

CITATION REPORT

List of articles citing

Kavosh: a new algorithm for finding network motifs

DOI: 10.1186/1471-2105-10-318

BMC Bioinformatics, 2009, 10, 318.

Source: <https://exaly.com/paper-pdf/45873501/citation-report.pdf>

Version: 2024-04-09

This report has been generated based on the citations recorded by exaly.com for the above article. 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.

| # | Paper | IF | Citations |
|-----|---|-----|-----------|
| 163 | MODA: an efficient algorithm for network motif discovery in biological networks. 2009 , 84, 385-95 | | 92 |
| 162 | A survey of current software for network analysis in molecular biology. 2010 , 4, 353-60 | | 138 |
| 161 | Good versus optimal: Why network analytic methods need more systematic evaluation. 2011 , 1, | | 6 |
| 160 | Degree-Based Sampling Method with Partition-Based Subgraph Finder for Larger Motif Detection. 2011 , 135-136, 509-515 | | |
| 159 | Querying subgraph sets with g-tries. 2012 , | | 15 |
| 158 | Biological network motif detection: principles and practice. 2012 , 13, 202-15 | | 99 |
| 157 | Detecting local network motifs. 2012 , 6, | | 6 |
| 156 | Motifs and Motif Generalization in Chinese Word Networks. 2012 , 9, 550-556 | | 3 |
| 155 | Accelerated Motif Detection Using Combinatorial Techniques. 2012 , | | 4 |
| 154 | Building blocks of biological networks: a review on major network motif discovery algorithms. <i>IET Systems Biology</i> , 2012 , 6, 164-74 | 1.4 | 48 |
| 153 | Machine-Learning Techniques. 2012 , 363-454 | | |
| 152 | Symmetry compression method for discovering network motifs. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012 , 9, 1776-89 | 3 | 10 |
| 151 | Motif Mining in Weighted Networks. 2012 , | | 8 |
| 150 | NetMODE: network motif detection without Nauty. <i>PLoS ONE</i> , 2012 , 7, e50093 | 3.7 | 34 |
| 149 | Parallel discovery of network motifs. 2012 , 72, 144-154 | | 21 |
| 148 | On the discovery of group-consistent graph substructure patterns from brain networks. 2013 , 213, 204-13 | | 9 |
| 147 | A subgraph isomorphism algorithm and its application to biochemical data. <i>BMC Bioinformatics</i> , 2013 , 14 Suppl 7, S13 | 3.6 | 77 |

| | | |
|-----|---|--------|
| 146 | Visual compression of workflow visualizations with automated detection of macro motifs. 2013 , 19, 2576-85 | 15 |
| 145 | RANGI: a fast list-colored graph motif finding algorithm. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013 , 10, 504-13 | 3 6 |
| 144 | Towards a faster network-centric subgraph census. 2013 , | 13 |
| 143 | Controllability in cancer metabolic networks according to drug targets as driver nodes. <i>PLoS ONE</i> , 2013 , 8, e79397 | 3-7 44 |
| 142 | Neutral forces acting on intragenomic variability shape the Escherichia coli regulatory network topology. 2013 , 110, 7754-9 | 9 |
| 141 | QuateXelero: an accelerated exact network motif detection algorithm. <i>PLoS ONE</i> , 2013 , 8, e68073 | 3-7 39 |
| 140 | NMDB: NETWORK MOTIF DATABASE ENVISAGED AND EXPLICATED FROM HUMAN DISEASE SPECIFIC PATHWAYS. 2014 , 22, 89-100 | 3 |
| 139 | On the impact of data integration and edge enrichment in mining significant signals from biological networks. 2014 , | |
| 138 | Efficiently Estimating Motif Statistics of Large Networks. <i>ACM Transactions on Knowledge Discovery From Data</i> , 2014 , 9, 1-27 | 4 48 |
| 137 | acc-Motif: Accelerated Network Motif Detection. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2014 , 11, 853-62 | 3 27 |
| 136 | A complex systems analysis of stick-slip dynamics of a laboratory fault. 2014 , 24, 013132 | 10 |
| 135 | CBOS-Clustering Base on the Score for Motif Discovery in Biological Network. 2014 , | |
| 134 | Efficient updates of network motif instances in the extended protein-protein interaction network. 2014 , | |
| 133 | G-Tries: a data structure for storing and finding subgraphs. 2014 , 28, 337-377 | 40 |
| 132 | GUISE: a uniform sampler for constructing frequency histogram of graphlets. 2014 , 38, 511-536 | 13 |
| 131 | Parallel Subgraph Counting for Multicore Architectures. 2014 , | 14 |
| 130 | CombiMotif: A new algorithm for network motifs discovery in protein-protein interaction networks. 2014 , 416, 309-320 | |
| 129 | FS3: A sampling based method for top-k frequent subgraph mining. 2015 , 8, 245-261 | 15 |

