

Quantitative genetics in structured populations

Goals:

- 1) Estimate the amount of genetic and environmental variation in the population.
- 2) Estimate the genetic and environmental effects on an individual.
- 3) Predict the phenotype of individuals using genome, pedigree, and environment.

Intermediate problems:

- 1) Genetic decompositions.
- 2) Estimating covariance matrices.

Where I am:

- Similar performance on allele frequency calling.
- Improved ROC for polymorphic sites.
 - Test with VG?
- Improved accuracy calculating genetic covariance matrices from genotypic likelihoods.
 - Including unique estimate of several matrices
- Improved accuracy calculating genetic covariance from use of individual specific priors.

TO DO LIST

- ☒ Formally derive covariance matrices.
- ☐ Estimate variances/covariances.
- ☐ Get the BLUP right.
- ☐ Implement model of DFE.
- ☐ Implement population structure in simulations.
- ☐ Check against GCTA in simulations.
- ☐ Check against GCTA on human data.

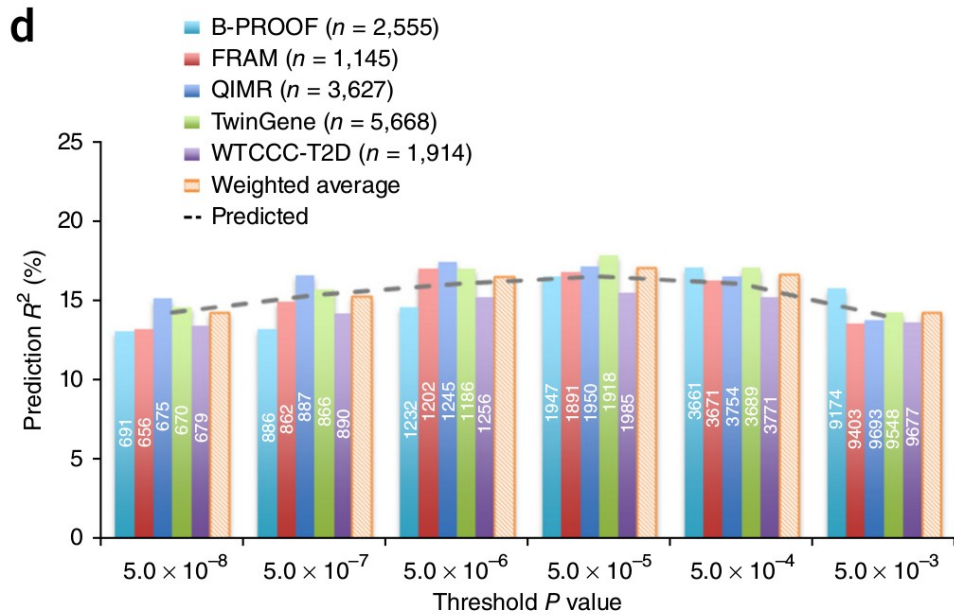
Potential future projects.

- 1) Phenotypic prediction
 - Ancient DNA
 - Works well with genetic likelihood data
- 2) Genetic architecture
- 3) Historic inbreeding
 - ROH?
- 4) Selection tests

Genetic architecture

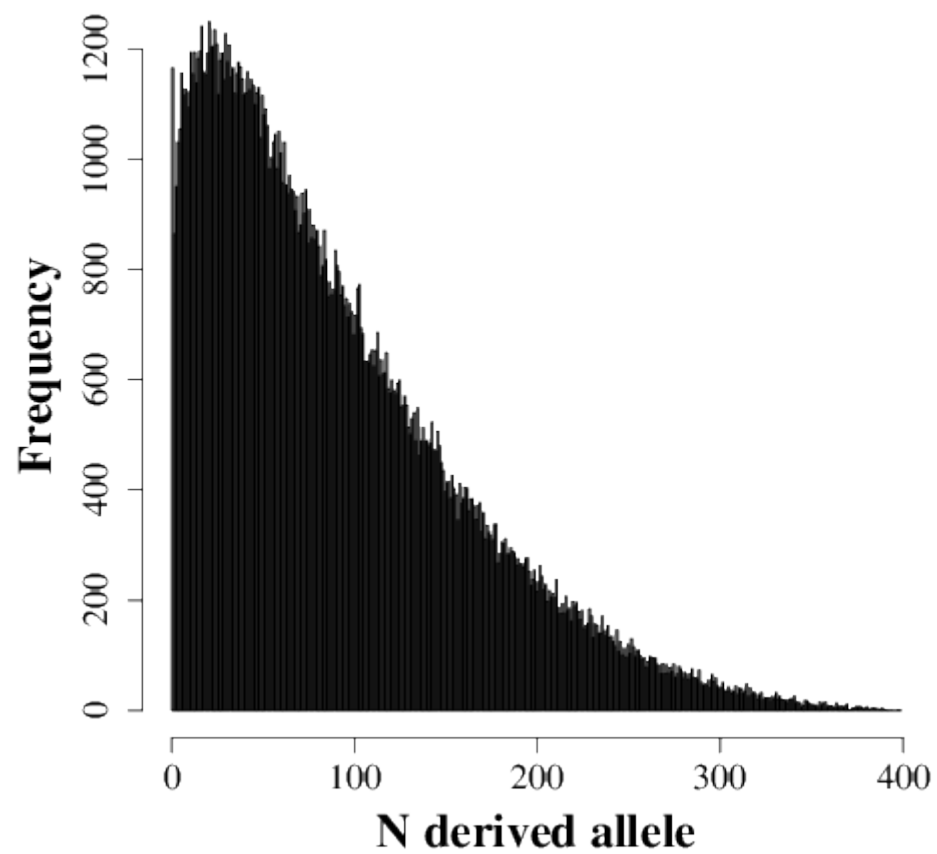
- Effects of inbreeding.
- Total amount of dominance variation
- Epistatic effects verse genetic distance
- Is GCTA really recovering narrow sense heritability?
- What is going on with linkage?
 - LDAK vs GCTA

Phenotypic prediction



Wood et. al 2014, Nature Genetics.

Allele frequency spectrum



Allele frequency spectrum

