

Frank Emmert-Streib

List of Publications by Citations

Source: <https://exaly.com/author-pdf/7537684/frank-emmert-streib-publications-by-citations.pdf>

Version: 2024-04-09

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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
3 ¹⁵	Inferring the conservative causal core of gene regulatory networks. <i>BMC Systems Biology</i> , 2010 , 4, 132	3.5	132
3 ¹⁴	An Introductory Review of Deep Learning for Prediction Models With Big Data. <i>Frontiers in Artificial Intelligence</i> , 2020 , 3, 4	3	114
3 ¹³	Fifty years of graph matching, network alignment and network comparison. <i>Information Sciences</i> , 2016 , 346-347, 180-197	7.7	112
3 ¹²	A review of connectivity map and computational approaches in pharmacogenomics. <i>Briefings in Bioinformatics</i> , 2018 , 19, 506-523	13.4	101
3 ¹¹	Networks for systems biology: conceptual connection of data and function. <i>IET Systems Biology</i> , 2011 , 5, 185-207	1.4	93
3 ¹⁰	Statistical inference and reverse engineering of gene regulatory networks from observational expression data. <i>Frontiers in Genetics</i> , 2012 , 3, 8	4.5	89
3 ⁰⁹	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	5.7	86
3 ⁰⁸	Unite and conquer: univariate and multivariate approaches for finding differentially expressed gene sets. <i>Bioinformatics</i> , 2009 , 25, 2348-54	7.2	86
3 ⁰⁷	Harnessing naturally randomized transcription to infer regulatory relationships among genes. <i>Genome Biology</i> , 2007 , 8, R219	18.3	83
3 ⁰⁶	Bagging statistical network inference from large-scale gene expression data. <i>PLoS ONE</i> , 2012 , 7, e33624	3.7	79
3 ⁰⁵	Pathway analysis of expression data: deciphering functional building blocks of complex diseases. <i>PLoS Computational Biology</i> , 2011 , 7, e1002053	5	79
3 ⁰⁴	Revealing differences in gene network inference algorithms on the network level by ensemble methods. <i>Bioinformatics</i> , 2010 , 26, 1738-44	7.2	76
3 ⁰³	On entropy-based molecular descriptors: statistical analysis of real and synthetic chemical structures. <i>Journal of Chemical Information and Modeling</i> , 2009 , 49, 1655-63	6.1	73
3 ⁰²	Gene Sets Net Correlations Analysis (GSNCA): a multivariate differential coexpression test for gene sets. <i>Bioinformatics</i> , 2014 , 30, 360-8	7.2	72
3 ⁰¹	The chronic fatigue syndrome: a comparative pathway analysis. <i>Journal of Computational Biology</i> , 2007 , 14, 961-72	1.7	68
3 ⁰⁰	Structural influence of gene networks on their inference: analysis of C3NET. <i>Biology Direct</i> , 2011 , 6, 31	7.2	45
299	Interrelations of graph distance measures based on topological indices. <i>PLoS ONE</i> , 2014 , 9, e94985	3.7	44

298	The gene regulatory network for breast cancer: integrated regulatory landscape of cancer hallmarks. <i>Frontiers in Genetics</i> , 2014 , 5, 15	4.5	42
297	Entropy bounds for dendrimers. <i>Applied Mathematics and Computation</i> , 2014 , 242, 462-472	2.7	42
296	Network biology: a direct approach to study biological function. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2011 , 3, 379-91	6.6	42
295	Gene set analysis approaches for RNA-seq data: performance evaluation and application guideline. <i>Briefings in Bioinformatics</i> , 2016 , 17, 393-407	13.4	37
294	A similarity measure for graphs with low computational complexity. <i>Applied Mathematics and Computation</i> , 2006 , 182, 447-459	2.7	34
293	Entropy bounds for hierarchical molecular networks. <i>PLoS ONE</i> , 2008 , 3, e3079	3.7	33
292	NetBioV: an R package for visualizing large network data in biology and medicine. <i>Bioinformatics</i> , 2014 , 30, 2834-6	7.2	32
291	Gene Coexpression Networks for the Analysis of DNA Microarray Data 2011 , 215-250		31
290	Graph Energy		31
289	Comprehensive molecular pathology analysis of small bowel adenocarcinoma reveals novel targets with potential for clinical utility. <i>Oncotarget</i> , 2015 , 6, 20863-74	3.3	31
288	Structural information content of networks: graph entropy based on local vertex functionals. <i>Computational Biology and Chemistry</i> , 2008 , 32, 131-8	3.6	30
287	2-(2-(2,4-dioxopentan-3-ylidene)hydrazineyl)benzonitrile as novel inhibitor of receptor tyrosine kinase and PI3K/AKT/mTOR signaling pathway in glioblastoma. <i>European Journal of Medicinal Chemistry</i> , 2019 , 166, 291-303	6.8	29
286	Functional and genetic analysis of the colon cancer network. <i>BMC Bioinformatics</i> , 2014 , 15 Suppl 6, S6	3.6	28
285	Inference and validation of predictive gene networks from biomedical literature and gene expression data. <i>Genomics</i> , 2014 , 103, 329-36	4.3	28
284	High-Dimensional LASSO-Based Computational Regression Models: Regularization, Shrinkage, and Selection. <i>Machine Learning and Knowledge Extraction</i> , 2019 , 1, 359-383	3.1	26
283	A computational approach to construct a multivariate complete graph invariant. <i>Information Sciences</i> , 2014 , 260, 200-208	7.7	26
282	Named Entity Recognition and Relation Detection for Biomedical Information Extraction. <i>Frontiers in Cell and Developmental Biology</i> , 2020 , 8, 673	5.7	26
281	Alkylaminophenol Induces G1/S Phase Cell Cycle Arrest in Glioblastoma Cells Through p53 and Cyclin-Dependent Kinase Signaling Pathway. <i>Frontiers in Pharmacology</i> , 2019 , 10, 330	5.6	25

