

# Package ‘martini’

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**Type** Package

**Title** GWAS Incorporating Networks

**Version** 1.14.0

**Description** martini deals with the low power inherent to GWAS studies by using prior knowledge represented as a network. SNPs are the vertices of the network, and the edges represent biological relationships between them (genomic adjacency, belonging to the same gene, physical interaction between protein products). The network is scanned using SConES, which looks for groups of SNPs maximally associated with the phenotype, that form a close subnetwork.

**License** GPL-3

**LazyData** TRUE

**Imports** igraph (>= 1.0.1), Matrix, methods (>= 3.3.2), Rcpp (>= 0.12.8), snpStats (>= 1.20.0), stats, utils,

**Suggests** biomaRt (>= 2.34.1), circlize (>= 0.4.11), STRINGdb (>= 2.2.0), httr (>= 1.2.1), IRanges (>= 2.8.2), S4Vectors (>= 0.12.2), memoise (>= 2.0.0), knitr, testthat, readr, rmarkdown

**Depends** R (>= 4.0)

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**BugReports** <https://github.com/hclimente/martini/issues>

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get_GI_network	<i>Get gene-interaction network.</i>
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### Description

Creates a network of SNPs where each SNP is connected as in the **GM** network and, in addition, to all the other SNPs pertaining to any interactor of the gene it is mapped to. Corresponds to the gene-interaction (GI) network described by Azencott et al.

**Usage**

```
get_GI_network(  
  gwas,  
  organism = 9606,  
  snpMapping = snp2ensembl(gwas, organism),  
  ppi = get_gxg("biogrid", organism, flush),  
  col_ppi = c("gene1", "gene2"),  
  col_genes = c("snp", "gene"),  
  flush = FALSE  
)
```

**Arguments**

gwas	A SnpMatrix object with the GWAS information.
organism	Tax ID of the studied organism. The default is 9606 (human).
snpMapping	A data.frame informing how SNPs map to genes. It contains minimum two columns: SNP id and a gene it maps to. Each row corresponds to one gene-SNP mapping. Unless column names are specified using col_genes, involved columns must be named 'snp' and 'gene'.
ppi	A data.frame describing protein-protein interactions with at least two columns. Gene ids must be the contained in snpMapping. Unless column names are specified using col_ppi, involved columns must be named gene1 and gene2.
col_ppi	Optional, length-2 character vector with the names of the two columns involving the protein-protein interactions.
col_genes	Optional, length-2 character vector with the names of the two columns involving the SNP-gene mapping. The first element is the column of the SNP, and the second is the column of the gene.
flush	Remove cached results? Boolean value.

**Value**

An igraph network of the GI network of the SNPs.

**References**

Azencott, C. A., Grimm, D., Sugiyama, M., Kawahara, Y., & Borgwardt, K. M. (2013). Efficient network-guided multi-locus association mapping with graph cuts. *Bioinformatics*, 29(13), 171-179. <https://doi.org/10.1093/bioinformatics/btt238>

**Examples**

```
get_GI_network(minigwas, snpMapping = minisnpMapping, ppi = minippi)
```

---

get_GM_network	<i>Get gene membership network.</i>
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---

### Description

Creates a network of SNPs where each SNP is connected as in the [GS](#) network and, in addition, to all the other SNPs pertaining to the same gene. Corresponds to the gene membership (GM) network described by Azencott et al.

### Usage

```
get_GM_network(  
  gwas,  
  organism = 9606,  
  snpMapping = snp2ensembl(gwas, organism),  
  col_genes = c("snp", "gene")  
)
```

### Arguments

gwas	A SnpMatrix object with the GWAS information.
organism	Tax ID of the studied organism. The default is 9606 (human).
snpMapping	A data.frame informing how SNPs map to genes. It contains minimum two columns: SNP id and a gene it maps to. Each row corresponds to one gene-SNP mapping. Unless column names are specified using col_genes, involved columns must be named 'snp' and 'gene'.
col_genes	Optional, length-2 character vector with the names of the two columns involving the SNP-gene mapping. The first element is the column of the SNP, and the second is the column of the gene.

### Value

An igraph network of the GM network of the SNPs.

