

Mohd Saberi Mohamad

List of Publications by Year in descending order

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162
papers

1,688
citations

489802

18
h-index

425179

34
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169
all docs

169
docs citations

169
times ranked

2056
citing authors

#	ARTICLE	IF	CITATIONS
1	A Hybrid of Bees Algorithm and Regulatory On/Off Minimization for Optimizing Lactate Production. Lecture Notes in Networks and Systems, 2022, , 95-104.	0.5	0
2	An Enhancement of Succinate Production Using a Hybrid of Bacterial Foraging Optimization Algorithm. Lecture Notes in Networks and Systems, 2022, , 591-601.	0.5	0
3	A hybrid of Bees algorithm and regulatory on/off minimization for optimizing lactate and succinate production. Journal of Integrative Bioinformatics, 2022, .	1.0	0
4	Deepint.net: A Rapid Deployment Platform for Smart Territories. Sensors, 2021, 21, 236.	2.1	36
5	Supervised and Unsupervised Machine Learning for Cancer Classification: Recent Development. , 2021, , .		2
6	<i>In silico</i> gene knockout prediction using a hybrid of Bat algorithm and minimization of metabolic adjustment. Journal of Integrative Bioinformatics, 2021, 18, .	1.0	0
7	SLC17A3 rs9379800 and Ischemic Stroke Susceptibility at the Northern Region of Malaysia. Journal of Stroke and Cerebrovascular Diseases, 2021, 30, 105908.	0.7	5
8	A Review on Recent Progress in Machine Learning and Deep Learning Methods for Cancer Classification on Gene Expression Data. Processes, 2021, 9, 1466.	1.3	16
9	Enhanced Directed Random Walk for the Identification of Breast Cancer Prognostic Markers from Multiclass Expression Data. Entropy, 2021, 23, 1232.	1.1	3
10	A Hybrid of Bat Algorithm and Minimization of Metabolic Adjustment for Succinate and Lactate Production. Advances in Intelligent Systems and Computing, 2021, , 166-175.	0.5	0
11	A Hybrid of Particle Swarm Optimization and Minimization of Metabolic Adjustment for Ethanol Production of Escherichia Coli. Advances in Intelligent Systems and Computing, 2020, , 36-44.	0.5	2
12	Comparative Study of One-Class Based Anomaly Detection Techniques for a Bicomponent Mixing Machine Monitoring. Cybernetics and Systems, 2020, 51, 649-667.	1.6	10
13	A Hybrid of Particle Swarm Optimization and Harmony Search to Estimate Kinetic Parameters in Arabidopsis thaliana. Processes, 2020, 8, 921.	1.3	2
14	A Diversity-Based Adaptive Synchronous-Asynchronous Switching Simulated Kalman Filter Optimizer. Lecture Notes in Electrical Engineering, 2020, , 113-126.	0.3	0
15	Gene Regulatory Network Construction of Ovarian Cancer Based on Passing Attributes between Network for Data Assimilation. , 2020, , .		0
16	Comparison of Optimization-Modelling Methods for Metabolites Production in <i>Escherichia coli</i> . Journal of Integrative Bioinformatics, 2020, 17, .	1.0	5
17	A Hybrid of Simple Constrained Artificial Bee Colony Algorithm and Flux Balance Analysis for Enhancing Lactate and Succinate in Escherichia Coli. Advances in Intelligent Systems and Computing, 2019, , 1-8.	0.5	1
18	Parameter Estimation of Essential Amino Acids in Arabidopsis thaliana Using Hybrid of Bees Algorithm and Harmony Search. Advances in Intelligent Systems and Computing, 2019, , 9-16.	0.5	1

