

ZIXIANG WEN

✉ wzxsoy@msu.edu ☎ 517-5755029

in <https://www.linkedin.com/in/zixiang-wen-403a4184/> 🌐 <https://github.com/wzxsoy>

SUMMARY

Data scientist with a strong math background and experience in big data, machine learning, statistics and quantitative genetics. Passionate about explaining data science to non-technical business audiences.

SKILLS

MACHINE LEARNING: Unsupervised Learning, Supervised learning, Classification, Regression, Clustering,

STATISTICAL METHODS: Hypothesis testing and confidence intervals, regression models,

Genetics, GWAS, Genomic Prediction and QTL mapping, principal component analysis and dimensionality reduction, Quantitative genetics

SOFTWARE AND PROGRAMMING LANGUAGES: Python (scikit-learn, numpy, scipy, pandas, gensim), R, SQL, Linux, Microsoft Excel

EDUCATION

Data Science Career Track, Springboard, San Francisco, CA · July 2019 to Current

6 month intensive course in data science, machine learning, Python, SQL. with 1:1 industry expert mentor oversight, and completion of 2 in-depth capstone projects. Mastering skills in Python, SQL, data analysis, data visualization, hypothesis testing, and machine learning.

Nanjing Agricultural University · Sept. 2004 to July 2008

Ph. D Plant Genetics 2008

Beijing Agricultural college · Sept. 2001 to June 2004

Master Plant breeding and genetics 2004

Xinjiang Agricultural University · Sept. 1997 to June 2001

Bachelor Agronomy 2001

PROJECTS

Incorporating molecular data-driven decisions towards soybean improvement

I assessed the usefulness of the genomic and phenotypic data collected on 9727 records from the USDA Soybean Germplasm Collection and our own breeding program for developing genomic prediction models to evaluate the genetic value of accessions for traits of protein, oil, and yield. Resulting genomic prediction models explained an appreciable amount of the variation in accession, with correlations between predicted and observed reaching up to 0.86 for yield, 0.70 and 0.67 for oil and protein respectively. The results reported on using comprehensive, extensive data gathered over time by the curators of a germplasm collection for making genomic predictions that will help breeders select accessions in a more rational manner

Beer Recommendation System

Current

There are more than 2,748 different breweries operating in the US as of June, 2018 and more than 5,000 unique brands in the U.S. which may cause newfound confusion for the average consumer when shopping for beer. Given the huge rise in the brewery scene in the United States, it can be overwhelming trying to decide which new brewery or beer to try. My recommendation system will help them decide which beer to try next given their unique tastes and historical ratings.

EMPLOYMENT

Michigan State University

Research Associate · Aug. 2011 to Current · East Lansing, Michigan

My present research project focuses on quantitative genetics and building genomic selection models for agronomic traits in soybean. The research rely heavily on quantitative data analysis, visualization, hypothesis testing and machine learning

Institute of Industrial Crops, Henan Academy of Agricultural Science

Assistant Researcher · Aug. 2008 to Aug. 2011 · Zheng Zhou, China

As a soybean breeder, I participated a province-wide program for development of soybean varieties with high yield, disease and insect resistance. I was also in charge of an NSF project about quantitative genetics of the soybean protein-related genes and exploration of functional polymorphic sequences.