280	Exploring statistical and population aspects of network complexity. <i>PLoS ONE</i> , 2012 , 7, e34523	3.7	25
279	Local network-based measures to assess the inferability of different regulatory networks. <i>IET Systems Biology</i> , 2010 , 4, 277-88	1.4	25
278	Information theoretic measures of UHG graphs with low computational complexity. <i>Applied Mathematics and Computation</i> , 2007 , 190, 1783-1794	2.7	25
277	Evaluation of Regression Models: Model Assessment, Model Selection and Generalization Error. <i>Machine Learning and Knowledge Extraction</i> , 2019 , 1, 521-551	3.1	24
276	Influence of the time scale on the construction of financial networks. <i>PLoS ONE</i> , 2010 , 5, e12884	3.7	24
275	Entropy of Weighted Graphs with Random Weights. <i>Entropy</i> , 2015 , 17, 3710-3723	2.8	23
274	Information processing in the transcriptional regulatory network of yeast: functional robustness. <i>BMC Systems Biology</i> , 2009 , 3, 35	3.5	23
273	GSAR: Bioconductor package for Gene Set analysis in R. <i>BMC Bioinformatics</i> , 2017 , 18, 61	3.6	22
272	Interfacing cellular networks of <i>S. cerevisiae</i> and <i>E. coli</i> : connecting dynamic and genetic information. <i>BMC Genomics</i> , 2013 , 14, 324	4.5	22
271	Quantitative Graph Theory: A new branch of graph theory and network science. <i>Information Sciences</i> , 2017 , 418-419, 575-580	7.7	22
270	Comparative evaluation of gene set analysis approaches for RNA-Seq data. <i>BMC Bioinformatics</i> , 2014 , 15, 397	3.6	22
269	The human disease network. <i>Systems Biomedicine (Austin, Tex.)</i> , 2013 , 1, 20-28		22
268	A BRCA1 deficient, NF κ B driven immune signal predicts good outcome in triple negative breast cancer. <i>Oncotarget</i> , 2016 , 7, 19884-96	3.3	22
267	Standardization of diagnostic biomarker concentrations in urine: the hematuria caveat. <i>PLoS ONE</i> , 2012 , 7, e53354	3.7	21
266	Ensuring the statistical soundness of competitive gene set approaches: gene filtering and genome-scale coverage are essential. <i>Nucleic Acids Research</i> , 2013 , 41, e82	20.1	21
265	Connections between classical and parametric network entropies. <i>PLoS ONE</i> , 2011 , 6, e15733	3.7	21
264	Graph distance measures based on topological indices revisited. <i>Applied Mathematics and Computation</i> , 2015 , 266, 623-633	2.7	20
263	Explainable artificial intelligence and machine learning: A reality rooted perspective. <i>Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery</i> , 2020 , 10, e1368	6.9	20

262	Identifying critical financial networks of the DJIA: Toward a network-based index. <i>Complexity</i> , 2010 , 16, 24-33	1.6	20
261	Influence of statistical estimators of mutual information and data heterogeneity on the inference of gene regulatory networks. <i>PLoS ONE</i> , 2011 , 6, e29279	3.7	20
260	Probabilistic inequalities for evaluating structural network measures. <i>Information Sciences</i> , 2014 , 288, 220-245	7.7	19
259	Harnessing the complexity of gene expression data from cancer: from single gene to structural pathway methods. <i>Biology Direct</i> , 2012 , 7, 44	7.2	19
258	Comparison of module detection algorithms in protein networks and investigation of the biological meaning of predicted modules. <i>BMC Bioinformatics</i> , 2016 , 17, 129	3.6	19
257	A Machine Learning Perspective on Personalized Medicine: An Automized, Comprehensive Knowledge Base with Ontology for Pattern Recognition. <i>Machine Learning and Knowledge Extraction</i> , 2018 , 1, 149-156	3.1	19
256	Multilayer Aggregation with Statistical Validation: Application to Investor Networks. <i>Scientific Reports</i> , 2018 , 8, 8198	4.9	19
255	Introduction to Survival Analysis in Practice. <i>Machine Learning and Knowledge Extraction</i> , 2019 , 1, 1013-1038	10.38	18
254	An efficient heuristic approach to detecting graph isomorphism based on combinations of highly discriminating invariants. <i>Advances in Computational Mathematics</i> , 2013 , 39, 311-325	1.6	18
253	Structural differentiation of graphs using Hosoya-based indices. <i>PLoS ONE</i> , 2014 , 9, e102459	3.7	18
252	Organizational structure and the periphery of the gene regulatory network in B-cell lymphoma. <i>BMC Systems Biology</i> , 2012 , 6, 38	3.5	18
251	A topological algorithm for identification of structural domains of proteins. <i>BMC Bioinformatics</i> , 2007 , 8, 237	3.6	18
250	Understanding Statistical Hypothesis Testing: The Logic of Statistical Inference. <i>Machine Learning and Knowledge Extraction</i> , 2019 , 1, 945-961	3.1	17
249	Defining Data Science by a Data-Driven Quantification of the Community. <i>Machine Learning and Knowledge Extraction</i> , 2018 , 1, 235-251	3.1	17
248	B-cell lymphoma gene regulatory networks: biological consistency among inference methods. <i>Frontiers in Genetics</i> , 2013 , 4, 281	4.5	16
247	Structural measures for network biology using QuACN. <i>BMC Bioinformatics</i> , 2011 , 12, 492	3.6	16
246	Comparing large graphs efficiently by margins of feature vectors. <i>Applied Mathematics and Computation</i> , 2007 , 188, 1699-1710	2.7	16
245	Assessment method for a power analysis to identify differentially expressed pathways. <i>PLoS ONE</i> , 2012 , 7, e37510	3.7	16

