

Curriculum Vitae
Gustavo de los Campos
(Jan, 2014)



SUMMARY. My academic interests center on statistical learning methods with emphasis on applications in the analysis and prediction of complex traits. I have an Agronomy degree from Universidad de la República-Uruguay, as well as two MS degrees (Statistics and Animal Sciences) and a joint doctoral degree (Animal Sciences and Agricultural & Applied Economics) from the University of Wisconsin-Madison. I am currently an Associate Professor at the [Section on Statistical Genetics](#) of the Biostatistics department at University of Alabama-Birmingham and my work focuses on the use of whole genome markers (e.g., SNPs), and other omics, for the prediction of complex traits in humans, animals and plants.

Contents

1. Education	2
2. Professional experience	2
<i>Current</i>	2
<i>Previous</i>	3
<i>Teaching</i>	4
<i>Editor/Reviewer</i>	5
3. Publications.....	5
<i>Peer-reviewed</i>	5
<i>Proceedings & abstracts</i>	11
<i>Extension publications</i>	15
4. Funding	16
<i>Active</i>	16
<i>Completed</i>	16
<i>Pending</i>	17
5. Selected Invited Presentations (2011 up-to-date)	18
6. Mentorship	19
7. Fellowships and awards	20
8. Personal information.....	20
9. Academic references	20

1. Education

2009. PhD, joint degree in [Animal Sciences](#) and [Agricultural & Applied Economics](#), UW-Madison. **Advisers:** [Daniel Gianola](#) and [Jeremy Foltz](#). **Dissertation:** *Semi-Parametric Methods with applications to Quantitative Genetics and Production Economics*. **Committee members:** [Daniel Gianola](#), [Jeremy Foltz](#), [Grace Wahba](#), [Jean Paul Chavas](#), [Guilherme Rosa](#), and [Kent Weigel](#).
2007. MS, [Statistics](#), UW-Madison. **Adviser:** [Jun Shao](#).
2005. MS, [Animal Sciences](#), UW-Madison. **Adviser:** [Daniel Gianola](#). **Thesis:** *Structural Equation Models with Applications to Quantitative Genetics*. **Committee members:** [Daniel Gianola](#), [Kent Weigel](#) and [Robert Hauser](#).
1998. B.A., Agronomy (plant and animal science), [Universidad de la República–Uruguay](#). **Adviser:** Guillermo Scarlatto. **Final project:** *Sustainability of the Recent Growth of Rice Production in Northern Uruguay*.

2. Professional experience

Current

- 2014 up-to-date. Associate Professor, [Section on Statistical Genetics](#), Biostatistics Department, University of Alabama-Birmingham.
- 2011-2014. **Assistant Professor**, [Section on Statistical Genetics](#), Biostatistics Department, University of Alabama-Birmingham.
- 2011 up-to-date. Member of the [Center for Aging](#) of University of Alabama at Birmingham.
- 2011 up-to-date. Member of the [Nutrition Obesity Research Center](#) of University of Alabama at Birmingham.
- 2009 up-to-date. **Consultant**, [CIMMYT](#). My consulting activities focus on: (a) development and evaluation parametric and non-parametric methods for the prediction of genomic values using dense marker panels and pedigree in Wheat and Maize, and (b) development of

customized pipelines data-analysis for implementing genome-wide selection on CIMMYT Maize and Wheat breeding programs.

2009 up-to-date. **Consultant**, [AVIAGEN](#), UK. My consulting activities focus on: (a) development of methods and of software for genome-wide selection in broilers and (b) development of a workflow for implementing genomic selection for broilers.

Previous

2010. **Post-Doctoral Fellow**, [Section on Statistical Genetics](#), Biostatistics Department, University of Alabama-Birmingham. Mentor: Dr. [David Allison](#). My research focused on use of dense molecular markers for prediction of likelihood of disease in humans.

2009. **Post-Doctoral Fellow**, [Dairy Science Department](#), UW-Madison. Supervisor: Dr. [Kent Weigel](#). My research focused on multiple-trait models for genomic selection in dairy cattle.

2003-09. **Research Assistant**, Animal Sciences and Agricultural and Applied Economics departments, UW-Madison.

1999-02. **Researcher**, National Institute of Agricultural Research ([INIA](#)), Uruguay. My research and extension activities focused on applied statistical methods with an emphasis on quantitative genetics and the economics of genetic programs.

1999. **Technical Member**, [EQUIPOS-MORI](#), Uruguay. The project aimed at characterizing the technological attitude and behavior of Uruguayan cattlemen, and was developed by EQUIPOS-MORI for INIA.

1996-99. **Research Assistant**, Interdisciplinary Center of Studies about Development ([CIEDUR](#)), Uruguay. At CIEDUR I worked as Research Assistant to several projects focusing on agricultural economics and development.

1994-95. **Technical Assistant**, SERAGRO, a private consulting firm. Here I worked in maintenance of the economics database.

Teaching

2013 Instructor, Intermediate Statistical Analysis, Biostatistics 612, University of Alabama at Birmingham.

2010-up-to-date. Co-Instructor, together with Dr. D. Gianola, in the short course *Statistical Learning Methods For Genome-based Prediction of Complex Traits*. This course has been/will be offered at the institutions listed below. The course has had between 30-90 participants per instance.