### References

Azencott, C. A., Grimm, D., Sugiyama, M., Kawahara, Y., & Borgwardt, K. M. (2013). Efficient network-guided multi-locus association mapping with graph cuts. *Bioinformatics*, 29(13), 171-179. <https://doi.org/10.1093/bioinformatics/btt238>

### Examples

```
get_GM_network(minigwas, snpMapping = minisnpMapping)
```

---

get_GS_network	<i>Get genomic sequence network</i>
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**Description**

Creates a network of SNPs where each SNP is connected to its adjacent SNPs in the genome sequence. Corresponds to the genomic sequence (GS) network described by Azencott et al.

**Usage**

```
get_GS_network(gwas)
```

**Arguments**

`gwas` A SnpMatrix object with the GWAS information.

**Value**

An igraph network of the GS network of the SNPs.

**References**

Azencott, C. A., Grimm, D., Sugiyama, M., Kawahara, Y., & Borgwardt, K. M. (2013). Efficient network-guided multi-locus association mapping with graph cuts. *Bioinformatics*, 29(13), 171-179. <https://doi.org/10.1093/bioinformatics/btt238>

**Examples**

```
get_GS_network(minigwas)
```

---

gwas2bed	<i>Converts a MAP data.frame to a BED data.frame</i>
----------	--

---

**Description**

Takes a map file and:

- column 1: Used as the chromosome column in the BED file.
- column 4: Used as start and end in the BED data.frame (as we work with SNPs).

**Usage**

```
gwas2bed(gwas)
```

**Arguments**

`gwas` A SnpMatrix object with the GWAS information.

**Value**

A BED data.frame.

---

ldweight_edges	<i>Include linkage disequilibrium information in the network.</i>
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**Description**

Include linkage disequilibrium information in the SNP network. The weight of the edges will be lower the higher the linkage is.

**Usage**

```
ldweight_edges(net, ld, method = "inverse")
```

**Arguments**

net	A SNP network.
ld	A dsCMatrix or dgCMatrix containing linkage disequilibrium measures, like the output of <a href="#">ld</a> .
method	How to incorporate linkage-disequilibrium values into the network.

**Value**

An copy of net where the edges weighted according to linkage disequilibrium.

**Examples**

```
ld <- snpStats::ld(minigwas[['genotypes']], depth = 2, stats = "R.squared")
# don't weight edges for which LD cannot be calculated
ld[is.na(ld)] <- 0
gi <- get_GI_network(minigwas, snpMapping = minisnpMapping, ppi = minippi)
ldGi <- ldweight_edges(gi, ld)
```

---

maxflow	<i>Maxflow algorithm</i>
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---

**Description**

Run the maxflow algorithm.

**Usage**

```
maxflow(A, As, At)
```

**Arguments**

A	A sparse matrix with the connectivity.
As	A vector containing the edges to the source.
At	A vector containing the edges to the sink.

**Value**

A list with vector indicating if the feature was selected and the objective score.

---

mincut_c	<i>Min-cut algorithm</i>
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**Description**

Run the mincut algorithm.

**Usage**

```
mincut_c(c, eta, lambda, W)
```

**Arguments**

c	A vector with the association of each SNP with the phenotype.
eta	A numeric with the value of the eta parameter.
lambda	A numeric with the value of the eta parameter.
W	A sparse matrix with the connectivity.

**Value**

A list with vector indicating if the feature was selected and the objective score.

---

minigwas	<i>Description of the minigwas dataset.</i>
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---

**Description**

Small GWAS example.

**Format**

A list with 3 items:

- genotypes** Genotype and phenotype information.
- fam** Simulated network.
- map** Result of running find\_cones with gwas and net.

**Examples**

```
data(minigwas)

# access different elements
minigwas[["genotypes"]]
minigwas[["map"]]
minigwas[["fam"]]
```

---

minippi	<i>PPIs for the minigwas dataset.</i>
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---

**Description**

data.frame describing pairs of proteins that interact for minigwas.

**Examples**

```
data(minippi)

head(minippi)
```

---

minisnpMapping	<i>Genes for the minigwas dataset.</i>
----------------	--

---

**Description**

data.frame that maps SNPs from minigwas to their gene.