#	ARTICLE	IF	CITATIONS
19	Evaluation of Different Horizon Lengths in Single-agent Finite Impulse Response Optimizer. , 2019, , .		0
20	A non-dominated sorting Differential Search Algorithm Flux Balance Analysis (ndsDSAFBA) for in silico multiobjective optimization in identifying reactions knockout. Computers in Biology and Medicine, 2019, 113, 103390.	3.9	7
21	Oppositional Learning Prediction Operator with Jumping Rate for Simulated Kalman Filter. , 2019, , .		1
22	Machine Learning Models for Electricity Consumption Forecasting: A Review. , 2019, , .		32
23	A Review of Computational Methods for Clustering Genes with Similar Biological Functions. Processes, 2019, 7, 550.	1.3	10
24	Missing-Values Imputation Algorithms for Microarray Gene Expression Data. Methods in Molecular Biology, 2019, 1986, 255-266.	0.4	14
25	Identifying a Gene Knockout Strategy Using a Hybrid of Simple Constrained Artificial Bee Colony Algorithm and Flux Balance Analysis to Enhance the Production of Succinate and Lactate in Escherichia Coli. Interdisciplinary Sciences, Computational Life Sciences, 2019, 11, 33-44.	2.2	4
26	Cooperative enhanced scatter search with opposition-based learning schemes for parameter estimation in high dimensional kinetic models of biological systems. Expert Systems With Applications, 2019, 116, 131-146.	4.4	11
27	An Improved Scatter Search Algorithm for Parameter Estimation in Large-Scale Kinetic Models of Biochemical Systems. Current Proteomics, 2019, 16, 427-438.	0.1	1
28	Topologically significant directed random walk with applied walker network in cancer environment. Pakistan Journal of Pharmaceutical Sciences, 2019, 32, 1395-1408.	0.2	0
29	NAHAL-Flex: A Numerical and Alphabetical Hinge Detection Algorithm for Flexible Protein Structure Alignment. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 934-943.	1.9	2
30	A hybrid of Cuckoo Search and Minimization of Metabolic Adjustment to optimize metabolites production in genome-scale models. Computers in Biology and Medicine, 2018, 102, 112-119.	3.9	9
31	Multi-Agent Systems Applications in Energy Optimization Problems: A State-of-the-Art Review. Energies, 2018, 11, 1928.	1.6	98
32	A Direct Proof of Improved Biased Random Walk with Gastric Cancer Dataset. , 2018, , .		1
33	Single-solution Simulated Kalman Filter algorithm for global optimisation problems. Sadhana - Academy Proceedings in Engineering Sciences, 2018, 43, 1.	0.8	9
34	Improving particle swarm optimization via adaptive switching asynchronous " synchronous update. Applied Soft Computing Journal, 2018, 72, 298-311.	4.1	24
35	An application of simulated Kalman filter optimization algorithm for parameter tuning in proportional-integral-derivative controllers for automatic voltage regulator system. , 2018, , .		11
36	A Review of Computational Approaches to Predict Gene Functions. Current Bioinformatics, 2018, 13, 373-386.	0.7	4

#	ARTICLE	IF	CITATIONS
37	An Effective Pre-Processing Phase for Gene Expression Classification. Indonesian Journal of Electrical Engineering and Computer Science, 2018, 11, 1223.	0.7	1
38	An enhanced scatter search with combined opposition-based learning for parameter estimation in large-scale kinetic models of biochemical systems. Engineering Applications of Artificial Intelligence, 2017, 62, 164-180.	4.3	28
39	Samira-VP: A simple protein alignment method with rechecking the alphabet vector positions. Journal of Bioinformatics and Computational Biology, 2017, 15, 1750004.	0.3	0
40	An improved hybrid of particle swarm optimization and the gravitational search algorithm to produce a kinetic parameter estimation of aspartate biochemical pathways. BioSystems, 2017, 162, 81-89.	0.9	11
41	An enhanced topologically significant directed random walk in cancer classification using gene expression datasets. Saudi Journal of Biological Sciences, 2017, 24, 1828-1841.	1.8	12
42	A Direct Proof of Significant Directed Random Walk. IOP Conference Series: Materials Science and Engineering, 2017, 235, 012004.	0.3	5
43	Classification of Colorectal Cancer Using Clustering and Feature Selection Approaches. Advances in Intelligent Systems and Computing, 2017, , 58-65.	0.5	1
44	Specific Tuning Parameter for Directed Random Walk Algorithm Cancer Classification. International Journal on Advanced Science, Engineering and Information Technology, 2017, 7, 176.	0.2	6
45	Improved Support Vector Machine Using Multiple SVM-RFE for Cancer Classification. International Journal on Advanced Science, Engineering and Information Technology, 2017, 7, 1589.	0.2	19
46	An Improved Parallelized mRMR for Gene Subset Selection in Cancer Classification. International Journal on Advanced Science, Engineering and Information Technology, 2017, 7, 1595.	0.2	3
47	Pathway-based Analysis with Support Vector Machine (SVM-LASSO) for Gene Selection and Classification. International Journal on Advanced Science, Engineering and Information Technology, 2017, 7, 1609.	0.2	2
48	A Review of Gene Selection Tools in Classifying Cancer Microarray Data. Current Bioinformatics, 2017, 12, 202-212.	0.7	11
49	Simulated Kalman Filter with Randomized Q and R Parameters. Proceedings of International Conference on Artificial Life and Robotics, 2017, 22, 711-714.	0.1	8
50	K-Means Clustering with Infinite Feature Selection for Classification Tasks in Gene Expression Data. Advances in Intelligent Systems and Computing, 2017, , 50-57.	0.5	4
51	Metaheuristic Optimization for Parameter Estimation in Kinetic Models of Biological Systems - Recent Development and Future Direction. Current Bioinformatics, 2017, 12, .	0.7	1
52	A Hybrid of Integer Differential Bees and Flux Balance Analysis for Improving Succinate and Lactate Production. International Journal on Advanced Science, Engineering and Information Technology, 2017, 7, 1615.	0.2	1
53	Multi-objective Optimization of Biochemical System Production Using an Improve Newton Competitive Differential Evolution Method. International Journal on Advanced Science, Engineering and Information Technology, 2017, 7, 1535.	0.2	6
54	Review on Local Binary Patterns Variants as Texture Descriptors for Copy-Move Forgery Detection. International Journal on Advanced Science, Engineering and Information Technology, 2017, 7, 1678.	0.2	1