Date	Institution
May. 2014	Kansas State University , Kansas, US.
Dec. 2013	Universidade Estadual Paulista , Jaboticabal, Brasil
Oct., 2013	Colegio de Postgraduados / CIMMYT , Mexico.
May, 2013	University of Wisconsin-Madison , US.
Dec., 2012	Universidad de la Republica , Uruguay.
Oct., 2012	Argentinean Biometric Society, Rosario, Argentina.
Sept., 2012	Technical University of Munich , Germany.
May, 2012	Iowa State University , US.
Feb., 2012	University of New England , Armidale, Australia.
May, 2011	University of Alabama at Birmingham , US.
Oct., 2011	Wageningen University , The Netherlands.
April, 2011	University of Aarhus , Denmark.
Sept., 2010	University of Padua , Italy.

2009. **Teaching Assistant**, Semi-parametric methods in genomic modeling (UW-Madison, ANSCI 875). *Instructor*: [Daniel Gianola](#). The lab activities I was involved on covered

computational techniques for implementing parametric and non-parametric models for the estimation of genetic values using dense marker panels and pedigree.

2007. **Teaching Assistant**, Bayesian Methods in Biology (UW-Madison, ANSCI 875). *Instructor:* [Daniel Gianola](#). The lab activities I was involved on focused on computational techniques for implementing several classes of Bayesian methods in biology.

1998-99. **Teaching Assistant**, Agricultural Economics Department, [Universidad de la Republica](#) under the supervision of Prof. Miguel Vasallo.

Editor/Reviewer

2010-up to date. Associate Editor of [Genetics Selection Evolution](#)

2011-up to date. Associate Editor of [Frontiers in Genetics](#).

2003-up to date. Reviewed scientific articles for the following journals: [PLoS Genetics](#), [Open Biology](#), [Genetics](#), [Genetics Research](#), [Genetics Selection Evolution](#), [Journal of Animal Sciences](#), [Livestock Science](#), [Obesity](#), [Animal Genetics](#), [Theoretical and Applied Genetics](#), [PLoS One](#), and [Preventive Veterinary Medicine](#).

3. Publications

Peer-reviewed

2014. Perez-Rodriguez, Paulino and Gustavo de los Campos. Genome-wide Regression & Prediction with the BGLR statistical package. *Genetics* (published online ahead of print (*Genetics*, pii: genetics.114.164442. [[PMID: 25009151](#)])

2014. Klimentidis, Yann, C., Nathan E. Wineinger, Ana I. Vazquez and **Gustavo de los Campos**. Multiple metabolic genetic risk scores and type 2 diabetes risk in three racial/ethnic groups (published online June 06, 2014 <http://dx.doi.org/10.1210/jc.2014-1818>).
2014. **de los Campos, Gustavo** and Daniel A. Sorensen. On the genomic analysis of data from structured populations (Editorial). *Journal of Animal Breeding and Genetics*, 131(3): 163-164. DOI: 10.1111/jbg.12091
2013. **de los Campos, Gustavo**, and Daniel A. Sorensen. A Commentary on Pitfalls of Predicting Complex Traits from SNPs. *Nature Reviews Genetics* 14 (12): 894–894. [[doi:10.1038/nrg3457-c1](https://doi.org/10.1038/nrg3457-c1)] [[PMID: 24240514](https://pubmed.ncbi.nlm.nih.gov/24240514/)]
2013. Jarquín, Diego, Crossa, José, Lacaze, Xavier, Cheyron, Philippe, Daucourt, Joëlle, Lorgeou, Josiane, Piraux, Piraux, Guerreiro, Laurent, Pérez, Paulino, Calus, Mario, Burgueño, Juan, **de los Campos, Gustavo**. A reaction norm model for genomic selection using high-dimensional genomic and environmental data. *Theor. Appl. Genet.*: 1–13. [[doi:10.1007/s00122-013-2243-1](https://doi.org/10.1007/s00122-013-2243-1)] [[PMID: 24337101](https://pubmed.ncbi.nlm.nih.gov/24337101/)] [[PMCID: PMC3931944](https://pubmed.ncbi.nlm.nih.gov/PMC3931944/)]
2013. **de los Campos, Gustavo**, Ana I. Vazquez, Rohan Fernando, Yann C. Klimentidis, and Daniel Sorensen. Prediction of Complex Human Traits Using the Genomic Best Linear Unbiased Predictor. Edited by Michael E. Goddard. *PLoS Genetics* 9 (7) (July 11): [e1003608] [[doi:10.1371/journal.pgen.1003608](https://doi.org/10.1371/journal.pgen.1003608)] [[PMID: 23874214](https://pubmed.ncbi.nlm.nih.gov/23874214/)] [[PMCID: PMC3815055](https://pubmed.ncbi.nlm.nih.gov/PMC3815055/)]
2013. **de los Campos, Gustavo**, Paulino Pérez, Ana I. Vazquez, and José Crossa. Genome-Enabled Prediction Using the BLR (Bayesian Linear Regression) R-Package. In *Genome-Wide Association Studies and Genomic Prediction*, edited by Cedric Gondro, Julius van der Werf, and Ben Hayes. *Methods in Molecular Biology* 1019: 299–320. Humana Press. [[PMID:23756896](https://pubmed.ncbi.nlm.nih.gov/23756896/)]
2013. **de los Campos, Gustavo**, John M. Hickey, Ricardo Pong-Wong, Hans D. Daetwyler, and Mario P. L. Calus. Whole Genome Regression and Prediction Methods Applied to Plant and Animal Breeding. *Genetics* 2: 327-345. [doi:[10.1534/genetics.112.143313](https://doi.org/10.1534/genetics.112.143313)] [[PMID: 22745228](https://pubmed.ncbi.nlm.nih.gov/22745228/)] [[PMCID: PMC3567727](https://pubmed.ncbi.nlm.nih.gov/PMC3567727/)]
2013. Klimentidis, Yann C., Ana I. Vazquez, Gustavo **de los Campos**, David B. Allison, Mark Dransfield, and Victor J. Thannickal. Heritability of Pulmonary Function Estimated from Pedigree and Whole-genome Markers. *Frontiers in Genetics* 4: 174. [[doi:10.3389/fgene.2013.00174](https://doi.org/10.3389/fgene.2013.00174)] [[PMID:24058366](https://pubmed.ncbi.nlm.nih.gov/24058366/)] [[PMCID: PMC3766834](https://pubmed.ncbi.nlm.nih.gov/PMC3766834/)]

