Package 'traseR'

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Description traseR performs GWAS trait-associated SNP enrichment analyses in genomic intervals using different hypothesis testing approaches, also provides various functionalities to explore and visualize the results.

License GPL

LazyLoad yes

biocViews Genetics,Sequencing, Coverage, Alignment, QualityControl, DataImport

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`traseR-package` *GWAS trait-associated SNP enrichment analyses in genomic intervals*

Description

Perform GWAS trait-associated SNP enrichment analyses in genomic intervals. Explore and visualize the results.

Details

Package:	traseR
Type:	Package
Version:	1.0
Date:	2015-11-18
License:	GPL

Author(s)

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`CEU` *Sampled SNPs from all SNPs of CEU population in 1000 genome project*

Description

A GRange object `CEU` contains 5% of all SNPs from CEU by controling genome-wide density is the same as all SNPs from CEU

Usage

```
data(CEU)
```

Value

The data frame CEU contains three columns,

SNP_ID	SNP rs number
seqnames	Chromosome number associated with rs number
ranges	Chromosomal position, in base pairs, associated with rs number

Author(s)

Li Chen <li.chen@emory.edu>, Zhaohui S.Qin<zhaohui.qin@emory.edu>

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plots *Visualize of trait-associated SNPs*

Description

These are a group of functions to generate plot to visualize the trait-associated SNPs.

Usage

```
plotContext(snpdb, region=NULL, keyword = NULL, pvalue = 1e-3)

plotPvalue(snpdb, region=NULL, keyword = NULL, plot.type = c("densityplot", "boxplot"), pvalue = 1e-3,

plotSNP(snpdb, snpid, ext = 10000)

plotGene(snpdb, gene, ext = 10000)

plotInterval(snpdb,interval,ext = 10000)
```

Arguments

snpdb	A GRange object or data frame, which is GWAS trait-associated SNPs downloaded from up-to-date dbGaP and NHGRI public database. It is maintained to be updated to the latest version. The data frame contains the following columns,Trait,SNP,p.value,Chr,Position,Context,GENE_NAME,GENE_START,GENE_END,GENE_STRAND. The data frame is in data subdirectory. Users are free to add more SNP records to the data frame for practical use.
region	A data frame, which is genomic intervals with three columns, chromosome, genomic start position, genomic end position.
keyword	The keyword is used when specific trait is of interest. If keyword is specified, only the SNPs associated to the trait are used for analyses. Otherwise, all traits will be analyzed.
snpid	SNP rs number

gene	Gene name
pvalue	SNPs with p-value less than this threshold are used for analyses.
plot.type	Either "densityplot" or "boxplot"
ext	Bp extended upstream and downstream
xymax	The maximum range on x-axis and y-axis
interval	A data frame, genomic interval:chromosome, genomic start position, genomic end position

Value

plotContext	A pie plot with the distribution of SNP function class
plotPvalue	A density plot of -logPvalue of trait-associated SNPs
plotSNP	A plot of trait-associated SNP on chromosome
plotGene	A plot with the gene and possible nearby trait-associated SNPs
plotInterval	A plot with chromosome interval with possible nearby genes and trait-associated SNPs

Author(s)

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Examples

```
data(taSNP)
plotContext(snpdb= taSNP,keyword="Autoimmune")
plotGene(snpdb= taSNP,gene="ZFP92",ext=50000)
plotSNP(snpdb= taSNP,snpid="rs766420",ext=50000)
plotInterval(snpdb= taSNP,data.frame(chr="chrX",start=152633780,end=152737085))
```

---

print.traseR *Print the outcome of taSNP enrichment analyses*

Description

Print the outcome of taSNP enrichment analyses. Print the overall taSNP enrichment, trait-specific taSNP enrichment,trait-class-specific taSNP enrichment.

Usage

```
 ## S3 method for class 'traseR'
print(x,isTopK1=FALSE,topK1=10,isTopK2=FALSE,topK2=10,trait.threshold=10,traitclass.threshold=10,..
```

Arguments

x	Object returned from traseR
isTopK1	If isTopK1 is TRUE, topK1 traits are printed; otherwise, traits with p-value below Bonferroni correction threshold are printed. Default is FALSE.
topK1	Top K1 traits are printed. Default is 10.
isTopK2	If isTopK2 is TRUE, topK2 trait class are printed; otherwise, trait class with p-value below Bonferroni correction threshold are printed. Default is FALSE.
topK2	Top K2 trait class are printed. Default is 10.
trait.threshold	Traits above this threshold are reported. Default is 10.
traitclass.threshold	Trait class above this threshold are reported. Default is 10.
...	Other parameters to print

Value

Print a data frame of traits ranked by p-value

Author(s)

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Examples

```
data(taSNP)
data(Tcell)
x=traseR(snpdb=taSNP,region=Tcell)
print(x)
```

