

Ola HÅssjer

List of Publications by Year in descending order

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Version: 2024-02-01

92
papers

1,220
citations

471509

17
h-index

454955

30
g-index

94
all docs

94
docs citations

94
times ranked

1058
citing authors

#	ARTICLE	IF	CITATIONS
1	Generalized S-Estimators. Journal of the American Statistical Association, 1994, 89, 1271-1281.	3.1	93
2	Generalizing univariate signed rank statistics for testing and estimating a multivariate location parameter. Journal of Nonparametric Statistics, 1995, 4, 293-308.	0.9	83
3	Rank-Based Estimates in the Linear Model with High Breakdown Point. Journal of the American Statistical Association, 1994, 89, 149-158.	3.1	55
4	Fast kriging of large data sets with Gaussian Markov random fields. Computational Statistics and Data Analysis, 2008, 52, 2331-2349.	1.2	55
5	Do estimates of contemporary effective population size tell us what we want to know?. Molecular Ecology, 2019, 28, 1904-1918.	3.9	53
6	On the optimality of S-estimators. Statistics and Probability Letters, 1992, 14, 413-419.	0.7	51
7	The Least Trimmed Differences Regression Estimator and Alternatives. Journal of the American Statistical Association, 2000, 95, 853-864.	3.1	50
8	LOCALLY WEIGHTED LEAST SQUARES KERNEL REGRESSION AND STATISTICAL EVALUATION OF LIDAR MEASUREMENTS. Environmetrics, 1996, 7, 401-416.	1.4	49
9	Samples from subdivided populations yield biased estimates of effective size that overestimate the rate of loss of genetic variation. Molecular Ecology Resources, 2014, 14, 87-99.	4.8	46
10	Rank-Based Estimates in the Linear Model with High Breakdown Point. Journal of the American Statistical Association, 1994, 89, 149.	3.1	45
11	The interaction between smoking and HLA genes in multiple sclerosis: replication and refinement. European Journal of Epidemiology, 2017, 32, 909-919.	5.7	45
12	Organic solvents and MS susceptibility. Neurology, 2018, 91, e455-e462.	1.1	37
13	Metapopulation effective size and conservation genetic goals for the Fennoscandian wolf (<i>Canis</i>) Tj ETQq1 1 0.784314 rgBT /Overloc 2.6 33	2.6	33
14	Generalized S-Estimators. Journal of the American Statistical Association, 1994, 89, 1271.	3.1	25
15	Methodological study of affine transformations of gene expression data with proposed robust non-parametric multi-dimensional normalization method. BMC Bioinformatics, 2006, 7, 100.	2.6	22
16	On the coefficient of determination for mixed regression models. Journal of Statistical Planning and Inference, 2008, 138, 3022-3038.	0.6	22
17	The relationship between nightmares, depression and suicide. Sleep Medicine, 2021, 77, 1-6.	1.6	18
18	Asymptotics for the Transformation Kernel Density Estimator. Annals of Statistics, 1995, 23, 1198.	2.6	17

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19	A general method for linkage disequilibrium correction for multipoint linkage and association. <i>Genetic Epidemiology</i> , 2008, 32, 647-657.	1.3	17
20	Insomnia in the context of short sleep increases suicide risk. <i>Sleep</i> , 2021, 44, .	1.1	17
21	A new general analytical approach for modeling patterns of genetic differentiation and effective size of subdivided populations over time. <i>Mathematical Biosciences</i> , 2014, 258, 113-133.	1.9	16
22	Interplay between alcohol, smoking and HLA genes in RA aetiology. <i>RMD Open</i> , 2019, 5, e000893.	3.8	16
23	Exact computation of the least trimmed squares estimate in simple linear regression. <i>Computational Statistics and Data Analysis</i> , 1995, 19, 265-282.	1.2	15
24	Effective sizes and time to migration "drift equilibrium in geographically subdivided populations. <i>Theoretical Population Biology</i> , 2016, 112, 139-156.	1.1	15
25	Metapopulation inbreeding dynamics, effective size and subpopulation differentiation "A general analytical approach for diploid organisms. <i>Theoretical Population Biology</i> , 2015, 102, 40-59.	1.1	13
26	Assessing accuracy in linkage analysis by means of confidence regions. <i>Genetic Epidemiology</i> , 2003, 25, 59-72.	1.3	12
27	Determining Inheritance Distributions via Stochastic Penetrances. <i>Journal of the American Statistical Association</i> , 2003, 98, 1035-1051.	3.1	12
28	Non-parametric and parametric bootstrap techniques for age-to-age development factor methods in stochastic claims reserving. <i>Scandinavian Actuarial Journal</i> , 2009, 2009, 306-331.	1.7	12
29	Quasi equilibrium, variance effective size and fixation index for populations with substructure. <i>Journal of Mathematical Biology</i> , 2014, 69, 1057-1128.	1.9	11
30	A generalized linear model with smoothing effects for claims reserving. <i>Insurance: Mathematics and Economics</i> , 2011, 49, 27-37.	1.2	10
31	Whole-genome resequencing confirms reproductive isolation between sympatric demes of brown trout (<i>Salmo trutta</i>) detected with allozymes. <i>Molecular Ecology</i> , 2022, 31, 498-511.	3.9	10
32	Asymptotic estimation theory of multipoint linkage analysis under perfect marker information. <i>Annals of Statistics</i> , 2003, 31, 1075.	2.6	9
33	Quasi equilibrium approximations of the fixation index under neutrality: The finite and infinite island models. <i>Theoretical Population Biology</i> , 2013, 84, 9-24.	1.1	9
34	Pricing catastrophe risk in life (re)insurance. <i>Scandinavian Actuarial Journal</i> , 2014, 2014, 352-367.	1.7	9
35	Multivariate time series modeling, estimation and prediction of mortalities. <i>Insurance: Mathematics and Economics</i> , 2015, 65, 156-171.	1.2	9
36	On the asymptotic variance of the continuous-time kernel density estimator. <i>Statistics and Probability Letters</i> , 1999, 44, 97-106.	0.7	8