2013. Robertson Henry, T., **Gustavo de los Campos** and David B. Allison. Turning the analysis of obesity–mortality associations upside down: Modeling years of life lost through conditional distributions. *Obesity* 21 (2): 398-404. [doi: [10.1002/oby.20019](https://doi.org/10.1002/oby.20019)] [PMCID: [PMC3610864](https://pubmed.ncbi.nlm.nih.gov/PMC3610864/)].
2013. Crossa, J., Y. Beyene, S. Kassa, P. Pérez, J.M. Hickey, C. Chen, G. **de los Campos**, et al. Genomic Prediction in Maize Breeding Populations with Genotyping-by-sequencing. *G3: GENES, GENOMES, GENETICS* 3(11):1903-1926 [doi: [10.1534/g3.113.008227](https://doi.org/10.1534/g3.113.008227)] [PMID:[24022750](https://pubmed.ncbi.nlm.nih.gov/24022750/)] [PMCID: [PMC3815055](https://pubmed.ncbi.nlm.nih.gov/PMC3815055/)]
2013. Daetwyler, Hans, Mario P.L. Calus, Ricardo Pong-Wong, **Gustavo de los Campos** and John M. Hickey . Simulation of Data, Validation, Reporting and Benchmarking of Genomic Prediction in Animals and Plants *Genetics* 2:347–365. Available online ahead of print: [doi:[10.1534/genetics.112.147983](https://doi.org/10.1534/genetics.112.147983)] [PMID: [23222650](https://pubmed.ncbi.nlm.nih.gov/23222650/)] [PMCID: [PMC3567728](https://pubmed.ncbi.nlm.nih.gov/PMC3567728/)]
2012. Vazquez, Ana I, **Gustavo de los Campos**, Yann C Klimentidis, Guilherme J M Rosa, Daniel Gianola, Nengjun Yi, and David B Allison. A Comprehensive Genetic Approach for Improving Prediction of Skin Cancer Risk in Humans. *Genetics* (October 10). [doi:[10.1534/genetics.112.141705](https://doi.org/10.1534/genetics.112.141705)]. [PMID: [23051645](https://pubmed.ncbi.nlm.nih.gov/23051645/)] [PMCID: [PMC3512154](https://pubmed.ncbi.nlm.nih.gov/PMC3512154/)]
2012. **de los Campos**, Gustavo, Yann C. Klimentidis, Ana I. Vazquez, and David B. Allison. Prediction of Expected Years of Life Using Whole-Genome Markers *PLoS ONE* (7) (July 25): e40964. [doi:[10.1371/journal.pone.0040964](https://doi.org/10.1371/journal.pone.0040964)] [PMID: [22848416](https://pubmed.ncbi.nlm.nih.gov/22848416/)] [PMCID:[PMC3405107](https://pubmed.ncbi.nlm.nih.gov/PMC3405107/)]
2012. Janss, L., **de los Campos, G.**, Sheehan, N. and Sorensen, D. Inferences from Genomic Models in Stratified Populations. *Genetics* [doi: [10.1534/genetics.112.141143](https://doi.org/10.1534/genetics.112.141143)] [PMID:[22813891](https://pubmed.ncbi.nlm.nih.gov/22813891/)] [PMCID: [PMC3454890](https://pubmed.ncbi.nlm.nih.gov/PMC3454890/)]
2012. Pérez, Paulino, **Gustavo de los Campos**, Susan Dreisigacker, Hector Sanchez-Villeda, and José Crossa. Application of Bayesian Elastic Net and Other Shrinkage Methods in Genomic Selection Adn QTL Mapping. *Journal of the Indian Society of Agricultural Statistics* 66 (3): 413–426.
2012. González-Camacho J. M., **de los Campos G.**, Pérez P., Gianola D., Cairns J. E., Mahuku G., Babu R. and Crossa J. Genome-enabled prediction of genetic values using radial basis function neural networks. *Theoretical & Applied Genetics* [doi:[10.1007/s00122-012-1876-9](https://doi.org/10.1007/s00122-012-1876-9)] [PMID:[22566067](https://pubmed.ncbi.nlm.nih.gov/22566067/)] [PMCID: [PMC3405257](https://pubmed.ncbi.nlm.nih.gov/PMC3405257/)].