244	The Process of Analyzing Data is the Emergent Feature of Data Science. <i>Frontiers in Genetics</i> , 2016 , 7, 12	4.5	16
243	Personalized medicine: Has it started yet? A reconstruction of the early history. <i>Frontiers in Genetics</i> , 2012 , 3, 313	4.5	15
242	Quantitative network measures as biomarkers for classifying prostate cancer disease states: a systems approach to diagnostic biomarkers. <i>PLoS ONE</i> , 2013 , 8, e77602	3.7	15
241	Information fusion as an integrative cross-cutting enabler to achieve robust, explainable, and trustworthy medical artificial intelligence. <i>Information Fusion</i> , 2022 , 79, 263-278	16.7	15
240	Hosoya entropy of fullerene graphs. <i>Applied Mathematics and Computation</i> , 2019 , 352, 88-98	2.7	14
239	Gene set analysis for self-contained tests: complex null and specific alternative hypotheses. <i>Bioinformatics</i> , 2012 , 28, 3073-80	7.2	14
238	Highly unique network descriptors based on the roots of the permanent polynomial. <i>Information Sciences</i> , 2017 , 408, 176-181	7.7	13
237	Comparing deep belief networks with support vector machines for classifying gene expression data from complex disorders. <i>FEBS Open Bio</i> , 2019 , 9, 1232-1248	2.7	13
236	Combining deep learning with token selection for patient phenotyping from electronic health records. <i>Scientific Reports</i> , 2020 , 10, 1432	4.9	13
235	On Properties of Distance-Based Entropies on Fullerene Graphs. <i>Entropy</i> , 2019 , 21,	2.8	12
234	The Hosoya Entropy of Graphs Revisited. <i>Symmetry</i> , 2019 , 11, 1013	2.7	12
233	Statistic complexity: combining kolmogorov complexity with an ensemble approach. <i>PLoS ONE</i> , 2010 , 5, e12256	3.7	12
232	A comprehensive survey of error measures for evaluating binary decision making in data science. <i>Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery</i> , 2019 , 9, e1303	6.9	12
231	Untangling statistical and biological models to understand network inference: the need for a genomics network ontology. <i>Frontiers in Genetics</i> , 2014 , 5, 299	4.5	11
230	Algorithmic computation of knot polynomials of secondary structure elements of proteins. <i>Journal of Computational Biology</i> , 2006 , 13, 1503-12	1.7	11
229	MetriIntMeas a novel metric for measuring the intelligence of a swarm of cooperating agents. <i>Cognitive Systems Research</i> , 2017 , 45, 17-29	4.8	10
228	Glioblastoma Multiforme Stem Cell Cycle Arrest by Alkylaminophenol Through the Modulation of EGFR and CSC Signaling Pathways. <i>Cells</i> , 2020 , 9,	7.9	10
227	ROBUSTNESS IN SCALE-FREE NETWORKS: COMPARING DIRECTED AND UNDIRECTED NETWORKS. <i>International Journal of Modern Physics C</i> , 2008 , 19, 717-726	1.1	10

226	Topological mappings between graphs, trees and generalized trees. <i>Applied Mathematics and Computation</i> , 2007 , 186, 1326-1333	2.7	10
225	A novel epidemic model considering demographics and intercity commuting on complex dynamical networks. <i>Applied Mathematics and Computation</i> , 2020 , 386, 125517	2.7	9
224	Comparing biological information contained in mRNA and non-coding RNAs for classification of lung cancer patients. <i>BMC Cancer</i> , 2019 , 19, 1176	4.8	9
223	Properties of Entropy-Based Topological Measures of Fullerenes. <i>Mathematics</i> , 2020 , 8, 740	2.3	8
222	Quantitative assessment and validation of network inference methods in bioinformatics. <i>Frontiers in Genetics</i> , 2014 , 5, 221	4.5	8
221	Exploratory analysis of spatiotemporal patterns of cellular automata by clustering compressibility. <i>Physical Review E</i> , 2010 , 81, 026103	2.4	8
220	Influence of the experimental design of gene expression studies on the inference of gene regulatory networks: environmental factors. <i>PeerJ</i> , 2013 , 1, e10	3.1	8
219	Graph-based exploitation of gene ontology using GOxploreR for scrutinizing biological significance. <i>Scientific Reports</i> , 2020 , 10, 16672	4.9	8
218	Against Dataism and for Data Sharing of Big Biomedical and Clinical Data with Research Parasites. <i>Frontiers in Genetics</i> , 2016 , 7, 154	4.5	8
217	Data Analytics Applications for Streaming Data From Social Media: What to Predict?. <i>Frontiers in Big Data</i> , 2018 , 1, 2	2.8	8
216	Urothelial cancer gene regulatory networks inferred from large-scale RNAseq, Bead and Oligo gene expression data. <i>BMC Systems Biology</i> , 2015 , 9, 21	3.5	7
215	The Orbit-Polynomial: A Novel Measure of Symmetry in Networks. <i>IEEE Access</i> , 2020 , 8, 36100-36112	3.5	7
214	L1000 Viewer: A Search Engine and Web Interface for the LINCS Data Repository. <i>Frontiers in Genetics</i> , 2019 , 10, 557	4.5	7
213	Entropy, Orbits, and Spectra of Graphs1-22		7
212	Generalized Shortest Path Trees: A Novel Graph Class by Example of Semiotic Networks175-220		7
211	The Structural Information Content of Chemical Networks. <i>Zeitschrift Fur Naturforschung - Section A Journal of Physical Sciences</i> , 2008 , 63, 155-158	1.4	7
210	Structural similarity of directed universal hierarchical graphs: A low computational complexity approach. <i>Applied Mathematics and Computation</i> , 2007 , 194, 7-20	2.7	7
209	A HETEROSYNAPTIC LEARNING RULE FOR NEURAL NETWORKS. <i>International Journal of Modern Physics C</i> , 2006 , 17, 1501-1520	1.1	7