| | | | |
|-----|--|-----|----|
| 128 | Fast Parallel All-Subgraph Enumeration Using Multicore Machines. 2015 , 2015, 1-11 | | 5 |
| 127 | Rand-FaSE: fast approximate subgraph census. <i>Social Network Analysis and Mining</i> , 2015 , 5, 1 | 2.2 | 5 |
| 126 | A Method of Motif Mining Based on Backtracking and Dynamic Programming. <i>Lecture Notes in Computer Science</i> , 2015 , 317-328 | 0.9 | 1 |
| 125 | Statistical approach to calculation of number of network motifs. 2015 , | | 1 |
| 124 | Motif mining based on network space compression. <i>BioData Mining</i> , 2015 , 8, 29 | 4.3 | 2 |
| 123 | Distributed discovery of frequent subgraphs of a network using MapReduce. 2015 , 97, 1101-1120 | | 16 |
| 122 | Sensible method for updating motif instances in an increased biological network. <i>Methods</i> , 2015 , 83, 71-9 | 4.6 | 0 |
| 121 | High-performance parallel frequent subgraph discovery. 2015 , 71, 2412-2432 | | 4 |
| 120 | A novel motif-discovery algorithm to identify co-regulatory motifs in large transcription factor and microRNA co-regulatory networks in human. 2015 , 31, 2348-55 | | 27 |
| 119 | P-Finder: Reconstruction of Signaling Networks from Protein-Protein Interactions and GO Annotations. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2015 , 12, 309-21 | 3 | 4 |
| 118 | COMMIT. 2015 , | | 28 |
| 117 | Network motif discovery: A GPU approach. 2015 , | | 11 |
| 116 | Structural templates of disordered granular media. 2015 , 54, 20-30 | | 4 |
| 115 | Network motifs that recur across species, including gene regulatory and protein-protein interaction networks. 2015 , 89, 489-99 | | 4 |
| 114 | Current innovations and future challenges of network motif detection. 2015 , 16, 497-525 | | 31 |
| 113 | Detecting multiple stochastic network motifs in network data. 2015 , 42, 49-74 | | 7 |
| 112 | On Efficient External-Memory Triangle Listing. 2016 , | | 9 |
| 111 | The exploration of network motifs as potential drug targets from post-translational regulatory networks. <i>Scientific Reports</i> , 2016 , 6, 20558 | 4.9 | 9 |

