

Jinliang Wang

List of Publications by Year in descending order

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Version: 2024-02-01

80
papers

9,893
citations

71061

41
h-index

64755

79
g-index

83
all docs

83
docs citations

83
times ranked

8775
citing authors

#	ARTICLE	IF	CITATIONS
1	COLONY: a program for parentage and sibship inference from multilocus genotype data. <i>Molecular Ecology Resources</i> , 2010, 10, 551-555.	2.2	1,394
2	Sibship Reconstruction From Genetic Data With Typing Errors. <i>Genetics</i> , 2004, 166, 1963-1979.	1.2	780
3	<scp>coancestry</scp>: a program for simulating, estimating and analysing relatedness and inbreeding coefficients. <i>Molecular Ecology Resources</i> , 2011, 11, 141-145.	2.2	758
4	An Estimator for Pairwise Relatedness Using Molecular Markers. <i>Genetics</i> , 2002, 160, 1203-1215.	1.2	575
5	Parentage and Sibship Inference From Multilocus Genotype Data Under Polygamy. <i>Genetics</i> , 2009, 181, 1579-1594.	1.2	400
6	Estimating Effective Population Size and Migration Rates From Genetic Samples Over Space and Time. <i>Genetics</i> , 2003, 163, 429-446.	1.2	378
7	Estimation of effective population sizes from data on genetic markers. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2005, 360, 1395-1409.	1.8	337
8	Triadic IBD coefficients and applications to estimating pairwise relatedness. <i>Genetical Research</i> , 2007, 89, 135-153.	0.3	333
9	A new method for estimating effective population sizes from a single sample of multilocus genotypes. <i>Molecular Ecology</i> , 2009, 18, 2148-2164.	2.0	319
10	related: an R package for analysing pairwise relatedness from codominant molecular markers. <i>Molecular Ecology Resources</i> , 2015, 15, 557-561.	2.2	298
11	Dynamics of inbreeding depression due to deleterious mutations in small populations: mutation parameters and inbreeding rate. <i>Genetical Research</i> , 1999, 74, 165-178.	0.3	249
12	The computer program <scp>structure</scp> for assigning individuals to populations: easy to use but easier to misuse. <i>Molecular Ecology Resources</i> , 2017, 17, 981-990.	2.2	239
13	A pseudo-likelihood method for estimating effective population size from temporally spaced samples. <i>Genetical Research</i> , 2001, 78, 243-257.	0.3	211
14	Application of the One-Migrant-per-Generation Rule to Conservation and Management. <i>Conservation Biology</i> , 2004, 18, 332-343.	2.4	185
15	Developments in predicting the effective size of subdivided populations. <i>Heredity</i> , 1999, 82, 212-226.	1.2	180
16	Bumblebee family lineage survival is enhanced in high-quality landscapes. <i>Nature</i> , 2017, 543, 547-549.	18.7	159
17	Recent Demographic History Inferred by High-Resolution Analysis of Linkage Disequilibrium. <i>Molecular Biology and Evolution</i> , 2020, 37, 3642-3653.	3.5	141
18	Maximum-Likelihood Estimation of Admixture Proportions From Genetic Data. <i>Genetics</i> , 2003, 164, 747-765.	1.2	139

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19	The effect of close relatives on unsupervised Bayesian clustering algorithms in population genetic structure analysis. <i>Molecular Ecology Resources</i> , 2012, 12, 873-884.	2.2	137
20	Genetic Effects of Multiple Generations of Supportive Breeding. <i>Conservation Biology</i> , 2001, 15, 1619-1631.	2.4	133
21	Sibship Reconstruction From Genetic Data With Typing Errors. <i>Genetics</i> , 2004, 166, 1963-1979.	1.2	131
22	Genetic and genomic monitoring with minimally invasive sampling methods. <i>Evolutionary Applications</i> , 2018, 11, 1094-1119.	1.5	126
23	Pedigrees or markers: Which are better in estimating relatedness and inbreeding coefficient?. <i>Theoretical Population Biology</i> , 2016, 107, 4-13.	0.5	119
24	Effects of habitat composition and landscape structure on worker foraging distances of five bumble bee species. <i>Ecological Applications</i> , 2016, 26, 726-739.	1.8	104
25	A comparison of single-sample estimators of effective population sizes from genetic marker data. <i>Molecular Ecology</i> , 2016, 25, 4692-4711.	2.0	101
26	Next-generation metrics for monitoring genetic erosion within populations of conservation concern. <i>Evolutionary Applications</i> , 2018, 11, 1066-1083.	1.5	93
27	Computationally Efficient Sibship and Parentage Assignment from Multilocus Marker Data. <i>Genetics</i> , 2012, 191, 183-194.	1.2	83
28	Informativeness of genetic markers for pairwise relationship and relatedness inference. <i>Theoretical Population Biology</i> , 2006, 70, 300-321.	0.5	72
29	Inbreeding and inbreeding depression of early life traits in a cooperative mammal. <i>Molecular Ecology</i> , 2012, 21, 2788-2804.	2.0	71
30	Bottleneck Effect on Genetic Variance: A Theoretical Investigation of the Role of Dominance. <i>Genetics</i> , 1998, 150, 435-447.	1.2	70
31	MHC, mate choice and heterozygote advantage in a wild social primate. <i>Molecular Ecology</i> , 2010, 19, no-no.	2.0	68
32	Does catch and release affect the mating system and individual reproductive success of wild Atlantic salmon (<i>Salmo salar</i> L.)?. <i>Molecular Ecology</i> , 2013, 22, 187-200.	2.0	68
33	Genetic analysis reveals promiscuity among female cheetahs. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2007, 274, 1993-2001.	1.2	64
34	Genetic consequences of historical anthropogenic and ecological events on giant pandas. <i>Ecology</i> , 2013, 94, 2346-2357.	1.5	64
35	Effects of sampling close relatives on some elementary population genetics analyses. <i>Molecular Ecology Resources</i> , 2018, 18, 41-54.	2.2	63
36	Effects of population structures and selection strategies on the purging of inbreeding depression due to deleterious mutations. <i>Genetical Research</i> , 2000, 76, 75-86.	0.3	62

