

# Package ‘fGWAS’

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**Title** Functional Genome-wide Association Study

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**Description** Analysis genetic effects to detect the significant SNPs associated with longitudinal traits based on fGWAS method.

**Depends**

R (>= 2.6.0), minpack.lm, snpStats, mvtnorm, parallel, methods, stats, graphics, grDevices, utils

**License** GPL-3

**Suggests** snow

**URL** <http://www.github.com/wzhy2000/fgwas>

**LazyLoad** no

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fg.load.phenotype	<i>Loading phenotypic data</i>
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## Description

Loading longitudinal phenotypic curve and covariate files.

## Usage

```
fg.load.phenotype(file.phe.long, file.phe.cov=NULL, file.phe.time=NULL,
  curve.type = NULL,
  covariance.type = NULL,
  file.plot.pdf = NULL,
  intercept = TRUE,
  options = list(verbose=F))
```

## Arguments

file.phe.long	string, indicating the file name of longitudinal curve for each individual.
file.phe.cov	string, indicating the file name of covariates.
file.phe.time	string, indicating the file name of observed time points for each individual. If this file is not specified, the column indexes are used as measured times.
curve.type	string, indicating the curve type, available options are in the details. Default is 'auto' which means the package selects the curve type using curve fitting.
covariance.type	string, indicating the covariance structure type, available options are in the details. Default is 'auto' which means the package selects the covariance type using MLE.
intercept	boolean, indicating whether intercept is included in the model.
file.plot.pdf	string, indicating a PDF file name to illustrate the performance of curve fitting.
options	list, including max.optim.failure, min.optim.success, R2.loop, and verbose, default values are max.optim.failure=100, min.optim.success=20, R2.loop=5, verbose=F.

## Details

The phenotype file(file.phe.long), observed time file(file.phe.time) and covariate file(file.phe.cov) must be a CSV file. The following sections illustrate the format of each data file.

1) The phenotype file. The first column is individual ID and the rest columns are sample data for each measurement. It looks like the following file. Please note missing data is coded as space or NA in all data files. For example:

```
ID, 1st, 2nd, 3rd, 4th, 5th, 6th, 7th
1, 2.9033, 4.118, 6.1495, 7.8161, 9.8379, 12.963, 14.918
2, 4.3306, 5.378, 7.0647, 9.3624, 11.439, NA, 15.701
3, 2.3997, 4.052, 5.5431, 7.6933, 9.8471, NA, 12.849
4, 3.3044, 4.154, 5.8924, 7.7133, 9.2144, 10.945, NA
...
```

2) The measurement time file. The first column is individual ID and the rest columns are observed times as the following format. For example:

```
ID, 1st, 2nd, 3rd, 4th, 5th, 6th, 7th
1, 1, 2, 3, 4, 5, 6, 7,
2, 1, 2, 3, 4, 5, NA, 7,
3, 1, 2, 3, 4, 5, NA, 7,
4, 1, 2, 3, 4, 5, 6, NA,
...
```

3) The covariate file. The first column is individual ID and the rest columns are covariate values as the following format. For example:

```
ID, X1, X2
1, 1.0, 0
2, 1.1, 1
3, 2.1, 1
4, 3.1, 0
...
```

The function returns a S3 object which details can be checked by the command `print` or `str`.

The following contents are exported by `print` command.

```
== Phenotype Object in fgWAS ==
Longitudal value : /tmp/Rtmp0lhMx2/file58b1776d8395.csv
-- Individual count : 1678
Longitudal time : /tmp/Rtmp0lhMx2/file58b1131b9b1.csv
-- Time count : 8
Covariate file : /tmp/Rtmp0lhMx2/file58b1246a670b.csv
-- Covariate count : 6
-- Intercept : YES
-- Estimate values : 36917.16 -1.553526 -2.702489 7.852712 -5.91549 7.210022 3.805883
Curve type : auto
-- Estimate type : Legendre2
-- Estimate values : -36888.65 1.081318 -1.852532
Covariate type : auto
-- Estimated type : TOEPH
-- Estimate values : 0.9082402 0.8627414 0.8142826 0.7713539 0.7200614 0.6669603 ...
```

9 curves have been implemented in current version, including:

### 1) "Logistic"

$$g(t) = \frac{a}{1 + b * e^{-r*t}}$$

### 2) "Bi-Logistic"

$$g(t) = \frac{a1}{1 + b1 * e^{-r1*t}} + \frac{a2}{1 + b2 * e^{-r2*t}}$$

### 3) "Pharmacology"

$$g(t) = \frac{E_{max} * t}{E_{c50} + t} + E_0$$

**4) "Exponential"**

$$g(t) = a * e^{-r*t}$$

**5) "Bi-Exponential"**

$$g(t) = a_1 * e^{-r_1*t} + a_2 * e^{-r_2*t}$$

**6) "Power"**

$$g(t) = a * t^b$$

**7) "Legendre2", Legendre Polynomial(2nd-order)**

$$g(t) = u_0 + u_1 * t + u_2 * (3 * t^2 - 1)/2$$

**8) "Legendre3", Legendre Polynomial(3rd-order)**

$$g(t) = u_0 + u_1 * t + u_2 * (2 * t^2 - 1)/2 + u_3 * (5 * t^3 - 3t)/2$$

**9) "Legendre4", Legendre Polynomial(4th-order)**

$$g(t) = u_0 + u_1 * t + u_2 * (2 * t^2 + 1)/2 + u_3 * (5 * t^3 - 3t)/2 + \dots$$

