KRISTY MA

kma1@unc.edu ◇ LinkedIn ◇ Github

EDUCATION

M.S. in Biostatistics. University of North Carolina at Chapel Hill — Expected May 2025

B.A. in Statistics. Macalester College — Aug 2019 - May 2023
Minors: Computer Science and Biology
GPA: 3.94

Coursework: Statistical Genetics, Mathematical Statistics, Causal Inference, Algorithm, Computational Biology, Machine Learning, Advanced Genetics, Molecular Biology

WORK AND RESEARCH EXPERIENCE

Maize Transposable Elements Linking Research — Sep 2022 - Dec 2022
Department of Plant and Microbial Biology, University of Minnesota — *Minneapolis, MN*

- Constructed pipelines using a combination of Shell and R scripting to classify 700+ structural variants into distinct categories based on TE annotations that intersected those variants
- Performed extensive data visualization exploring the proportions of these categories in recently diverged SNP-depleted regions across 26 inbred NAM lines to assess frequency of suspected insertion versus deletion events
- Compared differences in TE content at the class, superfamily, and family level in these SNP-depleted regions to see whether certain TEs are more common in putative insertions
- Inspected the putative insertion regions and test how TE insertions are correlated with differential expression of nearby genes

Maize Translational Genomics Research — Jun 2022 - Aug 2022
Department of Agronomy and Plant Genetics, University of Minnesota — *Saint Paul, MN*

- Carried out multiple GWAS analyses versus flowering times, yield, and moisture content, finding out two significant structural variations associated with late flowering time across 100+ maize domestic inbred lines
- Collected and validated data for a support vector machine model (Spearman's rank correlation 0.852) predicting moisture contents of nixtamalized maize, then visualized clustering of genotypes using PCA for 300+ hybrid maize genotypes in R
- Performed a scaled-down benchtop cook test with many steps in close succession with a high degree of fidelity to maximize the quality of the data collected
- Mastered molecular biology techniques including DNA extraction, DNA cloning, plasmid transformation
- Worked with E. coli DH10B cells for plasmid transformation, which were designed to be transformed into maize protoplasts for gene expression analysis

Cancer Immunology Research — Sep 2020 - Feb 2021
Jilin University National-Local Engineering Laboratory of Animal Models for Human Diseases — *Changchun, China*

- Analyzed time series regression to predict level changes of inflammatory cytokines to assess the cancerous effect of p53 knockout on thymus function in 6 months
- Applied Western Blot, immunofluorescence, Q-PCR, and flow cytometry to analyze the variation of thymus epithelial cells subgroup in p53 knockout mice across different ages
- Attended journal clubs, weekly research presentation sessions with graduates and principal investigator

Teaching and Lab Assistant — Sep 2021 - May 2023
Statistic Department, Biology department — *Saint Paul, MN*

- Assisted 200 students' learning in Machine Learning, Calculus II, Molecular Genetics, and Epidemiology
- Performed series of molecular biology lab techniques through the semesters

- Hold weekly office hours to work personally with students to strengthen their understanding of statistics; Prepared review material, proctored and evaluated exams, lab projects, homework, and quizzes

PROJECTS

Project 1 Applying linear mixed effect model in correlated family genetic data GitHub

- Conducted a small GWAS study involving simulation of genotypes using real genetic data to test out LMM's effectiveness in correcting family correlation and stratification structure
- Read and self-taught multiple R packages (GENESIS, SNPRelate, snpStats, GWASTools) to clean, prepare, and handle complicated HapMap data structure as desired by research questions
- Separated and filtered out uncorrelated individuals from the original data set by looking into correlation coefficient matrix between pairs of observations using KING tool set
- Determined effective, appropriate, significant genomic control in LMM model compared to OLS, supported by high quality output of Quantile-Quantile plot and and lambda GC numericals

Project 2 Exploration on breast cancer data using machine learning tools GitHub

- Extracted 600+ observations from Kaggle online resource and performed data wrangling for subsequent analysis
- Compared and evaluated the performance of GAM, Random Forest, LASSO and K-means predicting the area and malignancy of tumor using 30 variables
- Performed exhaustive data visualizations and identified ways to influence perspectives by manipulating data graphics
- Demonstrated high correlation for 4 predictors with tumor malignancy and implemented diagnostic matrix and ROC AUC graphs evidenced model optimization

Project 3 Literature review on genetic variants on SARS-CoV-2 Link

- Integrated and summarized the findings of 20+ high-quality published papers discussing various effects genetic variants of SARS-CoV-2
- Identified 13 mutant strains and 30+ specific amino acid or genetic mutations and loci related to variants' prevalence
- Thoroughly discussed the variants' impacts from aspects including respective characteristics, transmissibility, and clinical morbidity, also critically analyzed the limitations of investigation such as higher bias on epidemiology

PUBLICATION AND PRESENTATIONS

- *In progress:* Manisha Munasinghe, **Kristy Ma**, et.al. **Combined analysis of transposable elements and structural variation in maize genomes reveals genome contraction outpaces expansion.**
- **Kristy Ma**, Yuhua Wang, et.al. **Research on Effect of Storage Temperature on Microorganism of Eggshell Surface.** Farm Products Processing. Oct 2018. ISSN 1671-9646.
- Poster presentation: **Translational Genomics Research: Exploring Maize**. Summer 2022 Research Symposium. Macalester College, Saint Paul, MN, Sep 2022
- Poster and Oral presentation: **Genetic mutation and variants of SARS-CoV-2 and their relative effect on transmission, morbidity, and mortality: a systematic review.** 2021 Biology Department Capstone paper Presentation. Macalester College, Saint Paul, MN, Dec 2021

SKILLS

Programming Languages	Python, R, Unix Shell, Java, LaTex
Tools	Git, RStudio, Visual Studio Code, PyCharm, Jupyter Notebook
Soft Skills	Leadership, Teamwork, Communication, Problem Solving

ACTIVITIES

Admission Ambassdor and Admission Advisory Committee member at Macalester Student Board
Sep 2019 - May 2020

- Worked for Macalester international admission office
- Networked with incoming class of 2024 to help students accommodate to the campus
- Created a large chat group and answered questions for students regarding visa, school life, work balance
- Conducted weekly zoom advisory sessions recording the feedback from students to Macalester admission office
- Constantly collected students' feedback on admission including how they applied, decided, and enrolled
- Wrote weekly proposals summarizing possible solutions and advice for admission office