

Rohan Fernando

List of Publications by Year in descending order

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Version: 2024-02-01

65
papers

7,083
citations

159525

30
h-index

106281

65
g-index

72
all docs

72
docs citations

72
times ranked

4533
citing authors

#	ARTICLE	IF	CITATIONS
1	XSim version 2: simulation of modern breeding programs. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	6
2	Genome-wide association study of disease resilience traits from a natural polymicrobial disease challenge model in pigs identifies the importance of the major histocompatibility complex region. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	7
3	Cross-validation of best linear unbiased predictions of breeding values using an efficient leave-one-out strategy. <i>Journal of Animal Breeding and Genetics</i> , 2021, 138, 519-527.	0.8	16
4	Genomics of response to porcine reproductive and respiratory syndrome virus in purebred and crossbred sows: antibody response and performance following natural infection vs. vaccination. <i>Journal of Animal Science</i> , 2021, 99, .	0.2	2
5	Tests of association based on genomic windows can lead to spurious associations when using genotype panels with heterogeneous SNP densities. <i>Genetics Selection Evolution</i> , 2021, 53, 45.	1.2	3
6	Interpretable artificial neural networks incorporating Bayesian alphabet models for genome-wide prediction and association studies. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	13
7	Inferring trait-specific similarity among individuals from molecular markers and phenotypes with Bayesian regression. <i>Theoretical Population Biology</i> , 2020, 132, 47-59.	0.5	9
8	Genetic Analysis of Antibody Response to Porcine Reproductive and Respiratory Syndrome Vaccination as an Indicator Trait for Reproductive Performance in Commercial Sows. <i>Frontiers in Genetics</i> , 2020, 11, 1011.	1.1	16
9	A Multiple-Trait Bayesian Lasso for Genome-Enabled Analysis and Prediction of Complex Traits. <i>Genetics</i> , 2020, 214, 305-331.	1.2	25
10	Fast parallelized sampling of Bayesian regression models for whole-genome prediction. <i>Genetics Selection Evolution</i> , 2020, 52, 16.	1.2	8
11	Marker discovery and associations with β -carotene content in Indian dairy cattle and buffalo breeds. <i>Journal of Dairy Science</i> , 2019, 102, 10039-10055.	1.4	3
12	Efficient genetic value prediction using incomplete omics data. <i>Theoretical and Applied Genetics</i> , 2019, 132, 1211-1222.	1.8	8
13	Identification of recombination hotspots and quantitative trait loci for recombination rate in layer chickens. <i>Journal of Animal Science and Biotechnology</i> , 2019, 10, 20.	2.1	17
14	A certain invariance property of BLUE in a whole-genome regression context. <i>Journal of Animal Breeding and Genetics</i> , 2019, 136, 113-117.	0.8	2
15	Genomic Prediction from Multiple-Trait Bayesian Regression Methods Using Mixture Priors. <i>Genetics</i> , 2018, 209, 89-103.	1.2	61
16	Empirical Comparisons of Different Statistical Models To Identify and Validate Kernel Row Number-Associated Variants from Structured Multi-parent Mapping Populations of Maize. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3567-3575.	0.8	19
17	A nested mixture model for genomic prediction using whole-genome SNP genotypes. <i>PLoS ONE</i> , 2018, 13, e0194683.	1.1	9
18	Comparison of alternative approaches to single-trait genomic prediction using genotyped and non-genotyped Hanwoo beef cattle. <i>Genetics Selection Evolution</i> , 2017, 49, 2.	1.2	33

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19	Efficient strategies for leave-one-out cross validation for genomic best linear unbiased prediction. <i>Journal of Animal Science and Biotechnology</i> , 2017, 8, 38.	2.1	94
20	Application of Whole-Genome Prediction Methods for Genome-Wide Association Studies: A Bayesian Approach. <i>Journal of Agricultural, Biological, and Environmental Statistics</i> , 2017, 22, 172-193.	0.7	60
21	A comparison of identity-by-descent and identity-by-state matrices that are used for genetic evaluation and estimation of variance components. <i>Journal of Animal Breeding and Genetics</i> , 2017, 134, 213-223.	0.8	15
22	The Accuracy and Bias of Single-Step Genomic Prediction for Populations Under Selection. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2685-2694.	0.8	29
23	An Upper Bound for Accuracy of Prediction Using GBLUP. <i>PLoS ONE</i> , 2016, 11, e0161054.	1.1	53
24	Computational strategies for alternative single-step Bayesian regression models with large numbers of genotyped and non-genotyped animals. <i>Genetics Selection Evolution</i> , 2016, 48, 96.	1.2	57
25	Impact of fitting dominance and additive effects on accuracy of genomic prediction of breeding values in layers. <i>Journal of Animal Breeding and Genetics</i> , 2016, 133, 334-346.	0.8	24
26	An efficient exact method to obtain GBLUP and single-step GBLUP when the genomic relationship matrix is singular. <i>Genetics Selection Evolution</i> , 2016, 48, 80.	1.2	18
27	Contributions of linkage disequilibrium and co-segregation information to the accuracy of genomic prediction. <i>Genetics Selection Evolution</i> , 2016, 48, 77.	1.2	21
28	Effects of number of training generations on genomic prediction for various traits in a layer chicken population. <i>Genetics Selection Evolution</i> , 2016, 48, 22.	1.2	19
29	Mixture models detect large effect QTL better than GBLUP and result in more accurate and persistent predictions. <i>Journal of Animal Science and Biotechnology</i> , 2016, 7, 7.	2.1	23
30	Response and inbreeding from a genomic selection experiment in layer chickens. <i>Genetics Selection Evolution</i> , 2015, 47, 59.	1.2	67
31	Accuracy of prediction of simulated polygenic phenotypes and their underlying quantitative trait loci genotypes using real or imputed whole-genome markers in cattle. <i>Genetics Selection Evolution</i> , 2015, 47, 99.	1.2	6
32	XSim: Simulation of Descendants from Ancestors with Sequence Data. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1415-1417.	0.8	20
33	A fast and efficient Gibbs sampler for BayesB in whole-genome analyses. <i>Genetics Selection Evolution</i> , 2015, 47, 80.	1.2	31
34	A class of Bayesian methods to combine large numbers of genotyped and non-genotyped animals for whole-genome analyses. <i>Genetics Selection Evolution</i> , 2014, 46, 50.	1.2	147
35	Genome-wide association study for egg production and quality in layer chickens. <i>Journal of Animal Breeding and Genetics</i> , 2014, 131, 173-182.	0.8	72
36	The evolution of methodologies for genomic prediction. <i>Livestock Science</i> , 2014, 166, 10-18.	0.6	20

