

Frank Emmert-Streib

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7537684/publications.pdf>

Version: 2024-02-01

247
papers

5,420
citations

109321

35
h-index

128289

60
g-index

373
all docs

373
docs citations

373
times ranked

5357
citing authors

#	ARTICLE	IF	CITATIONS
1	An Introductory Review of Deep Learning for Prediction Models With Big Data. <i>Frontiers in Artificial Intelligence</i> , 2020, 3, 4.	3.4	316
2	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.	3.7	201
3	A review of connectivity map and computational approaches in pharmacogenomics. <i>Briefings in Bioinformatics</i> , 2018, 19, bbw112.	6.5	182
4	Inferring the conservative causal core of gene regulatory networks. <i>BMC Systems Biology</i> , 2010, 4, 132.	3.0	167
5	Fifty years of graph matching, network alignment and network comparison. <i>Information Sciences</i> , 2016, 346-347, 180-197.	6.9	158
6	Bagging Statistical Network Inference from Large-Scale Gene Expression Data. <i>PLoS ONE</i> , 2012, 7, e33624.	2.5	122
7	Statistical Inference and Reverse Engineering of Gene Regulatory Networks from Observational Expression Data. <i>Frontiers in Genetics</i> , 2012, 3, 8.	2.3	116
8	Harnessing naturally randomized transcription to infer regulatory relationships among genes. <i>Genome Biology</i> , 2007, 8, R219.	9.6	109
9	Networks for systems biology: conceptual connection of data and function. <i>IET Systems Biology</i> , 2011, 5, 185-207.	1.5	105
10	Pathway Analysis of Expression Data: Deciphering Functional Building Blocks of Complex Diseases. <i>PLoS Computational Biology</i> , 2011, 7, e1002053.	3.2	101
11	Gene Sets Net Correlations Analysis (GSNCA): a multivariate differential coexpression test for gene sets. <i>Bioinformatics</i> , 2014, 30, 360-368.	4.1	101
12	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.	19.1	100
13	Unite and conquer: univariate and multivariate approaches for finding differentially expressed gene sets. <i>Bioinformatics</i> , 2009, 25, 2348-2354.	4.1	98
14	Revealing differences in gene network inference algorithms on the network level by ensemble methods. <i>Bioinformatics</i> , 2010, 26, 1738-1744.	4.1	90
15	On Entropy-Based Molecular Descriptors: Statistical Analysis of Real and Synthetic Chemical Structures. <i>Journal of Chemical Information and Modeling</i> , 2009, 49, 1655-1663.	5.4	86
16	Named Entity Recognition and Relation Detection for Biomedical Information Extraction. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 673.	3.7	78
17	The Chronic Fatigue Syndrome: A Comparative Pathway Analysis. <i>Journal of Computational Biology</i> , 2007, 14, 961-972.	1.6	77
18	The gene regulatory network for breast cancer: integrated regulatory landscape of cancer hallmarks. <i>Frontiers in Genetics</i> , 2014, 5, 15.	2.3	74

#	ARTICLE	IF	CITATIONS
19	High-Dimensional LASSO-Based Computational Regression Models: Regularization, Shrinkage, and Selection. <i>Machine Learning and Knowledge Extraction</i> , 2019, 1, 359-383.	5.0	67
20	Evaluation of Regression Models: Model Assessment, Model Selection and Generalization Error. <i>Machine Learning and Knowledge Extraction</i> , 2019, 1, 521-551.	5.0	59
21	Gene set analysis approaches for RNA-seq data: performance evaluation and application guideline. <i>Briefings in Bioinformatics</i> , 2016, 17, 393-407.	6.5	57
22	Network biology: a direct approach to study biological function. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2011, 3, 379-391.	6.6	53
23	Introduction to Survival Analysis in Practice. <i>Machine Learning and Knowledge Extraction</i> , 2019, 1, 1013-1038.	5.0	53
24	Structural influence of gene networks on their inference: analysis of C3NET. <i>Biology Direct</i> , 2011, 6, 31.	4.6	51
25	2-(2-(2,4-dioxopentan-3-ylidene)hydrazineyl)benzotrile 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.	5.5	50
26	Interrelations of Graph Distance Measures Based on Topological Indices. <i>PLoS ONE</i> , 2014, 9, e94985.	2.5	49
27	Explainable artificial intelligence and machine learning: A reality rooted perspective. <i>Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery</i> , 2020, 10, e1368.	6.8	49
28	Entropy bounds for dendrimers. <i>Applied Mathematics and Computation</i> , 2014, 242, 462-472.	2.2	46
29	Quantitative Graph Theory: A new branch of graph theory and network science. <i>Information Sciences</i> , 2017, 418-419, 575-580.	6.9	46
30	NetBioV: an R package for visualizing large network data in biology and medicine. <i>Bioinformatics</i> , 2014, 30, 2834-2836.	4.1	44
31	A similarity measure for graphs with low computational complexity. <i>Applied Mathematics and Computation</i> , 2006, 182, 447-459.	2.2	42
32	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.	3.5	42
33	Comprehensive molecular pathology analysis of small bowel adenocarcinoma reveals novel targets with potential for clinical utility. <i>Oncotarget</i> , 2015, 6, 20863-20874.	1.8	41
34	Inference and validation of predictive gene networks from biomedical literature and gene expression data. <i>Genomics</i> , 2014, 103, 329-336.	2.9	40
35	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.	6.8	40
36	Robustness of differential gene expression analysis of RNA-seq. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 3470-3481.	4.1	39

