

Daniel Gianola

List of Publications by Year in descending order

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Version: 2024-02-01

99
papers

9,160
citations

50170

46
h-index

43802

91
g-index

105
all docs

105
docs citations

105
times ranked

5617
citing authors

#	ARTICLE	IF	CITATIONS
1	Rohan Fernando: a road from Sri Lanka to Ames. <i>Genetics Selection Evolution</i> , 2022, 54, 9.	1.2	0
2	Predictive assessment of single-step BLUP with linear and non-linear similarity RKHS kernels: A case study in chickens. <i>Journal of Animal Breeding and Genetics</i> , 2022, 139, 247-258.	0.8	3
3	Genome-Enabled Prediction Methods Based on Machine Learning. <i>Methods in Molecular Biology</i> , 2022, 2467, 189-218.	0.4	8
4	Feature Selection Stability and Accuracy of Prediction Models for Genomic Prediction of Residual Feed Intake in Pigs Using Machine Learning. <i>Frontiers in Genetics</i> , 2021, 12, 611506.	1.1	26
5	Prediction of biological age and evaluation of genome-wide dynamic methylomic changes throughout human aging. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	3
6	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
7	Machine Learning Prediction of Crossbred Pig Feed Efficiency and Growth Rate From Single Nucleotide Polymorphisms. <i>Frontiers in Genetics</i> , 2020, 11, 567818.	1.1	8
8	Deep learning versus parametric and ensemble methods for genomic prediction of complex phenotypes. <i>Genetics Selection Evolution</i> , 2020, 52, 12.	1.2	106
9	Integration of single nucleotide variants and whole-genome DNA methylation profiles for classification of rheumatoid arthritis cases from controls. <i>Heredity</i> , 2020, 124, 658-674.	1.2	10
10	A Multiple-Trait Bayesian Lasso for Genome-Enabled Analysis and Prediction of Complex Traits. <i>Genetics</i> , 2020, 214, 305-331.	1.2	25
11	Deep Kernel and Deep Learning for Genome-Based Prediction of Single Traits in Multienvironment Breeding Trials. <i>Frontiers in Genetics</i> , 2019, 10, 1168.	1.1	77
12	New Deep Learning Genomic-Based Prediction Model for Multiple Traits with Binary, Ordinal, and Continuous Phenotypes. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1545-1556.	0.8	81
13	A robust Bayesian genome-based median regression model. <i>Theoretical and Applied Genetics</i> , 2019, 132, 1587-1606.	1.8	1
14	Joint Use of Genome, Pedigree, and Their Interaction with Environment for Predicting the Performance of Wheat Lines in New Environments. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2925-2934.	0.8	13
15	A Benchmarking Between Deep Learning, Support Vector Machine and Bayesian Threshold Best Linear Unbiased Prediction for Predicting Ordinal Traits in Plant Breeding. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 601-618.	0.8	95
16	A certain invariance property of $\langle \text{scp} \rangle \text{BLUE} \langle / \text{scp} \rangle$ in a whole-genome regression context. <i>Journal of Animal Breeding and Genetics</i> , 2019, 136, 113-117.	0.8	2
17	Including Phenotypic Causal Networks in Genome-Wide Association Studies Using Mixed Effects Structural Equation Models. <i>Frontiers in Genetics</i> , 2018, 9, 455.	1.1	26
18	Multi-environment Genomic Prediction of Plant Traits Using Deep Learners With Dense Architecture. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3813-3828.	0.8	115

