Frank Emmert-Streib

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

315 papers	3,493 citations	29 h-index	48 g-index
373 ext. papers	4,538 ext. citations	4 avg, IF	6.14 L-index

#	Paper	IF	Citations
315	Information fusion as an integrative cross-cutting enabler to achieve robust, explainable, and trustworthy medical artificial intelligence. *Information Fusion*, **2022**, 79, 263-278	16.7	15
314	Identifying key interactions between process variables of different material categories using mutual information-based network inference method. *Procedia Computer Science*, **2022**, 200, 1550-1564	1.6	0
313	Comparison of Text Mining Models for Food and Dietary Constituent Named-Entity Recognition. *Machine Learning and Knowledge Extraction*, **2022**, 4, 254-275	3.1	3
312	A data-centric review of deep transfer learning with applications to text data. *Information Sciences*, **2021**, 585, 498-498	7.7	3
311	From the Digital Data Revolution toward a Digital Society: Pervasiveness of Artificial Intelligence. *Machine Learning and Knowledge Extraction*, **2021**, 3, 284-298	3.1	5
310	Analysis of the real number of infected people by COVID-19: A system dynamics approach. *PLoS ONE*, **2021**, 16, e0245728	3.7	0
309	Data-Driven Computational Social Network Science: Predictive and Inferential Models for Web-Enabled Scientific Discoveries. *Frontiers in Big Data*, **2021**, 4, 591749	2.8	4
308	Orbit Entropy and Symmetry Index Revisited. *Mathematics*, **2021**, 9, 1086	2.3	
307	Ensuring the Robustness and Reliability of Data-Driven Knowledge Discovery Models in Production and Manufacturing. *Frontiers in Artificial Intelligence*, **2021**, 4, 576892	3	3
306	Limitations of Explainability for Established Prognostic Biomarkers of Prostate Cancer. *Frontiers in Genetics*, **2021**, 12, 649429	4.5	0
305	Robustness of differential gene expression analysis of RNA-seq. *Computational and Structural Biotechnology Journal*, **2021**, 19, 3470-3481	6.8	4
304	Properties of Commuting Graphs over Semidihedral Groups. *Symmetry*, **2021**, 13, 103	2.7	1
303	Prognostic gene expression signatures of breast cancer are lacking a sensible biological meaning. *Scientific Reports*, **2021**, 11, 156	4.9	5
302	On the relationship between PageRank and automorphisms of a graph. *Information Sciences*, **2021**, 579, 401-417	7.7	0
301	Relationships between symmetry-based graph measures. *Information Sciences*, **2021**, 581, 291-303	7.7	0
300	In-flight Wind Field Identification and Prediction of Parafoil Systems. *Applied Sciences (Switzerland)*, **2020**, 10, 1958	2.6	2
299	Properties of Entropy-Based Topological Measures of Fullerenes. *Mathematics*, **2020**, 8, 740	2.3	8

298	Explainable artificial intelligence and machine learning: A reality rooted perspective. *Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery*, **2020**, 10, e1368	6.9	20
297	Relations and bounds for the zeros of graph polynomials using vertex orbits. *Applied Mathematics and Computation*, **2020**, 380, 125239	2.7	1
296	Glioblastoma Multiforme Stem Cell Cycle Arrest by Alkylaminophenol Through the Modulation of EGFR and CSC Signaling Pathways. *Cells*, **2020**, 9,	7.9	10
295	On the zeros of the partial Hosoya polynomial of graphs. *Information Sciences*, **2020**, 524, 199-215	7.7	4
294	The Orbit-Polynomial: A Novel Measure of Symmetry in Networks. *IEEE Access*, **2020**, 8, 36100-36112	3.5	7
293	Combining deep learning with token selection for patient phenotyping from electronic health records. *Scientific Reports*, **2020**, 10, 1432	4.9	13
292	The watching system as a generalization of identifying code. *Applied Mathematics and Computation*, **2020**, 380, 125302	2.7	1
291	Artificial Intelligence: A Clarification of Misconceptions, Myths and Desired Status. *Frontiers in Artificial Intelligence*, **2020**, 3, 524339	3	6
290	On graph entropy measures based on the number of independent sets and matchings. *Information Sciences*, **2020**, 516, 491-504	7.7	4
289	A novel epidemic model considering demographics and intercity commuting on complex dynamical networks. *Applied Mathematics and Computation*, **2020**, 386, 125517	2.7	9
288	On the Degeneracy of the Orbit Polynomial and Related Graph Polynomials. *Symmetry*, **2020**, 12, 1643	2.7	3
287	Graph-based exploitation of gene ontology using GOxploreR for scrutinizing biological significance. *Scientific Reports*, **2020**, 10, 16672	4.9	8
286	The Role of Symmetry in the Aesthetics of Residential Building Fa□des Using Cognitive Science Methods. *Symmetry*, **2020**, 12, 1438	2.7	2
285	Distributed Event-Triggered Circular Formation Control for Multiple Anonymous Mobile Robots With Order Preservation and Obstacle Avoidance. *IEEE Access*, **2020**, 8, 167288-167299	3.5	4
284	Named Entity Recognition and Relation Detection for Biomedical Information Extraction. *Frontiers in Cell and Developmental Biology*, **2020**, 8, 673	5.7	26
283	Partition and Colored Distances in Graphs Induced to Subsets of Vertices and Some of Its Applications. *Symmetry*, **2020**, 12, 2027	2.7	1
282	An Introductory Review of Deep Learning for Prediction Models With Big Data. *Frontiers in Artificial Intelligence*, **2020**, 3, 4	3	114
281	A Note on Distance-Based Entropy of Dendrimers. *Axioms*, **2019**, 8, 98	1.6	2

