Package 'FunciSNP'

March 26, 2013

Type Package

Title Integrating Functional Non-coding Datasets with Genetic Association Studies to Identify Candidate Regulatory SNPs

Version 1.1.8

Date 2013-01-19

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biocViews Infrastructure, DataRepresentation, DataImport,SequenceMatching, Annotation

Depends R (>= 2.14.0), ggplot2, TxDb.Hsapiens.UCSC.hg19.knownGene,FunciSNP.data

Imports AnnotationDbi, IRanges, Rsamtools (>= 1.6.1), rtracklayer(>= 1.14.1), methods, ChIPpeakAnno (>= 2.2.0), GenomicRanges,VariantAnnotation, plyr, org.Hs.eg.db, snpStats, ggplot2 (>= 0.9.0), reshape (>= 0.8.4), scales

Enhances parallel

Description FunciSNP integrates information from GWAS, 1000genomes and chromatin feature to identify functional SNP in coding or non-coding regions.

License GPL-3

URL http://coetzeeseq.usc.edu/publication/Coetzee_SG_et_al_2012/

LazyData yes

R topics documented:

FunciSNP-package *Functional Identification of SNPs with Phenotype by Coincidence with Chromatin Biofeatures*

Description

The package includes functions to identify and annotate putative functional SNPs using information derived from GWAS, 1000 genomes database, and sequences around peaks.

Details

Package:	FunciSNP
Type:	Package
Version:	0.99.0
Date:	2012-05-18
License:	GPL-3
LazyLoad:	yes

Author(s)

Simon G. Coetzee (maintainer: scoetzee@gmail.com); Houtan Noushmehr, PhD (houtan@usp.br)

References

SG. Coetzee, SK. Rhie, BP. Berman, GA. Coetzee and H. Noushmehr, FunciSNP: An R/Bioconductor Tool Integrating Functional Non-coding Datasets with Genetic Association Studies to Identify Candidate Regulatory SNPs., Nucleic Acids Research, In press, 2012 (doi:10.1093/nar/gks542).

See Also

FunciSNPplot, FunciSNPAnnotateSummary, FunciSNPtable, FunciSNPbed

Examples

```
##
## Glioblastoma analysis using FunciSNP
##
## Full path to the example regions file for Glioblastoma
#  (collected from SNPedia)
glioma.snp <- file.path(system.file('extdata',
  package='FunciSNP'),
  dir(system.file('extdata',package='FunciSNP'),
  pattern='.snp$'));
```

```
## Full path to the example biological features BED files
#  derived from the ENCODE project for Glioblastoma U-87
#  cell lines.
glioma.bio <- system.file('extdata',package='FunciSNP');

## FunciSNP analysis, extracts correlated SNPs from the
#  1000 genomes db ("ncbi") and finds overlaps between
#  correlated SNP and biological features and then
#  calculates LD (Rsquare, Dprime, distance, p-value).
# Do not run. Can take more than 5 min depending on internet connection and number of CPUs.
#glioma <- FunciSNP(snp.regions.file=glioma.snp,
#  bio.features.loc = glioma.bio, bio.features.TSS=FALSE);

##
data(glioma);
class(glioma);
glioma;
summary(glioma);
```

CorrelatedSNPs-class *Class* "CorrelatedSNPs"

Description

Class for CorrelatedSNPs

Usage

```
## S4 method for signature 'CorrelatedSNPs'
alt.allele(x)
## S4 replacement method for signature 'CorrelatedSNPs'
alt.allele(x) <- value
## S4 method for signature 'CorrelatedSNPs'
chr(x)
## S4 replacement method for signature 'CorrelatedSNPs'
chr(x) <- value
## S4 method for signature 'CorrelatedSNPs'
overlapping.features(x)
## S4 replacement method for signature 'CorrelatedSNPs'
overlapping.features(x) <- value
## S4 method for signature 'CorrelatedSNPs'
pop.genotype(x, population)
## S4 replacement method for signature 'CorrelatedSNPs'
pop.genotype(x) <- value
## S4 method for signature 'CorrelatedSNPs'
position(x)
## S4 replacement method for signature 'CorrelatedSNPs'
position(x) <- value
## S4 method for signature 'CorrelatedSNPs'
ref.allele(x)
```

```
## S4 replacement method for signature 'CorrelatedSNPs'
ref.allele(x) <- value
## S4 method for signature 'CorrelatedSNPs'
snpid(x)
## S4 replacement method for signature 'CorrelatedSNPs'
snpid(x) <- value
```

Arguments

x	The CorrelatedSNPs object from/on which to get/set snp information.
value	Examine the section "Slots" for the values taken by each method.
population	Population for which to set/get genotype information, either "AFR", "AMR", "ASN", "EUR" or "ALL".

