Korbinian Sebastian Strimmer

List of Publications by Year
in descending order

45 papers	24,413 citations	147566 31 h-index	253896 43 g-index
50 all docs	50 docs citations	50 times ranked	36573 citing authors

#	ARTICLE	IF	CITATIONS
1	Quantification of protein abundance and interaction defines a mechanism for operation of the circadian clock. ELife, 2022, 11, .	2.8	18
2	A whitening approach to probabilistic canonical correlation analysis for omics data integration. BMC Bioinformatics, 2019, 20, 15.	1.2	38
3	Optimal Whitening and Decorrelation. American Statistician, 2018, 72, 309-314.	0.9	210
4	Mass Spectrometry Analysis Using MALDIquant. , 2017, , 101-124.		18
5	Differential protein expression and peak selection in mass spectrometry data by binary discriminant analysis. Bioinformatics, 2015, 31, 3156-3162.	1.8	30
6	A simple data-adaptive probabilistic variant calling model. Algorithms for Molecular Biology, 2015, 10, 10.	0.3	3
7	Signal identification for rare and weak features: higher criticism or false discovery rates?. Biostatistics, 2013, 14, 129-143.	0.9	28
8	MALDIquant: a versatile R package for the analysis of mass spectrometry data. Bioinformatics, 2012, 28, 2270-2271.	1.8	525
9	A novel algorithm for simultaneous SNP selection in high-dimensional genome-wide association studies. BMC Bioinformatics, 2012, 13, 284.	1.2	15
10	High-Dimensional Regression and Variable Selection Using CAR Scores. Statistical Applications in Genetics and Molecular Biology, 2011, 10, .	0.2	104
11	Feature selection in omics prediction problems using cat scores and false nondiscovery rate control. Annals of Applied Statistics, 2010, 4, .	0.5	102
12	Over-optimism in bioinformatics: an illustration. Bioinformatics, 2010, 26, 1990-1998.	1.8	90
13	Genetic distances and nucleotide substitution models. , 2009, , 111-141.		20
14	Gene ranking and biomarker discovery under correlation. Bioinformatics, 2009, 25, 2700-2707.	1.8	82
15	A general modular framework for gene set enrichment analysis. BMC Bioinformatics, 2009, 10, 47.	1.2	300
16	Comments on: Augmenting the bootstrap to analyze high dimensional genomic data. Test, 2008, 17, 25-27.	0.7	8
17	A unified approach to false discovery rate estimation. BMC Bioinformatics, 2008, 9, 303.	1.2	351
18	Therapeutic vaccination reduces HIV sequence variability. FASEB Journal, 2008, 22, 437-444.	0.2	9

#	Article	IF	Citations
19	fdrtool: a versatile R package for estimating local and tail area-based false discovery rates. Bioinformatics, 2008, 24, 1461-1462.	1.8	592
20	Identifying periodically expressed transcripts in microarray time series data. Bioinformatics, 2008, 24, 2274-2274.	1.8	106
21	Accurate Ranking of Differentially Expressed Genes by a Distribution-Free Shrinkage Approach. Statistical Applications in Genetics and Molecular Biology, 2007, 6, Article9.	0.2	140
22	From correlation to causation networks: a simple approximate learning algorithm and its application to high-dimensional plant gene expression data. BMC Systems Biology, 2007, 1, 37.	3.0	304
23	Learning causal networks from systems biology time course data: an effective model selection procedure for the vector autoregressive process. BMC Bioinformatics, 2007, 8, S3.	1.2	106
24	Partial least squares: a versatile tool for the analysis of high-dimensional genomic data. Briefings in Bioinformatics, 2006, 8, 32-44.	3.2	611
25	Inference of demographic history from genealogical trees using reversible jump Markov chain Monte Carlo. BMC Evolutionary Biology, 2005, 5, 6.	3.2	75
26	Predicting transcription factor activities from combined analysis of microarray and ChIP data: a partial least squares approach. Theoretical Biology and Medical Modelling, 2005, 2, 23.	2.1	98
27	Learning Large-Scale Graphical Gaussian Models from Genomic Data. AIP Conference Proceedings, 2005, , .	0.3	24
28	An empirical Bayes approach to inferring large-scale gene association networks. Bioinformatics, 2005, 21, 754-764.	1.8	671
29	A Shrinkage Approach to Large-Scale Covariance Matrix Estimation and Implications for Functional Genomics. Statistical Applications in Genetics and Molecular Biology, 2005, 4, Article32.	0.2	1,128
30	Identifying periodically expressed transcripts in microarray time series data. Bioinformatics, 2004, 20, 5-20.	1.8	274
31	TREEFINDER: a powerful graphical analysis environment for molecular phylogenetics. BMC Evolutionary Biology, 2004, 4, 18.	3.2	978
32	APE: Analyses of Phylogenetics and Evolution in R language. Bioinformatics, 2004, 20, 289-290.	1.8	10,601
33	Modeling gene expression measurement error: a quasi-likelihood approach. BMC Bioinformatics, 2003, 4, 10.	1.2	23
34	A novel exploratory method for visual recombination detection. Genome Biology, 2003, 4, R33.	13.9	19
35	A CART-based approach to discover emerging patterns in microarray data. Bioinformatics, 2003, 19, 2465-2472.	1.8	74
36	TREE-PUZZLE: maximum likelihood phylogenetic analysis using quartets and parallel computing. Bioinformatics, 2002, 18, 502-504.	1.8	2,389

#	Article	IF	Citations
37	Inferring confidence sets of possibly misspecified gene trees. Proceedings of the Royal Society B: Biological Sciences, 2002, 269, 137-142.	1.2	441
38	Recombination Analysis Using Directed Graphical Models. Molecular Biology and Evolution, 2001, 18, 97-99.	3.5	36
39	Exploring the Demographic History of DNA Sequences Using the Generalized Skyline Plot. Molecular Biology and Evolution, 2001, 18, 2298-2305.	3.5	244
40	Dating the common ancestor of SIVcpz and HIVâ€1 group M and the origin of HIVâ€1 subtypes by using a new method to uncover clockâ€like molecular evolution. FASEB Journal, 2001, 15, 276-278.	0.2	111
41	Likelihood Analysis of Phylogenetic Networks Using Directed Graphical Models. Molecular Biology and Evolution, 2000, 17, 875-881.	3.5	78
42	Likelihood-mapping: A simple method to visualize phylogenetic content of a sequence alignment. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 6815-6819.	3.3	845
43	Accuracy of Neighbor Joining for n-Taxon Trees. Systematic Biology, 1996, 45, 516-523.	2.7	22
44	Quartet Puzzling: A Quartet Maximum-Likelihood Method for Reconstructing Tree Topologies. Molecular Biology and Evolution, 1996, 13, 964-969.	3.5	2,447
45	Accuracy of Neighbor Joining for n-Taxon Trees. , 0, .		2