280	Proteome-transcriptome alignment of molecular portraits achieved by self-contained gene set analysis: Consensus colon cancer subtypes case study. *PLoS ONE*, **2019**, 14, e0221444	3.7	1
279	Introduction to Survival Analysis in Practice. *Machine Learning and Knowledge Extraction*, **2019**, 1, 1013-1038	3.1	18
278	2-(2-(2,4-dioxopentan-3-ylidene)hydrazineyl)benzonitrile as novel inhibitor of receptor tyrosine kinase and PI3K/AKT/mTOR signaling pathway in glioblastoma. *European Journal of Medicinal Chemistry*, **2019**, 166, 291-303	6.8	29
277	Large-Scale Simultaneous Inference with Hypothesis Testing: Multiple Testing Procedures in Practice. *Machine Learning and Knowledge Extraction*, **2019**, 1, 653-683	3.1	5
276	Hermitian normalized Laplacian matrix for directed networks. *Information Sciences*, **2019**, 495, 175-184	7.7	4
275	Systems Pharmacogenomic Landscape of Drug Similarities from LINCS data: Drug Association Networks. *Scientific Reports*, **2019**, 9, 7849	4.9	4
274	A Graph Theoretic Approach to Construct Desired Cryptographic Boolean Functions. *Axioms*, **2019**, 8, 40	1.6	
273	Comparing deep belief networks with support vector machines for classifying gene expression data from complex disorders. *FEBS Open Bio*, **2019**, 9, 1232-1248	2.7	13
272	On Properties of Distance-Based Entropies on Fullerene Graphs. *Entropy*, **2019**, 21,	2.8	12
271	Evaluation of Regression Models: Model Assessment, Model Selection and Generalization Error. *Machine Learning and Knowledge Extraction*, **2019**, 1, 521-551	3.1	24
270	Global Genetics Research in Prostate Cancer: A Text Mining and Computational Network Theory Approach. *Frontiers in Genetics*, **2019**, 10, 70	4.5	4
269	Alkylaminophenol Induces G1/S Phase Cell Cycle Arrest in Glioblastoma Cells Through p53 and Cyclin-Dependent Kinase Signaling Pathway. *Frontiers in Pharmacology*, **2019**, 10, 330	5.6	25
268	Hosoya entropy of fullerene graphs. *Applied Mathematics and Computation*, **2019**, 352, 88-98	2.7	14
267	Graph entropy based on the number of spanning forests of c-cyclic graphs. *Applied Mathematics and Computation*, **2019**, 363, 124616	2.7	3
266	L1000 Viewer: A Search Engine and Web Interface for the LINCS Data Repository. *Frontiers in Genetics*, **2019**, 10, 557	4.5	7
265	On efficient network similarity measures. *Applied Mathematics and Computation*, **2019**, 362, 124521	2.7	1
264	High-Dimensional LASSO-Based Computational Regression Models: Regularization, Shrinkage, and Selection. *Machine Learning and Knowledge Extraction*, **2019**, 1, 359-383	3.1	26
263	Understanding Statistical Hypothesis Testing: The Logic of Statistical Inference. *Machine Learning and Knowledge Extraction*, **2019**, 1, 945-961	3.1	17

