Daniel Gianola

List of Publications by Citations

100 papers	6,515 citations	41 h-index	80 g-index
105 ext. papers	8,223 ext. citations	3.8 avg, IF	6.2 L-index

#	Paper	IF	Citations
100	Prediction of genetic values of quantitative traits in plant breeding using pedigree and molecular markers. *Genetics*, **2010**, 186, 713-24	4	508
99	Likelihood, Bayesian, and MCMC Methods in Quantitative Genetics **2002**,		422
98	Predicting quantitative traits with regression models for dense molecular markers and pedigree. *Genetics*, **2009**, 182, 375-85	4	392
97	Theory and Analysis of Threshold Characters. *Journal of Animal Science*, **1982**, 54, 1079-1096	0.7	330
96	Additive genetic variability and the Bayesian alphabet. *Genetics*, **2009**, 183, 347-63	4	308
95	Genomic-assisted prediction of genetic value with semiparametric procedures. *Genetics*, **2006**, 173, 1761-1776	4	287
94	Reproducing kernel hilbert spaces regression methods for genomic assisted prediction of quantitative traits. *Genetics*, **2008**, 178, 2289-303	4	271
93	Priors in whole-genome regression: the bayesian alphabet returns. *Genetics*, **2013**, 194, 573-96	4	248
92	Bayesian Methods in Animal Breeding Theory. *Journal of Animal Science*, **1986**, 63, 217-244	0.7	231
91	Semi-parametric genomic-enabled prediction of genetic values using reproducing kernel Hilbert spaces methods. *Genetical Research*, **2010**, 92, 295-308	1.1	221
90	Predicting genetic predisposition in humans: the promise of whole-genome markers. *Nature Reviews Genetics*, **2010**, 11, 880-6	30.1	205
89	Genomic heritability: what is it?. *PLoS Genetics*, **2015**, 11, e1005048	6	183
88	Genomic-Enabled Prediction Based on Molecular Markers and Pedigree Using the Bayesian Linear Regression Package in R. *Plant Genome*, **2010**, 3, 106-116	4.4	151
87	Using whole-genome sequence data to predict quantitative trait phenotypes in Drosophila melanogaster. *PLoS Genetics*, **2012**, 8, e1002685	6	144
86	Quantitative genetic models for describing simultaneous and recursive relationships between phenotypes. *Genetics*, **2004**, 167, 1407-24	4	140
85	Predicting complex quantitative traits with Bayesian neural networks: a case study with Jersey cows and wheat. *BMC Genetics*, **2011**, 12, 87	2.6	135
84	Comparison between linear and non-parametric regression models for genome-enabled prediction in wheat. *G3: Genes, Genomes, Genetics*, **2012**, 2, 1595-605	3.2	130

