Package 'kangar00'

March 24, 2016

Type Package

Title Kernel Approaches for Nonlinear Genetic Association Regression

Version 0.5

Date 2015-02-04

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Description This package includes methods to extract information on pathways, genes and SNPs from online databases. It provides functions for data preparation and evaluation of genetic influence on a binary outcome using the logistic kernel machine test (LKMT). Three different kernel functions are offered to analize genotype information in this variance component test: A linear kernel, a size-adjusted kernel and a network based kernel.

License GPL-2

Collate 'GWASdata.r'
'pathway.r'
'kernel.r'
'lkmt.r'

Depends R (>= 3.1.0)

Imports methods,
igraph,
biomaRt,
KEGGgraph,
sqldf,
CompQuadForm,
lattice

LazyData true

Suggests knitr,
gputools,
bigmemory,
rmarkdown

VignetteBuilder knitr

NeedsCompilation no

R topics documented:

`kangar00-package` *kangar00 package*

Description

This package includes methods to extract information on pathways, genes and SNPs from online databases and to evaluate these data using the logistic kernel machine test (LKMT) (Liu et al. 2008). We defined SNP sets representing genes and whole pathways using knowledge on gene membership and interaction from the Kyoto Encyclopedia of Genes and Genomes (KEGG) database (Kanehisa et al. 2014). SNPs are mapped to genes via base pair positions of SNPs and transcript start and end points of genes as documented in the Ensemble database (Cunningham et al. 2015).
In the LKMT, we employed the linear kernel (Wu et al. 2010) as well as two more advanced kernels, adjusting for size bias in the number of SNPs and genes in a pathway and incorporating the network structure of genes within the pathway, respectively (Freytag et al. 2012, 2014).
P-values are derived in a variance component test using a moment matching methode (Schaid, 2010) or Davies' algorithm (Davies, 1980).

Details

Package:	kangar00
Type:	Package
Version:	1.0
Date:	2015-02-04
License:	GPL-2
Depends:	methods, igraph, biomaRt, KEGGgraph, sqldf

Author(s)

Juliane Manitz, Stefanie Friedrichs, Patricia Burger, Benjamin Hofner
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References

- Schaid DJ: Genomic similarity and kernel methods I: advancements by building on mathematical and statistical foundations. Hum Hered 2010, 70:109-131.
- Davies R: Algorithm as 155: the distribution of a linear combination of chi-2 random variables. J R Stat Soc Ser C 1980, 29:323-333.
- Wu MC, Kraft P, Epstein MP, Taylor DM, Chanock SJ, Hunter DJ, Lin X: Powerful SNP-Set Analysis for Case-Control Genome-Wide Association Studies. Am J Hum Genet 2010, 86:929-42
- Fiona Cunningham, M. Ridwan Amode, Daniel Barrell et al. Ensembl 2015. Nucleic Acids Research 2015 43 Database issue:D662-D669
- Kanehisa, M., Goto, S., Sato, Y., Kawashima, M., Furumichi, M., and Tanabe, M.; Data, information, knowledge and principle: back to metabolism in KEGG. Nucleic Acids Res. 42, D199-D205 (2014).
- Freytag S, Bickeboeller H, Amos CI, Kneib T, Schlather M: A Novel Kernel for Correcting Size Bias in the Logistic Kernel Machine Test with an Application to Rheumatoid Arthritis. Hum Hered. 2012, 74(2):97-108.
- Freytag S, Manitz J, Schlather M, Kneib T, Amos CI, Risch A, Chang-Claude J, Heinrich J, Bickeboeller H: A network-based kernel machine test for the identification of risk pathways in genome-wide association studies. Hum Hered. 2013, 76(2):64-75.
- Liu D, Ghosh D, Lin X. Estimation and testing for the effect of a genetic pathway on a disease outcome using logistic kernel machine regression via logistic mixed models. BMC Bioinformatics. 2008 9:292.

`calc_kernel,GWASdata-method`

Calculates teh kernel-matrix for a pathway

Description

Uses individuals' genotypes to calculate a kernel-matrix for a specific pathway. Each numeric value within this matrix is calculated from two individuals' genotypevectors of the SNPs within the pathway by a kernelfunction. It can be interpreted as the genetic similiarity of the individuals. Association between the pathway and a binary phenotype (case-control status) can be evaluated in the logistic kernel machine test, based on the kernelmatrix. Three kernel functions are available.

