

Discovering functional relationships between RNA expression and disease susceptibility using relevance networks

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Mining gene expression data. Nature Reviews Genetics, 2000, 1, 165-165.	7.7	1
2	Gene expression profiling of cancer by use of DNA arrays: how far from the clinic?. Lancet Oncology, The, 2001, 2, 674-682.	5.1	69
3	Laboratory Adaptationsâ€”Changing Expectations. Clinical Chemistry, 2001, 47, 1509-1515.	1.5	1
4	Genomic approaches to the pathogenesis of hematologic malignancy. Current Opinion in Hematology, 2001, 8, 252-261.	1.2	29
5	Biomarker Identification by Feature Wrappers. Genome Research, 2001, 11, 1878-1887.	2.4	243
6	Functional genomic approaches to understanding molecular chaperones and stress responses. Advances in Protein Chemistry, 2001, 59, 345-390.	4.4	8
7	Integrated studies on plant biology using multiparallel techniques. Current Opinion in Biotechnology, 2001, 12, 82-86.	3.3	112
8	DNA microarrays: raising the profile. Current Opinion in Biotechnology, 2001, 12, 48-52.	3.3	45
9	Extracting Knowledge from Dynamics in Gene Expression. Journal of Biomedical Informatics, 2001, 34, 15-27.	2.5	18
10	Comparing the Similarity of Time-Series Gene Expression Using Signal Processing Metrics. Journal of Biomedical Informatics, 2001, 34, 396-405.	2.5	31
12	Impact of human genome sequencing for in silico target discovery. Drug Discovery Today, 2001, 6, 316-323.	3.2	19
13	Chemosensitivity prediction by transcriptional profiling. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 10787-10792.	3.3	619
14	DNA microarray gene expression analysis technology and its application to neurological disorders. Neurology, 2001, 57, 755-761.	1.5	65
15	Recursive partitioning for tumor classification with gene expression microarray data. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 6730-6735.	3.3	203
16	Transcriptional profiling in cancer: the path to clinical pharmacogenomics. Pharmacogenomics, 2001, 2, 123-136.	0.6	36
17	Cluster analysis of gene expression dynamics. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 9121-9126.	3.3	421
18	The Use of DNA Array Technology in Studies of Ocular Viral Pathogenesis. DNA and Cell Biology, 2002, 21, 483-490.	0.9	17
19	Analysis of matched mRNA measurements from two different microarray technologies. Bioinformatics, 2002, 18, 405-412.	1.8	441

#	ARTICLE	IF	CITATIONS
20	Global Analysis of Gene Expression: Methods, Interpretation, and Pitfalls. <i>Nephron Experimental Nephrology</i> , 2002, 10, 64-74.	2.4	48
21	Microarray technology and gene expression analysis for the study of angiogenesis. <i>Expert Opinion on Biological Therapy</i> , 2002, 2, 545-556.	1.4	9
22	DNA Hybridization Arrays for Gene Expression Analysis of Human Oral Cancer. <i>Journal of Dental Research</i> , 2002, 81, 89-97.	2.5	10
24	Control Genes and Variability: Absence of Ubiquitous Reference Transcripts in Diverse Mammalian Expression Studies. <i>Genome Research</i> , 2002, 12, 292-297.	2.4	315
25	Mining functional relationships in feature subspaces from gene expression profiles and drug activity profiles. <i>FEBS Letters</i> , 2002, 516, 113-118.	1.3	9
26	Identifying genes related to drug anticancer mechanisms using support vector machine. <i>FEBS Letters</i> , 2002, 521, 109-114.	1.3	51
27	Transcript array analysis in rheumatology. <i>Rheumatic Disease Clinics of North America</i> , 2002, 28, 151-176.	0.8	1
28	Time-dependent changes in ARE-driven gene expression by use of a noise-filtering process for microarray data. <i>Physiological Genomics</i> , 2002, 9, 137-144.	1.0	27
29	Expression microarray analysis of brain tumors what have we learned so far. <i>Frontiers in Bioscience - Landmark</i> , 2002, 7, c74-82.	3.0	2
30	Visualization and evaluation of clusters for exploratory analysis of gene expression data. <i>Journal of Biomedical Informatics</i> , 2002, 35, 25-36.	2.5	14
31	Wie mit Microarrays die Aktivität vieler Gene erfasst wird: Methodik der funktionellen Genomanalyse. <i>Biologie in Unserer Zeit</i> , 2002, 32, 20-29.	0.3	0
32	Role of gene expression microarray analysis in finding complex disease genes. <i>Genetic Epidemiology</i> , 2002, 23, 37-56.	0.6	31
33	"Seeing inside the body": MR imaging of gene expression. <i>European Journal of Nuclear Medicine and Molecular Imaging</i> , 2002, 29, 400-408.	3.3	28
34	From patterns to pathways: gene expression data analysis comes of age. <i>Nature Genetics</i> , 2002, 32, 502-508.	9.4	516
35	Better therapeutics through microarrays. <i>Nature Genetics</i> , 2002, 32, 547-552.	9.4	139
36	The use and analysis of microarray data. <i>Nature Reviews Drug Discovery</i> , 2002, 1, 951-960.	21.5	407
37	Interpretation of the complexity of innate immune responses by functional genomics. <i>Nature Reviews Immunology</i> , 2002, 2, 881-888.	10.6	105
38	Genetic network modeling. <i>Pharmacogenomics</i> , 2002, 3, 507-525.	0.6	158

#	ARTICLE	IF	CITATIONS
39	Self-Organizing Latent Lattice Models for Temporal Gene Expression Profiling. <i>Machine Learning</i> , 2003, 52, 67-89.	3.4	21
40	Global analysis of gene expression using GeneChip microarrays. <i>Current Opinion in Plant Biology</i> , 2003, 6, 418-425.	3.5	79
41	Drug sensitivity and resistance genes in cancer chemotherapy: a chemogenomics approach. <i>Drug Discovery Today</i> , 2003, 8, 356-363.	3.2	43
42	DNA microarray data and contextual analysis of correlation graphs. <i>BMC Bioinformatics</i> , 2003, 4, 15.	1.2	33
43	Cross-platform comparison and visualisation of gene expression data using co-inertia analysis. <i>BMC Bioinformatics</i> , 2003, 4, 59.	1.2	125
44	Pattern identification and classification in gene expression data using an autoassociative neural network model. <i>Biotechnology and Bioengineering</i> , 2003, 81, 594-606.	1.7	54
45	Gene profiling of hippocampal neuronal culture. <i>Journal of Neurochemistry</i> , 2003, 85, 1279-1288.	2.1	36
46	Classification of bladder cancer by microarray expression profiling: towards a general clinical use of microarrays in cancer diagnostics. <i>Expert Review of Molecular Diagnostics</i> , 2003, 3, 635-647.	1.5	39
48	Relevance Networks: A First Step Toward Finding Genetic Regulatory Networks Within Microarray Data. <i>Statistics in the Health Sciences</i> , 2003, , 428-446.	0.2	23
49	Pleiotropy, Homeostasis, and Functional Networks Based on Assays of Cardiovascular Traits in Genetically Randomized Populations. <i>Genome Research</i> , 2003, 13, 2082-2091.	2.4	67
50	Topology of gene expression networks as revealed by data mining and modeling. <i>Bioinformatics</i> , 2003, 19, 1909-1916.	1.8	30
51	Dysferlin Interacts with Annexins A1 and A2 and Mediates Sarcolemmal Wound-healing. <i>Journal of Biological Chemistry</i> , 2003, 278, 50466-50473.	1.6	336
52	Linking the growth inhibition response from the National Cancer Institute's anticancer screen to gene expression levels and other molecular target data. <i>Bioinformatics</i> , 2003, 19, 2212-2224.	1.8	29
53	DNA microarray and cancer. <i>Current Opinion in Oncology</i> , 2003, 15, 36-43.	1.1	53
54	Introduction: The Role of Genetic Bioinformatics. , 0, , 1-19.		0
55	Large Scale Expression Profiling in Cardiovascular Disease Using Microarrays: Prospects and Pitfalls. , 0, , 1-26.		1
56	Snomad: Biologist-Friendly Web Tools for the Standardization and Normalization of Microarray Data. <i>Statistics in the Health Sciences</i> , 2003, , 210-228.	0.2	1
57	TM4: A Free, Open-Source System for Microarray Data Management and Analysis. <i>BioTechniques</i> , 2003, 34, 374-378.	0.8	4,443

