

# Package ‘gwid’

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**Type** Package

**Title** Genome-Wide Identity-by-Descent

**Version** 0.2.0

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**Description** Methods and tools for the analysis of Genome Wide Identity-by-Descent ('gwid') mapping data, focusing on testing whether there is a higher occurrence of Identity-By-Descent (IBD) segments around potential causal variants in cases compared to controls, which is crucial for identifying rare variants. To enhance its analytical power, 'gwid' incorporates a Sliding Window Approach, allowing for the detection and analysis of signals from multiple Single Nucleotide Polymorphisms (SNPs).

**License** MIT + file LICENSE

**Encoding** UTF-8

**Imports** data.table, gdsfmt, SNPRelate, Matrix, ggplot2, plotly, utils, stats, RcppRoll, methods, piggyback, shiny, lattice, grid

**RoxygenNote** 7.3.1

**Suggests** knitr, magrittr, rmarkdown, testthat (>= 3.0.0)

**Config/testthat/edition** 3

**URL** <https://github.com/soroushmdg/gwid>,  
<https://soroushmdg.github.io/gwid/>

**BugReports** <https://github.com/soroushmdg/gwid/issues>

**VignetteBuilder** knitr

**NeedsCompilation** no

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**Repository** CRAN

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build_gwas	<i>Open a SNP GDS file and extract information.</i>
------------	---

---

**Description**

Open a SNP GDS file and extract information.

**Usage**

```
build_gwas(gds_data = "name.gds", caco = "name.Rda", gwas_generator = TRUE)
```

**Arguments**

gds_data	File name
caco	An object of class caco. Output of case_control function.
gwas_generator	logical; if TRUE an object of class result_snps will be saved inside output list.

**Value**

a list of seven objects; including smp.id, snp.id, snp.pos, smp.indx, smp.snp (a matrix with samples in rows and snp in columns), caco, snps(column sum of smp.snp for each case control)

---

build_gwid	<i>Open a ibd file and extract information.</i>
------------	---

---

**Description**

Open a ibd file and extract information.

**Usage**

```
build_gwid(
  ibd_data = "name.ibd",
  gwas = "object of class gwas",
  gwid_generator = TRUE
)
```

**Arguments**

ibd_data	a file name for output of <b>Refined IBD</b>
gwas	object of class gwas
gwid_generator	logical; if TRUE an object of class result_snps will be saved inside output list.

**Value**

the output will be a object(list) of class gwid contains profile object, IBD object and result\_snps object.

---

build_phase	<i>Read .vcf structured text format files and reduce the size of file.</i>
-------------	--

---

**Description**

Read .vcf structured text format files and reduce the size of file.

**Usage**

```
build_phase(phased_vcf = "name.vcf", caco)
```

**Arguments**

phased_vcf	A file name for a variant call format (vcf) file.
caco	An object of class caco. Output of case_control function.

**Value**

the output will be a a list of class phase contains two sparse matrix for each haplotype.

---

case_control	<i>Reload saved case-control list file</i>
--------------	--

---

**Description**

Reload saved case-control list file

**Usage**

```
case_control(case_control_rda, ...)
```

**Arguments**

case_control_rda	A character string giving the name of the case-control file to load. The file is a list of character vectors including subject names in each case-control groups or csv file including subject name for a disease.
...	name of a column (disease name) of csv file.

**Value**

The output will be a list of character vectors include subject names and groups. The class of returned object is caco.

---

extract	<i>Extract information from SNP GDS file.</i>
---------	---

---

**Description**

Extract information from SNP GDS file.

**Usage**

```
extract(obj, ...)
```

**Arguments**

obj	an object of class gwas
...	other arguments

**Value**

extract object instants

---

extract.gwas	<i>Extract information from SNP GDS file.</i>
--------------	---

---

**Description**

Extract information from SNP GDS file.

**Usage**

```
## S3 method for class 'gwas'
extract(obj, type = c("snps", "snp2", "nas"), snp_start, snp_end, ...)
```

**Arguments**

obj	object of class gwas.
type	indicate type of aggregation on sample-snp data and must be one of snps, snp2, or nas
snp_start	select starting position of snp, which we want to aggregate.
snp_end	select ending position of snp, which we want to aggregate.
...	other arguments

**Value**

the output will be a result\_snps (data.table) object including 3 columns including, snp\_pos, case\_control, and value

## Examples

```

piggyback::pb_download(repo = "soroushmdg/gwid", tag = "v0.0.1", dest = tempdir())
ibd_data_file <- paste0(tempdir(), "//chr3.ibd")
genome_data_file <- paste0(tempdir(), "//chr3.gds")
phase_data_file <- paste0(tempdir(), "//chr3.vcf")
case_control_data_file <- paste0(tempdir(), "//case-cont-RA.withmap.Rda")
# case-control data
case_control <- gwid::case_control(case_control_rda = case_control_data_file)
names(case_control) #cases and controls group
summary(case_control) # in here, we only consider cases,cont1,cont2,cont3 groups in the study
case_control$cases[1:3] # first three subject names of cases group
# read SNP data (use SNPRelate to convert it to gds) and count number of minor alleles
snp_data_gds <- gwid::build_gwas(gds_data = genome_data_file,
caco = case_control, gwas_generator = TRUE)
class(snp_data_gds)
names(snp_data_gds)
head(snp_data_gds$snp) # it has information about counts of minor alleles in each location.
# read haplotype data (output of beagle)
haplotype_data <- gwid::build_phase(phased_vcf = phase_data_file, caco = case_control)
class(haplotype_data)
names(haplotype_data)
dim(haplotype_data$Hap.1) #22302 SNP and 1911 subjects
# read IBD data (output of Refined-IBD)
ibd_data <- gwid::build_gwid(ibd_data = ibd_data_file, gwas = snp_data_gds)
class(ibd_data)
ibd_data$ibd # refined IBD output
ibd_data$res # count number of IBD for each SNP location
# plot count of IBD in chromosome 3
plot(ibd_data, y = c("cases", "cont1"), ly = FALSE)
# Further investigate location between 117M and 122M
# significant number of IBD's in group cases, compare to cont1, cont2 and cont3.
plot(ibd_data, y = c("cases", "cont1"), snp_start = 119026294, snp_end = 120613594, ly = FALSE)
model_fisher <- gwid::fisher_test(ibd_data, case_control, reference = "cases",
snp_start = 119026294, snp_end = 120613594)
class(model_fisher)
plot(model_fisher, y = c("cases", "cont1"), ly = FALSE)
hap_str <- gwid::haplotype_structure(ibd_data, phase = haplotype_data, w = 10,
snp_start = 119026294, snp_end = 120613594)
haplo_freq <- gwid::haplotype_frequency(hap_str)
plot(haplo_freq, y = c("cases", "cont1"), plot_type = "haplotype_structure_frequency",
nwin = 1, type = "version1", ly = FALSE)

```

---

extract.gwid

*Extract information from ibd data.*

---

## Description

Extract information from ibd data.

**Usage**

```
## S3 method for class 'gwid'
extract(obj = "object of class gwid", snp_start, snp_end, ...)
```

**Arguments**

```
obj          object of class gwid(output of function build_gwid)
snp_start    select starting position of snp, which we want to aggregate.
snp_end      select ending position of snp, which we want to aggregate.
...          other objects
```

**Value**

the output will be a result\_snps (data.table) object including 3 columns including, "snp\_pos", "case\_control", and "value"

**Examples**

```
piggyback::pb_download(repo = "soroushmdg/gwid", tag = "v0.0.1", dest = tempdir())
ibd_data_file <- paste0(tempdir(), "//chr3.ibd")
genome_data_file <- paste0(tempdir(), "//chr3.gds")
phase_data_file <- paste0(tempdir(), "//chr3.vcf")
case_control_data_file <- paste0(tempdir(), "//case-cont-RA.withmap.Rda")
# case-control data
case_control <- gwid::case_control(case_control_rda = case_control_data_file)
names(case_control) #cases and controls group
summary(case_control) # in here, we only consider cases, cont1, cont2, cont3 groups in the study
case_control$cases[1:3] # first three subject names of cases group
# read SNP data (use SNPRelate to convert it to gds) and count number of minor alleles
snp_data_gds <- gwid::build_gwas(gds_data = genome_data_file,
caco = case_control, gwas_generator = TRUE)
class(snp_data_gds)
names(snp_data_gds)
head(snp_data_gds$snps) # it has information about counts of minor alleles in each location.
# read haplotype data (output of beagle)
haplotype_data <- gwid::build_phase(phased_vcf = phase_data_file, caco = case_control)
class(haplotype_data)
names(haplotype_data)
dim(haplotype_data$Hap.1) #22302 SNP and 1911 subjects
# read IBD data (output of Refined-IBD)
ibd_data <- gwid::build_gwid(ibd_data = ibd_data_file, gwas = snp_data_gds)
class(ibd_data)
ibd_data$ibd # refined IBD output
ibd_data$res # count number of IBD for each SNP location
# plot count of IBD in chromosome 3
plot(ibd_data, y = c("cases", "cont1"), ly = FALSE)
# Further investigate location between 117M and 122M
# significant number of IBD's in group cases, compare to cont1, cont2 and cont3.
plot(ibd_data, y = c("cases", "cont1"), snp_start = 119026294, snp_end = 120613594, ly = FALSE)
model_fisher <- gwid::fisher_test(ibd_data, case_control, reference = "cases",
```

```

snp_start = 119026294,snp_end = 120613594)
class(model_fisher)
plot(model_fisher, y = c("cases", "cont1"),ly = FALSE)
hap_str <- gwid::haplotype_structure(ibd_data,phase = haplotype_data,w = 10,
snp_start = 119026294,snp_end = 120613594)
haplo_freq <- gwid::haplotype_frequency(hap_str)
plot(haplo_freq,y = c("cases", "cont1"),plot_type = "haplotype_structure_frequency",
nwin = 1, type = "version1",ly = FALSE)