2012. Hickey, J.M., Crossa, J., Babu, R. and **de los Campos, G.** Factors Affecting the Accuracy of Genotype Imputation in Populations from Several Maize Breeding Programs. [doi: 10.2135/cropsci2011.07.0358] [Crop Sci 52 654-663](#).
2011. Burgueño, J., **de los Campos, G.** Weigel, K., Crossa, J. Genomic Prediction of Breeding Values when Modeling Genotype \times Environment Interaction using Pedigree and Dense Molecular Markers. [doi: 10.2135/cropsci2011.06.0299] [Crop Sci 51:944-954](#).
2011. Fonseca Silva, F., Rosa, G.J.M., Guimarães, S.E.F., Lopes, P.S. and **de los Campos, G.** Three-step Bayesian factor analysis applied to QTL detection in crosses between outbred pig populations. [Livestock Science 142:210-215](#) [doi:10.1016/j.livsci.2011.07.012]
2011. Makowsky, R., Pajewski, N.M., Klimentidis, Y.C., Vazquez, A.I., Duarte, C.W., Allison, D.B. and **de los Campos, G.** Beyond Missing Heritability: Prediction of Complex Traits. [PLoS GENETICS 7\(4\):e1002051](#). [PMID: 21552331] [PMCID: PMC3084207]
2011. Inferring causal phenotype networks using structural equation models. Rosa, Guilherme, J.M., Valente B.D., de los Campos, G., Wu X.L., Gianola, D. and Silva M.A. Genetics Selection Evolution 43:6. [PMID 21310061] [PMCID PMC3056759]
2010. **de los Campos, G.**, Gianola, D. and Allison, D.B. Predicting genetic predisposition in humans: the promise of whole-genome markers. Nature Reviews Genetics 11, 880-886. [doi:10.1038/nrg2898][PMID: 21045869]
2010. **de los Campos, G.**, Gianola, D., Rosa, G.J.M., Weigel, K.A. and Crossa, J. Semi-parametric genomic-enabled prediction of genetic values using reproducing kernel Hilbert spaces methods. Genetics Research, 92:295-308. [doi: 10.1017/S0016672310000285] [PMID:20943010]
2010. Crossa, J., **de los Campos, G.**, Pérez, P., Gianola, D., Burgueño, J., Araus, J.L., Makumbi, D., Singh, R., Dreisigacker, S., Yan, J., Arief, V., Banziger, M., and Braun, H.J. Prediction of Genetic Values of Quantitative Traits in Plant Breeding Using Pedigree and Molecular Markers. [Genetics, 186: 713-724](#). [doi:10.1534/genetics.110.118521] [PMID: 20813882] [PMID: 20813882] [PMCID:PMC2954475]
2010. Pérez, P., **de los Campos, G.**, Crossa, J. and Gianola, D. Genomic-enabled prediction based on molecular markers and pedigree using the BLR package in R. The Plant Genome, 3:106-116. [doi: 10.3835/plantgenome2010.04.0005] [PMID:21566722]

[\[PMCID: PMC3091623\]](#)

2010. Weigel, K.A., **de los Campos**, G., Vazquez, A.I., Rosa, G.J.M., Gianola, D., Van Tassell, C.P. Accuracy of direct genomic values derived from imputed single nucleotide polymorphism genotypes in Jersey cattle. *Journal of Dairy Science* 93: 5423-5435. [\[doi:10.3168/jds.2010-3149\]](#) [\[PMID: 20965358\]](#)
2010. Vazquez, A.I., Rosa, G. J. M., Weigel, K.A., **de los Campos**, G., Gianola, D. and Allison, D.B. Predictive ability of subsets of single nucleotide polymorphisms with and without parent average in US Holsteins. *Journal of Dairy Science* 93: 5942-5949. [\[doi: 10.3168/jds.2010-3335\]](#) [\[PMID: 21094768\]](#) [\[PMCID:PMC3207239\]](#)
2010. Valente B.D., G.J.M. Rosa, **G. de los Campos**, D. Gianola, and M.A. Silva. Searching for Recursive Causal Structures in Multivariate Quantitative Genetics Mixed Models. *Genetics*, 185:633-644. [\[doi:10.1534/genetics.109.112979\]](#) [\[PMID: 20351220\]](#) [\[PMCID: PMC2881143\]](#)
2010. Cecchinato A., **G. de los Campos**, D. Gianola, L. Gallo and P. Carnier. The relevance of purebred information for predicting genetic merit of survival at birth of crossbred piglets. *Journal of animal Science*, 88: 481-490. [\[doi:10.2527/jas.2008-1744\]](#) [\[PMID: 19897636\]](#)
2010. Lopez de Maturana E., **G. de los Campos**, X. L. Wu, D. Gianola, K. A. Weigel and G. J. M. Rosa. Modeling Relationships between Calving Traits: a Comparison between Standard and Recursive Mixed Models. *Genetics Selection Evolution*, 42:1. [\[doi: 10.1186/1297-9686-42-1\]](#) [\[PMID: 20100345\]](#) [\[PMCID: PMC2830933\]](#)
2009. **de los Campos G.**, H. Naya, D. Gianola, J. Crossa, A. Legarra, E. Manfredi, and J. M. Cotes. Predicting quantitative traits with regression models for dense molecular markers and pedigree. *Genetics*, 182: 375-385. [\[doi:10.1534/genetics.109.101501\]](#) [\[PMID: 19293140\]](#) [\[PMCID:PMC2674834\]](#)
2009. **de los Campos G.**, D. Gianola, and G. J. M. Rosa. Reproducing kernel Hilbert spaces regression: A general framework for genetic evaluation. *Journal of Animal Science*, 87: 1883-1887. [\[doi:10.2527/jas.2008-1259\]](#) [\[PMID: 19213705\]](#)
2009. Gianola D., **G. de los Campos**, W. G. Hill, E. Manfredi and R. Fernando. Additive genetic variability and the Bayesian alphabet. *Genetics*, 183: 347-363. [\[doi: 10.1534/genetics.109.103952\]](#)[\[PMID: 19620397\]](#) [\[PMCID: PMC2746159\]](#)

