Christian L MÃ¼ller

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/4225699/publications.pdf

Version: 2024-02-01

38
papers

2,463
citations

567281

15
h-index

345221

36
g-index

48
all docs

48
docs citations

48
times ranked

3776
citing authors

#	Article	IF	Citations
1	Basin-scale biogeography of marine phytoplankton reflects cellular-scale optimization of metabolism and physiology. Science Advances, 2022, 8, eabl4930.	10.3	16
2	Topology Adaptive Graph Estimation in High Dimensions. Mathematics, 2022, 10, 1244.	2.2	0
3	Negative binomial factor regression with application to microbiome data analysis. Statistics in Medicine, 2022, 41, 2786-2803.	1.6	5
4	A randomization-based causal inference framework for uncovering environmental exposure effects on human gut microbiota. PLoS Computational Biology, 2022, 18, e1010044.	3.2	8
5	Stability selection enables robust learning of differential equations from limited noisy data. Proceedings of the Royal Society A: Mathematical, Physical and Engineering Sciences, 2022, 478, .	2.1	4
6	Ocean moverâ€™s distance: using optimal transport for analysing oceanographic data. Proceedings of the Royal Society A: Mathematical, Physical and Engineering Sciences, 2022, 478, .	2.1	3
7	NetCoMi: network construction and comparison for microbiome data in R. Briefings in Bioinformatics, 2021, 22, .	6.5	222
8	Regression Models for Compositional Data: General Log-Contrast Formulations, Proximal Optimization, and Microbiome Data Applications. Statistics in Biosciences, 2021, 13, 217-242.	1.2	15
9	Fast Computation of Latent Correlations. Journal of Computational and Graphical Statistics, 2021, 30, 1249-1256.	1.7	6
10	Learning physically consistent differential equation models from data using group sparsity. Physical Review E, 2021, 103, 042310.	2.1	12
11	Tree-aggregated predictive modeling of microbiome data. Scientific Reports, 2021, 11, 14505.	3.3	13
12	scCODA is a Bayesian model for compositional single-cell data analysis. Nature Communications, 2021, 12, 6876.	12.8	98
13	tascCODA: Bayesian Tree-Aggregated Analysis of Compositional Amplicon and Single-Cell Data. Frontiers in Genetics, 2021, 12, 766405.	2.3	4
14	Shrinkage improves estimation of microbial associations under different normalization methods. NAR Genomics and Bioinformatics, 2020, 2, lqaa100.	3.2	22
15	Perspective maximum likelihood-type estimation via proximal decomposition. Electronic Journal of Statistics, 2020, 14, .	0.7	14
16	Prediction error bounds for linear regression with the TREX. Test, 2019, 28, 451-474.	1.1	14
17	Microbial Networks in SPRING - Semi-parametric Rank-Based Correlation and Partial Correlation Estimation for Quantitative Microbiome Data. Frontiers in Genetics, 2019, 10, 516.	2.3	72
18	Temporal probabilistic modeling of bacterial compositions derived from 16S rRNA sequencing. Bioinformatics, 2018, 34, 372-380.	4.1	42

#	ARTICLE	IF	CITATIONS
19	Perspective functions: Proximal calculus and applications in high-dimensional statistics. Journal of Mathematical Analysis and Applications, 2018, 457, 1283-1306.	1.0	33
20	Non-Convex Global Minimization and False Discovery Rate Control for the TREX. Journal of Computational and Graphical Statistics, 2018, 27, 23-33.	1.7	13
21	Fungi stabilize connectivity in the lung and skin microbial ecosystems. Microbiome, 2018, 6, 12.	11.1	146
22	A single early-in-life macrolide course has lasting effects on murine microbial network topology and immunity. Nature Communications, 2017, 8, 518.	12.8	119
23	L p -Adaptation: Simultaneous Design Centering and Robustness Estimation of Electronic and Biological Systems. Scientific Reports, 2017, 7, 6660.	3.3	10
24	Identifying direct contacts between protein complex subunits from their conditional dependence in proteomics datasets. PLoS Computational Biology, 2017, 13, e1005625.	3.2	22
25	4C-ker: A Method to Reproducibly Identify Genome-Wide Interactions Captured by 4C-Seq Experiments. PLoS Computational Biology, 2016, 12, e1004780.	3.2	84
26	Fused Regression for Multi-source Gene Regulatory Network Inference. PLoS Computational Biology, 2016, 12, e1005157.	3.2	40
27	Antibiotic perturbation of the murine gut microbiome enhances the adiposity, insulin resistance, and liver disease associated with high-fat diet. Genome Medicine, 2016, 8, 48.	8.2	153
28	Robust classification of protein variation using structural modelling and large-scale data integration. Nucleic Acids Research, 2016, 44, 2501-2513.	14.5	52
29	Variable metric random pursuit. Mathematical Programming, 2016, 156, 549-579.	2.4	6
30	Sparse and Compositionally Robust Inference of Microbial Ecological Networks. PLoS Computational Biology, 2015, 11, e1004226.	3.2	1,089
31	Optimization of Convex Functions with Random Pursuit. SIAM Journal on Optimization, 2013, 23, 1284-1309.	2.0	20
32	Towards Functional Orthogonalisation of Protein Complexes: Individualisation of GroEL Monomers Leads to Distinct Quasihomogeneous Single Rings. ChemBioChem, 2013, 14, 2310-2321.	2.6	10
33	Energy Landscapes of Atomic Clusters as Black Box Optimization Benchmarks. Evolutionary Computation, 2012, 20, 543-573.	3.0	17
34	On Spectral Invariance of Randomized Hessian and Covariance Matrix Adaptation Schemes. Lecture Notes in Computer Science, 2012, , 448-457.	1.3	3
35	Global Parameter Identification of Stochastic Reaction Networks from Single Trajectories. Advances in Experimental Medicine and Biology, 2012, 736, 477-498.	1.6	2
36	Gaussian Adaptation as a unifying framework for continuous black-box optimization and adaptive Monte Carlo sampling. , 2010, , .		9

#	ARTICLE	IF	CITATIONS
37	Gaussian Adaptation Revisited â€“ An Entropic View on Covariance Matrix Adaptation. Lecture Notes in Computer Science, 2010, , 432-441.	1.3	9
38	In the eye of the beholder: Inhomogeneous distribution of high-resolution shapes within the random-walk ensemble. Journal of Chemical Physics, 2009, 130, 214904.	3.0	2