

User manual

Package R for execution steps:

1. Install R environment <https://cloud.r-project.org/>
2. Execute the code

```
# Test network environment
# Load network resources package and execute local code
source("http://106.13.144.206/psglmm/ggwas.txt")
# download Demo data and save them in GLMMG directory and run Demo Code
# Set the working directory, place the downloaded data files in the working directory
# setwd("GLMMG")
# gensv: gene csv file
# phecsv: phenotype csv file
# cvcsv: Covariate variables
# islinear: TRUE: continuous; FALSE: non-continuous(default) (optional)
# isexact: TRUE: exact method; FALSE: PSR (Pseudo response) method (default) (optional)
# phename: phename:name of the trait to be calculated
# phetype: trait type: binary (default), poisson, binomial (optional)
# phenameother: if the trait type is binomial, this trait needs to be specified, the actual program automatically uses
phetype/phenameother (optional)
# cores: number of threads used, default is 1
# output: output location for result files (optional)

# Optional continuous traits, non-continuous traits Binary, Binomial, Poisson using the EXACT method and PSR
(Pseudo response) method
ggwas(gensv,phecsv,cvcsv,islinear,isexact,
      phename,phetype,phenameother,cores,output)

# Ordinal traits EXACT method
pseudo_exact(gensv,phecsv,kkcsv,output)
```

```

# Ordinal traits PSR (Pseudo response) method
pseudo_approximate_fast(gencsv,phcsv,kkcsv,outpath)

# Binary, Binomial, Poisson traits using the P3D (Population parameter previously determined) method
method_c_binary_binomial_possion(gencsv,phcsv,kkcsv,phetype,outpath)

# Ordinal traits using the P3D (Population parameter previously determined) method
method_c_ordinal(gencsv=gencsv,phcsv,kkcsv,outpath)

# Binary, Binomial, Poisson traits using the Single method (no polygenic control)
glm(gencsv,phcsv,cvcsv,phename,phetype,phenameother,outpath)

# Ordinal traits using the Single method (no polygenic control)
ordinal(gencsv,phcsv,phename,phenameother,outpath)

# Test local resource environment
# Download resource package, place test files and resource files in the same path
source("ggwas.txt")
# Download demo data and save them in the GLMMG directory and run demo code
# Set the working directory, place the downloaded data files in the working directory
# setwd("GLMMG")
# gencsv: gene csv file
# phcsv: phenotype csv file
# cvcsv: Covariate variables
# islinear: TRUE: continuous; FALSE: non-continuous(default) (optional)
# isexact: TRUE: exact method; FALSE: PSR (Pseudo response) method (default) (optional)
# phename: name of the trait to be calculated
# phetype: trait type: binary (default), poisson, binomial (optional)
# phenameother: if the trait type is binomial, this trait needs to be specified, the actual program automatically uses
phetype/phenameother (optional)
# cores: number of threads used, default is 1
# outpath: output location for result files (optional)
# Optional continuous traits, non-continuous traits Binary, Binomial, Poisson using the EXACT method and PSR
(Pseudo response) method
ggwas(gencsv,phcsv,cvcsv,islinear,isexact,phename,phetype,phenameother,cores,outpath)

```

```
# Ordinal traits EXACT method
```

```
pseudo_exact(gencsv,phcsv,kkcsv,outpath)
```

```
# Ordinal traits PSR (Pseudo response) method
```

```
pseudo_approximate_fast(gencsv,phcsv,kkcsv,outpath)
```

```
# Binary, Binomial, Poisson traits using the P3D (Population parameter previously determined) method
```

```
method_c_binary_binomial_possion(gencsv,phcsv,kkcsv,phetype,outpath)
```

```
# Ordinal traits using the P3D (Population parameter previously determined) method
```

```
method_c_ordinal(gencsv=gencsv,phcsv,kkcsv,outpath)
```

```
# Binary, Binomial, Poisson traits using the Single method (no polygenic control)
```

```
glm(gencsv,phcsv,cvcsv,phename,phetype,phenameother,outpath)
```

```
# Ordinal traits using the Single method (no polygenic control)
```

```
ordinal(gencsv,phcsv,phename,phenameother,outpath)
```