#	ARTICLE	IF	CITATIONS
37	The human disease network. <i>Systems Biomedicine</i> (Austin, Tex), 2013, 1, 20-28.	0.7	38
38	Understanding Statistical Hypothesis Testing: The Logic of Statistical Inference. <i>Machine Learning and Knowledge Extraction</i> , 2019, 1, 945-961.	5.0	38
39	GSAR: Bioconductor package for Gene Set analysis in R. <i>BMC Bioinformatics</i> , 2017, 18, 61.	2.6	37
40	Combining deep learning with token selection for patient phenotyping from electronic health records. <i>Scientific Reports</i> , 2020, 10, 1432.	3.3	36
41	Structural information content of networks: Graph entropy based on local vertex functionals. <i>Computational Biology and Chemistry</i> , 2008, 32, 131-138.	2.3	35
42	A data-centric review of deep transfer learning with applications to text data. <i>Information Sciences</i> , 2022, 585, 498-528.	6.9	35
43	Entropy Bounds for Hierarchical Molecular Networks. <i>PLoS ONE</i> , 2008, 3, e3079.	2.5	34
44	Functional and genetic analysis of the colon cancer network. <i>BMC Bioinformatics</i> , 2014, 15, S6.	2.6	33
45	Multilayer Aggregation with Statistical Validation: Application to Investor Networks. <i>Scientific Reports</i> , 2018, 8, 8198.	3.3	33
46	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.	5.0	32
47	A BRCA1 deficient, NF κ B driven immune signal predicts good outcome in triple negative breast cancer. <i>Oncotarget</i> , 2016, 7, 19884-19896.	1.8	30
48	Exploring Statistical and Population Aspects of Network Complexity. <i>PLoS ONE</i> , 2012, 7, e34523.	2.5	29
49	A computational approach to construct a multivariate complete graph invariant. <i>Information Sciences</i> , 2014, 260, 200-208.	6.9	29
50	Information theoretic measures of UHG graphs with low computational complexity. <i>Applied Mathematics and Computation</i> , 2007, 190, 1783-1794.	2.2	28
51	Comparison of module detection algorithms in protein networks and investigation of the biological meaning of predicted modules. <i>BMC Bioinformatics</i> , 2016, 17, 129.	2.6	28
52	Local network-based measures to assess the inferability of different regulatory networks. <i>IET Systems Biology</i> , 2010, 4, 277-288.	1.5	27
53	Influence of the Time Scale on the Construction of Financial Networks. <i>PLoS ONE</i> , 2010, 5, e12884.	2.5	27
54	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.	2.8	27