208	Large-scale evaluation of molecular descriptors by means of clustering. <i>PLoS ONE</i> , 2013 , 8, e83956	3.7	7
207	Computational analysis of structural properties of economic and financial networks. <i>Journal of Network Theory in Finance</i> , 2018 , 1-32	1.5	7
206	samExploreR: exploring reproducibility and robustness of RNA-seq results based on SAM files. <i>Bioinformatics</i> , 2016 , 32, 3345-3347	7.2	7
205	Computational cancer biology: education is a natural key to many locks. <i>BMC Cancer</i> , 2015 , 15, 7	4.8	6
204	Measuring the complexity of directed graphs: A polynomial-based approach. <i>PLoS ONE</i> , 2019 , 14, e0223745	3.45	6
203	Collectives of diagnostic biomarkers identify high-risk subpopulations of hematuria patients: exploiting heterogeneity in large-scale biomarker data. <i>BMC Medicine</i> , 2013 , 11, 12	11.4	6
202	Influence of the neural network topology on the learning dynamics. <i>Neurocomputing</i> , 2006 , 69, 1179-1184	3.4	6
201	Extracting the dynamics of perceptual switching from 'noisy' behaviour: an application of hidden Markov modelling to pecking data from pigeons. <i>Journal of Physiology (Paris)</i> , 2000 , 94, 555-67		6
200	Artificial Intelligence: A Clarification of Misconceptions, Myths and Desired Status. <i>Frontiers in Artificial Intelligence</i> , 2020 , 3, 524339	3	6
199	Large-Scale Simultaneous Inference with Hypothesis Testing: Multiple Testing Procedures in Practice. <i>Machine Learning and Knowledge Extraction</i> , 2019 , 1, 653-683	3.1	5
198	MetrIntSimilAn Accurate and Robust Metric for Comparison of Similarity in Intelligence of Any Number of Cooperative Multiagent Systems. <i>Symmetry</i> , 2018 , 10, 48	2.7	5
197	Lessons from the Human Genome Project: Modesty, Honesty, and Realism. <i>Frontiers in Genetics</i> , 2017 , 8, 184	4.5	5
196	Relevance of different prior knowledge sources for inferring gene interaction networks. <i>Frontiers in Genetics</i> , 2014 , 5, 177	4.5	5
195	Limitations of gene duplication models: evolution of modules in protein interaction networks. <i>PLoS ONE</i> , 2012 , 7, e35531	3.7	5
194	Network nursing: connections between nursing and complex network science. <i>International Journal of Nursing Knowledge</i> , 2013 , 24, 150-6	1.1	5
193	Parametric construction of episode networks from pseudoperiodic time series based on mutual information. <i>PLoS ONE</i> , 2011 , 6, e27733	3.7	5
192	Fault tolerance of information processing in gene networks. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2009 , 388, 541-548	3.3	5
191	Reverse Engineering Gene Regulatory Networks with Various Machine Learning Methods101-142		5

190	A comparative analysis of multidimensional features of objects resembling sets of graphs. <i>Applied Mathematics and Computation</i> , 2008 , 196, 221-235	2.7	5
189	What Is Quantitative Graph Theory?. <i>Discrete Mathematics and Its Applications</i> , 2014 , 1-33		5
188	Predicting cell cycle regulated genes by causal interactions. <i>PLoS ONE</i> , 2009 , 4, e6633	3.7	5
187	From the Digital Data Revolution toward a Digital Society: Pervasiveness of Artificial Intelligence. <i>Machine Learning and Knowledge Extraction</i> , 2021 , 3, 284-298	3.1	5
186	Prostate Cancer Gene Regulatory Network Inferred from RNA-Seq Data. <i>Current Genomics</i> , 2019 , 20, 38-48	2.6	5
185	Towards detecting structural branching and cyclicity in graphs: A polynomial-based approach. <i>Information Sciences</i> , 2019 , 471, 19-28	7.7	5
184	Prognostic gene expression signatures of breast cancer are lacking a sensible biological meaning. <i>Scientific Reports</i> , 2021 , 11, 156	4.9	5
183	Harnessing the biological complexity of Big Data from LINCS gene expression signatures. <i>PLoS ONE</i> , 2018 , 13, e0201937	3.7	5
182	Hermitian normalized Laplacian matrix for directed networks. <i>Information Sciences</i> , 2019 , 495, 175-184	7.7	4
181	Systems Pharmacogenomic Landscape of Drug Similarities from LINCS data: Drug Association Networks. <i>Scientific Reports</i> , 2019 , 9, 7849	4.9	4
180	Global Genetics Research in Prostate Cancer: A Text Mining and Computational Network Theory Approach. <i>Frontiers in Genetics</i> , 2019 , 10, 70	4.5	4
179	On the zeros of the partial Hosoya polynomial of graphs. <i>Information Sciences</i> , 2020 , 524, 199-215	7.7	4
178	sgnesR: An R package for simulating gene expression data from an underlying real gene network structure considering delay parameters. <i>BMC Bioinformatics</i> , 2017 , 18, 325	3.6	4
177	Graph measures with high discrimination power revisited: A random polynomial approach. <i>Information Sciences</i> , 2018 , 467, 407-414	7.7	4
176	Comparing Biological Networks: A Survey on Graph Classifying Techniques 2013 , 43-63		4
175	Enhancing systems medicine beyond genotype data by dynamic patient signatures: having information and using it too. <i>Frontiers in Genetics</i> , 2013 , 4, 241	4.5	4
174	Graph Edit Distance [Optimal and Suboptimal Algorithms with Applications]113-143		4
173	Introduction to DNA Microarrays1-26		4