83	Application of site and haplotype-frequency based approaches for detecting selection signatures in cattle. *BMC Genomics*, **2011**, 12, 318	4.5	110
82	Nonparametric methods for incorporating genomic information into genetic evaluations: an application to mortality in broilers. *Genetics*, **2008**, 178, 2305-13	4	89
81	Kernel-based whole-genome prediction of complex traits: a review. *Frontiers in Genetics*, **2014**, 5, 363	4.5	88
80	On marker-assisted prediction of genetic value: beyond the ridge. *Genetics*, **2003**, 163, 347-65	4	81
79	Inferring causal phenotype networks using structural equation models. *Genetics Selection Evolution*, **2011**, 43, 6	4.9	77
78	Machine learning methods and predictive ability metrics for genome-wide prediction of complex traits. *Livestock Science*, **2014**, 166, 217-231	1.7	73
77	Applications of Machine Learning Methods to Genomic Selection in Breeding Wheat for Rust Resistance. *Plant Genome*, **2018**, 11, 170104	4.4	58
76	Multi-environment Genomic Prediction of Plant Traits Using Deep Learners With Dense Architecture. *G3: Genes, Genomes, Genetics*, **2018**, 8, 3813-3828	3.2	58
75	Multi-trait, Multi-environment Deep Learning Modeling for Genomic-Enabled Prediction of Plant Traits. *G3: Genes, Genomes, Genetics*, **2018**, 8, 3829-3840	3.2	55
74	Defining window-boundaries for genomic analyses using smoothing spline techniques. *Genetics Selection Evolution*, **2015**, 47, 30	4.9	51
73	Prediction of body mass index in mice using dense molecular markers and a regularized neural network. *Genetical Research*, **2011**, 93, 189-201	1.1	51
72	A Benchmarking Between Deep Learning, Support Vector Machine and Bayesian Threshold Best Linear Unbiased Prediction for Predicting Ordinal Traits in Plant Breeding. *G3: Genes, Genomes, Genetics*, **2019**, 9, 601-618	3.2	51
71	Inferring genetic values for quantitative traits non-parametrically. *Genetical Research*, **2008**, 90, 525-40	1.1	48
70	A genome-wide scan for evidence of selection in a maize population under long-term artificial selection for ear number. *Genetics*, **2014**, 196, 829-40	4	47
69	Prediction of Plant Height in Arabidopsis thaliana Using DNA Methylation Data. *Genetics*, **2015**, 201, 779-93	4	45
68	One hundred years of statistical developments in animal breeding. *Annual Review of Animal Biosciences*, **2015**, 3, 19-56	13.7	44
67	Deep learning versus parametric and ensemble methods for genomic prediction of complex phenotypes. *Genetics Selection Evolution*, **2020**, 52, 12	4.9	44
66	A high resolution genome-wide scan for significant selective sweeps: an application to pooled sequence data in laying chickens. *PLoS ONE*, **2012**, 7, e49525	3.7	44

65	Application of support vector regression to genome-assisted prediction of quantitative traits. *Theoretical and Applied Genetics*, **2011**, 123, 1065-74	6	44
64	Genome-assisted prediction of a quantitative trait measured in parents and progeny: application to food conversion rate in chickens. *Genetics Selection Evolution*, **2009**, 41, 3	4.9	44
63	A comprehensive genetic approach for improving prediction of skin cancer risk in humans. *Genetics*, **2012**, 192, 1493-502	4	44
62	Application of neural networks with back-propagation to genome-enabled prediction of complex traits in Holstein-Friesian and German Fleckvieh cattle. *Genetics Selection Evolution*, **2015**, 47, 22	4.9	43
61	Do Molecular Markers Inform About Pleiotropy?. *Genetics*, **2015**, 201, 23-9	4	42
60	New Deep Learning Genomic-Based Prediction Model for Multiple Traits with Binary, Ordinal, and Continuous Phenotypes. *G3: Genes, Genomes, Genetics*, **2019**, 9, 1545-1556	3.2	41
59	Genome-enabled prediction using probabilistic neural network classifiers. *BMC Genomics*, **2016**, 17, 208	4.5	35
58	Predicting expected progeny difference for marbling score in Angus cattle using artificial neural networks and Bayesian regression models. *Genetics Selection Evolution*, **2013**, 45, 34	4.9	35
57	Radial basis function regression methods for predicting quantitative traits using SNP markers. *Genetical Research*, **2010**, 92, 209-25	1.1	35
56	Enhancing genome-enabled prediction by bagging genomic BLUP. *PLoS ONE*, **2014**, 9, e91693	3.7	32
55	Genome-enabled prediction of quantitative traits in chickens using genomic annotation. *BMC Genomics*, **2014**, 15, 109	4.5	31
54	A two-step method for detecting selection signatures using genetic markers. *Genetical Research*, **2010**, 92, 141-55	1.1	30
53	An ensemble-based approach to imputation of moderate-density genotypes for genomic selection with application to Angus cattle. *Genetical Research*, **2012**, 94, 133-50	1.1	29
52	Cross-Validation Without Doing Cross-Validation in Genome-Enabled Prediction. *G3: Genes, Genomes, Genetics*, **2016**, 6, 3107-3128	3.2	28
51	Predicting complex traits using a diffusion kernel on genetic markers with an application to dairy cattle and wheat data. *Genetics Selection Evolution*, **2013**, 45, 17	4.9	28
50	Mixed effects linear models with t-distributions for quantitative genetic analysis: a Bayesian approach. *Genetics Selection Evolution*, **1999**, 31, 25	4.9	28
49	A predictive assessment of genetic correlations between traits in chickens using markers. *Genetics Selection Evolution*, **2017**, 49, 16	4.9	26
48	Sensitivity to prior specification in Bayesian genome-based prediction models. *Statistical Applications in Genetics and Molecular Biology*, **2013**, 12, 375-91	1.2	26