#	ARTICLE	IF	CITATIONS
58	Statistical Challenges in Functional Genomics. <i>Statistical Science</i> , 2003, 18, 33.	1.6	84
59	Analysis of DNA Microarray Data. <i>Current Topics in Medicinal Chemistry</i> , 2004, 4, 1355-1368.	1.0	23
60	Microarray Analysis of Human Nervous System Gene Expression in Neurological Disease. <i>International Review of Neurobiology</i> , 2004, 60, 135-151.	0.9	2
61	Chemical genetics for therapeutic target mining. <i>Expert Opinion on Therapeutic Targets</i> , 2004, 8, 653-661.	1.5	15
62	Methods for the Differential Integrative Omic Analysis of Plasma from a Transgenic Disease Animal Model. <i>OMICS A Journal of Integrative Biology</i> , 2004, 8, 267-288.	1.0	38
63	Integrative Biological Analysis of the APOE*3-Leiden Transgenic Mouse. <i>OMICS A Journal of Integrative Biology</i> , 2004, 8, 3-13.	1.0	108
64	Genomics and proteomics tools for compound mode-of-action studies in drug discovery. <i>Pharmacogenomics</i> , 2004, 5, 395-404.	0.6	13
65	A graph-theoretic approach to testing associations between disparate sources of functional genomics data. <i>Bioinformatics</i> , 2004, 20, 3353-3362.	1.8	42
66	Coexpression Analysis of Human Genes Across Many Microarray Data Sets. <i>Genome Research</i> , 2004, 14, 1085-1094.	2.4	688
67	Limited agreement among three global gene expression methods highlights the requirement for non-global validation. <i>Bioinformatics</i> , 2004, 20, 3431-3441.	1.8	19
68	Chemogenomics: an emerging strategy for rapid target and drug discovery. <i>Nature Reviews Genetics</i> , 2004, 5, 262-275.	7.7	340
69	DNA-microarray analysis of brain cancer: molecular classification for therapy. <i>Nature Reviews Neuroscience</i> , 2004, 5, 782-792.	4.9	189
70	Case study of a functional genomics application for an FPGA-based coprocessor. <i>Microprocessors and Microsystems</i> , 2004, 28, 213-222.	1.8	6
71	Genetic and Genomic Approaches to Identify and Study the Targets of Bioactive Small Molecules. <i>Chemistry and Biology</i> , 2004, 11, 609-618.	6.2	63
72	Predicting drug response based on gene expression. <i>Critical Reviews in Oncology/Hematology</i> , 2004, 51, 205-227.	2.0	15
73	Gene co-expression network topology provides a framework for molecular characterization of cellular state. <i>Bioinformatics</i> , 2004, 20, 2242-2250.	1.8	311
74	Genomic approaches to hematologic malignancies. <i>Blood</i> , 2004, 104, 923-932.	0.6	121
75	Primer on Medical Genomics Part XIV: Introduction to Systems Biology—A New Approach to Understanding Disease and Treatment. <i>Mayo Clinic Proceedings</i> , 2004, 79, 651-658.	1.4	72

#	ARTICLE	IF	CITATIONS
76	Phenotype Characterisation Using Integrated Gene Transcript, Protein and Metabolite Profiling. <i>Applied Bioinformatics</i> , 2004, 3, 205-217.	1.7	60
77	Estimating genomic coexpression networks using first-order conditional independence. <i>Genome Biology</i> , 2004, 5, R100.	13.9	115
78	Gene expression microarray technologies in the development of new therapeutic agents. <i>European Journal of Cancer</i> , 2004, 40, 2560-2591.	1.3	77
79	Genomics-based hypothesis generation: a novel approach to unravelling drug resistance in brain tumours?. <i>Lancet Oncology</i> , The, 2004, 5, 89-100.	5.1	15
80	Predicting drug response based on gene expression. <i>Critical Reviews in Oncology/Hematology</i> , 2004, 51, 205-227.	2.0	32
82	Microarray Data Analysis. , 2005, , 353-388.		4
83	Microarray-based gene expression profiling of hematologic malignancies: basic concepts and clinical applications. <i>Blood Reviews</i> , 2005, 19, 223-234.	2.8	47
84	Using genome-wide transcriptional profiling to elucidate small-molecule mechanism. <i>Current Opinion in Chemical Biology</i> , 2005, 9, 25-30.	2.8	50
85	Using In Vitro Models for Expression Profiling Studies on Ethanol and Drugs of Abuse. <i>Addiction Biology</i> , 2005, 10, 53-62.	1.4	12
86	The potential of proteomics and peptidomics for allergy and asthma research. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2005, 60, 1227-1237.	2.7	38
87	The future of microarray technology: networking the genome search. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2005, 60, 1219-1226.	2.7	14
88	Reverse engineering gene regulatory networks. <i>Nature Biotechnology</i> , 2005, 23, 554-555.	9.4	141
89	Reverse engineering of regulatory networks in human B cells. <i>Nature Genetics</i> , 2005, 37, 382-390.	9.4	1,268
90	Gene expression signature for angiogenic and nonangiogenic non-small-cell lung cancer. <i>Oncogene</i> , 2005, 24, 1212-1219.	2.6	83
91	Linking pathway gene expressions to the growth inhibition response from the National Cancer Institute's anticancer screen and drug mechanism of action. <i>Pharmacogenomics Journal</i> , 2005, 5, 381-399.	0.9	37
92	Potentials and pitfalls of DNA array analysis of the endothelial stress response. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2005, 1746, 73-84.	1.9	10
93	Sample phenotype clusters in high-density oligonucleotide microarray data sets are revealed using Isomap, a nonlinear algorithm. <i>BMC Bioinformatics</i> , 2005, 6, 195.	1.2	42
94	Gene analysis for exploring the effects of drugs in rheumatoid arthritis. <i>Arthritis and Rheumatism</i> , 2005, 52, 2248-2256.	6.7	12

#	ARTICLE	IF	CITATIONS
96	Linking tumor cell cytotoxicity to mechanism of drug action: An integrated analysis of gene expression, small-molecule screening and structural databases. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 59, 403-433.	1.5	39
97	Correlation-associated peptide networks of human cerebrospinal fluid. <i>Proteomics</i> , 2005, 5, 2789-2798.	1.3	29
98	Array lessons from the heart: focus on the genome and transcriptome of cardiomyopathies. <i>Physiological Genomics</i> , 2005, 21, 131-143.	1.0	34
100	Bioinformatic identification of novel early stress response genes in rodent models of lung injury. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2005, 289, L468-L477.	1.3	97
101	Datamining Methodology for LC-MALDI-MS Based Peptide Profiling. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2005, 8, 717-723.	0.6	17
102	The Hepatic Transcriptome as a Window on Whole-Body Physiology and Pathophysiology. <i>Toxicologic Pathology</i> , 2005, 33, 136-145.	0.9	23
103	Expression Profile of Malignant and Nonmalignant Lesions of Esophagus and Stomach: Differential Activity of Functional Modules Related to Inflammation and Lipid Metabolism. <i>Cancer Research</i> , 2005, 65, 7127-7136.	0.4	34
104	Signal Processing Challenges in The Post-Genomic Era. , 0, , .		0
105	High Throughput Screening of Co-Expressed Gene Pairs with Controlled False Discovery Rate (FDR) and Minimum Acceptable Strength (MAS). <i>Journal of Computational Biology</i> , 2005, 12, 1029-1045.	0.8	47
106	BAYESIAN NETWORK LEARNING WITH FEATURE ABSTRACTION FOR GENE-DRUG DEPENDENCY ANALYSIS. <i>Journal of Bioinformatics and Computational Biology</i> , 2005, 03, 61-77.	0.3	8
107	Reconstructing biological networks using conditional correlation analysis. <i>Bioinformatics</i> , 2005, 21, 765-773.	1.8	104
108	Targeting c-Myc-activated genes with a correlation method: Detection of global changes in large gene expression network dynamics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 6902-6906.	3.3	46
109	Network constrained clustering for gene microarray data. <i>Bioinformatics</i> , 2005, 21, 4014-4020.	1.8	53
110	Probabilities of spurious connections in gene networks: application to expression time series. <i>Bioinformatics</i> , 2005, 21, 1121-1128.	1.8	22
111	Identifying Genes Related to Chemosensitivity Using Support Vector Machine. , 2005, 111, 233-240.		0
112	Network constrained clustering for gene microarray data. , 0, , .		1
113	Topological-based classification using artificial gene networks. , 2005, , .		0
114	Gene Co-expression Networks Discovery with Controlled Statistical and Biological Significance. , 0, , .		2

#	ARTICLE	IF	CITATIONS
115	Functional Network Analysis Reveals Extended Gliomagenesis Pathway Maps and Three Novel MYC-Interacting Genes in Human Gliomas. <i>Cancer Research</i> , 2005, 65, 8679-8689.	0.4	285
117	A Shrinkage Approach to Large-Scale Covariance Matrix Estimation and Implications for Functional Genomics. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2005, 4, Article32.	0.2	1,128
118	Magnetic Resonance Imaging: Utility as a Molecular Imaging Modality. <i>Current Topics in Developmental Biology</i> , 2005, 70, 1-33.	1.0	18
120	Towards quantitative biology: Integration of biological information to elucidate disease pathways and to guide drug discovery. <i>Biotechnology Annual Review</i> , 2005, 11, 1-68.	2.1	51
121	Searching for differentially expressed gene combinations. <i>Genome Biology</i> , 2005, 6, R88.	13.9	57
122	Pathway and gene-set activation measurement from mRNA expression data: the tissue distribution of human pathways. <i>Genome Biology</i> , 2006, 7, R93.	13.9	93
124	OMICS and brain tumour biomarkers. <i>British Journal of Neurosurgery</i> , 2006, 20, 275-280.	0.4	19
125	Bayesian hierarchical model for estimating gene association network from microarray data. , 2006, , .		0
126	High Performance Liquid Chromatography~Mass Spectrometry for Metabonomics:~Potential Biomarkers for Acute Deterioration of Liver Function in Chronic Hepatitis B. <i>Journal of Proteome Research</i> , 2006, 5, 554-561.	1.8	153
127	A New Type of Stochastic Dependence Revealed in Gene Expression Data. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2006, 5, Article7.	0.2	32
128	A simple method for reverse engineering causal networks. <i>Journal of Physics A</i> , 2006, 39, L647-L655.	1.6	6
129	Creation and implications of a phenome-genome network. <i>Nature Biotechnology</i> , 2006, 24, 55-62.	9.4	190
130	The art of gene function prediction. <i>Nature Biotechnology</i> , 2006, 24, 1474-1475.	9.4	69
131	The future of dermatopathology. <i>Modern Pathology</i> , 2006, 19, S155-S163.	2.9	2
132	Utility of correlation measures in analysis of gene expression. <i>NeuroRx</i> , 2006, 3, 384-395.	6.0	32
133	Identification of lethal cluster of genes in the yeast transcription network. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2006, 364, 557-564.	1.2	20
134	Prediction of Anticancer Drug Potency from Expression of Genes Involved in Growth Factor Signaling. <i>Pharmaceutical Research</i> , 2006, 23, 336-349.	1.7	25
135	Hybridization interactions between probesets in short oligo microarrays lead to spurious correlations. <i>BMC Bioinformatics</i> , 2006, 7, 276.	1.2	143