| | | | |
|-----|---|-----|----|
| 110 | Syntactic complexity of Web search queries through the lenses of language models, networks and users. 2016 , 52, 923-948 | | 6 |
| 109 | CeFunMO: A centrality based method for discovering functional motifs with application in biological networks. 2016 , 76, 154-9 | | 1 |
| 108 | MASS-Based NemoProfile Construction for an Efficient Network Motif Search. 2016 , | | 4 |
| 107 | Identification of large disjoint motifs in biological networks. <i>BMC Bioinformatics</i> , 2016 , 17, 408 | 3.6 | 15 |
| 106 | Drivers of structural features in gene regulatory networks: From biophysical constraints to biological function. 2016 , 17, 124-58 | | 8 |
| 105 | Network Motif Discovery: A GPU Approach. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2017 , 29, 513-528 | 4.2 | 23 |
| 104 | Extending the Applicability of Graphlets to Directed Networks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017 , 14, 1302-1315 | 3 | 6 |
| 103 | Graph Theory at the Service of Electroencephalograms. 2017 , 7, 137-151 | | 6 |
| 102 | Triangular Alignment (TAME): A Tensor-Based Approach for Higher-Order Network Alignment. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017 , 14, 1446-1458 | 3 | 15 |
| 101 | MotifNet: a web-server for network motif analysis. 2017 , 33, 1907-1909 | | 11 |
| 100 | Homomorphisms are a good basis for counting small subgraphs. 2017 , | | 19 |
| 99 | Analytics in Human Resource Management The OpenSKIMR Approach. 2017 , 122, 727-734 | | 6 |
| 98 | NemoProfile as an efficient approach to network motif analysis with instance collection. <i>BMC Bioinformatics</i> , 2017 , 18, 423 | 3.6 | 1 |
| 97 | ParaMODA: Improving motif-centric subgraph pattern search in PPI networks. 2017 , | | 5 |
| 96 | . 2017 , | | 3 |
| 95 | Using k-Mix-Neighborhood Subdigraphs to Compute Canonical Labelings of Digraphs. 2017 , 19, 79 | | 1 |
| 94 | Network analysis of particles and grains. <i>Journal of Complex Networks</i> , 2018 , 6, 485-565 | 1.7 | 66 |
| 93 | Counting motifs in dynamic networks. 2018 , 12, 6 | | 6 |

| | | | |
|----|--|-----|----|
| 92 | An Efficient Sampling Algorithm for Network Motif Detection. 2018 , 27, 503-515 | | 7 |
| 91 | Community Detection Using Attribute Homogenous Motif. 2018 , 6, 47707-47716 | | 14 |
| 90 | Identifying Representative Network Motifs for Inferring Higher-order Structure of Biological Networks. 2018 , | | 1 |
| 89 | MTMO: an efficient network-centric algorithm for subtree counting and enumeration. 2018 , 6, 142-154 | | 3 |
| 88 | Clustering of proteins in interaction networks based on motif features. 2018 , | | 2 |
| 87 | Motif discovery in biological network using expansion tree. 2018 , 16, 1850024 | | 6 |
| 86 | Extensor-coding. 2018 , | | 5 |
| 85 | Profiling call changes via motif mining. 2018 , | | 1 |
| 84 | SuperNoder: a tool to discover over-represented modular structures in networks. <i>BMC Bioinformatics</i> , 2018 , 19, 318 | 3.6 | 4 |
| 83 | Grasping frequent subgraph mining for bioinformatics applications. <i>BioData Mining</i> , 2018 , 11, 20 | 4.3 | 13 |
| 82 | Formal Analysis of Network Motifs. <i>Lecture Notes in Computer Science</i> , 2018 , 111-128 | 0.9 | 4 |
| 81 | Edge sign prediction based on a combination of network structural topology and sign propagation. <i>Journal of Complex Networks</i> , 2019 , 7, 54-66 | 1.7 | 6 |
| 80 | PathEmb: Random Walk Based Document Embedding for Global Pathway Similarity Search. 2019 , 23, 1329-1335 | | 5 |
| 79 | Network Motifs: A Survey. 2019 , 80-91 | | 3 |
| 78 | Interaction pattern features and driving forces of intersectoral CO2 emissions in China: A network motif analysis. 2019 , 149, 391-412 | | 8 |
| 77 | A Survey of Measures for Network Motifs. 2019 , 7, 106576-106587 | | 10 |
| 76 | Research on interpersonal relationship network of pyramid scheme organization based on social network: A case study. 2019 , 30, 1940016 | | 2 |
| 75 | Use the K-Neighborhood Subgraphs to Compute Canonical Labelings of Graphs. 2019 , 7, 690 | | |

