

# Andreas Futschik

## List of Publications by Year in descending order

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Version: 2024-02-01

72  
papers

3,533  
citations

257450

24  
h-index

155660

55  
g-index

80  
all docs

80  
docs citations

80  
times ranked

5712  
citing authors

#	ARTICLE	IF	CITATIONS
1	Waves Out of the Korean Peninsula and Inter- and Intra-Species Replacements in Freshwater Fishes in Japan. <i>Genes</i> , 2021, 12, 303.	2.4	10
2	Multiple haplotype reconstruction from allele frequency data. <i>Nature Computational Science</i> , 2021, 1, 262-271.	8.0	6
3	Effects of restraint on heifers during gentle human-animal interactions. <i>Applied Animal Behaviour Science</i> , 2021, 243, 105445.	1.9	6
4	Disentangling observer error and climate change effects in long-term monitoring of alpine plant species composition and cover. <i>Journal of Vegetation Science</i> , 2020, 31, 14-25.	2.2	19
5	Talking to Cows: Reactions to Different Auditory Stimuli During Gentle Human-Animal Interactions. <i>Frontiers in Psychology</i> , 2020, 11, 579346.	2.1	10
6	Effects of Different Stroking Styles on Behaviour and Cardiac Parameters in Heifers. <i>Animals</i> , 2020, 10, 426.	2.3	15
7	Modifying the Chi-square and the CMH test for population genetic inference: Adapting to overdispersion. <i>Annals of Applied Statistics</i> , 2020, 14, .	1.1	22
8	Gentle interactions with restrained and free-moving cows: Effects on the improvement of the animal-human relationship. <i>PLoS ONE</i> , 2020, 15, e0242873.	2.5	4
9	Benchmarking software tools for detecting and quantifying selection in evolve and resequencing studies. <i>Genome Biology</i> , 2019, 20, 169.	8.8	33
10	The Effects of Play Behavior, Feeding, and Time of Day on Salivary Concentrations of sIgA in Calves. <i>Animals</i> , 2019, 9, 657.	2.3	3
11	<i>LDJump</i> : Estimating variable recombination rates from population genetic data. <i>Molecular Ecology Resources</i> , 2019, 19, 623-638.	4.8	22
12	An omnibus test for the global null hypothesis. <i>Statistical Methods in Medical Research</i> , 2019, 28, 2292-2304.	1.5	14
13	The impact of poly-A microsatellite heterologies in meiotic recombination. <i>Life Science Alliance</i> , 2019, 2, e201900364.	2.8	5
14	Caregiving and Caregiver Burden in Dementia Home Care: Results from the Prospective Dementia Registry (PRODEM) of the Austrian Alzheimer Society. <i>Journal of Alzheimer's Disease</i> , 2018, 63, 103-114.	2.6	41
15	Bounded risk estimation of a linear combination of location parameters in negative exponential distributions via three-stage sampling. <i>Communications in Statistics - Theory and Methods</i> , 2018, 47, 3728-3733.	1.0	1
16	The influence of gentle interactions with an experimenter during milking on dairy cows' avoidance distance and milk yield, flow and composition. <i>Animal</i> , 2018, 12, 340-349.	3.3	13
17	The long zinc finger domain of PRDM9 forms a highly stable and long-lived complex with its DNA recognition sequence. <i>Chromosome Research</i> , 2017, 25, 155-172.	2.2	17
18	Quantifying Selection with Pool-Seq Time Series Data. <i>Molecular Biology and Evolution</i> , 2017, 34, 3023-3034.	8.9	69