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37	Sensitive males: inbreeding depression in an endangered bird. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2010, 277, 3677-3684.	1.2	58
38	Effective Size and F_{ST} -Statistics of Subdivided Populations. II. Dioecious Species. <i>Genetics</i> , 1997, 146, 1465-1474.	1.2	57
39	ESTIMATION OF PARAMETERS OF INBREEDING AND GENETIC DRIFT IN POPULATIONS WITH OVERLAPPING GENERATIONS. <i>Evolution; International Journal of Organic Evolution</i> , 2010, 64, 1704-1718.	1.1	53
40	Individual identification from genetic marker data: developments and accuracy comparisons of methods. <i>Molecular Ecology Resources</i> , 2016, 16, 163-175.	2.2	51
41	Unbiased Relatedness Estimation in Structured Populations. <i>Genetics</i> , 2011, 187, 887-901.	1.2	49
42	Effective Size and F_{ST} -Statistics of Subdivided Populations. I. Monoecious Species with Partial Selfing. <i>Genetics</i> , 1997, 146, 1453-1463.	1.2	47
43	More efficient breeding systems for controlling inbreeding and effective size in animal populations. <i>Heredity</i> , 1997, 79, 591-599.	1.2	45
44	A parsimony estimator of the number of populations from a STRUCTURE-like analysis. <i>Molecular Ecology Resources</i> , 2019, 19, 970-981.	2.2	43
45	Fine-scale spatial genetic structure of common and declining bumble bees across an agricultural landscape. <i>Molecular Ecology</i> , 2014, 23, 3384-3395.	2.0	41
46	Parentage and sibship inference from markers in polyploids. <i>Molecular Ecology Resources</i> , 2014, 14, 541-553.	2.2	40
47	Banded mongooses avoid inbreeding when mating with members of the same natal group. <i>Molecular Ecology</i> , 2015, 24, 3738-3751.	2.0	38
48	Marker-Assisted Selection to Increase Effective Population Size by Reducing Mendelian Segregation Variance. <i>Genetics</i> , 2000, 154, 475-489.	1.2	38
49	Monitoring and managing genetic variation in group breeding populations without individual pedigrees. <i>Conservation Genetics</i> , 2004, 5, 813-825.	0.8	37
50	Mountains as barriers to gene flow in amphibians: Quantifying the differential effect of a major mountain ridge on the genetic structure of four sympatric species with different life history traits. <i>Journal of Biogeography</i> , 2018, 45, 318-331.	1.4	36
51	Estimating selfing rates from reconstructed pedigrees using multilocus genotype data. <i>Molecular Ecology</i> , 2012, 21, 100-116.	2.0	34
52	Effects of Sample Size and Full Sibs on Genetic Diversity Characterization: A Case Study of Three Syntopic Iberian Pond-Breeding Amphibians. <i>Journal of Heredity</i> , 2017, 108, 535-543.	1.0	33
53	Effects of genotyping errors on parentage exclusion analysis. <i>Molecular Ecology</i> , 2010, 19, 5061-5078.	2.0	30
54	A simulation module in the computer program <code>colony</code> for sibship and parentage analysis. <i>Molecular Ecology Resources</i> , 2013, 13, 734-739.	2.2	29

