Alencar Xavier, PhD.

Quantitative Geneticist, Corteva Agrisciences
Adjunct Faculty, Purdue University
8305 NW 62nd Ave, Johnston IA 50131
E-mail: Alencar.Xavier@Corteva.com
Website: http://alenxav.wix.com/home
OCRID: orcid.org/0000-0001-5034-9954

WORK EXPERIENCE

(2018-Current) Research Scientist. Seed Product Development, Corteva Agrisciences: Provide technical assistance to North America soybean breeding; Latin America and Africa corn and soybean breeding. Assist with the development and implementation of the genomic assisted breeding pipelines. Provide technical support to trait introgression and parent characterization. Curate and develop the standard analytical pipelines utilized for research and production. Implement machine learning approaches to automate SNP autoscoring. Develop and implement multi-trait methods, longitudinal and single-step analysis in the breeding pipeline. Build framework to utilizing environmental information for product placement and disease prediction for breeding and predictive agriculture. Incorporate elements of machine learning into breeding pipelines. Research statistical and computational methods for data analysis with high computational efficiency. Supervise interns and postdocs. Lead research projects and initiatives targeting changes in breeding pipeline. Ensure academic excellence and scientific rigor in all internal deliverables and external publications.

(2017-Current) Adjunct Faculty. Department of Agronomy, Purdue University: Collaboration with professors towards the training of plant breeding students. Give lectures pertinent to quantitative genetics, breeding analytics, and industry perspective on plant breeding. Contribute to writing grants under specific expertise. Be member of graduate students committee. Co-advise interns and postdocs. Answer general student questions about breeding.

(2016-2018) Research Scientist. Quantitative Genetics group, Dow AgroSciences: Worked on the implementation on the genomic prediction and selection pipeline in soybeans. Assisting and educate breeder on best practices for the deploying of genomic information for selection. Developed computational tools with high-performance computing for gene mapping, genomic prediction & selection. Develop customized apps for breeders and discovery breeders to perform genomic analysis. Germplasm analysis. Ensured transition of breeding operations from Dow to Corteva.

(2013-2015) Research Associate. Soybean Breeding, Purdue University: Worked on field breeding and the analysis of yield and yield components in the SoyNAM population. Pioneered the genetic evaluation of drone-derived canopy traits in soybean. Developed the analytical toolset utilized to perform mapping of QTLs in next-generation populations. Worked on incorporating multiple applications of machine learning into plant breeding. Implemented analytical pipelines including genomics and spatial adjustment under multi-trait settings.

EDUCATION

- B.Sc. Agronomic Engineering (2007-2011). Federal University of Santa Maria, RS, Brazil.
- Ph.D. Soybean Breeding and Statistical Genetics (2013-2016). Purdue University, IN, USA. GPA 4.

KEY EXPERTISES

- Soybean genetics and breeding, field breeding techniques, marked assisted breeding, and breeding pipeline workflow.
- Breeding designs: experimental designs, spatial statistics, adjustment of field variation and imputation methods.
- Predictive breeding analytics: Mixed models, multivariate models, machine learning and Bayesian methods.
- Routine breeding analysis: QTL mapping, genome-wide association mapping, genome-wide prediction methods.
- Computational breeding: algorithm development and high-performance computing, and user-friendly apps.
- Data collection: Phenomics and high-throughput phenotyping technologies in plant breeding.

SOFTWARE DEVELOPED

- BT-SAT-R: Interface to BT-SAT, package to analyze breeding data, phenotypic analysis, GS and GWAS. 2022.
- SoyOHV: App for prediction and recommendations of soybean crosses, combining TI and complex traits. Corteva 2022.
- Crux: A supervised machine learning approach for autoscoring and quality classification. Corteva 2021.
- GS: Fast and efficient implementation of multivariate models based on Tilde-Hat & Gauss-Seidel. In: BT-SAT 2020.
- EigenDNN: In-house implementation of deep neural networks for genomic prediction. Corteva Agrisciences 2020.
- eMM3: Efficient Mixed Models Solver for large datasets and multiple sources of data. Corteva Agrisciences 2016-2020.
- MDH2: Marker Data Hub R package to access Dow Agrosciences molecular data. Corteva Agrisciences 2018.
- HP: Hybrid prediction tool from Dow Agrosciences production pipeline. Corteva Agrisciences 2018.
- QG2: Quantitative Genetic Analytical Tools for Modeling, Mapping, Prediction. Dow Agrosciences. 2016.
- Xavier et al. (2015). NAM: Association analysis and breeding tools (CRAN.R-project.org/package=NAM)
- Xavier et al. (2015). bWGR: Bayesian Whole Genome Regression (CRAN.R-project.org/package=bWGR)
- Xavier et al. (2015). SoyNAM package: Data & Summary (CRAN.R-project.org/package=SoyNAM)

SELECTED PUBLICATIONS

A. Xavier and D. Habier. A new approach fits multivariate genomic prediction models efficiently. Genetics Selection Evolution (2022), 54.

A. Xavier, E. Silva, M. Faria. Impact of genomic prediction model, selection intensity and breeding strategy on the long-term genetic gain and genetic erosion in soybean breeding. Frontiers in Genetics (2021), 12, pp. 1577.

