Kenneth L Lange

List of Publications by Year
in descending order

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	A proximal distance algorithm for likelihood-based sparse covariance estimation. Biometrika, 2022, 109, 1047-1066.	2.4	4
2	Differential methods for assessing sensitivity in biological models. PLoS Computational Biology, 2022, 18, e1009598.	3.2	2
3	Orthogonal Trace-Sum Maximization: Applications, Local Algorithms, and Global Optimality. SIAM Journal on Matrix Analysis and Applications, 2021, 42, 859-882.	1.4	2
4	Stochastic simulation algorithms for Interacting Particle Systems. PLoS ONE, 2021, 16, e0247046.	2.5	1
5	An examination of school reopening strategies during the SARS-CoV-2 pandemic. PLoS ONE, 2021, 16, e0251242.	2.5	16
6	Modern simulation utilities for genetic analysis. BMC Bioinformatics, 2021, 22, 228.	2.6	3
7	A fast data-driven method for genotype imputation, phasing and local ancestry inference: MendelImpute.jl. Bioinformatics, 2021, 37, 4756-4763.	4.1	4
8	OpenMendel: a cooperative programming project for statistical genetics. Human Genetics, 2020, 139, 61-71.	3.8	29
9	Pooled analysis of radiation hybrids identifies loci for growth and drug action in mammalian cells. Genome Research, 2020, 30, 1458-1467.	5.5	6
10	Iterative hard thresholding in genome-wide association studies: Generalized linear models, prior weights, and double sparsity. GigaScience, 2020, 9, .	6.4	10
11	Exploring Population Structure with Admixture Models and Principal Component Analysis. Methods in Molecular Biology, 2020, 2090, 67-86.	0.9	23
12	Linear mixed models for association analysis of quantitative traits with next‐generation sequencing data. Genetic Epidemiology, 2019, 43, 189-206.	1.3	5
13	MM Algorithms for Variance Components Models. Journal of Computational and Graphical Statistics, 2019, 28, 350-361.	1.7	13
14	Proximal Distance Algorithms: Theory and Practice. Journal of Machine Learning Research, 2019, 20, .	62.4	0
15	BioSimulator.jl: Stochastic simulation in Julia. Computer Methods and Programs in Biomedicine, 2018, 167, 23-35.	4.7	12
16	A majorization–minimization algorithm for split feasibility problems. Computational Optimization and Applications, 2018, 71, 795-828.	1.6	7
17	Fast Genome‐Wide QTL Association Mapping on Pedigree and Population Data. Genetic Epidemiology, 2017, 41, 174-186.	1.3	10
18	Iterative hard thresholding for model selection in genome‐wide association studies. Genetic Epidemiology, 2017, 41, 756-768.	1.3	6

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19	Genome-wide QTL and eQTL analyses using Mendel. BMC Proceedings, 2016, 10, 239-244.	1.6	0
20	Coupling bounds for approximating birth–death processes by truncation. Statistics and Probability Letters, 2016, 109, 30-38.	0.7	4
21	Modeling of Cancer Stem Cell State Transitions Predicts Therapeutic Response. PLoS ONE, 2015, 10, e0135797.	2.5	34
22	Splitting Methods for Convex Clustering. Journal of Computational and Graphical Statistics, 2015, 24, 994-1013.	1.7	131
23	Polya's Random Walk Theorem Revisited. American Mathematical Monthly, 2015, 122, 1005.	0.3	0
24	Path following in the exact penalty method of convex programming. Computational Optimization and Applications, 2015, 61, 609-634.	1.6	4
25	Convex Clustering: An Attractive Alternative to Hierarchical Clustering. PLoS Computational Biology, 2015, 11, e1004228.	3.2	34
26	Matrix completion discriminant analysis. Computational Statistics and Data Analysis, 2015, 92, 115-125.	1.2	8
27	A multivariate Bernoulli model to predict DNaseI hypersensitivity status from haplotype data. Bioinformatics, 2015, 31, 3514-3521.	4.1	2
28	Distance majorization and its applications. Mathematical Programming, 2014, 146, 409-436.	2.4	22
29	MM algorithms for geometric and signomial programming. Mathematical Programming, 2014, 143, 339-356.	2.4	35
30	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
31	A Brief Survey of Modern Optimization for Statisticians. International Statistical Review, 2014, 82, 46-70.	1.9	31
32	Hadamard's Determinant Inequality. American Mathematical Monthly, 2014, 121, 258.	0.3	2
33	A Look at the Generalized Heron Problem through the Lens of Majorization-Minimization. American Mathematical Monthly, 2014, 121, 95.	0.3	7
34	Stable estimation of a covariance matrix guided by nuclear norm penalties. Computational Statistics and Data Analysis, 2014, 80, 117-128.	1.2	31
35	Fast genome-wide pedigree quantitative trait loci analysis using MENDEL. BMC Proceedings, 2014, 8, S93.	1.6	5
36	Fast spatial ancestry via flexible allele frequency surfaces. Bioinformatics, 2014, 30, 2915-2922.	4.1	16

