

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 (krailey@purdue.edu).
- 2010 - 2011: **RA Potato Breeding**, UFSM, Brazil. Supv. by Dilson Bisognin (dilsonb@mail.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

- Breeding business analytics: portfolio management, process mapping, simulations, resource optimization.
- 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*.
- New Frontiers conference. *Cell-to-Seed: Revolution in Breeding Technologies*, Corteva Agrisciences, 2023.
- 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

- Xavier and Xu (2023). MAS: Membership Association Studies (CRAN.R-project.org/package=mas)
- Real Time Analysis app: Insights of performance and stability for advancement. Corteva Agrisciences 2022.
- 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.
- 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 Agrosiences molecular data. Corteva Agrisciences 2018.
- HP: Hybrid prediction tool from Dow Agrosiences production pipeline. Corteva Agrisciences 2018.
- QG2: Quantitative Genetic Analytical Tools for Modeling, Mapping, Prediction. Dow Agrosiences. 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

- Genomic prediction, populations, machine learning. NDSU 2024. [LINK](#)
- Trends of predictive breeding. ASTA 2023 & NAPPN 2024. [LINK](#)
- Machine learning-based breeding. ASA-CSSA-SSSA 2023. [LINK](#)
- 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.
- Xavier, A. Good learners, faster learning. *IMPG3*, University of Sao Paulo, 2019.
- Xavier, A., Brito, L., Rainey, KM. Mixed models applied to breeding. *Purdue*, 2019. [LINK](#)
- Xavier, A. Good learners, faster learning. *PAG 2019* [LINK](#) and *IMPG3 2019* [LINK](#).
- Xavier, A. and Morota, G. Short course in mixed models. *UFV*, 2018. [LINK](#)
- Xavier, A. Learning from Data. *Purdue*. [LINK](#). 2015.

3. Selected articles

- Xavier et al (2024) Enriching genomic breeding with environmental covariates, crop models, and HTP. [LINK](#)
- 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](#)
- 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](#).