172	NONLINEAR TIME SERIES PREDICTION BASED ON A POWER-LAW NOISE MODEL. <i>International Journal of Modern Physics C</i> , 2007 , 18, 1839-1852	1.1	4
171	On graph entropy measures based on the number of independent sets and matchings. <i>Information Sciences</i> , 2020 , 516, 491-504	7.7	4
170	Distributed Event-Triggered Circular Formation Control for Multiple Anonymous Mobile Robots With Order Preservation and Obstacle Avoidance. <i>IEEE Access</i> , 2020 , 8, 167288-167299	3.5	4
169	Data-Driven Computational Social Network Science: Predictive and Inferential Models for Web-Enabled Scientific Discoveries. <i>Frontiers in Big Data</i> , 2021 , 4, 591749	2.8	4
168	The Need for Formally Defining "Modern Medicine" by Means of Experimental Design. <i>Frontiers in Genetics</i> , 2016 , 7, 60	4.5	4
167	Utilizing Social Media Data for Psychoanalysis to Study Human Personality. <i>Frontiers in Psychology</i> , 2019 , 10, 2596	3.4	4
166	Robustness of differential gene expression analysis of RNA-seq. <i>Computational and Structural Biotechnology Journal</i> , 2021 , 19, 3470-3481	6.8	4
165	Understanding the World Economy in Terms of Networks: A Survey of Data-Based Network Science Approaches on Economic Networks. <i>Frontiers in Applied Mathematics and Statistics</i> , 2018 , 4,	2.2	4
164	Properties of graph distance measures by means of discrete inequalities. <i>Applied Mathematical Modelling</i> , 2018 , 59, 739-749	4.5	3
163	Graph entropy based on the number of spanning forests of c-cyclic graphs. <i>Applied Mathematics and Computation</i> , 2019 , 363, 124616	2.7	3
162	Toward Measuring Network Aesthetics Based on Symmetry. <i>Axioms</i> , 2017 , 6, 12	1.6	3
161	Effects of subsampling on characteristics of RNA-seq data from triple-negative breast cancer patients. <i>Chinese Journal of Cancer</i> , 2015 , 34, 427-38		3
160	Netmes: assessing gene network inference algorithms by network-based measures. <i>Evolutionary Bioinformatics</i> , 2014 , 10, 1-9	1.9	3
159	Structural properties and complexity of a new network class: Collatz step graphs. <i>PLoS ONE</i> , 2013 , 8, e56461	3.7	3
158	Representing Cancer Cell Trajectories in a Phase-Space Diagram: Switching Cellular States by Biological Phase Transitions 2011 , 377-403		3
157	Hierarchical coordination of periodic genes in the cell cycle of <i>Saccharomyces cerevisiae</i> . <i>BMC Systems Biology</i> , 2009 , 3, 76	3.5	3
156	A constrained HMM-based approach to the estimation of perceptual switching dynamics in pigeons. <i>Neurocomputing</i> , 2001 , 38-40, 1495-1501	5.4	3
155	Frontiers in Data Science		3

154	A data-centric review of deep transfer learning with applications to text data. <i>Information Sciences</i> , 2021 , 585, 498-498	7.7	3
153	On the Degeneracy of the Orbit Polynomial and Related Graph Polynomials. <i>Symmetry</i> , 2020 , 12, 1643	2.7	3
152	Ensuring the Robustness and Reliability of Data-Driven Knowledge Discovery Models in Production and Manufacturing. <i>Frontiers in Artificial Intelligence</i> , 2021 , 4, 576892	3	3
151	Using the DiffCorr Package to Analyze and Visualize Differential Correlations in Biological Networks 2016 , 1-34		3
150	Constrained Covariance Matrices With a Biologically Realistic Structure: Comparison of Methods for Generating High-Dimensional Gaussian Graphical Models. <i>Frontiers in Applied Mathematics and Statistics</i> , 2019 , 5,	2.2	3
149	Impact of Variable RNA-Sequencing Depth on Gene Expression Signatures and Target Compound Robustness: Case Study Examining Brain Tumor (Glioma) Disease Progression. <i>JCO Precision Oncology</i> , 2018 , 2,	3.6	3
148	Comparison of Text Mining Models for Food and Dietary Constituent Named-Entity Recognition. <i>Machine Learning and Knowledge Extraction</i> , 2022 , 4, 254-275	3.1	3
147	A Note on Distance-Based Entropy of Dendrimers. <i>Axioms</i> , 2019 , 8, 98	1.6	2
146	In-flight Wind Field Identification and Prediction of Parafoil Systems. <i>Applied Sciences (Switzerland)</i> , 2020 , 10, 1958	2.6	2
145	Graph Entropy: Recent Results and Perspectives 2016 , 133-182		2
144	Application of Graph Entropy for Knowledge Discovery and Data Mining in Bibliometric Data 2016 , 259-273		2
143	The Maximum Hosoya Index of Unicyclic Graphs with Diameter at Most Four. <i>Symmetry</i> , 2019 , 11, 1034	2.7	2
142	Metros as Biological Systems: Complexity in Small Real-life Networks 2013 , 259-285		2
141	The Linear Complexity of a Graph 2013 , 155-175		2
140	Selection-Based Estimates of Complexity Unravel Some Mechanisms and Selective Pressures Underlying the Evolution of Complexity in Artificial Networks 2013 , 41-61		2
139	Discrimination Power of Polynomial-Based Descriptors for Graphs by Using Functional Matrices. <i>PLoS ONE</i> , 2015 , 10, e0139265	3.7	2
138	Universal construction mechanism for networks from one-dimensional symbol sequences. <i>Applied Mathematics and Computation</i> , 2012 , 219, 1020-1030	2.7	2
137	Evolutionary dynamics of the spatial Prisoner's Dilemma with self-inhibition. <i>Applied Mathematics and Computation</i> , 2012 , 218, 6482-6488	2.7	2