```

---

extract_window	<i>extract component of an object</i>
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---

### Description

extract component of an object

### Usage

```
extract_window(obj, ...)
```

### Arguments

obj	obj
...	other variables

### Value

the output will be a result\_snps (data.table) object including 3 columns including, "snp\_pos", "case\_control", and "value"

---

extract_window.gwid	<i>Extract information from ibd data in a moving window</i>
---------------------	---

---

### Description

Extract information from ibd data in a moving window

### Usage

```

## S3 method for class 'gwid'
extract_window(obj, w = 10, snp_start, snp_end, ...)

```



**Arguments**

obj	object of class gwid(output of function build_gwid)
w	window size
snp_start	select starting position of snp, which we want to aggregate.
snp_end	select ending position of snp, which we want to aggregate.
...	other variables

**Value**

the output will be a result\_snps (data.table) object including 3 columns including, "snp\_pos", "case\_control", and "value"

**Examples**

```

piggyback::pb_download(repo = "soroushmdg/gwid", tag = "v0.0.1", dest = tempdir())
ibd_data_file <- paste0(tempdir(), "//chr3.ibd")
genome_data_file <- paste0(tempdir(), "//chr3.gds")
phase_data_file <- paste0(tempdir(), "//chr3.vcf")
case_control_data_file <- paste0(tempdir(), "//case-cont-RA.withmap.Rda")
# case-control data
case_control <- gwid::case_control(case_control_rda = case_control_data_file)
names(case_control) #cases and controls group
summary(case_control) # in here, we only consider cases, cont1, cont2, cont3 groups in the study
case_control$cases[1:3] # first three subject names of cases group
# read SNP data (use SNPRelate to convert it to gds) and count number of minor alleles
snp_data_gds <- gwid::build_gwas(gds_data = genome_data_file,
caco = case_control, gwas_generator = TRUE)
class(snp_data_gds)
names(snp_data_gds)
head(snp_data_gds$snps) # it has information about counts of minor alleles in each location.
# read haplotype data (output of beagle)
haplotype_data <- gwid::build_phase(phased_vcf = phase_data_file, caco = case_control)
class(haplotype_data)
names(haplotype_data)
dim(haplotype_data$Hap.1) #22302 SNP and 1911 subjects
# read IBD data (output of Refined-IBD)
ibd_data <- gwid::build_gwid(ibd_data = ibd_data_file, gwas = snp_data_gds)
class(ibd_data)
ibd_data$ibd # refined IBD output
ibd_data$res # count number of IBD for each SNP location
# plot count of IBD in chromosome 3
plot(ibd_data, y = c("cases", "cont1"), ly = FALSE)
# Further investigate location between 117M and 122M
# significant number of IBD's in group cases, compare to cont1, cont2 and cont3.
plot(ibd_data, y = c("cases", "cont1"), snp_start = 119026294, snp_end = 120613594, ly = FALSE)
model_fisher <- gwid::fisher_test(ibd_data, case_control, reference = "cases",
snp_start = 119026294, snp_end = 120613594)
class(model_fisher)
plot(model_fisher, y = c("cases", "cont1"), ly = FALSE)
hap_str <- gwid::haplotype_structure(ibd_data, phase = haplotype_data, w = 10,

```

```
snp_start = 119026294,snp_end = 120613594)
haplo_freq <- gwid::haplotype_frequency(hap_str)
plot(haplo_freq,y = c("cases", "cont1"),plot_type = "haplotype_structure_frequency",
nwin = 1, type = "version1",ly = FALSE)
```

---

fisher_test	<i>Fisher test</i>
-------------	--------------------

---

### Description

Fisher test

### Usage

```
fisher_test(obj, ...)
```

### Arguments

obj	an object
...	other variables

### Value

the output will be a test\_snps (data.table) object including 3 columns: "snp\_pos", "case\_control", and "value" which is a p-values.

---

fisher_test.gwas	<i>Fisher's Exact Test for gwas count data</i>
------------------	--

---

### Description

Fisher's Exact Test for gwas count data

### Usage

```
## S3 method for class 'gwas'
fisher_test(
  obj,
  reference,
  snp_start,
  snp_end,
  alternative = c("two.sided", "greater", "less"),
  ...
)
```

**Arguments**

obj	object of class gwas
reference	reference group of subjects in which we want to perform fisher test test
snp_start	select starting position of snps.
snp_end	select ending position of snp.
alternative	indicates the alternative hypothesis and must be one of "two.sided", "greater" or "less". You can specify just the initial letter. Only used in the 2 by 2 case
...	optional arguments to fisher.test

**Value**

the output will be a test\_snps (data.table) object including 3 columns: "snp\_pos", "case\_control", and "value" which is a p-values.

**Examples**

```

piggyback::pb_download(repo = "soroushmdg/gwid", tag = "v0.0.1", dest = tempdir())
ibd_data_file <- paste0(tempdir(), "//chr3.ibd")
genome_data_file <- paste0(tempdir(), "//chr3.gds")
phase_data_file <- paste0(tempdir(), "//chr3.vcf")
case_control_data_file <- paste0(tempdir(), "//case-cont-RA.withmap.Rda")
# case-control data
case_control <- gwid::case_control(case_control_rda = case_control_data_file)
names(case_control) #cases and controls group
summary(case_control) # in here, we only consider cases,cont1,cont2,cont3 groups in the study
case_control$cases[1:3] # first three subject names of cases group
# read SNP data (use SNPRelate to convert it to gds) and count number of minor alleles
snp_data_gds <- gwid::build_gwas(gds_data = genome_data_file,
caco = case_control, gwas_generator = TRUE)
class(snp_data_gds)
names(snp_data_gds)
head(snp_data_gds$snps) # it has information about counts of minor alleles in each location.
# read haplotype data (output of beagle)
haplotype_data <- gwid::build_phase(phased_vcf = phase_data_file, caco = case_control)
class(haplotype_data)
names(haplotype_data)
dim(haplotype_data$Hap.1) #22302 SNP and 1911 subjects
# read IBD data (output of Refined-IBD)
ibd_data <- gwid::build_gwid(ibd_data = ibd_data_file, gwas = snp_data_gds)
class(ibd_data)
ibd_data$ibd # refined IBD output
ibd_data$res # count number of IBD for each SNP location
# plot count of IBD in chromosome 3
plot(ibd_data, y = c("cases", "cont1"), ly = FALSE)
# Further investigate location between 117M and 122M
# significant number of IBD's in group cases, compare to cont1, cont2 and cont3.
plot(ibd_data, y = c("cases", "cont1"), snp_start = 119026294, snp_end = 120613594, ly = FALSE)
model_fisher <- gwid::fisher_test(ibd_data, case_control, reference = "cases",
snp_start = 119026294, snp_end = 120613594)
class(model_fisher)

```

```

plot(model_fisher, y = c("cases", "cont1"),ly = FALSE)
hap_str <- gwid::haplotype_structure(ibd_data,phase = haplotype_data,w = 10,
snp_start = 119026294,snp_end = 120613594)
haplo_freq <- gwid::haplotype_frequency(hap_str)
plot(haplo_freq,y = c("cases", "cont1"),plot_type = "haplotype_structure_frequency",
nwin = 1, type = "version1",ly = FALSE)

```

---

fisher\_test.gwid

*Fisher's Exact Test for gwid count data*


---

## Description

Fisher's Exact Test for gwid count data

## Usage

```

## S3 method for class 'gwid'
fisher_test(
  obj,
  caco,
  snp_start,
  snp_end,
  reference,
  alternative = c("two.sided", "greater", "less"),
  ...
)

```

## Arguments

obj	An object of class gwid. Output of build_gwid function
caco	An object of class caco. Output of case_control function.
snp_start	select starting position of snps.
snp_end	select ending position of snp.
reference	reference group of subjects in which we want to perform fisher test
alternative	indicates the alternative hypothesis and must be one of "two.sided", "greater" or "less". You can specify just the initial letter. Only used in the 2 by 2 case
...	optional arguments to fisher.test

## Value

the output will be a test\_snps (data.table) object including 3 columns: "snp\_pos", "case\_control", and "value" which is a p-values.

