In what follows, we provide a guideline on how to use the R-based using GWAS experiment as an example.

1. Data in csv format that diameter\_ck, diameter\_salt and hysnp represent the diameter of the salt-free (control) group, the diameter of the salt-exposed (stress) group and marker of Euphrates populus , respectively.
2. Data processing.R is for loading data and processing phenotypic datas and markers.
3. Composite functional mapping.R is calculated by Funmap to get the fitting and Manhattan plot of log-likelihood ratios (LR).
4. Genetic effect.R is calculating the genetic standard deviation to get the genetic effect.
5. Functional cluster.R is to divide genetic effect into multiple distinct network communities.
6. Gene network.R is incorporating LASSO-based variable selection and decompose ODEs to obtain independent effect and dependent effect component.

Mapping experiment is the same as the above method.