**Examples**

```
data(minisnpMapping)

head(minisnpMapping)
```



---

plot\_ideogram                      *Ideogram of SConES results.*

---

### Description

Create a circular ideogram of the a network results using the circlize package (Gu et al., 2014).

### Usage

```
plot_ideogram(gwas, net, covars = data.frame(), genome = "hg19")
```

### Arguments

gwas	A SnpMatrix object with the GWAS information.
net	An igraph network that connects the SNPs.
covars	A data frame with the covariates. It must contain a column 'sample' containing the sample IDs, and an additional columns for each covariate.
genome	Abbreviations of the genome to use: hg19 for human (default), mm10 for mouse, etc.

### Value

A circular ideogram, including the manhattan plot, and the interactions between the selected SNPs.

### References

Gu, Z., Gu, L., Eils, R., Schlesner, M., & Brors, B. (2014). circlize Implements and enhances circular visualization in R. *Bioinformatics* (Oxford, England), 30(19), 2811-2. <https://doi.org/10.1093/bioinformatics/btu393>

---

scones                                      *Find connected explanatory SNPs*

---

### Description

Finds the SNPs maximally associated with a phenotype while being connected in an underlying network.

**Usage**

```
scones(
  gwas,
  net,
  eta,
  lambda,
  covars = data.frame(),
  score = c("chi2", "glm", "r2"),
  family = c("binomial", "poisson", "gaussian", "gamma"),
  link = c("logit", "log", "identity", "inverse")
)
```

**Arguments**

gwas	A SnpMatrix object with the GWAS information.
net	An igraph network that connects the SNPs.
eta	Value of the eta parameter.
lambda	Value of the lambda parameter.
covars	A data frame with the covariates. It must contain a column 'sample' containing the sample IDs, and an additional columns for each covariate.
score	Association score to measure association between genotype and phenotype. Possible values: chi2 (default), glm.
family	A string defining the generalized linear model family. This should match one of "binomial", "poisson", "gaussian" or "gamma". See <a href="#">snp.rhs.tests</a> for details.
link	A string defining the link function for the GLM. This should match one of "logit", "log", "identity" or "inverse". See <a href="#">snp.rhs.tests</a> for details.

**Value**

A copy of the SnpMatrix\$map data.frame, with the following additions:

- c: contains the univariate association score for every single SNP.
- selected: logical vector indicating if the SNP was selected by SConES or not.
- module: integer with the number of the module the SNP belongs to.

**References**

Azencott, C. A., Grimm, D., Sugiyama, M., Kawahara, Y., & Borgwardt, K. M. (2013). Efficient network-guided multi-locus association mapping with graph cuts. *Bioinformatics*, 29(13), 171-179. <https://doi.org/10.1093/bioinformatics/btt238>

**Examples**

```
gi <- get_GI_network(minigwas, snpMapping = minisnpMapping, ppi = minippi)
scones(minigwas, gi, 10, 1)
```

scones.cv

*Find connected explanatory SNPs.***Description**

Finds the SNPs maximally associated with a phenotype while being connected in an underlying network. Select the hyperparameters by cross-validation.

**Usage**

```
scones.cv(
  gwas,
  net,
  covars = data.frame(),
  score = c("chi2", "glm", "r2"),
  criterion = c("stability", "bic", "aic", "aicc", "global_clustering",
    "local_clustering"),
  etas = numeric(),
  lambdas = numeric(),
  family = c("binomial", "poisson", "gaussian", "gamma"),
  link = c("logit", "log", "identity", "inverse")
)
```

**Arguments**

gwas	A SnpMatrix object with the GWAS information.
net	An igraph network that connects the SNPs.
covars	A data frame with the covariates. It must contain a column 'sample' containing the sample IDs, and an additional columns for each covariate.
score	Association score to measure association between genotype and phenotype. Possible values: chi2 (default), glm.
criterion	String with the function to measure the quality of a split.
etas	Numeric vector with the etas to explore in the grid search. If omitted, it's automatically created based on the association scores.
lambdas	Numeric vector with the lambdas to explore in the grid search. If omitted, it's automatically created based on the association scores.
family	A string defining the generalized linear model family. This should match one of "binomial", "poisson", "gaussian" or "gamma". See <a href="#">snp.rhs.tests</a> for details.
link	A string defining the link function for the GLM. This should match one of "logit", "log", "identity" or "inverse". See <a href="#">snp.rhs.tests</a> for details.

