

# Kenneth L Lange

## List of Publications by Year in descending order

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97  
papers

15,146  
citations

126907

33  
h-index

45317

90  
g-index

107  
all docs

107  
docs citations

107  
times ranked

21822  
citing authors

#	ARTICLE	IF	CITATIONS
1	Fast model-based estimation of ancestry in unrelated individuals. <i>Genome Research</i> , 2009, 19, 1655-1664.	5.5	6,588
2	A Tutorial on MM Algorithms. <i>American Statistician</i> , 2004, 58, 30-37.	1.6	1,257
3	Localization of an ataxia-telangiectasia gene to chromosome 11q22-23. <i>Nature</i> , 1988, 336, 577-580.	27.8	677
4	Genome-wide association analysis by lasso penalized logistic regression. <i>Bioinformatics</i> , 2009, 25, 714-721.	4.1	639
5	Programs for pedigree analysis: Mendel, Fisher, and dGene. <i>Genetic Epidemiology</i> , 1988, 5, 471-472.	1.3	562
6	Coordinate descent algorithms for lasso penalized regression. <i>Annals of Applied Statistics</i> , 2008, 2, .	1.1	533
7	Prioritizing GWAS Results: A Review of Statistical Methods and Recommendations for Their Application. <i>American Journal of Human Genetics</i> , 2010, 86, 6-22.	6.2	531
8	Extensions to pedigree analysis III. Variance components by the scoring method. <i>Annals of Human Genetics</i> , 1976, 39, 485-491.	0.8	409
9	Optimization Transfer Using Surrogate Objective Functions. <i>Journal of Computational and Graphical Statistics</i> , 2000, 9, 1-20.	1.7	396
10	Detection and Integration of Genotyping Errors in Statistical Genetics. <i>American Journal of Human Genetics</i> , 2002, 70, 496-508.	6.2	317
11	A Theoretical Study of Some Maximum Likelihood Algorithms for Emission and Transmission Tomography. <i>IEEE Transactions on Medical Imaging</i> , 1987, 6, 106-114.	8.9	274
12	Extensions to pedigree analysis. IV. Covariance components models for multivariate traits. <i>American Journal of Medical Genetics Part A</i> , 1983, 14, 513-524.	2.4	253
13	Mathematical and Statistical Methods for Genetic Analysis. <i>Statistics in the Health Sciences</i> , 2002, , .	0.2	221
14	Numerical Analysis for Statisticians. <i>Statistics and Computing</i> , 2010, , .	0.2	202
15	Normal/Independent Distributions and Their Applications in Robust Regression. <i>Journal of Computational and Graphical Statistics</i> , 1993, 2, 175-198.	1.7	181
16	Splitting Methods for Convex Clustering. <i>Journal of Computational and Graphical Statistics</i> , 2015, 24, 994-1013.	1.7	131
17	A quasi-Newton acceleration for high-dimensional optimization algorithms. <i>Statistics and Computing</i> , 2011, 21, 261-273.	1.5	127
18	Association screening of common and rare genetic variants by penalized regression. <i>Bioinformatics</i> , 2010, 26, 2375-2382.	4.1	120

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19	Mendel: the Swiss army knife of genetic analysis programs. <i>Bioinformatics</i> , 2013, 29, 1568-1570.	4.1	104
20	EM algorithms without missing data. <i>Statistical Methods in Medical Research</i> , 1997, 6, 38-54.	1.5	68
21	The MM Alternative to EM. <i>Statistical Science</i> , 2010, 25, .	2.8	68
22	Central limit theorems of pedigrees. <i>Journal of Mathematical Biology</i> , 1978, 6, 59-66.	1.9	64
23	Association testing with Mendel. <i>Genetic Epidemiology</i> , 2005, 29, 36-50.	1.3	57
24	Gamete-Competition Models. <i>American Journal of Human Genetics</i> , 2000, 66, 1168-1172.	6.2	53
25	Stability selection for genome-wide association. <i>Genetic Epidemiology</i> , 2011, 35, 722-728.	1.3	51
26	Genotype imputation via matrix completion. <i>Genome Research</i> , 2013, 23, 509-518.	5.5	50
27	MM Algorithms for Some Discrete Multivariate Distributions. <i>Journal of Computational and Graphical Statistics</i> , 2010, 19, 645-665.	1.7	48
28	Linkage analysis without defined pedigrees. <i>Genetic Epidemiology</i> , 2011, 35, 360-370.	1.3	40
29	Imaging genetics via sparse canonical correlation analysis. , 2013, 2013, 740-743.		40
30	Next-Generation Statistical Genetics: Modeling, Penalization, and Optimization in High-Dimensional Data. <i>Annual Review of Statistics and Its Application</i> , 2014, 1, 279-300.	7.0	40
31	MM algorithms for geometric and signomial programming. <i>Mathematical Programming</i> , 2014, 143, 339-356.	2.4	35
32	Modeling of Cancer Stem Cell State Transitions Predicts Therapeutic Response. <i>PLoS ONE</i> , 2015, 10, e0135797.	2.5	34
33	Convex Clustering: An Attractive Alternative to Hierarchical Clustering. <i>PLoS Computational Biology</i> , 2015, 11, e1004228.	3.2	34
34	A maximum likelihood test of the two locus model for coeliac disease. <i>American Journal of Medical Genetics Part A</i> , 1982, 12, 75-82.	2.4	33
35	Graphics Processing Units and High-Dimensional Optimization. <i>Statistical Science</i> , 2010, 25, 311-324.	2.8	31
36	A Brief Survey of Modern Optimization for Statisticians. <i>International Statistical Review</i> , 2014, 82, 46-70.	1.9	31