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37	Short- and long-term mortality following hypnotic use. <i>Journal of Sleep Research</i> , 2020, 29, e13061.	3.2	8
38	Using statistical methods to model the fine-tuning of molecular machines and systems. <i>Journal of Theoretical Biology</i> , 2020, 501, 110352.	1.7	8
39	Conditional likelihood score functions for mixed models in linkage analysis. <i>Biostatistics</i> , 2005, 6, 313-332.	1.5	7
40	Estimating the parameters of the operational model of pharmacological agonism. <i>Statistics in Medicine</i> , 2006, 25, 2932-2945.	1.6	7
41	The genetic interacting landscape of 63 candidate genes in Major Depressive Disorder: an explorative study. <i>BioData Mining</i> , 2014, 7, 19.	4.0	7
42	On the eigenvalue effective size of structured populations. <i>Journal of Mathematical Biology</i> , 2015, 71, 595-646.	1.9	7
43	<scpgesp>: A computer program for modelling genetic effective population size, inbreeding and divergence in substructured populations. <i>Molecular Ecology Resources</i> , 2017, 17, 1378-1384.	4.8	7
44	Incomplete generalized L-statistics. <i>Annals of Statistics</i> , 1996, 24, 2631.	2.6	6
45	Using Importance Sampling to Improve Simulation in Linkage Analysis. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2004, 3, 1-22.	0.6	6
46	Information and effective number of meioses in linkage analysis. <i>Journal of Mathematical Biology</i> , 2005, 50, 208-232.	1.9	6
47	The influence of human leukocyte antigen-DRB1*15:01 and its interaction with smoking in MS development is dependent on DQA1*01:01 status. <i>Multiple Sclerosis Journal</i> , 2020, 26, 1638-1646.	3.0	6
48	On Computation of p-Values in Parametric Linkage Analysis. <i>Human Heredity</i> , 2004, 57, 207-219.	0.8	5
49	Combined Association and Linkage Analysis for General Pedigrees and Genetic Models. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2005, 4, Article11.	0.6	5
50	Improving the calculation of statistical significance in genome-wide scans. <i>Biostatistics</i> , 2005, 6, 520-538.	1.5	5
51	Modeling the effect of inbreeding among founders in linkage analysis. <i>Theoretical Population Biology</i> , 2006, 70, 146-163.	1.1	5
52	Spatial Autocorrelation for Subdivided Populations with Invariant Migration Schemes. <i>Methodology and Computing in Applied Probability</i> , 2014, 16, 777-810.	1.2	5
53	Equilibrium distributions and simulation methods for age structured populations. <i>Mathematical Biosciences</i> , 2015, 268, 45-51.	1.9	5
54	A monoecious and diploid Moran model of random mating. <i>Journal of Theoretical Biology</i> , 2016, 394, 182-196.	1.7	5