136	What if the Fit is Unfit? Criteria for Biological Systems Estimation beyond Residual Errors 2011 , 181-200		2
135	Gene Regulatory Networks Inference: Combining a Genetic Programming and HIFiltering Approach 2011 , 133-153		2
134	Transcriptional Network Inference Based on Information Theory 2011 , 67-89		2
133	Pathways and Networks as Functional Descriptors for Human Disease and Drug Response Endpoints 2011 , 415-442		2
132	Correlation Network Analysis and Knowledge Integration 2011 , 251-280		2
131	Statistical Mechanics of Complex Networks 23-45		2
130	Complexity of Phylogenetic Networks: Counting Cubes in Median Graphs and Related Problems 323-350		2
129	Analyzing and Modeling European R&D Collaborations: Challenges and Opportunities from a Large Social Network 401-423		2
128	Comparative Analysis of Clustering Methods for Microarray Data 27-50		2
127	Network-Based Methods for Computational Diagnostics by Means of R 2012 , 185-197		2
126	The Role of Symmetry in the Aesthetics of Residential Building Façades Using Cognitive Science Methods. <i>Symmetry</i> , 2020 , 12, 1438	2.7	2
125	Threshold Degradation in R Using iDEMO 2016 , 83-124		2
124	A Note on Graphs with Prescribed Orbit Structure. <i>Entropy</i> , 2019 , 21, 1118	2.8	2
123	Ensuring Quality Standards and Reproducible Research for Data Analysis Services in Oncology: A Cooperative Service Model. <i>Frontiers in Cell and Developmental Biology</i> , 2019 , 7, 349	5.7	2
122	Inference of Genome-Scale Gene Regulatory Networks: Are There Differences in Biological and Clinical Validations?. <i>Machine Learning and Knowledge Extraction</i> , 2018 , 1, 138-148	3.1	2
121	A Brief Introduction to Complex Networks and Their Analysis 2011 , 1-26		2
120	Proteome-transcriptome alignment of molecular portraits achieved by self-contained gene set analysis: Consensus colon cancer subtypes case study. <i>PLoS ONE</i> , 2019 , 14, e0221444	3.7	1
119	Relations and bounds for the zeros of graph polynomials using vertex orbits. <i>Applied Mathematics and Computation</i> , 2020 , 380, 125239	2.7	1

118	The watching system as a generalization of identifying code. <i>Applied Mathematics and Computation</i> , 2020 , 380, 125302	2.7	1
117	Graph Entropies in Texture Segmentation of Images 2016 , 203-231		1
116	On efficient network similarity measures. <i>Applied Mathematics and Computation</i> , 2019 , 362, 124521	2.7	1
115	Three Types of Network Complexity Pyramid 2013 , 63-98		1
114	[COMMODE] a large-scale database of molecular descriptors using compounds from PubChem. <i>Source Code for Biology and Medicine</i> , 2013 , 8, 22	1.9	1
113	Computational Complexity of Graphs 2013 , 99-153		1
112	Circumscribed Complexity in Ecological Networks 2013 , 249-258		1
111	Extracting the Strongest Signals from Omics Data: Differentially Expressed Pathways and Beyond. <i>Methods in Molecular Biology</i> , 2017 , 1613, 125-159	1.4	1
110	Colorectal Cancer and Its Molecular Subsystems: Construction, Interpretation, and Validation 2013 , 107-132		1
109	Network Analysis to Interpret Complex Phenotypes 2011 , 1-12		1
108	Elucidation of General and Condition-Dependent Gene Pathways Using Mixture Models and Bayesian Networks 2011 , 91-103		1
107	Multiple Testing Methods 2010 , 45-72		1
106	Kernel Classification Methods for Cancer Microarray Data 2010 , 279-303		1
105	Cancer Stem Cells [Finding and Capping the Roots of Cancer 2010 , 25-43		1
104	Community Detection in Biological Networks 2011 , 299-327		1
103	A Simple Integrated Approach to Network Complexity and Node Centrality47-53		1
102	Statistical Methods for Inference of Genetic Networks and Regulatory Modules143-167		1
101	A Model of Genetic Networks with Delayed Stochastic Dynamics169-204		1