Objects from the Class

Objects can be created by calls of the form new("CorrelatedSNPs", ...).

Slots

chromosome**:** Object of class "integer" ~~

position**:** Object of class "integer" ~~

snpid**:** Object of class "character" ~~

ref.allele**:** Object of class "character" ~~

alt.allele**:** Object of class "character" ~~

overlapping.features**:** Object of class "GRanges" ~~

genotype**:** Object of class "CorrGeno" ~~

Methods

alt.allele<- signature(x = "CorrelatedSNPs"): ...

alt.allele signature(x = "CorrelatedSNPs"): ...

chr<- signature(x = "CorrelatedSNPs"): ...

chr signature(x = "CorrelatedSNPs"): ...

overlapping.features<- signature(x = "CorrelatedSNPs"): ...

overlapping.features signature(x = "CorrelatedSNPs"): ...

pop.genotype<- signature(x = "CorrelatedSNPs"): ...

pop.genotype signature(x = "CorrelatedSNPs"): ...

position<- signature(x = "CorrelatedSNPs"): ...

position signature(x = "CorrelatedSNPs"): ...

ref.allele<- signature(x = "CorrelatedSNPs"): ...

ref.allele signature(x = "CorrelatedSNPs"): ...

snpid<- signature(x = "CorrelatedSNPs"): ...

snpid signature(x = "CorrelatedSNPs"): ...

Note

NA

Author(s)

Simon G. Coetzee (maintainer: scoetzee@gmail.com); Houtan Noushmehr, PhD (houtan@usp.br)

References

SG. Coetzee, SK. Rhie, BP. Berman, GA. Coetzee and H. Noushmehr, FunciSNP: An R/Bioconductor Tool Integrating Functional Non-coding Datasets with Genetic Association Studies to Identify Candidate Regulatory SNPs., Nucleic Acids Research, In press, 2012 (doi:10.1093/nar/gks542).

See Also

getFSNPs, FunciSNPplot, FunciSNPAnnotateSummary, FunciSNPtable, FunciSNPbed

Examples

```
showClass("CorrelatedSNPs")
```

FunciSNPAnnotateSummary

Genomic Annotation of YAFSNPs.

Description

This will annotate all identified YAFSNP for it's distance to the nearest known TSS, whether it overlapps a known exon, intron, 5'UTR, 3'UTR, promoter, lincRNA or in gene desert (intergentic) regions.

Usage

```
FunciSNPAnnotateSummary(snp.list)
```

Arguments

snp.list	a FunciSNP object: snp.list represents the FunciSNP object output from FunciSNP. See getFSNPs.

Details

All known genomic features (exon, intron, 5'UTR, 3'UTR, promoter, lincRNA or in gene desert (intergentic)) are used to annotate the newly identified YAFSNP. Information described in this data.frame is used for all summary plots, table, and bed file generations.

Value

data.frame with rows for each correlated SNP.

Note

NA

Author(s)

Simon G. Coetzee (maintainer: scoetzee@gmail.com); Houtan Noushmehr, PhD (houtan@usp.br)

References

SG. Coetzee, SK. Rhie, BP. Berman, GA. Coetzee and H. Noushmehr, FunciSNP: An R/Bioconductor Tool Integrating Functional Non-coding Datasets with Genetic Association Studies to Identify Candidate Regulatory SNPs., Nucleic Acids Research, In press, 2012 (doi:10.1093/nar/gks542).

See Also

getFSNPs, FunciSNPplot, FunciSNPAnnotateSummary, FunciSNPtable, FunciSNPbed

Examples

```
data(glioma);
gl <- FunciSNPAnnotateSummary(glioma);
dim(gl)
head(gl)
names(gl)
```

FunciSNPbed *Creates a BED file to view YAFSNPs in your favorite genome browser*

Description

FunciSNPbed will output a BED file to a specified folder. The BED file is in standard UCSC Genome Browser format (http://genome.ucsc.edu/FAQ/FAQformat). Each tagSNP is colored black and each YAFSNP is colored red.

