

This github contains the raw data and demonstration used in the original publication of OATH.

### **1 Get the data**

Please either "git clone <https://github.com/gc5k/OATH.git>" to have the whole data cloned to your local computer, or download it (notice the "clone or download", a green button?).

### **2 System requirements**

OATH has already been realized in GEAR [GEnetic Analysis Repository; gear.jar]. More details about GEAR can be found <https://github.com/gc5k/GEAR/wiki>. gear.jar requires java installed. To check the details, type "java -version". If it shows "java 1.7" or "java 1.8", then your computer is ready; otherwise please download java online and install it first (from oracle website).

### **3 Three demonstrations**

**a)** Run Figure2Demo.R.

DemonFig2 has an R script to generate Fig 2 as in the paper; and also it shows the kernel of OATH.

**b)** Run ArabAnalysis\_Fig6.R.

ArabData has the cleaned genotype data for generating results for Fig 6. Although genotype data are not really needed by OATH, to provide a more comprehensive experience for users we still include the data for 295 Arabidopsis lines.

**c)** Run GWAMA\_Fig7.R.

GWAMA analysis. Naive summary statistics provided two Chinese GWAS cohorts: NAc cohort and SLE cohort.

## **4. Data**

The 42 phenotypes in [Arab295Line.phe](#) are "RGT", "SGT", "Biomass", "PRL", "LRN", "EL", "RL", "K", "Ca", "Mg", "S", "Fe", "Mn", and "Na" under Low Mg (1-14), normal Mg (15-28), and high Mg (29-42), respectively.

The 10 covariates in [Arab295Line.eigenvec](#) are the top 10 eigenvectors.