

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	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
2	Sharp lower and upper bounds for the covariance of bounded random variables. <i>Statistics and Probability Letters</i> , 2022, 182, 109323.	0.7	2
3	Insomnia in the context of short sleep increases suicide risk. <i>Sleep</i> , 2021, 44, .	1.1	17
4	The relationship between nightmares, depression and suicide. <i>Sleep Medicine</i> , 2021, 77, 1-6.	1.6	18
5	Dynamical Systems and Fitness Maximization in Evolutionary Biology. , 2021, , 1-72.		1
6	Dynamical Systems and Fitness Maximization in Evolutionary Biology. , 2021, , 2097-2169.		0
7	Is cosmological tuning fine or coarse?. <i>Journal of Cosmology and Astroparticle Physics</i> , 2021, 2021, 020.	5.4	4
8	On the waiting time until coordinated mutations get fixed in regulatory sequences. <i>Journal of Theoretical Biology</i> , 2021, 524, 110657.	1.7	3
9	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
10	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
11	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
12	Short- and long-term mortality following hypnotic use. <i>Journal of Sleep Research</i> , 2020, 29, e13061.	3.2	8
13	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
14	Do estimates of contemporary effective population size tell us what we want to know?. <i>Molecular Ecology</i> , 2019, 28, 1904-1918.	3.9	53
15	Interplay between alcohol, smoking and HLA genes in RA aetiology. <i>RMD Open</i> , 2019, 5, e000893.	3.8	16
16	A spatio-temporal point process model for particle growth. <i>Journal of Applied Probability</i> , 2019, 56, 23-38.	0.7	0
17	A Single-Couple Human Origin is Possible. <i>BIO-complexity</i> , 2019, 2019, .	1.0	4
18	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

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19	Organic solvents and MS susceptibility. <i>Neurology</i> , 2018, 91, e455-e462.	1.1	37
20	Nonlinearly Perturbed Birth-Death-Type Models. <i>Springer Proceedings in Mathematics and Statistics</i> , 2018, , 189-244.	0.2	5
21	Continuous Approximations of Discrete Choice Models Using Point Process Theory. <i>Springer Proceedings in Mathematics and Statistics</i> , 2018, , 413-435.	0.2	0
22	Dmitrii S. Silvestrov. <i>Springer Proceedings in Mathematics and Statistics</i> , 2018, , 1-4.	0.2	0
23	<scp>gesp</scp>: 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
24	The interaction between smoking and HLA genes in multiple sclerosis: replication and refinement. <i>European Journal of Epidemiology</i> , 2017, 32, 909-919.	5.7	45
25	A General Framework for and New Normalization of Attributable Proportion. <i>Epidemiologic Methods</i> , 2017, 6, .	0.9	2
26	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
27	A monoecious and diploid Moran model of random mating. <i>Journal of Theoretical Biology</i> , 2016, 394, 182-196.	1.7	5
28	Effective sizes and time to migrationâ€œdrift equilibrium in geographically subdivided populations. <i>Theoretical Population Biology</i> , 2016, 112, 139-156.	1.1	15
29	Metapopulation effective size and conservation genetic goals for the Fennoscandian wolf (<i>Canis</i>) Tj ETQq1 1 0.784314 rgBT /Overloc 1	2.6	33
30	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
31	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
32	On the eigenvalue effective size of structured populations. <i>Journal of Mathematical Biology</i> , 2015, 71, 595-646.	1.9	7
33	Estimation of the variance effective population size in age structured populations. <i>Theoretical Population Biology</i> , 2015, 101, 9-23.	1.1	3
34	Metapopulation inbreeding dynamics, effective size and subpopulation differentiationâ€œA general analytical approach for diploid organisms. <i>Theoretical Population Biology</i> , 2015, 102, 40-59.	1.1	13
35	Multivariate time series modeling, estimation and prediction of mortalities. <i>Insurance: Mathematics and Economics</i> , 2015, 65, 156-171.	1.2	9
36	Equilibrium distributions and simulation methods for age structured populations. <i>Mathematical Biosciences</i> , 2015, 268, 45-51.	1.9	5

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37	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
38	Samples from subdivided populations yield biased estimates of effective size that overestimate the rate of loss of genetic variation. <i>Molecular Ecology Resources</i> , 2014, 14, 87-99.	4.8	46
39	Spatial Autocorrelation for Subdivided Populations with Invariant Migration Schemes. <i>Methodology and Computing in Applied Probability</i> , 2014, 16, 777-810.	1.2	5
40	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
41	Pricing catastrophe risk in life (re)insurance. <i>Scandinavian Actuarial Journal</i> , 2014, 2014, 352-367.	1.7	9
42	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
43	Analysis of the Stochasticity of Mortality Using Variance Decomposition. <i>Diabetes Therapy</i> , 2014, , 199-222.	2.5	2
44	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
45	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
46	A General Statistical Framework for Multistage Designs. <i>Scandinavian Journal of Statistics</i> , 2012, 39, 131-152.	1.4	3
47	A generalized linear model with smoothing effects for claims reserving. <i>Insurance: Mathematics and Economics</i> , 2011, 49, 27-37.	1.2	10
48	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
49	Efficient ascertainment schemes for maximum likelihood estimation. <i>Journal of Statistical Planning and Inference</i> , 2010, 140, 2078-2088.	0.6	2
50	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
51	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
52	Assessing Individual Unexplained Variation in Non-Life Insurance. <i>ASTIN Bulletin</i> , 2009, 39, 249-273.	1.0	2
53	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
54	A general method for linkage disequilibrium correction for multipoint linkage and association. <i>Genetic Epidemiology</i> , 2008, 32, 647-657.	1.3	17

