Marco Antônio de Amorim Peixoto

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Summary

I am a creative and self-motivated scientist with a solid foundation on theoretical and practical aspects of quantitative genetics, genomic selection, breeding program simulation, and linear mixed models. I generate data-driven evidence for the enhancement of genetics and breeding purposes, relying on statistics and genetic data.

Education background

- **Ph.D. in Genetics and breeding.** Federal University of Viçosa – Brazil (2019-2023).
  Dissertation: Applying quantitative genetics tools to breeding program optimization.
- **M.Sc. in Animal Biology.** Federal University of Viçosa – Brazil (2014-2016).
  Thesis: Biogeography and conservation of the anurofauna in the Mantiqueira mountain range.
- **B.S. in Biology Science.** Federal University of Viçosa – Brazil (2009-2014).

Experience

2023-present - Postdoctoral associate at Sweet Corn and Potato Breeding and Genomics Lab. University of Florida, USA. Supv. by Dr. Márcio Resende.
- Mate allocation of breeding crosses, via package development (SimpleMating package).
    Development of optimization algorithms.
    Non-additive effects estimation for crossing optimization.
- GWAS analyses for discovery breeding of traits in the Sweet Corn and in the Potato breeding programs
- Imputation of low-density marker data in Sweet Corn panel.
- Breeding program design and deployment of Genomic selection pipeline.
    Deployment of genomic selection in the Sweet Corn program.
    Simulation of potato breeding program with implementation of genomic selection for data-driven decisions.
- Mentoring students on quantitative genomics analyses and breeding-driven projects.
    Implementation of phenomic selection models through single-kernel NIR (Phenomics).
    Deployment of environmic models for TPE in potato breeding.

2021-2023 - Visiting Research Scholar at Sweet Corn and Potato Breeding and Genomics Lab. University of Florida, USA. Supv. by Dr. Márcio Resende.
- Planning and optimization of the sweet corn breeding program via stochastic simulations.
- Genetic data analyses (modelling, genomic prediction, and selection).
- Hybrid prediction under G×E interaction for recommendation purposes.
- Development of cross-prediction (mean, variance, and usefulness) algorithms and mate allocation optimization.
- Multidisciplinary activities through cross-functional teams.
    Functional biology: Identification GWAS hits for posterior functional identification.
    Evolutionary biology: Modelling, prediction/estimation of BLUEs/BLUPs and heritabilities for evolutionary studies.
- Nursery activities at sweet corn breeding program (phenotyping, selfing, crossing, and selection).

2021-2022 - Scientific coordinator, at GenMelhor. Federal University of Viçosa, Brazil.
- Coordination of the scientific sector of the study group, with emphasis on the promotion of events for the students from the genetics and breeding program and related areas.
- Working collaboratively with the team for symposiums, workshops, and short courses organization for students.

2019-2023 - Graduate research assistant at Biometry Lab. Supv. by Dr. Leonardo L. Bhering. Federal University of Viçosa.
- Development of statistical genetics approaches for genetic evaluation with emphasis on modeling, prediction, and selection via mixed models.
- Teaching short courses on mixed models, statistics, and plant breeding to companies, students, and professionals.
- Working collaboratively on the discussion and implementation of genetic assessment and breeding.

2016-2017 - Teaching Assistant. Institute of Technology of Minas Gerais State, Brazil
- Teaching classes for undergrads students from Agronomy and correlated areas.

2014-2016 - Graduate research assistant at biological data analysis Lab. Supv. Dr. Pedro S. Romano.
Federal University of Viçosa, Brazil.
- Definition of singular areas in species distribution from Mantiqueira mountain range region as surrogates to define target areas for conservation and protection.

2012-2014 - Fellowship intern, at Molecular Biology Lab. Federal University of Viçosa, Brazil.
- Development of molecular methods for genome sequencing and cytogenetics studies.
- Description of karyotypes of species and populations through classic and molecular techniques.