Usage

```
FunciSNPbed(dat, rsq, path = getwd(), filename = NULL)
```

Arguments

dat	FunciSNP data.frame: dat is a data.frame object from FunciSNPAnnotateSummary. Need to run FunciSNPAnnotateSummary first.
rsq	an interger (0-1): rsq is the Rsquared cutoff used to subset.
path	a character: path is the path to the folder where to save the BED file. Default to getwd() or current working directory.
filename	a character: filename is the name of the BED file. If NULL, filename is 'FunciSNP_results_rsq.RSQ value.bed'

Details

FunciSNPbed outputs a unique BED file which can be used to view in any genomic browser compatible with BED formats. To learn more about BED formats, see UCSC Genome Browser FAQ (http://genome.ucsc.edu/FAQ/FAQformat). Each tagSNP which is in LD to a corresponding YAFSNP overlapping at least one biofeature is colored black, while the YAFSNP is colored red. The initial position is provided by the first tagSNP and the first linked YAFSNP. We recommend using UCSC genome browser to view your BED files. This is useful so you can view all public and private tracks in relation to FunciSNP results.

Value

BED file is outputed as a tab-deliminated file in the specified 'path' folder. See example below.

Note

NA

Author(s)

Simon G. Coetzee (maintainer: scoetzee@gmail.com); Houtan Noushmehr, PhD (houtan@usp.br)

References

SG. Coetzee, SK. Rhie, BP. Berman, GA. Coetzee and H. Noushmehr, FunciSNP: An R/Bioconductor Tool Integrating Functional Non-coding Datasets with Genetic Association Studies to Identify Candidate Regulatory SNPs., Nucleic Acids Research, In press, 2012 (doi:10.1093/nar/gks542).

See Also

getFSNPs, FunciSNPplot, FunciSNPAnnotateSummary, FunciSNPtable, FunciSNPbed

Examples

```
##
data(glioma);
glioma.anno <- FunciSNPAnnotateSummary(glioma);
FunciSNPbed(glioma.anno, rsq=0.9);
####
#Bed file "FunciSNP_results_rsq.0.9.bed" created successfully.
#(See folder: "/home/houtan/Downloads/")
#Total corSNP (RED):  15
#Total tagSNP (BLK):  1

#To view results, submit bed file as a
#  custom track in UCSC Genome Browser (genome.ucsc.edu),

#Now have fun with your new Func-y SNPs!!
####
```

FunciSNPidsFromSummary

coming soon.

Description

placeholder«««

Usage

FunciSNPidsFromSummary(dat, tagsnpid = NULL, num.features, rsq = 0)

Arguments

dat	placeholder«««<
tagsnpid	placeholder«««<
num.features	placeholder«««<
rsq	placeholder«««< placeholder«««<

Details

placeholder«««<

Value

placeholder«««<

Note

NA

Author(s)

Simon G. Coetzee (maintainer: scoetzee@gmail.com); Houtan Noushmehr, PhD (houtan@usp.br)

References

SG. Coetzee, SK. Rhie, BP. Berman, GA. Coetzee and H. Noushmehr, FunciSNP: An R/Bioconductor Tool Integrating Functional Non-coding Datasets with Genetic Association Studies to Identify Candidate Regulatory SNPs., Nucleic Acids Research, In press, 2012 (doi:10.1093/nar/gks542).

See Also

getFSNPs, FunciSNPplot, FunciSNPAnnotateSummary, FunciSNPtable, FunciSNPbed

Examples

```
## coming soon
```

FunciSNPplot *FunciSNPplot to visualize YAFSNP summary.*

Description

FunciSNPplot is a function developed to plot various types of plots to summarize and assist end-user in making informed discoveries of FunciSNP results. Plots can be stored in a folder for future reference.