Usage

```
## S4 method for signature GWASdata
calc_kernel(object, pathway, knots = NULL,
  type = c("lin", "sia", "net"), parallel = c("none", "cpu", "gpu"), ...)

## S4 method for signature GWASdata
lin_kernel(object, pathway, knots = NULL,
  parallel = c("none", "cpu", "gpu"), ...)

## S4 method for signature GWASdata
sia_kernel(object, pathway, knots = NULL,
  parallel = c("none", "cpu", "gpu"), ...)

## S4 method for signature GWASdata
net_kernel(object, pathway, knots = NULL,
  parallel = c("none", "cpu", "gpu"), ...)
```

Arguments

`object`	`GWASdata` object containing the genotypes of the individuals for which a kernel will be calculated.
`pathway`	object of the class `pathway` specifying the SNP set for which a kernel will be calculated.
`knots`	`GWASdata` object, if specified a low-rank kernel will be computed
`type`	`character` indicating the kernel type: Use `"lin"` for linear kernel, `"sia"` for size-adjusted or `"net"` for network-based kernel.
`parallel`	`character` specifying if the kernel matrix is computed in parallel: Use `"none"` for non-parallel calculation on CPU. (other options not yet implemented)
`...`	further arguments to be passed to the kernel computations

Details

Different types of kernels can be constructed:

- `type=lin` creates the linear kernel assuming additive SNP effects to be evaluated in the logistic kernel machine test.
- `type=sia` calculates the size-adjusted kernel which takes into consideration the numbers of SNPs and genes in a pathway to correct for size bias.
- `type=net` calculates the network-based kernel. Here not only information on gene membership and gene/pathway size in number of SNPs is incorporated, but also the interaction structure of genes in the pathway.

For more details, check the references.

Value

Returns an object of class `kernel`, including the similarity matrix of the pathway for the considered individuals.
If `knots` are specified low-rank kernel of class `lowrank_kernel` will be returned, which is not necessarily quadratic and symmetric.

Methods (by class)

- GWASdata:
- GWASdata:
- GWASdata:

Author(s)

Stefanie Friedrichs, Juliane Manitz, Saskia Freytag, Ngoc Thuy Ha

References

- Wu MC, Kraft P, Epstein MP, Taylor DM, Chanock SJ, Hunter DJ, Lin X Powerful SNP-Set Analysis for Case-Control Genome-Wide Association Studies. Am J Hum Genet 2010, 86:929-42
- Freytag S, Bickeboeller H, Amos CI, Kneib T, Schlather M: A Novel Kernel for Correcting Size Bias in the Logistic Kernel Machine Test with an Application to Rheumatoid Arthritis. Hum Hered. 2012, 74(2):97-108.
- Freytag S, Manitz J, Schlather M, Kneib T, Amos CI, Risch A, Chang-Claude J, Heinrich J, Bickeboeller H: A network-based kernel machine test for the identification of risk pathways in genome-wide association studies. Hum Hered. 2013, 76(2):64-75.

See Also

kernel-class, GWASdata-class, pathway-class

Examples

```
data(gwas)
data(hsa04020)
K.net  <- calc_kernel(gwas, hsa04020, knots = NULL, type=net, parallel=none)
```

---

get_anno,snp_info,pathway_info-method

Annotates SNPs via genes to pathways

Description

A function to create the annotation for a GWASdata object. It combines a snp_info and a pathway_info object into an annotation data.frame used for pathway analysis on GWAS. SNPs are assigned to pathways via gene membership.

Usage

```
## S4 method for signature snp_info,pathway_info
get_anno(object1, object2, ...)
```

Arguments

object1	A snp_info object with SNP information as returned by the snp_info function. The included data frame contains the columns "chr", "position" and "rsnumber".
object2	A pathway_info object with information on genes contained in pathways. It is created by the pathway_info function and contains a data frame with columns "pathway", "gene_start", gene_end", "chr", "gene".
...	further arguments can be added.

Value

A data.frame including mapping SNPs to genes and genes to pathways. It includes the columns "pathway", "gene", "chr", "snp" and "position".

Author(s)

Stefanie Friedrichs, Saskia Freytag, Ngoc-Thuy Ha

See Also

snp_info, pathway_info

Examples

```
data(hsa04022_info)
data(rs10243170_info)
```

---

get_network_matrix,character-method

Function to calculate the network matrix

Description

This function creates the networkmatrix representing the gene-gene interaction structure within a particular pathway. In this process a KEGG kgml file is downloaded and saved in the working directory.

