Prof Guilherme J. M. Rosa Department of Animal Sciences Department of Biostatistics & Medical Informatics University of Wisconsin-Madison

Prof. Guilherme Rosa obtained an M.S. in Animal Sciences from Sao Paulo State University (UNESP) – Brazil in 1994, and a Ph.D. in Statistics and Agricultural Experimentation from the University of Sao Paulo (USP) – Brazil in 1998. Guilherme Rosa started his professional carrier as a faculty member of the Department of Biostatistics at UNESP



(1994-2001), then moved to the USA as a faculty member at Michigan State University (2002-2006), and is currently a Professor at the Department of Animal Sciences and the Department of Biostatistics & Medical Informatics at the University of Wisconsin-Madison (since 2006).

Guilherme Rosa teaches courses and develops research on quantitative genetics and statistical genomics, including design of experiments and data analysis tools. Some specific areas of interest include mixed effects models, Bayesian analysis, and Monte Carlo methods. More recently, Guilherme has been working also on the analysis of observational data in agriculture, using a variety of tools based either on the framework of potential outcomes, or graphical model tools, such as propensity score, instrumental variable, and Bayesian networks.

Guilherme has published 10 book chapters and over 150 refereed papers in scientific journals and has funded his program with outside grants valued at over \$10 million. He has been awarded with the LeClerg Rotary Lecturer from the Biometrics Program at the University of Maryland (2011) and the Pond Research Award from the University of Wisconsin-Madison (2013). He has also received the Rockefeller Prentice Memorial Award in Animal Breeding and Genetics, by the American Society of Animal Science (2016), the Vilas Faculty Mid-Career Investigator Award (2017) and the Excellence in International Activities Award, both from University of Wisconsin-Madison (2017), and was the Keynote Speaker at the KSU Conference on Applied Statistics in Agriculture (2018).

Papers in refereed journals

- Momen, M., Mehrgardi, A. A., Amiri Roudbar, M., Kranis, A., Pinto, R. M., Valente, B. D., Morota, G., Rosa, G. J. M. and Gianola, D. Including phenotypic causal networks in genome-wide association studies using mixed effects structural equation models. Frontiers in Genetics, 9:455, 2018.
- Töpner, K., Rosa, G. J. M., Gianola, D. and Schön, C.-C. Bayesian networks illustrate genomic and residual trait connections in maize (Zea mays L.). G3-Genes Genomes Genetics 7:2779-2789, 2017.

- Rosa, G. J. M., Felipe, V. P. S. and Peñagaricano, F. Applications of Graphical Models in Quantitative Genetics and Genomics. In: Systems Biology in Animal Production and Health, Volume 1. Kadarmideen, H. (Ed.) Springer, 2016.
- Inoue, K., Valente, B. D., Shoji, N., Honda, T., Oyama, K. and Rosa, G. J. M. Inferring phenotypic causal structures among meat quality traits and the application of a structural equation model in Japanese Black cattle. Journal of Animal Science 94: 4133-4142, 2016.
- Mokhtari, M. S., Moradi Shahrbabak, M., Nejati Javaremi, A. and Rosa, G. J. M. Relationship between calving difficulty and fertility traits in firstparity Iranian Holsteins under standard and recursive models. Journal of Animal Breeding and Genetics 133: 513-522, 2016.
- Peñagaricano, F., Valente, B. D., Steibel, J. P., Bates, R. O., Ernst, C. W., Khatib, H. and Rosa, G. J. M. Exploring causal networks underlying fat deposition and muscularity in pigs through the integration of phenotypic, genotypic and transcriptomic data. BMC Systems Biology 9: 58, 2015.
- Valente, B. D., Morota, G., Peñagaricano, F., Gianola, D., Weigel, K. A. and Rosa, G. J. M. The causal meaning of genomic predictors and how it affects the construction and comparison of genome-enabled selection models. Genetics 200: 483-494, 2015.
- Felipe, V. P. S., Silva, M. A., Valente, B. D. and Rosa, G. J. M. Using multiple regression, Bayesian networks and artificial neural networks for prediction of total egg production in European quails based on earlier expressed phenotypes. Poultry Science 94: 772-780, 2015.
- Peñagaricano, F., Valente, B. D., Steibel, J. P., Bates, R. O., Ernst, C. W., Khatib, H. and Rosa, G. J. M. Searching for causal networks involving latent variables in complex traits: Application to growth, carcass, and meat quality traits in pigs. Journal of Animal Science 93: 912-919, 2015.
- Rosa, G. J. M. and Valente, B. D. Structural Equation Models for Studying Causal Phenotype Networks in Quantitative Genetics. In: Probabilistic Graphical Models for Genetics, Genomics and Postgenomics. Sinoquet, C. and Mourad, R. (Eds.) Oxford University Press, 2014.
- Valente, B. D. and Rosa, G. J. M. Mixed effects structural equation models and phenotypic causal networks. In: Genome-Wide Association Studies. Gondro, C., van der Werf, J. and Hayes, B. (Eds.) Springer, 2013.
- Rosa, G. J. M. and Valente B. D. Inferring causal effects from observational data in livestock. Journal of Animal Science 91: 553-564, 2013.
- Valente, B. D., Rosa, G. J. M., Gianola, D., Wu, X.-L. and Weigel, K. A. Is structural equation modeling advantageous for the genetic improvement of multiple traits? Genetics 194: 561-572, 2013.
- Morota, G., Valente, B. D., Rosa, G. J. M., Weigel, K. A. and Gianola, D. An assessment of linkage disequilibrium in Holstein cattle using a Bayesian network. Journal of Animal Breeding and Genetics 129: 474-487, 2012.

- Valente, B. D., Rosa, G. J. M., Teixeira, R. B. and Torres, R. A. Searching for phenotypic causal networks involving complex traits: an application to European quails. Genet. Sel. Evol. 43:37, 2011.
- Rosa, G. J. M., Valente, B. D., de los Campos, G., Wu, X.-L., Gianola, D. and Silva, M. A. Inferring causal phenotype networks using structural equation models. Genetics Selection Evolution 43: 6, 2011.
- Maturana, E. L., de los Campos, G., Wu, X.-L., Gianola, D., Weigel, K. A. and Rosa, G. J.M. Modeling relationships between calving traits: a comparison between standard and recursive mixed models. Genetics Selection Evolution 42(1), 2010.
- Maturana, E. L., Wu, X.-L., Gianola, D., Weigel, K. A. and Rosa, G. J. M. Exploring biological relationships between calving traits in primiparous cattle with a Bayesian recursive model. Genetics 181: 277-287, 2009.