KEVIN STANFORD LIAO

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EDUCATION

University of Michigan, Ann Arbor, Michigan *Expected Graduation December 2022*
Ph.D. in Biostatistics
Dissertation Topic: Statistical and Machine Learning Methods to Analyze Genetic Architecture of Complex Traits Across Ancestral Populations
Supervised by: Dr. Sebastian Zoellner

University of Michigan, Ann Arbor, Michigan
Master of Science in Biostatistics, 2019
Research Topic: The Effect of Mutation Subtypes on the Allele Frequency Spectrum and Population Genetics Inference
Supervised by: Dr. Sebastian Zoellner

University of North Carolina, Chapel Hill, North Carolina
Bachelor of Science in Public Health in Biostatistics, 2017
Minor in Computer Science

RESEARCH INTERESTS

Statistical Genetics, Population Genetics, Polygenic Risk Scores, GWAS, Rare Variant Testing, Multi-Ethnic Genetic Research, Genetic Admixture
Machine Learning, Bayesian Methods, Statistical Inference for High-Dimensional Data

PROFESSIONAL EXPERIENCE

University of Michigan, Ann Arbor, MI
Graduate Research Assistant for Dr. Sebastian Zoellner, January 2018 - Present
· Analyzed high-dimensional whole genome sequencing and identified potential biases of current population genetics inference based on the allele frequency spectrum.
· Inferred local ancestry for 60,000 samples of diverse ancestry in the EHR-based Michigan Genomics Initiative.
· Developed novel machine learning stacking framework to combine GWAS summary statistics from multiple ancestries to optimize phenotype prediction in Admixed individuals.
· Developing novel composite null hypothesis framework to test for differences in estimated GWAS effect sizes for a given complex trait across ancestries.

University of Michigan, Ann Arbor, MI
Graduate Research Assistant for Drs. Mike Boehnke and Laura Scott, August 2020 - Present
· Conducted gene-based rare variant association tests to identify genes associated with Bipolar Disease and Schizophrenia in largest African American sample to date.
· Performed stratified LD score regression to estimate heritability enrichment in annotations identified from regional rare variant testing.

PROFESSIONAL SKILLS SUMMARY

Software
· Statistical: R, Python, SAS, SQL Computational: Java, C++, Linux

Statistical and Machine Learning Methods
· Generalized Linear Regression, Mixed Effects Models, Statistical Inference, Bayesian Methods
· Parallel Computing, Penalized Regression, Decision Trees, Neural Networks, Ensemble Methods

Data Experience

· High-Dimensional Whole Genome Sequencing Data

—- Deep whole genome sequencing data from TOPMed, 1000 Genomes, European samples in BRIDGES, African Americans in InPSYght

· Eletronic Health Records

—- Genotype and phenotype (Phecodes) data from UK Biobank and Michigan Genomics Initiative

Language

· English (native), Chinese (conversational)

TEACHING EXPERIENCE

University of Michigan, Ann Arbor, MI Sep 2017 - Dec 2017

Graduate Student Instructor for Biostat 501: Introduction to Biostatistics

· Taught statistical computing lab using SPSS to graduate students in school of public health.

University of Michigan, Ann Arbor, MI Mar 2021

Guest Lecturer for Biostat 666: Statistical Models And Numerical Methods In Human Genetics

· Developed curriculum and gave guest lecture on ”Estimating GWAS Effect Sizes and Polygenic Risk Scores”

AWARDS AND RECOGNITION

· T32 Genome Science Training Program Fellow	2018-2020
· MSSISS Student Award for Best Poster	2019
· Rackham Graduate School Conference Travel Grant	2018-2021
· Integrated Biological Sciences Certificate of Achievement	2016
· UNC Business Essentials Certificate, Kenan-Flagler Business School	2014

MANUSCRIPTS IN PROGRESS

1. **Liao, K.**, Carlson, J., Zoellner, S. The Effect of Mutation Subtypes on the Allele Frequency Spectrum and Population Genetics Inference.
2. Gagliano Taliun, S., **Liao, K.** ... Zoellner, S., Boehnke, M., Scott, L. Whole Genome Sequencing of African Americans with Bipolar Disease and Schizophrenia.
3. **Liao, K.**, Zoellner, S. A Novel Stacking Framework for Polygenic Risk Prediction in Admixed Individuals.

SELECTED PRESENTATIONS

1. American Society of Human Genetics Meeting, Virtual, October 2021. “A Stacking Framework for Polygenic Risk Prediction in Admixed Individuals” (Poster).
2. American Society of Human Genetics Meeting, Houston, October 2019. “The Effect of Mutation Subtypes on the Allele Frequency Spectrum and Population Genetics Inference” (Platform Talk.)
3. Midwest Popgen Conference, Chicago, August 2019. ”The Effect of Mutation Subtypes on the Allele Frequency Spectrum and Population Genetics Inference” (Poster). MidWest PopGen, .
4. Michigan Students Symposium on Interdisciplinary Statistical Sciences, Ann Arbor, March 2019. “The Effect of Mutation Subtypes on the Allele Frequency Spectrum and Population Genetics Inference” (Poster).

LEADERSHIP AND SERVICE

Department of Biostatistics, University of Michigan, Ann Arbor

· Study Group Tutor of core Biostatistics 601 and 602 courses for 1st year students	Aug 2020 - Present
· Member of Biostatistics Diversity Equity and Inclusion Committee	Aug 2020 - Present
· Organizer of Biostatistics Brown Bag Seminars	Aug 2018 - Aug 2020
· Co-founder and Editor of NHGRI online journal Genomics: Insights	Jan 2019 - June 2019