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37	Genomic BLUP Decoded: A Look into the Black Box of Genomic Prediction. <i>Genetics</i> , 2013, 194, 597-607.	1.2	279
38	Pedigree and genomic analyses of feed consumption and residual feed intake in laying hens. <i>Poultry Science</i> , 2013, 92, 2270-2275.	1.5	25
39	Bayesian Methods Applied to GWAS. <i>Methods in Molecular Biology</i> , 2013, 1019, 237-274.	0.4	115
40	Implementing a QTL Detection Study (GWAS) Using Genomic Prediction Methodology. <i>Methods in Molecular Biology</i> , 2013, 1019, 275-298.	0.4	80
41	Dissecting the genetic architecture of frost tolerance in Central European winter wheat. <i>Journal of Experimental Botany</i> , 2013, 64, 4453-4460.	2.4	69
42	Prediction of Complex Human Traits Using the Genomic Best Linear Unbiased Predictor. <i>PLoS Genetics</i> , 2013, 9, e1003608.	1.5	318
43	Genomic Prediction of Hybrid Wheat Performance. <i>Crop Science</i> , 2013, 53, 802-810.	0.8	127
44	Accuracy of Genomic Selection Methods in a Standard Data Set of Loblolly Pine (<i>Pinus taeda</i> L.). <i>Genetics</i> , 2012, 190, 1503-1510.	1.2	363
45	A Fast EM Algorithm for BayesA-Like Prediction of Genomic Breeding Values. <i>PLoS ONE</i> , 2012, 7, e49157.	1.1	27
46	Genomic breeding value prediction and QTL mapping of QTLMAS2010 data using Bayesian Methods. <i>BMC Proceedings</i> , 2011, 5, S13.	1.8	45
47	Persistence of accuracy of genomic estimated breeding values over generations in layer chickens. <i>Genetics Selection Evolution</i> , 2011, 43, 23.	1.2	86
48	Accuracies of genomic breeding values in American Angus beef cattle using K-means clustering for cross-validation. <i>Genetics Selection Evolution</i> , 2011, 43, 40.	1.2	174
49	Breeding value prediction for production traits in layer chickens using pedigree or genomic relationships in a reduced animal model. <i>Genetics Selection Evolution</i> , 2011, 43, 5.	1.2	130
50	Extension of the bayesian alphabet for genomic selection. <i>BMC Bioinformatics</i> , 2011, 12, 186.	1.2	942
51	A gene frequency model for QTL mapping using Bayesian inference. <i>Genetics Selection Evolution</i> , 2010, 42, 21.	1.2	6
52	Genomic prediction of simulated multibreed and purebred performance using observed fifty thousand single nucleotide polymorphism genotypes1. <i>Journal of Animal Science</i> , 2010, 88, 544-551.	0.2	228
53	A Two-Stage Approximation for Analysis of Mixture Genetic Models in Large Pedigrees. <i>Genetics</i> , 2010, 185, 655-670.	1.2	9
54	Additive Genetic Variability and the Bayesian Alphabet. <i>Genetics</i> , 2009, 183, 347-363.	1.2	398

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55	Extent and consistency of linkage disequilibrium and identification of DNA markers for production and egg quality traits in commercial layer chicken populations. BMC Genomics, 2009, 10, S2.	1.2	44
56	Deregressing estimated breeding values and weighting information for genomic regression analyses. Genetics Selection Evolution, 2009, 41, 55.	1.2	500
57	Genomic selection. Acta Agriculturae Scandinavica - Section A: Animal Science, 2007, 57, 192-195.	0.2	24
58	The Impact of Genetic Relationship Information on Genome-Assisted Breeding Values. Genetics, 2007, 177, 2389-2397.	1.2	1,077
59	Genomic-Assisted Prediction of Genetic Value With Semiparametric Procedures. Genetics, 2006, 173, 1761-1776.	1.2	401
60	Controlling the Proportion of False Positives in Multiple Dependent Tests. Genetics, 2004, 166, 611-619.	1.2	147
61	Quantitative Trait Locus Analysis in Crosses Between Outbred Lines With Dominance and Inbreeding. Genetics, 2001, 159, 413-422.	1.2	16
62	Genetic Evaluation by Best Linear Unbiased Prediction Using Marker and Trait Information in a Multibreed Population. Genetics, 1998, 148, 507-515.	1.2	24
63	Covariance between relatives in multibreed populations: additive model. Theoretical and Applied Genetics, 1993, 87, 423-430.	1.8	69
64	On the principle underlying the tabular method to compute coancestry. Theoretical and Applied Genetics, 1991, 81, 233-238.	1.8	10
65	Bayesian Methods in Animal Breeding Theory. Journal of Animal Science, 1986, 63, 217-244.	0.2	311