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37	Stable estimation of a covariance matrix guided by nuclear norm penalties. <i>Computational Statistics and Data Analysis</i> , 2014, 80, 117-128.	1.2	31
38	Cohabitation, convergence, and environmental covariances. <i>American Journal of Medical Genetics Part A</i> , 1986, 24, 483-491.	2.4	30
39	On the Bumpy Road to the Dominant Mode. <i>Scandinavian Journal of Statistics</i> , 2010, 37, 612-631.	1.4	30
40	An MM Algorithm for Multicategory Vertex Discriminant Analysis. <i>Journal of Computational and Graphical Statistics</i> , 2008, 17, 527-544.	1.7	29
41	OpenMendel: a cooperative programming project for statistical genetics. <i>Human Genetics</i> , 2020, 139, 61-71.	3.8	29
42	Haplotyping Algorithms. , 1996, , 89-110.		29
43	Association Testing in a Linked Region Using Large Pedigrees. <i>American Journal of Human Genetics</i> , 2005, 76, 538-542.	6.2	25
44	A Poisson model for random multigraphs. <i>Bioinformatics</i> , 2010, 26, 2004-2011.	4.1	25
45	Exploring Population Structure with Admixture Models and Principal Component Analysis. <i>Methods in Molecular Biology</i> , 2020, 2090, 67-86.	0.9	23
46	Distance majorization and its applications. <i>Mathematical Programming</i> , 2014, 146, 409-436.	2.4	22
47	Computing Estimates in the Proportional Odds Model. <i>Annals of the Institute of Statistical Mathematics</i> , 2002, 54, 155-168.	0.8	19
48	Multicategory vertex discriminant analysis for high-dimensional data. <i>Annals of Applied Statistics</i> , 2010, 4, .	1.1	19
49	Penalized estimation of haplotype frequencies. <i>Bioinformatics</i> , 2008, 24, 1596-1602.	4.1	16
50	Fast spatial ancestry via flexible allele frequency surfaces. <i>Bioinformatics</i> , 2014, 30, 2915-2922.	4.1	16
51	An examination of school reopening strategies during the SARS-CoV-2 pandemic. <i>PLoS ONE</i> , 2021, 16, e0251242.	2.5	16
52	MM Algorithms for Variance Components Models. <i>Journal of Computational and Graphical Statistics</i> , 2019, 28, 350-361.	1.7	13
53	BioSimulator.jl: Stochastic simulation in Julia. <i>Computer Methods and Programs in Biomedicine</i> , 2018, 167, 23-35.	4.7	12
54	Accurate Stochastic Simulation via the Step Anticipation <i>Leaping (SAL) Algorithm. <i>Journal of Computational Biology</i> , 2009, 16, 1195-1208.	1.6	11

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55	Mendel-GPU: haplotyping and genotype imputation on graphics processing units. <i>Bioinformatics</i> , 2012, 28, 2979-2980.	4.1	11
56	Variance component models for X-linked QTLs. <i>Genetic Epidemiology</i> , 2006, 30, 380-383.	1.3	10
57	Fast Genome-Wide QTL Association Mapping on Pedigree and Population Data. <i>Genetic Epidemiology</i> , 2017, 41, 174-186.	1.3	10
58	Iterative hard thresholding in genome-wide association studies: Generalized linear models, prior weights, and double sparsity. <i>GigaScience</i> , 2020, 9, .	6.4	10
59	The Pedigree Trimming Problem. <i>Human Heredity</i> , 2004, 58, 108-111.	0.8	9
60	Computational Statistics and Optimization Theory at UCLA. <i>American Statistician</i> , 2004, 58, 9-11.	1.6	9
61	A heterozygote-homozygote test of Hardy-Weinberg equilibrium. <i>European Journal of Human Genetics</i> , 2009, 17, 1495-1500.	2.8	9
62	The MM Algorithm. <i>Springer Texts in Statistics</i> , 2013, , 185-219.	6.7	9
63	A dictionary model for haplotyping, genotype calling, and association testing. <i>Genetic Epidemiology</i> , 2007, 31, 672-683.	1.3	8
64	Modeling maternal-offspring gene-gene interactions: the extended-MFG test. <i>Genetic Epidemiology</i> , 2010, 34, 512-521.	1.3	8
65	Quantitative Trait Loci Association Mapping by Imputation of Strain Origins in Multifounder Crosses. <i>Genetics</i> , 2012, 190, 459-473.	2.9	8
66	Matrix completion discriminant analysis. <i>Computational Statistics and Data Analysis</i> , 2015, 92, 115-125.	1.2	8
67	A cross-population extended haplotype-based homozygosity score test to detect positive selection in genome-wide scans. <i>Statistics and Its Interface</i> , 2011, 4, 51-63.	0.3	8
68	Bayesian Gaussian Mixture Models for High-Density Genotyping Arrays. <i>Journal of the American Statistical Association</i> , 2008, 103, 89-100.	3.1	7
69	Mixed Effects Models for Quantitative Trait Loci Mapping With Inbred Strains. <i>Genetics</i> , 2008, 180, 1743-1761.	2.9	7
70	A Look at the Generalized Heron Problem through the Lens of Majorization-Minimization. <i>American Mathematical Monthly</i> , 2014, 121, 95.	0.3	7
71	A majorization-minimization algorithm for split feasibility problems. <i>Computational Optimization and Applications</i> , 2018, 71, 795-828.	1.6	7
72	Estimating Ethnic Admixture from Pedigree Data. <i>American Journal of Human Genetics</i> , 2008, 82, 748-755.	6.2	6