47	Genome-wide association analysis in dogs implicates 99 loci as risk variants for anterior cruciate ligament rupture. *PLoS ONE*, **2017**, 12, e0173810	3.7	25
46	Predictive ability of genome-assisted statistical models under various forms of gene action. *Scientific Reports*, **2018**, 8, 12309	4.9	25
45	Deep Kernel and Deep Learning for Genome-Based Prediction of Single Traits in Multienvironment Breeding Trials. *Frontiers in Genetics*, **2019**, 10, 1168	4.5	25
44	Accuracy of Genome-Enabled Prediction in a Dairy Cattle Population using Different Cross-Validation Layouts. *Frontiers in Genetics*, **2012**, 3, 27	4.5	24
43	Kernel-based variance component estimation and whole-genome prediction of pre-corrected phenotypes and progeny tests for dairy cow health traits. *Frontiers in Genetics*, **2014**, 5, 56	4.5	21
42	Differential contribution of genomic regions to marked genetic variation and prediction of quantitative traits in broiler chickens. *Genetics Selection Evolution*, **2016**, 48, 10	4.9	20
41	Marker-assisted prediction of non-additive genetic values. *Genetica*, **2011**, 139, 843-54	1.5	20
40	L2-Boosting algorithm applied to high-dimensional problems in genomic selection. *Genetical Research*, **2010**, 92, 227-37	1.1	20
39	The Causal Meaning of Genomic Predictors and How It Affects Construction and Comparison of Genome-Enabled Selection Models. *Genetics*, **2015**, 200, 483-94	4	17
38	Genome-Wide Association Studies with a Genomic Relationship Matrix: A Case Study with Wheat and Arabidopsis. *G3: Genes, Genomes, Genetics*, **2016**, 6, 3241-3256	3.2	16
37	Contribution of an additive locus to genetic variance when inheritance is multi-factorial with implications on interpretation of GWAS. *Theoretical and Applied Genetics*, **2013**, 126, 1457-72	6	16
36	Comparison of classification methods for detecting associations between SNPs and chick mortality. *Genetics Selection Evolution*, **2009**, 41, 18	4.9	15
35	Attenuating effects of preferential treatment with Student-t mixed linear models: a simulation study. *Genetics Selection Evolution*, **1998**, 30, 565	4.9	15
34	Including Phenotypic Causal Networks in Genome-Wide Association Studies Using Mixed Effects Structural Equation Models. *Frontiers in Genetics*, **2018**, 9, 455	4.5	15
33	Assessing genomic prediction accuracy for Holstein sires using bootstrap aggregation sampling and leave-one-out cross validation. *Journal of Dairy Science*, **2017**, 100, 453-464	4	14
32	A primer on high-throughput computing for genomic selection. *Frontiers in Genetics*, **2011**, 2, 4	4.5	14
31	On the quantitative genetics of mixture characters. *Genetics*, **2006**, 173, 2247-55	4	14
30	Long-term impacts of genome-enabled selection. *Journal of Applied Genetics*, **2011**, 52, 467-80	2.5	12