262	The Hosoya Entropy of Graphs Revisited. *Symmetry*, **2019**, 11, 1013	2.7	12
261	The Maximum Hosoya Index of Unicyclic Graphs with Diameter at Most Four. *Symmetry*, **2019**, 11, 1034	2.7	2
260	Measuring the complexity of directed graphs: A polynomial-based approach. *PLoS ONE*, **2019**, 14, e0223745	3.7	6
259	Prostate Cancer Gene Regulatory Network Inferred from RNA-Seq Data. *Current Genomics*, **2019**, 20, 38-48	2.6	5
258	A comprehensive survey of error measures for evaluating binary decision making in data science. *Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery*, **2019**, 9, e1303	6.9	12
257	A Note on Graphs with Prescribed Orbit Structure. *Entropy*, **2019**, 21, 1118	2.8	2
256	Utilizing Social Media Data for Psychoanalysis to Study Human Personality. *Frontiers in Psychology*, **2019**, 10, 2596	3.4	4
255	Ensuring Quality Standards and Reproducible Research for Data Analysis Services in Oncology: A Cooperative Service Model. *Frontiers in Cell and Developmental Biology*, **2019**, 7, 349	5.7	2
254	Comparing biological information contained in mRNA and non-coding RNAs for classification of lung cancer patients. *BMC Cancer*, **2019**, 19, 1176	4.8	9
253	Constrained Covariance Matrices With a Biologically Realistic Structure: Comparison of Methods for Generating High-Dimensional Gaussian Graphical Models. *Frontiers in Applied Mathematics and Statistics*, **2019**, 5,	2.2	3
252	Towards detecting structural branching and cyclicity in graphs: A polynomial-based approach. *Information Sciences*, **2019**, 471, 19-28	7.7	5
251	On the degeneracy of the Randi entropy and related graph measures. *Information Sciences*, **2019**, 501, 680-687	7.7	0
250	A review of connectivity map and computational approaches in pharmacogenomics. *Briefings in Bioinformatics*, **2018**, 19, 506-523	13.4	101
249	Properties of graph distance measures by means of discrete inequalities. *Applied Mathematical Modelling*, **2018**, 59, 739-749	4.5	3
248	Graph measures with high discrimination power revisited: A random polynomial approach. *Information Sciences*, **2018**, 467, 407-414	7.7	4
247	MetrIntSimil An Accurate and Robust Metric for Comparison of Similarity in Intelligence of Any Number of Cooperative Multiagent Systems. *Symmetry*, **2018**, 10, 48	2.7	5
246	Comments to Quantification of network structural dissimilarities published by Schieber et al. *Mathematical Methods in the Applied Sciences*, **2018**, 41, 5711-5713	2.3	
245	Computational analysis of structural properties of economic and financial networks. *Journal of Network Theory in Finance*, **2018**, 1-32	1.5	7

244	A Machine Learning Perspective on Personalized Medicine: An Automized, Comprehensive Knowledge Base with Ontology for Pattern Recognition. *Machine Learning and Knowledge Extraction*, **2018**, 1, 149-156	3.1	19
243	Defining Data Science by a Data-Driven Quantification of the Community. *Machine Learning and Knowledge Extraction*, **2018**, 1, 235-251	3.1	17
242	Harnessing the biological complexity of Big Data from LINCS gene expression signatures. *PLoS ONE* , **2018**, 13, e0201937	3.7	5
241	Data Analytics Applications for Streaming Data From Social Media: What to Predict?. *Frontiers in Big Data*, **2018**, 1, 2	2.8	8
240	Impact of Variable RNA-Sequencing Depth on Gene Expression Signatures and Target Compound Robustness: Case Study Examining Brain Tumor (Glioma) Disease Progression. *JCO Precision Oncology*, **2018**, 2,	3.6	3
239	Inference of Genome-Scale Gene Regulatory Networks: Are There Differences in Biological and Clinical Validations?. *Machine Learning and Knowledge Extraction*, **2018**, 1, 138-148	3.1	2
238	Understanding the World Economy in Terms of Networks: A Survey of Data-Based Network Science Approaches on Economic Networks. *Frontiers in Applied Mathematics and Statistics*, **2018**, 4,	2.2	4
237	Multilayer Aggregation with Statistical Validation: Application to Investor Networks. *Scientific Reports*, **2018**, 8, 8198	4.9	19
236	GSAR: Bioconductor package for Gene Set analysis in R. *BMC Bioinformatics*, **2017**, 18, 61	3.6	22
235	MetrIntMeas a novel metric for measuring the intelligence of a swarm of cooperating agents. *Cognitive Systems Research*, **2017**, 45, 17-29	4.8	10
234	Highly unique network descriptors based on the roots of the permanental polynomial. *Information Sciences*, **2017**, 408, 176-181	7.7	13
233	sgnesR: An R package for simulating gene expression data from an underlying real gene network structure considering delay parameters. *BMC Bioinformatics*, **2017**, 18, 325	3.6	4
232	Extracting the Strongest Signals from Omics Data: Differentially Expressed Pathways and Beyond. *Methods in Molecular Biology*, **2017**, 1613, 125-159	1.4	1
231	Quantitative Graph Theory: A new branch of graph theory and network science. *Information Sciences*, **2017**, 418-419, 575-580	7.7	22
230	Toward Measuring Network Aesthetics Based on Symmetry. *Axioms*, **2017**, 6, 12	1.6	3
229	Lessons from the Human Genome Project: Modesty, Honesty, and Realism. *Frontiers in Genetics*, **2017**, 8, 184	4.5	5
228	Mathematical Modeling in Systems Biology. *Communications in Computer and Information Science*, **2017**, 161-166	0.3	
227	Gene set analysis approaches for RNA-seq data: performance evaluation and application guideline. *Briefings in Bioinformatics*, **2016**, 17, 393-407	13.4	37