Usage

```
FunciSNPplot(dat, rsq = 0, split = FALSE, splitbysnp = FALSE, tagSummary = FALSE, heatmap = FALSE, he
```

Arguments

dat	FunciSNP data.frame: dat is a data.frame object from FunciSNPAnnotateSummary. Need to run FunciSNPAnnotateSummary first.
rsq	an interger (0-1): rsq is the Rsquared cutoff used to subset.
split	logical: split will generate distribution plot of all Correlated SNPs by Rsquare values.
splitbysnp	logical: splitbysnp is similar to split but instead split the distribution by tagSNP.
tagSummary	logical: tagSummary Will output two plots per biofeature. The first one is a scatter plot showing the relationship between Rsquare and Distance to tagSNP for each YAFSNP. The second plot is a histogram distribution of number of correlated SNPs at each Rsquare value. Each set of plot is further divided by tagSNP. Best if used with rsq value.
heatmap	logical: heatmap correlation heatmap to visualize the number of correlated SNPs at each tagSNP overlapping each biological feature. Most informative if used with a rsq value.
heatmap.key	logical: heatmap.key Places the count of each cell on the heatmap.
genomicSum	logical: genomicSum Stacked bar chart summarizing all correlated SNPs for each of the identified genomie features (exon, intron, 5'UTR, 3'UTR, promoter, lincRNA or in gene desert (intergentic)). Most informative if used with a rsq value.
save	logical: save to save outputs to folder. Set at getwd(), in folder 'FunciSNP.VERSION/plots
pathplot	a character: pathplot is the path to the folder where to save the plots. Default to getwd() or current working directory.
text.size	Text size passed to graphing functions
save.width	Width of saved images in inches
save.height	Height of saved images in inches

Details

NA

Value

Plots are generated either in X11 or in specified folder.

Note

NA

Author(s)

Simon G. Coetzee (maintainer: scoetzee@gmail.com); Houtan Noushmehr, PhD (houtan@usp.br)

References

SG. Coetzee, SK. Rhie, BP. Berman, GA. Coetzee and H. Noushmehr, FunciSNP: An R/Bioconductor Tool Integrating Functional Non-coding Datasets with Genetic Association Studies to Identify Candidate Regulatory SNPs., Nucleic Acids Research, In press, 2012 (doi:10.1093/nar/gks542).

See Also

getFSNPs, FunciSNPplot, FunciSNPAnnotateSummary, FunciSNPtable, FunciSNPbed

Examples

```
data(glioma)
gl <- FunciSNPAnnotateSummary(glioma)
FunciSNPplot(gl)
FunciSNPplot(gl, rsq=0, genomicSum=TRUE, save=FALSE)
FunciSNPplot(gl, rsq=0.5, genomicSum=TRUE, save=FALSE)
# DO NOT RUN
#FunciSNPplot(gl, tagSummary=TRUE, rsq=0.5)
#
```

FunciSNPsummaryOverlaps

Summarizes FunciSNP results by overlaps

Description

This will summarize the total number of YAFSNPs identified by the number of biofeatures per tagSNP

Usage

```
FunciSNPsummaryOverlaps(dat, rsq = 0)
```

Arguments

dat	FunciSNP data object
rsq	Rsquare value used to filter the summary report

Note

NA

Author(s)

Simon G. Coetzee (maintainer: scoetzee@gmail.com); Houtan Noushmehr, PhD (houtan@usp.br)

References

SG. Coetzee, SK. Rhie, BP. Berman, GA. Coetzee and H. Noushmehr, FunciSNP: An R/Bioconductor Tool Integrating Functional Non-coding Datasets with Genetic Association Studies to Identify Candidate Regulatory SNPs., Nucleic Acids Research, In press, 2012 (doi:10.1093/nar/gks542).

See Also

getFSNPs, FunciSNPplot, FunciSNPAnnotateSummary, FunciSNPtable, FunciSNPbed

Examples

```
data(glioma);
glioma.anno <- FunciSNPAnnotateSummary(glioma);
FunciSNPsummaryOverlaps(glioma.anno, rsq = 0.2);
```

FunciSNPtable *Will output a summary report from FunciSNP at specified Rsquare cut-offs.*

Description

Using a specified Rsquare value (0-1) to subset the data, a table is generated which summarizes the total number of YAFSNPs, associated tagSNPs, and number of overlapping biofeatures.

Usage

```
FunciSNPtable(dat, rsq, geneSum = FALSE)
```

Arguments

dat	FunciSNP data.frame: dat is a data.frame object from FunciSNPAnnotateSummary. Need to run FunciSNPAnnotateSummary first.
rsq	an interger (0-1): rsq is the Rsquared cutoff used to subset.
geneSum	logical: geneSum is set to FALSE. Setting to TRUE will output a list of Gene names which are nearest to the YAFSNP.