**Examples**

```

piggyback::pb_download(repo = "soroushmdg/gwid",tag = "v0.0.1",dest = tempdir())
ibd_data_file <- paste0(tempdir(),"//chr3.ibd")
genome_data_file <- paste0(tempdir(),"//chr3.gds")
phase_data_file <- paste0(tempdir(),"//chr3.vcf")
case_control_data_file <- paste0(tempdir(),"//case-cont-RA.withmap.Rda")
# case-control data
case_control <- gwid::case_control(case_control_rda = case_control_data_file)
names(case_control) #cases and controls group
summary(case_control) # in here, we only consider cases,cont1,cont2,cont3 groups in the study
case_control$cases[1:3] # first three subject names of cases group
# read SNP data (use SNPRelate to convert it to gds) and count number of minor alleles
snp_data_gds <- gwid::build_gwas(gds_data = genome_data_file,
caco = case_control,gwas_generator = TRUE)
class(snp_data_gds)
names(snp_data_gds)
head(snp_data_gds$snp) # it has information about counts of minor alleles in each location.
# read haplotype data (output of beagle)
haplotype_data <- gwid::build_phase(phased_vcf = phase_data_file,caco = case_control)
class(haplotype_data)
names(haplotype_data)
dim(haplotype_data$Hap.1) #22302 SNP and 1911 subjects
# read IBD data (output of Refined-IBD)
ibd_data <- gwid::build_gwid(ibd_data = ibd_data_file,gwas = snp_data_gds)
class(ibd_data)
ibd_data$ibd # refined IBD output
ibd_data$res # count number of IBD for each SNP location
# plot count of IBD in chromosome 3
plot(ibd_data,y = c("cases","cont1"),ly = FALSE)
# Further investigate location between 117M and 122M
# significant number of IBD's in group cases, compare to cont1, cont2 and cont3.
plot(ibd_data,y = c("cases","cont1"),snp_start = 119026294,snp_end = 120613594,ly = FALSE)
model_fisher <- gwid::fisher_test(ibd_data,case_control,reference = "cases",
snp_start = 119026294,snp_end = 120613594)
class(model_fisher)
plot(model_fisher, y = c("cases","cont1"),ly = FALSE)
hap_str <- gwid::haplotype_structure(ibd_data,phase = haplotype_data,w = 10,
snp_start = 119026294,snp_end = 120613594)
haplo_freq <- gwid::haplotype_frequency(hap_str)
plot(haplo_freq,y = c("cases", "cont1"),plot_type = "haplotype_structure_frequency",
nwin = 1, type = "version1",ly = FALSE)

```

---

fisher\_test.result\_snps

*fisher exact test for result\_snps count data*


---

**Description**

fisher exact test for result\_snps count data

**Usage**

```
## S3 method for class 'result_snps'
fisher_test(
  obj,
  caco,
  reference,
  alternative = c("two.sided", "greater", "less"),
  ...
)
```

**Arguments**

obj	An object of class result_snps
caco	An object of class caco. Output of case_control function.
reference	reference group of subjects in which we want to perform fisher test.
alternative	indicates the alternative hypothesis and must be one of "two.sided", "greater" or "less". You can specify just the initial letter. Only used in the 2 by 2 case
...	optional arguments to fisher.test

**Value**

the output will be a test\_snps (data.table) object including 3 columns: "snp\_pos", "case\_control", and "value" which is a p-values.

**Examples**

```
piggyback::pb_download(repo = "soroushmdg/gwid", tag = "v0.0.1", dest = tempdir())
ibd_data_file <- paste0(tempdir(), "//chr3.ibd")
genome_data_file <- paste0(tempdir(), "//chr3.gds")
phase_data_file <- paste0(tempdir(), "//chr3.vcf")
case_control_data_file <- paste0(tempdir(), "//case-cont-RA.withmap.Rda")
# case-control data
case_control <- gwid::case_control(case_control_rda = case_control_data_file)
names(case_control) #cases and controls group
summary(case_control) # in here, we only consider cases,cont1,cont2,cont3 groups in the study
case_control$cases[1:3] # first three subject names of cases group
# read SNP data (use SNPrelate to convert it to gds) and count number of minor alleles
snp_data_gds <- gwid::build_gwas(gds_data = genome_data_file,
caco = case_control, gwas_generator = TRUE)
class(snp_data_gds)
names(snp_data_gds)
head(snp_data_gds$snps) # it has information about counts of minor alleles in each location.
# read haplotype data (output of beagle)
haplotype_data <- gwid::build_phase(phased_vcf = phase_data_file, caco = case_control)
class(haplotype_data)
names(haplotype_data)
dim(haplotype_data$Hap.1) #22302 SNP and 1911 subjects
# read IBD data (output of Refined-IBD)
ibd_data <- gwid::build_gwid(ibd_data = ibd_data_file, gwas = snp_data_gds)
```

```

class(ibd_data)
ibd_data$ibd # refined IBD output
ibd_data$res # count number of IBD for each SNP location
# plot count of IBD in chromosome 3
plot(ibd_data,y = c("cases", "cont1"),ly = FALSE)
# Further investigate location between 117M and 122M
# significant number of IBD's in group cases, compare to cont1, cont2 and cont3.
plot(ibd_data,y = c("cases", "cont1"),snp_start = 119026294,snp_end = 120613594,ly = FALSE)
model_fisher <- gwid::fisher_test(ibd_data,case_control,reference = "cases",
snp_start = 119026294,snp_end = 120613594)
model_permutation <- permutation_test(ibd_data,snp_data_gds,
snp_start = 119026294,snp_end = 120613594,nperm=20,reference = "cases")
class(model_fisher)
plot(model_fisher, y = c("cases", "cont1"),ly = FALSE)
hap_str <- gwid::haplotype_structure(ibd_data,phase = haplotype_data,w = 10,
snp_start = 119026294,snp_end = 120613594)
haplo_freq <- gwid::haplotype_frequency(hap_str)
plot(haplo_freq,y = c("cases", "cont1"),plot_type = "haplotype_structure_frequency",
nwin = 1, type = "version1",ly = FALSE)

```

---

gtest

*perform gtest*


---

## Description

perform gtest

## Usage

```
gtest(haplotype_structure, ...)
```

## Arguments

haplotype_structure	object of a class
...	other variables

## Value

the output will be a test\_snps (data.table) object including 3 columns: "snp\_pos", "case\_control", and "value" which is a p-values.

---

```
gtest.haplotype_structure
```

*Perform G-test on haplotype structures extracted from haplotype\_structure function*

---

### Description

Perform G-test on haplotype structures extracted from haplotype\_structure function

### Usage

```
## S3 method for class 'haplotype_structure'
gtest(haplotype_structure, reference, ...)
```

### Arguments

haplotype_structure	An object of class haplotype_structure. Output of haplotype_structure function.
reference	reference group of subjects in which we want to perform G-test
...	other variables

### Value

the output will be a test\_snps (data.table) object including 3 columns: “snp\_pos”, “case\_control”, and “value” which is a p-values.

---

```
haplotype_frequency    haplotype frequency
```

---

### Description

haplotype frequency

### Usage

```
haplotype_frequency(haplotype_structure, ...)
```

### Arguments

haplotype_structure	object of class haplotype structure
...	other variables



**Value**

An object of class `haplotype_frequency` contains of two objects. first one is object of `haplotype_structure_frequency` (`data.table`) and second one is object of class `result_snps`(`data.table`)

**Examples**

```

piggyback::pb_download(repo = "soroushmdg/gwid",tag = "v0.0.1",dest = tempdir())
ibd_data_file <- paste0(tempdir(),"//chr3.ibd")
genome_data_file <- paste0(tempdir(),"//chr3.gds")
phase_data_file <- paste0(tempdir(),"//chr3.vcf")
case_control_data_file <- paste0(tempdir(),"//case-cont-RA.withmap.Rda")
# case-control data
case_control <- gwid::case_control(case_control_rda = case_control_data_file)
names(case_control) #cases and controls group
summary(case_control) # in here, we only consider cases,cont1,cont2,cont3 groups in the study
case_control$cases[1:3] # first three subject names of cases group
# read SNP data (use SNPRelate to convert it to gds) and count number of minor alleles
snp_data_gds <- gwid::build_gwas(gds_data = genome_data_file,
caco = case_control,gwas_generator = TRUE)
class(snp_data_gds)
names(snp_data_gds)
head(snp_data_gds$snps) # it has information about counts of minor alleles in each location.
# read haplotype data (output of beagle)
haplotype_data <- gwid::build_phase(phased_vcf = phase_data_file,caco = case_control)
class(haplotype_data)
names(haplotype_data)
dim(haplotype_data$Hap.1) #22302 SNP and 1911 subjects
# read IBD data (output of Refined-IBD)
ibd_data <- gwid::build_gwid(ibd_data = ibd_data_file,gwas = snp_data_gds)
class(ibd_data)
ibd_data$ibd # refined IBD output
ibd_data$res # count number of IBD for each SNP location
# plot count of IBD in chromosome 3
plot(ibd_data,y = c("cases","cont1"),ly = FALSE)
# Further investigate location between 117M and 122M
# significant number of IBD's in group cases, compare to cont1, cont2 and cont3.
plot(ibd_data,y = c("cases","cont1"),snp_start = 119026294,snp_end = 120613594,ly = FALSE)
model_fisher <- gwid::fisher_test(ibd_data,case_control,reference = "cases",
snp_start = 119026294,snp_end = 120613594)
class(model_fisher)
plot(model_fisher, y = c("cases","cont1"),ly = FALSE)
hap_str <- gwid::haplotype_structure(ibd_data,phase = haplotype_data,w = 10,
snp_start = 119026294,snp_end = 120613594)
haplo_freq <- gwid::haplotype_frequency(hap_str)
plot(haplo_freq,y = c("cases", "cont1"),plot_type = "haplotype_structure_frequency",
nwin = 1, type = "version1",ly = FALSE)

```

---

haplotype\_frequency.haplotype\_structure  
*haplotype frequency in sliding windows*

---

## Description

haplotype frequency in sliding windows

## Usage

```
## S3 method for class 'haplotype_structure'
haplotype_frequency(haplotype_structure, ...)
```

## Arguments

haplotype\_structure  
 An object of class haplotype\_structure. Output of haplotype\_structure function.