2009. Weigel K. A., **G. de los Campos**, O. González-Recio, H. Naya, X. L. Wu, N. Long, G. J. M. Rosa, and D. Gianola. Predictive ability of direct genomic values for Lifetime Net Merit of Holstein sires using selected subsets of single nucleotide polymorphism markers. *Journal of Dairy Science*, 92: 5239-5247. [[doi:10.3168/jds.2009-2092](https://doi.org/10.3168/jds.2009-2092)] [[PMID: 19762843](https://pubmed.ncbi.nlm.nih.gov/19762843/)]
2009. Forni S., D. Gianola, G. J. M. Rosa and **G. de los Campos**. A dynamic linear model for genetic analysis of longitudinal traits. *Journal Animal Science* 87: 3845-3853. [[doi:10.2527/jas.2008-1514](https://doi.org/10.2527/jas.2008-1514)] [[PMID: 19684262](https://pubmed.ncbi.nlm.nih.gov/19684262/)]
2009. Pérez-Cabal M. A., **G. de los Campos**, A. I. Vazquez, D. Gianola, G. J. M. Rosa, K. A. Weigel, and R. Alenda. Genetic evaluation of susceptibility to clinical mastitis in Spanish Holstein cows. *Journal of Dairy Science*, 92: 3472-3480. [[doi: 10.3168/jds.2008-1978](https://doi.org/10.3168/jds.2008-1978)] [[PMID: 19528625](https://pubmed.ncbi.nlm.nih.gov/19528625/)]
2008. Gianola D. and **G. de los Campos**. Inferring genetic values for quantitative traits non-parametrically. *Genetics Research*, 90: 525-540. [[doi:10.1017/S0016672308009890](https://doi.org/10.1017/S0016672308009890)] [[PMID: 19123970](https://pubmed.ncbi.nlm.nih.gov/19123970/)]
2007. **de los Campos G.** and D. Gianola. Factor analysis models for structuring covariance matrices of additive genetic effects: A Bayesian implementation. *Genetics Selection Evolution*, 39: 481-494. [[PMID: 17897592](https://pubmed.ncbi.nlm.nih.gov/17897592/)] [[PMCID: PMC2682801](https://pubmed.ncbi.nlm.nih.gov/PMC2682801/)]
2007. Wu X. L., B. Heringstad, Y. M. Chang, **G. de los Campos** and D. Gianola. Inferring relationships between somatic cell score and milk yield using simultaneous and recursive models. *Journal of Dairy Science*, 90: 3508-3521. [[PMID: 17582135](https://pubmed.ncbi.nlm.nih.gov/17582135/)]
2006. **de los Campos G.**, D. Gianola, P. Boettcher, and P. A. Moroni. A structural equation model for describing relationships between somatic cell score and milk yield in dairy goats. *Journal of Animal Science*, 84: 2934-2941. [[PMID: 17032786](https://pubmed.ncbi.nlm.nih.gov/17032786/)]
2006. **de los Campos G.**, D. Gianola and B. Heringstad. A structural equation model for describing relationships between somatic cell score and milk yield in first-lactation dairy cows. *Journal of Dairy Science*, 89: 4445-4455. [[PMID: 17033034](https://pubmed.ncbi.nlm.nih.gov/17033034/)]

Proceedings & abstracts

2014. de los Campos G., D. Sorensen and G. de los Campos. Genomic Heritability: What is it?
In: Proceedings of the 10th WCGALP, Vancouver, Canada, August 17-22.
2013. Klimentidis, Y.C., **de los Campos**, G. and A.I. Vazquez. Prediction of human height with GWAS-identified SNPs – insights into genetic architecture. Annual Meeting of the American Society of Human Genetics, Boston, Massachusetts, October 22-26.
2012. **de los Campos**, G. Vazquez A.I., Klimentidis Y.C., Sorensen D. Whole-genome regression and prediction of human complex traits using data from related and unrelated individuals. 4th International Conference of Quantitative Genetics: Understanding Variation in Complex Traits. O-24. Edinburgh, U.K, June, 2012.
2012. **de los Campos**, Gustavo, Ana Ines Vazquez, Andreas Kranis, Watson Kellie, Santiago Avendaño, and Mario P. L. Calus. Factors Affecting Prediction Accuracy of Genome-Enabled Prediction: Lessons Learnt from Empirical Studies & Implications for Breeding Programs. In *2012 Poultry Breeders' Roundtable*. St. Louis, Missouri.
2012. **de los Campos G.** Whole Genome regression and prediction of complex human traits using family data and data from nominally-unrelated individuals. European Mathematical Genetics Meeting, Georg-August-University, April 12&13, Göttingen, Germany.
2012. Aslibekyan S., Wiener H.W., Wu G., Zhi D., Shrestha S., **de los Campos G.**, Vazquez A.I. Estimating Proportions of Explained Variance: a Comparison of Whole Genome Subsets Genetic Analysis Workshop, October-2012.
2012. Vazquez A.I., **de los Campos G.**, Klimentidis Y.C., Allison D.B. Whole-genome enabled prediction in moderately heritable complex human traits. 4th International Conference of Quantitative Genetics: Understanding Variation in Complex Traits. P-146, Edinburgh, U.K., June, 2012.
2012. Crossa, J., P. Pérez, J. M. Hickey, J. Burgueño, and de los Campos, G. 2012. Next Generation Breeding Using Genotyping-By-Sequencing. *4th International Conference on Quantitative Genetics*: 56. Edinburgh, U.K, June, 2012.
2012. Klimentidis Y.C., Vazquez A.I., **de los Campos G.** Prediction of human height with large panels of SNPs – insights into genetic architecture. American Society of Human Genetics, San Francisco, Nov./2012.

