

# Comparison of Association Mapping Methods in Admixed Populations

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## Background

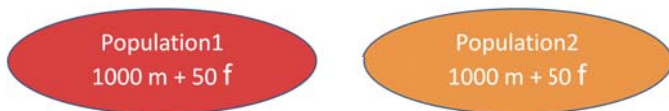
Population stratification occurs when the individuals in a sample differ in their genetic backgrounds. If these differences are not accounted for, this leads to false positive results in genome-wide association studies (GWAS). We have compared GWAS methods for power and type-I error in the presence of stratification in a pedigreed population.

## Simulation

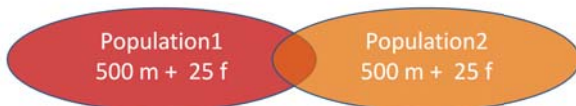
### Historic Population ; 1000 Generations



### Separation for 30 generations



### Admixture for 3 generations



- 2,000 individuals from an admixed population, typed for 40,000 SNP markers on 20 chromosomes.
- 2 QTL on a chromosome jointly explained 10% of the phenotypic variation.
- Four methods compared (100 replicates each).
  1. Linear mixed model including pedigree based relationship (**LMMped**).
  2. Linear mixed model including genomic relationship (**LMMgmat**).
  3. LMMped including population structure using STRUCTURE (**LMMstr**).
  4. LMMped including population structure through principal components (**LMMpca**).
- False positive rates were assessed from 5 chromosomes with no simulated QTL.

## Main findings

- LMMped, LMMstr and LMMpca showed similar power (35%) and LMMgmat had a slightly lower power (32.5%).
- All four methods controlled false positives.
- Incorporating the relationship in the model was sufficient to control the type-I error rate when there was both admixture and relationship, however incorporating structure alone was not sufficient.
- LMMgmat was the most conservative – probably due to the use of SNPs at the QTL region to estimate the genomic relationship.
- All models had low power (~5%) to detect small effect QTL (<5% of  $\sigma_p^2$ ) and a high power (60-65%) to detect large effect QTL (5% - 10% of  $\sigma_p^2$ ).

## Results