Details

Using a specified Rsquare value (0-1) to subset the data, a table is generated which summarizes the total number of YAFSNPs, associated tagSNPs, and number of overlapping biofeatures. This will provide user a first look at the total number of available YAFSNP at a particular Rsquare cutoff. If geneSum is set to TRUE, a list of gene names is reported instead.

Value

Standard output which summarizes FunciSNP results.

Note

NA

Author(s)

Simon G. Coetzee (maintainer: scoetzee@gmail.com); Houtan Noushmehr, PhD (houtan@usp.br)

References

SG. Coetzee, SK. Rhie, BP. Berman, GA. Coetzee and H. Noushmehr, FunciSNP: An R/Bioconductor Tool Integrating Functional Non-coding Datasets with Genetic Association Studies to Identify Candidate Regulatory SNPs., Nucleic Acids Research, In press, 2012 (doi:10.1093/nar/gks542).

See Also

getFSNPs, FunciSNPplot, FunciSNPAnnotateSummary, FunciSNPtable, FunciSNPbed

Examples

```
data(glioma);
gl <- FunciSNPAnnotateSummary(glioma);
FunciSNPtable(gl, rsq=0.5);
FunciSNPtable(gl, rsq=0.5, geneSum=TRUE);
```

---

getFSNPs *Functional Identification of SNPs with Phenotype by Coincidence with Chromatin Biofeatures*

Description

Given a set of known tag-SNPs associated with a particular phenotype (e.g. disease, trait), and a set of available biological features (e.g. peaks derived from ChIP-seq experiments for phenotype), returns correlated SNPs (from the 1000 genomes db) which are in linkage disequilibrium (LD) to a known disease associated tag-SNP and overlaps chromatin biological features. These identified correlated SNPs are characterized as putative functional SNPs for a particular trait.

Usage

```
getFSNPs(snp.regions.file, bio.features.loc = NULL,
                built.in.biofeatures = TRUE,
                par.threads=detectCores()/2,
                verbose = par.threads < 2, method.p = "BH",
                search.window = 200000)
```

Arguments

snp.regions.file	path: Location of the regions file: Regions file is tab-deliminated and contains three elements per row. First element defines the genomic location of the tagSNP, 'chr:position' (e.g. 5:5420030). Second element contains the tagSNP name, 'rsID' (e.g. rs6010620). Third element defines the 'POPULATION' (ASN, EUR, AFR, ALL) where the tagSNP was identified (e.g. ASN, EUR, AFR, ALL). SNP Region file is imported and each row element (tagSNP element) is parsed for tagSNP name (rsXXXX), population (ASN, EUR, AFR, or ALL), and genomic location. Genomic location is used to define the window size (see 'search.window' argument). See example file here: file.path(system.file('data',package='FunciSNP'), dir(system.file('data',package='FunciSNP'), pattern='.snp$'));
bio.features.loc	path: Location of the biological features folder: Each biological feature for a particular genomic phenotype should be separated as individual BED files (tab deliminated file with chr, start and end). See UCSC for more information about BED formats http://genome.ucsc.edu/FAQ/FAQformat.html#format1. See example below. Default set to NULL.

built.in.biofeatures
: logical: To include promoter regions, Encode DNaseI and CTCF sites as an additional biofeature in the analysis. Promoters defined as -1000 to +100 bp of a known TSS. File extracted on Feb. 9, 2012 from UCSC genome table browser. Default set to TRUE.

par.threads
: an integer: Number of CPU cores to use for FunciSNP analysis. Default set at detectCores()/2. If par.threads > 1, then by default "verbose" = FALSE.

verbose
: logical: If set to TRUE, then regardless of par.threads value, all verbose message will output to terminal. If set to FALSE, no verbose message will output to terminal, except for warnings(). Default setting depends on number of 'par.threads' value.

method.p
: method: p-value correction (or adjustment) method (see ?p.adjust). Default set at "BH" (Benjamini & Hochberg (1995)).

search.window
: an integer: genomic window size used to extract all available correlated SNPs from the 1000 genomes db. The window size is centered around the tagSNP position as defined in the regions.file.