#	ARTICLE	IF	CITATIONS
55	IN SILICO GENE DELETION OF ESCHERICHIA COLI FOR OPTIMAL ETHANOL PRODUCTION USING A HYBRID ALGORITHM OF PARTICLE SWARM OPTIMIZATION AND FLUX BALANCE ANALYSIS. Jurnal Teknologi (Sciences) Tj ETQq1 1 0.764314 rsB	1.0	1
56	A Kalman Filter approach to PCB drill path optimization problem. , 2016, , .		21
57	Identification of informative genes and pathways using an improved penalized support vector machine with a weighting scheme. Computers in Biology and Medicine, 2016, 77, 102-115.	3.9	23
58	An improved gSVM-SCADL2 with firefly algorithm for identification of informative genes and pathways. International Journal of Bioinformatics Research and Applications, 2016, 12, 72.	0.1	8
59	Investigation of the Effects of Imputation Methods for Gene Regulatory Networks Modelling Using Dynamic Bayesian Networks. Advances in Intelligent Systems and Computing, 2016, , 413-421.	0.5	3
60	A Hybrid of Harmony Search and Minimization of Metabolic Adjustment for Optimization of Succinic Acid Production. Advances in Intelligent Systems and Computing, 2016, , 183-191.	0.5	1
61	Simulated Kalman Filter: A Novel Estimation-Based Metaheuristic Optimization Algorithm. Advanced Science Letters, 2016, 22, 2941-2946.	0.2	30
62	A Review of Gene Knockout Strategies for Microbial Cells. Recent Patents on Biotechnology, 2016, 9, 176-197.	0.4	6
63	A Newton Cooperative Genetic Algorithm Method for In Silico Optimization of Metabolic Pathway Production. PLoS ONE, 2015, 10, e0126199.	1.1	12
64	A Review on Bioinformatics Enrichment Analysis Tools Towards Functional Analysis of High Throughput Gene Set Data. Current Proteomics, 2015, 12, 14-27.	0.1	19
65	Gene Knockout Identification Using an Extension of Bees Hill Flux Balance Analysis. BioMed Research International, 2015, 2015, 1-10.	0.9	9
66	Modelling the Longevity of Dental Restorations by means of a CBR System. BioMed Research International, 2015, 2015, 1-10.	0.9	21
67	Metabolites production improvement by identifying minimal genomes and essential genes using flux balance analysis. International Journal of Data Mining and Bioinformatics, 2015, 12, 85.	0.1	0
68	Software for detecting gene-gene interactions in genome wide association studies. Biotechnology and Bioprocess Engineering, 2015, 20, 662-676.	1.4	4
69	Optimising the production of succinate and lactate in Escherichia coli using a hybrid of artificial bee colony algorithm and minimisation of metabolic adjustment. Journal of Bioscience and Bioengineering, 2015, 119, 363-368.	1.1	14
70	BIOLOGICAL ANALYSIS OF MICROARRAY DATA USING ORTHOGONAL FORWARD SELECTION WITH A CLUSTERING APPROACH. Journal of Biological Systems, 2015, 23, 275-288.	0.5	1
71	A Review of Software for Predicting Gene Function. International Journal of Bio-Science and Bio-Technology, 2015, 7, 57-70.	0.2	3
72	Identifying a gene knockout strategy using a hybrid of the bat algorithm and flux balance analysis to enhance the production of succinate and lactate in Escherichia coli. Biotechnology and Bioprocess Engineering, 2015, 20, 349-357.	1.4	11