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55	Exact Markov chain and approximate diffusion solution for haploid genetic drift with one-way mutation. <i>Mathematical Biosciences</i> , 2016, 272, 100-112.	1.9	5
56	Nonlinearly Perturbed Birth-Death-Type Models. <i>Springer Proceedings in Mathematics and Statistics</i> , 2018, , 189-244.	0.2	5
57	Local Polynomial Variance Function Estimation. <i>SSRN Electronic Journal</i> , 0, , .	0.4	5
58	The Least Trimmed Differences Regression Estimator and Alternatives. <i>Journal of the American Statistical Association</i> , 2000, 95, 853.	3.1	5
59	Asymptotic bias and variance for a general class of varying bandwidth density estimators. <i>Probability Theory and Related Fields</i> , 1996, 105, 159-192.	1.8	4
60	Fine Mapping of Disease Genes Using Tagging SNPs. <i>Annals of Human Genetics</i> , 2007, 71, 815-827.	0.8	4
61	Characteristics of the variance effective population size over time using an age structured model with variable size. <i>Theoretical Population Biology</i> , 2013, 90, 91-103.	1.1	4
62	Phase-Type Distribution Approximations of the Waiting Time Until Coordinated Mutations Get Fixed in a Population. <i>Springer Proceedings in Mathematics and Statistics</i> , 2018, , 245-313.	0.2	4
63	Is cosmological tuning fine or coarse?. <i>Journal of Cosmology and Astroparticle Physics</i> , 2021, 2021, 020.	5.4	4
64	A Single-Couple Human Origin is Possible. <i>BIO-complexity</i> , 2019, 2019, .	1.0	4
65	A test for singularity. <i>Statistics and Probability Letters</i> , 1998, 40, 215-226.	0.7	3
66	A General Statistical Framework for Multistage Designs. <i>Scandinavian Journal of Statistics</i> , 2012, 39, 131-152.	1.4	3
67	Estimation of the variance effective population size in age structured populations. <i>Theoretical Population Biology</i> , 2015, 101, 9-23.	1.1	3
68	Local fluctuations of genetic processes defined on two time scales, with applications to effective size estimation. <i>Theoretical Population Biology</i> , 2020, 131, 79-99.	1.1	3
69	On the waiting time until coordinated mutations get fixed in regulatory sequences. <i>Journal of Theoretical Biology</i> , 2021, 524, 110657.	1.7	3
70	Spectral decomposition of score functions in linkage analysis. <i>Bernoulli</i> , 2005, 11, .	1.3	3
71	Delta method for long-range dependent observations. <i>Journal of Nonparametric Statistics</i> , 1995, 5, 75-82.	0.9	2
72	A Shot-Noise Model for Paper Fibres with Non-uniform Random Orientations. <i>Scandinavian Journal of Statistics</i> , 2005, 32, 351-363.	1.4	2

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73	Strategies for Conditional Two-Locus Nonparametric Linkage Analysis. <i>Human Heredity</i> , 2008, 66, 138-156.	0.8	2
74	Assessing Individual Unexplained Variation in Non-Life Insurance. <i>ASTIN Bulletin</i> , 2009, 39, 249-273.	1.0	2
75	Utilizing identity-by-descent probabilities for genetic fine-mapping in population based samples, via spatial smoothing of haplotype effects. <i>Computational Statistics and Data Analysis</i> , 2009, 53, 1802-1817.	1.2	2
76	A Stochastic EM Type Algorithm for Parameter Estimation in Models with Continuous Outcomes, under Complex Ascertainment. <i>International Journal of Biostatistics</i> , 2010, 6, Article 23.	0.7	2
77	Efficient ascertainment schemes for maximum likelihood estimation. <i>Journal of Statistical Planning and Inference</i> , 2010, 140, 2078-2088.	0.6	2
78	A significant risk locus on 19q13 for bipolar disorder identified using a combined genome-wide linkage and copy number variation analysis. <i>BioData Mining</i> , 2015, 8, 42.	4.0	2
79	A General Framework for and New Normalization of Attributable Proportion. <i>Epidemiologic Methods</i> , 2017, 6, .	0.9	2
80	Novel bounds for causal effects based on sensitivity parameters on the risk difference scale. <i>Journal of Causal Inference</i> , 2021, 9, 190-210.	1.2	2
81	Analysis of the Stochasticity of Mortality Using Variance Decomposition. <i>Diabetes Therapy</i> , 2014, , 199-222.	2.5	2
82	Sharp lower and upper bounds for the covariance of bounded random variables. <i>Statistics and Probability Letters</i> , 2022, 182, 109323.	0.7	2
83	Recursive U-quantiles. <i>Sequential Analysis</i> , 1997, 16, 119-129.	0.5	1
84	Dimension spectra for multifractal measures with connections to nonparametric density estimation. <i>Journal of Nonparametric Statistics</i> , 2001, 13, 351-395.	0.9	1
85	Ancestral Recombination Graphs under Non-Random Ascertainment, with Applications to Gene Mapping. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2009, 8, 1-44.	0.6	1
86	Dynamical Systems and Fitness Maximization in Evolutionary Biology. , 2021, , 1-72.		1
87	Asymptotic bias and variance for a general class of varying bandwidth density estimators. <i>Probability Theory and Related Fields</i> , 1996, 105, 159-192.	1.8	1
88	A spatio-temporal point process model for particle growth. <i>Journal of Applied Probability</i> , 2019, 56, 23-38.	0.7	0
89	Dynamical Systems and Fitness Maximization in Evolutionary Biology. , 2021, , 2097-2169.		0
90	Quantifying and estimating additive measures of interaction from case-control data. <i>Modern Stochastics: Theory and Applications</i> , 2017, 4, 109-125.	0.4	0

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91	Continuous Approximations of Discrete Choice Models Using Point Process Theory. Springer Proceedings in Mathematics and Statistics, 2018, , 413-435.	0.2	0
92	Dmitrii S. Silvestrov. Springer Proceedings in Mathematics and Statistics, 2018, , 1-4.	0.2	0