... other variables

## Value

An object of class haplotype\_frequency contains of two objects. first one is object of haplotype\_structure\_frequency (data.table) and second one is object of class result\_snps(data.table)

## Examples

```
piggyback::pb_download(repo = "soroushmdg/gwid", tag = "v0.0.1", dest = tempdir())
ibd_data_file <- paste0(tempdir(), "//chr3.ibd")
genome_data_file <- paste0(tempdir(), "//chr3.gds")
phase_data_file <- paste0(tempdir(), "//chr3.vcf")
case_control_data_file <- paste0(tempdir(), "//case-cont-RA.withmap.Rda")
# case-control data
case_control <- gwid::case_control(case_control_rda = case_control_data_file)
names(case_control) #cases and controls group
summary(case_control) # in here, we only consider cases, cont1, cont2, cont3 groups in the study
case_control$cases[1:3] # first three subject names of cases group
# read SNP data (use SNPrelate to convert it to gds) and count number of minor alleles
snp_data_gds <- gwid::build_gwas(gds_data = genome_data_file,
caco = case_control, gwas_generator = TRUE)
class(snp_data_gds)
names(snp_data_gds)
head(snp_data_gds$snps) # it has information about counts of minor alleles in each location.
# read haplotype data (output of beagle)
haplotype_data <- gwid::build_phase(phased_vcf = phase_data_file, caco = case_control)
class(haplotype_data)
names(haplotype_data)
dim(haplotype_data$Hap.1) #22302 SNP and 1911 subjects
# read IBD data (output of Refined-IBD)
```

```
ibd_data <- gwid::build_gwid(ibd_data = ibd_data_file,gwas = snp_data_gds)
class(ibd_data)
ibd_data$ibd # refined IBD output
ibd_data$res # count number of IBD for each SNP location
# plot count of IBD in chromosome 3
plot(ibd_data,y = c("cases","cont1"),ly = FALSE)
# Further investigate location between 117M and 122M
# significant number of IBD's in group cases, compare to cont1, cont2 and cont3.
plot(ibd_data,y = c("cases","cont1"),snp_start = 119026294,snp_end = 120613594,ly = FALSE)
model_fisher <- gwid::fisher_test(ibd_data,case_control,reference = "cases",
snp_start = 119026294,snp_end = 120613594)
class(model_fisher)
plot(model_fisher, y = c("cases","cont1"),ly = FALSE)
hap_str <- gwid::haplotype_structure(ibd_data,phase = haplotype_data,w = 10,
snp_start = 119026294,snp_end = 120613594)
haplo_freq <- gwid::haplotype_frequency(hap_str)
plot(haplo_freq,y = c("cases", "cont1"),plot_type = "haplotype_structure_frequency",
nwin = 1, type = "version1",ly = FALSE)
```

---

haplotype\_structure    *haplotype structures in a window*

---

## Description

haplotype structures in a window

## Usage

```
haplotype_structure(obj, ...)
```

## Arguments

obj	object
...	other variables

## Value

The output will be an object of class `haplotype_structure` (`data.table`) that has information about subjects haplotype structures in a window.

---

 haplotype\_structure.gwas

*extract haplotype structures of individuals in a window*


---

## Description

extract haplotype structures of individuals in a window

## Usage

```
## S3 method for class 'gwas'
haplotype_structure(obj, phase, w = 10, snp_start, snp_end, ...)
```

## Arguments

obj	object of class gwas
phase	An object of class phase. Output of build_phase function
w	window size
snp_start	select starting position of snps.
snp_end	select ending position of snps.
...	other variables

## Value

The output will be an object of class haplotype\_structure (data.table) that has information about subjects haplotype structures in a a window.

## Examples

```
piggyback::pb_download(repo = "soroshmdg/gwid", tag = "v0.0.1", dest = tempdir())
ibd_data_file <- paste0(tempdir(), "//chr3.ibd")
genome_data_file <- paste0(tempdir(), "//chr3.gds")
phase_data_file <- paste0(tempdir(), "//chr3.vcf")
case_control_data_file <- paste0(tempdir(), "//case-cont-RA.withmap.Rda")
# case-control data
case_control <- gwid::case_control(case_control_rda = case_control_data_file)
names(case_control) #cases and controls group
summary(case_control) # in here, we only consider cases,cont1,cont2,cont3 groups in the study
case_control$cases[1:3] # first three subject names of cases group
# read SNP data (use SNPRelate to convert it to gds) and count number of minor alleles
snp_data_gds <- gwid::build_gwas(gds_data = genome_data_file,
caco = case_control, gwas_generator = TRUE)
class(snp_data_gds)
names(snp_data_gds)
head(snp_data_gds$snps) # it has information about counts of minor alleles in each location.
# read haplotype data (output of beagle)
haplotype_data <- gwid::build_phase(phased_vcf = phase_data_file, caco = case_control)
```

```

class(haplotype_data)
names(haplotype_data)
dim(haplotype_data$Hap.1) #22302 SNP and 1911 subjects
# read IBD data (output of Refined-IBD)
ibd_data <- gwid::build_gwid(ibd_data = ibd_data_file,gwas = snp_data_gds)
class(ibd_data)
ibd_data$ibd # refined IBD output
ibd_data$res # count number of IBD for each SNP location
# plot count of IBD in chromosome 3
plot(ibd_data,y = c("cases","cont1"),ly = FALSE)
# Further investigate location between 117M and 122M
# significant number of IBD's in group cases, compare to cont1, cont2 and cont3.
plot(ibd_data,y = c("cases","cont1"),snp_start = 119026294,snp_end = 120613594,ly = FALSE)
model_fisher <- gwid::fisher_test(ibd_data,case_control,reference = "cases",
snp_start = 119026294,snp_end = 120613594)
class(model_fisher)
plot(model_fisher, y = c("cases","cont1"),ly = FALSE)
hap_str <- gwid::haplotype_structure(ibd_data,phase = haplotype_data,w = 10,
snp_start = 119026294,snp_end = 120613594)
haplo_freq <- gwid::haplotype_frequency(hap_str)
plot(haplo_freq,y = c("cases", "cont1"),plot_type = "haplotype_structure_frequency",
nwin = 1, type = "version1",ly = FALSE)

```

---

haplotype\_structure.gwid

*extract haplotype structures of pairwise ibd samples in a window*

---

## Description

extract haplotype structures of pairwise ibd samples in a window

## Usage

```

## S3 method for class 'gwid'
haplotype_structure(obj, phase, w = 10, snp_start, snp_end, ...)

```

## Arguments

obj	An object of class gwid. Output of build_gwid function.
phase	An object of class phase. Output of build_phase function.
w	window size
snp_start	select starting position of snps.
snp_end	select ending position of snps.
...	other variables

**Value**

The output will be an object of class `haplotype_structure` (`data.table`) that has information about subjects haplotype structures in a window.

**Examples**

```

piggyback::pb_download(repo = "soroshmdg/gwid", tag = "v0.0.1", dest = tempdir())
ibd_data_file <- paste0(tempdir(), "//chr3.ibd")
genome_data_file <- paste0(tempdir(), "//chr3.gds")
phase_data_file <- paste0(tempdir(), "//chr3.vcf")
case_control_data_file <- paste0(tempdir(), "//case-cont-RA.withmap.Rda")
# case-control data
case_control <- gwid::case_control(case_control_rda = case_control_data_file)
names(case_control) #cases and controls group
summary(case_control) # in here, we only consider cases, cont1, cont2, cont3 groups in the study
case_control$cases[1:3] # first three subject names of cases group
# read SNP data (use SNPRelate to convert it to gds) and count number of minor alleles
snp_data_gds <- gwid::build_gwas(gds_data = genome_data_file,
caco = case_control, gwas_generator = TRUE)
class(snp_data_gds)
names(snp_data_gds)
head(snp_data_gds$snps) # it has information about counts of minor alleles in each location.
# read haplotype data (output of beagle)
haplotype_data <- gwid::build_phase(phased_vcf = phase_data_file, caco = case_control)
class(haplotype_data)
names(haplotype_data)
dim(haplotype_data$Hap.1) #22302 SNP and 1911 subjects
# read IBD data (output of Refined-IBD)
ibd_data <- gwid::build_gwid(ibd_data = ibd_data_file, gwas = snp_data_gds)
class(ibd_data)
ibd_data$ibd # refined IBD output
ibd_data$res # count number of IBD for each SNP location
# plot count of IBD in chromosome 3
plot(ibd_data, y = c("cases", "cont1"), ly = FALSE)
# Further investigate location between 117M and 122M
# significant number of IBD's in group cases, compare to cont1, cont2 and cont3.
plot(ibd_data, y = c("cases", "cont1"), snp_start = 119026294, snp_end = 120613594, ly = FALSE)
model_fisher <- gwid::fisher_test(ibd_data, case_control, reference = "cases",
snp_start = 119026294, snp_end = 120613594)
class(model_fisher)
plot(model_fisher, y = c("cases", "cont1"), ly = FALSE)
hap_str <- gwid::haplotype_structure(ibd_data, phase = haplotype_data, w = 10,
snp_start = 119026294, snp_end = 120613594)
haplo_freq <- gwid::haplotype_frequency(hap_str)
plot(haplo_freq, y = c("cases", "cont1"), plot_type = "haplotype_structure_frequency",
nwin = 1, type = "version1", ly = FALSE)

```

**Description**

lauchn a shiny app

**Usage**

```
launch_app(data_folder_address, ...)
```

**Arguments**

data\_folder\_address

address of the folder that your data folders are. for example if you have two sets of data such as data1 and data2 and they are in mydata folder then your data\_folder\_address should be "./mydata"

... other variables

**Value**

open a shiny app

---

mcnemar\_test

*mcnemar test*

---

**Description**

mcnemar test

**Usage**

```
mcnemar_test(roh, ...)
```

**Arguments**

roh roh as class result\_snp

... other variables

**Value**

the output will be a test\_snps (data.table) object including 3 columns: "snp\_pos", "case\_control", and "value" which is a p-values.

---

```
mcnemar_test.result_snps
      mcnemar test
```

---

**Description**

mcnemar test

**Usage**

```
## S3 method for class 'result_snps'
mcnemar_test(
  roh = "object of class result_snps (output of function roh with fun=sum)",
  reference,
  w = 10,
  ...
)
```

**Arguments**

roh	An object of class result_snps (output of function roh with fun=sum)
reference	reference group of subjects in which we want to perform fisher test.
w	window size
...	other variables

**Value**

the output will be a test\_snps (data.table) object including 3 columns: "snpos", "case\_control", and "value" which is a p-values.

