Alencar Xavier

E-mail: alenxav@gmail.com	**Website**: http://alenxav.wix.com/home	**ORCID**: orcid.org/0000-0001-5034-9954
Phone: 765-631-2572	**GitHub**: https://github.com/alenxav/	**linkedin**: www.linkedin.com/in/alenxav

EXPERIENCE

- 2022 - Current: **Principal Investigator**, Breeding Analyst, Latin America and Africa. Corteva Agrisciences.
- 2017 - Current: **Adjunct Faculty**, Department of Agronomy, Purdue University.
- 2016 - 2022: **Research Scientist**, Quantitative Geneticist group at Corteva Agrisciences.
- 2013 - 2016: **RA Population Genetics**, Purdue University. Supv. by William Muir (bmuir@purdue.edu).
- 2013 - 2016: **RA Soybean Breeding**, Purdue University. Supv. by Katy Rainey (krainey@purdue.edu).
- 2010 - 2011: **RA Potato Breeding**, UFSM, Brazil. Supv. by Dilson Bisognin (dilsonb@smail.ufsm.br).
- 2009 - 2011: **RA Soil Physics**, UFSM, Brazil. Supv. by Jose Miguel Reichert (reichert.jm@gmail.com).

ACADEMICS

1. **Academic Background**
   - *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.*
2. **Computational**
   - Advanced R programming and related tools (Markdown, Shiny, Rcpp Eigen/Armadillo, Tidyverse).
   - Background in C++, parallel computing, and commercial software (Eigen, SAS, ASReml, BLUPF90).
   - Familiarity with machine learning computation and libraries (AWS, Docker, Keras, h2o, XGBoost).
   - Basic coding in Python, Shell, SQL, Perl/regex and LaTeX.
3. **Key areas of Expertise**
   - Plant genetics and breeding, field breeding techniques and selection theory;
   - Phenomics and high-throughput technologies in plant breeding;
   - Mixed models, multivariate models, machine learning and Bayesian methods;
   - Spatial statistics, adjustment of field variation and imputation methods;
   - QTL mapping, Genome-wide association mapping, genome-wide prediction methods;
   - Computational breeding, algorithm development and high-performance computing;
   - Software development using R/C++ coding with R Shiny app interface;
4. **Editor**
   - Scientia Agricola (2019-Current)
   - Frontiers special issue (2022-2023) *Enriching Genomic Breeding with Crop Models, Enviromics, and Phenomics*
5. **Awards and Recognitions**
   - *1st place.* Genomes to Fields (G2F) Genotype by Environment Prediction Competition. 2023.
   - *2022 ACE Process Innovation Award Global Impact.* 2022 Seed Product Development Awards, Corteva Agrisciences.
   - *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.* International Conference of Quantitative Genetics. 2020.
   - *Summer Institute of Statistical Genetics (SISG) Scholarship*, University of Washington. 2016.
   - *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.
   - *Summer Institute in Statistics for Big Data (SISBID) Scholarship*, University of Washington. 2015.
   - *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.
   - *Wyman E. Nyquist Quantitative Genetics Scholarship* . Purdue 2014 Graduate Student Award.
   - *Soy2014 Student Award* - MCBS: 15th Biennial Conference. University of Minnesota, 2014.
   - *Summer Institute of Statistical Genetics (SISG) Scholarship*, University of Washington. 2013.
6. **Grants**
   - Rainey, et al. (2016). Development of pipeline & tools for drone-based canopy phenotyping in crop breeding. LINK
   - Rainey, et al. (2021). Application of uas biomass longitudinal phenotypes to selection in soybean breeding trials. LINK.

7. **Patents**
   - Rainey, et al. (2018). Method of using genetic architecture of phenomic-enabled canopy coverage in glycine max. LINK
8. **Community Leader**
   - 2023 ASA Symposium Co-chair: *Quantitative Genetics and Phenotype Prediction.*
   - 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.*