226	Graph Entropy: Recent Results and Perspectives **2016**, 133-182		2
225	Graph Entropies in Texture Segmentation of Images **2016**, 203-231		1
224	Application of Graph Entropy for Knowledge Discovery and Data Mining in Bibliometric Data **2016**, 259-273		2
223	Fifty years of graph matching, network alignment and network comparison. *Information Sciences*, **2016**, 346-347, 180-197	7.7	112
222	A BRCA1 deficient, NFB driven immune signal predicts good outcome in triple negative breast cancer. *Oncotarget*, **2016**, 7, 19884-96	3.3	22
221	The Process of Analyzing Data is the Emergent Feature of Data Science. *Frontiers in Genetics*, **2016**, 7, 12	4.5	16
220	The Need for Formally Defining "Modern Medicine" by Means of Experimental Design. *Frontiers in Genetics*, **2016**, 7, 60	4.5	4
219	Against Dataism and for Data Sharing of Big Biomedical and Clinical Data with Research Parasites. *Frontiers in Genetics*, **2016**, 7, 154	4.5	8
218	samExploreR: exploring reproducibility and robustness of RNA-seq results based on SAM files. *Bioinformatics*, **2016**, 32, 3345-3347	7.2	7
217	Comparison of module detection algorithms in protein networks and investigation of the biological meaning of predicted modules. *BMC Bioinformatics*, **2016**, 17, 129	3.6	19
216	Inference and Analysis of Gene Regulatory Networks in R **2016**, 289-306		0
215	Using the DiffCorr Package to Analyze and Visualize Differential Correlations in Biological Networks **2016**, 1-34		3
214	Visualization of Biological Networks Using NetBioV **2016**, 307-333		1
213	Bayesian Computational Algorithms for Social Network Analysis **2016**, 63-82		
212	Threshold Degradation in R Using iDEMO **2016**, 83-124		2
211	Optimization of Stratified Sampling with the R Package SamplingStrata: Applications to Network Data **2016**, 125-150		
210	Exploring the Role of Small Molecules in Biological Systems Using Network Approaches **2016**, 151-172		
209	Performing Network Alignments with R **2016**, 173-200		

208	1-Penalized Methods in High-Dimensional Gaussian Markov Random Fields **2016**, 201-265		1
207	Cluster Analysis of Social Networks Using R **2016**, 267-288		
206	Analytical Models and Methods for Anomaly Detection in Dynamic, Attributed Graphs **2016**, 35-61		
205	Computational cancer biology: education is a natural key to many locks. *BMC Cancer*, **2015**, 15, 7	4.8	6
204	Using shRNA experiments to validate gene regulatory networks. *Genomics Data*, **2015**, 4, 123-6		
203	Graph distance measures based on topological indices revisited. *Applied Mathematics and Computation*, **2015**, 266, 623-633	2.7	20
202	Urothelial cancer gene regulatory networks inferred from large-scale RNAseq, Bead and Oligo gene expression data. *BMC Systems Biology*, **2015**, 9, 21	3.5	7
201	Effects of subsampling on characteristics of RNA-seq data from triple-negative breast cancer patients. *Chinese Journal of Cancer*, **2015**, 34, 427-38		3
200	Entropy of Weighted Graphs with Randi c Weights. *Entropy*, **2015**, 17, 3710-3723	2.8	23
199	Biological networks: the microscope of the twenty-first century?. *Frontiers in Genetics*, **2015**, 6, 307	4.5	
198	Structural Analysis of Treatment Cycles Representing Transitions between Nursing Organizational Units Inferred from Diabetes. *PLoS ONE*, **2015**, 10, e0127152	3.7	
197	Discrimination Power of Polynomial-Based Descriptors for Graphs by Using Functional Matrices. *PLoS ONE*, **2015**, 10, e0139265	3.7	2
196	Comprehensive molecular pathology analysis of small bowel adenocarcinoma reveals novel targets with potential for clinical utility. *Oncotarget*, **2015**, 6, 20863-74	3.3	31
195	Gene Sets Net Correlations Analysis (GSNCA): a multivariate differential coexpression test for gene sets. *Bioinformatics*, **2014**, 30, 360-8	7.2	72
194	Functional and genetic analysis of the colon cancer network. *BMC Bioinformatics*, **2014**, 15 Suppl 6, S6	3.6	28
193	Inference and validation of predictive gene networks from biomedical literature and gene expression data. *Genomics*, **2014**, 103, 329-36	4.3	28
192	Report from the 2nd Summer School in Computational Biology organized by the Queen's University of Belfast. *Genomics Data*, **2014**, 2, 37-9		
191	NetBioV: an R package for visualizing large network data in biology and medicine. *Bioinformatics*, **2014**, 30, 2834-6	7.2	32