---

```
mcnemar_test_permut      mcnemar permutation
```

---

**Description**

mcnemar permutation

**Usage**

```
mcnemar_test_permut(mcnemar, ...)
```

**Arguments**

mcnemar	macnemar test output
...	other variables



**Value**

the output will be a test\_snps (data.table) object including 3 columns: “snp\_pos”, “case\_control”, and “value” which is a p-values.

---

```
mcnemar_test_permut.result_snps
      mcnemar permutation test
```

---

**Description**

mcnemar permutation test

**Usage**

```
## S3 method for class 'result_snps'
mcnemar_test_permut(
  mcnemar = "object of class result_snps (output of function mcnemar_test with fun=sum)",
  roh_mat = "output of roh function when roh_mat = TRUE",
  gwas = "object of class gwas",
  nperm = 1000,
  reference = "cases",
  w,
  ...
)
```

**Arguments**

mcnemar	macnemar test output
roh_mat	roh matrix
gwas	gwas
nperm	number of permutation
reference	reference group
w	window
...	other variables

**Value**

the output will be a test\_snps (data.table) object including 3 columns: “snp\_pos”, “case\_control”, and “value” which is a p-values.

permutation\_test      *permutation test*

---

**Description**

permutation test

**Usage**

```
permutation_test(obj, ...)
```

**Arguments**

obj	object
...	other variables

**Value**

the output will be a test\_snps (data.table) object including 3 columns: “snp\_pos”, “case\_control”, and “value” which is a p-values.

---

permutation\_test.gwas      *Permutation test for gwas object*

---

**Description**

Permutation test for gwas object

**Usage**

```
## S3 method for class 'gwas'  
permutation_test(  
  obj,  
  snp_start,  
  snp_end,  
  nperm = 1000,  
  reference = "cases",  
  ...  
)
```

**Arguments**

obj	object of class gwas
snp_start	select starting position of snps.
snp_end	select ending position of snp.
nperm	Number of permutations.
reference	reference group of subjects in which we want to perform fisher test
...	other variables

**Value**

the output will be a test\_snps (data.table) object including 3 columns: "snp\_pos", "case\_control", and "value" which is a p-values.

**Examples**

```

piggyback::pb_download(repo = "soroushmdg/gwid", tag = "v0.0.1", dest = tempdir())
ibd_data_file <- paste0(tempdir(), "//chr3.ibd")
genome_data_file <- paste0(tempdir(), "//chr3.gds")
phase_data_file <- paste0(tempdir(), "//chr3.vcf")
case_control_data_file <- paste0(tempdir(), "//case-cont-RA.withmap.Rda")
# case-control data
case_control <- gwid::case_control(case_control_rda = case_control_data_file)
names(case_control) #cases and controls group
summary(case_control) # in here, we only consider cases, cont1, cont2, cont3 groups in the study
case_control$cases[1:3] # first three subject names of cases group
# read SNP data (use SNPRelate to convert it to gds) and count number of minor alleles
snp_data_gds <- gwid::build_gwas(gds_data = genome_data_file,
caco = case_control, gwas_generator = TRUE)
class(snp_data_gds)
names(snp_data_gds)
head(snp_data_gds$snps) # it has information about counts of minor alleles in each location.
# read haplotype data (output of beagle)
haplotype_data <- gwid::build_phase(phased_vcf = phase_data_file, caco = case_control)
class(haplotype_data)
names(haplotype_data)
dim(haplotype_data$Hap.1) #22302 SNP and 1911 subjects
# read IBD data (output of Refined-IBD)
ibd_data <- gwid::build_gwid(ibd_data = ibd_data_file, gwas = snp_data_gds)
class(ibd_data)
ibd_data$ibd # refined IBD output
ibd_data$res # count number of IBD for each SNP location
# plot count of IBD in chromosome 3
plot(ibd_data, y = c("cases", "cont1"), ly = FALSE)
# Further investigate location between 117M and 122M
# significant number of IBD's in group cases, compare to cont1, cont2 and cont3.
plot(ibd_data, y = c("cases", "cont1"), snp_start = 119026294, snp_end = 120613594, ly = FALSE)
model_fisher <- gwid::fisher_test(ibd_data, case_control, reference = "cases",
snp_start = 119026294, snp_end = 120613594)
model_permutation <- permutation_test(ibd_data, snp_data_gds,
snp_start = 119026294, snp_end = 120613594, nperm=20, reference = "cases")

```

```

class(model_fisher)
plot(model_fisher, y = c("cases", "cont1"), ly = FALSE)
hap_str <- gwid::haplotype_structure(ibd_data, phase = haplotype_data, w = 10,
snp_start = 119026294, snp_end = 120613594)
haplo_freq <- gwid::haplotype_frequency(hap_str)
plot(haplo_freq, y = c("cases", "cont1"), plot_type = "haplotype_structure_frequency",
nwin = 1, type = "version1", ly = FALSE)

```

---

permutation\_test.gwid *permutation test for gwid count data*

---

### Description

permutation test for gwid count data

### Usage

```

## S3 method for class 'gwid'
permutation_test(
  obj,
  gwas,
  snp_start,
  snp_end,
  nperm = 100,
  reference = "cases",
  ...
)

```

### Arguments

obj	An object of class gwid. Output of build_gwid function
gwas	object of class gwas
snp_start	select starting position of snps.
snp_end	select ending position of snp.
nperm	Number of permutations.
reference	reference group
...	other variables

### Value

the output will be a test\_snps (data.table) object including 3 columns: "snp\_pos", "case\_control", and "value" which is a p-values.

**Examples**

```

piggyback::pb_download(repo = "soroushmdg/gwid",tag = "v0.0.1",dest = tempdir())
ibd_data_file <- paste0(tempdir(),"//chr3.ibd")
genome_data_file <- paste0(tempdir(),"//chr3.gds")
phase_data_file <- paste0(tempdir(),"//chr3.vcf")
case_control_data_file <- paste0(tempdir(),"//case-cont-RA.withmap.Rda")
# case-control data
case_control <- gwid::case_control(case_control_rda = case_control_data_file)
names(case_control) #cases and controls group
summary(case_control) # in here, we only consider cases,cont1,cont2,cont3 groups in the study
case_control$cases[1:3] # first three subject names of cases group
# read SNP data (use SNPRelate to convert it to gds) and count number of minor alleles
snp_data_gds <- gwid::build_gwas(gds_data = genome_data_file,
caco = case_control,gwas_generator = TRUE)
class(snp_data_gds)
names(snp_data_gds)
head(snp_data_gds$snps) # it has information about counts of minor alleles in each location.
# read haplotype data (output of beagle)
haplotype_data <- gwid::build_phase(phased_vcf = phase_data_file,caco = case_control)
class(haplotype_data)
names(haplotype_data)
dim(haplotype_data$Hap.1) #22302 SNP and 1911 subjects
# read IBD data (output of Refined-IBD)
ibd_data <- gwid::build_gwid(ibd_data = ibd_data_file,gwas = snp_data_gds)
class(ibd_data)
ibd_data$ibd # refined IBD output
ibd_data$res # count number of IBD for each SNP location
# plot count of IBD in chromosome 3
plot(ibd_data,y = c("cases","cont1"),ly = FALSE)
# Further investigate location between 117M and 122M
# significant number of IBD's in group cases, compare to cont1, cont2 and cont3.
plot(ibd_data,y = c("cases","cont1"),snp_start = 119026294,snp_end = 120613594,ly = FALSE)
model_fisher <- gwid::fisher_test(ibd_data,case_control,reference = "cases",
snp_start = 119026294,snp_end = 120613594)
model_permutation <- permutation_test(ibd_data,snp_data_gds,
snp_start = 119026294,snp_end = 120613594,nperm=20,reference = "cases")
class(model_fisher)
plot(model_fisher, y = c("cases","cont1"),ly = FALSE)
hap_str <- gwid::haplotype_structure(ibd_data,phase = haplotype_data,w = 10,
snp_start = 119026294,snp_end = 120613594)
haplo_freq <- gwid::haplotype_frequency(hap_str)
plot(haplo_freq,y = c("cases", "cont1"),plot_type = "haplotype_structure_frequency",
nwin = 1, type = "version1",ly = FALSE)

```

---

permutation\_test.haplotype\_structure

*Permutation test for 'haplotype\_structure' object*


---

**Description**

Permutation test for ‘haplotype\_structure’ object

**Usage**

```
## S3 method for class 'haplotype_structure'
permutation_test(obj, nperm, reference, ...)
```

**Arguments**

obj	object of class ‘haplotype_structure’
nperm	Number of permutations.
reference	reference group of subjects in which we want to perform ‘gtest’
...	other variables

**Value**

the output will be a test\_snps (data.table) object including 3 columns: “snps\_pos”, “case\_control”, and “value” which is a p-values.