2012. Vazquez A.I., Dhurandhar E.J., Bray M.S., **de los Campos** G., Klimentidis Y.C., Allison D.B., Argyropoulos G., Gonzalez M.N.. Genetic predisposition to obesity predicted with thousands of single nucleotide polymorphisms. Obesity Society Meeting, San Antonio, Texas, Control id: 1375685, 9/2012.
2012. Vazquez A.I., **de los Campos** G., Klimentidis Y.C., Rosa G.J.M., Gianola D., Yi N., Allison D.B. Whole genome-enabled prediction of skin cancer liability vs. family-based prediction. UAB SOPH, Research Day, Birmingham, AL, April/2012; Awarded: First Place Post Doctoral/Fellow Category.
2011. **de los Campos**, G., Klimentidis, Y.C., Makowsky, R., Vazquez, A.I., Pajewski, N.M., Duarte, C.W. and D.B. Allison. Predicting Complex Human Traits Using Whole-Genome Markers: Proof of Principle with Human Height and Human Longevity. [Joint Statistical Meetings, Miami, 2011](#).
2011. Mehta, T., Fontaine, K.R., Keith, S.W., Bangalore, S.S., **de los Campos**, G., Bartolucci, A., Pajewski, N.M. and D.B. David B. Allison. Has the Relationship Between Obesity and Mortality Changed Over Calendar Time? Evidence From a Raw Data Meta-Analysis of Eighteen Prospective Cohorts in US. The Obesity Society Annual Meeting 2011, Orlando, Florida.
2011. Vazquez, A.I., **de los Campos**, G., Rosa, G.M.J., Gianola, D., Klimentidis, Y.C. and D.B. Allison. Whole genome enabled prediction of liability to cancer related outcomes. Eastern North American Region, Miami, FL, Spring 2011, book of abstracts, p 202.
2011. Makowsky, R., Pajewski, N. M. , Klimentidis, Y. C., Vazquez, A.I., Duarte, C. W., Allison, D. B. and G. **de los Campos**. Beyond missing heritability: prediction of complex traits. Eastern North American Region, Miami, FL, Spring 2011, book of abstracts, p 202.
2010. de los Campos G., D. Gianola, G.J.M. Rosa, K.A. Weigel, A.I. Vazquez and D.B. Allison. Semi-Parametric Marker-enabled Prediction of Genetic Values using Gaussian Processes. 2010 [World Congress on Genetics Applied to Livestock Production](#), Invited article.
2010. Weigel, K.de los Campos, G., Vazquez, A., Van Tassell, C., Rosa, G., Gianola, D., O'Connell, J., VanRaden, P., Wiggans, G. Genomic Selection and its Effects on Dairy

- Cattle Breeding Programs. 2010 World Congress on Genetics Applied to Livestock Production. 2010 [World Congress on Genetics Applied to Livestock Production](#).
2010. Rosa, G.Valente, B., de los Campos, G., Wu, X.-L., Gianola, D., Silva, M. Inferring causal phenotype networks using structural equation models. 2010 [World Congress on Genetics Applied to Livestock Production](#).
2010. Peñagaricano, F.Urioste, J.I., Naya, H., de los Campos, G., Gianola, D. Genetic analysis of black spots in Corriedale sheep using Poisson, Probit and linear models. 2010 [World Congress on Genetics Applied to Livestock Production](#).
2010. Valente, B.Rosa, G., de los Campos, G., Gianola, D., Silva, M. Searching for Recursive Causal Structures in Multivariate Quantitative Genetics Mixed Models. 2010 [World Congress on Genetics Applied to Livestock Production](#).
2010. Yokoo, M.de los Campos, G.; Rosa, G.; Magnabosco, C.; Sainz, R.; Lobo, R.; Albuquerque, L. Recursive Models for the Analyses of Growth And Ultrasound Carcass Traits In Nelore Cattle. 2010 [World Congress on Genetics Applied to Livestock Production](#).
2009. de los Campos G., G. J. M. Rosa, D. Gianola, K. Weigel, A. I. Vazquez, J. Crossa, and J. M. Cotes. Choosing regularization parameters in marker-assisted prediction of genetic values: Cross-validation versus Bayesian methods. In: Statistical Genetics of Livestock for the Post-Genomic Era, University of Wisconsin-Madison ([poster](#)).
2009. de los Campos G., D. Gianola, K. A. Weigel and G. J. M. Rosa. Automatic model selection via kernel averaging: Application to marker-assisted prediction. In: Statistical Genetics of Livestock for the Post-Genomic Era, University of Wisconsin-Madison ([poster](#)).
2009. de los Campos G., H. Naya, D. Gianola, J. Crossa, A. Legarra, E. Manfredi, K. A. Weigel and J. M. Cotes. Predicting quantitative traits with regression models for dense molecular markers and pedigrees. In: Statistical Genetics of Livestock for the Post-Genomic Era, University of Wisconsin-Madison ([poster](#)).
2009. Silva F. F., G. J. M. Rosa, G. de los Campos, S. E. F. Guilmarães, and P. S. Lopes. Bayesian factor analysis applied to QTL detection in crosses between outbred populations. In: Statistical Genetics of Livestock for the Post-Genomic Era, University of Wisconsin-Madison ([poster](#)).

2009. Vazquez A. I., G. J. M. Rosa, G. de los Campos, K. A. Weigel and D. Gianola. Biologically informed models for microarray gene expression data analysis. In: Statistical Genetics of Livestock for the Post-Genomic Era, University of Wisconsin-Madison ([poster](#)).
2009. Vazquez A. I., G. de los Campos, K. A. Weigel and D. Gianola. Selection of SNPs for an optimal low-density assay for genetic prediction of transmitting abilities. In: ADSA-CSAS-ASAS Joint Annual Meeting, Montreal, Canada ([abstract](#)).
2008. Cecchinato A., G. de los Campos, D. Gianola, L. Gallo and P. Carnier. Genetic parameters of farrowing survival in purebred and crossbred pigs. In: [2008 Joint ADSA-ASAS-CSAS Meeting, Indianapolis, USA.](#)
2005. de los Campos G., D. Gianola and B. Heringstad. Bivariate recursive and simultaneous models for milk yield and somatic cell scores. In: [2005 Joint ADSA-ASAS-CSAS Meeting, Cincinnati, USA.](#)
2000. San Julián R., G. de los Campos and F. Montossi. Lamb classification systems to meet Uruguayan export market demands. In: Proceedings of the 46th International Meat Science Congress, Buenos Aires, Argentina.
1998. Pérez, J. and G. de los Campos. Sustainability of the rice development in the north zone of Uruguay (translated from Spanish). In: Proceedings of the 29th Congress of the Argentinean Association of Agricultural Economics, La Plata, Argentina.