PUBLICATIONS

1. **Software**
   - BT-SAT-R: Package interface to analyze and model 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. *github*. 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, A. et al. (2015). NAM: Nested Association Mapping. LINK
   - Xavier, A. et al. (2015). SoyNAM Dataset. LINK
   - Xavier, A. et al. (2015). bWGR: Bayesian Whole-Genome Regression. LINK
2. **Presentations & Short Courses**
   - Machine learning-based AI applied to breeding. Purdue 2023. LINK
   - Leveraging correlated information under multivariate settings. UGA 2023. LINK
   - Xavier, A. Maize Yield Predictions: 2022 G2F prediction competition. MGC 2023. LINK
   - Xavier, A. Leveraging correlated information under multivariate settings. Plant Science symposium, UIUC, 2022. LINK
   - Xavier, A. Modeling white mold with more than genomics. *SBW*, 2022. LINK
   - Xavier, A. Implementation and Validation of supervised methods in GS, *2021 ASA CSSA SSSA meetings.* LINK
   - Xavier, A. Efficient computation of multivariate ridge regression, *2021 ASA CSSA SSSA meetings.* LINK
   - Xavier, A. Technical Nuances of Machine Learning. *Iowa State University, 2021.* LINK
   - Xavier, A. Overview on Plant Breeding Analytics (lecture), *Purdue University, 2021.* LINK
   - Xavier, A. Technical Nuances of Machine Learning in Plant Breeding, *Iowa State Symposium, 2021.* VIDEO, SLIDES.
   - ANSC595, Quantitative Genomics Applied to Breeding (1 lecture), Purdue University, Fall 2019. LINK
   - Xavier, A. Good learners, faster learning. *IMPG3*, University of Sao Paulo, 2019. LINK
   - Xavier, A., Brito, L., Rainey, KM. Mixed models applied to breeding. *Purdue*, 2019. LINK
   - Xavier, A. Good learners, faster learning. *PAG*, 2019. LINK
   - Xavier, A. and Morota, G. Short course in mixed models. *UFV*, 2018. LINK
   - Xavier, A. Learning from Data: Machine Learning in Plant Breeding. *UFV*, 2018.
   - AGRY611, Quantitative Genetics (7 lectures), Purdue University, Fall 2017. LINK
   - AGRY620, Advanced Plant Breeding (3 lectures), Purdue University, Spring 2017.
   - Xavier, A. Analytical Methods for Phenomics. *Purdue Phenomic Workshop*, 2017. LINK
   - Xavier, A. Learning from Data. Purdue. LINK. 2015.
3. **Selected articles**
   - Xavier and Habier (2022) A new approach fits multivariate genomic prediction models efficiently LINK
   - Xavier et al. (2021) Breeding Strategy on the Long-Term Genetic Gain in Soybean Breeding LINK
   - Xavier et al. (2021) Modeling of Genetics and Field Variation in Breeding Trials LINK
   - Xavier (2021) Implementation and validation of supervised methods for genomic prediction in plant breeding. LINK
   - Xavier and Rainey (2020). Quantitative Genomic Dissection of Soybean Yield Components. G3. LINK
   - Xavier et al (2019). bWGR: Bayesian Whole-Genome Regression. Bioinformatics. LINK
   - Xavier (2019). Efficient Estimation of Marker Effects in Plant Breeding. G3. LINK
   - Diers et al (2018). Genetic architecture of soybean yield and agronomic traits. G3. LINK
   - Xavier et al (2018). Genomic properties of the USDA soybean germplasm collection. Plant Genetic Resources. LINK
   - Xavier et al (2018). Genome-Wide Analysis of Grain Yield Stability in Soybeans. G3. LINK
   - Xavier et al (2017). Genetic Architecture of Phenomic-enabled Canopy Coverage in *Glycine max.* Genetics. LINK
   - Xavier et al (2017). Genomic Prediction using Subsampling. BMC Bioinformatics. LINK.
   - Xavier et al (2017). Unsupervised learning techniques to dissect associations of soybean traits. Euphytica. LINK.
   - Xavier et al (2016). Walking through the Black Boxes of Statistical Plant Breeding. TAG. LINK.
   - Xavier et al (2016). Assessment of Predictive Properties of Genome-wide Selection in Soybeans. G3. LINK.
   - Xavier et al (2016). Genetic variation captured by a SNP panel in soybean. BMC Informatics. LINK
   - Xavier (2016). Learning from data: Plant breeding applications of machine learning. Purdue University. LINK
   - Xavier et al (2015). Association Studies in Multiple Populations. Bioinformatics. LINK.
   - **See all publications on Google scholar**: LINK.