| | | | |
|----|---|------|----|
| 74 | Antimodularity: Pragmatic Consequences of Computational Complexity on Scientific Explanation. 2019 , 97-122 | | |
| 73 | Enumerating Connected Induced Subgraphs: Improved Delay and Experimental Comparison. <i>Lecture Notes in Computer Science</i> , 2019 , 272-284 | 0.9 | 1 |
| 72 | Detecting list-colored graph motifs in biological networks using branch-and-bound strategy. 2019 , 107, 1-9 | | 4 |
| 71 | . 2019 , 7, 49778-49789 | | 10 |
| 70 | Online Estimation of Motif Distribution in Dynamic Networks. 2019 , | | 3 |
| 69 | . <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2019 , 31, 1555-1568 | 4.2 | 4 |
| 68 | . 2019 , | | |
| 67 | Motifs in Big Networks: Methods and Applications. 2019 , 7, 183322-183338 | | 7 |
| 66 | NemoMapPy: Motif-centric network motif search on a web. 2019 , | | 1 |
| 65 | Higher-Order Brain Network Analysis for Auditory Disease. 2019 , 49, 879-897 | | 5 |
| 64 | System Network Complexity: Network Evolution Subgraphs of System State Series. 2020 , 4, 130-139 | | 5 |
| 63 | FSM: Fast and scalable network motif discovery for exploring higher-order network organizations. <i>Methods</i> , 2020 , 173, 83-93 | 4.6 | 11 |
| 62 | The short-term roles of sectors during a carbon tax on Chinese economy based on complex network: An in-process analysis. <i>Journal of Cleaner Production</i> , 2020 , 251, 119560 | 10.3 | 6 |
| 61 | Enumerating connected induced subgraphs: Improved delay and experimental comparison. <i>Discrete Applied Mathematics</i> , 2020 , 303, 262-262 | 1 | 2 |
| 60 | Motif discovery in networks: A survey. <i>Computer Science Review</i> , 2020 , 37, 100267 | 8.3 | 10 |
| 59 | Searching and inferring colorful topological motifs in vertex-colored graphs. <i>Journal of Combinatorial Optimization</i> , 2020 , 40, 379-411 | 0.9 | |
| 58 | An Efficient Multiresolution Clustering for Motif Discovery in Complex Networks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020 , PP, | 3 | 1 |
| 57 | A new method for organizational process model discovery through the analysis of workflows and data exchange networks. <i>Social Network Analysis and Mining</i> , 2020 , 10, 1 | 2.2 | 2 |