#	ARTICLE	IF	CITATIONS
55	Entropy of Weighted Graphs with Random Weights. <i>Entropy</i> , 2015, 17, 3710-3723.	2.2	27
56	Artificial Intelligence: A Clarification of Misconceptions, Myths and Desired Status. <i>Frontiers in Artificial Intelligence</i> , 2020, 3, 524339.	3.4	27
57	Prognostic gene expression signatures of breast cancer are lacking a sensible biological meaning. <i>Scientific Reports</i> , 2021, 11, 156.	3.3	26
58	Influence of Statistical Estimators of Mutual Information and Data Heterogeneity on the Inference of Gene Regulatory Networks. <i>PLoS ONE</i> , 2011, 6, e29279.	2.5	26
59	Information processing in the transcriptional regulatory network of yeast: Functional robustness. <i>BMC Systems Biology</i> , 2009, 3, 35.	3.0	25
60	Identifying critical financial networks of the DJIA: Toward a network-based index. <i>Complexity</i> , 2010, 16, 24-33.	1.6	25
61	Comparative evaluation of gene set analysis approaches for RNA-Seq data. <i>BMC Bioinformatics</i> , 2014, 15, 397.	2.6	25
62	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.	2.3	25
63	A novel epidemic model considering demographics and intercity commuting on complex dynamical networks. <i>Applied Mathematics and Computation</i> , 2020, 386, 125517.	2.2	25
64	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-e82.	14.5	24
65	Connections between Classical and Parametric Network Entropies. <i>PLoS ONE</i> , 2011, 6, e15733.	2.5	23
66	Harnessing the complexity of gene expression data from cancer: from single gene to structural pathway methods. <i>Biology Direct</i> , 2012, 7, 44.	4.6	23
67	Probabilistic inequalities for evaluating structural network measures. <i>Information Sciences</i> , 2014, 288, 220-245.	6.9	23
68	Graph distance measures based on topological indices revisited. <i>Applied Mathematics and Computation</i> , 2015, 266, 623-633.	2.2	23
69	Defining Data Science by a Data-Driven Quantification of the Community. <i>Machine Learning and Knowledge Extraction</i> , 2018, 1, 235-251.	5.0	23
70	Glioblastoma Multiforme Stem Cell Cycle Arrest by Alkylaminophenol through the Modulation of EGFR and CSC Signaling Pathways. <i>Cells</i> , 2020, 9, 681.	4.1	23
71	Organizational structure and the periphery of the gene regulatory network in B-cell lymphoma. <i>BMC Systems Biology</i> , 2012, 6, 38.	3.0	22
72	Standardization of Diagnostic Biomarker Concentrations in Urine: The Hematuria Caveat. <i>PLoS ONE</i> , 2012, 7, e53354.	2.5	22

#	ARTICLE	IF	CITATIONS
73	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	22
74	B-cell lymphoma gene regulatory networks: biological consistency among inference methods. <i>Frontiers in Genetics</i> , 2013, 4, 281.	2.3	21
75	The Process of Analyzing Data is the Emergent Feature of Data Science. <i>Frontiers in Genetics</i> , 2016, 7, 12.	2.3	21
76	A topological algorithm for identification of structural domains of proteins. <i>BMC Bioinformatics</i> , 2007, 8, 237.	2.6	20
77	Structural Differentiation of Graphs Using Hosoya-Based Indices. <i>PLoS ONE</i> , 2014, 9, e102459.	2.5	19
78	Graph-based exploitation of gene ontology using GOxploreR for scrutinizing biological significance. <i>Scientific Reports</i> , 2020, 10, 16672.	3.3	19
79	Quantitative Network Measures as Biomarkers for Classifying Prostate Cancer Disease States: A Systems Approach to Diagnostic Biomarkers. <i>PLoS ONE</i> , 2013, 8, e77602.	2.5	18
80	Comparing large graphs efficiently by margins of feature vectors. <i>Applied Mathematics and Computation</i> , 2007, 188, 1699-1710.	2.2	17
81	Structural Measures for Network Biology Using QuACN. <i>BMC Bioinformatics</i> , 2011, 12, 492.	2.6	17
82	Gene set analysis for self-contained tests: complex null and specific alternative hypotheses. <i>Bioinformatics</i> , 2012, 28, 3073-3080.	4.1	17
83	Personalized medicine: Has it started yet? A reconstruction of the early history. <i>Frontiers in Genetics</i> , 2012, 3, 313.	2.3	17
84	Ensuring the Robustness and Reliability of Data-Driven Knowledge Discovery Models in Production and Manufacturing. <i>Frontiers in Artificial Intelligence</i> , 2021, 4, 576892.	3.4	17
85	Hosoya entropy of fullerene graphs. <i>Applied Mathematics and Computation</i> , 2019, 352, 88-98.	2.2	16
86	Assessment Method for a Power Analysis to Identify Differentially Expressed Pathways. <i>PLoS ONE</i> , 2012, 7, e37510.	2.5	16
87	Statistic Complexity: Combining Kolmogorov Complexity with an Ensemble Approach. <i>PLoS ONE</i> , 2010, 5, e12256.	2.5	15
88	Untangling statistical and biological models to understand network inference: the need for a genomics network ontology. <i>Frontiers in Genetics</i> , 2014, 5, 299.	2.3	15
89	Entropy, Orbits, and Spectra of Graphs. , 0, , 1-22.		14
90	Highly unique network descriptors based on the roots of the permanental polynomial. <i>Information Sciences</i> , 2017, 408, 176-181.	6.9	14