#	ARTICLE	IF	CITATIONS
136	From multi-scale methodology to systems biology: to integrate strain improvement and fermentation optimization. <i>Journal of Chemical Technology and Biotechnology</i> , 2006, 81, 734-745.	1.6	28
137	Statistical challenges with gene expression studies. <i>Pharmacogenomics</i> , 2006, 7, 511-519.	0.6	3
138	Innovative computational methods for transcriptomic data analysis. , 2006, , .		4
139	A scalable method for integration and functional analysis of multiple microarray datasets. <i>Bioinformatics</i> , 2006, 22, 2890-2897.	1.8	127
140	Behavioral Profiling of Human Transitional Cell Carcinoma Ex vivo. <i>Cancer Research</i> , 2006, 66, 3078-3086.	0.4	18
141	Topology-based cancer classification and related pathway mining using microarray data. <i>Nucleic Acids Research</i> , 2006, 34, 4069-4080.	6.5	39
142	NETWORKS FROM GENE EXPRESSION TIME SERIES: CHARACTERIZATION OF CORRELATION PATTERNS. <i>International Journal of Bifurcation and Chaos in Applied Sciences and Engineering</i> , 2007, 17, 2477-2483.	0.7	5
143	Systematic construction of gene coexpression networks with applications to human T helper cell differentiation process. <i>Bioinformatics</i> , 2007, 23, 2096-2103.	1.8	94
144	Large-Scale Mapping and Validation of Escherichia coli Transcriptional Regulation from a Compendium of Expression Profiles. <i>PLoS Biology</i> , 2007, 5, e8.	2.6	1,308
145	Chemogenomics of Sensitivity and Resistance to Anticancer Drugs. <i>Current Pharmacogenomics and Personalized Medicine: the International Journal for Expert Reviews in Pharmacogenomics</i> , 2007, 5, 11-19.	0.3	0
146	Information theory applied to the sparse gene ontology annotation network to predict novel gene function. <i>Bioinformatics</i> , 2007, 23, i529-i538.	1.8	148
147	A Network of Genes Regulated by Light in Cyanobacteria. <i>OMICS A Journal of Integrative Biology</i> , 2007, 11, 166-185.	1.0	12
148	Information-Theoretic Inference of Large Transcriptional Regulatory Networks. <i>Eurasip Journal on Bioinformatics and Systems Biology</i> , 2007, 2007, 1-9.	1.4	320
149	Estimation of a covariance matrix with zeros. <i>Biometrika</i> , 2007, 94, 199-216.	1.3	80
150	Advanced Computing. , 0, , 165-188.		0
151	Connexin43 and the brain transcriptome of newborn mice. <i>Genomics</i> , 2007, 89, 113-123.	1.3	49
152	Innovative Computational Methods for Transcriptomic Data Analysis: A Case Study in the Use of FPT for Practical Algorithm Design and Implementation. <i>Computer Journal</i> , 2007, 51, 26-38.	1.5	26
153	Strategy for encoding and comparison of gene expression signatures. <i>Genome Biology</i> , 2007, 8, R133.	3.8	24

#	ARTICLE	IF	CITATIONS
155	Multiple Testing and Error Control in Gaussian Graphical Model Selection. <i>Statistical Science</i> , 2007, 22, .	1.6	81
157	From correlation to causation networks: a simple approximate learning algorithm and its application to high-dimensional plant gene expression data. <i>BMC Systems Biology</i> , 2007, 1, 37.	3.0	304
158	New insights about host response to smallpox using microarray data. <i>BMC Systems Biology</i> , 2007, 1, 38.	3.0	5
159	Correlation analysis reveals the emergence of coherence in the gene expression dynamics following system perturbation. <i>BMC Bioinformatics</i> , 2007, 8, S16.	1.2	6
160	Validating module network learning algorithms using simulated data. <i>BMC Bioinformatics</i> , 2007, 8, S5.	1.2	34
161	Testing whether genetic variation explains correlation of quantitative measures of gene expression, and application to genetic network analysis. <i>Statistics in Medicine</i> , 2008, 27, 3847-3867.	0.8	1
162	Identification of mouse heart transcriptomic network sensitive to various heart diseases. <i>Biotechnology Journal</i> , 2008, 3, 648-658.	1.8	6
163	Binary Models for Marginal Independence. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , 2008, 70, 287-309.	1.1	37
164	Conditional clustering of temporal expression profiles. <i>BMC Bioinformatics</i> , 2008, 9, 147.	1.2	14
165	minet: A R/Bioconductor Package for Inferring Large Transcriptional Networks Using Mutual Information. <i>BMC Bioinformatics</i> , 2008, 9, 461.	1.2	460
166	Learning transcriptional regulatory networks from high throughput gene expression data using continuous three-way mutual information. <i>BMC Bioinformatics</i> , 2008, 9, 467.	1.2	60
167	An integrative approach to characterize disease-specific pathways and their coordination: a case study in cancer. <i>BMC Genomics</i> , 2008, 9, S12.	1.2	43
168	Multivariate gene expression analysis reveals functional connectivity changes between normal/tumoral prostates. <i>BMC Systems Biology</i> , 2008, 2, 106.	3.0	22
169	Biomolecular network querying: a promising approach in systems biology. <i>BMC Systems Biology</i> , 2008, 2, 5.	3.0	30
170	Constructing disease-specific gene networks using pair-wise relevance metric: Application to colon cancer identifies interleukin 8, desmin and enolase 1 as the central elements. <i>BMC Systems Biology</i> , 2008, 2, 72.	3.0	64
171	SIRENE: supervised inference of regulatory networks. <i>Bioinformatics</i> , 2008, 24, i76-i82.	1.8	155
173	Advanced Data-Mining Strategies for the Analysis of Direct-Infusion Ion Trap Mass Spectrometry Data from the Association of Perennial Ryegrass with Its Endophytic Fungus, <i>Neotyphodium lolii</i> . <i>Plant Physiology</i> , 2008, 146, 1501-1514.	2.3	42
174	Pharmacogenomics of the National Cancer Institute's 60-Tumor Cell Panel. , 2008, , 57-74.		0

#	ARTICLE	IF	CITATIONS
175	Heuristic Approach to Sparse Approximation of Gene Regulatory Networks. <i>Journal of Computational Biology</i> , 2008, 15, 1173-1186.	0.8	15
176	EVIDENCE OF SCALE-FREE TOPOLOGY IN GENE REGULATORY NETWORK OF HUMAN TISSUES. <i>International Journal of Modern Physics C</i> , 2008, 19, 283-290.	0.8	7
177	Functional meta-analysis of double connectivity in gene coexpression networks in mammals. <i>Physiological Genomics</i> , 2008, 34, 34-41.	1.0	21
178	A Semi-Supervised Method for Predicting Transcription Factor-Gene Interactions in <i>Escherichia coli</i> . <i>PLoS Computational Biology</i> , 2008, 4, e1000044.	1.5	85
179	Geometric Interpretation of Gene Coexpression Network Analysis. <i>PLoS Computational Biology</i> , 2008, 4, e1000117.	1.5	719
180	Early detection of ovarian cancer using group biomarkers. <i>Molecular Cancer Therapeutics</i> , 2008, 7, 27-37.	1.9	35
181	Inference algorithms for gene networks: a statistical mechanics analysis. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2008, 2008, P12001.	0.9	21
182	TOWARDS A CYTOKINE-CELL INTERACTION KNOWLEDGEBASE OF THE ADAPTIVE IMMUNE SYSTEM. , 2008, , .		10
183	Gene-network inference by message passing. <i>Journal of Physics: Conference Series</i> , 2008, 95, 012016.	0.3	10
184	Systems Pharmacology, Biomarkers, and Biomolecular Networks. , 0, , 75-113.		0
185	Evolutionarily Conserved Transcriptional Co-Expression Guiding Embryonic Stem Cell Differentiation. <i>PLoS ONE</i> , 2008, 3, e3406.	1.1	43
186	Modulated Modularity Clustering as an Exploratory Tool for Functional Genomic Inference. <i>PLoS Genetics</i> , 2009, 5, e1000479.	1.5	118
187	From Modules to Models: Advanced Analysis Methods for Large-Scale Data. , 2009, , 59-83.		0
188	COMPARING PEARSON, SPEARMAN AND Hoeffding's D Measure for Gene Expression Association Analysis. <i>Journal of Bioinformatics and Computational Biology</i> , 2009, 07, 663-684.	0.3	46
189	Towards Systems Biology of Heterosis: A Hypothesis about Molecular Network Structure Applied for the Arabidopsis Metabolome. <i>Eurasip Journal on Bioinformatics and Systems Biology</i> , 2009, 2009, 1-12.	1.4	9
190	Reconstructing transcriptional regulatory networks through genomics data. <i>Statistical Methods in Medical Research</i> , 2009, 18, 595-617.	0.7	19
191	Detecting Gene Regulatory Networks from Microarray Data Using Fuzzy Logic. <i>Studies in Fuzziness and Soft Computing</i> , 2009, , 141-163.	0.6	6
193	Textual data compression in computational biology: a synopsis. <i>Bioinformatics</i> , 2009, 25, 1575-1586.	1.8	83