190	Structural differentiation of graphs using Hosoya-based indices. *PLoS ONE*, **2014**, 9, e102459	3.7	18
189	Interrelations of graph distance measures based on topological indices. *PLoS ONE*, **2014**, 9, e94985	3.7	44
188	Gene regulatory networks and their applications: understanding biological and medical problems in terms of networks. *Frontiers in Cell and Developmental Biology*, **2014**, 2, 38	5.7	86
187	The gene regulatory network for breast cancer: integrated regulatory landscape of cancer hallmarks. *Frontiers in Genetics*, **2014**, 5, 15	4.5	42
186	Enhancing our understanding of ways to analyze metagenomes. *Frontiers in Genetics*, **2014**, 5, 108	4.5	
185	Quantitative assessment and validation of network inference methods in bioinformatics. *Frontiers in Genetics*, **2014**, 5, 221	4.5	8
184	Comparative evaluation of gene set analysis approaches for RNA-Seq data. *BMC Bioinformatics*, **2014**, 15, 397	3.6	22
183	Untangling statistical and biological models to understand network inference: the need for a genomics network ontology. *Frontiers in Genetics*, **2014**, 5, 299	4.5	11
182	Entropy bounds for dendrimers. *Applied Mathematics and Computation*, **2014**, 242, 462-472	2.7	42
181	Relevance of different prior knowledge sources for inferring gene interaction networks. *Frontiers in Genetics*, **2014**, 5, 177	4.5	5
180	Probabilistic inequalities for evaluating structural network measures. *Information Sciences*, **2014**, 288, 220-245	7.7	19
179	Netmes: assessing gene network inference algorithms by network-based measures. *Evolutionary Bioinformatics*, **2014**, 10, 1-9	1.9	3
178	A computational approach to construct a multivariate complete graph invariant. *Information Sciences*, **2014**, 260, 200-208	7.7	26
177	What Is Quantitative Graph Theory?. *Discrete Mathematics and Its Applications*, **2014**, 1-33		5
176	Metros as Biological Systems: Complexity in Small Real-life Networks **2013**, 259-285		2
175	Three Types of Network Complexity Pyramid **2013**, 63-98		1
174	Information-Based Complexity of Networks **2013**, 209-227		
173	Thermodynamic Depth in Undirected and Directed Networks **2013**, 229-247		

172	Functional Complexity Based on Topology **2013**, 1-15		
171	Interfacing cellular networks of S. cerevisiae and E. coli: connecting dynamic and genetic information. *BMC Genomics*, **2013**, 14, 324	4.5	22
170	Collectives of diagnostic biomarkers identify high-risk subpopulations of hematuria patients: exploiting heterogeneity in large-scale biomarker data. *BMC Medicine*, **2013**, 11, 12	11.4	6
169	An efficient heuristic approach to detecting graph isomorphism based on combinations of highly discriminating invariants. *Advances in Computational Mathematics*, **2013**, 39, 311-325	1.6	18
168	Comparing Biological Networks: A Survey on Graph Classifying Techniques **2013**, 43-63		4
167	[COMMODE] a large-scale database of molecular descriptors using compounds from PubChem. *Source Code for Biology and Medicine*, **2013**, 8, 22	1.9	1
166	Kirchhoff's Matrix-Tree Theorem Revisited: Counting Spanning Trees with the Quantum Relative Entropy **2013**, 177-190		
165	Computational Complexity of Graphs **2013**, 99-153		1
164	The Linear Complexity of a Graph **2013**, 155-175		2
163	Dimension Measure for Complex Networks **2013**, 191-208		
162	Connections Between Artificial Intelligence and Computational Complexity and the Complexity of Graphs **2013**, 17-40		
161	Circumscribed Complexity in Ecological Networks **2013**, 249-258		1
160	Selection-Based Estimates of Complexity Unravel Some Mechanisms and Selective Pressures Underlying the Evolution of Complexity in Artificial Networks **2013**, 41-61		2
159	Learning Systems Biology: Conceptual Considerations toward a Web-Based Learning Platform. *Education Sciences*, **2013**, 3, 158-171	2.2	
158	Discriminant and Network Analysis to Study Origin of Cancer **2013**, 193-214		
157	Intervention and Control of Gene Regulatory Networks: Theoretical Framework and Application to Human Melanoma Gene Regulation **2013**, 215-238		
156	Colorectal Cancer and Its Molecular Subsystems: Construction, Interpretation, and Validation **2013**, 107-132		1
155	Semisupervised Methods for Analyzing High-dimensional Genomic Data **2013**, 93-106		