#	ARTICLE	IF	CITATIONS
91	The Hosoya Entropy of Graphs Revisited. <i>Symmetry</i> , 2019, 11, 1013.	2.2	14
92	Comparing biological information contained in mRNA and non-coding RNAs for classification of lung cancer patients. <i>BMC Cancer</i> , 2019, 19, 1176.	2.6	14
93	Algorithmic Computation of Knot Polynomials of Secondary Structure Elements of Proteins. <i>Journal of Computational Biology</i> , 2006, 13, 1503-1512.	1.6	13
94	ROBUSTNESS IN SCALE-FREE NETWORKS: COMPARING DIRECTED AND UNDIRECTED NETWORKS. <i>International Journal of Modern Physics C</i> , 2008, 19, 717-726.	1.7	13
95	On Properties of Distance-Based Entropies on Fullerene Graphs. <i>Entropy</i> , 2019, 21, 482.	2.2	13
96	Computational analysis of structural properties of economic and financial networks. <i>Journal of Network Theory in Finance</i> , 2018, , 1-32.	0.7	13
97	Topological mappings between graphs, trees and generalized trees. <i>Applied Mathematics and Computation</i> , 2007, 186, 1326-1333.	2.2	12
98	MetrlntMeas a novel metric for measuring the intelligence of a swarm of cooperating agents. <i>Cognitive Systems Research</i> , 2017, 45, 17-29.	2.7	12
99	L1000 Viewer: A Search Engine and Web Interface for the LINCS Data Repository. <i>Frontiers in Genetics</i> , 2019, 10, 557.	2.3	12
100	Prostate Cancer Gene Regulatory Network Inferred from RNA-Seq Data. <i>Current Genomics</i> , 2019, 20, 38-48.	1.6	12
101	The Orbit-Polynomial: A Novel Measure of Symmetry in Networks. <i>IEEE Access</i> , 2020, 8, 36100-36112.	4.2	12
102	From the Digital Data Revolution toward a Digital Society: Pervasiveness of Artificial Intelligence. <i>Machine Learning and Knowledge Extraction</i> , 2021, 3, 284-298.	5.0	12
103	Large-Scale Evaluation of Molecular Descriptors by Means of Clustering. <i>PLoS ONE</i> , 2013, 8, e83956.	2.5	12
104	Urothelial cancer gene regulatory networks inferred from large-scale RNAseq, Bead and Oligo gene expression data. <i>BMC Systems Biology</i> , 2015, 9, 21.	3.0	11
105	samExploreR: exploring reproducibility and robustness of RNA-seq results based on SAM files. <i>Bioinformatics</i> , 2016, 32, 3345-3347.	4.1	11
106	Comparison of Text Mining Models for Food and Dietary Constituent Named-Entity Recognition. <i>Machine Learning and Knowledge Extraction</i> , 2022, 4, 254-275.	5.0	11
107	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.	5.5	10
108	Data Analytics Applications for Streaming Data From Social Media: What to Predict?. <i>Frontiers in Big Data</i> , 2018, 1, 2.	2.9	10