**Value**

A copy of the `SnpMatrix$map` data.frame, with the following additions:

- `c`: contains the univariate association score for every single SNP.
- `selected`: logical vector indicating if the SNP was selected by SConES or not.
- `module`: integer with the number of the module the SNP belongs to.

**References**

Azencott, C. A., Grimm, D., Sugiyama, M., Kawahara, Y., & Borgwardt, K. M. (2013). Efficient network-guided multi-locus association mapping with graph cuts. *Bioinformatics*, 29(13), 171-179. <https://doi.org/10.1093/bioinformatics/btt238>

**Examples**

```
gi <- get_GI_network(minigwas, snpMapping = minisnpMapping, ppi = minippi)
scones.cv(minigwas, gi)
scones.cv(minigwas, gi, score = "glm")
```

---

scones.cv\_

*Find connected explanatory features*

---

**Description**

Finds the features maximally associated with a phenotype while being connected in an underlying network. Select the hyperparameters by cross-validation.

**Usage**

```
scones.cv_(X, y, featnames, net)
```

**Arguments**

<code>X</code>	n x d design matrix
<code>y</code>	Vector of length n with the outcomes
<code>featnames</code>	Vector of length d with the feature names
<code>net</code>	An igraph network that connects the SNPs.

**Value**

A copy of the `SnpMatrix$map` data.frame, with the following additions:

- `c`: contains the univariate association score for every single SNP.
- `selected`: logical vector indicating if the SNP was selected by SConES or not.
- `module`: integer with the number of the module the SNP belongs to.

**Examples**

```
X <- as(minigwas[['genotypes']], 'numeric')
X <- X + matrix(rnorm(2500, sd = 0.1), nrow(X), ncol(X))
gi <- get_GI_network(minigwas, snpMapping = minisnpMapping, ppi = minippi)
scones.cv_(X, minigwas[['fam']]$affected, minigwas[['map']]$snp, gi)
```

scones\_

*Find connected explanatory features***Description**

Finds the features maximally associated with a phenotype while being connected in an underlying network.

**Usage**

```
scones_(X, y, featnames, net, eta, lambda)
```

**Arguments**

X	n x d design matrix
y	Vector of length n with the outcomes
featnames	Vector of length d with the feature names
net	An igraph network that connects the SNPs.
eta	Value of the eta parameter.
lambda	Value of the lambda parameter.

**Value**

A copy of the `SnpMatrix`\$map data.frame, with the following additions:

- c: contains the univariate association score for every single SNP.
- selected: logical vector indicating if the SNP was selected by SConES or not.
- module: integer with the number of the module the SNP belongs to.

**Examples**

```
X <- as(minigwas[['genotypes']], 'numeric')
X <- X + matrix(rnorm(2500, sd = 0.1), nrow(X), ncol(X))
gi <- get_GI_network(minigwas, snpMapping = minisnpMapping, ppi = minippi)
scones_(X, minigwas[['fam']]$affected, minigwas[['map']]$snp, gi, 10, 1)
```

---

search_cones	<i>Find connected explanatory SNPs.</i>
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---

### Description

Finds the SNPs maximally associated with a phenotype while being connected in an underlying network (Azencott et al., 2013).