#	ARTICLE	IF	CITATIONS
194	Prestige centrality-based functional outlier detection in gene expression analysis. <i>Bioinformatics</i> , 2009, 25, 2222-2228.	1.8	5
195	Statistical Estimation of Correlated Genome Associations to a Quantitative Trait Network. <i>PLoS Genetics</i> , 2009, 5, e1000587.	1.5	160
196	A multivariate regression approach to association analysis of a quantitative trait network. <i>Bioinformatics</i> , 2009, 25, i204-i212.	1.8	101
197	Using a mutual information-based site transition network to map the genetic evolution of influenza A/H3N2 virus. <i>Bioinformatics</i> , 2009, 25, 2309-2317.	1.8	31
198	Gaussian process regression bootstrapping: exploring the effects of uncertainty in time course data. <i>Bioinformatics</i> , 2009, 25, 1300-1306.	1.8	62
199	Variable selection and dependency networks for genomewide data. <i>Biostatistics</i> , 2009, 10, 621-639.	0.9	24
200	Sparse canonical methods for biological data integration: application to a cross-platform study. <i>BMC Bioinformatics</i> , 2009, 10, 34.	1.2	219
201	Threshold selection in gene co-expression networks using spectral graph theory techniques. <i>BMC Bioinformatics</i> , 2009, 10, S4.	1.2	71
202	A graphical model approach for inferring large-scale networks integrating gene expression and genetic polymorphism. <i>BMC Systems Biology</i> , 2009, 3, 55.	3.0	31
203	Comparison of threshold selection methods for microarray gene co-expression matrices. <i>BMC Research Notes</i> , 2009, 2, 240.	0.6	37
204	Fuzzy logic and related methods as a screening tool for detecting gene regulatory networks. <i>Information Fusion</i> , 2009, 10, 250-259.	11.7	13
205	Data-Driven Methods to Discover Molecular Determinants of Serious Adverse Drug Events. <i>Clinical Pharmacology and Therapeutics</i> , 2009, 85, 259-268.	2.3	46
206	Reverse engineering and verification of gene networks: Principles, assumptions, and limitations of present methods and future perspectives. <i>Journal of Biotechnology</i> , 2009, 144, 190-203.	1.9	67
207	Recovering context-specific gene network modules from expression data: A brief review. <i>Frontiers of Biology in China: Selected Publications From Chinese Universities</i> , 2009, 4, 414-418.	0.2	1
208	Inferring Dynamic Genetic Networks with Low Order Independencies. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2009, 8, 1-38.	0.2	97
209	Algebraic Models of Biochemical Networks. <i>Methods in Enzymology</i> , 2009, 467, 163-196.	0.4	3
210	A linear programming approach for estimating the structure of a sparse linear genetic network from transcript profiling data. <i>Algorithms for Molecular Biology</i> , 2009, 4, 5.	0.3	4
211	Correlating measurements across samples improves accuracy of large-scale expression profile experiments. <i>Genome Biology</i> , 2009, 10, R143.	13.9	14

#	ARTICLE	IF	CITATIONS
212	Reverse Engineering Molecular Regulatory Networks from Microarray Data with qp-Graphs. Journal of Computational Biology, 2009, 16, 213-227.	0.8	59
213	ROBUST GENE NETWORK ANALYSIS REVEALS ALTERATION OF THE STAT5a NETWORK AS A HALLMARK OF PROSTATE CANCER. , 2010, , .		3
214	Enriched partial correlations in genome-wide gene expression profiles of hybrids (<i>A. thaliana</i>): a systems biological approach towards the molecular basis of heterosis. Theoretical and Applied Genetics, 2010, 120, 249-259.	1.8	26
215	Drug Discovery in a Multidimensional World: Systems, Patterns, and Networks. Journal of Cardiovascular Translational Research, 2010, 3, 438-447.	1.1	59
216	Local network-based measures to assess the inferability of different regulatory networks. IET Systems Biology, 2010, 4, 277-288.	0.8	27
217	Mapping transcription mechanisms from multimodal genomic data. BMC Bioinformatics, 2010, 11, S2.	1.2	7
218	Inferring the conservative causal core of gene regulatory networks. BMC Systems Biology, 2010, 4, 132.	3.0	167
219	Co-expression module analysis reveals biological processes, genomic gain, and regulatory mechanisms associated with breast cancer progression. BMC Systems Biology, 2010, 4, 74.	3.0	117
221	DREAM3: Network Inference Using Dynamic Context Likelihood of Relatedness and the Inferelator. PLoS ONE, 2010, 5, e9803.	1.1	95
222	Gene Regulatory Networks from Multifactorial Perturbations Using Graphical Lasso: Application to the DREAM4 Challenge. PLoS ONE, 2010, 5, e14147.	1.1	54
223	Incorporating Network Topology Improves Prediction of Protein Interaction Networks from Transcriptomic Data. International Journal of Knowledge Discovery in Bioinformatics, 2010, 1, 1-19.	0.8	3
224	Reducing the Computational Complexity of Information Theoretic Approaches for Reconstructing Gene Regulatory Networks. Journal of Computational Biology, 2010, 17, 169-176.	0.8	6
225	Discovery and assessment of gene-disease associations by integrated analysis of scientific literature and microarray data. , 2010, , .		2
227	Computational modeling of the effects of oxidative stress on the IGF-1 signaling pathway in human articular chondrocytes. , 2010, , .		0
228	Biomarker and Drug Discovery for Gastroenterology Through Translational Bioinformatics. Gastroenterology, 2010, 139, 735-741.e1.	0.6	7
229	Gene Association Networks from Microarray Data Using a Regularized Estimation of Partial Correlation Based on PLS Regression. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2010, 7, 251-262.	1.9	31
230	Bioinformatic and Computational Analysis for Genomic Medicine. , 2010, , 111-130.		0
232	Comparison of Co-temporal Modeling Algorithms on Sparse Experimental Time Series Data Sets. , 2010, 2010, 79-85.		2

#	ARTICLE	IF	CITATIONS
233	A parallel algorithm for reverse engineering of biological networks. Integrative Biology (United Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 74)	0.6	13
234	Gene network inference via sparse structural equation modeling with genetic perturbations. , 2011, , .		5
237	Weighted Network Analysis. , 2011, , .		241
238	Differential C3NET reveals disease networks of direct physical interactions. BMC Bioinformatics, 2011, 12, 296.	1.2	35
239	A comparison of the functional modules identified from time course and static PPI network data. BMC Bioinformatics, 2011, 12, 339.	1.2	103
240	Sparse estimation of a covariance matrix. Biometrika, 2011, 98, 807-820.	1.3	223
241	A Systematic Comparison of Genome Scale Clustering Algorithms. Lecture Notes in Computer Science, 2011, , 416-427.	1.0	2
242	Parametric Construction of Episode Networks from Pseudoperiodic Time Series Based on Mutual Information. PLoS ONE, 2011, 6, e27733.	1.1	5
246	Modeling mutations of influenza virus with IBM Blue Gene. IBM Journal of Research and Development, 2011, 55, 7:1-7:11.	3.2	2
248	Structural influence of gene networks on their inference: analysis of C3NET. Biology Direct, 2011, 6, 31.	1.9	51
249	Gene network analyses point to the importance of human tissue kallikreins in melanoma progression. BMC Medical Genomics, 2011, 4, 76.	0.7	22
250	Link-based quantitative methods to identify differentially coexpressed genes and gene Pairs. BMC Bioinformatics, 2011, 12, 315.	1.2	82
251	<i>parmigene</i> a parallel R package for mutual information estimation and gene network reconstruction. Bioinformatics, 2011, 27, 1876-1877.	1.8	82
252	Inferring Functional Relationships and Causal Network Structure from Gene Expression Profiles. Methods in Enzymology, 2011, 487, 133-146.	0.4	1
253	Transcriptome Data Analysis for Cell Culture Processes. , 2011, 127, 27-70.		2
254	Experiment Specific Expression Patterns. Journal of Computational Biology, 2011, 18, 1423-1435.	0.8	0
256	Review of Weighted Gene Coexpression Network Analysis. , 2011, , 369-388.		19
257	Wishart distributions for decomposable covariance graph models. Annals of Statistics, 2011, 39, .	1.4	47