A. Xavier, E. Silva, M. Faria. Joint Modeling of Genetics and Field Variation in Plant Breeding Trials Using Relationship and Different Spatial Methods: A Simulation Study of Accuracy and Bias. Agronomy (2021), 11(7), pp. 1397.

A. Xavier. Technical nuances of machine learning: implementation and validation of supervised methods for genomic prediction in plant breeding. In: Crop Breeding and Applied Biotechnology (2021).

A. Xavier, B. P. Hall, F. Moreira, et al. Quantitative characterization of Proximate Sensing Canopy Traits in the Soynam Population. In: Crop Science (2020).

A. Xavier and K. M. Rainey. Quantitative Genomic Dissection of Soybean Yield Components. In: G3: Genes, Genomes, Genetics 10.2 (2020), pp. 665-675.

A. Xavier. Efficient estimation of marker effects in plant breeding. In: G3: Genes, Genomes, Genetics 9.11 (2019), pp. 3855-3866.

A. Xavier, W. M. Muir, and K. M. Rainey. bWGR: Bayesian whole-genome regression. In: Bioinformatics 36.6 (2019), pp. 1957-1959.

A. Xavier, et al. Population and quantitative genomic properties of the USDA soybean germplasm collection. In: Plant Genetic Resources (2018), pp. 1-11.

A. Xavier, et al. Genetic architecture of phenomic-enabled canopy coverage in Glycine max. In: Genetics (2017), pp.116.

A. Xavier, D. Jarquin, R. Howard, et al. Genome-Wide analysis of grain yield stability and environmental interactions in a multi-parental soybean population. In: G3: Genes, Genomes, Genetics (2017).

A. Xavier, et al. Using unsupervised learning techniques to assess interactions among complex traits in soybeans. In: Euphytica 213.8 (2017), p. 200.

A. Xavier, et al. Genomic prediction using subsampling. In: BMC bioinformatics 18.1 (2017), p. 191.

A. Xavier, et al. Walking through the statistical black boxes of plant breeding. In: Theoretical and applied genetics 129.10 (2016), pp. 1933-1949.

A. Xavier, W. M. Muir, and K. M. Rainey. Assessing predictive properties of genome-wide selection in soybeans. In: G3: Genes, Genomes, Genetics (2016), pp. g3-116.

A. Xavier, W. M. Muir, and K. M. Rainey. Impact of imputation methods on the amount of genetic variation captured by a single-nucleotide polymorphism panel in soybeans. In: BMC bioinformatics 17.1 (2016), p. 55.

A. Xavier, et al. NAM: association studies in multiple populations. In: Bioinformatics 31.23 (2015), pp. 3862-3864.

GRANTS

- Rainey, et al. (2020). Application of UAS biomass longitudinal phenotypes to selection in soybean breeding trials. National. Institute of Food and Agriculture, USDA.

PATENTS

- Rainey, et al. (2018). Method of using genetic architecture of phenomic-enabled canopy coverage in glycine max. US20180232579A1

EDITOR

- Associated Editor at Scientia Agricola (ISSN 1678-992X) since 2019.
- Frontiers (2023) "Enriching Genomic Breeding with Environmental Covariates, Crop Models, and High-Throughput Phenotyping"

COMMUNITY LEADER

- 2023 ASA Symposium Chair, "2022 ASA Symposium Chair, "Quantitative Analytics Using Machine Learning".
- 2022 Biometrics Community Leader for the Biometry and Statistical Computing Section, American Society of Agronomy.
- 2022 ASA Symposium Chair, "Quantitative Analytics Using Machine Learning".
- 2022 ASA Symposium Co-chair, "Advances in High-Throughput Phenotyping".

AWARDS AND RECOGNITIONS

- 1st place Genomes to Fields (G2F) Genotype by Environment Prediction Competition. 2023.
- 2022 Breakthrough Innovation Award. AgCon 2022, Corteva Agrisciences.
- 2022 NAPPN Industry Award. The North American Plant Phenotyping Network 2022.
- Best Early-Mid Career Researcher Poster Slide, Intern. Conference of Quantitative Genetics 6. 2020.
- John Axtell Graduate Student Award in Plant Breeding and Genetics, Purdue University. 2016.
- ICQG5 Fellowship. Support for graduate students in plant breeding. Sponsored by USDA. 2016.
- Dow AgroSciences Graduate Scholarship. Integrity, academic excellence, initiative and leadership, 2016.
- Outstanding Graduate Research Award (PhD). Purdue 2015 Graduate Student Award.
- AG Spotlight - Graduate AG Research Spotlight. College of Agriculture, Purdue University. Feb 2015.
- Bauman-Doolittle Endowment - Support for graduate students in breeding and genetics. 2015.
- Loyal F. Pete Bauman Memorial Fund - Support for graduate students in breeding and genetics. 2014.
- Wyman E. Nyquist Scholarship - Quantitative Genetics. Purdue 2014 Graduate Student Award.
- Soy2014 Student Award - MCBS: 15th Biennial Conference. University of Minnesota, 2014.