Extension publications

2010. Navajas, E. and de los Campos, G. [Congreso Mundial de Mejoramiento Genético Animal: La Celeste Marco Presencia](#). Suplemento Agropecuario, Diario El País, Uruguay.
2006. (With several authors). How much is your ram worth? Economic evaluation of the use of Merino rams (translated from Spanish). In: [Revista INIA, 9: 2-6](#).
2002. (With several authors). Economic evaluation of fine-Merino rams using estimated breeding values (translated from Spanish). In: [Extension Activities 305, INIA \(poster 001, poster 002\)](#).
2002. (With several authors). Contributions to a value-based carcass evaluation system (translated from Spanish). [In: Extension Activities 295, INIA](#).
2001. de los Campos G. and F. Montossi. The sheep-meat production and transformation chain: Analysis of the evolution in the last decade and outlook (translated from Spanish). In: Technical Bulletin No 126, INIA ([poster 012](#)).
2001. (With several authors). Estimation of valuable lamb cuts based on carcass measurements (translated from Spanish). [In: Diffusion Activities 253, INIA \(poster 005\)](#).
2001. (With several authors). Estimation of the industrial value and yield of fattening steers (translated from Spanish). [In: Extension Activities No 261, INIA](#).
2001. (With several authors). Introducing market signals in the genetic decision making process (translated from Spanish). In: Extension Activities No 246, INIA.
2000. (With several authors). Seasonality was that of the good old times (translated from Spanish). In: Plan Agropecuario, extension monthly magazine, December.
1998. de los Campos G. and J. Pérez. Horizontal and vertical coordination in the Rice complex of Northern Uruguay (translated from Spanish). In: Revista Arroz, N° 17, Year IV, IV era, December.
1998. de los Campos G. and J. Pérez. Agents, natural resources and rice production technology in Northern Uruguay (translated from Spanish). In: Revista Arroz, N° 16, Year IV, IV era, October.
1997. Buxedas M. and G. de los Campos. Agricultural activities will grow selectively (translated from Spanish). In: *agora* Finanzas & Agronegocios, N° 1, Vol. 1, August.

1997. Buxedas M. and G. de los Campos. The future of agro industrial complexes and changes in the financial pattern (translated from Spanish). In: *agora* Finanzas & Agronegocios, N° 1, Vol. 1, August.

4. Funding

Active

- NIH R01 grant (R01GM099992-01A1) *Factors Affecting Prediction Accuracy of Complex Human Traits and Diseases*. **PI:** G. de los Campos. Year one direct costs **USD 224,352** (consortium not included). August-2012/July-2016.
- NIH R01 grant (R01GM101219-01) *Statistical Tools for Whole-Genome Prediction of Complex Traits and Diseases*. **PI:** G. de los Campos. Year one direct costs **USD 200,000**. **Period:** March-2012/Jan-2015.
- **2012-13**. ARVALIS. *Models and Software Development for Incorporation of Genetic by Environmental Interactions in Whole Genome Regression Models*. Direct Costs **PI:** G. de los Campos. Year one direct costs **USD 90,000**. **Period:** March2012/Feb-2013.

Completed

- **2010-11**. NIH UAB-NORC P30 Administrative Supplement. *Development of Methods and Software for Whole Genome Prediction of Obesity-related Health Outcomes*. **PI:** G. de los Campos & David Allison. **USD 87,263**. **Period:** 2012
- 2010**. UAB-Nutrition Obesity Research Center Pilot Feasibility Grant. *Identification and Quantification of Genetic Factors Affecting the Effect of BMI as a Risk Factor for Relevant Human Diseases and Mortality* **PI:** G. de los Campos. **USD 25,000**.
- 2010**. UAB-School of Public Health. 2010 Back of the Envelope Award. *Genomic Medicine: From Utopias to Deliverables*. **PI:** G. de los Campos. **USD 20,000**.

2010. UAB-CIMMYT Contract for Service Agreement. *Development and Evaluation of Models for Genome Enabled Prediction in Maize and Wheat.* PI. G. de los Campos. USD 18,000.

Pending

None.

