

Rohan Fernando

List of Publications by Year in descending order

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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	The Impact of Genetic Relationship Information on Genome-Assisted Breeding Values. <i>Genetics</i> , 2007, 177, 2389-2397.	1.2	1,077
2	Extension of the bayesian alphabet for genomic selection. <i>BMC Bioinformatics</i> , 2011, 12, 186.	1.2	942
3	Deregressing estimated breeding values and weighting information for genomic regression analyses. <i>Genetics Selection Evolution</i> , 2009, 41, 55.	1.2	500
4	Genomic-Assisted Prediction of Genetic Value With Semiparametric Procedures. <i>Genetics</i> , 2006, 173, 1761-1776.	1.2	401
5	Additive Genetic Variability and the Bayesian Alphabet. <i>Genetics</i> , 2009, 183, 347-363.	1.2	398
6	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
7	Prediction of Complex Human Traits Using the Genomic Best Linear Unbiased Predictor. <i>PLoS Genetics</i> , 2013, 9, e1003608.	1.5	318
8	Bayesian Methods in Animal Breeding Theory. <i>Journal of Animal Science</i> , 1986, 63, 217-244.	0.2	311
9	Genomic BLUP Decoded: A Look into the Black Box of Genomic Prediction. <i>Genetics</i> , 2013, 194, 597-607.	1.2	279
10	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
11	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
12	Controlling the Proportion of False Positives in Multiple Dependent Tests. <i>Genetics</i> , 2004, 166, 611-619.	1.2	147
13	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
14	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
15	Genomic Prediction of Hybrid Wheat Performance. <i>Crop Science</i> , 2013, 53, 802-810.	0.8	127
16	Bayesian Methods Applied to GWAS. <i>Methods in Molecular Biology</i> , 2013, 1019, 237-274.	0.4	115
17	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
18	Persistence of accuracy of genomic estimated breeding values over generations in layer chickens. <i>Genetics Selection Evolution</i> , 2011, 43, 23.	1.2	86

#	ARTICLE	IF	CITATIONS
19	Implementing a QTL Detection Study (GWAS) Using Genomic Prediction Methodology. <i>Methods in Molecular Biology</i> , 2013, 1019, 275-298.	0.4	80
20	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
21	Covariance between relatives in multibreed populations: additive model. <i>Theoretical and Applied Genetics</i> , 1993, 87, 423-430.	1.8	69
22	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
23	Response and inbreeding from a genomic selection experiment in layer chickens. <i>Genetics Selection Evolution</i> , 2015, 47, 59.	1.2	67
24	Genomic Prediction from Multiple-Trait Bayesian Regression Methods Using Mixture Priors. <i>Genetics</i> , 2018, 209, 89-103.	1.2	61
25	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
26	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
27	An Upper Bound for Accuracy of Prediction Using GBLUP. <i>PLoS ONE</i> , 2016, 11, e0161054.	1.1	53
28	Genomic breeding value prediction and QTL mapping of QTLMAS2010 data using Bayesian Methods. <i>BMC Proceedings</i> , 2011, 5, S13.	1.8	45
29	Extent and consistency of linkage disequilibrium and identification of DNA markers for production and egg quality traits in commercial layer chicken populations. <i>BMC Genomics</i> , 2009, 10, S2.	1.2	44
30	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
31	A fast and efficient Gibbs sampler for BayesB in whole-genome analyses. <i>Genetics Selection Evolution</i> , 2015, 47, 80.	1.2	31
32	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
33	A Fast EM Algorithm for BayesA-Like Prediction of Genomic Breeding Values. <i>PLoS ONE</i> , 2012, 7, e49157.	1.1	27
34	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
35	A Multiple-Trait Bayesian Lasso for Genome-Enabled Analysis and Prediction of Complex Traits. <i>Genetics</i> , 2020, 214, 305-331.	1.2	25
36	Genomic selection. <i>Acta Agriculturae Scandinavica - Section A: Animal Science</i> , 2007, 57, 192-195.	0.2	24

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37	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
38	Genetic Evaluation by Best Linear Unbiased Prediction Using Marker and Trait Information in a Multibreed Population. <i>Genetics</i> , 1998, 148, 507-515.	1.2	24
39	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
40	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
41	The evolution of methodologies for genomic prediction. <i>Livestock Science</i> , 2014, 166, 10-18.	0.6	20
42	XSim: Simulation of Descendants from Ancestors with Sequence Data. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1415-1417.	0.8	20
43	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
44	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
45	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
46	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
47	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
48	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
49	Quantitative Trait Locus Analysis in Crosses Between Outbred Lines With Dominance and Inbreeding. <i>Genetics</i> , 2001, 159, 413-422.	1.2	16
50	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
51	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
52	On the principle underlying the tabular method to compute coancestry. <i>Theoretical and Applied Genetics</i> , 1991, 81, 233-238.	1.8	10
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	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

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55	A nested mixture model for genomic prediction using whole-genome SNP genotypes. PLoS ONE, 2018, 13, e0194683.	1.1	9
56	Efficient genetic value prediction using incomplete omics data. Theoretical and Applied Genetics, 2019, 132, 1211-1222.	1.8	8
57	Fast parallelized sampling of Bayesian regression models for whole-genome prediction. Genetics Selection Evolution, 2020, 52, 16.	1.2	8
58	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. G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	7
59	A gene frequency model for QTL mapping using Bayesian inference. Genetics Selection Evolution, 2010, 42, 21.	1.2	6
60	Accuracy of prediction of simulated polygenic phenotypes and their underlying quantitative trait loci genotypes using real or imputed whole-genome markers in cattle. Genetics Selection Evolution, 2015, 47, 99.	1.2	6
61	XSim version 2: simulation of modern breeding programs. G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	6
62	Marker discovery and associations with β -carotene content in Indian dairy cattle and buffalo breeds. Journal of Dairy Science, 2019, 102, 10039-10055.	1.4	3
63	Tests of association based on genomic windows can lead to spurious associations when using genotype panels with heterogeneous SNP densities. Genetics Selection Evolution, 2021, 53, 45.	1.2	3
64	A certain invariance property of BLUE in a whole-genome regression context. Journal of Animal Breeding and Genetics, 2019, 136, 113-117.	0.8	2
65	Genomics of response to porcine reproductive and respiratory syndrome virus in purebred and crossbred sows: antibody response and performance following natural infection vs. vaccination. Journal of Animal Science, 2021, 99, .	0.2	2