**Polygenic prediction and health disparities among diverse populations**

The vast majority of participants in genetic studies are of European descent, and a key open question is the extent to which findings from these studies generalize across globally diverse populations. While the fundamental biology discovered by genetic studies at individual sites in the genome are mostly shared across humanity, Eurocentric study biases mean we miss low-hanging fruit in other populations, and limit the utility of genomic prediction across globally diverse populations. We are currently capable of predicting heritable risk of complex diseases several-fold more accurately in European populations than in non-Europeans. As genomic studies increase in sample size and explain a greater proportion of heritable variation, they hold greater potential for clinical translation, but their implementation today would exacerbate health disparities more than many other clinical tests. To increase the transferability of genetic prediction, we are performing increasingly diverse genomic studies and building statistical methods that consider population genetic differences among globally diverse populations.

Ongoing work:

* MAMA

Published research in this area:

* Hidden ‘risk’ PRS disparities
* 1kG PRS paper
* Need/challenges of genetic architecture Africa
* Mashaal/Robert
* Sini
* Stanley Global

**Human evolution and fine-scale population history**

I am interested in using genetic data to look back through time to learn about how demographic dynamics—e.g., migration, admixture, and population size changes—shaped human history. Understanding human evolutionary history has implications for study design, interpreting and accounting for population stratification, learning about the genetic architecture of complex traits, and gaining insights into forces of natural selection. I am especially interested in understanding the genetic basis of traits that have been evolutionarily important throughout human history, such as skin pigmentation and height, and how they changed throughout the human diaspora. To this end, I have focused in several geographic areas, including on very recent admixture in the Americas, recent history for the bottlenecked Finnish population, and with a particular emphasis on deeper and more complex history in sub-Saharan Africa.

Published research in this area:

* Sini Finland
* Me Finland
* KhoeSan pigmentation
* Uren et al
* Lemon’s pigmentation

**Genetic basis of psychiatric disorders**

I am also researching the genetic basis of psychiatric disorders as an analyst in the Psychiatric Genomics Consortium (PGC). Like most GWAS, gene discovery efforts in psychiatric disease have largely focused on individuals of European descent, and my work assesses current findings

from an evolutionary lens. I am especially interested in increasing the scale of multi-ethnic data to uncover new genetic associations, aid in the identification of causal variants, and to build more transferable genetic risk prediction models. To this end, my work focuses primarily on the genetics of more heritable, early onset psychiatric disorders including schizophrenia, bipolar disorder, ADHD, and autism.

* PRS psych review
* Hailiang
* ADHD
* ASD
* PTSD