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19	Multi-trait, Multi-environment Deep Learning Modeling for Genomic-Enabled Prediction of Plant Traits. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3829-3840.	0.8	108
20	Applications of Machine Learning Methods to Genomic Selection in Breeding Wheat for Rust Resistance. <i>Plant Genome</i> , 2018, 11, 170104.	1.6	94
21	Prediction of Complex Traits: Robust Alternatives to Best Linear Unbiased Prediction. <i>Frontiers in Genetics</i> , 2018, 9, 195.	1.1	29
22	Predictive ability of genome-assisted statistical models under various forms of gene action. <i>Scientific Reports</i> , 2018, 8, 12309.	1.6	38
23	A predictive assessment of genetic correlations between traits in chickens using markers. <i>Genetics Selection Evolution</i> , 2017, 49, 16.	1.2	30
24	Assessing genomic prediction accuracy for Holstein sires using bootstrap aggregation sampling and leave-one-out cross validation. <i>Journal of Dairy Science</i> , 2017, 100, 453-464.	1.4	23
25	It is unlikely that genomic selection will ever be 100% accurate. <i>Journal of Animal Breeding and Genetics</i> , 2017, 134, 438-440.	0.8	10
26	Genome-wide association analysis in dogs implicates 99 loci as risk variants for anterior cruciate ligament rupture. <i>PLoS ONE</i> , 2017, 12, e0173810.	1.1	39
27	Cross-Validation Without Doing Cross-Validation in Genome-Enabled Prediction. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 3107-3128.	0.8	50
28	Genome-Wide Association Studies with a Genomic Relationship Matrix: A Case Study with Wheat and <i>Arabidopsis</i> . <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 3241-3256.	0.8	32
29	Incorporating parent-of-origin effects in whole-genome prediction of complex traits. <i>Genetics Selection Evolution</i> , 2016, 48, 34.	1.2	8
30	Differential contribution of genomic regions to marked genetic variation and prediction of quantitative traits in broiler chickens. <i>Genetics Selection Evolution</i> , 2016, 48, 10.	1.2	26
31	Genome-enabled prediction using probabilistic neural network classifiers. <i>BMC Genomics</i> , 2016, 17, 208.	1.2	51
32	Improving reliability of genomic predictions for Jersey sires using bootstrap aggregation sampling. <i>Journal of Dairy Science</i> , 2016, 99, 3632-3645.	1.4	7
33	Do Molecular Markers Inform About Pleiotropy?. <i>Genetics</i> , 2015, 201, 23-29.	1.2	53
34	The Causal Meaning of Genomic Predictors and How It Affects Construction and Comparison of Genome-Enabled Selection Models. <i>Genetics</i> , 2015, 200, 483-494.	1.2	24
35	Genomic Heritability: What Is It?. <i>PLoS Genetics</i> , 2015, 11, e1005048.	1.5	298
36	Application of neural networks with back-propagation to genome-enabled prediction of complex traits in Holstein-Friesian and German Fleckvieh cattle. <i>Genetics Selection Evolution</i> , 2015, 47, 22.	1.2	62

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37	Defining window-boundaries for genomic analyses using smoothing spline techniques. <i>Genetics Selection Evolution</i> , 2015, 47, 30.	1.2	72
38	A GWAS assessment of the contribution of genomic imprinting to the variation of body mass index in mice. <i>BMC Genomics</i> , 2015, 16, 576.	1.2	8
39	Prediction of Plant Height in <i>Arabidopsis thaliana</i> Using DNA Methylation Data. <i>Genetics</i> , 2015, 201, 779-793.	1.2	61
40	One Hundred Years of Statistical Developments in Animal Breeding. <i>Annual Review of Animal Biosciences</i> , 2015, 3, 19-56.	3.6	81
41	Enhancing Genome-Enabled Prediction by Bagging Genomic BLUP. <i>PLoS ONE</i> , 2014, 9, e91693.	1.1	41
42	Meta-Analysis of Candidate Gene Effects Using Bayesian Parametric and Non-Parametric Approaches. <i>Journal of Genomics</i> , 2014, 2, 1-19.	0.6	3
43	Kernel-based whole-genome prediction of complex traits: a review. <i>Frontiers in Genetics</i> , 2014, 5, 363.	1.1	127
44	Kernel-based variance component estimation and whole-genome prediction of pre-corrected phenotypes and progeny tests for dairy cow health traits. <i>Frontiers in Genetics</i> , 2014, 5, 56.	1.1	25
45	Bayesian Genomic-Enabled Prediction as an Inverse Problem. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 1991-2001.	0.8	6
46	Effect of genotype imputation on genome-enabled prediction of complex traits: an empirical study with mice data. <i>BMC Genomics</i> , 2014, 15, 149.	2.7	12
47	Bayesian analysis of additive epistasis arising from new mutations in mice. <i>Genetical Research</i> , 2014, 96, e008.	0.3	3
48	Genome-enabled prediction of quantitative traits in chickens using genomic annotation. <i>BMC Genomics</i> , 2014, 15, 109.	1.2	52
49	Machine learning methods and predictive ability metrics for genome-wide prediction of complex traits. <i>Livestock Science</i> , 2014, 166, 217-231.	0.6	123
50	Whole Genome Prediction of Bladder Cancer Risk With the Bayesian LASSO. <i>Genetic Epidemiology</i> , 2014, 38, 467-476.	0.6	11
51	A Genome-Wide Scan for Evidence of Selection in a Maize Population Under Long-Term Artificial Selection for Ear Number. <i>Genetics</i> , 2014, 196, 829-840.	1.2	63
52	Priors in Whole-Genome Regression: The Bayesian Alphabet Returns. <i>Genetics</i> , 2013, 194, 573-596.	1.2	374
53	Predicting complex traits using a diffusion kernel on genetic markers with an application to dairy cattle and wheat data. <i>Genetics Selection Evolution</i> , 2013, 45, 17.	1.2	33
54	Evaluation of linkage disequilibrium in wheat with an L1-regularized sparse Markov network. <i>Theoretical and Applied Genetics</i> , 2013, 126, 1991-2002.	1.8	4