**Examples**

```
piggyback::pb_download(repo = "sorushmdg/gwid", tag = "v0.0.1", dest = tempdir())
ibd_data_file <- paste0(tempdir(), "//chr3.ibd")
genome_data_file <- paste0(tempdir(), "//chr3.gds")
phase_data_file <- paste0(tempdir(), "//chr3.vcf")
case_control_data_file <- paste0(tempdir(), "//case-cont-RA.withmap.Rda")
# case-control data
case_control <- gwid::case_control(case_control_rda = case_control_data_file)
names(case_control) #cases and controls group
summary(case_control) # in here, we only consider cases, cont1, cont2, cont3 groups in the study
case_control$cases[1:3] # first three subject names of cases group
# read SNP data (use SNPRelate to convert it to gds) and count number of minor alleles
snp_data_gds <- gwid::build_gwas(gds_data = genome_data_file,
caco = case_control, gwas_generator = TRUE)
class(snp_data_gds)
names(snp_data_gds)
head(snp_data_gds$snps) # it has information about counts of minor alleles in each location.
# read haplotype data (output of beagle)
haplotype_data <- gwid::build_phase(phased_vcf = phase_data_file, caco = case_control)
class(haplotype_data)
names(haplotype_data)
dim(haplotype_data$Hap.1) #22302 SNP and 1911 subjects
# read IBD data (output of Refined-IBD)
ibd_data <- gwid::build_gwid(ibd_data = ibd_data_file, gwas = snp_data_gds)
class(ibd_data)
ibd_data$ibd # refined IBD output
ibd_data$res # count number of IBD for each SNP location
# plot count of IBD in chromosome 3
plot(ibd_data, y = c("cases", "cont1"), ly = FALSE)
```

```

# Further investigate location between 117M and 122M
# significant number of IBD's in group cases, compare to cont1, cont2 and cont3.
plot(ibd_data,y = c("cases", "cont1"),snp_start = 119026294,snp_end = 120613594,ly = FALSE)
model_fisher <- gwid::fisher_test(ibd_data,case_control,reference = "cases",
snp_start = 119026294,snp_end = 120613594)
model_permutation <- permutation_test(ibd_data,snp_data_gds,
snp_start = 119026294,snp_end = 120613594,nperm=20,reference = "cases")
class(model_fisher)
plot(model_fisher, y = c("cases", "cont1"),ly = FALSE)
hap_str <- gwid::haplotype_structure(ibd_data,phase = haplotype_data,w = 10,
snp_start = 119026294,snp_end = 120613594)
haplo_freq <- gwid::haplotype_frequency(hap_str)
plot(haplo_freq,y = c("cases", "cont1"),plot_type = "haplotype_structure_frequency",
nwin = 1, type = "version1",ly = FALSE)

```

---

plot.gwas

*Line plot of gwas objects*


---

## Description

Line plot of gwas objects

## Usage

```

## S3 method for class 'gwas'
plot(x, y = NA, title = "number of snps", ...)

```

## Arguments

x	object of class gwas.
y	default value is NA, if specified it should be a vector of names of subject groups i.e. y = c("case","control")
title	title of the plot.
...	optional argument of plot

## Value

an interactive line plot of gwas objects for each case control subjects.

## Examples

```

piggyback::pb_download(repo = "soroushmdg/gwid",tag = "v0.0.1",dest = tempdir())
ibd_data_file <- paste0(tempdir(),"//chr3.ibd")
genome_data_file <- paste0(tempdir(),"//chr3.gds")
phase_data_file <- paste0(tempdir(),"//chr3.vcf")
case_control_data_file <- paste0(tempdir(),"//case-cont-RA.withmap.Rda")
# case-control data

```

```

case_control <- gwid::case_control(case_control_rda = case_control_data_file)
names(case_control) #cases and controls group
summary(case_control) # in here, we only consider cases,cont1,cont2,cont3 groups in the study
case_control$cases[1:3] # first three subject names of cases group
# read SNP data (use SNPRelate to convert it to gds) and count number of minor alleles
snp_data_gds <- gwid::build_gwas(gds_data = genome_data_file,
caco = case_control,gwas_generator = TRUE)
class(snp_data_gds)
names(snp_data_gds)
head(snp_data_gds$snps) # it has information about counts of minor alleles in each location.
# read haplotype data (output of beagle)
haplotype_data <- gwid::build_phase(phased_vcf = phase_data_file,caco = case_control)
class(haplotype_data)
names(haplotype_data)
dim(haplotype_data$Hap.1) #22302 SNP and 1911 subjects
# read IBD data (output of Refined-IBD)
ibd_data <- gwid::build_gwid(ibd_data = ibd_data_file,gwas = snp_data_gds)
class(ibd_data)
ibd_data$ibd # refined IBD output
ibd_data$res # count number of IBD for each SNP location
# plot count of IBD in chromosome 3
plot(ibd_data,y = c("cases","cont1"),ly = FALSE)
# Further investigate location between 117M and 122M
# significant number of IBD's in group cases, compare to cont1, cont2 and cont3.
plot(ibd_data,y = c("cases","cont1"),snp_start = 119026294,snp_end = 120613594,ly = FALSE)
model_fisher <- gwid::fisher_test(ibd_data,case_control,reference = "cases",
snp_start = 119026294,snp_end = 120613594)
class(model_fisher)
plot(model_fisher, y = c("cases","cont1"),ly = FALSE)
hap_str <- gwid::haplotype_structure(ibd_data,phase = haplotype_data,w = 10,
snp_start = 119026294,snp_end = 120613594)
haplo_freq <- gwid::haplotype_frequency(hap_str)
plot(haplo_freq,y = c("cases", "cont1"),plot_type = "haplotype_structure_frequency",
nwin = 1, type = "version1",ly = FALSE)

```

---

plot.gwid

*Line plot of gwid objects*


---

## Description

Line plot of gwid objects

## Usage

```

## S3 method for class 'gwid'
plot(
  x,
  y = NA,
  title = "number of IBD in each snp",

```



```

    plot_type = c("result_snps", "profile"),
    reference,
    ...
  )

```

### Arguments

x	An object of class gwid. Output of build_gwid function.
y	default value is NA, if specified it should be a vector of names of subject groups i.e. y = c("case","control")
title	title of the plot.
plot_type	either "result_snps" or "profile".
reference	reference group of subjects in which we want to have profile plot.
...	if plot_type is "result_snps" it is optional argument of plot. if plot_type is "profile" we can subset plot based on snp_start and snp_end locations.

### Value

if plot\_type is "result\_snps" an interactive line plot of result\_snps for each case control subjects. if plot\_type is "profile" an interactive profile plot of identity by descent subjects in subset of locations.

### Examples

```

piggyback::pb_download(repo = "soroshmdg/gwid", tag = "v0.0.1", dest = tempdir())
ibd_data_file <- paste0(tempdir(), "//chr3.ibd")
genome_data_file <- paste0(tempdir(), "//chr3.gds")
phase_data_file <- paste0(tempdir(), "//chr3.vcf")
case_control_data_file <- paste0(tempdir(), "//case-cont-RA.withmap.Rda")
# case-control data
case_control <- gwid::case_control(case_control_rda = case_control_data_file)
names(case_control) #cases and controls group
summary(case_control) # in here, we only consider cases, cont1, cont2, cont3 groups in the study
case_control$cases[1:3] # first three subject names of cases group
# read SNP data (use SNPRelate to convert it to gds) and count number of minor alleles
snp_data_gds <- gwid::build_gwas(gds_data = genome_data_file,
caco = case_control, gwas_generator = TRUE)
class(snp_data_gds)
names(snp_data_gds)
head(snp_data_gds$snps) # it has information about counts of minor alleles in each location.
# read haplotype data (output of beagle)
haplotype_data <- gwid::build_phase(phased_vcf = phase_data_file, caco = case_control)
class(haplotype_data)
names(haplotype_data)
dim(haplotype_data$Hap.1) #22302 SNP and 1911 subjects
# read IBD data (output of Refined-IBD)
ibd_data <- gwid::build_gwid(ibd_data = ibd_data_file, gwas = snp_data_gds)
class(ibd_data)
ibd_data$ibd # refined IBD output
ibd_data$res # count number of IBD for each SNP location
# plot count of IBD in chromosome 3

```

```

plot(ibd_data,y = c("cases","cont1"),ly = FALSE)
# Further investigate location between 117M and 122M
# significant number of IBD's in group cases, compare to cont1, cont2 and cont3.
plot(ibd_data,y = c("cases","cont1"),snp_start = 119026294,snp_end = 120613594,ly = FALSE)
model_fisher <- gwid::fisher_test(ibd_data,case_control,reference = "cases",
snp_start = 119026294,snp_end = 120613594)
class(model_fisher)
plot(model_fisher, y = c("cases","cont1"),ly = FALSE)
hap_str <- gwid::haplotype_structure(ibd_data,phase = haplotype_data,w = 10,
snp_start = 119026294,snp_end = 120613594)
haplo_freq <- gwid::haplotype_frequency(hap_str)
plot(haplo_freq,y = c("cases", "cont1"),plot_type = "haplotype_structure_frequency",
nwin = 1, type = "version1",ly = FALSE)

```

---

plot.haplotype\_frequency

*Line plot of haplotype\_frequency object*

---

## Description

Line plot of haplotype\_frequency object

## Usage

```

## S3 method for class 'haplotype_frequency'
plot(
  x,
  y = NA,
  plot_type = c("haplotype_structure_frequency", "result_snps"),
  type = c("version1", "version2"),
  ly = TRUE,
  nwin,
  title,
  line_size = 0.6,
  ...
)

```

## Arguments

x	an object of class haplotype_frequency
y	default value is 'NA', if specified it should be a vector of names of subject groups i.e. 'y = c("case","control")'
plot_type	either "result_snps" or ""haplotype_structure_frequency""
type	either "version1" or "version2" when plot_type is ""haplotype_structure_frequency""
ly	if TRUE, we have a plotly object and if it is false plot is going to be a ggplot object.

nwin	window number
title	title of the plot.
line_size	geom_line size
...	optional argument of plot

### Value

an interactive line plot of haplotype\_frequency objects for each case control subjects.

