Kenneth Lange

List of Publications by Year in descending order

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

#	Article	IF	CITATIONS
1	Fast model-based estimation of ancestry in unrelated individuals. Genome Research, 2009, 19, 1655-1664.	5.5	6,588
2	A Tutorial on MM Algorithms. American Statistician, 2004, 58, 30-37.	1.6	1,257
3	Enhancements to the ADMIXTURE algorithm for individual ancestry estimation. BMC Bioinformatics, 2011, 12, 246.	2.6	990
4	Localization of an ataxia-telangiectasia gene to chromosome 11q22–23. Nature, 1988, 336, 577-580.	27.8	677
5	Genome-wide association analysis by lasso penalized logistic regression. Bioinformatics, 2009, 25, 714-721.	4.1	639
6	Coordinate descent algorithms for lasso penalized regression. Annals of Applied Statistics, 2008, 2, .	1.1	533
7	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
8	Extensions to pedigree analysis III. Variance components by the scoring method. Annals of Human Genetics, 1976, 39, 485-491.	0.8	409
9	Optimization Transfer Using Surrogate Objective Functions. Journal of Computational and Graphical Statistics, 2000, 9, 1-20.	1.7	396
10	Use of population isolates for mapping complex traits. Nature Reviews Genetics, 2000, 1, 182-190.	16.3	348
11	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
12	Optimization Transfer Using Surrogate Objective Functions. Journal of Computational and Graphical Statistics, 2000, 9, 1.	1.7	219
13	A Conditional Inference Framework for Extending the Transmission/Disequilibrium Test. Human Heredity, 1998, 48, 67-81.	0.8	137
14	A quasi-Newton acceleration for high-dimensional optimization algorithms. Statistics and Computing, 2011, 21, 261-273.	1.5	127
15	Quantile Regression via an MM Algorithm. Journal of Computational and Graphical Statistics, 2000, 9, 60-77.	1.7	117
16	Quantile Regression via an MM Algorithm. Journal of Computational and Graphical Statistics, 2000, 9, 60.	1.7	102
17	Assessment of Chronic \hat{I}^3 Radiosensitivity as an in Vitro Assay for Heterozygote Identification of Ataxia-Telangiectasia. Radiation Research, 1991, 128, 90.	1.5	74
18	Normal/Independent Distributions and Their Applications in Robust Regression. Journal of Computational and Graphical Statistics, 1993, 2, 175.	1.7	74

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19	EM algorithms without missing data. Statistical Methods in Medical Research, 1997, 6, 38-54.	1.5	68
20	The MM Alternative to EM. Statistical Science, 2010, 25, .	2.8	68
21	Central limit theorems of pedigrees. Journal of Mathematical Biology, 1978, 6, 59-66.	1.9	64
22	Association testing with Mendel. Genetic Epidemiology, 2005, 29, 36-50.	1.3	57
23	Gamete-Competition Models. American Journal of Human Genetics, 2000, 66, 1168-1172.	6.2	53
24	MM Algorithms for Some Discrete Multivariate Distributions. Journal of Computational and Graphical Statistics, 2010, 19, 645-665.	1.7	48
25	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
26	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
27	Efficient analysis of large datasets and sex bias with ADMIXTURE. BMC Bioinformatics, 2016, 17, 218.	2.6	38
28	Genetic Mapping of Complex Traits: Promises, Problems, and Prospects. Theoretical Population Biology, 2000, 57, 1-11.	1.1	36
29	Sharp quadratic majorization in one dimension. Computational Statistics and Data Analysis, 2009, 53, 2471-2484.	1.2	35
30	MM algorithms for geometric and signomial programming. Mathematical Programming, 2014, 143, 339-356.	2.4	35
31	Convex Clustering: An Attractive Alternative to Hierarchical Clustering. PLoS Computational Biology, 2015, 11, e1004228.	3.2	34
32	A primary linkage map of the human chromosome 11q22–23 region. Genomics, 1990, 6, 316-323.	2.9	33
33	A Brief Survey of Modern Optimization for Statisticians. International Statistical Review, 2014, 82, 46-70.	1.9	31
34	Cohabitation, convergence, and environmental covariances. American Journal of Medical Genetics Part A, 1986, 24, 483-491.	2.4	30
35	An MM Algorithm for Multicategory Vertex Discriminant Analysis. Journal of Computational and Graphical Statistics, 2008, 17, 527-544.	1.7	29
36	OpenMendel: a cooperative programming project for statistical genetics. Human Genetics, 2020, 139, 61-71.	3.8	29