**Value**

This function returns a S3 object with the class label of `fgwas.phe.obj`:

<code>pheY</code>	Matrix, the longitudinal curve data with the rowname indicating the individuals' id.
<code>pheX</code>	Matrix, the covariate with the rowname indicating the individuals' id.
<code>pheT</code>	Matrix, the observed time points with the rowname indicating the individuals' id.
<code>ids</code>	Vector, the common individuals' id in all data file
<code>obj.curve</code>	Curve object, S4 object inherited from <code>fg.curve.base</code>
<code>obj.covar</code>	Covariance object, S4 object inherited from <code>fg.covariance.base</code>
<code>est.curve</code>	List, including the curve type and estimated parameters.
<code>est.covar</code>	List, including the covariance type and estimated parameters.
<code>summary.curve</code>	List, including the result of curve fitting.
<code>summary.covar</code>	List, including the result of covariance fitting.
<code>params</code>	List, the parameters of function calling, including the file names of longitudinal data and covariate, curve type and covariance type
<code>options</code>	List, not used currently

You can plot the curve by the function `plot` or print summary information by the function `print`.

## Examples

```
# use simulation to make a phenotype object and genotype object and generate the files.
obj.sim <- fg.simulate( "Logistic", "SAD1", 2000, 800, 1:6,
  phe.missing=0.05, snp.missing=0.05,
  sig.pos=301, plink.format=TRUE, file.prefix = "temp.fwgas.test1" );

# show the brief information for the phenotype object
obj.sim$obj.phe

# load the phenotype traits generated by the simulation
obj.phe <- fg.load.phenotype("temp.fwgas.test1.pheY.csv", NULL, "temp.fwgas.test1.pheT.csv",
  curve.type = "Logistic", "SAD1", file.plot.pdf = NULL,
  intercept = FALSE, options = list(verbose=TRUE))

# show the brief information, this object is equal to 'obj.sim$obj.phe'
obj.phe;

# plot the phenotype traits into a PDF file without the curving fitting information.
plot( obj.phe, curve.fitting=FALSE, file.pdf = "temp.fwgas.test1.phe.pdf");

# remove all test files
unlink("temp.fwgas.test1.*");
```

---

fg.load.plink	<i>Loading PLINK data set.</i>
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---

## Description

Loading genotype data from PLINK data set.

## Usage

```
fg.load.plink(file.plink.bed, file.plink.bim, file.plink.fam,
  plink.command = NULL,
  chr = NULL,
  options = list(verbose=F))
```

## Arguments

file.plink.bed	string, the name of PLINK bed file, containing the packed binary SNP genotype data
file.plink.bim	string, the name of PLINK bim file, containing the SNP descriptions
file.plink.fam	string, the name of PLINK fam file, containing subject(and, possibly, family) identifiers
plink.command	string, indicating PLINK command path, for the large PLINK data, the package loads partial PLINK data extracted by the 'plink' command rather than the whole data set.
chr	vector of string, indicating the chromosome number involved to do hypothesis test.
options	list, including force.split and verbose

## Details

This function try to avoid loading all genotype data in memory. The optional parameter `force.split` indicates to use the `plink` command to split the genotype data according to chromosome unit and then load the partial genotype data gradually.

The following example show the contents exported by `print` command.

```
== Genotype Object in fGWAS ==
Plink bed : /home/userx/proj/gwas2/bmi-c1c2-qc2.bed
Plink bim : /home/userx/proj/gwas2/bmi-c1c2-qc2.bim
Plink fam : /home/userx/proj/gwas2/bmi-c1c2-qc2.fam
Data file :
SNP count : 431670
Total individuals : 1678
Reference matrix object of class "fg.dm.plink"
Data type:
Description:
SNP Count: 431670
Individual Count: 1678
Individual Used: 1678
Plink Command: plink
chromosome: all
```

## Value

This function returns a S3 object with the class label of `fgwas.gen.obj`, including:

<code>reader</code>	a reference class <code>fg.dm.plink</code> , the reader object for plink data, the structure is demonstrated in the details.
<code>n.snp</code>	integer value, indicating the total SNP number.
<code>n.ind.total</code>	integer value, indicating the total individual number.
<code>n.ind.used</code>	integer value, indicating the used individual number except the missing data.
<code>params</code>	list, including the PLINK file names and 'plink' command assigned to this function calling.
<code>options</code>	list, two options: <code>force.split</code> and <code>verbose</code> , default values are TRUE.