100	Probabilistic Boolean Networks as Models for Gene Regulation	205-242		1
99	STOCHASTIC SZNAJD MODEL IN OPEN COMMUNITY. <i>International Journal of Modern Physics C</i> , 2005 , 16, 1693-1699		1.1	1
98	Towards Network Complexity. <i>Lecture Notes of the Institute for Computer Sciences, Social-Informatics and Telecommunications Engineering</i> , 2009 , 707-714		0.2	1
97	Partition and Colored Distances in Graphs Induced to Subsets of Vertices and Some of Its Applications. <i>Symmetry</i> , 2020 , 12, 2027		2.7	1
96	Visualization of Biological Networks Using NetBioV	2016 , 307-333		1
95	ℓ_1 -Penalized Methods in High-Dimensional Gaussian Markov Random Fields	2016 , 201-265		1
94	Properties of Commuting Graphs over Semidihedral Groups. <i>Symmetry</i> , 2021 , 13, 103		2.7	1
93	Influence of Statistical Estimators on the Large-Scale Causal Inference of Regulatory Networks	131-152		1
92	Spectral Theory of Networks: From Biomolecular to Ecological Systems	55-83		0
91	Computational Reconstruction of Transcriptional Regulatory Modules of the Yeast Cell Cycle	331-354		0
90	Analysis of the real number of infected people by COVID-19: A system dynamics approach. <i>PLoS ONE</i> , 2021 , 16, e0245728		3.7	0
89	Limitations of Explainability for Established Prognostic Biomarkers of Prostate Cancer. <i>Frontiers in Genetics</i> , 2021 , 12, 649429		4.5	0
88	Inference and Analysis of Gene Regulatory Networks in R	2016 , 289-306		0
87	On the degeneracy of the Randi entropy and related graph measures. <i>Information Sciences</i> , 2019 , 501, 680-687		7.7	0
86	On the relationship between PageRank and automorphisms of a graph. <i>Information Sciences</i> , 2021 , 579, 401-417		7.7	0
85	Relationships between symmetry-based graph measures. <i>Information Sciences</i> , 2021 , 581, 291-303		7.7	0
84	Identifying key interactions between process variables of different material categories using mutual information-based network inference method. <i>Procedia Computer Science</i> , 2022 , 200, 1550-1564		1.6	0
83	Taxonomy of machine learning paradigms: A data-centric perspective. <i>Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery</i> ,		6.9	0

- 82 A Graph Theoretic Approach to Construct Desired Cryptographic Boolean Functions. *Axioms*, **2019**, 8, 40 1.6
- 81 Using shRNA experiments to validate gene regulatory networks. *Genomics Data*, **2015**, 4, 123-6
- 80 Comments to Quantification of network structural dissimilarities published by Schieber et al. *Mathematical Methods in the Applied Sciences*, **2018**, 41, 5711-5713 2.3
- 79 Report from the 2nd Summer School in Computational Biology organized by the Queen's University of Belfast. *Genomics Data*, **2014**, 2, 37-9
- 78 Information-Based Complexity of Networks **2013**, 209-227
- 77 Thermodynamic Depth in Undirected and Directed Networks **2013**, 229-247
- 76 Functional Complexity Based on Topology **2013**, 1-15
- 75 Kirchhoff's Matrix-Tree Theorem Revisited: Counting Spanning Trees with the Quantum Relative Entropy **2013**, 177-190
- 74 Dimension Measure for Complex Networks **2013**, 191-208
- 73 Connections Between Artificial Intelligence and Computational Complexity and the Complexity of Graphs **2013**, 17-40
- 72 Biological networks: the microscope of the twenty-first century?. *Frontiers in Genetics*, **2015**, 6, 307 4.5
- 71 Structural Analysis of Treatment Cycles Representing Transitions between Nursing Organizational Units Inferred from Diabetes. *PLoS ONE*, **2015**, 10, e0127152 3.7
- 70 Learning Systems Biology: Conceptual Considerations toward a Web-Based Learning Platform. *Education Sciences*, **2013**, 3, 158-171 2.2
- 69 Enhancing our understanding of ways to analyze metagenomes. *Frontiers in Genetics*, **2014**, 5, 108 4.5
- 68 Detecting sequence dependent transcriptional pauses from RNA and protein number time series. *BMC Bioinformatics*, **2012**, 13, 152 3.6
- 67 Discriminant and Network Analysis to Study Origin of Cancer **2013**, 193-214
- 66 Intervention and Control of Gene Regulatory Networks: Theoretical Framework and Application to Human Melanoma Gene Regulation **2013**, 215-238
- 65 Semisupervised Methods for Analyzing High-dimensional Genomic Data **2013**, 93-106