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73	Iterative hard thresholding for model selection in genome-wide association studies. <i>Genetic Epidemiology</i> , 2017, 41, 756-768.	1.3	6
74	Pooled analysis of radiation hybrids identifies loci for growth and drug action in mammalian cells. <i>Genome Research</i> , 2020, 30, 1458-1467.	5.5	6
75	Fast genome-wide pedigree quantitative trait loci analysis using MENDEL. <i>BMC Proceedings</i> , 2014, 8, S93.	1.6	5
76	Linear mixed models for association analysis of quantitative traits with next-generation sequencing data. <i>Genetic Epidemiology</i> , 2019, 43, 189-206.	1.3	5
77	Path following in the exact penalty method of convex programming. <i>Computational Optimization and Applications</i> , 2015, 61, 609-634.	1.6	4
78	Coupling bounds for approximating birth-death processes by truncation. <i>Statistics and Probability Letters</i> , 2016, 109, 30-38.	0.7	4
79	A fast data-driven method for genotype imputation, phasing and local ancestry inference: MendelImpute.jl. <i>Bioinformatics</i> , 2021, 37, 4756-4763.	4.1	4
80	A proximal distance algorithm for likelihood-based sparse covariance estimation. <i>Biometrika</i> , 2022, 109, 1047-1066.	2.4	4
81	Estimation for the Simple Linear Boolean Model. <i>Methodology and Computing in Applied Probability</i> , 2006, 8, 559-571.	1.2	3
82	Modern simulation utilities for genetic analysis. <i>BMC Bioinformatics</i> , 2021, 22, 228.	2.6	3
83	Efficiency of Protein Production from mRNA. <i>Journal of Statistical Theory and Practice</i> , 2008, 2, 173-182.	0.5	2
84	A fast procedure for calculating importance weights in bootstrap sampling. <i>Computational Statistics and Data Analysis</i> , 2011, 55, 26-33.	1.2	2
85	Hadamard's Determinant Inequality. <i>American Mathematical Monthly</i> , 2014, 121, 258.	0.3	2
86	A multivariate Bernoulli model to predict DNaseI hypersensitivity status from haplotype data. <i>Bioinformatics</i> , 2015, 31, 3514-3521.	4.1	2
87	Orthogonal Trace-Sum Maximization: Applications, Local Algorithms, and Global Optimality. <i>SIAM Journal on Matrix Analysis and Applications</i> , 2021, 42, 859-882.	1.4	2
88	Differential methods for assessing sensitivity in biological models. <i>PLoS Computational Biology</i> , 2022, 18, e1009598.	3.2	2
89	Sex differences in recombination fraction estimates and their effect on ordering of chromosome 11 markers. <i>Genetic Epidemiology</i> , 1986, 3, 185-190.	1.3	1
90	Stochastic simulation algorithms for Interacting Particle Systems. <i>PLoS ONE</i> , 2021, 16, e0247046.	2.5	1

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91	A Look at the Generalized Heron Problem through the Lens of Majorization-Minimization. American Mathematical Monthly, 2014, 121, 95-108.	0.3	1
92	Genomewide Motif Identification Using a Dictionary Model. , 0, , 157-172.		0
93	Feasibility and Duality. Springer Texts in Statistics, 2013, , 383-414.	6.7	0
94	Penalty and Barrier Methods. Springer Texts in Statistics, 2013, , 313-339.	6.7	0
95	Polya's Random Walk Theorem Revisited. American Mathematical Monthly, 2015, 122, 1005.	0.3	0
96	Genome-wide QTL and eQTL analyses using Mendel. BMC Proceedings, 2016, 10, 239-244.	1.6	0
97	Proximal Distance Algorithms: Theory and Practice. Journal of Machine Learning Research, 2019, 20, .	62.4	0