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55	On the coefficient of determination for mixed regression models. <i>Journal of Statistical Planning and Inference</i> , 2008, 138, 3022-3038.	0.6	22
56	Fast kriging of large data sets with Gaussian Markov random fields. <i>Computational Statistics and Data Analysis</i> , 2008, 52, 2331-2349.	1.2	55
57	Strategies for Conditional Two-Locus Nonparametric Linkage Analysis. <i>Human Heredity</i> , 2008, 66, 138-156.	0.8	2
58	Fine Mapping of Disease Genes Using Tagging SNPs. <i>Annals of Human Genetics</i> , 2007, 71, 815-827.	0.8	4
59	Modeling the effect of inbreeding among founders in linkage analysis. <i>Theoretical Population Biology</i> , 2006, 70, 146-163.	1.1	5
60	Estimating the parameters of the operational model of pharmacological agonism. <i>Statistics in Medicine</i> , 2006, 25, 2932-2945.	1.6	7
61	Methodological study of affine transformations of gene expression data with proposed robust non-parametric multi-dimensional normalization method. <i>BMC Bioinformatics</i> , 2006, 7, 100.	2.6	22
62	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
63	Information and effective number of meioses in linkage analysis. <i>Journal of Mathematical Biology</i> , 2005, 50, 208-232.	1.9	6
64	Conditional likelihood score functions for mixed models in linkage analysis. <i>Biostatistics</i> , 2005, 6, 313-332.	1.5	7
65	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
66	Improving the calculation of statistical significance in genome-wide scans. <i>Biostatistics</i> , 2005, 6, 520-538.	1.5	5
67	Spectral decomposition of score functions in linkage analysis. <i>Bernoulli</i> , 2005, 11, .	1.3	3
68	On Computation of p-Values in Parametric Linkage Analysis. <i>Human Heredity</i> , 2004, 57, 207-219.	0.8	5
69	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
70	Assessing accuracy in linkage analysis by means of confidence regions. <i>Genetic Epidemiology</i> , 2003, 25, 59-72.	1.3	12
71	Determining Inheritance Distributions via Stochastic Penetrances. <i>Journal of the American Statistical Association</i> , 2003, 98, 1035-1051.	3.1	12
72	Asymptotic estimation theory of multipoint linkage analysis under perfect marker information. <i>Annals of Statistics</i> , 2003, 31, 1075.	2.6	9

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73	Dimension spectra for multifractal measures with connections to nonparametric density estimation— Journal of Nonparametric Statistics, 2001, 13, 351-395.	0.9	1
74	The Least Trimmed Differences Regression Estimator and Alternatives. Journal of the American Statistical Association, 2000, 95, 853-864.	3.1	50
75	The Least Trimmed Differences Regression Estimator and Alternatives. Journal of the American Statistical Association, 2000, 95, 853.	3.1	5
76	On the asymptotic variance of the continuous-time kernel density estimator. Statistics and Probability Letters, 1999, 44, 97-106.	0.7	8
77	A test for singularity. Statistics and Probability Letters, 1998, 40, 215-226.	0.7	3
78	Recursive U-quantiles. Sequential Analysis, 1997, 16, 119-129.	0.5	1
79	Incomplete generalized L-statistics. Annals of Statistics, 1996, 24, 2631.	2.6	6
80	LOCALLY WEIGHTED LEAST SQUARES KERNEL REGRESSION AND STATISTICAL EVALUATION OF LIDAR MEASUREMENTS. Environmetrics, 1996, 7, 401-416.	1.4	49
81	Asymptotic bias and variance for a general class of varying bandwidth density estimators. Probability Theory and Related Fields, 1996, 105, 159-192.	1.8	4
82	Asymptotic bias and variance for a general class of varying bandwidth density estimators. Probability Theory and Related Fields, 1996, 105, 159-192.	1.8	1
83	Exact computation of the least trimmed squares estimate in simple linear regression. Computational Statistics and Data Analysis, 1995, 19, 265-282.	1.2	15
84	Asymptotics for the Transformation Kernel Density Estimator. Annals of Statistics, 1995, 23, 1198.	2.6	17
85	Generalizing univariate signed rank statistics for testing and estimating a multivariate location parameter. Journal of Nonparametric Statistics, 1995, 4, 293-308.	0.9	83
86	Delta method for long-range dependent observations. Journal of Nonparametric Statistics, 1995, 5, 75-82.	0.9	2
87	Rank-Based Estimates in the Linear Model with High Breakdown Point. Journal of the American Statistical Association, 1994, 89, 149-158.	3.1	55
88	Generalized S-Estimators. Journal of the American Statistical Association, 1994, 89, 1271-1281.	3.1	93
89	Rank-Based Estimates in the Linear Model with High Breakdown Point. Journal of the American Statistical Association, 1994, 89, 149.	3.1	45
90	Generalized S-Estimators. Journal of the American Statistical Association, 1994, 89, 1271.	3.1	25

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91	On the optimality of S-estimators. <i>Statistics and Probability Letters</i> , 1992, 14, 413-419.	0.7	51
92	Local Polynomial Variance Function Estimation. <i>SSRN Electronic Journal</i> , 0, , .	0.4	5