You can print summary information by the function `print`.

## Examples

```
# use simulation to generate PLINK data files.
objx <- fg.simulate( "Logistic", "SAD1", 2000, 800, 1:6,
  phe.missing=0.05, snp.missing=0.05,
  sig.pos=301, plink.format=TRUE,
  file.prefix = "temp.fgwas" );

# load genotype data from PLINK data file and return a genotype object
obj.gen <- fg.load.plink("temp.fgwas.geno.bed", "temp.fgwas.geno.bim", "temp.fgwas.geno.fam" );

# show the brief information of genotype object
```

```
obj.gen;
```

---

fg.load.simple	<i>Loading simple SNP file</i>
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---

## Description

Loading the SNP data from a text file in simple format.

## Usage

```
fg.load.simple( file.simple.snp, options=list(verbose=F))
```

## Arguments

file.simple.snp	string, file name of SNP data table, the format is described in the details.
options	list, only including the item verbose.

## Details

This table file contains SNP information and individual SNPs. The SNP information, including SNP name, chromosome, position, reference allele and alternate allele are located from the 1st column to 5rd column. The individual SNPs follow the SNP information at each row, encoding genotype type as 0,1,2 or NA (for missing data). For example:

```
SNP  CHR POS RefAllele AltAllele Sub1 Sub2 Sub3 Sub4 Sub5 ...
SNP1 1 1  A T   2  0  1  1  1  ...
SNP2 1 2  A G   2  1  1  0  0  ...
...
```

## Value

A S3 object (fgwas.gen.obj) is returned by this function, including:

options	List,
reader	A reference class , indicating the reader object for simple data format.
params	List, including the file names and other optional parameters.
n.snp	Numeric, indicating the total SNP number.
n.ind.total	Numeric, indicating the total individual number.
n.ind.used	Nuermic, indicating the used individual number except the missing data.

## Examples

```
# make a simple SNP data table
snp <- matrix( round( runif(20000, 0, 2) ), nrow=100)
colnames(snp) <- paste("sub", 1:200, sep="");
snp.name <- paste("snp", 1:100, sep="");
# make a data frame including snp information and snp data table
snp.mat <- data.frame(snp.name, chr=1, pos=1:100, Allele1="A", Allele2="B", snp);
# write the data frame into a tab-seperated table file
write.table(snp.mat, file="temp.fgwas.snp.mat.csv",
            row.names=FALSE, col.names=TRUE, quote=FALSE, sep="\t");
# load the snp data from a simple snp data file.
obj.gen <- fg.load.simple("temp.fgwas.snp.mat.csv");

# simulate the phenotype and genotype data and generate a simple snp data file
objx <- fg.simulate( "Logistic", "SAD1", 2000, 800, 1:6, phe.missing=0.05, snp.missing=0.05,
                    sig.pos=301, plink.format=FALSE, file.prefix = "test1.fgwas" );
# load the snp data generated from the simulation
obj.gen <- fg.load.simple("test1.fgwas.geno.tab");
# call SNP scanning
r1 <- fg.snpscan(obj.gen, objx$obj.phe, snp.sub=c(290:310), options=list(ncores=1));

# simulate the phenotype and genotype data and generate PLINK data file
objx <- fg.simulate( "Logistic", "SAD1", 2000, 800, 1:6, phe.missing=0.05, snp.missing=0.05,
                    sig.pos=301, plink.format=TRUE, file.prefix = "test1.fgwas" );

# load PLINK data file using the function in the snpStats package
obj.plink <- read.plink( "test1.fgwas.geno.bed", "test1.fgwas.geno.bim", "test1.fgwas.geno.fam");
# convert the PLINK data object into SNP data table
x0 <- as.data.frame( obj.plink$map[,c(2,1,4,5,6)])
x1 <- matrix( as.numeric( t(obj.plink$genotypes ) ), nrow=800)
x1[which(x1==0)]<-NA
x1 <- x1 - 1;
x1 <- matrix( x1, nrow=800);
colnames(x1) <- paste("N", 1:2000, sep="_");
snp.mat <- data.frame(x0, x1) ;
# write snp data table into a tab-seperated table file.
write.table(snp.mat, file="temp.fgwas.snp.mat.csv",
            row.names=FALSE, col.names=TRUE, quote=FALSE, sep="\t");

# load the snp data converted from the PLINK files
obj.gen <- fg.load.simple("temp.fgwas.snp.mat.csv");
# call SNP scanning in a short range(290:310)
r2 <- fg.snpscan(obj.gen, objx$obj.phe, snp.sub=c(290:310), options=list(ncores=1));
```

---

fg.select.sigsnp

Selecting significant SNPs

---

## Description

Selecting significant SNPs



**Usage**

```
fg.select.sigsnp( fgwas.scan.obj, sig.level=0.05, pv.adjust="bonferroni", options=list() )
```

**Arguments**

fgwas.scan.obj	A S3 object of scanning result returned by <a href="#">fg.snpscan</a> .
sig.level	Numeric value indicating the p-value of criteria.
pv.adjust	string indicating whether p-value is adjusted value for multiple Comparisons, the optional values are holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none" defined in <a href="#">p.adjust</a> .
options	Not used

**Value**

The function returns a sub-matrix including the significant SNPs.

