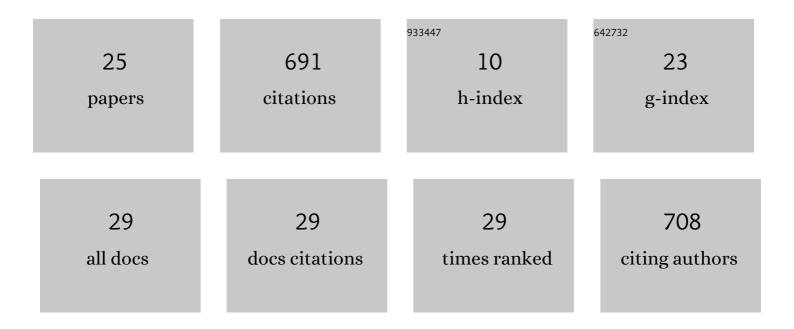
## Marco Grzegorczyk

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	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
2	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
3	Modelling non-stationary gene regulatory processes with a non-homogeneous Bayesian network and the allocation sampler. Bioinformatics, 2008, 24, 2071-2078.	4.1	55
4	Non-homogeneous dynamic Bayesian networks forÂcontinuous data. Machine Learning, 2011, 83, 355-419.	5.4	50
5	An Introduction to Gaussian Bayesian Networks. Methods in Molecular Biology, 2010, 662, 121-147.	0.9	28
6	Statistical inference of regulatory networks for circadian regulation. Statistical Applications in Genetics and Molecular Biology, 2014, 13, 227-73.	0.6	22
7	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
8	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
9	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
10	Approximate Bayesian inference in semi-mechanistic models. Statistics and Computing, 2017, 27, 1003-1040.	1.5	12
11	Non-homogeneous dynamic Bayesian networks with edge-wise sequentially coupled parameters. Bioinformatics, 2020, 36, 1198-1207.	4.1	10
12	Modelling non-stationary dynamic gene regulatory processes with the BGM model. Computational Statistics, 2011, 26, 199-218.	1.5	9
13	Comparative evaluation of various frequentist and Bayesian non-homogeneous Poisson counting models. Computational Statistics, 2017, 32, 1-33.	1.5	9
14	Improving nonhomogeneous dynamic Bayesian networks with sequentially coupled parameters. Statistica Neerlandica, 2018, 72, 281-305.	1.6	9
15	Partially non-homogeneous dynamic Bayesian networks based on Bayesian regression models with partitioned design matrices. Bioinformatics, 2019, 35, 2108-2117.	4.1	9
16	Exact hypothesis testing for shrinkage-based Gaussian graphical models. Bioinformatics, 2019, 35, 5011-5017.	4.1	8
17	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
18	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

#	Article	IF	CITATIONS
19	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
20	A new Bayesian piecewise linear regression model for dynamic network reconstruction. BMC Bioinformatics, 2021, 22, 196.	2.6	5
21	A Bayesian Network Analysis of the Diagnostic Process and its Accuracy to Determine How Clinicians Estimate Cardiac Function in Critically III Patients: Prospective Observational Cohort Study. JMIR Medical Informatics, 2019, 7, e15358.	2.6	3
22	Targeting Bayes factors with direct-path non-equilibrium thermodynamic integration. Computational Statistics, 2017, 32, 717-761.	1.5	2
23	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
24	The â€~un-shrunk' partial correlation in Gaussian graphical models. BMC Bioinformatics, 2021, 22, 424.	2.6	0
25	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