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73	Gene knockout identification for metabolite production improvement using a hybrid of genetic ant colony optimization and flux balance analysis. <i>Biotechnology and Bioprocess Engineering</i> , 2015, 20, 685-693.	1.4	10
74	A Review of Cancer Classification Software for Gene Expression Data. <i>International Journal of Bio-Science and Bio-Technology</i> , 2015, 7, 89-108.	0.2	7
75	A Review on Metabolic Pathway Analysis in Biological Production. <i>Mini-Reviews in Organic Chemistry</i> , 2015, 12, 506-523.	0.6	2
76	A Review on the Bioinformatics Tools for Neuroimaging. <i>The Malaysian Journal of Medical Sciences</i> , 2015, 22, 9-19.	0.3	3
77	A Review on Missing Value Imputation Algorithms for Microarray Gene Expression Data. <i>Current Bioinformatics</i> , 2014, 9, 18-22.	0.7	48
78	Differential Bees Flux Balance Analysis with OptKnock for In Silico Microbial Strains Optimization. <i>PLoS ONE</i> , 2014, 9, e102744.	1.1	56
79	A Synchronous-Asynchronous Particle Swarm Optimisation Algorithm. <i>Scientific World Journal, The</i> , 2014, 2014, 1-17.	0.8	11
80	Feature Selection and Classifier Parameters Estimation for EEG Signals Peak Detection Using Particle Swarm Optimization. <i>Scientific World Journal, The</i> , 2014, 2014, 1-13.	0.8	33
81	Parameter Estimation by Using an Improved Bee Memory Differential Evolution Algorithm (IBMDE) to Simulate Biochemical Pathways. <i>Current Bioinformatics</i> , 2014, 9, 65-75.	0.7	5
82	USING AN IMPROVED BEE MEMORY DIFFERENTIAL EVOLUTION ALGORITHM FOR PARAMETER ESTIMATION TO SIMULATE BIOCHEMICAL PATHWAYS. <i>Journal of Biological Systems</i> , 2014, 22, 101-121.	0.5	1
83	A gene knockout strategy for succinate production using a hybrid algorithm of bees algorithm and minimization of metabolic adjustment. , 2014, , .		1
84	A Dynamic Bayesian Network-based Model for Inferring Gene Regulatory Networks from Gene Expression Data. <i>International Journal of Bio-Science and Bio-Technology</i> , 2014, 6, 41-52.	0.2	2
85	A group-specific tuning parameter for hybrid of SVM and SCAD in identification of informative genes and pathways. <i>International Journal of Data Mining and Bioinformatics</i> , 2014, 10, 146.	0.1	7
86	Continuous Dynamic Bayesian Network for gene regulatory network modelling. , 2014, , .		2
87	Inferring gene regulatory networks from perturbed gene expression data using a dynamic Bayesian network with a Markov Chain Monte Carlo algorithm. , 2014, , .		1
88	Random Forest and Gene Ontology for functional analysis of microarray data. , 2014, , .		2
89	A Review of Feature Extraction Software for Microarray Gene Expression Data. <i>BioMed Research International</i> , 2014, 2014, 1-15.	0.9	18
90	A hybrid of bees algorithm and flux balance analysis with OptKnock as a platform for in silico optimization of microbial strains. <i>Bioprocess and Biosystems Engineering</i> , 2014, 37, 521-532.	1.7	28