| | | | |
|----|--|------|----|
| 56 | Intrinsic limitations in mainstream methods of identifying network motifs in biology. <i>BMC Bioinformatics</i> , 2020 , 21, 165 | 3.6 | 2 |
| 55 | Parallelization of network motif discovery using star contraction. <i>Parallel Computing</i> , 2021 , 101, 102734 | 1 | 1 |
| 54 | HM-Modularity: A Harmonic Motif Modularity Approach for Multi-Layer Network Community Detection. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2021 , 33, 2520-2533 | 4.2 | 5 |
| 53 | Formal Analysis of Network Motifs Links Structure to Function in Biological Programs. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021 , 18, 261-271 | 3 | 4 |
| 52 | Research on Motif Mining Based on Neighborhood Equivalence Class. <i>Journal of Physics: Conference Series</i> , 2021 , 1738, 012076 | 0.3 | |
| 51 | A Fast and Exact Motif Enumeration Algorithm for Dynamic Networks. <i>Advances in Intelligent Systems and Computing</i> , 2021 , 123-141 | 0.4 | |
| 50 | Network motifs: A key variable in the equation of dynamic flow between macro and micro layers in Complex Networks. <i>Knowledge-Based Systems</i> , 2021 , 213, 106648 | 7.3 | 1 |
| 49 | RASMA: a reverse search algorithm for mining maximal frequent subgraphs. <i>BioData Mining</i> , 2021 , 14, 19 | 4.3 | 2 |
| 48 | A Survey on Subgraph Counting. <i>ACM Computing Surveys</i> , 2021 , 54, 1-36 | 13.4 | 10 |
| 47 | Network Subgraph Pattern Mining. <i>Journal of Physics: Conference Series</i> , 2021 , 1881, 032043 | 0.3 | |
| 46 | Functional network motifs defined through integration of protein-protein and genetic interactions. | | |
| 45 | Hepatoenteric recycling is a new disposition mechanism for orally administered phenolic drugs and phytochemicals in rats. <i>ELife</i> , 2021 , 10, | 8.9 | 1 |
| 44 | CTD: An information-theoretic algorithm to interpret sets of metabolomic and transcriptomic perturbations in the context of graphical models. <i>PLoS Computational Biology</i> , 2021 , 17, e1008550 | 5 | 1 |
| 43 | Motifs in Biological Networks. 2021 , 101-123 | | 1 |
| 42 | A survey of pattern mining in dynamic graphs. <i>Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery</i> , 2020 , 10, e1372 | 6.9 | 8 |
| 41 | Discovering Colored Network Motifs. <i>Studies in Computational Intelligence</i> , 2014 , 107-118 | 0.8 | 13 |
| 40 | A Scalable Parallel Approach for Subgraph Census Computation. <i>Lecture Notes in Computer Science</i> , 2014 , 194-205 | 0.9 | 4 |
| 39 | Finding Network Motifs Using MCMC Sampling. <i>Studies in Computational Intelligence</i> , 2015 , 13-24 | 0.8 | 16 |

| | | | |
|----|--|-----|----|
| 38 | StreaM - A Stream-Based Algorithm for Counting Motifs in Dynamic Graphs. <i>Lecture Notes in Computer Science</i> , 2015 , 53-67 | 0.9 | 9 |
| 37 | Efficient Subgraph Frequency Estimation with G-Tries. <i>Lecture Notes in Computer Science</i> , 2010 , 238-249 | 0.9 | 11 |
| 36 | Frequent Subpatterns Distribution in Social Network Analysis. <i>Advances in Intelligent Systems and Computing</i> , 2019 , 393-403 | 0.4 | 2 |
| 35 | Review of tools and algorithms for network motif discovery in biological networks. <i>IET Systems Biology</i> , 2020 , 14, 171-189 | 1.4 | 3 |
| 34 | Motif discovery algorithms in static and temporal networks: A survey. <i>Journal of Complex Networks</i> , 2020 , 8, | 1.7 | 5 |
| 33 | Formal Analysis of Network Motifs. | | 1 |
| 32 | Community Detection by Motif-Aware Label Propagation. <i>ACM Transactions on Knowledge Discovery From Data</i> , 2020 , 14, 1-19 | 4 | 14 |
| 31 | CytoKavosh: a cytoscape plug-in for finding network motifs in large biological networks. <i>PLoS ONE</i> , 2012 , 7, e43287 | 3.7 | 10 |
| 30 | Directed network motifs in Alzheimer's disease and mild cognitive impairment. <i>PLoS ONE</i> , 2015 , 10, e0124453 | 3.7 | 9 |
| 29 | Complex Networks, Gene Expression and Cancer Complexity: A Brief Review of Methodology and Applications. <i>Current Bioinformatics</i> , 2020 , 15, 629-655 | 4.7 | 5 |
| 28 | NemoMap: Improved Motif-centric Network Motif Discovery Algorithm. <i>Advances in Science, Technology and Engineering Systems</i> , 2018 , 3, 186-199 | 0.3 | 5 |
| 27 | NemoSuite: Web-based Network Motif Analytic Suite. <i>Advances in Science, Technology and Engineering Systems</i> , 2020 , 5, 1545-1553 | 0.3 | 0 |
| 26 | Application of dynamic expansion tree for finding large network motifs in biological networks. <i>PeerJ</i> , 2019 , 7, e6917 | 3.1 | 5 |
| 25 | References. 157-176 | | |
| 24 | Network Motif Discovery. 2014 , 169-199 | | |
| 23 | Network Motif Search. <i>Computational Biology</i> , 2015 , 275-302 | 0.7 | |
| 22 | NemoLib: A Java Library for Efficient Network Motif Detection. <i>Lecture Notes in Computer Science</i> , 2017 , 403-407 | 0.9 | 3 |
| 21 | Impact of Memory Space Optimization Technique on Fast Network Motif Search Algorithm. <i>Advances in Intelligent Systems and Computing</i> , 2017 , 559-567 | 0.4 | 0 |