5. Selected Invited Presentations (2011 up-to-date)

Date	Place/Event/Institution	Place	Title
May-2013	Epidemiology and Biostatistics Seminar, Michigan State University	Lansing, Michigan	Genomic Analysis of Data from Structured Populations
May-2013	Conference on Applied Statistics in Agrigulture, Kansas State University (Keynote speaker)	Manhattan, Kansas	Analysis & Prediction of Complex Traits Using High Dimensional Genomic Data http://www.dce.k-state.edu/conf/applied-stats/speakers
Oct-13	4 th Bioinformatics Meetings of Colegio de Postgraduados.	Texcoco, Mexico	Analysis and Prediction of Complex Traits Using Whole-Genome Regression Methods
Aug-13	Genomic Prediction Workshop, University of Florida Genomic Institute	Gainesville, FL	Methods for Whole-Genome Regression/Prediction & Factors Affecting Prediction Accuracy
Feb-13	Gordon Conference on Quantitative Genetics & Genomics	Galveston, Texas	Genomic Prediction: the Forces that Drive Prediction Accuracy of Genomic BLUP.
Dec-12	Seminar: Plant Breeding Webinar	Virtual Seminar	Factors Affecting Prediction Accuracy of Genome-Enabled Prediction & Implications for Breeding Programs.
Oct-12	Conference of the Latin-American Genetic Society	Rosario, Argentina	Prediction of Complex Traits Using Genomic-BLUP With Data From Related and Unrelated Individuals.
Sep-12	Seminar: Plant Breeding Department, University of Wisconsin-Madison	Madison, Wisconsin	Prediction of Complex Traits Using Data of Related and Unrelated Individuals.
Jun-12	4 th International Quantitative Genetics Conference	Edinburgh, Scotland	Whole Genome regression and prediction of complex human traits using data from related and un-related individuals.
May-12	Poultry Breeders' Roundtable, St. Louis, Missouri.	St. Louis, Missouri	Factors Affecting Prediction Accuracy of Genome-Enabled Prediction & Implications for Breeding Programs.
Apr-12	European Mathematical Genetics Meeting	Gottingen, Germany	Whole Genome regression and prediction of complex human traits using family data and data from nominally-unrelated individuals.
Apr-12	Seminar: Plant Breeding Department, Cornell University	Ithaca, NY, US	Genomic Selection: Lessons Learned From Empirical Analysis & Implications for Breeding Programs.
Apr-12	Seminar: Statistics Department, Colegio de Postgraduados	Texcoco, Mexico	Prediction of Complex Traits Using Reproducing Kernel Hilbert Spaces Regressions.
Dec-11	Seminar: Statistics Department, Iowa State University	Ames, Iowa	Prediction of Complex Traits Using Reproducing Kernel Hilbert Spaces Regressions.

6. Mentorship

Year	Student	Degree seeking	Institution	Role	Country of birth
2013-14	Alessandro Ferragina	PhD	University of Padua, Italy	Mentor during his stance at UAB	Italy
2013	Swetlana Miller	PhD	Georg-August-Universität, Germany	Mentor during her stance at UAB	Kazakhstan
2012-	Bertha Hidalgo	Postdoctoral Fellow	Biostatistics, UAB	2ndary mentor	US
2012-	Marcio Resende	PhD	University of Florida Genetics Institute	Committee member	Brazil
2012-	Mallick Himel	PhD	Biostatistics, UAB	Committee member	India
2012-	Yogasudha Veturi	PhD	Biostatistics, UAB	Mentor	India
2013	Paulino Pérez	Visiting Scholar	Colegio de Postgraduados, Mexico	Mentor	Mexico
2012	Peter Sorensen	Visiting Scholar	Aarhus University, Denmark	Mentor	Denmark
2012	Diego Hernandez-Jarquin	Postdoctoral Fellow	Biostatistics, UAB	Mentor	Mexico
2011	Mohammad Shariati	Visiting Post. Doc. Fellow	Aarhus University, Denmark	Mentor	Iran
2012	Anna C. Flores Maddox	Summer Internship	Universidad Metropolitana, Puerto Rico	Mentor	Puerto Rico
2011	Kamil Suliveres	Summer Internship	Universidad Metropolitana, Puerto Rico	Co-Mentor	Puerto Rico
2010	Maggie González Delgado	Summer Internship	Universidad de Turabo, Puerto Rico	Co-Mentor	Puerto Rico

7. Fellowships and awards

2011. Best scientific article by a University of Alabama at Birmingham-based investigator. The award was given by the [Science Unbound Foundation](#) in recognition of the article Predicting genetic predisposition in humans: the promise of whole-genome markers was published November 20, 2010 in *Nature Reviews Genetics*, <http://dx.doi.org/doi:10.1038/nrg2898>
2010. [Back of the Envelop Award](#) of the UAB-School of Public Health.
2010. Best 2009 Dissertation, [Agricultural and Applied Economics, UW-Madison](#).
2008. [Mueller Graduate Fellowship, Agricultural and Applied Economics, UW-Madison](#).

8. Personal information

Date of birth: 3/21/1973

Place of birth: Montevideo, Uruguay.

Address: 1665 University Boulevard, Ryals Public Health Building 414, Birmingham, AL 35294.

Phone: +1 (205) 975-9248

Fax: +1 (205) 975-2541

E-mail: gcampos@uab.edu

Webpage: <http://www.soph.uab.edu/ssg/people/campos>

9. Academic references

Daniel Gianola, PhD. Sewall Wright Professor of Animal Breeding and Quantitative Genetics of University of Wisconsin-Madison. Address: 1675 Observatory Drive Madison, WI 53706-1284 2. Phone: (608)265-2054 . Fax: (608)262-5157 . E-mail: gianola@ansci.wisc.edu

David Allison, PhD. Distinguished Professor, Associate Dean for Science, Director of Nutrition Obesity Research Center of University of Alabama at Birmingham

Address: 1665 University Blvd, RPHB 140J Birmingham, AL 35294-0022. Phone: (205) 975-9169. Fax: (205) 975-7536. E-mail: dallison@uab.edu

Daniel Sorensen, PhD. Professor Department of Molecular Biology and Genetics - Genetics and Biotechnology, Foulum. Address: Blichers Allé 20, 8830, Tjele, Denmark. Phone: 89991215. E-mail: daniel.sorensen@agrsci.dk

Jack Dekkers, PhD. Professor, Animal Science, Iowa State University. Address: 239 Kildee Hall, Ames, IA 50011-3150. Phone: 515-294-7509. Fax: 515-294-9150.
Email: jdekkers@iastate.edu