Eric F Lock

List of Publications by Year
in descending order

41 papers	1,377 citations	623734 14 h-index	361022 35 g-index
41 all docs	41 docs citations	41 times ranked	2532 citing authors

#	Article	IF	Citations
1	Multiway Sparse Distance Weighted Discrimination. Journal of Computational and Graphical Statistics, 2023, 32, 730-743.	1.7	0
2	Bayesian modeling of associations in bivariate piecewise linear mixed-effects models.. Psychological Methods, 2022, 27, 44-64.	3.5	6
3	Multiomic profiling of iron-deficient infant monkeys reveals alterations in neurologically important biochemicals in serum and cerebrospinal fluid before the onset of anemia. American Journal of Physiology - Regulatory Integrative and Comparative Physiology, 2022, 322, R486-R500.	1.8	10
4	Bidimensional linked matrix factorization for pan-omics pan-cancer analysis. Annals of Applied Statistics, 2022, 16, 193-215.	1.1	9
5	Bayesian Distance Weighted Discrimination. Journal of Computational and Graphical Statistics, 2022, 31, 1177-1188.	1.7	1
6	Identification of shared and disease-specific host geneâ€“microbiome associations across human diseases using multi-omic integration. Nature Microbiology, 2022, 7, 780-795.	13.3	57
7	A hierarchical spike-and-slab model for pan-cancer survival using pan-omic data. BMC Bioinformatics, 2022, 23, .	2.6	0
8	sJIVE: Supervised joint and individual variation explained. Computational Statistics and Data Analysis, 2022, 175, 107547.	1.2	6
9	Predictors of severe intraventricular hemorrhage in preterm infants under 29-weeks gestation. Journal of Maternal-Fetal and Neonatal Medicine, 2021, 34, 195-200.	1.5	9
10	Correcting iron deficiency anemia with iron dextran alters the serum metabolomic profile of the infant Rhesus Monkey. American Journal of Clinical Nutrition, 2021, 113, 915-923.	4.7	13
11	Bayesian nonparametric multiway regression for clustered binomial data. Stat, 2021, 10, e378.	0.4	0
12	Bayesian variable selection in hierarchical difference-in-differences models. Statistical Methods in Medical Research, 2021, , 096228022110510.	1.5	1
13	Generalized integrative principal component analysis for multi-type data with block-wise missing structure. Biostatistics, 2020, 21, 302-318.	1.5	15
14	Bayesian GWAS with Structured and Non-Local Priors. Bioinformatics, 2020, 36, 17-25.	4.1	3
15	Early-Life Iron Deficiency and Its Natural Resolution Are Associated with Altered Serum Metabolomic Profiles in Infant Rhesus Monkeys. Journal of Nutrition, 2020, 150, 685-693.	2.9	14
16	Integrative factorization of bidimensionally linked matrices. Biometrics, 2020, 76, 61-74.	1.4	12
17	A Pan-Cancer and Polygenic Bayesian Hierarchical Model for the Effect of Somatic Mutations on Survival. Cancer Informatics, 2020, 19, 117693512090739.	1.9	2
18	Single-cell RNA sequencing reveals that lung mesenchymal progenitor cells in IPF exhibit pathological features early in their differentiation trajectory. Scientific Reports, 2020, 10, 11162.	3.3	25

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19	A Bayesian Difference-in-Difference Framework for the Impact of Primary Care Redesign on Diabetes Outcomes. Statistics and Public Policy (Philadelphia, Pa), 2019, 6, 55-66.	1.6	5
20	Linked Matrix Factorization. Biometrics, 2019, 75, 582-592.	1.4	6
21	Metabolomic analysis of CSF indicates brain metabolic impairment precedes hematological indices of anemia in the iron-deficient infant monkey. Nutritional Neuroscience, 2018, 21, 40-48.	3.1	29
22	Tensor-on-Tensor Regression. Journal of Computational and Graphical Statistics, 2018, 27, 638-647.	1.7	49
23	Multi-omic molecular profiling of lung cancer in COPD. European Respiratory Journal, 2018, 52, 1702665.	6.7	25
24	Supervised multiway factorization. Electronic Journal of Statistics, 2018, 12, 1150-1180.	0.7	7
25	Detecting Multiple Random Changepoints in Bayesian Piecewise Growth Mixture Models. Psychometrika, 2018, 83, 733-750.	2.1	11
26	Bayesian Genome- and Epigenome-Wide Association Studies with Gene Level Dependence. Biometrics, 2017, 73, 1018-1028.	1.4	9
27	Discriminating sample groups with multi-way data. Biostatistics, 2017, 18, kxw057.	1.5	10
28	Prediction With Dimension Reduction of Multiple Molecular Data Sources for Patient Survival. Cancer Informatics, 2017, 16, 117693511771851.	1.9	17
29	R.JIVE for exploration of multi-source molecular data. Bioinformatics, 2016, 32, 2877-2879.	4.1	54
30	Shared kernel Bayesian screening. Biometrika, 2015, 102, 829-842.	2.4	10
31	Analysis of multi-source metabolomic data using joint and individual variation explained (JIVE). Analyst, The, 2015, 140, 4521-4529.	3.5	21
32	Joint eQTL assessment of whole blood and dura mater tissue from individuals with Chiari type I malformation. BMC Genomics, 2015, 16, 11.	2.8	10
33	Identification of Chiari Type I Malformation subtypes using whole genome expression profiles and cranial base morphometrics. BMC Medical Genomics, 2014, 7, 39.	1.5	24
34	The genomic landscape of mantle cell lymphoma is related to the epigenetically determined chromatin state of normal B cells. Blood, 2014, 123, 2988-2996.	1.4	224
35	Chemical Genomics Reveals JAK STAT Activation As a Mechanism of Resistance to HDAC Inhibitors in B Cell Lymphomas. Blood, 2014, 124, 271-271.	1.4	1
36	Bayesian consensus clustering. Bioinformatics, 2013, 29, 2610-2616.	4.1	211

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37	Joint and individual variation explained (JIVE) for integrated analysis of multiple data types. Annals of Applied Statistics, 2013, 7, 523-542.	1.1	367
38	The Genetic Landscape Of Mantle Cell Lymphoma and The Epigenetic Origins Of Lineage Specific Mutations. Blood, 2013, 122, 347-347.	1.4	0
39	Quantitative High-Throughput Screening for Chemical Toxicity in a Population-Based In Vitro Model. Toxicological Sciences, 2012, 126, 578-588.	3.1	47
40	Interstrain Differences in the Liver Effects of Trichloroethylene in a Multistrain Panel of Inbred Mice. Toxicological Sciences, 2011, 120, 206-217.	3.1	49
41	Exploratory Analysis of Exercise Adherence Patterns With Sedentary Pregnant Women. Nursing Research, 2010, 59, 280-287.	1.7	8