#	ARTICLE	IF	CITATIONS
109	Systems Pharmacogenomic Landscape of Drug Similarities from LINCS data: Drug Association Networks. <i>Scientific Reports</i> , 2019, 9, 7849.	3.3	10
110	Utilizing Social Media Data for Psychoanalysis to Study Human Personality. <i>Frontiers in Psychology</i> , 2019, 10, 2596.	2.1	10
111	Properties of Entropy-Based Topological Measures of Fullerenes. <i>Mathematics</i> , 2020, 8, 740.	2.2	10
112	A HETEROSYNAPTIC LEARNING RULE FOR NEURAL NETWORKS. <i>International Journal of Modern Physics C</i> , 2006, 17, 1501-1520.	1.7	9
113	Computational cancer biology: education is a natural key to many locks. <i>BMC Cancer</i> , 2015, 15, 7.	2.6	9
114	Against Dataism and for Data Sharing of Big Biomedical and Clinical Data with Research Parasites. <i>Frontiers in Genetics</i> , 2016, 7, 154.	2.3	9
115	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.	2.6	9
116	Harnessing the biological complexity of Big Data from LINCS gene expression signatures. <i>PLoS ONE</i> , 2018, 13, e0201937.	2.5	9
117	On graph entropy measures based on the number of independent sets and matchings. <i>Information Sciences</i> , 2020, 516, 491-504.	6.9	9
118	The Role of Symmetry in the Aesthetics of Residential Building Façades Using Cognitive Science Methods. <i>Symmetry</i> , 2020, 12, 1438.	2.2	9
119	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.	4.2	9
120	Influence of the experimental design of gene expression studies on the inference of gene regulatory networks: environmental factors. <i>PeerJ</i> , 2013, 1, e10.	2.0	9
121	Taxonomy of machine learning paradigms: A data-centric perspective. <i>Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery</i> , 2022, 12, .	6.8	9
122	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, 555-567.	2.1	8
123	Influence of the neural network topology on the learning dynamics. <i>Neurocomputing</i> , 2006, 69, 1179-1182.	5.9	8
124	The Structural Information Content of Chemical Networks. <i>Zeitschrift Fur Naturforschung - Section A Journal of Physical Sciences</i> , 2008, 63, 155-158.	1.5	8
125	Exploratory analysis of spatiotemporal patterns of cellular automata by clustering compressibility. <i>Physical Review E</i> , 2010, 81, 026103.	2.1	8
126	Quantitative assessment and validation of network inference methods in bioinformatics. <i>Frontiers in Genetics</i> , 2014, 5, 221.	2.3	8

#	ARTICLE	IF	CITATIONS
127	Large-Scale Simultaneous Inference with Hypothesis Testing: Multiple Testing Procedures in Practice. Machine Learning and Knowledge Extraction, 2019, 1, 653-683.	5.0	8
128	The usefulness of topological indices. Information Sciences, 2022, 606, 143-151.	6.9	8
129	Structural similarity of directed universal hierarchical graphs: A low computational complexity approach. Applied Mathematics and Computation, 2007, 194, 7-20.	2.2	7
130	Fault tolerance of information processing in gene networks. Physica A: Statistical Mechanics and Its Applications, 2009, 388, 541-548.	2.6	7
131	Relevance of different prior knowledge sources for inferring gene interaction networks. Frontiers in Genetics, 2014, 5, 177.	2.3	7
132	Lessons from the Human Genome Project: Modesty, Honesty, and Realism. Frontiers in Genetics, 2017, 8, 184.	2.3	7
133	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, .	1.3	7
134	Graph entropy based on the number of spanning forests of c-cyclic graphs. Applied Mathematics and Computation, 2019, 363, 124616.	2.2	7
135	Measuring the complexity of directed graphs: A polynomial-based approach. PLoS ONE, 2019, 14, e0223745.	2.5	7
136	Towards detecting structural branching and cyclicity in graphs: A polynomial-based approach. Information Sciences, 2019, 471, 19-28.	6.9	7
137	What Is Quantitative Graph Theory?. Discrete Mathematics and Its Applications, 2014, , 1-33.	0.1	7
138	Predicting Cell Cycle Regulated Genes by Causal Interactions. PLoS ONE, 2009, 4, e6633.	2.5	7
139	Editorial: Artificial Intelligence for Precision Medicine. Frontiers in Artificial Intelligence, 2021, 4, 834645.	3.4	7
140	A comparative analysis of multidimensional features of objects resembling sets of graphs. Applied Mathematics and Computation, 2008, 196, 221-235.	2.2	6
141	Graph measures with high discrimination power revisited: A random polynomial approach. Information Sciences, 2018, 467, 407-414.	6.9	6
142	MetrIntSimilâ€”An Accurate and Robust Metric for Comparison of Similarity in Intelligence of Any Number of Cooperative Multiagent Systems. Symmetry, 2018, 10, 48.	2.2	6
143	Hermitian normalized Laplacian matrix for directed networks. Information Sciences, 2019, 495, 175-184.	6.9	6
144	Global Genetics Research in Prostate Cancer: A Text Mining and Computational Network Theory Approach. Frontiers in Genetics, 2019, 10, 70.	2.3	6

