

Alice H. MacQueen, Ph.D.

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Relevant Experience

ADAPTIVE BIOTECHNOLOGIES, Seattle, WA

2022-2024

Computational Biologist II

- Worked with computational and wet lab research teams to develop wet lab assays and bioinformatic pipelines for use on human immunologic data.
- Identified issues with important assay metrics after change to the sequencing platform and proposed an effective solution to the issue.
- Trained and validated statistical models of T-cell sequence annotations across multiple diagnostic assay versions.
- Prototyped software to make T-cell sequence annotations statistically comparable for regulated and in-development diagnostic assay versions.
- Maintained rigorous, comprehensive documentation of projects via electronic lab notebooks and version control.
- Delivered regular reports and presentations to cross-functional groups to support business decision-making and alterations to standard operating procedures.

THE UNIVERSITY OF TEXAS AT AUSTIN, Austin, TX

2019 - 2022

Research Associate

- Developed software that delivered a 200-fold speed improvement for genome-wide association in polyploid switchgrass, an important biofuel species.
- Analyzed large genetic datasets with supervised modeling of genetic effects on traits (linear and logistic regression, random forest models) and Bayesian statistical models (multivariate adaptive shrinkage).
- Major contributor to statistical genomics analysis and co-first author on a publication in Nature: <https://doi.org/10.1038/s41586-020-03127-1>

THE UNIVERSITY OF TEXAS AT AUSTIN, Austin, TX

2016 - 2019

Post-doctoral fellow

- Led effort involving crop scientists and bioinformaticians to conduct statistical genetic analyses in common bean to identify areas for genetic improvement for this crop plant.
- Collected, cleaned, and preprocessed large multi-decadal multi-site phenotypic dataset: http://rpubs.com/alice_macqueen/CDBN_Phenotype_Standardization
- Built large relational database of genotypes, phenotypes, sites, and weather data and delivered database to key stakeholders in the project.
- Used of unsupervised modeling for exploratory data analysis and supervised modeling for analysis of genetic and genomic datasets
- Won Editors' Choice Award for an Outstanding Quantitative Genetics Article: <https://doi.org/10.1534/genetics.120.303038>

THE UNIVERSITY OF CHICAGO, Chicago, IL

2009 - 2016

Graduate Student

- Developed bioinformatic pipeline for analysis of m6A RNA editing in plant transcriptomic data, published in: <https://doi.org/10.1038/ncomms6630>
- Conducted analyses of RNA-seq data to investigate mechanism of gene action, published in: <https://doi.org/10.1038/nplants.2016.110>

Teaching & Presentation Experience

SOFTWARE & DATA CARPENTRY WORKSHOPS, Austin, TX

2019 - 2021

Instructor

Trained 50 graduate and undergraduate students in the use of git and R's ggplot2 package.

CROPS , Huntsville, AL <i>Invited Presentation</i> “Finding conditionally neutral alleles to harness “harmless” local adaptation in common bean (<i>Phaseolus vulgaris</i>)”	2019
PAG , San Diego, CA <i>Invited Presentation</i> “Genetics of Genotype-by-Environment Interactions in the Switchgrass Diversity Panel”	2020
Plant Soils and Microbial Sciences Department, MSU , East Lansing, MI <i>Invited Presentation</i> “Finding conditionally neutral alleles to harness “harmless” local adaptation in common bean (<i>Phaseolus vulgaris</i>)”	2020

Open Source Software

switchgrassGWAS: <https://github.com/Alice-MacQueen/switchgrassGWAS>.

An R package to conduct genome-wide association and other genomic analyses on the *Panicum virgatum* diversity panel.

CDBNgenomics: <https://github.com/Alice-MacQueen/CDBNgenomics>.

An R package to conduct genome-wide association and other genomic work using individuals from the Cooperative Dry Bean Nursery phenotypic dataset.

Education

UNIVERSITY OF CHICAGO , Chicago, IL <i>Ph.D., Ecology and Evolution</i> National Science Foundation Graduate Research Fellowship	2016
UNIVERSITY OF VIRGINIA , Charlottesville, VA <i>B.Sc. Chemistry; B.Sc. Biology with Highest Distinction</i> Distinguished Major Research in Biology	2009

Skills & Interests

- Dual citizen: US and New Zealand
- Technologies: R, tidyverse, Quarto, Shiny, git, Unix/Linux, Python, poetry, Jupyter, Docker, Azure, AWS.
- Distance running, feminist science fiction, Dungeons & Dragons.