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55	Role of evolutionary and ecological factors in the reproductive success and the spatial genetic structure of the temperate gorgonian <i>Paramuricea clavata</i> . <i>Ecology and Evolution</i> , 2013, 3, 1765-1779.	0.8	29
56	Estimating genotyping errors from genotype and reconstructed pedigree data. <i>Methods in Ecology and Evolution</i> , 2018, 9, 109-120.	2.2	29
57	Optimal Marker-Assisted Selection to Increase the Effective Size of Small Populations. <i>Genetics</i> , 2001, 157, 867-874.	1.2	26
58	Postcopulatory mechanisms of inbreeding avoidance in the island endemic hihi (<i>Notiomystis cincta</i>). <i>Behavioral Ecology</i> , 2012, 23, 278-284.	1.0	25
59	A comparison of four methods for detecting weak genetic structure from marker data. <i>Ecology and Evolution</i> , 2012, 2, 1048-1055.	0.8	25
60	Estimation of migration rates from marker-based parentage analysis. <i>Molecular Ecology</i> , 2014, 23, 3191-3213.	2.0	25
61	Evaluating a multi-generational reintroduction program for threatened salmon using genetic parentage analysis. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 2016, 73, 844-852.	0.7	25
62	Deviation from Hardy-Weinberg proportions in finite populations. <i>Genetical Research</i> , 1996, 68, 249-257.	0.3	21
63	Pedigree reconstruction from poor quality genotype data. <i>Heredity</i> , 2019, 122, 719-728.	1.2	21
64	Effect of Selection Against Deleterious Mutations on the Decline in Heterozygosity at Neutral Loci in Closely Inbreeding Populations. <i>Genetics</i> , 1999, 153, 1475-1489.	1.2	20
65	Rapid selection against inbreeding in a wild population of a rare frog. <i>Evolutionary Applications</i> , 2011, 4, 30-38.	1.5	18
66	A Coalescent-Based Estimator of Admixture From DNA Sequences. <i>Genetics</i> , 2006, 173, 1679-1692.	1.2	16
67	Distinct and Diverse: Range-Wide Phylogeography Reveals Ancient Lineages and High Genetic Variation in the Endangered Okapi (<i>Okapia johnstoni</i>). <i>PLoS ONE</i> , 2014, 9, e101081.	1.1	16
68	Improving the inference of population genetic structure in the presence of related individuals. <i>Genetical Research</i> , 2014, 96, e003.	0.3	15
69	Do marker-based paternity assignments favour heterozygous and unrelated males?. <i>Molecular Ecology</i> , 2010, 19, 1898-1913.	2.0	14
70	Predictive Model and Software for Inbreeding-Purging Analysis of Pedigreed Populations. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 3593-3601.	0.8	14
71	Reliable effective number of breeders/adult census size ratios in seasonal-breeding species: Opportunity for integrative demographic inferences based on capture-recapture data and multilocus genotypes. <i>Ecology and Evolution</i> , 2017, 7, 10301-10314.	0.8	14
72	Prediction of the minimum effective size of a population viable in the long term. <i>Biodiversity and Conservation</i> , 2022, 31, 2763-2780.	1.2	14

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73	Detection of genetic purging and predictive value of purging parameters estimated in pedigreed populations. <i>Heredity</i> , 2018, 121, 38-51.	1.2	12
74	Genetic Family Reconstruction Characterizes Lake Sturgeon Use of Newly Constructed Spawning Habitat and Larval Dispersal. <i>Transactions of the American Fisheries Society</i> , 2020, 149, 266-283.	0.6	12
75	Genealogical Relationship among Members of Selection and Production Populations of Yellow Cedar (<i>Callitropsis nootkatensis</i> [D. Don] Oerst.) in the Absence of Parental Information. <i>Journal of Heredity</i> , 2010, 101, 154-163.	1.0	10
76	Genetic structure of captive and free-ranging okapi (<i>Okapia johnstoni</i>) with implications for management. <i>Conservation Genetics</i> , 2015, 16, 1115-1126.	0.8	7
77	Non-invasive genetic identification confirms the presence of the Endangered okapi <i>Okapia johnstoni</i> south-west of the Congo River. <i>Oryx</i> , 2016, 50, 134-137.	0.5	7
78	Evaluating the effect of forest loss and agricultural expansion on Sumatran tigers from scat surveys. <i>Biological Conservation</i> , 2018, 221, 270-278.	1.9	7
79	Fast and accurate population admixture inference from genotype data from a few microsatellites to millions of SNPs. <i>Heredity</i> , 2022, 129, 79-92.	1.2	4
80	Obituary in memoriam of Professor William G. (Bill) Hill. <i>Heredity</i> , 2022, 128, 77-78.	1.2	0