### Examples

```

piggyback::pb_download(repo = "soroushmdg/gwid", tag = "v0.0.1",
  dest = tempdir())
ibd_data_file <- paste0(tempdir(), "//chr3.ibd")
genome_data_file <- paste0(tempdir(), "//chr3.gds")
phase_data_file <- paste0(tempdir(), "//chr3.vcf")
case_control_data_file <- paste0(tempdir(), "//case-cont-RA.withmap.Rda")
# case-control data
case_control <- gwid::case_control(case_control_rda = case_control_data_file)
names(case_control) #cases and controls group
summary(case_control)
case_control$cases[1:3] # first three subject names of cases group
# read SNP data (use SNPRelate to convert it to gds) and count number of minor alleles
snp_data_gds <- gwid::build_gwas(gds_data = genome_data_file,
  caco = case_control, gwas_generator = TRUE)
class(snp_data_gds)
names(snp_data_gds)
head(snp_data_gds$snps) # it has information about counts of minor alleles in each location.
# read haplotype data (output of beagle)
haplotype_data <- gwid::build_phase(phased_vcf = phase_data_file, caco = case_control)
class(haplotype_data)
names(haplotype_data)
dim(haplotype_data$Hap.1) #22302 SNP and 1911 subjects
# read IBD data (output of Refined-IBD)
ibd_data <- gwid::build_gwid(ibd_data = ibd_data_file, gwas = snp_data_gds)
class(ibd_data)
ibd_data$ibd # refined IBD output
ibd_data$res # count number of IBD for each SNP location
# plot count of IBD in chromosome 3
plot(ibd_data, y = c("cases", "cont1"), ly = FALSE)
# Further investigate location between 117M and 122M
# significant number of IBD's in group cases, compare to cont1, cont2 and cont3.
plot(ibd_data, y = c("cases", "cont1"), snp_start = 119026294, snp_end = 120613594, ly = FALSE)
model_fisher <- gwid::fisher_test(ibd_data, case_control, reference = "cases",
  snp_start = 119026294, snp_end = 120613594)
class(model_fisher)
plot(model_fisher, y = c("cases", "cont1"), ly = FALSE)
hap_str <- gwid::haplotype_structure(ibd_data, phase = haplotype_data, w = 10,
  snp_start = 119026294, snp_end = 120613594)
haplo_freq <- gwid::haplotype_frequency(hap_str)
plot(haplo_freq, y = c("cases", "cont1"), plot_type = "haplotype_structure_frequency",

```

```
nwin = 1, type = "version1",ly = FALSE)
```

---

```
plot.haplotype_structure_frequency
```

*Two type of line plots for haplotype\_structure\_frequency objects .*

---

### Description

Two type of line plots for haplotype\_structure\_frequency objects .

### Usage

```
## S3 method for class 'haplotype_structure_frequency'
plot(
  x,
  y = NA,
  type = c("version1", "version2"),
  nwin,
  ly = TRUE,
  line_size = 0.6,
  ...
)
```

### Arguments

x	an object of class haplotype_structure_frequency
y	default value is NA, if specified it should be a vector of names of subject groups i.e. y = c("case","control")
type	either "version1" or "version2"
nwin	window number
ly	if 'TRUE', we have a 'plotly' object and if it is 'FALSE' plot is going to be a 'ggplot' object.
line_size	geom_line size
...	other variables

### Value

an interactive line plot of haplotype\_structure\_frequency objects for each case control subjects.

**Examples**

```

piggyback::pb_download(repo = "soroushmdg/gwid", tag = "v0.0.1", dest = tempdir())
ibd_data_file <- paste0(tempdir(), "//chr3.ibd")
genome_data_file <- paste0(tempdir(), "//chr3.gds")
phase_data_file <- paste0(tempdir(), "//chr3.vcf")
case_control_data_file <- paste0(tempdir(), "//case-cont-RA.withmap.Rda")
# case-control data
case_control <- gwid::case_control(case_control_rda = case_control_data_file)
names(case_control) #cases and controls group
summary(case_control) # in here, we only consider cases,cont1,cont2,cont3 groups in the study
case_control$cases[1:3] # first three subject names of cases group
# read SNP data (use SNPRelate to convert it to gds) and count number of minor alleles
snp_data_gds <- gwid::build_gwas(gds_data = genome_data_file,
caco = case_control, gwas_generator = TRUE)
class(snp_data_gds)
names(snp_data_gds)
head(snp_data_gds$snp) # it has information about counts of minor alleles in each location.
# read haplotype data (output of beagle)
haplotype_data <- gwid::build_phase(phased_vcf = phase_data_file, caco = case_control)
class(haplotype_data)
names(haplotype_data)
dim(haplotype_data$Hap.1) #22302 SNP and 1911 subjects
# read IBD data (output of Refined-IBD)
ibd_data <- gwid::build_gwid(ibd_data = ibd_data_file, gwas = snp_data_gds)
class(ibd_data)
ibd_data$ibd # refined IBD output
ibd_data$res # count number of IBD for each SNP location
# plot count of IBD in chromosome 3
plot(ibd_data, y = c("cases", "cont1"), ly = FALSE)
# Further investigate location between 117M and 122M
# significant number of IBD's in group cases, compare to cont1, cont2 and cont3.
plot(ibd_data, y = c("cases", "cont1"), snp_start = 119026294, snp_end = 120613594, ly = FALSE)
model_fisher <- gwid::fisher_test(ibd_data, case_control, reference = "cases",
snp_start = 119026294, snp_end = 120613594)
class(model_fisher)
plot(model_fisher, y = c("cases", "cont1"), ly = FALSE)
hap_str <- gwid::haplotype_structure(ibd_data, phase = haplotype_data, w = 10,
snp_start = 119026294, snp_end = 120613594)
haplo_freq <- gwid::haplotype_frequency(hap_str)
plot(haplo_freq, y = c("cases", "cont1"), plot_type = "haplotype_structure_frequency",
nwin = 1, type = "version1", ly = FALSE)

```

---

plot.result\_snps

*Line plot of result\_snps objects*


---

**Description**

Line plot of result\_snps objects

**Usage**

```
## S3 method for class 'result_snps'
plot(x, y = NA, title, snp_start, snp_end, ly = TRUE, line_size = 0.6, ...)
```

**Arguments**

x	An object of class result_snps.
y	default value is NA, if specified it should be a vector of names of subject groups i.e. y = c("case","control")
title	title of the plot.
snp_start	select starting position of snps.
snp_end	select ending position of snps.
ly	if TRUE, we have a plotly object and if it is false plot is going to be a ggplot object.
line_size	geom_line size
...	other variables

**Value**

an interactive line plot of result\_snps for each case control subjects.

**Examples**

```
piggyback::pb_download(repo = "soroushmdg/gwid", tag = "v0.0.1", dest = tempdir())
ibd_data_file <- paste0(tempdir(), "//chr3.ibd")
genome_data_file <- paste0(tempdir(), "//chr3.gds")
phase_data_file <- paste0(tempdir(), "//chr3.vcf")
case_control_data_file <- paste0(tempdir(), "//case-cont-RA.withmap.Rda")
# case-control data
case_control <- gwid::case_control(case_control_rda = case_control_data_file)
names(case_control) #cases and controls group
summary(case_control) # in here, we only consider cases, cont1, cont2, cont3 groups in the study
case_control$cases[1:3] # first three subject names of cases group
# read SNP data (use SNPRelate to convert it to gds) and count number of minor alleles
snp_data_gds <- gwid::build_gwas(gds_data = genome_data_file,
caco = case_control, gwas_generator = TRUE)
class(snp_data_gds)
names(snp_data_gds)
head(snp_data_gds$snps)
# read haplotype data (output of beagle)
haplotype_data <- gwid::build_phase(phased_vcf = phase_data_file, caco = case_control)
class(haplotype_data)
names(haplotype_data)
dim(haplotype_data$Hap.1) #22302 SNP and 1911 subjects
# read IBD data (output of Refined-IBD)
ibd_data <- gwid::build_gwid(ibd_data = ibd_data_file, gwas = snp_data_gds)
class(ibd_data)
ibd_data$ibd # refined IBD output
ibd_data$res # count number of IBD for each SNP location
```

```

# plot count of IBD in chromosome 3
plot(ibd_data,y = c("cases","cont1"),ly = FALSE)
# Further investigate location between 117M and 122M
# significant number of IBD's in group cases, compare to cont1, cont2 and cont3.
plot(ibd_data,y = c("cases","cont1"),snp_start = 119026294,snp_end = 120613594,ly = FALSE)
model_fisher <- gwid::fisher_test(ibd_data,case_control,reference = "cases",
snp_start = 119026294,snp_end = 120613594)
class(model_fisher)
plot(model_fisher, y = c("cases","cont1"),ly = FALSE)
hap_str <- gwid::haplotype_structure(ibd_data,phase = haplotype_data,w = 10,
snp_start = 119026294,snp_end = 120613594)
haplo_freq <- gwid::haplotype_frequency(hap_str)
plot(haplo_freq,y = c("cases", "cont1"),plot_type = "haplotype_structure_frequency",
nwin = 1, type = "version1",ly = FALSE)

```

---

plot.test\_snps

*Line plot of test\_snps objects*


---

## Description

Line plot of test\_snps objects

## Usage

```

## S3 method for class 'test_snps'
plot(
  x,
  y = NA,
  title,
  snp_start,
  snp_end,
  ly = TRUE,
  line_size = 0.6,
  log_transformation = TRUE,
  QQplot = FALSE,
  ...
)

```

## Arguments

x	an object of class test_snps.
y	default value is NA, if specified it should be a vector of names of subject groups i.e. y = c("case","control")
title	title of the plot.
snp_start	select starting position of snps.
snp_end	select ending position of snps.

ly                    if 'TRUE', we have a 'plotly' object and if it is 'FALSE' plot is going to be a 'ggplot' object.

line\_size            geom\_line size

log\_transformation            if 'TRUE' plot -log10 transformation of p\_values.

QQplot                if TRUE, plot QQplot of P-values

...                    other variables

## Value

an interactive line plot of test\_snps objects for each case control subjects.