**Examples**

```
# simulate the phenotype object and genotype object.
r<-fg.simulate("Logistic", "AR1", 2000, 500, 1:7 );
# call SNP scanning using 'fast' method
obj.scan <- fg.snpscan(r$obj.gen, r$obj.phe, covariance.type="AR1", method="fast");
# select the significant SNPs from the result object
tb<-fg.select.sigsnp(obj.scan, sig.level=1e-10, "fdr")

# show 5 lines of significant SNP table
head(tb);
# show SNP indexes in significant SNP table
show(tb$INDEX);
# show SNP names in significant SNP table
show(tb$NAME);
```

fg.simulate

*Data Simulation***Description**

Data simulation is for demonstration or power test in the fGWAS package.

**Usage**

```
fg.simulate(curve.type, covariance.type, n.obs, n.snp, time.points,
  par0 = NULL,
  par1 = NULL,
  par2 = NULL,
  par.covar = NULL,
  par.X = NULL,
  sig.pos = NULL,
  phe.missing = 0.03,
  snp.missing = 0.03,
  plink.format = FALSE,
  file.prefix = NULL )
```

## Arguments

curve.type	String, indicating the curve type, such as "Logistic", "Legendre2", available options are described in the details of <a href="#">fg.load.phenotype</a> .
covariance.type	String, indicating the covariance structure type, such as "SAD1", "AR1", available options are described in the details of <a href="#">fg.load.phenotype</a> .
n.obs	Numeric, indicating the individual number.
n.snp	Numeric, indicating the SNP number.
time.points	Numeric, indicating the measure time points for the longitudinal traits.
par0	Numeric vector, indicating the curve parameters for the genotype AA.
par1	Numeric vector, indicating the curve parameters for the genotype Aa.
par2	Numeric vector, indicating the curve parameters for the genotype aa.
par.covar	Numeric vector, indicating the parameters of the covariance matrix.
par.X	Numeric vector, indicating the covariate coefficients.
sig.pos	Numeric, indicating the significant SNP position.
phe.missing	Numeric, the missing rate of phenotype data.
snp.missing	Numeric, the missing rate of genotype data.
plink.format	Logical variable, indicating whether the PLINK data files are generated.
file.prefix	String, the prefix file name for the simulation data.

## Details

The object structures of two S3 object, phenotype data object([fg.load.phenotype](#)) and genotype object([fg.load.plink](#))

The mathematics model can be illustrated as the following formulas:

$$Y = X \%*\% \text{par.X} + \text{curve\_function}(\text{par0}, T) + e \text{ if snp is AA } \backslash \text{cr}$$

$$Y = X \%*\% \text{par.X} + \text{curve\_function}(\text{par1}, T) + e \text{ if snp is Aa } \backslash \text{cr}$$

$$Y = X \%*\% \text{par.X} + \text{curve\_function}(\text{par2}, T) + e \text{ if snp is aa } \backslash \text{cr}$$

In above formulas, X and snp are generated randomly, curve\_function is selected by the curve.type, the residuals e follow the multivariate normal distribution  $N(0, \text{covar})$ , covariance matrix is built by the parameter covariance.type and par.covar.

## Value

The function return a list containing two objects, including

obj.gen	genotype data object, S3 object with class name 'fgas.gen.obj', the format is identical with return of <a href="#">fg.load.simple</a> .
obj.phe	phenotype data object, S3 object with class name 'fgas.phe.obj', the format is identical with return of <a href="#">fg.load.phenotype</a> .

If plink.format is set to TRUE, the plink data set generated by the simulation process will be stored in the file specified by obj.gen\$files.

## Examples

```
# simulate the Logistic traits and genotype data.
obj1 <- fg.simulate( "Logistic", "AR1", 2000, 1000, 1:8,
  phe.missing=0.05, snp.missing=0.05,
  sig.pos=501, plink.format=FALSE, file.prefix = NULL );

# show the genotype object
print(obj1$obj.gen);
# show the phenotype object
print(obj1$obj.phe);
# plot the phenotype object
plot(obj1$obj.phe, curve.fitting=FALSE);

# simulate the Logistic traits and genotype data and save the data into PLINK files
obj2 <- fg.simulate( "Logistic", "SAD1", 2000, 800, 1:6,
  phe.missing=0.05, snp.missing=0.05, sig.pos=301,
  plink.format=TRUE, file.prefix = "temp.fgwas" );

# show the genotype object
print(obj2$obj.gen);
# show the phenotype object
print(obj2$obj.phe);
# plot the phenotype object
plot(obj2$obj.phe, curve.fitting=FALSE);

# remove the phenotype files and PLINK files
unlink(c("temp.fgwas.geno.bed", "temp.fgwas.geno.bed", "temp.fgwas.geno.bed",
  "temp.fgwas.pheT.csv", "temp.fgwas.pheY.csv"));
```

---

fg.snpscan

---

*Detecting significant SNPs by fGWAS model*


---

## Description

Scanning SNPs with the fGWAS model and detect the significant SNPs.