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37	A Poisson model for random multigraphs. Bioinformatics, 2010, 26, 2004-2011.	4.1	25
38	[Optimization Transfer Using Surrogate Objective Functions]: Rejoinder. Journal of Computational and Graphical Statistics, 2000, 9, 52.	1.7	23
39	Exploring Population Structure with Admixture Models and Principal Component Analysis. Methods in Molecular Biology, 2020, 2090, 67-86.	0.9	23
40	Distance majorization and its applications. Mathematical Programming, 2014, 146, 409-436.	2.4	22
41	An adaptive barrier method for convex programming. Methods and Applications of Analysis, 1994, 1, 392-402.	0.5	21
42	Computing Estimates in the Proportional Odds Model. Annals of the Institute of Statistical Mathematics, 2002, 54, 155-168.	0.8	19
43	Penalized estimation of haplotype frequencies. Bioinformatics, 2008, 24, 1596-1602.	4.1	16
44	Fast spatial ancestry via flexible allele frequency surfaces. Bioinformatics, 2014, 30, 2915-2922.	4.1	16
45	MM Algorithms for Variance Components Models. Journal of Computational and Graphical Statistics, 2019, 28, 350-361.	1.7	13
46	Rating Movies and Rating the Raters Who Rate Them. American Statistician, 2009, 63, 297-307.	1.6	12
47	Variance component models for X-linked QTLs. Genetic Epidemiology, 2006, 30, 380-383.	1.3	10
48	Fast Genomeâ€Wide QTL Association Mapping on Pedigree and Population Data. Genetic Epidemiology, 2017, 41, 174-186.	1.3	10
49	Iterative hard thresholding in genome-wide association studies: Generalized linear models, prior weights, and double sparsity. GigaScience, 2020, 9, .	6.4	10
50	Computational Statistics and Optimization Theory at UCLA. American Statistician, 2004, 58, 9-11.	1.6	9
51	The MM Algorithm. Springer Texts in Statistics, 2013, , 185-219.	6.7	9
52	Accommodating Chromosome Inversions in Linkage Analysis. American Journal of Human Genetics, 2006, 79, 238-251.	6.2	8
53	Quantitative Trait Loci Association Mapping by Imputation of Strain Origins in Multifounder Crosses. Genetics, 2012, 190, 459-473.	2.9	8
54	Cluster and propensity based approximation of a network. BMC Systems Biology, 2013, 7, 21.	3.0	8

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55	Matrix completion discriminant analysis. Computational Statistics and Data Analysis, 2015, 92, 115-125.	1.2	8
56	A majorization–minimization algorithm for split feasibility problems. Computational Optimization and Applications, 2018, 71, 795-828.	1.6	7
57	How Many Ataxia-Telangiectasia Genes?. , 1993, , 37-54.		6
58	A fast data-driven method for genotype imputation, phasing and local ancestry inference: MendelImpute.jl. Bioinformatics, 2021, 37, 4756-4763.	4.1	4
59	Genetic Identity Coefficients. Statistics in the Health Sciences, 1997, , 70-84.	0.2	4
60	Genetic Identity Coefficients. Statistics in the Health Sciences, 2002, , 81-96.	0.2	3
61	A fast procedure for calculating importance weights in bootstrap sampling. Computational Statistics and Data Analysis, 2011, 55, 26-33.	1.2	2
62	The MM Algorithm. Statistics and Computing, 2010, , 189-221.	0.2	1
63	The Polygenic Model. Statistics in the Health Sciences, 1997, , 123-141.	0.2	1
64	Feasibility and Duality. Springer Texts in Statistics, 2013, , 383-414.	6.7	0
65	Advanced Optimization Topics. Statistics and Computing, 2010, , 297-332.	0.2	O