Thomas Thorne

List of Publications by Year
in descending order

26 papers	1,367 citations	567281 15 h-index	642732 23 g-index
28 all docs	28 docs citations	28 times ranked	2053 citing authors

#	Article	IF	Citations
1	Topological approximate Bayesian computation for parameter inference of an angiogenesis model. Bioinformatics, 2022, 38, 2529-2535.	4.1	6
2	Gene Regulatory Network Inference. , 2021, , 86-95.		2
3	A Dynamic Bayesian Network Approach for Analysing Topic-Sentiment Evolution. IEEE Access, 2020, 8, 54164-54174.	4.2	35
4	Approximate inference of gene regulatory network models from RNA-Seq time series data. BMC Bioinformatics, 2018, 19, 127.	2.6	16
5	Lipoprotein markers associated with disability from multiple sclerosis. Scientific Reports, 2018, 8, 17026.	3.3	35
6	NetDiff â€" Bayesian model selection for differential gene regulatory network inference. Scientific Reports, 2016, 6, 39224.	3.3	8
7	Empirical likelihood tests for nonparametric detection of differential expression from RNA-seq data. Statistical Applications in Genetics and Molecular Biology, 2015, 14, 575-83.	0.6	1
8	Derivative processes for modelling metabolic fluxes. Bioinformatics, 2014, 30, 1892-1898.	4.1	5
9	Bayesian non-parametric approaches to reconstructing oscillatory systems and the Nyquist limit. Physica A: Statistical Mechanics and Its Applications, 2014, 407, 33-42.	2.6	3
10	Model selection in systems and synthetic biology. Current Opinion in Biotechnology, 2013, 24, 767-774.	6.6	100
11	Graphical modelling of molecular networks underlying sporadic inclusion body myositis. Molecular BioSystems, 2013, 9, 1736.	2.9	10
12	Graph spectral analysis of protein interaction network evolution. Journal of the Royal Society Interface, 2012, 9, 2653-2666.	3.4	23
13	Inference of temporally varying Bayesian Networks. Bioinformatics, 2012, 28, 3298-3305.	4.1	23
14	Parameter-free model discrimination criterion based on steady-state coplanarity. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 15746-15751.	7.1	28
15	Considerate approaches to constructing summary statistics for ABC model selection. Statistics and Computing, 2012, 22, 1181-1197.	1.5	45
16	Calibrating spatio-temporal models of leukocyte dynamics against in vivo live-imaging data using approximate Bayesian computation. Integrative Biology (United Kingdom), 2012, 4, 335.	1.3	31
17	Combinatorial stresses kill pathogenic *Candida* species. Medical Mycology, 2012, 50, 699-709.	0.7	79
18	A systems biology analysis of long and short-term memories of osmotic stress adaptation in fungi. BMC Research Notes, 2012, 5, 258.	1.4	28

#	Article	IF	Citations
19	Prediction of putative protein interactions through evolutionary analysis of osmotic stress response in the model yeast Saccharomyces cerevisae. Fungal Genetics and Biology, 2011, 48, 504-511.	2.1	9
20	The Evolution of the Phage Shock Protein Response System: Interplay between Protein Function, Genomic Organization, and System Function. Molecular Biology and Evolution, 2011, 28, 1141-1155.	8.9	56
21	Estimating the size of the human interactome. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 6959-6964.	7.1	692
22	Evolution at the system level: the natural history of protein interaction networks. Trends in Ecology and Evolution, 2007, 22, 366-373.	8.7	46
23	Generating confidence intervals on biological networks. BMC Bioinformatics, 2007, 8, 467.	2.6	20
24	Multi-model inference of network properties from incomplete data. Journal of Integrative Bioinformatics, 2006, 3, 123-136.	1.5	6
25	The effects of incomplete protein interaction data on structural and evolutionary inferences. BMC Biology, 2006, 4, 39.	3.8	58
26	Multi-model inference of network properties from incomplete data. , 0, .		2