## Usage

```
fg.snpscan( fgwas.gen.obj, fgwas.phe.obj,
  method = "optim-fgwas",
  curve.type = NULL,
  covariance.type = NULL,
  snp.sub = NULL,
  options = list(verbose=F) )
```

## Arguments

fgwas.gen.obj    S3 object fgwas.gen.obj, indicating the genotype object generated by the [fg.load.plink](#), [fg.load.simple](#) or [fg.simulate](#).

fgwas.phe.obj	S3 object fgwas.phe.obj, indicating the phenotype object generated by the <a href="#">fg.load.phenotype</a> or <a href="#">fg.simulate</a> .
method	string, indicating the statistical model used in the scanning process, available options are "gls", "mixed", "fast", "fgwas", "optim-fgwas". Default is 'optim-fgwas'.
curve.type	string, indicating the curve type used in the scanning process for the method "fast", "fgwas" and "optim-fast", instead of the original curve type in phenotype object. The full optional values are listed in <a href="#">fg.load.phenotype</a>
covariance.type	string, indicating the type of covariance structure used in the scanning process for the method "fast", "fgwas" and "optim-fast", instead of the curve type in phenotype object. The full optional values are listed in <a href="#">fg.load.phenotype</a>
snp.sub	vector of SNP index or SNP name, indicating the selected SNPs will be scanned, not the whole data set.
options	list, including verbose, ncores, max.optim.failure, min.optim.success, use.gradient, degree, default values are verbose=F, ncores=1, max.optim.failure=20 min.optim.success=2 use.gradient=FALSE degree=3.

## Details

The parallel computing is available in Lunix or Linux compatible OS using the optional ncores item. **fgWAS** uses the **snowfall** for the method "gls" and **parallel** for the method "fast", "fgwas", and "optim-fgwas".

Due to the difficulty to estimate and provide initial parameters for the function optim, **fgWAS** sets the maximum optim failure time and minimum optim success time in the optional items.

For the method "fgwas" and "optim-fgwas", **fgWAS** performs the MLE using the numerical derivation by default use.gradient=FALSE, If use.gradient=TRUE, the gradient function is provided and used in the MLE.

For the method mixed, the default polynomial degree is 3, it can be customized with the optional item degree.

## Value

A S3 object with the class name (fgwas.scan.obj) is returned by this function, including:

obj.gen	S3 object fgwas.gen.obj processed in this function
obj.phe	S3 object fgwas.phe.obj processed in this function
ret.gls	Matrix, results for each SNP scanned by the 'gls' method.
ret.mixed	Matrix, results for each SNP scanned by the 'mixed' method.
ret.fast	Matrix, results for each SNP scanned by the 'fast' method.
ret.fgwas	Matrix, results for each SNP scanned by the 'fgwas' or 'fgwas-optim' method.

If 'gls' is used to scan the SNPs, the result is stored in ret.gls with the following items:

INDEX	SNP index.
-------	------------

NAME	SNP name.
CHR	Chromosome.
POS	Base position.
NMISS	Number of missing.
MAF	Minor allele frequency.
LR	Likelihood ratio.
pv	p-value of Fisher.

If 'mixed' is used to scan the SNPs, the result is stored in `ret.mixed` with the following items:

INDEX	SNP index.
NAME	SNP name.
CHR	Chromosome.
POS	Base position.
Allel1	Allel 1.
Allel2	Allel 2.
MAF	Minor allele frequency.
NMISS	Number of missing.
pv	p-value of Fisher .
p.min	p-value of minimum values.
p.join	p-value of joint value.
p0	p-value of 0th-degree Legendre polynomial.
p1	p-value of 1st-degree Legendre polynomial.
p2	p-value of 2nd-degree Legendre polynomial.
p3	p-value of 3rd-degree Legendre polynomial.
p4	p-value of 4th-degree Legendre polynomial.

