAPP: Architectural Similarity-based Automated Pathway Prediction System and its Application in Host-Pathogen Interactions. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 17, 1-1.	3.0	0
62	Expected return time to the initial state for biochemical systems with linear cyclic chains: unidirectional and bidirectional reactions. Sadhana - Academy Proceedings in Engineering Sciences, 2019, 44, 1.	1.3	0
63	Two-Class in Silico Categorization of Intermediate Epileptic EEG Data. Lecture Notes in Computer Science, 2019, , 184-192.	1.3	0
64	Pattern and Rule Mining for Identifying Signatures of Epileptic Patients from Clinical EEG Data. Fundamenta Informaticae, 2020, 176, 141-166.	0.4	0
65	Computational neuroscience and neuroinformatics: Recent progress and resources. Journal of Biosciences, 2018, 43, 1037-1054.	1.1	0