154	Identification of Recurrent DNA Copy Number Aberrations in Tumors **2013**, 239-260		
153	The Cancer Cell, Its Entropy, and High-Dimensional Molecular Data **2013**, 261-285		
152	Control of Type I Error Rates for Oncology Biomarker Discovery with High-Throughput Platforms **2013**, 1-26		
151	Overview of Public Cancer Databases, Resources, and Visualization Tools **2013**, 27-40		
150	Discovery of Expression Signatures in Chronic Myeloid Leukemia by Bayesian Model Averaging **2013**, 41-55		
149	Bayesian Ranking and Selection Methods in Microarray Studies **2013**, 57-74		
148	Multiclass Classification via Bayesian Variable Selection with Gene Expression Data **2013**, 75-92		
147	Network Medicine: Disease Genes in Molecular Networks **2013**, 133-151		
146	Inference of Gene Regulatory Networks in Breast and Ovarian Cancer by Integrating Different Genomic Data **2013**, 153-171		
145	Network-Module-Based Approaches in Cancer Data Analysis **2013**, 173-192		
144	Ensuring the statistical soundness of competitive gene set approaches: gene filtering and genome-scale coverage are essential. *Nucleic Acids Research*, **2013**, 41, e82	20.1	21
143	Network nursing: connections between nursing and complex network science. *International Journal of Nursing Knowledge*, **2013**, 24, 150-6	1.1	5
142	The human disease network. *Systems Biomedicine (Austin, Tex)*, **2013**, 1, 20-28		22
141	Structural properties and complexity of a new network class: Collatz step graphs. *PLoS ONE*, **2013**, 8, e56461	3.7	3
140	Enhancing systems medicine beyond genotype data by dynamic patient signatures: having information and using it too. *Frontiers in Genetics*, **2013**, 4, 241	4.5	4
139	B-cell lymphoma gene regulatory networks: biological consistency among inference methods. *Frontiers in Genetics*, **2013**, 4, 281	4.5	16
138	Quantitative network measures as biomarkers for classifying prostate cancer disease states: a systems approach to diagnostic biomarkers. *PLoS ONE*, **2013**, 8, e77602	3.7	15
137	Large-scale evaluation of molecular descriptors by means of clustering. *PLoS ONE*, **2013**, 8, e83956	3.7	7

136	Influence of the experimental design of gene expression studies on the inference of gene regulatory networks: environmental factors. *PeerJ*, **2013**, 1, e10	3.1	8
135	Detecting sequence dependent transcriptional pauses from RNA and protein number time series. *BMC Bioinformatics*, **2012**, 13, 152	3.6	
134	Harnessing the complexity of gene expression data from cancer: from single gene to structural pathway methods. *Biology Direct*, **2012**, 7, 44	7.2	19
133	Organizational structure and the periphery of the gene regulatory network in B-cell lymphoma. *BMC Systems Biology*, **2012**, 6, 38	3.5	18
132	Universal construction mechanism for networks from one-dimensional symbol sequences. *Applied Mathematics and Computation*, **2012**, 219, 1020-1030	2.7	2
131	Bagging statistical network inference from large-scale gene expression data. *PLoS ONE*, **2012**, 7, e33624	3.7	79
130	Exploring statistical and population aspects of network complexity. *PLoS ONE*, **2012**, 7, e34523	3.7	25
129	Limitations of gene duplication models: evolution of modules in protein interaction networks. *PLoS ONE*, **2012**, 7, e35531	3.7	5
128	Standardization of diagnostic biomarker concentrations in urine: the hematuria caveat. *PLoS ONE*, **2012**, 7, e53354	3.7	21
127	Statistical inference and reverse engineering of gene regulatory networks from observational expression data. *Frontiers in Genetics*, **2012**, 3, 8	4.5	89
126	Evolutionary dynamics of the spatial Prisoner Dilemma with self-inhibition. *Applied Mathematics and Computation*, **2012**, 218, 6482-6488	2.7	2
125	Personalized medicine: Has it started yet? A reconstruction of the early history. *Frontiers in Genetics* , **2012**, 3, 313	4.5	15
124	Gene set analysis for self-contained tests: complex null and specific alternative hypotheses. *Bioinformatics*, **2012**, 28, 3073-80	7.2	14
123	A Bayesian analysis of the chromosome architecture of human disorders by integrating reductionist data. *Scientific Reports*, **2012**, 2, 513	4.9	
122	Assessment method for a power analysis to identify differentially expressed pathways. *PLoS ONE*, **2012**, 7, e37510	3.7	16
121	Network-Based Methods for Computational Diagnostics by Means of R **2012**, 185-197		2
120	What if the Fit is Unfit? Criteria for Biological Systems Estimation beyond Residual Errors **2011**, 181-200		2
119	Connections between classical and parametric network entropies. *PLoS ONE*, **2011**, 6, e15733	3.7	21