### Usage

```
search_cones(
  gwas,
  net,
  encoding = "additive",
  sigmod = FALSE,
  covars = data.frame(),
  associationScore = c("chi2", "glm"),
  modelScore = c("stability", "bic", "aic", "aicc", "global_clustering",
    "local_clustering"),
  etas = numeric(),
  lambdas = numeric()
)
```

### Arguments

<code>gwas</code>	A SnpMatrix object with the GWAS information.
<code>net</code>	An igraph network that connects the SNPs.
<code>encoding</code>	SNP encoding (unused argument).
<code>sigmod</code>	Boolean. If TRUE, use the Sigmod variant of SConES, meant to prioritize tightly connected clusters of SNPs.
<code>covars</code>	A data frame with the covariates. It must contain a column 'sample' containing the sample IDs, and an additional columns for each covariate.
<code>associationScore</code>	Association score to measure association between genotype and phenotype.
<code>modelScore</code>	String with the function to measure the quality of a split.
<code>etas</code>	Numeric vector with the etas to explore in the grid search. If omitted, it's automatically created based on the association scores.
<code>lambdas</code>	Numeric vector with the lambdas to explore in the grid search. If omitted, it's automatically created based on the association scores.

### Value

A copy of the SnpMatrix\$map data.frame, with the following additions:

- `c`: contains the univariate association score for every single SNP.
- `selected`: logical vector indicating if the SNP was selected by SConES or not.
- `module`: integer with the number of the module the SNP belongs to.

## References

Azencott, C. A., Grimm, D., Sugiyama, M., Kawahara, Y., & Borgwardt, K. M. (2013). Efficient network-guided multi-locus association mapping with graph cuts. *Bioinformatics*, 29(13), 171-179. <https://doi.org/10.1093/bioinformatics/btt238>

## Examples

```
## Not run: gi <- get_GI_network(minigwas, snpMapping = minisnpMapping, ppi = minippi)
search_cones(minigwas, gi)
search_cones(minigwas, gi, encoding = "recessive")
search_cones(minigwas, gi, associationScore = "skat")
## End(Not run)
```

---

sigmod

*Find connected explanatory SNPs*


---

## Description

Finds the SNPs maximally associated with a phenotype while being connected in an underlying network.

## Usage

```
sigmod(
  gwas,
  net,
  eta,
  lambda,
  covars = data.frame(),
  score = c("chi2", "glm", "r2"),
  family = c("binomial", "poisson", "gaussian", "gamma"),
  link = c("logit", "log", "identity", "inverse")
)
```

## Arguments

gwas	A SnpMatrix object with the GWAS information.
net	An igraph network that connects the SNPs.
eta	Value of the eta parameter.
lambda	Value of the lambda parameter.
covars	A data frame with the covariates. It must contain a column 'sample' containing the sample IDs, and an additional columns for each covariate.
score	Association score to measure association between genotype and phenotype. Possible values: chi2 (default), glm.
family	A string defining the generalized linear model family. This should match one of "binomial", "poisson", "gaussian" or "gamma". See <a href="#">snp.rhs.tests</a> for details.

link            A string defining the link function for the GLM. This should match one of "logit", "log", "identity" or "inverse". See [snp.rhs.tests](#) for details.

### Value

A copy of the `SnpMatrix$map` data.frame, with the following additions:

- `c`: contains the univariate association score for every single SNP.
- `selected`: logical vector indicating if the SNP was selected by SConES or not.
- `module`: integer with the number of the module the SNP belongs to.

### References

Liu, Y., Brossard, M., Roqueiro, D., Margaritte-Jeannin, P., Sarnowski, C., Bouzigon, E., Demenais, F. (2017). SigMod: an exact and efficient method to identify a strongly interconnected disease-associated module in a gene network. *Bioinformatics*, 33(10), 1536–1544. <https://doi.org/10.1093/bioinformatics/btx004>

### Examples

```
gi <- get_GI_network(minigwas, snpMapping = minisnpMapping, ppi = minippi)
sigmod(minigwas, gi, 10, 1)
```

---

sigmod.cv

*Find connected explanatory SNPs.*

---

### Description

Finds the SNPs maximally associated with a phenotype while being connected in an underlying network. Select the hyperparameters by cross-validation.