Details

This is the main funtion of FunciSNP. It will identify correlated SNPs which are in linkage disequilibrium (LD) to a known disease associated tagSNP. It will also determine if the correlated SNP in LD to the tagSNP overlaps a genomic biological feature. Correlated SNPs are directly imported from the current public release of the 1000 genomes database. 1000 genomes ftp servers available for the 1000 genomes public data: 1) National Center for Biotechnology Information (NCBI) ftp://ftp-trace.ncbi.nih.gov/1000genomes/; 2) European Bioinformatics Institute (EBI) ftp://ftp.1000genomes.ebi.ac.uk/vol1/.

Correlated SNPs in LD to a tagSNP and overlapping genomic biological features are known as putative functional SNPs (also defined as 'YAFSNP' elsewhere in the package.).

Value

TSList
: FunciSNP object.

Note

NA

Author(s)

Simon G. Coetzee (maintainer: scoetzee@gmail.com); Houtan Noushmehr, PhD (houtan@usp.br)

References

SG. Coetzee, SK. Rhie, BP. Berman, GA. Coetzee and H. Noushmehr, FunciSNP: An R/Bioconductor Tool Integrating Functional Non-coding Datasets with Genetic Association Studies to Identify Candidate Regulatory SNPs., Nucleic Acids Research, In press, 2012 (doi:10.1093/nar/gks542).

See Also

FunciSNPplot, FunciSNPAnnotateSummary, FunciSNPtable, FunciSNPbed

Examples

```
##
## Glioblastoma analysis using FunciSNP
##
## Full path to the example regions file for Glioblastoma
#  (collected from SNPedia)
glioma.snp <- file.path(system.file('extdata',
  package='FunciSNP'),
  dir(system.file('extdata',package='FunciSNP'),
  pattern='.snp$'));

## Full path to the example biological features BED files
#  derived from the ENCODE project for Glioblastoma U-87
#  cell lines.
glioma.bio <- system.file('extdata',package='FunciSNP');

## FunciSNP analysis, extracts correlated SNPs from the
#  1000 genomes db ("ncbi") and finds overlaps between
#  correlated SNP and biological features and then
#  calculates LD (Rsquare, Dprime, distance, p-value).
# Do not run. Can take more than 5 min depending on internet connection and number of CPUs.
#glioma <- getFSNPs(snp.regions.file=glioma.snp,
#  bio.features.loc = glioma.bio);

##
data(glioma);
class(glioma);
glioma;
summary(glioma);
```

TagSNP-class *Class* "TagSNP"

Description

In the code snippets below, x is a TagSNP object. for the usage of alt.allele, chr, position, ref.allele, and snpid for the object CorrelatedSNPs, see ?CorrelatedSNPs-class

Usage

```
## S4 method for signature 'TagSNP'
alt.allele(x)
## S4 replacement method for signature 'TagSNP'
alt.allele(x) <- value
## S4 method for signature 'TagSNP'
chr(x)
## S4 replacement method for signature 'TagSNP'
chr(x) <- value
## S4 method for signature 'TagSNP'
correlated.snps(x)
## S4 replacement method for signature 'TagSNP'
```

```
correlated.snps(x) <- value
## S4 method for signature 'TagSNP'
genotype(x)
## S4 replacement method for signature 'TagSNP'
genotype(x) <- value
## S4 method for signature 'TagSNP'
population(x)
## S4 replacement method for signature 'TagSNP'
population(x) <- value
## S4 method for signature 'TagSNP'
position(x)
## S4 replacement method for signature 'TagSNP'
position(x) <- value
## S4 method for signature 'TagSNP'
ref.allele(x)
## S4 replacement method for signature 'TagSNP'
ref.allele(x) <- value
## S4 method for signature 'TagSNP'
snpid(x)
## S4 replacement method for signature 'TagSNP'
snpid(x) <- value
## S4 method for signature 'TagSNP'
yafsnp.rsq(x)
## S4 replacement method for signature 'TagSNP'
yafsnp.rsq(x) <- value
## S4 method for signature 'TagSNP'
yafsnp.dprime(x)
## S4 replacement method for signature 'TagSNP'
yafsnp.dprime(x) <- value
## S4 method for signature 'TagSNP'
yafsnp.pvalue(x)
## S4 replacement method for signature 'TagSNP'
yafsnp.pvalue(x) <- value
## S4 method for signature 'TagSNP'
AFR.overlapping.snps.geno(x)
## S4 method for signature 'TagSNP'
AMR.overlapping.snps.geno(x)
## S4 method for signature 'TagSNP'
ASN.overlapping.snps.geno(x)
## S4 method for signature 'TagSNP'
EUR.overlapping.snps.geno(x)
```

Arguments

x	The TagSNP object from/on which to get/set snp information.
value	Examine the section "Slots" for the values taken by each method.