Usage

```
## S4 method for signature character
get_network_matrix(x, directed, keep.kgml)
```

Arguments

x	A character identifying the pathway for which gene infomation should be extracted. Here KEGG IDs ('hsa00100') are used.
directed	A logic argument, stating whether the networkmatrix should be returned directed (TRUE) or undirected (FALSE).
keep.kgml	A logic argument, specifying whether the downloaded KEGG kgml file of the pathway should be kept in the working directory after calculation of the network matrix. For (FALSE) the file is deleted, for (TRUE) not.

Value

A matrix representing the interaction network in the pathway.

Author(s)

Stefanie Friedrichs

GWASdata *S4 class for an object representing a Genome-wide Assocaition Study.*

Description

S4 class for an object representing a Genome-wide Assocaition Study.

GWASdata is a GWASdata object constructor

show displays basic information on GWASdata object

summary summarizes the content of a GWASdata object and gives an overview about the information included in a GWASdata object. Summary statistics for phenotype and genotype data are calculated.

GeneSNPsize creates a data.frame of pathway names with numbers of snps and genes in each pathway.

Usage

```
GWASdata(object, ...)

## S4 method for signature ANY
GWASdata(geno, anno, pheno = NULL, desc = "")

## S4 method for signature GWASdata
show(object)

## S4 method for signature GWASdata
summary(object)

## S4 method for signature GWASdata
GeneSNPsize(object)
```

Arguments

object	A GWASdata object.

Slots

geno An object of any type, including genotype information. The format needs to be one line per individual and on colum per SNP in minor-allele coding (0,1,2). Other values between 0 and 2, as from impute dosages, are allowed. Missing values must be imputed prior to creation of a GWAS object.

anno A data.frame mapping SNPs to genes and genes to pathways. Needs to include the columns 'pathway' (pathway ID, e.g. hsa number from KEGG database), 'gene' (gene name (hgnc_symbol)), 'chr' (chromosome), 'snp' (rsnumber) and 'position' (base pair position of SNP).

pheno A data.frame specifying individual IDs, phenotypes and covariates to be included in the regression model e.g. ID, pheno, sex, pack.years. Note: IDs have to be in the first column!

desc A character giving the GWAS description, e.g. name of study.

Author(s)

Juliane Manitz, Stefanie Friedrichs

Examples

```
data(pheno)
data(geno)
data(anno)
gwas <- new(GWASdata, pheno=pheno, geno=geno, anno=anno, desc="some study")
# show method
data(gwas)
gwas
# summary method
data(gwas)
summary(gwas)
# SNPs and genes in pathway
data(gwas)
GeneSNPsize(gwas)
```

---

kernel-class *An S4 class representing the kernel of a pathway*

Description

An S4 class representing the kernel of a pathway

show displays the kernel object briefly

summary generates a kernel object summary including the number of individuals and genes for the pathway

plot creates an image plot of a kernel object

Usage

```
## S4 method for signature kernel
show(object)

## S4 method for signature kernel
summary(object)

## S4 method for signature kernel,missing
plot(x, y = NA, hclust = FALSE, ...)
```

Arguments

object	kernel object
y	missing (placeholder)
hclust	logical, indicating whether a dendrogram should be added

Slots

`type` A `character` representing the kernel type: Use `"lin"` for linear kernels, `"sia"` for size-adjusted or `"net"` for network-based kernels.

`kernel` A kernel matrix of dimension equal to the number of individuals

`pathway` A pathway object

Author(s)

Juliane Manitz

---

lkmt *An S4 class to represent the variance component test.*

Description

An S4 class to represent the variance component test.

`show` Shows basic information on `lkmt` object

`summary` Summarizes information on `lkmt` object

Usage

```
lkmt(formula, kernel, GWASdata, method = c("satt", "davies"), ...)

## S4 method for signature lkmt
show(object)

## S4 method for signature lkmt
summary(object)
```

Value

`show` Basic information on `lkmt` object.

`summary` Summarized information on `lkmt` object.

Slots

`formula` A formula stating the regression nullmodel that will be used in the variance component test.

`kernel` An object of class `kernel` representing the similarity matrix of the individuals based on which the pathways influence is evaluated.

`GWASdata` An object of class `GWASdata` including the data on which the test is conducted.

`statistic` A `vector` giving the value of the variance component test statistic.