If 'fgwas', 'fgwas-optim' or 'fast' are used to scan the SNPs, the result is stored in `ret.fast` or `ret.fgwas` with the following items:

INDEX	SNP index.
NAME	SNP name.
CHR	Chromosome.
POS	Base position.
MAF	Minor allele frequency.
NMISS	Number of missing.
SNP0	Individual count of genotype 0.
SNP1	Individual count of genotype 1.
SNP2	Individual count of genotype 2.
GEN0	Genotype count.
LR	Likelihood Ratio.

pv	p-value based on LR.
h0.X0	the 1st covariate coefficient under NULL hypothesis.
...	the other covariate coefficients under NULL hypothesis.
h0.a	the parameter 'a' in curve function( e.g. Logistic curve) under NULL hypothesis.
h0.b	the parameter 'b' in curve function( e.g. Logistic curve) under NULL hypothesis.
...	the other curve parameters in the curve function under NULL hypothesis.
h0X.rho	the parameter 'rho' in covariance structure ( e.g. AR1 ) under NULL hypothesis.
...	the other parameters in covariance structure ( e.g. AR1 ) under NULL hypothesis.
h1.X0	the 1st covariate coefficient under alternative hypothesis.
...	the other covariate coefficients under alternative hypothesis.
h1.G0.a	the parameter 'a' for genotype 0 in curve function (e.g. Logistic curve) under alternative hypothesis.
h1.G0.b	the parameter 'b' for genotype 0 in curve function (e.g. Logistic curve) under alternative hypothesis.
...	the other parameters for genotype 0 in curve function (e.g. logistic curve) under alternative hypothesis.
h1.G1.a	the parameter 'a' for genotype 1 in curve function (e.g. Logistic curve) under alternative hypothesis.
h1.G1.b	the parameter 'b' for genotype 1 in curve function (e.g. Logistic curve) under alternative hypothesis.
...	the other parameters for genotype 1 in curve function (e.g. logistic curve) under alternative hypothesis.
h1.G2.a	the parameter 'a' for genotype 2 in curve function (e.g. Logistic curve) under alternative hypothesis.
h1.G2.b	the parameter 'b' for genotype 2 in curve function (e.g. Logistic curve) under alternative hypothesis.
...	the other parameters for genotype 2 in curve function (e.g. logistic curve) under alternative hypothesis.
h1X.rho	the parameter 'rho' in covariance structure ( e.g. AR1 ) under alternative hypothesis.
...	the other parameters in covariance structure ( e.g. AR1 ) under alternative hypothesis.
h0.R2	R2 under NULL hypothesis.
h1.R2	R2 under alternative hypothesis.

**See Also**

[fg.load.phenotype](#), [fg.load.plink](#), [fg.load.simple](#), [fg.select.sigsnp](#)

## Examples

```
# simulate the phenotype object and genotype object
r<-fg.simulate("Logistic", "AR1", 2000, 500, 1:7, sig.pos=250 );
# SNP scanning in a short range (245:255) using 'fast' method
obj1.scan <- fg.snpscan(r$obj.gen, r$obj.phe, method="fast", snp.sub=c(245:255) );
# show the summary information of result object
obj1.scan;

# SNP scanning in a short range (245:255) using 'fgwas' method
obj2.scan <- fg.snpscan(r$obj.gen, r$obj.phe, method="fgwas", snp.sub=c(245:255) );
obj2.scan;

# check the full result table.
tb.full <- obj2.scan$obj.fgwas$results;

# plot Manhattan figure
plot(obj2.scan, file.pdf="temp.fgwas.obj2.scan.pdf");

# select significant SNPs
tb.sig <- fg.select.sigsnp(obj2.scan, sig.level=0.001, pv.adjust = "bonferroni")
# plot the genetic curve effect for the significant SNPs
plot.fgwas.curve( obj2.scan, tb.sig$INDEX, file.pdf="temp.fgwas.obj2.curve.pdf");
```

---

plot.fgwas.curve

*Plotting the genetic curve effects associated with SNP.*


---

## Description

Plot the genetic curve effects based on the parameter estimation in the fGWAS model for each genotype.

## Usage

```
plot.fgwas.curve( object, snp.sub, file.pdf)
```

## Arguments

object	Result object returned by the <a href="#">fg.snpscan</a> .
snp.sub	Vector of SNP index or SNP name.
file.pdf	String indicating the PDF file name.

## Details

This function will apply to the result obtained from 'fgwas', 'fgwas-optin' or 'fast' method.

## Value

No return values.

## Examples

```
# simulate phenotype object and genotype object
r <- fg.simulate("Logistic", "AR1", 2000, 500, 1:7, sig.pos=250 );
# SNP scanning
obj.scan <- fg.snpscan(r$obj.gen, r$obj.phe, method="fast", snp.sub=c(245:255) );
# select significant SNPs by default.
tb.sig <- fg.select.sigsnp(obj.scan)
# plot the genteic curves for each significant SNP.
plot.fgwas.curve( obj.scan, tb.sig$INDEX, file.pdf="test.plot.pdf");
# remove the PDF file
unlink("test.plot.pdf")
```

---

plot.fgwas.phe.obj	<i>Ploting the longitudinal curves</i>
--------------------	--

---

## Description

Ploting the longitudinal curves.

## Usage

```
## S3 method for class 'fgwas.phe.obj'
plot(x, y, ..., curve.fitting = T, file.pdf = NULL)
```

## Arguments

x	a phenotype object return by <a href="#">fg.load.phenotype</a> or <a href="#">fg.simulate</a>
y	required parameter in the generic plot function, not used.
...	additional arguments affecting the summary produced.
curve.fitting	boolean value indicating whether the fitted curve is plot.
file.pdf	string indicating the output pdf file name.

