

Christoph Lippert

List of Publications by Year in descending order

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Version: 2024-02-01

31
papers

4,034
citations

304743

22
h-index

454955

30
g-index

39
all docs

39
docs citations

39
times ranked

7426
citing authors

#	ARTICLE	IF	CITATIONS
1	Self-Supervised Learning Methods for Label-Efficient Dental Caries Classification. <i>Diagnostics</i> , 2022, 12, 1237.	2.6	8
2	transferGWAS: GWAS of images using deep transfer learning. <i>Bioinformatics</i> , 2022, 38, 3621-3628.	4.1	15
3	Multimodal Self-supervised Learning for Medical Image Analysis. <i>Lecture Notes in Computer Science</i> , 2021, , 661-673.	1.3	40
4	Predicting the SARS-CoV-2 effective reproduction number using bulk contact data from mobile phones. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	19
5	Time to reality check the promises of machine learning-powered precision medicine. <i>The Lancet Digital Health</i> , 2020, 2, e677-e680.	12.3	126
6	Deep learning of genomic variation and regulatory network data. <i>Human Molecular Genetics</i> , 2018, 27, R63-R71.	2.9	64
7	Ensembles of Lasso Screening Rules. <i>IEEE Transactions on Pattern Analysis and Machine Intelligence</i> , 2018, 40, 2841-2852.	13.9	12
8	easyGWAS: A Cloud-Based Platform for Comparing the Results of Genome-Wide Association Studies. <i>Plant Cell</i> , 2017, 29, 5-19.	6.6	98
9	Profiling of Short-Tandem-Repeat Disease Alleles in 12,632 Human Whole Genomes. <i>American Journal of Human Genetics</i> , 2017, 101, 700-715.	6.2	142
10	Identification of individuals by trait prediction using whole-genome sequencing data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 10166-10171.	7.1	118
11	Sparse probit linear mixed model. <i>Machine Learning</i> , 2017, 106, 1621-1642.	5.4	4
12	Accurate liability estimation improves power in ascertained case-control studies. <i>Nature Methods</i> , 2015, 12, 332-334.	19.0	36
13	Efficient set tests for the genetic analysis of correlated traits. <i>Nature Methods</i> , 2015, 12, 755-758.	19.0	97
14	Computational and statistical issues in personalized medicine. <i>Xrds</i> , 2015, 21, 24-27.	0.3	0
15	Warped linear mixed models for the genetic analysis of transformed phenotypes. <i>Nature Communications</i> , 2014, 5, 4890.	12.8	47
16	Quantifying the uncertainty in heritability. <i>Journal of Human Genetics</i> , 2014, 59, 269-275.	2.3	21
17	Greater power and computational efficiency for kernel-based association testing of sets of genetic variants. <i>Bioinformatics</i> , 2014, 30, 3206-3214.	4.1	35
18	Epigenome-wide association studies without the need for cell-type composition. <i>Nature Methods</i> , 2014, 11, 309-311.	19.0	205

#	ARTICLE	IF	CITATIONS
19	Further Improvements to Linear Mixed Models for Genome-Wide Association Studies. Scientific Reports, 2014, 4, 6874.	3.3	61
20	A Lasso multi-marker mixed model for association mapping with population structure correction. Bioinformatics, 2013, 29, 206-214.	4.1	99
21	FaST-LMM-Select for addressing confounding from spatial structure and rare variants. Nature Genetics, 2013, 45, 470-471.	21.4	88
22	An Exhaustive Epistatic SNP Association Analysis on Expanded Wellcome Trust Data. Scientific Reports, 2013, 3, 1099.	3.3	59
23	Patterns of methylation heritability in a genome-wide analysis of four brain regions. Nucleic Acids Research, 2013, 41, 2095-2104.	14.5	44
24	The benefits of selecting phenotype-specific variants for applications of mixed models in genomics. Scientific Reports, 2013, 3, 1815.	3.3	43
25	A powerful and efficient set test for genetic markers that handles confounders. Bioinformatics, 2013, 29, 1526-1533.	4.1	72
26	Detecting regulatory gene-environment interactions with unmeasured environmental factors. Bioinformatics, 2013, 29, 1382-1389.	4.1	12
27	A genome-to-genome analysis of associations between human genetic variation, HIV-1 sequence diversity, and viral control. ELife, 2013, 2, e01123.	6.0	126
28	Improved linear mixed models for genome-wide association studies. Nature Methods, 2012, 9, 525-526.	19.0	292
29	Whole-genome sequencing of multiple Arabidopsis thaliana populations. Nature Genetics, 2011, 43, 956-963.	21.4	910
30	FaST linear mixed models for genome-wide association studies. Nature Methods, 2011, 8, 833-835.	19.0	1,021
31	Gene function prediction from synthetic lethality networks via ranking on demand. Bioinformatics, 2010, 26, 912-918.	4.1	23