`df` A `vector` containing the number of degrees of freedom.

`p.value` A `vector` giving the p-value calculated for the pathway in the variance component test. For details on the variance component test see the references.

Author(s)

Juliane Manitz, Stefanie Friedrichs

References

- Liu D, Lin X, Ghosh D: Semiparametric regression of multidimensional genetic pathway data: least-squares kernel machines and linear mixed models. Biometrics 2007, 63(4):1079-88.
- Wu MC, Kraft P, Epstein MP, Taylor DM, Chanock SJ, Hunter DJ, Lin X: Powerful SNP-Set Analysis for Case-Control Genome-Wide Association Studies. Am J Hum Genet 2010, 86:929-42

`lkmt` *A function to calculate the p-values for kernel-matrices.*

Description

A function to calculate the p-values for kernel-matrices.

This function evaluates a pathways influence on an individuals probability of beeing a case using the logistic kernel machine test. P-values are determined using a Sattherthwaite Approximation as described by Dan Schaid.

This function evaluates a pathways influence on an individuals probability of beeing a case using the logistic kernel machine test. P-values are determined using the method described by Davies as implemented in the function `davies()` from package `CompQuadForm`.

Usage

```
lkmt(formula, kernel, GWASdata, method = c("satt", "davies"), ...)

## S4 method for signature matrix
score_test(x1, x2)

## S4 method for signature matrix
davies_test(x1, x2)
```

Arguments

`formula`	The formula to be used for the regression nullmodel.
`kernel`	An object of class `kernel` including the pathway representing kernel-matrix based on which the test statistic will be calculated.
`GWASdata`	A `GWASdata` object stating the data used in analysis.
`method`	A `character` specifying which method will be used for p-value calculation. Available are `satt` for the Satterthwaite approximation and `davies` for Davies' algorithm. For more details see the references.

Value

An `lkmt` object including the following test results

- The formula of the regression nullmodel used in the variance component test.
- An object of class `kernel` including the similarity matrix of the individuals based on which the pathways influence is evaluated.
- An object of class `GWASdata` stating the data on which the test was conducted.

- statistic A `vector` giving the value of the variance component test statistic.
- df A `vector` giving the number of degrees of freedom.
- p.value A `vector` giving the p-value calculated for the pathway in the variance component test.

Author(s)

Stefanie Friedrichs,Juliane Manitz , Saskia Freytag, Ngoc-Thuy Ha

References

For details on the variance component test

- Wu MC, Kraft P, Epstein MP, Taylor DM, Chanock SJ, Hunter DJ, Lin X: Powerful SNP-Set Analysis for Case-Control Genome-Wide Association Studies. Am J Hum Genet 2010, 86:929-42
- Liu D, Lin X, Ghosh D: Semiparametric regression of multidimensional genetic pathway data: least-squares kernel machines and linear mixed models. Biometrics 2007, 63(4):1079-88.

For details on the p-value calculation see

- Schaid DJ: Genomic Similarity and Kernel Methods I: Advancements by Building on Mathematical and Statistical Foundations. Hum Hered 2010, 70:109-31
- Davies R: Algorithm as 155: the distribution of a linear combination of chi-2 random variables. J R Stat Soc Ser C 1980, 29:323-333.

`lowrank_kernel-class` *An S4 class to represent a low-rank kernel for a SNPset at specified knots*

Description

An S4 class to represent a low-rank kernel for a SNPset at specified knots

Details

This kernel is used for predictions. If observations and knots are equal, better construct a full-rank kernel of class `kernel`.

Slots

`type` character, kernel type: Use `"lin"` for linear kernels, `"sia"` for size-adjusted or `"net"` for network-based kernels.

`kernel` kernel matrix of dimension equal to individuals

`pathway` pathway object

Author(s)

Juliane Manitz

`make_psd,matrix-method` *Adjust network matrix to be positive semi-definite*

Description

Adjust network matrix to be positive semi-definite

Usage

```
## S4 method for signature matrix
make_psd(x, eps = sqrt(.Machine$double.eps))
```

Arguments

`x`	A `matrix` specifying the network adjacency matrix.
`eps`	A `numeric` value, setting the tolance for smallest eigenvalue adjustment

Details

For a matrix N, the closest positive semi-definite matrix is calculated as N* = rho*N + (1+rho)*I, where I is the identity matrix and rho = 1/(1 - lambda) with lambda the smallest eigenvalue of N. For more details check the references.