### Usage

```
sigmod.cv(
  gwas,
  net,
  covars = data.frame(),
  score = c("chi2", "glm", "r2"),
  criterion = c("stability", "bic", "aic", "aicc", "global_clustering",
    "local_clustering"),
  etas = numeric(),
  lambdas = numeric(),
  family = c("binomial", "poisson", "gaussian", "gamma"),
  link = c("logit", "log", "identity", "inverse")
)
```



**Arguments**

<code>gwas</code>	A <code>SnpMatrix</code> object with the GWAS information.
<code>net</code>	An <code>igraph</code> network that connects the SNPs.
<code>covars</code>	A data frame with the covariates. It must contain a column 'sample' containing the sample IDs, and an additional columns for each covariate.
<code>score</code>	Association score to measure association between genotype and phenotype. Possible values: <code>chi2</code> (default), <code>glm</code> .
<code>criterion</code>	String with the function to measure the quality of a split.
<code>etas</code>	Numeric vector with the <code>etas</code> to explore in the grid search. If omitted, it's automatically created based on the association scores.
<code>lambdas</code>	Numeric vector with the <code>lambdas</code> to explore in the grid search. If omitted, it's automatically created based on the association scores.
<code>family</code>	A string defining the generalized linear model family. This should match one of "binomial", "poisson", "gaussian" or "gamma". See <a href="#">snp.rhs.tests</a> for details.
<code>link</code>	A string defining the link function for the GLM. This should match one of "logit", "log", "identity" or "inverse". See <a href="#">snp.rhs.tests</a> for details.

**Value**

A copy of the `SnpMatrix$map` data frame, with the following additions:

- `c`: contains the univariate association score for every single SNP.
- `selected`: logical vector indicating if the SNP was selected by SConES or not.
- `module`: integer with the number of the module the SNP belongs to.

**References**

Liu, Y., Brossard, M., Roqueiro, D., Margaritte-Jeannin, P., Sarnowski, C., Bouzigon, E., Demenais, F. (2017). SigMod: an exact and efficient method to identify a strongly interconnected disease-associated module in a gene network. *Bioinformatics*, 33(10), 1536–1544. <https://doi.org/10.1093/bioinformatics/btx004>

**Examples**

```
gi <- get_GI_network(minigwas, snpMapping = minisnpMapping, ppi = minippi)
sigmod.cv(minigwas, gi)
sigmod.cv(minigwas, gi, score = "glm")
```

---

sigmod.cv\_ *Find connected explanatory features*

---

### Description

Finds the features maximally associated with a phenotype while being connected in an underlying network. Select the hyperparameters by cross-validation.

### Usage

```
sigmod.cv_(X, y, featnames, net)
```

### Arguments

X	n x d design matrix
y	Vector of length n with the outcomes
featnames	Vector of length d with the feature names
net	An igraph network that connects the SNPs.

### Value

A copy of the `SnpMatrix$map` data.frame, with the following additions:

- `c`: contains the univariate association score for every single SNP.
- `selected`: logical vector indicating if the SNP was selected by SConES or not.
- `module`: integer with the number of the module the SNP belongs to.

### Examples

```
X <- as(minigwas[['genotypes']], 'numeric')
X <- X + matrix(rnorm(2500, sd = 0.1), nrow(X), ncol(X))
gi <- get_GI_network(minigwas, snpMapping = minisnpMapping, ppi = minippi)
sigmod.cv_(X, minigwas[['fam']]$affected, minigwas[['map']]$snp, gi)
```

---

sigmod\_ *Find connected explanatory features*

---

### Description

Finds the features maximally associated with a phenotype while being connected in an underlying network.

### Usage

```
sigmod_(X, y, featnames, net, eta, lambda)
```

**Arguments**

<code>X</code>	n x d design matrix
<code>y</code>	Vector of length n with the outcomes
<code>featnames</code>	Vector of length d with the feature names
<code>net</code>	An igraph network that connects the SNPs.
<code>eta</code>	Value of the eta parameter.
<code>lambda</code>	Value of the lambda parameter.

**Value**

A copy of the `SnpMatrix$map` data.frame, with the following additions:

- `c`: contains the univariate association score for every single SNP.
- `selected`: logical vector indicating if the SNP was selected by SConES or not.
- `module`: integer with the number of the module the SNP belongs to.

**Examples**

```
X <- as(minigwas[['genotypes']], 'numeric')
X <- X + matrix(rnorm(2500, sd = 0.1), nrow(X), ncol(X))
gi <- get_GI_network(minigwas, snpMapping = minisnpMapping, ppi = minippi)
sigmod(X, minigwas[['fam']]$affected, minigwas[['map']]$snp, gi, 10, 1)
```

---

simulate\_causal\_snps    *Simulate causal SNPs*

---

**Description**

Selects randomly interconnected genes as causal, then selects a proportion of them as causal.