#	ARTICLE	IF	CITATIONS
258	Applications of Translational Bioinformatics in Transplantation. <i>Clinical Pharmacology and Therapeutics</i> , 2011, 90, 323-327.	2.3	9
259	Assessing Modularity Using a Random Matrix Theory Approach. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2011, 10, .	0.2	1
260	A NEW METHOD OF DETERMINING THRESHOLD OF GENE NETWORK BASED ON PHENOTYPES. <i>Journal of Biological Systems</i> , 2011, 19, 607-616.	0.5	1
262	Quantitative Epistasis Analysis and Pathway Inference from Genetic Interaction Data. <i>PLoS Computational Biology</i> , 2011, 7, e1002048.	1.5	15
263	Quantifying the white blood cell transcriptome as an accessible window to the multiorgan transcriptome. <i>Bioinformatics</i> , 2012, 28, 538-545.	1.8	52
264	Mining Gene Expression Signature for the Detection of Pre-Malignant Melanocytes and Early Melanomas with Risk for Metastasis. <i>PLoS ONE</i> , 2012, 7, e44800.	1.1	20
265	Efficient Reverse-Engineering of a Developmental Gene Regulatory Network. <i>PLoS Computational Biology</i> , 2012, 8, e1002589.	1.5	82
266	Integrative systems biology approaches in asthma pharmacogenomics. <i>Pharmacogenomics</i> , 2012, 13, 1387-1404.	0.6	23
267	Background gene expression networks significantly enhance drug response prediction by transcriptional profiling. <i>Pharmacogenomics Journal</i> , 2012, 12, 446-452.	0.9	7
268	Quantifying the white blood cell transcriptome as an accessible window to the multiorgan transcriptome. <i>Bioinformatics</i> , 2012, 28, 905-905.	1.8	22
269	Inference and characterization of multi-attribute networks with application to computational biology. <i>Annals of Applied Statistics</i> , 2012, 6, .	0.5	14
270	Genome-wide transcriptome analysis of rice genes responsive to chilling stress. <i>Canadian Journal of Plant Science</i> , 2012, 92, 447-460.	0.3	13
272	Transcriptional Network Analysis Identifies BACH1 as a Master Regulator of Breast Cancer Bone Metastasis. <i>Journal of Biological Chemistry</i> , 2012, 287, 33533-33544.	1.6	118
273	Negative Correlation Aided Network Module Extraction. <i>Procedia Technology</i> , 2012, 6, 658-665.	1.1	4
274	Module extraction from subspace co-expression networks. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2012, 1, 183-195.	1.2	5
275	GSGS: A Computational Approach to Reconstruct Signaling Pathway Structures from Gene Sets. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012, 9, 438-450.	1.9	10
276	Reverse engineering of gene regulatory networks from biological data. <i>Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery</i> , 2012, 2, 365-385.	4.6	12
277	Molecular ecological network analyses. <i>BMC Bioinformatics</i> , 2012, 13, 113.	1.2	1,917

#	ARTICLE	IF	CITATIONS
278	Spice: discovery of phenotype-determining component interplays. BMC Systems Biology, 2012, 6, 40.	3.0	11
279	Bioenergy grass feedstock: current options and prospects for trait improvement using emerging genetic, genomic, and systems biology toolkits. Biotechnology for Biofuels, 2012, 5, 80.	6.2	53
280	Inference of Regulatory Networks from Microarray Data with R and the Bioconductor Package qppgraph. Methods in Molecular Biology, 2012, 802, 215-233.	0.4	5
281	Next Generation Microarray Bioinformatics. Methods in Molecular Biology, 2012, , .	0.4	8
282	Utilizing RNA-Seq data for cancer network inference. , 2012, , .		4
283	An effective method for network module extraction from microarray data. BMC Bioinformatics, 2012, 13, S4.	1.2	25
284	Comparison of co-expression measures: mutual information, correlation, and model based indices. BMC Bioinformatics, 2012, 13, 328.	1.2	406
285	TIGRESS: Trustful Inference of Gene REgulation using Stability Selection. BMC Systems Biology, 2012, 6, 145.	3.0	338
286	Visualising associations between paired "omics" data sets. BioData Mining, 2012, 5, 19.	2.2	261
287	Cell Cycle Gene Networks Are Associated with Melanoma Prognosis. PLoS ONE, 2012, 7, e34247.	1.1	32
288	Textual data compression in computational biology: Algorithmic techniques. Computer Science Review, 2012, 6, 1-25.	10.2	19
289	Ethanol modulation of gene networks: Implications for alcoholism. Neurobiology of Disease, 2012, 45, 115-121.	2.1	23
290	Additional role of <i>O</i> -acetylserine as a sulfur status-independent regulator during plant growth. Plant Journal, 2012, 70, 666-677.	2.8	104
291	A systematic comparison of genome-scale clustering algorithms. BMC Bioinformatics, 2012, 13, S7.	1.2	55
292	Genomic survey, expression profile and co-expression network analysis of OsWD40 family in rice. BMC Genomics, 2012, 13, 100.	1.2	78
293	Maximizing capture of gene co-expression relationships through pre-clustering of input expression samples: an Arabidopsis case study. BMC Systems Biology, 2013, 7, 44.	3.0	22
294	Altering physiological networks using drugs: steps towards personalized physiology. BMC Medical Genomics, 2013, 6, S7.	0.7	6
295	The integrative expression and co-expression analysis of the AGO gene family in rice. Gene, 2013, 528, 221-235.	1.0	24

#	ARTICLE	IF	CITATIONS
296	Evaluation of linkage disequilibrium in wheat with an L1-regularized sparse Markov network. <i>Theoretical and Applied Genetics</i> , 2013, 126, 1991-2002.	1.8	4
298	Data Mining for Systems Biology. <i>Methods in Molecular Biology</i> , 2013, , .	0.4	2
299	Modularity of a leaf moth-wing pattern and a versatile characteristic of the wing-pattern ground plan. <i>BMC Evolutionary Biology</i> , 2013, 13, 158.	3.2	28
300	Reconstructing biological networks using low order partial correlation. , 2013, , .		2
301	Network analysis: tackling complex data to study plant metabolism. <i>Trends in Biotechnology</i> , 2013, 31, 29-36.	4.9	87
302	A comparative study of covariance selection models for the inference of gene regulatory networks. <i>Journal of Biomedical Informatics</i> , 2013, 46, 894-904.	2.5	12
303	Supervised Inference of Gene Regulatory Networks from Positive and Unlabeled Examples. <i>Methods in Molecular Biology</i> , 2013, 939, 47-58.	0.4	2
304	Translational Bioinformatics for Genomic Medicine. , 2013, , 272-286.		4
305	Identification of self-consistent modulons from bacterial microarray expression data with the help of structured regulon gene sets. <i>Journal of Biomolecular Structure and Dynamics</i> , 2013, 31, 115-124.	2.0	1
306	Collections of Simultaneously Altered Genes as Biomarkers of Cancer Cell Drug Response. <i>Cancer Research</i> , 2013, 73, 1699-1708.	0.4	46
307	Global assessment of network inference algorithms based on available literature of gene/protein interactions. <i>Turkish Journal of Biology</i> , 2013, 37, 547-555.	2.1	14
308	Systems Biology Approach to the Dissection of the Complexity of Regulatory Networks in the <i>S. scrofa</i> Cardiocirculatory System. <i>International Journal of Molecular Sciences</i> , 2013, 14, 23160-23187.	1.8	7
309	Inference of Gene Regulatory Networks with Sparse Structural Equation Models Exploiting Genetic Perturbations. <i>PLoS Computational Biology</i> , 2013, 9, e1003068.	1.5	115
310	Fatigue-Related Gene Networks Identified in CD14 ⁺ Cells Isolated From HIV-Infected Patientsâ€™ Part II. <i>Biological Research for Nursing</i> , 2013, 15, 152-159.	1.0	2
311	Reverse Engineering Cellular Networks with Information Theoretic Methods. <i>Cells</i> , 2013, 2, 306-329.	1.8	54
312	Fatigue-Related Gene Networks Identified in CD14 ⁺ Cells Isolated From HIV-Infected Patientsâ€™ Part I. <i>Biological Research for Nursing</i> , 2013, 15, 137-151.	1.0	8
314	When Is Hub Gene Selection Better than Standard Meta-Analysis?. <i>PLoS ONE</i> , 2013, 8, e61505.	1.1	243
315	Impact of Noise on Molecular Network Inference. <i>PLoS ONE</i> , 2013, 8, e80735.	1.1	8