29	Prediction of Complex Traits: Robust Alternatives to Best Linear Unbiased Prediction. *Frontiers in Genetics*, **2018**, 9, 195	4.5	11
28	A Thurstonian model for quantitative genetic analysis of ranks: a Bayesian approach. *Genetics*, **2006**, 174, 1613-24	4	11
27	Whole genome prediction of bladder cancer risk with the Bayesian LASSO. *Genetic Epidemiology*, **2014**, 38, 467-76	2.6	10
26	Effect of genotype imputation on genome-enabled prediction of complex traits: an empirical study with mice data. *BMC Genetics*, **2014**, 15, 149	2.6	10
25	On measures of association among genetic variables. *Animal Genetics*, **2012**, 43 Suppl 1, 19-35	2.5	9
24	Statistics in Animal Breeding. *Journal of the American Statistical Association*, **2000**, 95, 296-299	2.8	9
23	A GWAS assessment of the contribution of genomic imprinting to the variation of body mass index in mice. *BMC Genomics*, **2015**, 16, 576	4.5	8
22	Integration of single nucleotide variants and whole-genome DNA methylation profiles for classification of rheumatoid arthritis cases from controls. *Heredity*, **2020**, 124, 658-674	3.6	8
21	A non-parametric mixture model for genome-enabled prediction of genetic value for a quantitative trait. *Genetica*, **2010**, 138, 959-77	1.5	8
20	Incorporating parent-of-origin effects in whole-genome prediction of complex traits. *Genetics Selection Evolution*, **2016**, 48, 34	4.9	7
19	Joint Use of Genome, Pedigree, and Their Interaction with Environment for Predicting the Performance of Wheat Lines in New Environments. *G3: Genes, Genomes, Genetics*, **2019**, 9, 2925-2934	3.2	7
18	Improving reliability of genomic predictions for Jersey sires using bootstrap aggregation sampling. *Journal of Dairy Science*, **2016**, 99, 3632-3645	4	6
17	A Multiple-Trait Bayesian Lasso for Genome-Enabled Analysis and Prediction of Complex Traits. *Genetics*, **2020**, 214, 305-331	4	5
16	Bayesian genomic-enabled prediction as an inverse problem. *G3: Genes, Genomes, Genetics*, **2014**, 4, 1991-2001	3.2	5
15	Feature Selection Stability and Accuracy of Prediction Models for Genomic Prediction of Residual Feed Intake in Pigs Using Machine Learning. *Frontiers in Genetics*, **2021**, 12, 611506	4.5	5
14	Evaluation of linkage disequilibrium in wheat with an L1-regularized sparse Markov network. *Theoretical and Applied Genetics*, **2013**, 126, 1991-2002	6	4
13	Inferring trait-specific similarity among individuals from molecular markers and phenotypes with Bayesian regression. *Theoretical Population Biology*, **2020**, 132, 47-59	1.2	4
12	Machine Learning Prediction of Crossbred Pig Feed Efficiency and Growth Rate From Single Nucleotide Polymorphisms. *Frontiers in Genetics*, **2020**, 11, 567818	4.5	4

LIST OF PUBLICATIONS

11	Genome-wide methylation prediction of biological age using reproducing kernel Hilbert spaces and Bayesian ridge regressions		3
10	It is unlikely that genomic selection will ever be 100% accurate. *Journal of Animal Breeding and Genetics*, **2017**, 134, 438-440	2.9	2
9	Bayesian analysis of additive epistasis arising from new mutations in mice. *Genetical Research*, **2014**, 96, e008	1.1	2
8	Statistics in Animal Breeding		2
7	A certain invariance property of BLUE in a whole-genome regression context. *Journal of Animal Breeding and Genetics*, **2019**, 136, 113-117	2.9	2
6	A robust Bayesian genome-based median regression model. *Theoretical and Applied Genetics*, **2019**, 132, 1587-1606	6	1
5	Meta-analysis of candidate gene effects using bayesian parametric and non-parametric approaches. *Journal of Genomics*, **2014**, 2, 1-19	0.9	1
4	Including phenotypic causal networks in genome-wide association studies using mixed effects structural equation models		1
3	Prediction of biological age and evaluation of genome-wide dynamic methylomic changes throughout human aging. *G3: Genes, Genomes, Genetics*, **2021**,	3.2	1
2	Genome-Enabled Prediction Methods Based on Machine Learning.. *Methods in Molecular Biology*, **2022**, 2467, 189-218	1.4	0
1	Inferring fixed effects in a mixed linear model from an integrated likelihood. *Acta Agriculturae Scandinavica - Section A: Animal Science*, **2007**, 57, 183-191	0.6	