118	Parametric construction of episode networks from pseudoperiodic time series based on mutual information. *PLoS ONE*, **2011**, 6, e27733	3.7	5
117	Network Analysis to Interpret Complex Phenotypes **2011**, 1-12		1
116	Network Screening: A New Method to Identify Active Networks from an Ensemble of Known Networks **2011**, 281-298		
115	Protein Network Analysis for Disease Gene Identification and Prioritization **2011**, 405-413		
114	Modeling Expression Quantitative Trait Loci in Multiple Populations **2011**, 39-65		
113	Elucidation of General and Condition-Dependent Gene Pathways Using Mixture Models and Bayesian Networks **2011**, 91-103		1
112	Multiscale Network Reconstruction from Gene Expression Measurements: Correlations, Perturbations, and A Priori Biological Knowledge **2011**, 105-131		
111	Gene Regulatory Networks Inference: Combining a Genetic Programming and H Filtering Approach **2011**, 133-153		2
110	Computational Reconstruction of Protein Interaction Networks **2011**, 155-180		
109	Transcriptional Network Inference Based on Information Theory **2011**, 67-89		2
108	Representing Cancer Cell Trajectories in a Phase-Space Diagram: Switching Cellular States by Biological Phase Transitions **2011**, 377-403		3
107	On Some Inverse Problems in Generating Probabilistic Boolean Networks **2011**, 329-348		
106	Boolean Analysis of Gene Expression Datasets **2011**, 349-375		
105	Networks for systems biology: conceptual connection of data and function. *IET Systems Biology*, **2011**, 5, 185-207	1.4	93
104	Structural measures for network biology using QuACN. *BMC Bioinformatics*, **2011**, 12, 492	3.6	16
103	Pathways and Networks as Functional Descriptors for Human Disease and Drug Response Endpoints **2011**, 415-442		2
102	Structural influence of gene networks on their inference: analysis of C3NET. *Biology Direct*, **2011**, 6, 31	7.2	45
101	Network biology: a direct approach to study biological function. *Wiley Interdisciplinary Reviews: Systems Biology and Medicine*, **2011**, 3, 379-91	6.6	42

100	Stochastic Modeling of Gene Regulatory Networks **2011**, 13-37		
99	Correlation Network Analysis and Knowledge Integration **2011**, 251-280		2
98	Machine Learning Methods for Identifying Essential Genes and Proteins in Networks **2011**, 201-214		
97	Gene Coexpression Networks for the Analysis of DNA Microarray Data **2011**, 215-250		31
96	Community Detection in Biological Networks **2011**, 299-327		1
95	Pathway analysis of expression data: deciphering functional building blocks of complex diseases. *PLoS Computational Biology*, **2011**, 7, e1002053	5	79
94	Influence of statistical estimators of mutual information and data heterogeneity on the inference of gene regulatory networks. *PLoS ONE*, **2011**, 6, e29279	3.7	20
93	Large-Scale Statistical Inference of Gene Regulatory Networks: Local Network-Based Measures. *Intelligent Systems Reference Library*, **2011**, 179-193	0.8	
92	A Brief Introduction to Complex Networks and Their Analysis **2011**, 1-26		2
91	Statistic complexity: combining kolmogorov complexity with an ensemble approach. *PLoS ONE*, **2010**, 5, e12256	3.7	12
90	Influence of the time scale on the construction of financial networks. *PLoS ONE*, **2010**, 5, e12884	3.7	24
89	Revealing differences in gene network inference algorithms on the network level by ensemble methods. *Bioinformatics*, **2010**, 26, 1738-44	7.2	76
88	Exploratory analysis of spatiotemporal patterns of cellular automata by clustering compressibility. *Physical Review E*, **2010**, 81, 026103	2.4	8
87	Making Mountains out of Molehills: Moving from Single Gene to Pathway Based Models of Colon Cancer Progression **2010**, 73-87		
86	Multivariate Analysis of Microarray Data Using Hotelling's T2 Test **2010**, 113-130		
85	Gene-Set Expression Analysis: Challenges and Tools **2010**, 89-112		
84	Interpreting Differential Coexpression of Gene Sets **2010**, 131-150		
83	Multivariate Analysis of Microarray Data: Application of MANOVA **2010**, 151-166		

82	Testing Significance of a Class of Genes **2010**, 167-184		
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80	Predicting Cancer Survival Using Expression Patterns **2010**, 305-323		
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78	A Systems Biology Approach to Construct a Cancer-Perturbed Protein–Protein Interaction Network for Apoptosis by Means of Microarray and Database Mining **2010**, 231-251		
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76	Model Averaging for Biological Networks with Prior Information **2010**, 347-372		
75	Multiple Testing Methods **2010**, 45-72		1
74	Integration of Microarray Datasets **2010**, 325-345		
73	Kernel Classification Methods for Cancer Microarray Data **2010**, 279-303		1
72	Cancer Stem Cells – Finding and Capping the Roots of Cancer **2010**, 25-43		1
71	Mining Graph Patterns in Web-based Systems: A Conceptual View. *Text, Speech and Language Technology*, **2010**, 237-253		
70	The Biology of MYC in Health and Disease: A High Altitude View **2010**, 1-24		
69	Local network-based measures to assess the inferability of different regulatory networks. *IET Systems Biology*, **2010**, 4, 277-88	1.4	25
68	Inferring the conservative causal core of gene regulatory networks. *BMC Systems Biology*, **2010**, 4, 132	3.5	132
67	Identifying critical financial networks of the DJIA: Toward a network-based index. *Complexity*, **2010**, 16, 24-33	1.6	20
66	Unite and conquer: univariate and multivariate approaches for finding differentially expressed gene sets. *Bioinformatics*, **2009**, 25, 2348-54	7.2	86
65	Information processing in the transcriptional regulatory network of yeast: functional robustness. *BMC Systems Biology*, **2009**, 3, 35	3.5	23

