

Christian L MÃ¼ller

List of Publications by Year in descending order

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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 | Sparse and Compositionally Robust Inference of Microbial Ecological Networks. PLoS Computational Biology, 2015, 11, e1004226. | 3.2 | 1,089 |
| 2 | NetCoMi: network construction and comparison for microbiome data in R. Briefings in Bioinformatics, 2021, 22, . | 6.5 | 222 |
| 3 | 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 |
| 4 | Fungi stabilize connectivity in the lung and skin microbial ecosystems. Microbiome, 2018, 6, 12. | 11.1 | 146 |
| 5 | 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 |
| 6 | scCODA is a Bayesian model for compositional single-cell data analysis. Nature Communications, 2021, 12, 6876. | 12.8 | 98 |
| 7 | 4C-ker: A Method to Reproducibly Identify Genome-Wide Interactions Captured by 4C-Seq Experiments. PLoS Computational Biology, 2016, 12, e1004780. | 3.2 | 84 |
| 8 | 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 |
| 9 | Robust classification of protein variation using structural modelling and large-scale data integration. Nucleic Acids Research, 2016, 44, 2501-2513. | 14.5 | 52 |
| 10 | Temporal probabilistic modeling of bacterial compositions derived from 16S rRNA sequencing. Bioinformatics, 2018, 34, 372-380. | 4.1 | 42 |
| 11 | Fused Regression for Multi-source Gene Regulatory Network Inference. PLoS Computational Biology, 2016, 12, e1005157. | 3.2 | 40 |
| 12 | Perspective functions: Proximal calculus and applications in high-dimensional statistics. Journal of Mathematical Analysis and Applications, 2018, 457, 1283-1306. | 1.0 | 33 |
| 13 | Shrinkage improves estimation of microbial associations under different normalization methods. NAR Genomics and Bioinformatics, 2020, 2, lqaa100. | 3.2 | 22 |
| 14 | Identifying direct contacts between protein complex subunits from their conditional dependence in proteomics datasets. PLoS Computational Biology, 2017, 13, e1005625. | 3.2 | 22 |
| 15 | Optimization of Convex Functions with Random Pursuit. SIAM Journal on Optimization, 2013, 23, 1284-1309. | 2.0 | 20 |
| 16 | Energy Landscapes of Atomic Clusters as Black Box Optimization Benchmarks. Evolutionary Computation, 2012, 20, 543-573. | 3.0 | 17 |
| 17 | Basin-scale biogeography of marine phytoplankton reflects cellular-scale optimization of metabolism and physiology. Science Advances, 2022, 8, eabl4930. | 10.3 | 16 |
| 18 | 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 |

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 19 | Prediction error bounds for linear regression with the TREX. <i>Test</i> , 2019, 28, 451-474. | 1.1 | 14 |
| 20 | Perspective maximum likelihood-type estimation via proximal decomposition. <i>Electronic Journal of Statistics</i> , 2020, 14, . | 0.7 | 14 |
| 21 | Non-Convex Global Minimization and False Discovery Rate Control for the TREX. <i>Journal of Computational and Graphical Statistics</i> , 2018, 27, 23-33. | 1.7 | 13 |
| 22 | Tree-aggregated predictive modeling of microbiome data. <i>Scientific Reports</i> , 2021, 11, 14505. | 3.3 | 13 |
| 23 | Learning physically consistent differential equation models from data using group sparsity. <i>Physical Review E</i> , 2021, 103, 042310. | 2.1 | 12 |
| 24 | Towards Functional Orthogonalisation of Protein Complexes: Individualisation of GroEL Monomers Leads to Distinct Quasihomogeneous Single Rings. <i>ChemBioChem</i> , 2013, 14, 2310-2321. | 2.6 | 10 |
| 25 | L_p -Adaptation: Simultaneous Design Centering and Robustness Estimation of Electronic and Biological Systems. <i>Scientific Reports</i> , 2017, 7, 6660. | 3.3 | 10 |
| 26 | Gaussian Adaptation as a unifying framework for continuous black-box optimization and adaptive Monte Carlo sampling. , 2010, , . | | 9 |
| 27 | Gaussian Adaptation Revisited – An Entropic View on Covariance Matrix Adaptation. <i>Lecture Notes in Computer Science</i> , 2010, , 432-441. | 1.3 | 9 |
| 28 | A randomization-based causal inference framework for uncovering environmental exposure effects on human gut microbiota. <i>PLoS Computational Biology</i> , 2022, 18, e1010044. | 3.2 | 8 |
| 29 | Variable metric random pursuit. <i>Mathematical Programming</i> , 2016, 156, 549-579. | 2.4 | 6 |
| 30 | Fast Computation of Latent Correlations. <i>Journal of Computational and Graphical Statistics</i> , 2021, 30, 1249-1256. | 1.7 | 6 |
| 31 | Negative binomial factor regression with application to microbiome data analysis. <i>Statistics in Medicine</i> , 2022, 41, 2786-2803. | 1.6 | 5 |
| 32 | tascCODA: Bayesian Tree-Aggregated Analysis of Compositional Amplicon and Single-Cell Data. <i>Frontiers in Genetics</i> , 2021, 12, 766405. | 2.3 | 4 |
| 33 | Stability selection enables robust learning of differential equations from limited noisy data. <i>Proceedings of the Royal Society A: Mathematical, Physical and Engineering Sciences</i> , 2022, 478, . | 2.1 | 4 |
| 34 | On Spectral Invariance of Randomized Hessian and Covariance Matrix Adaptation Schemes. <i>Lecture Notes in Computer Science</i> , 2012, , 448-457. | 1.3 | 3 |
| 35 | Ocean mover’s distance: using optimal transport for analysing oceanographic data. <i>Proceedings of the Royal Society A: Mathematical, Physical and Engineering Sciences</i> , 2022, 478, . | 2.1 | 3 |
| 36 | In the eye of the beholder: Inhomogeneous distribution of high-resolution shapes within the random-walk ensemble. <i>Journal of Chemical Physics</i> , 2009, 130, 214904. | 3.0 | 2 |

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|----|--|-----|-----------|
| 37 | Global Parameter Identification of Stochastic Reaction Networks from Single Trajectories. <i>Advances in Experimental Medicine and Biology</i> , 2012, 736, 477-498. | 1.6 | 2 |
| 38 | Topology Adaptive Graph Estimation in High Dimensions. <i>Mathematics</i> , 2022, 10, 1244. | 2.2 | 0 |