- 64 Identification of Recurrent DNA Copy Number Aberrations in Tumors **2013**, 239-260
- 63 The Cancer Cell, Its Entropy, and High-Dimensional Molecular Data **2013**, 261-285
- 62 Control of Type I Error Rates for Oncology Biomarker Discovery with High-Throughput Platforms **2013**, 1-26
- 61 Overview of Public Cancer Databases, Resources, and Visualization Tools **2013**, 27-40
- 60 Discovery of Expression Signatures in Chronic Myeloid Leukemia by Bayesian Model Averaging **2013**, 41-55
- 59 Bayesian Ranking and Selection Methods in Microarray Studies **2013**, 57-74
- 58 Multiclass Classification via Bayesian Variable Selection with Gene Expression Data **2013**, 75-92
- 57 Network Medicine: Disease Genes in Molecular Networks **2013**, 133-151
- 56 Inference of Gene Regulatory Networks in Breast and Ovarian Cancer by Integrating Different Genomic Data **2013**, 153-171
- 55 Network-Module-Based Approaches in Cancer Data Analysis **2013**, 173-192
- 54 Network Screening: A New Method to Identify Active Networks from an Ensemble of Known Networks **2011**, 281-298
- 53 Protein Network Analysis for Disease Gene Identification and Prioritization **2011**, 405-413
- 52 Modeling Expression Quantitative Trait Loci in Multiple Populations **2011**, 39-65
- 51 Multiscale Network Reconstruction from Gene Expression Measurements: Correlations, Perturbations, and A Priori Biological Knowledge **2011**, 105-131
- 50 Computational Reconstruction of Protein Interaction Networks **2011**, 155-180
- 49 On Some Inverse Problems in Generating Probabilistic Boolean Networks **2011**, 329-348
- 48 Boolean Analysis of Gene Expression Datasets **2011**, 349-375
- 47 Making Mountains out of Molehills: Moving from Single Gene to Pathway Based Models of Colon Cancer Progression **2010**, 73-87

- 46 Multivariate Analysis of Microarray Data Using Hotelling's T2 Test **2010**, 113-130
- 45 Gene-Set Expression Analysis: Challenges and Tools **2010**, 89-112
- 44 Interpreting Differential Coexpression of Gene Sets **2010**, 131-150
- 43 Multivariate Analysis of Microarray Data: Application of MANOVA **2010**, 151-166
- 42 Testing Significance of a Class of Genes **2010**, 167-184
- 41 Differential Dependency Network Analysis to Identify Topological Changes in Biological Networks **2010**, 185-203
- 40 Predicting Cancer Survival Using Expression Patterns **2010**, 305-323
- 39 An Introduction to Time-Varying Connectivity Estimation for Gene Regulatory Networks **2010**, 205-230
- 38 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
- 37 A New Gene Expression Meta-Analysis Technique and its Application to Co-Analyze Three Independent Lung Cancer Datasets **2010**, 253-277
- 36 Model Averaging for Biological Networks with Prior Information **2010**, 347-372
- 35 Integration of Microarray Datasets **2010**, 325-345
- 34 Mining Graph Patterns in Web-based Systems: A Conceptual View. *Text, Speech and Language Technology*, **2010**, 237-253
- 33 Stochastic Modeling of Gene Regulatory Networks **2011**, 13-37
- 32 Machine Learning Methods for Identifying Essential Genes and Proteins in Networks **2011**, 201-214
- 31 A Bayesian analysis of the chromosome architecture of human disorders by integrating reductionist data. *Scientific Reports*, **2012**, 2, 513 4.9
- 30 On the Structure of Neutral Networks of RNA Pseudoknot Structures 85-112
- 29 Applications of Graph Theory in Chemo- and Bioinformatics 221-243

- 28 Structural and Functional Dynamics in Cortical and Neuronal Networks 245-269
- 27 Network Mapping of Metabolic Pathways 271-293
- 26 Graph Structure Analysis and Computational Tractability of Scheduling Problems 295-322
- 25 Elementary Elliptic (R, q) -Polycycles 351-376
- 24 Optimal Dynamic Flows in Networks and Algorithms for Finding Them 377-400
- 23 Analytic Combinatorics on Random Graphs 425-450
- 22 The Biology of MYC in Health and Disease: A High Altitude View **2010**, 1-24
- 21 Structural Equation for Identification of Genetic Networks 243-283
- 20 Detecting Pathological Pathways of a Complex Disease by a Comparative Analysis of Networks 285-305
- 19 Finding Verified Edges in Genetic/Gene Networks: Bilayer Verification for Network Recovery in the Presence of Hidden Confounders 51-81
- 18 Pathway-Based Methods for Analyzing Microarray Data 355-384
- 17 Predicting Functional Modules Using Microarray and Protein Interaction Data 307-329
- 16 Computational Inference of Biological Causal Networks I Analysis of Therapeutic Compound Effects 83-99
- 15 Optimization Procedure for Predicting Nonlinear Time Series Based on a Non-Gaussian Noise Model **2007**, 540-549
- 14 A Neurobiologically Motivated Model for Self-organized Learning. *Lecture Notes in Computer Science*, **2005**, 415-424 0.9
- 13 A Novel Stochastic Learning Rule for Neural Networks. *Lecture Notes in Computer Science*, **2006**, 414-423 0.9
- 12 Mathematical Modeling in Systems Biology. *Communications in Computer and Information Science*, **2017**, 161-166 0.3
- 11 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

- 10 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
- 9 Large-Scale Statistical Inference of Gene Regulatory Networks: Local Network-Based Measures. *Intelligent Systems Reference Library*, **2011**, 179-193 0.8
- 8 Orbit Entropy and Symmetry Index Revisited. *Mathematics*, **2021**, 9, 1086 2.3
- 7 Bayesian Computational Algorithms for Social Network Analysis **2016**, 63-82
- 6 Optimization of Stratified Sampling with the R Package SamplingStrata: Applications to Network Data **2016**, 125-150
- 5 Exploring the Role of Small Molecules in Biological Systems Using Network Approaches **2016**, 151-172
- 4 Performing Network Alignments with R **2016**, 173-200
- 3 Cluster Analysis of Social Networks Using R **2016**, 267-288
- 2 Analytical Models and Methods for Anomaly Detection in Dynamic, Attributed Graphs **2016**, 35-61
- 1 The Most Probable Genetic Interaction Networks Inferred from Gene Expression Patterns 385-412