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55	Predicting expected progeny difference for marbling score in Angus cattle using artificial neural networks and Bayesian regression models. <i>Genetics Selection Evolution</i> , 2013, 45, 34.	1.2	50
56	Contribution of an additive locus to genetic variance when inheritance is multi-factorial with implications on interpretation of GWAS. <i>Theoretical and Applied Genetics</i> , 2013, 126, 1457-1472.	1.8	17
57	Sensitivity to prior specification in Bayesian genome-based prediction models. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2013, 12, 375-91.	0.2	27
58	Using Whole-Genome Sequence Data to Predict Quantitative Trait Phenotypes in <i>Drosophila melanogaster</i> . <i>PLoS Genetics</i> , 2012, 8, e1002685.	1.5	191
59	Comparison Between Linear and Non-parametric Regression Models for Genome-Enabled Prediction in Wheat. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 1595-1605.	0.8	187
60	A Comprehensive Genetic Approach for Improving Prediction of Skin Cancer Risk in Humans. <i>Genetics</i> , 2012, 192, 1493-1502.	1.2	50
61	An ensemble-based approach to imputation of moderate-density genotypes for genomic selection with application to Angus cattle. <i>Genetical Research</i> , 2012, 94, 133-150.	0.3	40
62	A High Resolution Genome-Wide Scan for Significant Selective Sweeps: An Application to Pooled Sequence Data in Laying Chickens. <i>PLoS ONE</i> , 2012, 7, e49525.	1.1	65
63	Accuracy of Genome-Enabled Prediction in a Dairy Cattle Population using Different Cross-Validation Layouts. <i>Frontiers in Genetics</i> , 2012, 3, 27.	1.1	33
64	On measures of association among genetic variables. <i>Animal Genetics</i> , 2012, 43, 19-35.	0.6	9
65	Predicting complex quantitative traits with Bayesian neural networks: a case study with Jersey cows and wheat. <i>BMC Genetics</i> , 2011, 12, 87.	2.7	223
66	A Primer on High-Throughput Computing for Genomic Selection. <i>Frontiers in Genetics</i> , 2011, 2, 4.	1.1	18
67	Marker-assisted prediction of non-additive genetic values. <i>Genetica</i> , 2011, 139, 843-854.	0.5	26
68	Application of support vector regression to genome-assisted prediction of quantitative traits. <i>Theoretical and Applied Genetics</i> , 2011, 123, 1065-1074.	1.8	82
69	Long-term impacts of genome-enabled selection. <i>Journal of Applied Genetics</i> , 2011, 52, 467-480.	1.0	16
70	Inferring causal phenotype networks using structural equation models. <i>Genetics Selection Evolution</i> , 2011, 43, 6.	1.2	101
71	Application of site and haplotype-frequency based approaches for detecting selection signatures in cattle. <i>BMC Genomics</i> , 2011, 12, 318.	1.2	135
72	Prediction of body mass index in mice using dense molecular markers and a regularized neural network. <i>Genetical Research</i> , 2011, 93, 189-201.	0.3	67