Objects from the Class

Objects can be created by calls of the form new("TagSNP", ...).

Slots

chromosome: Object of class "integer" ~~
position: Object of class "integer" ~~
snpid: Object of class "character" ~~
population: Object of class "character" ~~
ref.allele: Object of class "character" ~~
alt.allele: Object of class "character" ~~
genotype: Object of class "SnpMatrix" ~~
yafsnp.rsq: Object of class "dgCMatrix" ~~
yafsnp.dprime: Object of class "dgCMatrix" ~~
yafsnp.pvalue: Object of class "list" ~~
correlated.snps: Object of class "CorrelatedSNPs" ~~

Methods

alt.allele<- signature(x = "TagSNP"): ...
alt.allele signature(x = "TagSNP"): ...
chr<- signature(x = "TagSNP"): ...
chr signature(x = "TagSNP"): ...
correlated.snps<- signature(x = "TagSNP"): ...
correlated.snps signature(x = "TagSNP"): ...
genotype<- signature(x = "TagSNP"): ...
genotype signature(x = "TagSNP"): ...
population<- signature(x = "TagSNP"): ...
population signature(x = "TagSNP"): ...
position<- signature(x = "TagSNP"): ...
position signature(x = "TagSNP"): ...
ref.allele<- signature(x = "TagSNP"): ...
ref.allele signature(x = "TagSNP"): ...
R.squared.corrsnps<- signature(x = "TagSNP"): ...
R.squared.corrsnps signature(x = "TagSNP"): ...
show signature(object = "TagSNP"): ...
snpid<- signature(x = "TagSNP"): ...
snpid signature(x = "TagSNP"): ...
yafsnp.rsq<- signature(x = "TagSNP"): ...
yafsnp.rsq signature(x = "TagSNP"): ...
yafsnp.dprime<- signature(x = "TagSNP"): ...
yafsnp.dprime signature(x = "TagSNP"): ...
yafsnp.pvalue<- signature(x = "TagSNP"): ...
yafsnp.pvalue signature(x = "TagSNP"): ...
AFR.overlapping.snps.geno signature(x = "TagSNP"): ...
AMR.overlapping.snps.geno signature(x = "TagSNP"): ...
ASN.overlapping.snps.geno signature(x = "TagSNP"): ...
EUR.overlapping.snps.geno signature(x = "TagSNP"): ...

Note

NA

Author(s)

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References

SG. Coetzee, SK. Rhie, BP. Berman, GA. Coetzee and H. Noushmehr, FunciSNP: An R/Bioconductor Tool Integrating Functional Non-coding Datasets with Genetic Association Studies to Identify Candidate Regulatory SNPs., Nucleic Acids Research, In press, 2012 (doi:10.1093/nar/gks542).

See Also

getFSNPs, FunciSNPplot, FunciSNPAnnotateSummary, FunciSNPtable, FunciSNPbed

Examples

```
showClass("TagSNP")
```

TSList-class *Class* "TSList"

Description

ffff

Objects from the Class

Objects can be created by calls of the form new("TSList", ...).

Slots

snp.data**:** Object of class "list" ~~

summary.data**:** Object of class "data.frame" ~~

elementType**:** Object of class "character" ~~

elementMetadata**:** Object of class "DataTableORNULL" ~~

metadata**:** Object of class "list" ~~

Methods

show signature(object = "TSList"): ...

summary signature(object = "TSList"): ...

Note

NA

Author(s)

Simon G. Coetzee and Houtan Noushmehr, PhD

References

SG. Coetzee, SK. Rhie, BP. Berman, GA. Coetzee and H. Noushmehr, FunciSNP: An R/Bioconductor Tool Integrating Functional Non-coding Datasets with Genetic Association Studies to Identify Candidate Regulatory SNPs., Nucleic Acids Research, In press, 2012 (doi:10.1093/nar/gks542).

See Also

getFSNPs, FunciSNPplot, FunciSNPAnnotateSummary, FunciSNPtable, FunciSNPbed

Examples

```
showClass("TSList")
```

Index