Skills

Computational:

- Advanced R programming and related tools (Markdown/Quarto, Shiny, Tidyverse).
- Background on parallel computing (linux), Git version control system (GitHub), and commercial software (*i.e.* ASReml, BLUPF90 family).
- Basic coding in C++ (Rcpp Eigen/Armadillo), Python, shell/bash, LaTeX, and VCFtools/BCFtools.
- Background on marker data imputation programs: BEAGLE, AlphaPlantImpute2, and Impute5.

Key-areas of expertise:

- Plant genetics and breeding: field breeding techniques, selection theory, and breeding program simulations (stochastic process).
- Quantitative genetics, Mixed models, Multivariate models, and Bayesian methods.
- Software development using R coding with R Shiny app interface.
- Imputation methods based on hidden Markov models.
- Genome-wide association, genetic evaluation, genome-wide prediction methods, cross-prediction and mate pair allocation.
- Phenomics (NIR-based methods) and environmic-based prediction models.

Awards and Recognitions

- 1st place: Larry Darrah Student presentation contest (best oral presentation). Corn breeding and research meeting (2023), Saint Louis, Missouri, USA.
- 1st place: best dissertation in Genetics and Breeding. Federal University of Viçosa (2023). Viçosa, Minas Gerais, Brazil.
- PrInt-CAPES scholarship (1st place - 2021). Federal University of Viçosa. Viçosa, Minas Gerais, Brazil.

Publications

Software

- **SimpleMating**: R package for breeding crosses prediction and optimization. Access: https://github.com/Resende-Lab/SimpleMating

Teaching and short talks

- Short course in 'Breeding Programs simulations,' University of Florida (2023).
- Teaching assistant of 'Molecular markers applied to plant breeding', graduate level, University of Florida (2023).
- Short course in 'Multi-Omic integration for AI Genomic Prediction Breeding'. University of Florida (2023).
- Teaching assistant of Quantitative genetics, graduate level, University of Florida (2022).
- Guest lecture "Artificial intelligence in the big data era: insights and applications", Federal University of Juiz de Fora (2021).
- Guest lecture "Forest genetics: present and perspectives", Sistemas integrados Florestais, Brazil (2020).
- Short course in Spatial statistics applied to plant breeding, Federal University of Viçosa, Brazil (2020).
- Short course in experimental statistics applied to plant breeding, CMPC company, Brazil (2020).
- Short course in mixed models applied to plant breeding, Sistemas integrados Florestais, Brazil (2020).
- Teaching assistant of experimental statistics, graduate level, Federal University of Viçosa, Brazil (2020).

Selected publications

- Peixoto, MA, Amadeu RR, Bhering, LL, Munoz, PR, Ferrao, LF, Resende, M. SimpleMating: R-package for prediction and optimization of breeding crosses using genomic selection. In prep. 2024.
- Peixoto, MA, Coelho, I, Leach, K, Lubberstedt, T, Bhering, LL, Resende, M. (2024). Use of simulation to optimize a sweet corn breeding program: implementing genomic selection and doubled haploid technology. G3: Genes | Genome | Genetics.