## Details

The phenotype object is described in [fg.load.phenotype](#).

## Value

No return values, only figure is exported to PDF file.

## Examples

```
# data simulation
r<-fg.simulate( "Logistic", "SAD1", 2000, 1000, c(2,4,6,8,10) );
# plot phenotype traits
plot(r$obj.phe, file.pdf="temp.fg.test.pdf");
# remove the PDF file
unlink("temp.fg.test.pdf");
```



---

plot.fgwas.scan.obj     *Drawing Manhattan plot*


---

**Description**

Drawing p-values in Manhattan plot.

**Usage**

```
## S3 method for class 'fgwas.scan.obj'
plot(x, y, ..., file.pdf = NULL)
```

**Arguments**

x	a result object return by <a href="#">fg.snpscan</a>
y	required parameter in the generic plot function, but unused in this function.
...	additional arguments affecting the summary produced.
file.pdf	string indicating output PDF file name.

**Details**

N/A

**Value**

No return values, only figure is exported into PDF file.

**Examples**

```
# data simulation
r<-fg.simulate("Logistic", "AR1", 2000, 500, 1:7 );
# SNP scanning using 'fast' method
obj.scan <- fg.snpscan(r$obj.gen, r$obj.phe, method="fast");
# plot the Manhattan figure
plot(obj.scan, file.pdf="temp.fgwas.plot.pdf");
# remove the PDF file
unlink("temp.fgwas.plot.pdf");
```

---

print.fgwas.gen.obj     *Printing brief information for the genotype object*


---

**Description**

Printing brief information for the genotype object.

**Usage**

```
## S3 method for class 'fgwas.gen.obj'
print( x, ..., useS4 = FALSE )
```

## Arguments

x	a genotype object returned by <code>fg.load.plink</code> or <code>fg.load.simple</code>
...	additional arguments affecting the summary produced.
useS4	an argument used to match showDefault function. Fixed as FALSE.

## Details

The genotype object is described in `fg.load.plink` or `fg.load.simple`.

The following example demonstrates the output of `print` command for a genotype object.

```
== Genotype Object in fGWAS ==
Plink bed : /demo.bed
Plink bim : /demo.bim
Plink fam : /demo.fam
Data file :
SNP count : 431670
Total individuals : 1678
Reference matrix object of class "fg.dm.plink"
Data type:
Description:
Chromosome: all
SNP Count: 431670
Individual Count: 1678
Individual Used: 1678
Plink Command: plink
```

## Value

No return values, only output the brief information on the R console.

## Examples

```
# data simulation
r<-fg.simulate("Logistic", "AR1", 2000, 500, 1:7 );
# call this function to print the genotype information
r$obj.gen;
# summarize the genotype object
summary(r$obj.gen);
```

---

```
print.fgwas.phe.obj    Printing brief information for the phenotype object
```

---

## Description

Printing brief information for the phenotype object.

## Usage

```
## S3 method for class 'fgwas.phe.obj'
print( x, ..., useS4=FALSE )
```

## Arguments

x	a phenotype data object returned by <a href="#">fg.load.phenotype</a> or obj.phe in the <a href="#">fg.simulate</a>
...	additional arguments affecting the summary produced.
useS4	an argument used to match showDefault function. Fixed as FALSE.

## Details

The phenotype object is described in [fg.load.phenotype](#).

The following example demonstrates the output of print command for a phenotype object.

```
== Phenotype Object in fGWAS ==
Longitudal value : /tmp/Rtmp0lhMx2/file58b1776d8395.csv
-- Individual count : 1678
Longitudal time : /tmp/Rtmp0lhMx2/file58b1131b9b1.csv
-- Time count : 8
Covariate file : /tmp/Rtmp0lhMx2/file58b1246a670b.csv
-- Covariate count : 6
-- Intercept : YES
-- Estimate values : 36917.16 -1.553526 -2.702489 7.852712 -5.91549 7.210022 3.805883
Curve type : auto
-- Estimate type : Legendre2
-- Estimate values : -36888.65 1.081318 -1.852532
Covariate type : auto
-- Estimated type : TOEPH
-- Estimate values : 0.9082402 0.8627414 0.8142826 0.7713539 0.7200614 0.6669603 ...
```

## Value

No return values, only output the brief information on the R console.

## Examples

```
# data simulation
r<-fg.simulate("Logistic", "AR1", 2000, 500, 1:7 );
# print brief phenotype information
r$obj.phe;
```

---

```
print.fgwas.scan.obj
```

*Printing the significant SNPs or top SNPs.*

---

## Description

Printing the significant SNPs or top SNPs.

