Kenneth Lange

List of Publications by Year
in descending order

65 papers	14,638 citations	136950 32 h-index	114465 63 g-index
69 all docs	69 docs citations	69 times ranked	21173 citing authors

#	Article	IF	Citations
1	A fast data-driven method for genotype imputation, phasing and local ancestry inference: MendelImpute.jl. Bioinformatics, 2021, 37, 4756-4763.	4.1	4
2	OpenMendel: a cooperative programming project for statistical genetics. Human Genetics, 2020, 139, 61-71.	3.8	29
3	Iterative hard thresholding in genome-wide association studies: Generalized linear models, prior weights, and double sparsity. GigaScience, 2020, 9, .	6.4	10
4	Exploring Population Structure with Admixture Models and Principal Component Analysis. Methods in Molecular Biology, 2020, 2090, 67-86.	0.9	23
5	MM Algorithms for Variance Components Models. Journal of Computational and Graphical Statistics, 2019, 28, 350-361.	1.7	13
6	A majorization–minimization algorithm for split feasibility problems. Computational Optimization and Applications, 2018, 71, 795-828.	1.6	7
7	Fast Genome‐Wide QTL Association Mapping on Pedigree and Population Data. Genetic Epidemiology, 2017, 41, 174-186.	1.3	10
8	Efficient analysis of large datasets and sex bias with ADMIXTURE. BMC Bioinformatics, 2016, 17, 218.	2.6	38
9	Convex Clustering: An Attractive Alternative to Hierarchical Clustering. PLoS Computational Biology, 2015, 11, e1004228.	3.2	34
10	Matrix completion discriminant analysis. Computational Statistics and Data Analysis, 2015, 92, 115-125.	1.2	8
11	Distance majorization and its applications. Mathematical Programming, 2014, 146, 409-436.	2.4	22
12	MM algorithms for geometric and signomial programming. Mathematical Programming, 2014, 143, 339-356.	2.4	35
13	Next-Generation Statistical Genetics: Modeling, Penalization, and Optimization in High-Dimensional Data. Annual Review of Statistics and Its Application, 2014, 1, 279-300.	7.0	40
14	A Brief Survey of Modern Optimization for Statisticians. International Statistical Review, 2014, 82, 46-70.	1.9	31
15	Fast spatial ancestry via flexible allele frequency surfaces. Bioinformatics, 2014, 30, 2915-2922.	4.1	16
16	Cluster and propensity based approximation of a network. BMC Systems Biology, 2013, 7, 21.	3.0	8
17	The MM Algorithm. Springer Texts in Statistics, 2013, , 185-219.	6.7	9
18	Feasibility and Duality. Springer Texts in Statistics, 2013, , 383-414.	6.7	0

#	Article	IF	Citations
19	Quantitative Trait Loci Association Mapping by Imputation of Strain Origins in Multifounder Crosses. Genetics, 2012, 190, 459-473.	2.9	8
20	A quasi-Newton acceleration for high-dimensional optimization algorithms. Statistics and Computing, 2011, 21, 261-273.	1.5	127
21	Enhancements to the ADMIXTURE algorithm for individual ancestry estimation. BMC Bioinformatics, 2011, 12, 246.	2.6	990
22	A fast procedure for calculating importance weights in bootstrap sampling. Computational Statistics and Data Analysis, 2011, 55, 26-33.	1.2	2
23	The MM Alternative to EM. Statistical Science, 2010, 25, .	2.8	68
24	Prioritizing GWAS Results: A Review of Statistical Methods and Recommendations for Their Application. American Journal of Human Genetics, 2010, 86, 6-22.	6.2	531
25	A Poisson model for random multigraphs. Bioinformatics, 2010, 26, 2004-2011.	4.1	25
26	MM Algorithms for Some Discrete Multivariate Distributions. Journal of Computational and Graphical Statistics, 2010, 19, 645-665.	1.7	48
27	The MM Algorithm. Statistics and Computing, 2010, , 189-221.	0.2	1
28	Advanced Optimization Topics. Statistics and Computing, 2010, , 297-332.	0.2	0
29	Genome-wide association analysis by lasso penalized logistic regression. Bioinformatics, 2009, 25, 714-721.	4.1	639
30	Fast model-based estimation of ancestry in unrelated individuals. Genome Research, 2009, 19, 1655-1664.	5.5	6,588
31	Sharp quadratic majorization in one dimension. Computational Statistics and Data Analysis, 2009, 53, 2471-2484.	1.2	35
32	Rating Movies and Rating the Raters Who Rate Them. American Statistician, 2009, 63, 297-307.	1.6	12
33	Penalized estimation of haplotype frequencies. Bioinformatics, 2008, 24, 1596-1602.	4.1	16
34	An MM Algorithm for Multicategory Vertex Discriminant Analysis. Journal of Computational and Graphical Statistics, 2008, 17, 527-544.	1.7	29
35	Coordinate descent algorithms for lasso penalized regression. Annals of Applied Statistics, 2008, 2, .	1.1	533
36	Accommodating Chromosome Inversions in Linkage Analysis. American Journal of Human Genetics, 2006, 79, 238-251.	6.2	8