#	ARTICLE	IF	CITATIONS
316	Maximal information component analysis: a novel non-linear network analysis method. <i>Frontiers in Genetics</i> , 2013, 4, 28.	1.1	22
319	The Inferred Cardiogenic Gene Regulatory Network in the Mammalian Heart. <i>PLoS ONE</i> , 2014, 9, e100842.	1.1	8
320	Gene regulatory networks and their applications: understanding biological and medical problems in terms of networks. <i>Frontiers in Cell and Developmental Biology</i> , 2014, 2, 38.	1.8	201
322	Condensing Biochemistry into Gene Regulatory Networks. <i>International Journal of Natural Computing Research</i> , 2014, 4, 1-25.	0.5	0
323	CompareSVM: supervised, Support Vector Machine (SVM) inference of gene regularity networks. <i>BMC Bioinformatics</i> , 2014, 15, 395.	1.2	42
325	Information theoretic approach to complex biological network reconstruction: application to cytokine release in RAW 264.7 macrophages. <i>BMC Systems Biology</i> , 2014, 8, 77.	3.0	11
326	Reverse Engineering of High-Throughput Genomic and Genetic Data. , 2014, , 189-205.		1
327	MicroRNAs in bovine adipogenesis: genomic context, expression and function. <i>BMC Genomics</i> , 2014, 15, 137.	1.2	77
328	Systems genetics: A paradigm to improve discovery of candidate genes and mechanisms underlying complex traits. <i>Plant Science</i> , 2014, 223, 45-48.	1.7	37
329	Biological network inference using low order partial correlation. <i>Methods</i> , 2014, 69, 266-273.	1.9	35
330	Network-based approach reveals Y chromosome influences prostate cancer susceptibility. <i>Computers in Biology and Medicine</i> , 2014, 54, 24-31.	3.9	21
331	Reverse engineering and identification in systems biology: strategies, perspectives and challenges. <i>Journal of the Royal Society Interface</i> , 2014, 11, 20130505.	1.5	194
332	Scalable Combinatorial Tools for Health Disparities Research. <i>International Journal of Environmental Research and Public Health</i> , 2014, 11, 10419-10443.	1.2	22
333	Joint estimation of multiple related biological networks. <i>Annals of Applied Statistics</i> , 2014, 8, .	0.5	13
334	Transcriptional regulatory networks controlling woolliness in peach in response to preharvest gibberellin application and cold storage. <i>BMC Plant Biology</i> , 2015, 15, 279.	1.6	14
335	Inferring interaction type in gene regulatory networks using co-expression data. <i>Algorithms for Molecular Biology</i> , 2015, 10, 23.	0.3	22
336	An Overview of NCA-Based Algorithms for Transcriptional Regulatory Network Inference. <i>Microarrays (Basel, Switzerland)</i> , 2015, 4, 596-617.	1.4	7
337	Computational Models for Transplant Biomarker Discovery. <i>Frontiers in Immunology</i> , 2015, 6, 458.	2.2	11

#	ARTICLE	IF	CITATIONS
338	Semi-Supervised Multi-View Learning for Gene Network Reconstruction. PLoS ONE, 2015, 10, e0144031.	1.1	32
339	Reverse Engineering of Genome-wide Gene Regulatory Networks from Gene Expression Data. Current Genomics, 2015, 16, 3-22.	0.7	79
340	Integrative approach for inference of gene regulatory networks using lasso-based random featuring and application to Psychiatric disorders. , 2015, , .		0
341	Solving the inverse problem of noise-driven dynamic networks. Physical Review E, 2015, 91, 012814.	0.8	44
342	Identifying functional gene regulatory network phenotypes underlying single cell transcriptional variability. Progress in Biophysics and Molecular Biology, 2015, 117, 87-98.	1.4	19
343	Comprehensive meta-analysis, co-expression, and miRNA nested network analysis identifies gene candidates in citrus against Huanglongbing disease. BMC Plant Biology, 2015, 15, 184.	1.6	51
344	An argument for mechanism-based statistical inference in cancer. Human Genetics, 2015, 134, 479-495.	1.8	9
345	Exploring the Genomic Roadmap and Molecular Phylogenetics Associated with MODY Cascades Using Computational Biology. Cell Biochemistry and Biophysics, 2015, 71, 1491-1502.	0.9	2
346	A Multi-Method Approach for Proteomic Network Inference in 11 Human Cancers. PLoS Computational Biology, 2016, 12, e1004765.	1.5	32
347	DTW-MIC Coexpression Networks from Time-Course Data. PLoS ONE, 2016, 11, e0152648.	1.1	7
348	Graph reconstruction using covariance-based methods. Eurasip Journal on Bioinformatics and Systems Biology, 2016, 2016, 19.	1.4	7
349	Understanding the progression of atherosclerosis through gene profiling and co-expression network analysis in Apob tm2Sgy Ldlr tm1Her double knockout mice. Genomics, 2016, 107, 239-247.	1.3	14
350	Analysis of bHLH coding genes using gene co-expression network approach. Molecular Biology Reports, 2016, 43, 677-685.	1.0	5
351	PathCellNet: Cell-type specific pathogen-response network explorer. Journal of Immunological Methods, 2016, 439, 15-22.	0.6	9
353	A Two-Stage Approach to Spatio-Temporal Analysis with Strong and Weak Cross-Sectional Dependence. Journal of Applied Econometrics, 2016, 31, 249-280.	1.3	123
354	Exploring the molecular basis of age-related disease comorbidities using a multi-omics graphical model. Scientific Reports, 2016, 6, 37646.	1.6	45
355	Inference of Gene Regulatory Network Based on Legendre Neural Network. , 2016, , .		1
356	Unexpected links reflect the noise in networks. Biology Direct, 2016, 11, 52.	1.9	35

#	ARTICLE	IF	CITATIONS
357	A comparative evaluation of data-merging and meta-analysis methods for reconstructing gene-gene interactions. BMC Bioinformatics, 2016, 17, 194.	1.2	16
358	Integrative approach for inference of gene regulatory networks using lasso-based random featuring and application to psychiatric disorders. BMC Medical Genomics, 2016, 9, 50.	0.7	5
359	Detecting the large entries of a sparse covariance matrix in sub-quadratic time. Information and Inference, 2016, 5, 304-330.	0.9	1
360	Data based identification and prediction of nonlinear and complex dynamical systems. Physics Reports, 2016, 644, 1-76.	10.3	268
361	Depicting network structures from variable data produced by unknown colored-noise driven dynamics. Europhysics Letters, 2016, 113, 18005.	0.7	11
362	Sparse factor model for co-expression networks with an application using prior biological knowledge. Statistical Applications in Genetics and Molecular Biology, 2016, 15, 253-272.	0.2	5
363	<i>CCor</i> : A Whole Genome Network-Based Similarity Measure Between Two Genes. Biometrics, 2016, 72, 1216-1225.	0.8	3
364	Estimation of Directed Acyclic Graphs Through Two-Stage Adaptive Lasso for Gene Network Inference. Journal of the American Statistical Association, 2016, 111, 1004-1019.	1.8	36
365	Windowing improvements towards more comprehensible models. Knowledge-Based Systems, 2016, 92, 9-22.	4.0	2
366	Oxygen and tissue culture affect placental gene expression. Placenta, 2017, 55, 13-20.	0.7	10
367	Effects of low dose ionizing radiation on DNA damage-caused pathways by reverse-phase protein array and Bayesian networks. Journal of Bioinformatics and Computational Biology, 2017, 15, 1750006.	0.3	4
368	Comprehensive discovery of subsample gene expression components by information explanation: therapeutic implications in cancer. BMC Medical Genomics, 2017, 10, 12.	0.7	18
369	Reconstruction of noise-driven nonlinear networks from node outputs by using high-order correlations. Scientific Reports, 2017, 7, 44639.	1.6	16
370	Gene Regulatory Network Inference from Single-Cell Data Using Multivariate Information Measures. Cell Systems, 2017, 5, 251-267.e3.	2.9	414
371	Supervised Learning for Gene Regulatory Network Based on Flexible Neural Tree Model. Communications in Computer and Information Science, 2017, , 293-301.	0.4	0
372	Discovering Condition-Specific Gene Co-Expression Patterns Using Gaussian Mixture Models: A Cancer Case Study. Scientific Reports, 2017, 7, 8617.	1.6	44
373	Inference of targeted interactions of networks with data of driving and driven nodes only by applying fast-varying noise signals. Physics Letters, Section A: General, Atomic and Solid State Physics, 2017, 381, 2502-2509.	0.9	2
374	Efficient Ad-Hoc Graph Inference and Matching in Biological Databases. , 2017, , .		0

#	ARTICLE	IF	CITATIONS
375	Proteome Profiling Outperforms Transcriptome Profiling for Coexpression Based Gene Function Prediction. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 121-134.	2.5	111
377	Uncovering robust patterns of microRNA co-expression across cancers using Bayesian Relevance Networks. <i>PLoS ONE</i> , 2017, 12, e0183103.	1.1	6
378	A composite network of conserved and tissue specific gene interactions reveals possible genetic interactions in glioma. <i>PLoS Computational Biology</i> , 2017, 13, e1005739.	1.5	15
379	A link prediction approach to cancer drug sensitivity prediction. <i>BMC Systems Biology</i> , 2017, 11, 94.	3.0	47
380	A Generalized Approach for Measuring Relationships Among Genes. <i>Journal of Integrative Bioinformatics</i> , 2017, 14, .	1.0	2
381	Introduction to Environment and Exposome-Wide Association Studies: A Data-Driven Method to Identify Multiple Environmental Factors Associated with Phenotypes in Human Populations. , 2018, , 129-149.		3
382	Reconstruction of dynamic structures of experimental setups based on measurable experimental data only. <i>Chinese Physics B</i> , 2018, 27, 030503.	0.7	3
383	Large-deviation theory for diluted Wishart random matrices. <i>Physical Review E</i> , 2018, 97, 032124.	0.8	11
384	NF \hat{P} B pathway analysis: An approach to analyze gene co-expression networks employing feedback cycles. <i>Computational Biology and Chemistry</i> , 2018, 72, 62-76.	1.1	1
385	Systems Biology Approaches to Redox Metabolism in Stress and Disease States. <i>Antioxidants and Redox Signaling</i> , 2018, 29, 953-972.	2.5	44
386	Meal and habitual dietary networks identified through Semiparametric Gaussian Copula Graphical Models in a German adult population. <i>PLoS ONE</i> , 2018, 13, e0202936.	1.1	16
387	Bioinformatics and Systems Biology in Bioengineering. , 2018, , 223-243.		1
388	Recent developments in high dimensional covariance estimation and its related issues, a review. <i>Journal of the Korean Statistical Society</i> , 2018, 47, 239-247.	0.3	5
389	Characterizing functional consequences of DNA copy number alterations in breast and ovarian tumors by spaceMap. <i>Journal of Genetics and Genomics</i> , 2018, 45, 361-371.	1.7	1
390	A statistical method for measuring activation of gene regulatory networks. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2018, 17, .	0.2	1
391	Biological Pathways. , 2019, , 1047-1062.		0
392	Network Inference and Reconstruction in Bioinformatics. , 2019, , 805-813.		38
393	Moving Just Enough Deep Sequencing Data to Get the Job Done. <i>Bioinformatics and Biology Insights</i> , 2019, 13, 117793221985635.	1.0	2