Value

The matrix x, if it is positive definite and the closest positive semi-definite matrix if x is not positive semi-definite.

Author(s)

Juliane Manitz, Saskia Freytag, Stefanie Friedrichs

References

- Freytag S, Manitz J, Schlather M, Kneib T, Amos CI, Risch A, Chang-Claude J, Heinrich J, Bickeboeller H: A network-based kernel machine test for the identification of risk pathways in genome-wide association studies. Hum Hered. 2013, 76(2):64-75.

pathway-class *An S4 class to represent a gene-gene interaction network*

Description

An S4 class to represent a gene-gene interaction network

show displays the pathway object briefly

summary generates a pathway object summary including basic network properties.

pathway2igraph converts a pathway object into an igraph object with edge attribute sign

analyze pathway network properties

get_genes is a helper function that extracts the gene names in a pathway and returns a vector of character containing gene names

plot plots pathway as igraph object

sample_genes function randomly selects effect genes in pathway and returns a vector of length no with vertex id's of sampled genes

Usage

```
## S4 method for signature pathway
show(object)

## S4 method for signature pathway
summary(object)

## S4 method for signature pathway
pathway2igraph(object)

## S4 method for signature pathway
analyze(object, ...)

## S4 method for signature pathway
get_genes(object)

## S4 method for signature pathway,missing
plot(x, y = NA, highlight.genes = NULL,
  gene.names = c("legend", "nodes", NA), main = NULL, asp = 0.95,
  vertex.size = 11, vertex.color = "khaki1", vertex.label.cex = 0.8,
  edge.width = 2, edge.color = "olivedrab4", ...)

## S4 method for signature pathway
sample_genes(object, no = 3)
```

Arguments

object	pathway object
...	further arguments specifying plotting options in plot.igraph
x	pathway object
y	missing (placeholder)

`highlight.genes`
: vector of gene names or node id's, which should be highlighted in a different color, default is `NULL` so that no genes are highlighted

`gene.names`
: character indicating whether the genes names should appear in a legend (`legend`), as vertex label (`nodes`), or should be omitted (`NA`)

`main`
: optional overall main title, default is `NULL`, which uses the pathway id

`asp`
: a numeric constant, which gives the aspect ratio parameter for plot, default is 0.95

`vertex.size`
: a numeric constant specifying the vertex size, default is 11

`vertex.color`
: a character or numeric constant specifying the vertex color, default is 'khaki1'

`vertex.label.cex`
: a numeric constant specifying the the vertex label size, default is 0.8,

`edge.width`
: a numeric constant specifying the edge width, default is 2

`edge.color`
: a character or numeric constant specifying the edge color, default is 'olivedrab4'

`no`
: a numeric constant specifying the number of genes to be sampled, default is 3

`object`
: A pathway object

Value

`analyze` returns a `data.frame` consisting of

id pathway id,

vcount number of genes,

ecount number of links,

inh_ecount number of inhibition links,

density network density,

av_deg average degree,

inh_deg average degree of inhibition links,

diam network diamter,

trans transitivity, and

s_trans signed transitivity (Kunegis et al., 2009).

Slots

`id` A character repesenting the pathway id, e.g. hsa00100 as used in the KEGG database.

`adj` A matrix respresenting the network adjacency matrix of dimension equaling the number of genes (1 interaction, 0 otherwise)

`sign` A numeric vector indicating the interaction type for each link (1 activation, -1 inhibition) in the interaction network for the pathway.

Author(s)

Juliane Manitz

References

Details to the computation and interpretation can be found in:

- Kolaczyk, E. D. (2009). Statistical analysis of network data: methods and models. Springer series in statistics. Springer.
- Kunegis, J., A. Lommatzsch, and C. Bauckhage (2009). The slashdot zoo: Mining a social network with negative egdes. In Proceedings of the 18th international conference on World wide web, pp. 741-750. ACM Press.