#	ARTICLE	IF	CITATIONS
145	On the zeros of the partial Hosoya polynomial of graphs. <i>Information Sciences</i> , 2020, 524, 199-215.	6.9	6
146	Data-Driven Computational Social Network Science: Predictive and Inferential Models for Web-Enabled Scientific Discoveries. <i>Frontiers in Big Data</i> , 2021, 4, 591749.	2.9	6
147	Parametric Construction of Episode Networks from Pseudoperiodic Time Series Based on Mutual Information. <i>PLoS ONE</i> , 2011, 6, e27733.	2.5	5
148	Limitations of Gene Duplication Models: Evolution of Modules in Protein Interaction Networks. <i>PLoS ONE</i> , 2012, 7, e35531.	2.5	5
149	Network Nursing: Connections Between Nursing and Complex Network Science. <i>International Journal of Nursing Knowledge</i> , 2013, 24, 150-156.	1.0	5
150	The Need for Formally Defining "Modern Medicine" by Means of Experimental Design. <i>Frontiers in Genetics</i> , 2016, 7, 60.	2.3	5
151	The Maximum Hosoya Index of Unicyclic Graphs with Diameter at Most Four. <i>Symmetry</i> , 2019, 11, 1034.	2.2	5
152	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, .	1.3	5
153	Properties of Commuting Graphs over Semidihedral Groups. <i>Symmetry</i> , 2021, 13, 103.	2.2	5
154	Analysis of the real number of infected people by COVID-19: A system dynamics approach. <i>PLoS ONE</i> , 2021, 16, e0245728.	2.5	5
155	Limitations of Explainability for Established Prognostic Biomarkers of Prostate Cancer. <i>Frontiers in Genetics</i> , 2021, 12, 649429.	2.3	5
156	A Brief Introduction to Complex Networks and Their Analysis. , 2011, , 1-26.		5
157	NONLINEAR TIME SERIES PREDICTION BASED ON A POWER-LAW NOISE MODEL. <i>International Journal of Modern Physics C</i> , 2007, 18, 1839-1852.	1.7	4
158	Comparing Biological Networks: A Survey on Graph Classifying Techniques. , 2013, , 43-63.		4
159	Structural Properties and Complexity of a New Network Class: Collatz Step Graphs. <i>PLoS ONE</i> , 2013, 8, e56461.	2.5	4
160	Enhancing systems medicine beyond genotype data by dynamic patient signatures: having information and using it too. <i>Frontiers in Genetics</i> , 2013, 4, 241.	2.3	4
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.	4.9	4
162	Toward Measuring Network Aesthetics Based on Symmetry. <i>Axioms</i> , 2017, 6, 12.	1.9	4

#	ARTICLE	IF	CITATIONS
163	Properties of graph distance measures by means of discrete inequalities. Applied Mathematical Modelling, 2018, 59, 739-749.	4.2	4
164	On the Degeneracy of the Orbit Polynomial and Related Graph Polynomials. Symmetry, 2020, 12, 1643.	2.2	4
165	Towards Network Complexity. Lecture Notes of the Institute for Computer Sciences, Social-Informatics and Telecommunications Engineering, 2009, , 707-714.	0.3	4
166	A constrained HMM-based approach to the estimation of perceptual switching dynamics in pigeons. Neurocomputing, 2001, 38-40, 1495-1501.	5.9	3
167	Global information processing in gene networks: Fault tolerance. , 2007, , .		3
168	Hierarchical coordination of periodic genes in the cell cycle of Saccharomyces cerevisiae. BMC Systems Biology, 2009, 3, 76.	3.0	3
169	Netmes: Assessing Gene Network Inference Algorithms by Network-Based Measures. Evolutionary Bioinformatics, 2014, 10, EBO.S13481.	1.2	3
170	Extracting the Strongest Signals from Omics Data: Differentially Expressed Pathways and Beyond. Methods in Molecular Biology, 2017, 1613, 125-159.	0.9	3
171	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, 1-17.	3.0	3
172	Inference of Genome-Scale Gene Regulatory Networks: Are There Differences in Biological and Clinical Validations?. Machine Learning and Knowledge Extraction, 2018, 1, 138-148.	5.0	3
173	A Note on Distance-Based Entropy of Dendrimers. Axioms, 2019, 8, 98.	1.9	3
174	In-flight Wind Field Identification and Prediction of Parafoil Systems. Applied Sciences (Switzerland), 2020, 10, 1958.	2.5	3
175	On the relationship between PageRank and automorphisms of a graph. Information Sciences, 2021, 579, 401-417.	6.9	3
176	Prognostic modeling of predictive maintenance with survival analysis for mobile work equipment. Scientific Reports, 2022, 12, .	3.3	3
177	Universal construction mechanism for networks from one-dimensional symbol sequences. Applied Mathematics and Computation, 2012, 219, 1020-1030.	2.2	2
178	Evolutionary dynamics of the spatial Prisoner's Dilemma with self-inhibition. Applied Mathematics and Computation, 2012, 218, 6482-6488.	2.2	2
179	[COMMODE] a large-scale database of molecular descriptors using compounds from PubChem. Source Code for Biology and Medicine, 2013, 8, 22.	1.7	2
180	Discrimination Power of Polynomial-Based Descriptors for Graphs by Using Functional Matrices. PLoS ONE, 2015, 10, e0139265.	2.5	2

