

# Learning Graphical Models With Hubs

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Network assisted analysis to reveal the genetic basis of autism. <i>Annals of Applied Statistics</i> , 2015, 9, 1571-1600.	0.5	43
2	Consistency of biological networks inferred from microarray and sequencing data. <i>BMC Bioinformatics</i> , 2016, 17, 254.	1.2	4
3	Graph reconstruction using covariance-based methods. <i>Eurasip Journal on Bioinformatics and Systems Biology</i> , 2016, 2016, 19.	1.4	7
4	Incorporating prior information into differential network analysis using non-paranormal graphical models. <i>Bioinformatics</i> , 2017, 33, 2436-2445.	1.8	40
5	Node-based learning of differential networks from multi-platform gene expression data. <i>Methods</i> , 2017, 129, 41-49.	1.9	16
6	Node-based differential network analysis in genomics. <i>Computational Biology and Chemistry</i> , 2017, 69, 194-201.	1.1	10
7	Robust sparse Gaussian graphical modeling. <i>Journal of Multivariate Analysis</i> , 2017, 161, 172-190.	0.5	15
8	Frobenius Norm Regularization for the Multivariate Von Mises Distribution. <i>International Journal of Intelligent Systems</i> , 2017, 32, 153-176.	3.3	3
9	JRmGRN: joint reconstruction of multiple gene regulatory networks with common hub genes using data from multiple tissues or conditions. <i>Bioinformatics</i> , 2018, 34, 3470-3478.	1.8	19
10	Edge selection for undirected graphs. <i>Journal of Statistical Computation and Simulation</i> , 2018, 88, 3291-3322.	0.7	2
11	A structural Markov property for decomposable graph laws that allows control of clique intersections. <i>Biometrika</i> , 2018, 105, 19-29.	1.3	4
12	Data-driven graph construction and graph learning: A review. <i>Neurocomputing</i> , 2018, 312, 336-351.	3.5	93
13	Bayesian Inference of Hub Nodes Across Multiple Networks. <i>Biometrics</i> , 2019, 75, 172-182.	0.8	2
14	Identifying gene-environment interactions incorporating prior information. <i>Statistics in Medicine</i> , 2019, 38, 1620-1633.	0.8	9
15	Inferring gene expression networks with hubs using a degree weighted Lasso approach. <i>Bioinformatics</i> , 2019, 35, 987-994.	1.8	16
16	Structure learning of sparse directed acyclic graphs incorporating the scale-free property. <i>Computational Statistics</i> , 2019, 34, 713-742.	0.8	0
17	Low Rank and Structured Modeling of High-Dimensional Vector Autoregressions. <i>IEEE Transactions on Signal Processing</i> , 2019, 67, 1207-1222.	3.2	37
18	Certifiably optimal sparse inverse covariance estimation. <i>Mathematical Programming</i> , 2020, 184, 491-530.	1.6	6

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19	Integrating approximate single factor graphical models. <i>Statistics in Medicine</i> , 2020, 39, 146-155.	0.8	3
20	Open eyes and closed eyes elicit different temporal properties of brain functional networks. <i>NeuroImage</i> , 2020, 222, 117230.	2.1	36
21	Estimating sparse networks with hubs. <i>Journal of Multivariate Analysis</i> , 2020, 179, 104655.	0.5	3
22	Sparse principal component regression via singular value decomposition approach. <i>Advances in Data Analysis and Classification</i> , 2021, 15, 795-823.	0.9	2
25	Fused Graphical Lasso for Brain Networks with Symmetries. <i>Journal of the Royal Statistical Society Series C: Applied Statistics</i> , 2021, 70, 1299-1322.	0.5	2
26	Identifying Hub Wastewater Propagation Chains in China's National Economic System: A Model Coupled Input-Output Analysis with Graphical Theory. <i>Water (Switzerland)</i> , 2021, 13, 2351.	1.2	1
27	Network analysis methods for studying microbial communities: A mini review. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 2687-2698.	1.9	130
29	Extended graphical lasso for multiple interaction networks for high dimensional omics data. <i>PLoS Computational Biology</i> , 2021, 17, e1008794.	1.5	0
30	Inference of genetic regulatory networks with regulatory hubs using vector autoregressions and automatic relevance determination with model selections. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2021, 20, 121-143.	0.2	2