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73	A two-step method for detecting selection signatures using genetic markers. <i>Genetical Research</i> , 2010, 92, 141-155.	0.3	53
74	Genomic-Enabled Prediction Based on Molecular Markers and Pedigree Using the Bayesian Linear Regression Package in R. <i>Plant Genome</i> , 2010, 3, 106-116.	1.6	183
75	A non-parametric mixture model for genome-enabled prediction of genetic value for a quantitative trait. <i>Genetica</i> , 2010, 138, 959-977.	0.5	10
76	Predicting genetic predisposition in humans: the promise of whole-genome markers. <i>Nature Reviews Genetics</i> , 2010, 11, 880-886.	7.7	250
77	Semi-parametric genomic-enabled prediction of genetic values using reproducing kernel Hilbert spaces methods. <i>Genetical Research</i> , 2010, 92, 295-308.	0.3	319
78	<i>L</i> ₂ -Boosting algorithm applied to high-dimensional problems in genomic selection. <i>Genetical Research</i> , 2010, 92, 227-237.	0.3	27
79	Radial basis function regression methods for predicting quantitative traits using SNP markers. <i>Genetical Research</i> , 2010, 92, 209-225.	0.3	43
80	Prediction of Genetic Values of Quantitative Traits in Plant Breeding Using Pedigree and Molecular Markers. <i>Genetics</i> , 2010, 186, 713-724.	1.2	664
81	Additive Genetic Variability and the Bayesian Alphabet. <i>Genetics</i> , 2009, 183, 347-363.	1.2	398
82	Comparison of classification methods for detecting associations between SNPs and chick mortality. <i>Genetics Selection Evolution</i> , 2009, 41, 18.	1.2	17
83	Genome-assisted prediction of a quantitative trait measured in parents and progeny: application to food conversion rate in chickens. <i>Genetics Selection Evolution</i> , 2009, 41, 3.	1.2	54
84	Predicting Quantitative Traits With Regression Models for Dense Molecular Markers and Pedigree. <i>Genetics</i> , 2009, 182, 375-385.	1.2	514
85	Inferring genetic values for quantitative traits non-parametrically. <i>Genetical Research</i> , 2008, 90, 525-540.	0.3	59
86	Nonparametric Methods for Incorporating Genomic Information Into Genetic Evaluations: An Application to Mortality in Broilers. <i>Genetics</i> , 2008, 178, 2305-2313.	1.2	110
87	Reproducing Kernel Hilbert Spaces Regression Methods for Genomic Assisted Prediction of Quantitative Traits. <i>Genetics</i> , 2008, 178, 2289-2303.	1.2	368
88	Inferring fixed effects in a mixed linear model from an integrated likelihood. <i>Acta Agriculturae Scandinavica - Section A: Animal Science</i> , 2007, 57, 183-191.	0.2	0
89	Genomic-Assisted Prediction of Genetic Value With Semiparametric Procedures. <i>Genetics</i> , 2006, 173, 1761-1776.	1.2	401
90	On the Quantitative Genetics of Mixture Characters. <i>Genetics</i> , 2006, 173, 2247-2255.	1.2	19

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91	A Thurstonian Model for Quantitative Genetic Analysis of Ranks: A Bayesian Approach. <i>Genetics</i> , 2006, 174, 1613-1624.	1.2	14
92	Quantitative Genetic Models for Describing Simultaneous and Recursive Relationships Between Phenotypes This article is dedicated to Arthur B. Chapman, teacher and mentor of numerous animal breeding students and disciple and friend of Sewall Wright.. <i>Genetics</i> , 2004, 167, 1407-1424.	1.2	172
93	On Marker-Assisted Prediction of Genetic Value: Beyond the Ridge. <i>Genetics</i> , 2003, 163, 347-365.	1.2	94
94	Statistics in Animal Breeding. <i>Journal of the American Statistical Association</i> , 2000, 95, 296-299.	1.8	10
95	Mixed effects linear models with t-distributions for quantitative genetic analysis: a Bayesian approach. <i>Genetics Selection Evolution</i> , 1999, 31, 1.	1.2	47
96	Attenuating effects of preferential treatment with Student-t mixed linear models: a simulation study. <i>Genetics Selection Evolution</i> , 1998, 30, 1.	1.2	29
97	Bayesian Methods in Animal Breeding Theory. <i>Journal of Animal Science</i> , 1986, 63, 217-244.	0.2	311
98	Theory and Analysis of Threshold Characters. <i>Journal of Animal Science</i> , 1982, 54, 1079-1096.	0.2	409
99	Statistics in Animal Breeding. , 0, .		3