

One of the greatest promises of modern genetics is the ability to identify loci responsible for, or at least highly correlated with, important physical traits and disease susceptibility. This will enable benefits ranging from improved disease risk assessment and crop design to ultimately a better understanding of how genotype variation effects variations in phenotypes. A key component in this task is association mapping where correlations between the clustering in the trait of interest and the clustering observed in the genealogy of a set of sampled sequences has the potential to localise causative genomic locations with relatively high precision. This project pursues this with focus on a genomewide data set from Arabidopsis.