

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	CASSL: A cell-type annotation method for single cell transcriptomics data using semi-supervised learning. Applied Intelligence, 2023, 53, 1287-1305.	5.3	7
2	GenSeg and MR-GenSeg: A Novel Segmentation Algorithm and its Parallel MapReduce Based Approach for Identifying Genomic Regions With Copy Number Variations. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 443-454.	3.0	4
3	Block Search Stochastic Simulation Algorithm (<i>BLSSA</i>): 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
4	Epidemiological challenges in pandemic coronavirus disease (<i>COVID-19</i>): Role of artificial intelligence. Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery, 2022, 12, .	6.8	3
5	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
6	Metabolic pathway engineering: Perspectives and applications. Computer Methods and Programs in Biomedicine, 2020, 192, 105436.	4.7	18
7	Catestatin improves insulin sensitivity by attenuating endoplasmic reticulum stress: In vivo and in silico validation. Computational and Structural Biotechnology Journal, 2020, 18, 464-481.	4.1	21
8	Estimating gene expression from DNA methylation and copy number variation: A deep learning regression model for multi-omics integration. Genomics, 2020, 112, 2833-2841.	2.9	36
9	Pattern and Rule Mining for Identifying Signatures of Epileptic Patients from Clinical EEG Data. Fundamenta Informaticae, 2020, 176, 141-166.	0.4	0
10	PyPredT6: A python-based prediction tool for identification of Type VI effector proteins. Journal of Bioinformatics and Computational Biology, 2019, 17, 1950019.	0.8	11
11	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
12	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
13	A Model for Distributed Processing and Analyses of NGS Data under Map-Reduce Paradigm. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 827-840.	3.0	5
14	Two-Class in Silico Categorization of Intermediate Epileptic EEG Data. Lecture Notes in Computer Science, 2019, , 184-192.	1.3	0
15	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
16	Computational neuroscience and neuroinformatics: Recent progress and resources. Journal of Biosciences, 2018, 43, 1037-1054.	1.1	8
17	Succinate aggravates NAFLD progression to liver cancer on the onset of obesity: An in silico model. Journal of Bioinformatics and Computational Biology, 2018, 16, 1850008.	0.8	3
18	Computational neuroscience and neuroinformatics: Recent progress and resources. Journal of Biosciences, 2018, 43, 1037-1054.	1.1	0

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19	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
20	Feature Selection and Fuzzy Rule Mining for Epileptic Patients from Clinical EEG Data. <i>Lecture Notes in Computer Science</i> , 2017, , 87-95.	1.3	2
21	Slow update stochastic simulation algorithms for modeling complex biochemical networks. <i>BioSystems</i> , 2017, 162, 135-146.	2.0	2
22	OCDD: an obesity and co-morbid disease database. <i>BioData Mining</i> , 2017, 10, 33.	4.0	10
23	Obesity: An Immunometabolic Perspective. <i>Frontiers in Endocrinology</i> , 2016, 7, 157.	3.5	77
24	Wnt signal transduction pathways: modules, development and evolution. <i>BMC Systems Biology</i> , 2016, 10, 44.	3.0	23
25	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
26	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
27	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
28	Concepts of relative sample outlier (RSO) and weighted sample similarity (WSS) for improving performance of clustering genes: co-function and co-regulation. <i>International Journal of Data Mining and Bioinformatics</i> , 2015, 11, 314.	0.1	0
29	A module tree of Wnt signal transduction pathways. , 2015, , .		0
30	Evolutionary growth of certain metabolic pathways involved in the functioning of GAD and INS genes in Type 1 Diabetes Mellitus: Their architecture and stability. <i>Computers in Biology and Medicine</i> , 2015, 61, 19-35.	7.0	2
31	A novel locally guided genome reassembling technique using an artificial ant system. <i>Applied Intelligence</i> , 2015, 43, 397-411.	5.3	2
32	Identification of certain cancer-mediating genes using Gaussian fuzzy cluster validity index. <i>Journal of Biosciences</i> , 2015, 40, 741-754.	1.1	6
33	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
34	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
35	Development of a fuzzy entropy based method for detecting altered gene-gene interactions in carcinogenic state. <i>Journal of Intelligent and Fuzzy Systems</i> , 2014, 26, 2731-2746.	1.4	3
36	Second order optimization for the inference of gene regulatory pathways. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2014, 13, 19-33.	0.6	0