#	ARTICLE	IF	CITATIONS
394	Estimating the Mutual Information between Two Discrete, Asymmetric Variables with Limited Samples. <i>Entropy</i> , 2019, 21, 623.	1.1	11
395	EdgeScaping: Mapping the spatial distribution of pairwise gene expression intensities. <i>PLoS ONE</i> , 2019, 14, e0220279.	1.1	2
396	Challenges in the Multivariate Analysis of Mass Cytometry Data: The Effect of Randomization. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2019, 95, 1178-1190.	1.1	12
397	Estimating Brain Connectivity Using Copula Gaussian Graphical Models. , 2019, , .		2
398	Coordinated Activity of Transcriptional Networks Responding to the Pattern of Action Potential Firing in Neurons. <i>Genes</i> , 2019, 10, 754.	1.0	24
399	Reconstructing nonlinear networks subject to fast-varying noises by using linearization with expanded variables. <i>Communications in Nonlinear Science and Numerical Simulation</i> , 2019, 72, 407-416.	1.7	8
400	Reconstruction and inference of the <i>Lactococcus lactis</i> MG1363 gene co-expression network. <i>PLoS ONE</i> , 2019, 14, e0214868.	1.1	5
401	Gene Regulatory Networks from Single Cell Data for Exploring Cell Fate Decisions. <i>Methods in Molecular Biology</i> , 2019, 1975, 211-238.	0.4	3
402	Efficient proximal gradient algorithm for inference of differential gene networks. <i>BMC Bioinformatics</i> , 2019, 20, 224.	1.2	3
403	Inferring Gene Regulatory Networks from a Population of Yeast Segregants. <i>Scientific Reports</i> , 2019, 9, 1197.	1.6	11
404	Host Transcriptomics as a Tool to Identify Diagnostic and Mechanistic Immune Signatures of Tuberculosis. <i>Frontiers in Immunology</i> , 2019, 10, 221.	2.2	31
405	Reconstructing of Networks With Binary-State Dynamics via Generalized Statistical Inference. <i>IEEE Transactions on Circuits and Systems I: Regular Papers</i> , 2019, 66, 1608-1619.	3.5	26
406	Compressed Covariance Estimation with Automated Dimension Learning. <i>Sankhya A</i> , 2019, 81, 466-481.	0.4	0
407	Effective Data-Aware Covariance Estimator From Compressed Data. <i>IEEE Transactions on Neural Networks and Learning Systems</i> , 2020, 31, 1-14.	7.2	2
408	Statistical genomics in rare cancer. <i>Seminars in Cancer Biology</i> , 2020, 61, 1-10.	4.3	15
409	Deep learning of pharmacogenomics resources: moving towards precision oncology. <i>Briefings in Bioinformatics</i> , 2020, 21, 2066-2083.	3.2	43
410	Quantitative proteomics and reverse engineer analysis identified plasma exosome derived protein markers related to osteoporosis.. <i>Journal of Proteomics</i> , 2020, 228, 103940.	1.2	14
411	Differential analysis of gene regulatory networks modeled with structural equation models. <i>Journal of Ambient Intelligence and Humanized Computing</i> , 2021, 12, 9181-9192.	3.3	0

#	ARTICLE	IF	CITATIONS
412	The Nexus Between Plant and Plant Microbiome: Revelation of the Networking Strategies. <i>Frontiers in Microbiology</i> , 2020, 11, 548037.	1.5	39
413	Extraction and Integration of Genetic Networks from Short-Profile Omic Data Sets. <i>Metabolites</i> , 2020, 10, 435.	1.3	6
414	Information Theory in Computational Biology: Where We Stand Today. <i>Entropy</i> , 2020, 22, 627.	1.1	27
415	Bayesian correlation is a robust gene similarity measure for single-cell RNA-seq data. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa002.	1.5	17
416	Supervised learning of gene-regulatory networks based on graph distance profiles of transcriptomics data. <i>Npj Systems Biology and Applications</i> , 2020, 6, 21.	1.4	22
417	Detecting network structures from measurable data produced by dynamics with hidden variables. <i>Chaos</i> , 2020, 30, 013138.	1.0	10
418	A powerful framework for an integrative study with heterogeneous omics data: from univariate statistics to multi-block analysis. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	10
419	Detection of hubs in complex networks by the Laplacian matrix. <i>Journal of the Korean Statistical Society</i> , 2021, 50, 431-446.	0.3	1
420	Gene Regulatory Network Inference. , 2021, , 86-95.		2
421	The effect of tissue composition on gene co-expression. <i>Briefings in Bioinformatics</i> , 2021, 22, 127-139.	3.2	25
422	An Early Stage Researcher's Primer on Systems Medicine Terminology. <i>Network and Systems Medicine</i> , 2021, 4, 2-50.	2.7	9
423	Identification of human glucocorticoid response markers using integrated multi-omic analysis from a randomized crossover trial. <i>ELife</i> , 2021, 10, .	2.8	22
424	Highly connected, non-redundant microRNA functional control in breast cancer molecular subtypes. <i>Interface Focus</i> , 2021, 11, 20200073.	1.5	6
426	Mechanism-Centric Approaches for Biomarker Detection and Precision Therapeutics in Cancer. <i>Frontiers in Genetics</i> , 2021, 12, 687813.	1.1	10
427	IonFlow: a galaxy tool for the analysis of ionomics data sets. <i>Metabolomics</i> , 2021, 17, 91.	1.4	3
428	ONAC066, A Stress-Responsive NAC Transcription Activator, Positively Contributes to Rice Immunity Against <i>Magnaporthe oryzae</i> Through Modulating Expression of OsWRKY62 and Three Cytochrome P450 Genes. <i>Frontiers in Plant Science</i> , 2021, 12, 749186.	1.7	6
429	An integrated workflow for biomarker development using microRNAs in extracellular vesicles for cancer precision medicine. <i>Seminars in Cancer Biology</i> , 2021, 74, 134-155.	4.3	9
430	Bacterial community demonstrates stronger network connectivity than fungal community in desert-grassland salt marsh. <i>Science of the Total Environment</i> , 2021, 798, 149118.	3.9	24

#	ARTICLE	IF	CITATIONS
431	HB-PLS: A statistical method for identifying biological process or pathway regulators by integrating Huber loss and Berhu penalty with partial least squares regression. <i>Forestry Research</i> , 2021, 1, 0-0.	0.5	1
432	Bayesian Clustering of Gene Expression Dynamics. <i>Statistics in the Health Sciences</i> , 2003, , 409-427.	0.2	2
433	Correlation and Gene Co-Expression Networks. , 2011, , 91-121.		2
434	Taking Bioinformatics to Systems Medicine. <i>Methods in Molecular Biology</i> , 2016, 1386, 17-41.	0.4	9
435	cDNA Microarrays. <i>Springer Protocols</i> , 2008, , 269-289.	0.1	1
436	Reconstructing Transcriptional Regulatory Networks Using Three-Way Mutual Information and Bayesian Networks. <i>Methods in Molecular Biology</i> , 2010, 674, 401-418.	0.4	2
437	Knowledge Integration: Its Meaning and Measurement. <i>Springer Handbooks</i> , 2019, , 69-94.	0.3	18
438	Inference of Gene Regulatory Network Based on Radial Basis Function Neural Network. <i>Lecture Notes in Computer Science</i> , 2016, , 442-450.	1.0	1
439	Combinatorial Genetic Regulatory Network Analysis Tools for High Throughput Transcriptomic Data. , 2005, , 150-165.		27
440	Biological Network Inference Using Redundancy Analysis. , 2007, , 16-27.		8
441	gPrune: A Constraint Pushing Framework for Graph Pattern Mining. , 2007, , 388-400.		45
442	Inferring Gene Regulatory Networks from Expression Data. <i>Studies in Computational Intelligence</i> , 2008, , 33-74.	0.7	24
443	Reverse Engineering of Gene Regulation Networks with an Application to the DREAM4 in silico Network Challenge. , 2011, , 461-477.		1
444	Shrinkage improves estimation of microbial associations under different normalization methods. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa100.	1.5	22
450	A Network Biology Approach Identifies Molecular Cross-Talk between Normal Prostate Epithelial and Prostate Carcinoma Cells. <i>PLoS Computational Biology</i> , 2016, 12, e1004884.	1.5	5
451	Biological Process Linkage Networks. <i>PLoS ONE</i> , 2009, 4, e5313.	1.1	34
452	Towards a Rigorous Assessment of Systems Biology Models: The DREAM3 Challenges. <i>PLoS ONE</i> , 2010, 5, e9202.	1.1	337
453	A Scale-Free Structure Prior for Graphical Models with Applications in Functional Genomics. <i>PLoS ONE</i> , 2010, 5, e13580.	1.1	23