64	Hierarchical coordination of periodic genes in the cell cycle of Saccharomyces cerevisiae. *BMC Systems Biology*, **2009**, 3, 76	3.5	3
63	Fault tolerance of information processing in gene networks. *Physica A: Statistical Mechanics and Its Applications*, **2009**, 388, 541-548	3.3	5
62	On entropy-based molecular descriptors: statistical analysis of real and synthetic chemical structures. *Journal of Chemical Information and Modeling*, **2009**, 49, 1655-63	6.1	73
61	Predicting cell cycle regulated genes by causal interactions. *PLoS ONE*, **2009**, 4, e6633	3.7	5
60	Towards a Partitioning of the Input Space of Boolean Networks: Variable Selection Using Bagging. *Lecture Notes of the Institute for Computer Sciences, Social-Informatics and Telecommunications Engineering*, **2009**, 715-723	0.2	
59	Organizational Structure of the Transcriptional Regulatory Network of Yeast: Periodic Genes. *Lecture Notes of the Institute for Computer Sciences, Social-Informatics and Telecommunications Engineering*, **2009**, 140-148	0.2	
58	Towards Network Complexity. *Lecture Notes of the Institute for Computer Sciences, Social-Informatics and Telecommunications Engineering*, **2009**, 707-714	0.2	1
57	ROBUSTNESS IN SCALE-FREE NETWORKS: COMPARING DIRECTED AND UNDIRECTED NETWORKS. *International Journal of Modern Physics C*, **2008**, 19, 717-726	1.1	10
56	The Structural Information Content of Chemical Networks. *Zeitschrift Fur Naturforschung - Section A Journal of Physical Sciences*, **2008**, 63, 155-158	1.4	7
55	A comparative analysis of multidimensional features of objects resembling sets of graphs. *Applied Mathematics and Computation*, **2008**, 196, 221-235	2.7	5
54	Structural information content of networks: graph entropy based on local vertex functionals. *Computational Biology and Chemistry*, **2008**, 32, 131-8	3.6	30
53	Entropy bounds for hierarchical molecular networks. *PLoS ONE*, **2008**, 3, e3079	3.7	33
52	The chronic fatigue syndrome: a comparative pathway analysis. *Journal of Computational Biology*, **2007**, 14, 961-72	1.7	68
51	Topological mappings between graphs, trees and generalized trees. *Applied Mathematics and Computation*, **2007**, 186, 1326-1333	2.7	10
50	Comparing large graphs efficiently by margins of feature vectors. *Applied Mathematics and Computation*, **2007**, 188, 1699-1710	2.7	16
49	Information theoretic measures of UHG graphs with low computational complexity. *Applied Mathematics and Computation*, **2007**, 190, 1783-1794	2.7	25
48	Structural similarity of directed universal hierarchical graphs: A low computational complexity approach. *Applied Mathematics and Computation*, **2007**, 194, 7-20	2.7	7
47	A topological algorithm for identification of structural domains of proteins. *BMC Bioinformatics*, **2007**, 8, 237	3.6	18

46	NONLINEAR TIME SERIES PREDICTION BASED ON A POWER-LAW NOISE MODEL. *International Journal of Modern Physics C*, **2007**, 18, 1839-1852	1.1	4
45	Harnessing naturally randomized transcription to infer regulatory relationships among genes. *Genome Biology*, **2007**, 8, R219	18.3	83
44	Optimization Procedure for Predicting Nonlinear Time Series Based on a Non-Gaussian Noise Model **2007**, 540-549		
43	Influence of the neural network topology on the learning dynamics. *Neurocomputing*, **2006**, 69, 1179-1182	3.4	6
42	A HETEROSYNAPTIC LEARNING RULE FOR NEURAL NETWORKS. *International Journal of Modern Physics C*, **2006**, 17, 1501-1520	1.1	7
41	Algorithmic computation of knot polynomials of secondary structure elements of proteins. *Journal of Computational Biology*, **2006**, 13, 1503-12	1.7	11
40	A similarity measure for graphs with low computational complexity. *Applied Mathematics and Computation*, **2006**, 182, 447-459	2.7	34
39	A Novel Stochastic Learning Rule for Neural Networks. *Lecture Notes in Computer Science*, **2006**, 414-423	0.9	
38	STOCHASTIC SZNAJD MODEL IN OPEN COMMUNITY. *International Journal of Modern Physics C*, **2005**, 16, 1693-1699	1.1	1
37	A Neurobiologically Motivated Model for Self-organized Learning. *Lecture Notes in Computer Science*, **2005**, 415-424	0.9	
36	A constrained HMM-based approach to the estimation of perceptual switching dynamics in pigeons. *Neurocomputing*, **2001**, 38-40, 1495-1501	5.4	3
35	Extracting the dynamics of perceptual switching from 'noisy' behaviour: an application of hidden Markov modelling to pecking data from pigeons. *Journal of Physiology (Paris)*, **2000**, 94, 555-67		6
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