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37	A Look at the Generalized Heron Problem through the Lens of Majorization-Minimization. American Mathematical Monthly, 2014, 121, 95-108.	0.3	1
38	Imaging genetics via sparse canonical correlation analysis. , 2013, 2013, 740-743.		40
39	Genotype imputation via matrix completion. Genome Research, 2013, 23, 509-518.	5.5	50
40	The MM Algorithm. Springer Texts in Statistics, 2013, , 185-219.	6.7	9
41	Feasibility and Duality. Springer Texts in Statistics, 2013, , 383-414.	6.7	0
42	Penalty and Barrier Methods. Springer Texts in Statistics, 2013, , 313-339.	6.7	0
43	Mendel: the Swiss army knife of genetic analysis programs. Bioinformatics, 2013, 29, 1568-1570.	4.1	104
44	Mendel-GPU: haplotyping and genotype imputation on graphics processing units. Bioinformatics, 2012, 28, 2979-2980.	4.1	11
45	Quantitative Trait Loci Association Mapping by Imputation of Strain Origins in Multifounder Crosses. Genetics, 2012, 190, 459-473.	2.9	8
46	A quasi-Newton acceleration for high-dimensional optimization algorithms. Statistics and Computing, 2011, 21, 261-273.	1.5	127
47	Linkage analysis without defined pedigrees. Genetic Epidemiology, 2011, 35, 360-370.	1.3	40
48	Stability selection for genome-wide association. Genetic Epidemiology, 2011, 35, 722-728.	1.3	51
49	A fast procedure for calculating importance weights in bootstrap sampling. Computational Statistics and Data Analysis, 2011, 55, 26-33.	1.2	2
50	A cross-population extended haplotype-based homozygosity score test to detect positive selection in genome-wide scans. Statistics and Its Interface, 2011, 4, 51-63.	0.3	8
51	Multicategory vertex discriminant analysis for high-dimensional data. Annals of Applied Statistics, 2010, 4, .	1.1	19
52	The MM Alternative to EM. Statistical Science, 2010, 25, .	2.8	68
53	Graphics Processing Units and High-Dimensional Optimization. Statistical Science, 2010, 25, 311-324.	2.8	31
54	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

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55	Modeling maternal–offspring gene–gene interactions: the extended–MFG test. Genetic Epidemiology, 2010, 34, 512-521.	1.3	8
56	On the Bumpy Road to the Dominant Mode. Scandinavian Journal of Statistics, 2010, 37, 612-631.	1.4	30
57	A Poisson model for random multigraphs. Bioinformatics, 2010, 26, 2004-2011.	4.1	25
58	Association screening of common and rare genetic variants by penalized regression. Bioinformatics, 2010, 26, 2375-2382.	4.1	120
59	MM Algorithms for Some Discrete Multivariate Distributions. Journal of Computational and Graphical Statistics, 2010, 19, 645-665.	1.7	48
60	Numerical Analysis for Statisticians. Statistics and Computing, 2010, , .	0.2	202
61	Accurate Stochastic Simulation via the Step Anticipation τ-Leaping (SAL) Algorithm. Journal of Computational Biology, 2009, 16, 1195-1208.	1.6	11
62	Genome-wide association analysis by lasso penalized logistic regression. Bioinformatics, 2009, 25, 714-721.	4.1	639
63	Fast model-based estimation of ancestry in unrelated individuals. Genome Research, 2009, 19, 1655-1664.	5.5	6,588
64	A heterozygote–homozygote test of Hardy–Weinberg equilibrium. European Journal of Human Genetics, 2009, 17, 1495-1500.	2.8	9
65	Estimating Ethnic Admixture from Pedigree Data. American Journal of Human Genetics, 2008, 82, 748-755.	6.2	6
66	Bayesian Gaussian Mixture Models for High-Density Genotyping Arrays. Journal of the American Statistical Association, 2008, 103, 89-100.	3.1	7
67	Penalized estimation of haplotype frequencies. Bioinformatics, 2008, 24, 1596-1602.	4.1	16
68	Efficiency of Protein Production from mRNA. Journal of Statistical Theory and Practice, 2008, 2, 173-182.	0.5	2
69	Mixed Effects Models for Quantitative Trait Loci Mapping With Inbred Strains. Genetics, 2008, 180, 1743-1761.	2.9	7
70	An MM Algorithm for Multicategory Vertex Discriminant Analysis. Journal of Computational and Graphical Statistics, 2008, 17, 527-544.	1.7	29
71	Coordinate descent algorithms for lasso penalized regression. Annals of Applied Statistics, 2008, 2, .	1.1	533
72	A dictionary model for haplotyping, genotype calling, and association testing. Genetic Epidemiology, 2007, 31, 672-683.	1.3	8