**Usage**

```
simulate_causal_snps(net, ngenes = 20, pcausal = 1)
```

**Arguments**

<code>net</code>	An igraph gene-interaction (GI) network that connects the SNPs.
<code>ngenes</code>	Number of causal genes.
<code>pcausal</code>	Number between 0 and 1, proportion of the SNPs in causal genes that are causal themselves.

**Value**

A vector with the ids of the simulated causal SNPs.

**Examples**

```
gi <- get_GI_network(minigwas, snpMapping = minisnpMapping, ppi = minippi)
simulate_causal_snps(gi, ngenes=2)
```

---

simulate\_phenotype      *Simulate phenotype*

---

**Description**

Simulates a phenotype from a GWAS experiment and a specified set of causal SNPs. If the data is qualitative, only controls are used.

**Usage**

```
simulate_phenotype(
  gwas,
  snps,
  h2,
  model = "additive",
  effectSize = rnorm(length(snps)),
  qualitative = FALSE,
  ncases,
  ncontrols,
  prevalence
)
```

**Arguments**

gwas	A SnpMatrix object with the GWAS information.
snps	Character vector with the SNP ids of the causal SNPs. Must match SNPs in <code>gwas[["map"]][["snp.name"]]</code> .
h2	Heritability of the phenotype (between 0 and 1).
model	String specifying the genetic model under the phenotype. Accepted values: "additive".
effectSize	Numeric vector with the same length as the number of causal SNPs. It indicates the effect size of each of the SNPs; if absent, they are sampled from a normal distribution.
qualitative	Bool indicating if the phenotype is qualitative or not (quantitative).
ncases	Integer specifying the number of cases to simulate in a qualitative phenotype. Required if <code>qualitative = TRUE</code> .
ncontrols	Integer specifying the number of controls to simulate in a qualitative phenotype. Required if <code>qualitative = TRUE</code> .
prevalence	Value between 0 and 1 specifying the population prevalence of the disease. Note that <code>ncases</code> cannot be greater than <code>prevalence * number of samples</code> . Required if <code>qualitative = TRUE</code> .

**Value**

A copy of the GWAS experiment with the new phenotypes in `gwas[["fam"]][["affected"]]`.

**References**

Inspired from GCTA simulation tool: <http://cnsgenomics.com/software/gcta/Simu.html>.

**Examples**

```
gi <- get_GI_network(minigwas, snpMapping = minisnpMapping, ppi = minippi)
causal <- simulate_causal_snps(gi, ngenes = 2)
simulate_phenotype(minigwas, causal, h2 = 1)
```

---

subvert	<i>Vertices with an attribute</i>
---------	-----------------------------------

---

**Description**

Returns the nodes matching some condition.

**Usage**

```
subvert(net, attr, values, affirmative = TRUE)
```

**Arguments**

<code>net</code>	An igraph network.
<code>attr</code>	An attribute of the vertices.
<code>values</code>	Possible values of <code>attr</code>
<code>affirmative</code>	Logical. States if a condition must be its affirmation (e.g. all nodes with gene name "X"), or its negation (all nodes not with gene name "X").

**Value**

The vertices with attribute equal to any of the values in `values`.

**Examples**

```
gi <- get_GI_network(minigwas, snpMapping = minisnpMapping, ppi = minippi)
martini:::subvert(gi, "gene", "A")
martini:::subvert(gi, "name", c("1A1", "1A3"))
```

---

`wrap_Xy`*Make pseudo SnpMatrix object*

---

**Description**

Wrap design matrix and outcome vector into a pseudo SnpMatrix object.

**Usage**

```
wrap_Xy(X, y, featnames, net)
```

**Arguments**

<code>X</code>	n x d design matrix
<code>y</code>	Vector of length n with the outcomes
<code>featnames</code>	Vector of length d with the feature names
<code>net</code>	An igraph network that connects the SNPs.

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