- Peixoto, MA, Leach, K, Jarquin, D, Flannery, P, Zystro, J, Tracy, W, Bhering LL., Resende, M. (2024). Utilizing genomic prediction to boost hybrid performance in a sweet corn breeding program. Frontiers in Plant Science.
- Peixoto, MA, Coelho, I, Leach, K, Bhering, LL, Resende, M. (2023). Simulation-Based Decision Making and Implementation of Tools in Hybrid Crop Breeding Pipelines. Crop Science.
- Santana A, Marçal T, Salvador F, Souza M, Silva L, Silva B, Peixoto, MA, Carneiro P, Carneiro J. (2023). Analysis of advanced generation multistage field trials data in autogamous plant breeding: An evaluation in common Bean. Crop Science.
- Evangelista J, Peixoto, MA, Coelho I, Ferreira F, Marçal T, Alves R, Chaves S, Rodrigues E, Laviola B, Resende M, Dias K, Bhering L. (2023). Modeling covariance structures and optimizing Jatropha curcas breeding. Tree Genetics & Genomes.
- Malikouski R, Alves R, Peixoto MA, Ferreira F, do Nascimento E, de Morais A, Zucoloto M, Dias K, Bhering L. (2023). Selection index based on random regression model in 'Tahiti'acid lime. Euphytica.
- Santos I, Peixoto MA, Cruz C, Ferreira R, Nascimento M, Rosado R, Sant'Anna I. (2022). A novel approach to determine tropical persistence on alfalfa germplasm. Agronomy Journal.
- Marinho C, Coelho I, Peixoto MA, Junior G, Resende M. (2022). Genomic Selection As A Tool For Maize Cultivars Development. Revista Brasileira De Milho E Sorgo.
- Ferreira F, Rodrigo V, Malikouski R, Peixoto MA, Bernardeli A, Alves R, Magalhães-Jr W, Andrade R, Bhering L, Machado J. (2021). Bioenergy Elephant Grass Genotype Selection Leveraged by Spatial Modeling of Conventional and High-Throughput Phenotyping Data. Journal of Cleaner Production.
- Peixoto MA, Evangelista J, Coelho I, Alves R, Laviola B, Fonseca-e-Silva F, Resende M, Bhering L. (2021). Multiple-Trait Model Through Bayesian Inference Applied to Jatropha Curcas Breeding for Bioenergy. Plos One.
- Silva L. Peixoto MA, Peixoto L. Romero J, Bhering L. (2021). Multi-Trait Genomic Selection Indexes Applied to Identification of Superior Genotypes. Bragantia.
- Peixoto MA, Coelho, I, Evangelista J, Santos S, Alves R, Pinto J, Reis E, Bhering L. (2021). Selection of Maize Hybrids: An Approach with Multi-Trait, Multi-Environment, and Ideotype-Design. Crop Breeding and Applied Biotechnology.
- Peixoto MA, Malikouski R, Evangelista J, Alves R, Morais A, Barbosa D, Zucoloto M, Bhering L. (2021). Multitrait and Multiharvest Analyses for Genetic Assessment and Selection of Tahiti Acid Lime Genotypes Through Bayesian Inference. Scientia Horticulturae.
- Coelho I, Peixoto MA, Marçal T, Bernardeli A, Alves R, De-Lima R, Reis E, Bhering L. (2021). Accounting for Spatial Trends in Multi-Environment Diallel Analysis in Maize Breeding. Plos One.
- Evangelista J. Peixoto MA, Coelho I, Alves R, Laviola B, Fonseca-e-Silva F, Resende M, Silva F, Bhering L. (2020). Environmental Stratification and Genotype Recommendation Toward the Soybean ideotype: A Bayesian Approach. Crop Breeding and Applied Biotechnology.
- Peixoto MA, Coelho IF, Evangelista JS, Alves RS, Rocha JRASC, Farias FJC, Carvalho LP, Teodoro PE, Bhering L. (2020). Reaction Norms-Based Approach Applied to Optimizing Recommendations of Cotton Genotypes. Agronomy Journal.
- Coelho IF, Peixoto MA, Evangelista JS, Alves RS, Sales S, Resende MD, Pinto JF, Reis EF, Bhering L. (2020). Multiple-Trait, Random Regression, and Compound Symmetry Models for Analyzing Multi-Environment Trials in Maize Breeding. Plos One.
- Peixoto MA, Alves R, Coelho I, Evangelista J, Resende M, Carvalho J, Fonseca-e-Silva F, Laviola B, Bhering L. (2020). Random Regression for Modeling Yield Genetic Trajectories in Jatropha Curcas Breeding. Plos One.
- **See all publications at my website:** https://marcopxt.github.io/publications/

References

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