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73	Estimation for the Simple Linear Boolean Model. Methodology and Computing in Applied Probability, 2006, 8, 559-571.	1.2	3
74	Variance component models for X-linked QTLs. Genetic Epidemiology, 2006, 30, 380-383.	1.3	10
75	Association testing with Mendel. Genetic Epidemiology, 2005, 29, 36-50.	1.3	57
76	Association Testing in a Linked Region Using Large Pedigrees. American Journal of Human Genetics, 2005, 76, 538-542.	6.2	25
77	The Pedigree Trimming Problem. Human Heredity, 2004, 58, 108-111.	0.8	9
78	Computational Statistics and Optimization Theory at UCLA. American Statistician, 2004, 58, 9-11.	1.6	9
79	A Tutorial on MM Algorithms. American Statistician, 2004, 58, 30-37.	1.6	1,257
80	Mathematical and Statistical Methods for Genetic Analysis. Statistics in the Health Sciences, 2002, , .	0.2	221
81	Computing Estimates in the Proportional Odds Model. Annals of the Institute of Statistical Mathematics, 2002, 54, 155-168.	0.8	19
82	Detection and Integration of Genotyping Errors in Statistical Genetics. American Journal of Human Genetics, 2002, 70, 496-508.	6.2	317
83	Optimization Transfer Using Surrogate Objective Functions. Journal of Computational and Graphical Statistics, 2000, 9, 1-20.	1.7	396
84	Gamete-Competition Models. American Journal of Human Genetics, 2000, 66, 1168-1172.	6.2	53
85	EM algorithms without missing data. Statistical Methods in Medical Research, 1997, 6, 38-54.	1.5	68
86	Haplotyping Algorithms. , 1996, , 89-110.		29
87	Normal/Independent Distributions and Their Applications in Robust Regression. Journal of Computational and Graphical Statistics, 1993, 2, 175-198.	1.7	181
88	Programs for pedigree analysis: Mendel, Fisher, and dGene. Genetic Epidemiology, 1988, 5, 471-472.	1.3	562
89	Localization of an ataxia-telangiectasia gene to chromosome 11q22â€"23. Nature, 1988, 336, 577-580.	27.8	677
90	A Theoretical Study of Some Maximum Likelihood Algorithms for Emission and Transmission Tomography. IEEE Transactions on Medical Imaging, 1987, 6, 106-114.	8.9	274

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91	Cohabitation, convergence, and environmental covariances. American Journal of Medical Genetics Part A, 1986, 24, 483-491.	2.4	30
92	Sex differences in recombination fraction estimates and their effect on ordering of chromosome 11 markers. Genetic Epidemiology, 1986, 3, 185-190.	1.3	1
93	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
94	A maximum likelihood test of the two locus model for coeliac disease. American Journal of Medical Genetics Part A, 1982, 12, 75-82.	2.4	33
95	Central limit theorems of pedigrees. Journal of Mathematical Biology, 1978, 6, 59-66.	1.9	64
96	Extensions to pedigree analysis III. Variance components by the scoring method. Annals of Human Genetics, 1976, 39, 485-491.	0.8	409
97	Genomewide Motif Identification Using a Dictionary Model. , 0, , 157-172.		0