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37	Selection of genes mediating certain cancers, using a neuro-fuzzy approach. <i>Neurocomputing</i> , 2014, 133, 122-140.	5.9	22
38	Analyzing methods for path mining with applications in metabolomics. <i>Gene</i> , 2014, 534, 125-138.	2.2	18
39	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
40	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
41	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
42	Comparing methods for metabolic network analysis and an application to metabolic engineering. <i>Gene</i> , 2013, 521, 1-14.	2.2	47
43	Simulating an Infection Growth Model in Certain Healthy Metabolic Pathways of <i>Homo sapiens</i> for Highlighting Their Role in Type I Diabetes mellitus Using Fire-Spread Strategy, Feedbacks and Sensitivities. <i>PLoS ONE</i> , 2013, 8, e69724.	2.5	0
44	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. <i>Lecture Notes in Computer Science</i> , 2013, , 680-687.	1.3	1
45	A Model of an Integrated Immune System Pathway in <i>Homo sapiens</i> and Its Interaction with Superantigen Producing Expression Regulatory Pathway in <i>Staphylococcus aureus</i> : Comparing Behavior of Pathogen Perturbed and Unperturbed Pathway. <i>PLoS ONE</i> , 2013, 8, e80918.	2.5	2
46	Modeling host-pathogen interactions: <i>H. sapiens</i> as a host and <i>C. difficile</i> as a pathogen. <i>Journal of Molecular Recognition</i> , 2012, 25, 474-485.	2.1	0
47	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
48	SAGPAR: Structural Grammar-based automated pathway reconstruction. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2012, 4, 116-127.	3.6	2
49	Detecting breakdown points in metabolic networks. <i>Computational Biology and Chemistry</i> , 2011, 35, 371-380.	2.3	2
50	A novel noise handling method to improve clustering of gene expression patterns. <i>BMC Bioinformatics</i> , 2011, 12, .	2.6	0
51	Neuro-fuzzy Methodology for Selecting Genes Mediating Lung Cancer. <i>Lecture Notes in Computer Science</i> , 2011, , 388-393.	1.3	4
52	Developmental Trend Derived from Modules of Wnt Signaling Pathways. <i>Lecture Notes in Computer Science</i> , 2011, , 400-405.	1.3	1
53	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
54	Immunoinformatics: an integrated scenario. <i>Immunology</i> , 2010, 131, 153-168.	4.4	116

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55	Gradient Descent Optimization in Gene Regulatory Pathways. PLoS ONE, 2010, 5, e12475.	2.5	8
56	Interval based fuzzy systems for identification of important genes from microarray gene expression data: Application to carcinogenic development. Journal of Biomedical Informatics, 2009, 42, 1022-1028.	4.3	10
57	Linguistic recognition system for identification of some possible genes mediating the development of lung adenocarcinoma. Information Fusion, 2009, 10, 260-269.	19.1	10
58	Incorporation of enzyme concentrations into FBA and identification of optimal metabolic pathways. BMC Systems Biology, 2008, 2, 65.	3.0	12
59	Divisive Correlation Clustering Algorithm (DCCA) for grouping of genes: detecting varying patterns in expression profiles. Bioinformatics, 2008, 24, 1359-1366.	4.1	56
60	An algorithm for modularization of MAPK and calcium signaling pathways: Comparative analysis among different species. Journal of Biomedical Informatics, 2007, 40, 726-749.	4.3	12
61	Modularized study of human calcium signalling pathway. Journal of Biosciences, 2007, 32, 1009-1017.	1.1	2
62	Unsupervised feature extraction using neuro-fuzzy approach. Fuzzy Sets and Systems, 2002, 126, 277-291.	2.7	14
63	A connectionist model for selection of cases. Information Sciences, 2001, 132, 179-194.	6.9	3
64	Unsupervised feature selection using a neuro-fuzzy approach. Pattern Recognition Letters, 1998, 19, 997-1006.	4.2	75
65	Feature analysis: Neural network and fuzzy set theoretic approaches. Pattern Recognition, 1997, 30, 1579-1590.	8.1	90