#	ARTICLE	IF	CITATIONS
454	Conserved Non-Coding Regulatory Signatures in Arabidopsis Co-Expressed Gene Modules. PLoS ONE, 2012, 7, e45041.	1.1	7
455	Massive-Scale Gene Co-Expression Network Construction and Robustness Testing Using Random Matrix Theory. PLoS ONE, 2013, 8, e55871.	1.1	49
456	Stability Indicators in Network Reconstruction. PLoS ONE, 2014, 9, e89815.	1.1	20
457	Bayesian Correlation Analysis for Sequence Count Data. PLoS ONE, 2016, 11, e0163595.	1.1	10
458	Prophetic Granger Causality to infer gene regulatory networks. PLoS ONE, 2017, 12, e0170340.	1.1	10
459	Estimation of Gene Regulatory Networks. Postdoc Journal, 0, , .	0.4	6
460	Maximum likelihood degree of the two-dimensional linear Gaussian covariance model. Algebraic Statistics, 2020, 11, 107-123.	0.5	2
461	Complex Networks, Gene Expression and Cancer Complexity: A Brief Review of Methodology and Applications. Current Bioinformatics, 2020, 15, 629-655.	0.7	8
462	Clustering Techniques for Revealing Gene Expression Patterns. , 2015, , 438-447.		3
463	What are Gene Regulatory Networks?. , 2010, , 1-27.		9
464	A Linear Programming Framework for Inferring Gene Regulatory Networks by Integrating Heterogeneous Data. , 2010, , 450-475.		1
465	Microarray applications in nephrology with special focus on transplantation. Journal of Nephrology, 2012, 25, 589-602.	0.9	9
466	Microarrays. , 2003, , 665-692.		0
467	Strategies for Clustering, Classifying, Integrating, Standardizing and Visualizing Microarray Gene Expression Data. , 2003, , 277-340.		1
468	Toxicogenomic Dissection of the Antioxidant Response. , 2003, , .		0
469	Expression Profiling Uses in Antibacterial Chemotherapy Development. , 2003, , 187-199.		0
470	Information economics and the Internet. , 2003, , 347-356.		0
471	Lipidomic Analysis of Plasma and Tissues. , 2005, , 185-202.		0

#	ARTICLE	IF	CITATIONS
472	Statistical Methodologies for Analyzing Genomic Data. , 2006, , 607-621.		0
473	AN INFORMATION THEORETIC METHOD FOR RECONSTRUCTING LOCAL REGULATORY NETWORK MODULES FROM POLYMORPHIC SAMPLES. , 2007, , .		0
474	Using Gene Expression Modeling to Determine Biological Relevance of Putative Regulatory Networks. Lecture Notes in Computer Science, 2009, , 40-51.	1.0	0
475	Bioinformatic and Computational Analysis for Genomic Medicine. , 2009, , 206-225.		0
476	Complexity in Systems Level Biology and Genetics: Statistical Perspectives. , 2009, , 1226-1244.		0
477	Gaussian Graphical Models to Infer Putative Genes Involved in Nitrogen Catabolite Repression in <i>S. cerevisiae</i> . Lecture Notes in Computer Science, 2009, , 13-24.	1.0	0
478	Learning Network from High-Dimensional Array Data. Computational Biology, 2010, , 133-156.	0.1	0
479	Designing Microarray Experiments. , 2010, , 271-290.		0
480	Networks Between Categorical or Discretized Numeric Variables. , 2011, , 373-400.		0
481	Large-Scale Statistical Inference of Gene Regulatory Networks: Local Network-Based Measures. Intelligent Systems Reference Library, 2011, , 179-193.	1.0	0
482	Network module extraction with positive and negative co-regulation. , 2012, , .		0
483	Complexity in Systems Level Biology and Genetics: Statistical Perspectives. , 2012, , 561-578.		0
484	A Model-Based Method for Gene Dependency Measurement. PLoS ONE, 2012, 7, e40918.	1.1	3
485	Divergence Weighted Independence Graphs for the Exploratory Analysis of Biological Expression Data. Journal of Health & Medical Informatics, 2013, 04, .	0.2	0
487	Computational Methods for Analysis of Transcriptional Regulation. , 2014, , 327-353.		0
488	RSEM: Accurate Transcript Quantification from RNA-Seq Data With or Without a Reference Genome. , 2014, , 69-102.		4
489	Recent developments of constructing adjacency matrix in network analysis. Journal of the Korean Data and Information Science Society, 2014, 25, 1107-1116.	0.0	4
493	Inferring Genome-Wide Interaction Networks. Methods in Molecular Biology, 2017, 1526, 99-117.	0.4	2

#	ARTICLE	IF	CITATIONS
497	Building Gene Networks by Analyzing Gene Expression Profiles. , 2018, , 440-454.		0
502	Building Gene Networks by Analyzing Gene Expression Profiles. Advances in Medical Diagnosis, Treatment, and Care, 2019, , 27-44.	0.1	0
505	Identification of Common Gene Signatures in Microarray and RNA-Sequencing Data Using Network-Based Regularization. Lecture Notes in Computer Science, 2020, , 15-26.	1.0	0
507	Incorporating Network Topology Improves Prediction of Protein Interaction Networks from Transcriptomic Data. , 0, , 203-221.		0
508	Nested q-Partial Graphs for Genetic Network Inference from "Small n, Large p" Microarray Data. Communications in Computer and Information Science, 2008, , 273-287.	0.4	0
509	Evolutionary Search for Improved Path Diagrams. , 2007, , 114-121.		0
510	Utility of correlation measures in analysis of gene expression. Neurotherapeutics, 2006, 3, 384-395.	2.1	0
512	NetExtractor: Extracting a Cerebellar Tissue Gene Regulatory Network Using Differentially Expressed High Mutual Information Binary RNA Profiles. G3: Genes, Genomes, Genetics, 2020, 10, 2953-2963.	0.8	2
513	Functional relationships between gene pairs in oral squamous cell carcinoma. AMIA ... Annual Symposium proceedings, 2003, , 371-5.	0.2	4
514	Towards a cytokine-cell interaction knowledgebase of the adaptive immune system. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2009, , 439-50.	0.7	10
515	Identifying gene networks underlying the neurobiology of ethanol and alcoholism. , 2012, 34, 306-17.		26
516	Analysis of candidate genes has proposed the role of y chromosome in human prostate cancer. Iranian Journal of Cancer Prevention, 2014, 7, 204-11.	0.7	3
517	Comparative Analysis of Prostate Cancer Gene Regulatory Networks via Hub Type Variation. Avicenna Journal of Medical Biotechnology, 2015, 7, 8-15.	0.2	2
518	Estimation of Gene Regulatory Networks. Postdoc Journal, 2013, 1, 60-69.	0.4	2
519	Robust gene network analysis reveals alteration of the STAT5a network as a hallmark of prostate cancer. Genome Informatics, 2010, 24, 139-53.	0.4	5
520	Inferring linear and nonlinear Interaction networks using neighborhood support vector machines. , 2021, , .		0
521	Identification of the Association Between Toll-Like Receptors and T-Cell Activation in Takayasu's Arteritis. Frontiers in Immunology, 2021, 12, 792901.	2.2	3
522	Identifying large-scale interaction atlases using probabilistic graphs and external knowledge. Journal of Clinical and Translational Science, 2022, 6, e27.	0.3	1

#	ARTICLE	IF	CITATIONS
524	Using the co-expression network of T cell-activation-related genes to assess the disease activity in Takayasu's arteritis patients. <i>Arthritis Research and Therapy</i> , 2021, 23, 303.	1.6	6
525	Bayesian multistudy factor analysis for high-throughput biological data. <i>Annals of Applied Statistics</i> , 2021, 15, .	0.5	10
526	Application of modular response analysis to medium- to large-size biological systems. <i>PLoS Computational Biology</i> , 2022, 18, e1009312.	1.5	1
529	Clique Selection and its Effect on Paraclique Enrichment: An Experimental Study. , 0, , .		0
531	Signed and unsigned partial information decompositions of continuous network interactions. <i>Journal of Complex Networks</i> , 2022, 10, .	1.1	0
533	Inferencing Bulk Tumor and Single-Cell Multi-Omics Regulatory Networks for Discovery of Biomarkers and Therapeutic Targets. <i>Cells</i> , 2023, 12, 101.	1.8	0
535	Identification of a novel gene signature for neuroblastoma differentiation using a Boolean implication network. <i>Genes Chromosomes and Cancer</i> , 2023, 62, 313-331.	1.5	0
536	A multimodal deep learning model to infer cell-type-specific functional gene networks. <i>BMC Bioinformatics</i> , 2023, 24, .	1.2	1
537	Statistical Methodologies for Analyzing Genomic Data. <i>Springer Handbooks</i> , 2023, , 621-634.	0.3	0