Marco Grzegorczyk

List of Publications by Year
in descending order

25 papers	691 citations	933447 10 h-index	642732 23 g-index
29 all docs	29 docs citations	29 times ranked	708 citing authors

#	Article	IF	Citations
1	On the Bayesian network based data mining framework for the choice of appropriate time scale for regional analysis of drought Hazard. Theoretical and Applied Climatology, 2021, 143, 1677-1695.	2.8	5
2	A new Bayesian piecewise linear regression model for dynamic network reconstruction. BMC Bioinformatics, 2021, 22, 196.	2.6	5
3	The 'un-shrunk' partial correlation in Gaussian graphical models. BMC Bioinformatics, 2021, 22, 424.	2.6	0
4	Non-homogeneous dynamic Bayesian networks with edge-wise sequentially coupled parameters. Bioinformatics, 2020, 36, 1198-1207.	4.1	10
5	A New Partially Segment-Wise Coupled Piece-Wise Linear Regression Model for Statistical Network Structure Inference. Lecture Notes in Computer Science, 2020, , 139-152.	1.3	0
6	Exact hypothesis testing for shrinkage-based Gaussian graphical models. Bioinformatics, 2019, 35, 5011-5017.	4.1	8
7	A new Bayesian multivariate exponentially weighted moving average control chart for phase II monitoring of multivariate multiple linear profiles. Quality and Reliability Engineering International, 2019, 35, 2152-2177.	2.3	2
8	Overview and Evaluation of Recent Methods for Statistical Inference of Gene Regulatory Networks from Time Series Data. Methods in Molecular Biology, 2019, 1883, 49-94.	0.9	6
9	Partially non-homogeneous dynamic Bayesian networks based on Bayesian regression models with partitioned design matrices. Bioinformatics, 2019, 35, 2108-2117.	4.1	9
10	A Bayesian Network Analysis of the Diagnostic Process and its Accuracy to Determine How Clinicians Estimate Cardiac Function in Critically Ill Patients: Prospective Observational Cohort Study. JMIR Medical Informatics, 2019, 7, e15358.	2.6	3
11	Improving nonhomogeneous dynamic Bayesian networks with sequentially coupled parameters. Statistica Neerlandica, 2018, 72, 281-305.	1.6	9
12	Approximate Bayesian inference in semi-mechanistic models. Statistics and Computing, 2017, 27, 1003-1040.	1.5	12
13	Comparative evaluation of various frequentist and Bayesian non-homogeneous Poisson counting models. Computational Statistics, 2017, 32, 1-33.	1.5	9
14	Targeting Bayes factors with direct-path non-equilibrium thermodynamic integration. Computational Statistics, 2017, 32, 717-761.	1.5	2
15	A non-homogeneous dynamic Bayesian network with a hidden Markov model dependency structure among the temporal data points. Machine Learning, 2016, 102, 155-207.	5.4	22
16	Inferring bi-directional interactions between circadian clock genes and metabolism with model ensembles. Statistical Applications in Genetics and Molecular Biology, 2015, 14, 143-67.	0.6	5
17	Statistical inference of regulatory networks for circadian regulation. Statistical Applications in Genetics and Molecular Biology, 2014, 13, 227-73.	0.6	22
18	Regularization of non-homogeneous dynamic Bayesian networks with global information-coupling based on hierarchical Bayesian models. Machine Learning, 2013, 91, 105-154.	5.4	19

#	Article	IF	Citations
19	A Non-Homogeneous Dynamic Bayesian Network with Sequentially Coupled Interaction Parameters for Applications in Systems and Synthetic Biology. Statistical Applications in Genetics and Molecular Biology, 2012, 11, .	0.6	21
20	Non-homogeneous dynamic Bayesian networks forÂcontinuous data. Machine Learning, 2011, 83, 355-419.	5.4	50
21	Modelling non-stationary dynamic gene regulatory processes with the BGM model. Computational Statistics, 2011, 26, 199-218.	1.5	9
22	Improvements in the reconstruction of time-varying gene regulatory networks: dynamic programming and regularization by information sharing among genes. Bioinformatics, 2011, 27, 693-699.	4.1	77
23	An Introduction to Gaussian Bayesian Networks. Methods in Molecular Biology, 2010, 662, 121-147.	0.9	28
24	Modelling non-stationary gene regulatory processes with a non-homogeneous Bayesian network and the allocation sampler. Bioinformatics, 2008, 24, 2071-2078.	4.1	55
25	Comparative evaluation of reverse engineering gene regulatory networks with relevance networks, graphical gaussian models and bayesian networks. Bioinformatics, 2006, 22, 2523-2531.	4.1	301