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19	Approximate maximum likelihood estimation for population genetic inference. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2017, 16, 387-405.	0.6	8
20	Gentle interactions decrease the fear of humans in dairy heifers independently of early experience of stroking. <i>Applied Animal Behaviour Science</i> , 2016, 178, 16-22.	1.9	29
21	Estimating the Effective Population Size from Temporal Allele Frequency Changes in Experimental Evolution. <i>Genetics</i> , 2016, 204, 723-735.	2.9	58
22	Improved Versions of Common Estimators of the Recombination Rate. <i>Journal of Computational Biology</i> , 2016, 23, 756-768.	1.6	6
23	Choosing summary statistics by least angle regression for approximate Bayesian computation. <i>Journal of Applied Statistics</i> , 2016, 43, 2191-2202.	1.3	1
24	Exact Likelihood Calculation under the Infinite Sites Model. <i>Computation</i> , 2015, 3, 701-713.	2.0	1
25	The influence of gentle interactions on avoidance distance towards humans, weight gain and physiological parameters in group-housed dairy calves. <i>Applied Animal Behaviour Science</i> , 2015, 172, 9-16.	1.9	39
26	Effects of gentle interactions on the relationship with humans and on stress-related parameters in group-housed calves. <i>Animal Welfare</i> , 2015, 24, 475-484.	0.7	14
27	Effects of mother versus artificial rearing during the first 12 weeks of life on challenge responses of dairy cows. <i>Applied Animal Behaviour Science</i> , 2015, 164, 1-11.	1.9	36
28	Head partitions at the feed barrier affect behaviour of goats. <i>Applied Animal Behaviour Science</i> , 2015, 167, 9-19.	1.9	7
29	Multiscale DNA partitioning: statistical evidence for segments. <i>Bioinformatics</i> , 2014, 30, 2255-2262.	4.1	17
30	mtDNA Segregation in Heteroplasmic Tissues Is Common In Vivo and Modulated by Haplotype Differences and Developmental Stage. <i>Cell Reports</i> , 2014, 7, 2031-2041.	6.4	99
31	A new approach to choose acceptance cutoff for approximate Bayesian computation. <i>Journal of Applied Statistics</i> , 2013, 40, 862-869.	1.3	7
32	Introducing young dairy goats into the adult herd after parturition reduces social stress. <i>Journal of Dairy Science</i> , 2013, 96, 5644-5655.	3.4	9
33	Mother rearing of dairy calves: Reactions to isolation and to confrontation with an unfamiliar conspecific in a new environment. <i>Applied Animal Behaviour Science</i> , 2013, 147, 43-54.	1.9	48
34	A Genome-Wide, Fine-Scale Map of Natural Pigmentation Variation in <i>Drosophila melanogaster</i> . <i>PLoS Genetics</i> , 2013, 9, e1003534.	3.5	146
35	A Fast Estimate for the Population Recombination Rate Based on Regression. <i>Genetics</i> , 2013, 194, 473-484.	2.9	37
36	Approximate Bayesian computation for modular inference problems with many parameters: the example of migration rates. <i>Molecular Ecology</i> , 2013, 22, 987-1002.	3.9	15

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37	Poolâ€œmm: a Python program for estimating the allele frequency spectrum and detecting selective sweeps from next generation sequencing of pooled samples. <i>Molecular Ecology Resources</i> , 2013, 13, 337-340.	4.8	55
38	Allelic imbalance metre ( A llim), a new tool for measuring alleleâ€œspecific gene expression with RNA â€œseq data. <i>Molecular Ecology Resources</i> , 2013, 13, 740-745.	4.8	36
39	Intra-Specific Regulatory Variation in <i>Drosophila pseudoobscura</i> . <i>PLoS ONE</i> , 2013, 8, e83547.	2.5	23
40	Detecting Selective Sweeps from Pooled Next-Generation Sequencing Samples. <i>Molecular Biology and Evolution</i> , 2012, 29, 2177-2186.	8.9	75
41	A Novel Approach for Choosing Summary Statistics in Approximate Bayesian Computation. <i>Genetics</i> , 2012, 192, 1027-1047.	2.9	82
42	Integration into the dairy cow herd: Long-term effects of mother contact during the first twelve weeks of life. <i>Applied Animal Behaviour Science</i> , 2012, 141, 117-129.	1.9	60
43	DNA Pooling and Statistical Tests for the Detection of Single Nucleotide Polymorphisms. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2012, 11, Article 1.	0.6	2
44	Continent-wide response of mountain vegetation to climate change. <i>Nature Climate Change</i> , 2012, 2, 111-115.	18.8	941
45	PoPoolation: A Toolbox for Population Genetic Analysis of Next Generation Sequencing Data from Pooled Individuals. <i>PLoS ONE</i> , 2011, 6, e15925.	2.5	556
46	Distinguishing Positive Selection From Neutral Evolution: Boosting the Performance of Summary Statistics. <i>Genetics</i> , 2011, 187, 229-244.	2.9	102
47	Behaviour of smaller and larger dogs: Effects of training methods, inconsistency of owner behaviour and level of engagement in activities with the dog. <i>Applied Animal Behaviour Science</i> , 2010, 123, 131-142.	1.9	148
48	Sequential estimation of a linear function of location parameters of two negative exponential distributions. <i>Journal of Statistical Planning and Inference</i> , 2010, 140, 2416-2424.	0.6	4
49	The Next Generation of Molecular Markers From Massively Parallel Sequencing of Pooled DNA Samples. <i>Genetics</i> , 2010, 186, 207-218.	2.9	329
50	Hidden Markov Models in Biology. <i>Methods in Molecular Biology</i> , 2010, 609, 241-253.	0.9	2
51	Detecting Selective Sweeps: A New Approach Based on Hidden Markov Models. <i>Genetics</i> , 2009, 181, 1567-1578.	2.9	48
52	On the convergence rate of sequential fixed-width confidence intervals for normal parameters. <i>Statistics and Probability Letters</i> , 2008, 78, 1826-1834.	0.7	0
53	On the inadmissibility of Wattersonâ€™s estimator. <i>Theoretical Population Biology</i> , 2008, 73, 212-221.	1.1	8
54	A Uniform Improvement of Bonferroni-Type Tests by Sequential Tests. <i>Journal of the American Statistical Association</i> , 2008, 103, 299-308.	3.1	7

