

Korbinian Sebastian Strimmer

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1397440/publications.pdf>

Version: 2024-02-01

45
papers

24,413
citations

147801

31
h-index

243625

44
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. <i>ELife</i> , 2022, 11, .	6.0	18
2	A whitening approach to probabilistic canonical correlation analysis for omics data integration. <i>BMC Bioinformatics</i> , 2019, 20, 15.	2.6	38
3	Optimal Whitening and Decorrelation. <i>American Statistician</i> , 2018, 72, 309-314.	1.6	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. <i>Bioinformatics</i> , 2015, 31, 3156-3162.	4.1	30
6	A simple data-adaptive probabilistic variant calling model. <i>Algorithms for Molecular Biology</i> , 2015, 10, 10.	1.2	3
7	Signal identification for rare and weak features: higher criticism or false discovery rates?. <i>Biostatistics</i> , 2013, 14, 129-143.	1.5	28
8	MALDIquant: a versatile R package for the analysis of mass spectrometry data. <i>Bioinformatics</i> , 2012, 28, 2270-2271.	4.1	525
9	A novel algorithm for simultaneous SNP selection in high-dimensional genome-wide association studies. <i>BMC Bioinformatics</i> , 2012, 13, 284.	2.6	15
10	High-Dimensional Regression and Variable Selection Using CAR Scores. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2011, 10, .	0.6	104
11	Feature selection in omics prediction problems using cat scores and false nondiscovery rate control. <i>Annals of Applied Statistics</i> , 2010, 4, .	1.1	102
12	Over-optimism in bioinformatics: an illustration. <i>Bioinformatics</i> , 2010, 26, 1990-1998.	4.1	90
13	Genetic distances and nucleotide substitution models. , 2009, , 111-141.		20
14	Gene ranking and biomarker discovery under correlation. <i>Bioinformatics</i> , 2009, 25, 2700-2707.	4.1	82
15	A general modular framework for gene set enrichment analysis. <i>BMC Bioinformatics</i> , 2009, 10, 47.	2.6	300
16	Comments on: Augmenting the bootstrap to analyze high dimensional genomic data. <i>Test</i> , 2008, 17, 25-27.	1.1	8
17	A unified approach to false discovery rate estimation. <i>BMC Bioinformatics</i> , 2008, 9, 303.	2.6	351
18	Therapeutic vaccination reduces HIV sequence variability. <i>FASEB Journal</i> , 2008, 22, 437-444.	0.5	9

#	ARTICLE	IF	CITATIONS
19	fdrtool: a versatile R package for estimating local and tail area-based false discovery rates. <i>Bioinformatics</i> , 2008, 24, 1461-1462.	4.1	592
20	Identifying periodically expressed transcripts in microarray time series data. <i>Bioinformatics</i> , 2008, 24, 2274-2274.	4.1	106
21	Accurate Ranking of Differentially Expressed Genes by a Distribution-Free Shrinkage Approach. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2007, 6, Article9.	0.6	140
22	From correlation to causation networks: a simple approximate learning algorithm and its application to high-dimensional plant gene expression data. <i>BMC Systems Biology</i> , 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. <i>BMC Bioinformatics</i> , 2007, 8, S3.	2.6	106
24	Partial least squares: a versatile tool for the analysis of high-dimensional genomic data. <i>Briefings in Bioinformatics</i> , 2006, 8, 32-44.	6.5	611
25	Inference of demographic history from genealogical trees using reversible jump Markov chain Monte Carlo. <i>BMC Evolutionary Biology</i> , 2005, 5, 6.	3.2	75
26	Predicting transcription factor activities from combined analysis of microarray and ChIP data: a partial least squares approach. <i>Theoretical Biology and Medical Modelling</i> , 2005, 2, 23.	2.1	98
27	Learning Large-Scale Graphical Gaussian Models from Genomic Data. <i>AIP Conference Proceedings</i> , 2005, , .	0.4	24
28	An empirical Bayes approach to inferring large-scale gene association networks. <i>Bioinformatics</i> , 2005, 21, 754-764.	4.1	671
29	A Shrinkage Approach to Large-Scale Covariance Matrix Estimation and Implications for Functional Genomics. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2005, 4, Article32.	0.6	1,128
30	Identifying periodically expressed transcripts in microarray time series data. <i>Bioinformatics</i> , 2004, 20, 5-20.	4.1	274
31	TREEFINDER: a powerful graphical analysis environment for molecular phylogenetics. <i>BMC Evolutionary Biology</i> , 2004, 4, 18.	3.2	978
32	APE: Analyses of Phylogenetics and Evolution in R language. <i>Bioinformatics</i> , 2004, 20, 289-290.	4.1	10,601
33	Modeling gene expression measurement error: a quasi-likelihood approach. <i>BMC Bioinformatics</i> , 2003, 4, 10.	2.6	23
34	A novel exploratory method for visual recombination detection. <i>Genome Biology</i> , 2003, 4, R33.	9.6	19
35	A CART-based approach to discover emerging patterns in microarray data. <i>Bioinformatics</i> , 2003, 19, 2465-2472.	4.1	74
36	TREE-PUZZLE: maximum likelihood phylogenetic analysis using quartets and parallel computing. <i>Bioinformatics</i> , 2002, 18, 502-504.	4.1	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.	2.6	441
38	Recombination Analysis Using Directed Graphical Models. Molecular Biology and Evolution, 2001, 18, 97-99.	8.9	36
39	Exploring the Demographic History of DNA Sequences Using the Generalized Skyline Plot. Molecular Biology and Evolution, 2001, 18, 2298-2305.	8.9	244
40	Dating the common ancestor of SIVcpz and HIV-1 group M and the origin of HIV-1 subtypes by using a new method to uncover clock-like molecular evolution. FASEB Journal, 2001, 15, 276-278.	0.5	111
41	Likelihood Analysis of Phylogenetic Networks Using Directed Graphical Models. Molecular Biology and Evolution, 2000, 17, 875-881.	8.9	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.	7.1	845
43	Accuracy of Neighbor Joining for n-Taxon Trees. Systematic Biology, 1996, 45, 516-523.	5.6	22
44	Quartet Puzzling: A Quartet Maximum-Likelihood Method for Reconstructing Tree Topologies. Molecular Biology and Evolution, 1996, 13, 964-969.	8.9	2,447
45	Accuracy of Neighbor Joining for n-Taxon Trees. Systematic Biology, 1996, 45, 516.	5.6	2