#	ARTICLE	IF	CITATIONS
181	Exploiting Genomic Relations in Big Data Repositories by Graph-Based Search Methods. Machine Learning and Knowledge Extraction, 2018, 1, 205-210.	5.0	2
182	A Note on Graphs with Prescribed Orbit Structure. Entropy, 2019, 21, 1118.	2.2	2
183	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.	3.7	2
184	On the degeneracy of the RandiÄž entropy and related graph measures. Information Sciences, 2019, 501, 680-687.	6.9	2
185	Relations and bounds for the zeros of graph polynomials using vertex orbits. Applied Mathematics and Computation, 2020, 380, 125239.	2.2	2
186	The watching system as a generalization of identifying code. Applied Mathematics and Computation, 2020, 380, 125302.	2.2	2
187	Editorial: AI and Multi-Omics for Rare Diseases: Challenges, Advances and Perspectives. Frontiers in Molecular Biosciences, 2021, 8, 719978.	3.5	2
188	Relationships between symmetry-based graph measures. Information Sciences, 2021, 581, 291-303.	6.9	2
189	Network-Based Methods for Computational Diagnostics by Means of R. , 2012, , 185-197.		2
190	Mathematical Modeling in Systems Biology. Communications in Computer and Information Science, 2017, , 161-166.	0.5	2
191	STOCHASTIC SZNAJD MODEL IN OPEN COMMUNITY. International Journal of Modern Physics C, 2005, 16, 1693-1699.	1.7	1
192	Network Classes and Graph Complexity Measures. , 2008, , .		1
193	Comments to "Quantification of network structural dissimilarities" published by Schieber et al. Mathematical Methods in the Applied Sciences, 2018, 41, 5711-5713.	2.3	1
194	On efficient network similarity measures. Applied Mathematics and Computation, 2019, 362, 124521.	2.2	1
195	Proteome-transcriptome alignment of molecular portraits achieved by self-contained gene set analysis: Consensus colon cancer subtypes case study. PLoS ONE, 2019, 14, e0221444.	2.5	1
196	Partition and Colored Distances in Graphs Induced to Subsets of Vertices and Some of Its Applications. Symmetry, 2020, 12, 2027.	2.2	1
197	Orbit Entropy and Symmetry Index Revisited. Mathematics, 2021, 9, 1086.	2.2	1
198	Grand Challenges for Artificial Intelligence in Molecular Medicine. Frontiers in Molecular Medicine, 2021, 1, .	1.9	1

#	ARTICLE	IF	CITATIONS
199	Are There Limits in Explainability of Prognostic Biomarkers? Scrutinizing Biological Utility of Established Signatures. <i>Cancers</i> , 2021, 13, 5087.	3.7	1
200	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.	2.0	1
201	Towards a Channel Capacity of Communication Networks. , 2008, , .		0
202	Finding Verified Edges in Genetic/Gene Networks: Bilayer Verification for Network Recovery in the Presence of Hidden Confounders. , 0, , 51-81.		0
203	Predicting Functional Modules Using Microarray and Protein Interaction Data. , 0, , 307-329.		0
204	Graph Structure Analysis and Computational Tractability of Scheduling Problems. , 0, , 295-322.		0
205	Elementary Elliptic (R, q)-Polycycles. , 0, , 351-376.		0
206	Mining Graph Patterns in Web-based Systems: A Conceptual View. <i>Text, Speech and Language Technology</i> , 2010, , 237-253.	0.2	0
207	A Bayesian analysis of the chromosome architecture of human disorders by integrating reductionist data. <i>Scientific Reports</i> , 2012, 2, 513.	3.3	0
208	Detecting sequence dependent transcriptional pauses from RNA and protein number time series. <i>BMC Bioinformatics</i> , 2012, 13, 152.	2.6	0
209	Semisupervised Methods for Analyzing High-dimensional Genomic Data. , 2013, , 93-106.		0
210	Network Medicine: Disease Genes in Molecular Networks. , 2013, , 133-151.		0
211	Learning Systems Biology: Conceptual Considerations toward a Web-Based Learning Platform. <i>Education Sciences</i> , 2013, 3, 158-171.	2.6	0
212	Enhancing our understanding of ways to analyze metagenomes. <i>Frontiers in Genetics</i> , 2014, 5, 108.	2.3	0
213	Report from the 2nd Summer School in Computational Biology organized by the Queen's University of Belfast. <i>Genomics Data</i> , 2014, 2, 37-39.	1.3	0
214	Biological networks: the microscope of the twenty-first century?. <i>Frontiers in Genetics</i> , 2015, 6, 307.	2.3	0
215	Structural Analysis of Treatment Cycles Representing Transitions between Nursing Organizational Units Inferred from Diabetes. <i>PLoS ONE</i> , 2015, 10, e0127152.	2.5	0
216	Network signatures based on gene pair expression ratios improve classification and the analysis of muscle-invasive urothelial cancer. , 2015, , .		0