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91	Identification of gene knockout strategies using a hybrid of an ant colony optimization algorithm and flux balance analysis to optimize microbial strains. <i>Computational Biology and Chemistry</i> , 2014, 53, 175-183.	1.1	4
92	Database and tools for metabolic network analysis. <i>Biotechnology and Bioprocess Engineering</i> , 2014, 19, 568-585.	1.4	19
93	A hybrid of ant colony optimization and minimization of metabolic adjustment to improve the production of succinic acid in <i>Escherichia coli</i> . <i>Computers in Biology and Medicine</i> , 2014, 49, 74-82.	3.9	12
94	A review on the computational approaches for gene regulatory network construction. <i>Computers in Biology and Medicine</i> , 2014, 48, 55-65.	3.9	216
95	A hybrid of bees algorithm and flux balance analysis (BAFBA) for the optimisation of microbial strains. <i>International Journal of Data Mining and Bioinformatics</i> , 2014, 10, 225.	0.1	9
96	An improved differential evolution algorithm for enhancing biochemical pathways simulation and production. <i>International Journal of Data Mining and Bioinformatics</i> , 2014, 10, 424.	0.1	0
97	Multiagent Application in Mobile Environments to Data Collection in Park Zones. <i>Advances in Intelligent Systems and Computing</i> , 2014, , 251-259.	0.5	2
98	A Review on Modelling Methods, Pathway Simulation Software and Recent Development on Differential Evolution Algorithms for Metabolic Pathways in Systems Biology. <i>Current Bioinformatics</i> , 2014, 9, 509-521.	0.7	6
99	Current Development and Review of Dynamic Bayesian Network-Based Methods for Inferring Gene Regulatory Networks from Gene Expression Data. <i>Current Bioinformatics</i> , 2014, 9, 531-539.	0.7	9
100	HomeCare, Elder People Monitoring System and TV Communication. <i>Communications in Computer and Information Science</i> , 2014, , 111-120.	0.4	0
101	Parameter Estimation Using Improved Differential Evolution And Bacterial Foraging Algorithms To Model Tyrosine Production In <i>Mus Musculus</i> (Mouse). <i>Jurnal Teknologi (Sciences and Engineering)</i> , 2014, 72, .	0.3	0
102	Investigating the effects of imputation methods for modelling gene networks using a dynamic bayesian network from gene expression data. <i>The Malaysian Journal of Medical Sciences</i> , 2014, 21, 20-7.	0.3	7
103	An enhancement of binary particle swarm optimization for gene selection in classifying cancer classes. <i>Algorithms for Molecular Biology</i> , 2013, 8, 15.	0.3	33
104	Multiple Gene Sets for Cancer Classification Using Gene Range Selection Based on Random Forest. <i>Lecture Notes in Computer Science</i> , 2013, , 385-393.	1.0	5
105	A Review for Detecting Gene-Gene Interactions Using Machine Learning Methods in Genetic Epidemiology. <i>BioMed Research International</i> , 2013, 2013, 1-13.	0.9	52
106	Producing Succinic Acid in Yeast using A Hybrid of Differential Evolution and Flux Balance Analysis. <i>International Journal of Bio-Science and Bio-Technology</i> , 2013, 5, 91-100.	0.2	5
107	Parameter Estimation Using Improved Differential Evolution (IDE) and Bacterial Foraging Algorithm to Model Tyrosine Production in <i>Mus Musculus</i> (Mouse). <i>Lecture Notes in Computer Science</i> , 2013, , 179-190.	1.0	0
108	A Method to Construct Gene Regulatory Networks to Estimate and Calculate Time Delays. <i>Jurnal Teknologi (Sciences and Engineering)</i> , 2013, 62, .	0.3	0