Examples

```
#show method
data(hsa04020)
hsa04020
#summary method
data(hsa04020)
summary(hsa04020)
# convert to igraph object
data(hsa04020)
str(hsa04020)
g <- pathway2igraph(hsa04020)
str(g)
data(hsa04020)
summary(hsa04020)
analyze(hsa04020)
# extract gene names from pathway
get_genes(hsa04020)
# plot pathway as igraph object
plot(hsa04020)
sample3 <- sample_genes(hsa04020, no = 3)
plot(hsa04020, highlight.genes = sample3)
# sample effect genes
sample3 <- sample_genes(hsa04020, no = 3)
plot(hsa04020, highlight.genes = sample3)
sample5 <- sample_genes(hsa04020, no = 5)
plot(hsa04020, highlight.genes = sample5)
```

---

pathway_info *An S4 class for an object assigning genes to pathways*

Description

An S4 class for an object assigning genes to pathways

This function lists all genes formig a particular pathway. Start and end positions of these genes are extracted from the Ensemble database. The database is accessed via the R-package `biomaRt`.

`show` Shows basic information on `pathway_info` object

`summary` Summarizes information on `pathway_info` object

Usage

```
pathway_info(x, ...)

## S4 method for signature character
pathway_info(x)

## S4 method for signature pathway_info
show(object)

## S4 method for signature pathway_info
summary(object)
```

Arguments

x	A character identifying the pathway for which gene infomation should be extracted. Here KEGG IDs ('hsa00100') are used.
object	An object of class pathway_info.

Value

A data.frame including as many rows as genes appear in the pathway. for each gene its name, the start and end point and the chromosome it lies on are given.

show Basic information on pathway_info object.

summary Summarized information on pathway_info object.

Slots

info A data.frame including information on genes contained in pathways with columns 'pathway', 'gene_start', 'gene_end', 'chr' and 'gene'.

Author(s)

Stefanie Friedrichs

Stefanie Friedrichs

Examples

```
data(hsa04022_info)
pathway_info("hsa04022")
# show method
data(hsa04022_info)
hsa04022_info
# summary method
data(hsa04022_info)
summary(hsa04022_info)
```

`read_geno,character-method`

read genotype data from file to one of several available objects, which can be passed to a GWASdata object `GWASdata-class`

Description

read genotype data from file to one of several available objects, which can be passed to a GWASdata object `GWASdata-class`

Usage

```
## S4 method for signature character
read_geno(file.path, save.path = NULL, sep = " ",
  header = TRUE, use.fread = TRUE, row.names = TRUE, ...)
```

Arguments

`file.path`	character, which contains the path to the data file to be read
`save.path`	character, which contains the path for the backingfile
`sep`	character. A field delimeter. See `bigmemory::read.big.matrix` for details.
`header`	logical. Does the data set contain column names?
`...`	further arguments to be passed to `bigmemory::read.big.matrix`.

Details

If the data set contains rownames specified, set option `has.row.names = TRUE`.

See Also

`GWASdata-class`

`rewire_network,matrix-method`

Rewires interactions in a pathway, which go through a gene not represented by any SNPs in the considered `GWASdata` *object. (for internal use)*

Description

Rewires interactions in a pathway, which go through a gene not represented by any SNPs in the considered `GWASdata` object. (for internal use)

Usage

```
## S4 method for signature matrix
rewire_network(x, remov)
```

Arguments

x	Adjacency matrix
remov	A vector of gene names, indicating which genes are not represented by SNPs in the considered GWASdata and will be removed

Value

An adjacency matrix containing the rewired network

Author(s)

Juliane Manitz

---

snp_info *An S4 class for an object assigning SNP positions to rs-numbers (for internal use)*

Description

An S4 class for an object assigning SNP positions to rs-numbers (for internal use)

This function gives for a vector of SNP identifiers the position of each SNP as extracted from the Ensemble database. The database is accessed via the R-package biomaRt.

show Shows basic information on snp_info object

summary Summarizes information on snp_info object

Usage

```
snp_info(x, ...)

## S4 method for signature character
snp_info(x)

## S4 method for signature snp_info
show(object)

## S4 method for signature snp_info
summary(object)
```

Arguments

x	A character vector of SNP rsnumbers for which positions will be extracted.
...	further arguments can be added.

Value

A data.frame including the SNP positions with columns 'chromosome', #position' and 'rsnumber'. SNPs not found in the Ensemble database will not be listed in the returned snp_info object, SNPs with multiple positions will appear several times.

show Basic information on snp_info object.

summary Summarized information on snp_info object.

Slots

`info` A `data.frame` including information on SNP positions

Author(s)

Stefanie Friedrichs

Examples

```
# snp_info
data(rs10243170_info)
snp_info(c("rs234"))
# show
data(rs10243170_info)
rs10243170_info
# summary
data(rs10243170_info)
summary(rs10243170_info)
```

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