#	ARTICLE	IF	CITATIONS
217	Using shRNA experiments to validate gene regulatory networks. <i>Genomics Data</i> , 2015, 4, 123-126.	1.3	0
218	A Graph Theoretic Approach to Construct Desired Cryptographic Boolean Functions. <i>Axioms</i> , 2019, 8, 40.	1.9	0
219	A Neurobiologically Motivated Model for Self-organized Learning. <i>Lecture Notes in Computer Science</i> , 2005, , 415-424.	1.3	0
220	A Novel Stochastic Learning Rule for Neural Networks. <i>Lecture Notes in Computer Science</i> , 2006, , 414-423.	1.3	0
221	Global Information Processing in Gene Networks: Fault Tolerance. , 2007, ,		0
222	Towards a Partitioning of the Input Space of Boolean Networks: Variable Selection Using Bagging. <i>Lecture Notes of the Institute for Computer Sciences, Social-Informatics and Telecommunications Engineering</i> , 2009, , 715-723.	0.3	0
223	Organizational Structure of the Transcriptional Regulatory Network of Yeast: Periodic Genes. <i>Lecture Notes of the Institute for Computer Sciences, Social-Informatics and Telecommunications Engineering</i> , 2009, , 140-148.	0.3	0
224	Large-Scale Statistical Inference of Gene Regulatory Networks: Local Network-Based Measures. <i>Intelligent Systems Reference Library</i> , 2011, , 179-193.	1.2	0
225	Urinary Thrombomodulin Levels Were Significantly Higher Following Occupational Exposure to Chemicals, In The Presence of Dipstick Protein, But Not in the Presence of Dipstick Blood. <i>Biology and Medicine (Aligarh)</i> , 2016, 08, .	0.3	0
226	Abstract 2270: A BRCA1 deficient, NF κ B driven immune signal predicts good outcome in triple negative breast cancer. , 2016, ,		0
227	Network Science: From Chemistry to Digital Society. <i>Frontiers for Young Minds</i> , 0, 7, .	0.8	0
228	14. Differential equations. , 2020, , 253-266.		0
229	4. Installation of R packages. , 2020, , 27-30.		0
230	5. Introduction to programming in R. , 2020, , 31-78.		0
231	17. Probability theory. , 2020, , 331-374.		0
232	3. Setting up and installing the R program. , 2020, , 23-26.		0
233	7. Basic plotting functions. , 2020, , 97-116.		0
234	9. Visualization of networks. , 2020, , 133-150.		0

#	ARTICLE	IF	CITATIONS
235	18. Optimization. , 2020, , 375-402.		0
236	8. Advanced plotting functions: ggplot2. , 2020, , 117-132.		0
237	2. Overview of programming paradigms. , 2020, , 11-22.		0
238	10. Mathematics as a language for science. , 2020, , 153-170.		0
239	12. Linear algebra. , 2020, , 181-228.		0
240	15. Dynamical systems. , 2020, , 267-304.		0
241	13. Analysis. , 2020, , 229-252.		0
242	16. Graph theory and network analysis. , 2020, , 305-330.		0
243	6. Creating R packages. , 2020, , 79-94.		0
244	11. Computability and complexity. , 2020, , 171-180.		0
245	Optimization Procedure for Predicting Nonlinear Time Series Based on a Non-Gaussian Noise Model. , 2007, , 540-549.		0
246	Automorphism Groups of Alkane Graphs. Croatica Chemica Acta, 2021, 94, .	0.4	0
247	The Most Probable Genetic Interaction Networks Inferred from Gene Expression Patterns. , 0, , 385-412.		0