## Examples

```

piggyback::pb_download(repo = "soroushmdg/gwid", tag = "v0.0.1", dest = tempdir())
ibd_data_file <- paste0(tempdir(), "//chr3.ibd")
genome_data_file <- paste0(tempdir(), "//chr3.gds")
phase_data_file <- paste0(tempdir(), "//chr3.vcf")
case_control_data_file <- paste0(tempdir(), "//case-cont-RA.withmap.Rda")
# case-control data
case_control <- gwid::case_control(case_control_rda = case_control_data_file)
names(case_control) #cases and controls group
summary(case_control) # in here, we only consider cases, cont1, cont2, cont3 groups in the study
case_control$cases[1:3] # first three subject names of cases group
# read SNP data (use SNPRelate to convert it to gds) and count number of minor alleles
snp_data_gds <- gwid::build_gwas(gds_data = genome_data_file,
caco = case_control, gwas_generator = TRUE)
class(snp_data_gds)
names(snp_data_gds)
head(snp_data_gds$snp) # it has information about counts of minor alleles in each location.
# read haplotype data (output of beagle)
haplotype_data <- gwid::build_phase(phased_vcf = phase_data_file, caco = case_control)
class(haplotype_data)
names(haplotype_data)
dim(haplotype_data$Hap.1) #22302 SNP and 1911 subjects
# read IBD data (output of Refined-IBD)
ibd_data <- gwid::build_gwid(ibd_data = ibd_data_file, gwas = snp_data_gds)
class(ibd_data)
ibd_data$ibd # refined IBD output
ibd_data$res # count number of IBD for each SNP location
# plot count of IBD in chromosome 3
plot(ibd_data, y = c("cases", "cont1"), ly = FALSE)
# Further investigate location between 117M and 122M
# significant number of IBD's in group cases, compare to cont1, cont2 and cont3.
plot(ibd_data, y = c("cases", "cont1"), snp_start = 119026294, snp_end = 120613594, ly = FALSE)
model_fisher <- gwid::fisher_test(ibd_data, case_control, reference = "cases",
snp_start = 119026294, snp_end = 120613594)
class(model_fisher)
plot(model_fisher, y = c("cases", "cont1"), ly = FALSE)
hap_str <- gwid::haplotype_structure(ibd_data, phase = haplotype_data, w = 10,
snp_start = 119026294, snp_end = 120613594)

```



```
haplo_freq <- gwid::haplotype_frequency(hap_str)
plot(haplo_freq, y = c("cases", "cont1"), plot_type = "haplotype_structure_frequency",
     nwin = 1, type = "version1", ly = FALSE)
```

---

print

*print*


---

**Description**

print

**Usage**

print(x, ...)

**Arguments**

x	an object
...	other objects

**Value**

print an object

---

print.gwas

*print gwas instants*


---

**Description**

print gwas instants

**Usage**

```
## S3 method for class 'gwas'
print(x, ...)
```

**Arguments**

x	object gwas
...	other objects

**Value**

print number of subjects and number of SNPs of a GWAS object

## Examples

```

piggyback::pb_download(repo = "soroushmdg/gwid",tag = "v0.0.1",dest = tempdir())
ibd_data_file <- paste0(tempdir(),"//chr3.ibd")
genome_data_file <- paste0(tempdir(),"//chr3.gds")
phase_data_file <- paste0(tempdir(),"//chr3.vcf")
case_control_data_file <- paste0(tempdir(),"//case-cont-RA.withmap.Rda")
# case-control data
case_control <- gwid::case_control(case_control_rda = case_control_data_file)
names(case_control) #cases and controls group
summary(case_control) # in here, we only consider cases,cont1,cont2,cont3 groups in the study
case_control$cases[1:3] # first three subject names of cases group
# read SNP data (use SNPrelate to convert it to gds) and count number of minor alleles
snp_data_gds <- gwid::build_gwas(gds_data = genome_data_file,
caco = case_control,gwas_generator = TRUE)
print(snp_data_gds)
class(snp_data_gds)
names(snp_data_gds)
head(snp_data_gds$snps) # it has information about counts of minor alleles in each location.
# read haplotype data (output of beagle)
haplotype_data <- gwid::build_phase(phased_vcf = phase_data_file,caco = case_control)
class(haplotype_data)
names(haplotype_data)
dim(haplotype_data$Hap.1) #22302 SNP and 1911 subjects
# read IBD data (output of Refined-IBD)
ibd_data <- gwid::build_gwid(ibd_data = ibd_data_file,gwas = snp_data_gds)
class(ibd_data)
ibd_data$ibd # refined IBD output
ibd_data$res # count number of IBD for each SNP location
# plot count of IBD in chromosome 3
plot(ibd_data,y = c("cases","cont1"),ly = FALSE)
# Further investigate location between 117M and 122M
# significant number of IBD's in group cases, compare to cont1, cont2 and cont3.
plot(ibd_data,y = c("cases","cont1"),snp_start = 119026294,snp_end = 120613594,ly = FALSE)
model_fisher <- gwid::fisher_test(ibd_data,case_control,reference = "cases",
snp_start = 119026294,snp_end = 120613594)
class(model_fisher)
plot(model_fisher, y = c("cases","cont1"),ly = FALSE)
hap_str <- gwid::haplotype_structure(ibd_data,phase = haplotype_data,w = 10,
snp_start = 119026294,snp_end = 120613594)
haplo_freq <- gwid::haplotype_frequency(hap_str)
plot(haplo_freq,y = c("cases", "cont1"),plot_type = "haplotype_structure_frequency",
nwin = 1, type = "version1",ly = FALSE)

```

roh

*runs of homozygosity*

## Description

runs of homozygosity

**Usage**

```
roh(phase, ...)
```

**Arguments**

```
phase      object of phase
...        other variables
```

**Value**

runs of homozygosity data table or matrix

---

roh.phase	<i>runs of homozygosity</i>
-----------	-----------------------------

---

**Description**

runs of homozygosity

**Usage**

```
## S3 method for class 'phase'
roh(
  phase,
  gwas,
  w = 10,
  fun = c("sum", "mean"),
  snp_start,
  snp_end,
  roh_mat = FALSE,
  ...
)
```

**Arguments**

```
phase      An object of class phase. Output of build_phase function
gwas       object of class gwas
w          window size
fun        an aggregate function. either "sum" or "mean"
snp_start  select starting position of snps.
snp_end    select ending position of snps.
roh_mat    return roh as matrix
...        other variables
```

**Value**

the output will be a result\_snps (data.table) object including 3 columns including, “snps\_pos”, “case\_control”, and “value”

---

subset	<i>subset an object</i>
--------	-------------------------

---

**Description**

subset an object

**Usage**

```
subset(obj, ...)
```

**Arguments**

obj	object
...	other variables

**Value**

the output will be a object(list) of class gwid contains profile object and result\_snps object.

---

subset.gwid	<i>subset gwid object based on snp position</i>
-------------	---

---

**Description**

subset gwid object based on snp position

**Usage**

```
## S3 method for class 'gwid'
subset(obj, snp_start, snp_end, ...)
```

**Arguments**

obj	object of class gwid(output of function build_gwid)
snp_start	select starting position of snp, which we want to aggregate.
snp_end	select ending position of snp, which we want to aggregate.
...	other variables

**Value**

the output will be a object(list) of class gwid contains profile object and result\_snps object.

**Examples**

```

piggyback::pb_download(repo = "soroshmdg/gwid",tag = "v0.0.1",dest = tempdir())
ibd_data_file <- paste0(tempdir(),"//chr3.ibd")
genome_data_file <- paste0(tempdir(),"//chr3.gds")
phase_data_file <- paste0(tempdir(),"//chr3.vcf")
case_control_data_file <- paste0(tempdir(),"//case-cont-RA.withmap.Rda")
# case-control data
case_control <- gwid::case_control(case_control_rda = case_control_data_file)
names(case_control) #cases and controls group
summary(case_control) # in here, we only consider cases,cont1,cont2,cont3 groups in the study
case_control$cases[1:3] # first three subject names of cases group
# read SNP data (use SNPRelate to convert it to gds) and count number of minor alleles
snp_data_gds <- gwid::build_gwas(gds_data = genome_data_file,
caco = case_control,gwas_generator = TRUE)
class(snp_data_gds)
names(snp_data_gds)
head(snp_data_gds$snps) # it has information about counts of minor alleles in each location.
# read haplotype data (output of beagle)
haplotype_data <- gwid::build_phase(phased_vcf = phase_data_file,caco = case_control)
class(haplotype_data)
names(haplotype_data)
dim(haplotype_data$Hap.1) #22302 SNP and 1911 subjects
# read IBD data (output of Refined-IBD)
ibd_data <- gwid::build_gwid(ibd_data = ibd_data_file,gwas = snp_data_gds)
class(ibd_data)
ibd_data$ibd # refined IBD output
ibd_data$res # count number of IBD for each SNP location
# plot count of IBD in chromosome 3
plot(ibd_data,y = c("cases","cont1"),ly = FALSE)
# Further investigate location between 117M and 122M
# significant number of IBD's in group cases, compare to cont1, cont2 and cont3.
plot(ibd_data,y = c("cases","cont1"),snp_start = 119026294,snp_end = 120613594,ly = FALSE)
model_fisher <- gwid::fisher_test(ibd_data,case_control,reference = "cases",
snp_start = 119026294,snp_end = 120613594)
class(model_fisher)
plot(model_fisher, y = c("cases","cont1"),ly = FALSE)
hap_str <- gwid::haplotype_structure(ibd_data,phase = haplotype_data,w = 10,
snp_start = 119026294,snp_end = 120613594)
haplo_freq <- gwid::haplotype_frequency(hap_str)
plot(haplo_freq,y = c("cases", "cont1"),plot_type = "haplotype_structure_frequency",
nwin = 1, type = "version1",ly = FALSE)

```

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