

## Alencar Xavier, PhD.

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### EXPERIENCE

- (2018-Current) **Research Scientist. Biostatistics, Corteva Agrisciences:** Ensured transition of breeding operations from legacy Dow to Corteva. Provide technical assistance to soybean and cotton breeders and discovery breeders. Assist with the development of the genomic assisted breeding pipeline in soybeans and cotton. Provide guidance and technical support to trait introgression in soybeans. Curate and develop the standard analytical pipelines utilized for research and production. Implement automated autoscoring system based on machine learning. Implement multi-trait analysis in the breeding pipeline to leverage information of correlated traits. 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.
- (2017-Current) **Adjunct Faculty. Department of Agronomy, Purdue University:** Work in close 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. 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 guiding breeder on how to utilize genomic information for selection. Developed a set of computational tools with high-performance computing for mapping, prediction and selection. Created a set of customized apps for breeders and discovery breeders to perform genomic analysis. Contributed to the cotton germplasm analysis and quality traits.
- (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 for the SoyNAM project. Worked on multiple applications of machine learning in plant breeding. Implemented analytical pipelines including genomics and spatial adjustment under multi-trait settings.

### EDUCATION

- Technical degree in agriculture and livestock (2004-2006). E.E.T. Celeste Gobbato, RS, Brazil.
- 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

- GS: Fast and efficient implementation of multivariate models based on Tilde-Hat & Gauss-Seidel. In: BT-SAT 2020.
- Eigen DNN: In-house implementation of a deep neural networks. Corteva Agrisciences 2020.
- eMM3: Efficient Mixed Models Solver. Corteva Agrisciences 2016-2020.
- MDH2: Marker Data Hub R package to access Dow Agrisciences molecular data. Corteva Agrisciences 2018.
- HP: Hybrid prediction tool from Dow Agrisciences production pipeline. Corteva Agrisciences 2018.
- QG2: Quantitative Genetic Analytical Tools for Modeling, Mapping, Prediction. Dow Agrisciences. 2016.
- Xavier et al. (2015). NAM: Association analysis and breeding tools ([CRAN.R-project.org/package=NAM](http://CRAN.R-project.org/package=NAM))
- Xavier et al. (2015). bWGR: Bayesian Whole genome regression ([CRAN.R-project.org/package=bWGR](http://CRAN.R-project.org/package=bWGR))
- Xavier et al. (2015). SoyNAM package: data & summary functions ([CRAN.R-project.org/package=SoyNAM](http://CRAN.R-project.org/package=SoyNAM))

## SELECTION PUBLICATIONS

- S. S. Gangurde, H. Wang, S. Yaduru, et al. Nested-association mapping(NAM)-based genetic dissection uncovers candidate genes for seed and pod weights in peanut. In: Plant Biotechnology Journal 18.6 (2020), pp. 1457-1471.
- B. P. Hall, A. Xavier, F. Moreira, et al. Quantitative characterization of Proximate Sensing Canopy Traits in the Soynam Population. In: Crop Science (2020).
- M. Mohammadi, A. Xavier, T. Beckett, et al. Identification, Deployment, and Transferability of Quantitative Trait Loci from Genome-Wide Association Studies in Plants. In: Current Plant Biology (2020), p. 100145.
- 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.
- D. Jarquin, R. Howard, A. Xavier, et al. Increasing Predictive Ability by Modeling Interactions between Environments, Genotype and Canopy Coverage Image Data for Soybeans. In: Agronomy 8.4 (2018), p. 51.
- A. Xavier, R. Thapa, W. M. Muir, et al. Population and quantitative genomic properties of the USDA soybean germplasm collection. In: Plant Genetic Resources (2018), pp. 1-11.
- A. Xavier, B. Hall, A. A. Hearst, 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, B. Hall, S. Casteel, et al. Using unsupervised learning techniques to assess interactions among complex traits in soybeans. In: Euphytica 213.8 (2017), p. 200.
- A. Xavier, S. Xu, W. Muir, et al. Genomic prediction using subsampling. In: BMC bioinformatics 18.1 (2017), p. 191.
- A. Xavier, W. M. Muir, B. Craig, 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, S. Xu, W. M. Muir, 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.

## AWARDS AND RECOGNITIONS

- 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.