#	ARTICLE	IF	CITATIONS
37	Variance component models for X-linked QTLs. Genetic Epidemiology, 2006, 30, 380-383.	1.3	10
38	Association testing with Mendel. Genetic Epidemiology, 2005, 29, 36-50.	1.3	57
39	Computational Statistics and Optimization Theory at UCLA. American Statistician, 2004, 58, 9-11.	1.6	9
40	A Tutorial on MM Algorithms. American Statistician, 2004, 58, 30-37.	1.6	1,257
41	Computing Estimates in the Proportional Odds Model. Annals of the Institute of Statistical Mathematics, 2002, 54, 155-168.	0.8	19
42	Genetic Identity Coefficients. Statistics in the Health Sciences, 2002, , 81-96.	0.2	3
43	[Optimization Transfer Using Surrogate Objective Functions]: Rejoinder. Journal of Computational and Graphical Statistics, 2000, 9, 52.	1.7	23
44	Optimization Transfer Using Surrogate Objective Functions. Journal of Computational and Graphical Statistics, 2000, 9, 1.	1.7	219
45	Use of population isolates for mapping complex traits. Nature Reviews Genetics, 2000, 1, 182-190.	16.3	348
46	Optimization Transfer Using Surrogate Objective Functions. Journal of Computational and Graphical Statistics, 2000, 9, 1-20.	1.7	396
47	Genetic Mapping of Complex Traits: Promises, Problems, and Prospects. Theoretical Population Biology, 2000, 57, 1-11.	1.1	36
48	Gamete-Competition Models. American Journal of Human Genetics, 2000, 66, 1168-1172.	6.2	53
49	Quantile Regression via an MM Algorithm. Journal of Computational and Graphical Statistics, 2000, 9, 60-77.	1.7	117
50	Quantile Regression via an MM Algorithm. Journal of Computational and Graphical Statistics, 2000, 9, 60.	1.7	102
51	A Conditional Inference Framework for Extending the Transmission/Disequilibrium Test. Human Heredity, 1998, 48, 67-81.	0.8	137
52	EM algorithms without missing data. Statistical Methods in Medical Research, 1997, 6, 38-54.	1.5	68
53	Genetic Identity Coefficients. Statistics in the Health Sciences, 1997, , 70-84.	0.2	4
54	The Polygenic Model. Statistics in the Health Sciences, 1997, , 123-141.	0.2	1

#	Article	IF	Citations
55	An adaptive barrier method for convex programming. Methods and Applications of Analysis, 1994, 1, 392-402.	0.5	21
56	Normal/Independent Distributions and Their Applications in Robust Regression. Journal of Computational and Graphical Statistics, 1993, 2, 175.	1.7	74
57	How Many Ataxia-Telangiectasia Genes?. , 1993, , 37-54.		6
58	Assessment of Chronic Î³ Radiosensitivity as an in Vitro Assay for Heterozygote Identification of Ataxia-Telangiectasia. Radiation Research, 1991, 128, 90.	1.5	74
59	A primary linkage map of the human chromosome 11q22â€"23 region. Genomics, 1990, 6, 316-323.	2.9	33
60	Localization of an ataxia-telangiectasia gene to chromosome 11q22â€"23. Nature, 1988, 336, 577-580.	27.8	677
61	Univariate and bivariate analyses of cholesterol and triglyceride levels in pedigrees. American Journal of Medical Genetics Part A, 1986, 23, 775-792.	2.4	42
62	Cohabitation, convergence, and environmental covariances. American Journal of Medical Genetics Part A, 1986, 24, 483-491.	2.4	30
63	Extensions to pedigree analysis. IV. Covariance components models for multivariate traits. American Journal of Medical Genetics Part A, 1983, 14, 513-524.	2.4	253
64	Central limit theorems of pedigrees. Journal of Mathematical Biology, 1978, 6, 59-66.	1.9	64
65	Extensions to pedigree analysis III. Variance components by the scoring method. Annals of Human Genetics, 1976, 39, 485-491.	0.8	409