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109	Estimating Kinetic Parameters for Essential Amino Acid Production in Arabidopsis Thaliana by Using Particle Swarm Optimization. Jurnal Teknologi (Sciences and Engineering), 2013, 64, .	0.3	2
110	An Improved Swarm Optimization for Parameter Estimation and Biological Model Selection. PLoS ONE, 2013, 8, e61258.	1.1	16
111	Identifying Minimal Genomes and Essential Genes in Metabolic Model Using Flux Balance Analysis. Lecture Notes in Computer Science, 2013, , 414-423.	1.0	4
112	Prediction of Vanillin Production in Yeast Using a Hybrid of Continuous Bees Algorithm and Flux Balance Analysis (CBAFBA). Studies in Computational Intelligence, 2013, , 101-116.	0.7	3
113	Identifying Gene Knockout Strategy Using Bees Hill Flux Balance Analysis (BHFBA) for Improving the Production of Ethanol in Bacillus Subtilis. Studies in Computational Intelligence, 2013, , 117-126.	0.7	2
114	A Hybrid of Artificial Bee Colony and Flux Balance Analysis for Identifying Optimum Knockout Strategies for Producing High Yields of Lactate in Echerichia Coli. Studies in Computational Intelligence, 2013, , 127-137.	0.7	3
115	A Constraint and Rule in an Enhancement of Binary Particle Swarm Optimization to Select Informative Genes for Cancer Classification. Lecture Notes in Computer Science, 2013, , 168-178.	1.0	2
116	Multiclass Prediction for Cancer Microarray Data Using Various Variables Range Selection Based on Random Forest. Lecture Notes in Computer Science, 2013, , 247-257.	1.0	4
117	A Hybrid of SVM and SCAD with Group-Specific Tuning Parameters in Identification of Informative Genes and Biological Pathways. Lecture Notes in Computer Science, 2013, , 258-269.	1.0	1
118	A Review of Computational Approaches for In Silico Metabolic Engineering for Microbial Fuel Production. Current Bioinformatics, 2013, 8, 253-258.	0.7	6
119	Threonine Biosynthesis Pathway Simulation Using IBMDE with Parameter Estimation. Lecture Notes in Computer Science, 2013, , 191-200.	1.0	0
120	Identifying Gene Knockout Strategy Using Bees Hill Flux Balance Analysis (BHFBA) for Improving the Production of Succinic Acid and Glycerol in Saccharomyces cerevisiae. Lecture Notes in Computer Science, 2013, , 223-233.	1.0	0
121	Using Particle Swarm Optimization for Estimating Kinetics Parameters on Essential Amino Acid Production of Arabidopsis Thaliana. Studies in Computational Intelligence, 2013, , 51-61.	0.7	1
122	Inferring Gene Networks from Gene Expression Data Using Dynamic Bayesian Network with Different Scoring Metric Approaches. Studies in Computational Intelligence, 2013, , 77-86.	0.7	1
123	Using Ant Colony Optimization (ACO) on Kinetic Modeling of the Acetoin Production in Lactococcus Lactis C7. Studies in Computational Intelligence, 2013, , 25-35.	0.7	3
124	Validation of Hierarchical Gene Clusters Using Repeated Measurements. Jurnal Teknologi (Sciences) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.3	0
125	A New Hybrid Firefly Algorithm for Complex and Nonlinear Problem. Advances in Intelligent and Soft Computing, 2012, , 673-680.	0.2	48
126	Random Forest for Gene Selection and Microarray Data Classification. Communications in Computer and Information Science, 2012, , 174-183.	0.4	12