## Usage

```
## S3 method for class 'fgwas.scan.obj'
print( x, ..., useS4 = FALSE )
```

## Arguments

x	a result object return by <a href="#">fg.snpscan</a>
...	additional arguments affecting the summary produced.
useS4	an argument used to match showDefault function. Fixed as FALSE.

## Details

The result object is described in [fg.snpscan](#).

The following example demonstrates the output of print command for a result object.

```
== Result from 'fGWAS' method ==
SNP = 431670
      INDEX      NAME CHR      POS      MAF NMISS      pv
rs11081728 386746 rs11081728 18 29511663 0.169253731      3 5.413541e-15
rs11051162 301826 rs11051162 12 31074982 0.034090909      6 3.997973e-14
rs7876945 423711 rs7876945 23 13134844 0.292572464     22 5.341771e-14
rs12652390 146007 rs12652390  5 126322102 0.014379868      9 2.143879e-13
rs6029168 407076 rs6029168 20 39158207 0.324880668      2 2.182798e-13
rs7876326 424440 rs7876326 23 23626268 0.470481928     18 3.074301e-13
...
```

## Value

No return values, only output the significant SNPs or top SNPs on the R console.

## Examples

```
# data simulation
r <- fg.simulate("Logistic", "AR1", 2000, 500, 1:7 );
# SNP scanning
obj.scan <- fg.snpscan(r$obj.gen, r$obj.phe, method="fast");
# print the top or significant SNPs.
obj.scan;
```

---

summary.fgwas.gen.obj *Summarizing genotype object*


---

**Description**

Printing the summary information of the genotype object.

**Usage**

```
## S3 method for class 'fgwas.gen.obj'
summary( object, ... )
```

**Arguments**

object	a data object returned by <a href="#">fg.load.plink</a> or <a href="#">fg.load.simple</a>
...	additional arguments affecting the summary produced.

**Details**

The genotype object is described in [fg.load.plink](#) or [fg.load.simple](#).

**Value**

A numeric vector including snp count, individual count and used individual count.

**Examples**

```
# data simulation
r<-fg.simulate("Logistic", "AR1", 2000, 500, 1:7 );
# print the brief information of gthe genotype object
r$obj.gen;
# output the sumamry information
summary(r$obj.gen);
```

---

summary.fgwas.phe.obj *Summarizing phenotype object.*


---

**Description**

Summarizing phenotype object.

**Usage**

```
## S3 method for class 'fgwas.phe.obj'
summary( object, ... )
```

**Arguments**

object            a phenotype object returned by `fg.load.phenotype` or `obj.phe` in the `fg.simulate`  
 ...              additional arguments affecting the summary produced.

**Details**

None

**Value**

This function returns an extend table containing the covariate data , the longitudinal curve data and the measured times.

**Examples**

```
# data simulation
r<-fg.simulate("Logistic", "AR1", 2000, 500, 1:7 );

# print the brief information of the phenotype object
r$obj.phe;

# output the summary information
ext_phe <- summary(r$obj.phe);

# show the summary table
head(ext_phe);
```

---

summary.fgwas.scan.obj

*Summarizing the result object*


---

**Description**

Summarizing the result object.

**Usage**

```
## S3 method for class 'fgwas.scan.obj'
summary( object, ... )
```

**Arguments**

object            a result object return by `fg.snpscan`  
 ...              additional arguments affecting the summary produced.

## Details

Below lists all columns for the analysis with curve 'Legendre2' and covariance 'AR1':

```
#obj.fgwas is result object of 'fgwas' method.
> colnames(summary(obj.fgwas))
[1] "INDEX"      "NAME"      "CHR"      "POS"      "MAF"
[6] "NMISS"      "SNP0"      "SNP1"      "SNP2"      "GEN0"
[11] "LR"         "pv"        "L0"        "h0.X0"     "h0.X1"
[16] "h0.X2"      "h0.X3"     "h0.X4"     "h0.X5"     "h0.X6"
[21] "h0.u0"      "h0.u1"     "h0.u2"     "h0X.rho"   "h0X.sigma2"
[26] "L1"         "h1.X0"     "h1.X1"     "h1.X2"     "h1.X3"
[31] "h1.X4"      "h1.X5"     "h1.X6"     "h1.G0.u0"  "h1.G0.u1"
[36] "h1.G0.u2"   "h1.G1.u0"  "h1.G1.u1"  "h1.G1.u2"  "h1.G2.u0"
[41] "h1.G2.u1"   "h1.G2.u2"  "h1X.rho"   "h1X.sigma2" "h0.R2"
[46] "h1.R2"
```

## Value

This function returns a data frame including the results of scanned SNPs and excluding covariate and curve object.

## Examples

```
# data simulation
r<-fg.simulate("Logistic", "AR1", 2000, 500, 1:7, sig.pos=190 );

# SNP scanning
obj.scan <- fg.snpscan(r$obj.gen, r$obj.phe, covariance.type="AR1", method="fast");

# summarize the result object
tb <- summary(obj.scan);

# show the summary table
head(tb);
```

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