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55	Locating Multiple Interacting Quantitative Trait Loci Using Rank-Based Model Selection. <i>Genetics</i> , 2007, 176, 1845-1854.	2.9	18
56	Locating multiple interacting quantitative trait loci using robust model selection. <i>Computational Statistics and Data Analysis</i> , 2007, 51, 6423-6434.	1.2	7
57	On the convergence of Newton's method when estimating higher dimensional parameters. <i>Journal of Multivariate Analysis</i> , 2007, 98, 916-931.	1.0	2
58	On Locating Multiple Interacting Quantitative Trait Loci in Intercross Designs. <i>Genetics</i> , 2006, 173, 1693-1703.	2.9	46
59	Power analysis of database search using multiple scoring matrices. <i>Computational Statistics and Data Analysis</i> , 2006, 51, 1656-1663.	1.2	0
60	On the consistency of kernel density estimates under modality constraints. <i>Statistics and Probability Letters</i> , 2006, 76, 431-437.	0.7	1
61	Confidence sets for the maximizers of intensity functions. <i>Journal of Statistical Planning and Inference</i> , 2005, 134, 549-567.	0.6	0
62	On the significance of sequence alignments when using multiple scoring matrices. <i>Bioinformatics</i> , 2004, 20, 881-887.	4.1	10
63	On the Dependence Structure of Sequence Alignment Scores Calculated with Multiple Scoring Matrices. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2004, 3, 1-12.	0.6	1
64	Improving bandwidth selection methods by adding qualitative constraints. <i>Computational Statistics</i> , 2004, 19, 445-453.	1.5	1
65	A Data Driven Smooth Test for Circular Uniformity. <i>Annals of the Institute of Statistical Mathematics</i> , 2002, 54, 29-44.	0.8	44
66	Confidence regions for the set of global maximizers of nonparametrically estimated curves. <i>Journal of Statistical Planning and Inference</i> , 1999, 82, 237-250.	0.6	1
67	A new estimate of the mode based on the quantile density. <i>Statistics and Probability Letters</i> , 1999, 43, 145-152.	0.7	1
68	Distance Testing for Selecting the Best Population. <i>Australian and New Zealand Journal of Statistics</i> , 1998, 40, 443-464.	0.9	1
69	The likelihood ratio test for simple tree order: A useful asymptotic expansion. <i>Journal of Statistical Planning and Inference</i> , 1998, 70, 57-68.	0.6	4
70	Rotation invariant tests for discrete uniformity against peak shaped alternatives. <i>Communications in Statistics Part B: Simulation and Computation</i> , 1998, 27, 431-457.	1.2	0
71	Optimal allocation of simulation experiments in discrete stochastic optimization and approximative algorithms. <i>European Journal of Operational Research</i> , 1997, 101, 245-260.	5.7	18
72	Confidence sets for discrete stochastic optimization. <i>Annals of Operations Research</i> , 1995, 56, 95-108.	4.1	10