| | | | |
|----|--|-----|---|
| 20 | Intrinsic limitations in mainstream methods of identifying network motifs in biology. | | |
| 19 | Discovery of Large Disjoint Motif in Biological Network using Dynamic Expansion Tree. | | |
| 18 | Identifying Representative Network Motifs for Inferring Higher-order Structure of Biological Networks. | | |
| 17 | Mining Network Motif Discovery by Learning Techniques. <i>Lecture Notes in Computer Science</i> , 2019 , 73-84. | 0.9 | |
| 16 | Disjoint motif discovery in biological network using pattern join method. <i>IET Systems Biology</i> , 2019 , 13, 213-224 | 1.4 | 2 |
| 15 | NemoLib: Network Motif Libraries for Network Motif Detection and Analysis. <i>Lecture Notes in Computer Science</i> , 2020 , 327-334 | 0.9 | |
| 14 | Diffusion Dynamics Prediction on Networks Using Sub-graph Motif Distribution. <i>Studies in Computational Intelligence</i> , 2021 , 482-493 | 0.8 | 0 |
| 13 | A Fast Counting Method for 6-Motifs with Low Connectivity. <i>Lecture Notes in Computer Science</i> , 2020 , 324-332 | 0.9 | |
| 12 | Topological parameters, patterns, and motifs in biological networks. 2022 , 367-380 | | |
| 11 | Extreme vulnerability of high-order organization in complex networks. <i>Physics Letters, Section A: General, Atomic and Solid State Physics</i> , 2021 , 424, 127829 | 2.3 | 0 |
| 10 | Identification of patterns for space-time event networks. <i>Applied Network Science</i> , 2022 , 7, | 2.9 | |
| 9 | Influence Maximization Based on Network Motifs in Mobile Social Networks. <i>IEEE Transactions on Network Science and Engineering</i> , 2022 , 1-1 | 4.9 | 0 |
| 8 | Functional network motifs defined through integration of protein-protein and genetic interactions.. <i>PeerJ</i> , 2022 , 10, e13016 | 3.1 | 2 |
| 7 | The brainstem connectome database.. <i>Scientific Data</i> , 2022 , 9, 168 | 8.2 | |
| 6 | Detecting Anomalous Graphs in Labeled Multi-Graph Databases. <i>ACM Transactions on Knowledge Discovery From Data</i> , | 4 | 1 |
| 5 | Graph convolutional networks fusing motif-structure information. <i>Scientific Reports</i> , 2022 , 12, | 4.9 | |
| 4 | Edge-colored directed subgraph enumeration on the connectome. <i>Scientific Reports</i> , 2022 , 12, | 4.9 | 0 |
| 3 | A Survey of Visualization and Analysis in High-Resolution Connectomics. 2022 , 41, 573-607 | | 0 |

- 2 BFS-based distributed algorithm for parallel local-directed subgraph enumeration. **2022**, 10, o
- 1 PATRICIA trie based time and memory optimization for fast network motif Search. **2017**, 87, o