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127	The emerging field of synthetic biology: A review. , 2012, , .		2
128	Identifying Gene Knockout Strategies Using a Hybrid of Bees Algorithm and Flux Balance Analysis for in Silico Optimization of Microbial Strains. Advances in Intelligent and Soft Computing, 2012, , 371-378.	0.2	11
129	Using Bayesian Networks to Construct Gene Regulatory Networks from Microarray Data. Jurnal Teknologi (Sciences and Engineering), 2012, , 1-6.	0.3	4
130	Inferring Gene Regulatory Networks from Gene Expression Data by a Dynamic Bayesian Network-Based Model. Advances in Intelligent and Soft Computing, 2012, , 379-386.	0.2	10
131	Improved Differential Evolution Algorithm for Parameter Estimation to Improve the Production of Biochemical Pathway. International Journal of Interactive Multimedia and Artificial Intelligence, 2012, 1, 22.	1.0	10
132	A Hybrid of SVM and SCAD with Group-Specific Tuning Parameter for Pathway-Based Microarray Analysis. Advances in Intelligent and Soft Computing, 2012, , 387-394.	0.2	0
133	Parameter Estimation for Simulation of Glycolysis Pathway by Using an Improved Differential Evolution. Communications in Computer and Information Science, 2012, , 352-355.	0.4	0
134	Prediction of Protein Residue Contact Using Support Vector Machine. Communications in Computer and Information Science, 2012, , 323-332.	0.4	0
135	Identifying Metabolic Pathway within Microarray Gene Expression Data Using Combination of Probabilistic Models. Communications in Computer and Information Science, 2012, , 52-61.	0.4	0
136	Optimized Local Protein Structure with Support Vector Machine to Predict Protein Secondary Structure. Communications in Computer and Information Science, 2012, , 333-342.	0.4	0
137	Performance Measurement of Thresholding Algorithms in Printed Circuit Board Inspection System. , 2011, , .		1
138	A Modified Binary Particle Swarm Optimization for Selecting the Small Subset of Informative Genes From Gene Expression Data. IEEE Transactions on Information Technology in Biomedicine, 2011, 15, 813-822.	3.6	74
139	An improved local best searching in Particle Swarm Optimization using Differential Evolution. , 2011, , .		8
140	Random forest for gene selection and microarray data classification. Bioinformation, 2011, 7, 142-146.	0.2	45
141	An improved hybrid of SVM and SCAD for pathway analysis. Bioinformation, 2011, 7, 169-175.	0.2	3
142	Particle swarm optimization with a modified sigmoid function for gene selection from gene expression data. Artificial Life and Robotics, 2010, 15, 21-24.	0.7	7
143	A Three-Stage Method to Select Informative Genes from Gene Expression Data in Classifying Cancer Classes. , 2010, , .		1
144	Selecting Informative Genes from Microarray Data by Using a Cyclic GA-Based Method. , 2010, , .		4

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145	Pathway-Based Microarray Analysis for Defining Statistical Significant Phenotype-Related Pathways: A Review of Common Approaches. , 2009, , .		9
146	A Study of Network-based Approach for Cancer Classification. , 2009, , .		2
147	A multi-objective strategy in genetic algorithms for gene selection of gene expression data. Artificial Life and Robotics, 2009, 13, 410-413.	0.7	27
148	Selecting informative genes from microarray data by using hybrid methods for cancer classification. Artificial Life and Robotics, 2009, 13, 414-417.	0.7	11
149	Gene subset selection using an iterative approach based on genetic algorithms. Artificial Life and Robotics, 2009, 14, 12-15.	0.7	0
150	Particle swarm optimization for gene selection in classifying cancer classes. Artificial Life and Robotics, 2009, 14, 16-19.	0.7	28
151	Three-Stage Method for Selecting Informative Genes for Cancer Classification. IEEJ Transactions on Electrical and Electronic Engineering, 2009, 4, 725-730.	0.8	1
152	An Improved Binary Particle Swarm Optimisation for Gene Selection in Classifying Cancer Classes. Lecture Notes in Computer Science, 2009, , 495-502.	1.0	2
153	An Iterative GASVM-Based Method: Gene Selection and Classification of Microarray Data. Lecture Notes in Computer Science, 2009, , 187-194.	1.0	1
154	A Three-Stage Method to Select Informative Genes for Cancer Classification. Proceedings of the ISCIE International Symposium on Stochastic Systems Theory and Its Applications, 2009, 2009, 243-247.	0.1	0
155	An Approach Using Hybrid Methods to Select Informative Genes from Microarray Data for Cancer Classification. , 2008, , .		10
156	Multi-objective optimization using genetic algorithm for gene selection from microarray data. , 2008, , .		3
157	A model for gene selection and classification of gene expression data. Artificial Life and Robotics, 2007, 11, 219-222.	0.7	18
158	Selecting Informative Genes from Leukemia Gene Expression Data using a Hybrid Approach for Cancer Classification. IFMBE Proceedings, 2007, , 528-532.	0.2	0
159	A HYBRID OF GENETIC ALGORITHM AND SUPPORT VECTOR MACHINE FOR FEATURES SELECTION AND CLASSIFICATION OF GENE EXPRESSION MICROARRAY. International Journal of Computational Intelligence and Applications, 2005, 05, 91-107.	0.6	34
160	An Improved Algorithm for Optimising the Production of Biochemical Systems. , 0, , .		0
161	A brief review of simulated Kalman Filter Algorithm and its variants and applications. F1000Research, 0, 10, 1081.	0.8	0
162	A Recursive Genetic Algorithm to Automatically Select Genes for Cancer Classification. Advances in Soft Computing, 0, , 166-174.	0.4	0