---

querys *Retrieve trait-associated SNPs based*

Description

These are a group of functions to retrieve the trait-associated SNPs based on input

Usage

```
queryKeyword(snpdb, region=NULL, keyword = NULL, returnby = c("SNP_ID", "trait"), pvalue = 1e-3)

queryGene(snpdb, genes = NULL)

querySNP(snpdb, snpid, region = NULL)
```

Arguments

snpdb	A GRange object or data frame, which is GWAS trait-associated SNPs downloaded from up-to-date dbGaP and NHGRI public database. It is maintained to be updated to the latest version. The data frame contains the following columns,Trait,SNP_ID,p.value,Chr,Position,Context,GENE_NAME,GENE_START,GENE_END,GENE_STRA The data frame is in data subdirectory. Users are free to add more SNP records to the data frame for practical use.
region	A data frame, which is genomic intervals with three columns, chromosome, genomic start position, genomic end position.
keyword	The keyword is used when specific trait is of interest. If keyword is specified, only the SNPs associated to the trait are used for analyses. Otherwise, all traits will be analyzed.
snpid	SNP rs number
genes	Gene name
pvalue	SNPs with p-value less than this threshold are used for analyses.
returnby	Either SNP or trait. If returnby is specified as 'SNP_ID', a data frame based on 'SNP_ID' is returned. If returnby is specified as 'trait', a data frame based on 'trait' is returned.

Value

queryKeyword: Return a data frame of traits containing the keyword queryGene: Return a data frame of traits associated with the gene querySNP: Return a data frame of traits associated with the SNP

Author(s)

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Examples

```
data(taSNP)
data(Tcell)
x=queryKeyword(snpdb=taSNP,region=Tcell,keyword="Autoimmune",returnby="SNP_ID")
x=queryGene(snpdb=taSNP,genes=c("AGRN","UBE2J2","SSU72"))
x=querySNP(snpdb=taSNP,snpid=c("rs3766178","rs880051"))
```

---

taSNP *trait-associated SNPs in dbGaP and NHGRI downloaded from Association Results Browser*

Description

A GRange object taSNP contains trait-associated SNPs from dbGaP and NHGRI downloaded from Association Results Browser.

Usage

```
data(taSNP)
```

Value

The data frame taSNP contains the following columns

Trait	Trait
Trait Class	Trait class which is formed based on the phenotype tree. Close traits are grouped together to form one class
SNP_ID	SNP rs number
p.value	GWAS SNP p-value
seqnames	Chromosome
ranges	Chromosome position
Context	SNP functional class
GENE_NAME	Nearest gene name
GENE_START	Gene start genomic position
GENE_END	Gene end genomic position
GENE_STRAND	Gene strand

Author(s)

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taSNPLD *linkage disequilibrium (>0.8) within 100kb SNPs of all trait-associated SNPs from dbGaP and NHGRI*

Description

A GRange object taSNPLD contains linkage disequilibrium (>0.8) SNPs of all trait-associated SNPs from dbGaP and NHGRI.

Usage

```
data(taSNPLD)
```

Value

The data frame taSNPLD contains four columns,

SNP_ID	SNP rs number
seqnames	Chromosome number associated with rs number
ranges	Chromosomal position, in base pairs, associated with rs number
Trait	Trait the SNP is associated with
Trait Class	Trait class which is formed based on the phenotype tree. Close traits are grouped together to form one class

Author(s)

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`Tcell` *Peak regions of H3K4me1 in Peripheral blood T cell*

Description

A GRange object `Tcell` contains three columns: chromosome, genomic start position and genomic end position.

Usage

```
data(Tcell)
```

Value

The data frame `Tcell` contains three columns,

`seqnames`	Chromosome id
`ranges`	Chromosome position

Author(s)

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`traseR` *TRait-Associated SNP EnRichment analyses*

Description

Perform GWAS trait-associated SNP enrichment analyses in genomic intervals using different approaches

Usage

```
traseR(snpdb, region, snpdb.bg=NULL, keyword = NULL, rankby = c("pvalue", "odds.ratio"),
test.method = c("binomial", "fisher","chisq", "nonparametric"), alternative = c("greater", "less", "tw
ntimes=100,nbatch=1,
trait.threshold = 0, traitclass.threshold=0, pvalue = 1e-3)
```

Arguments

snpdb	A GRange object. It could be GWAS trait-associated SNPs downloaded from up-to-date dbGaP and NHGRI public database. It is maintained to be updated to the latest version. The data frame contains the following columns,Source,Trait,SNP,p.value,Chr,Posit The data frame is in data subdirectory. Users are free to add more SNP records to the data frame for practical use. It could also be a data frame with columns as, SNP,Chr,Position.
region	A GRange object or data frame, which is genomic intervals with three columns, chromosome, genomic start position, genomic end position.
snpdb.bg	A GRange object contains non-trait-associated SNPs. They are treated as background for statistical testing instead of whole genome as background if specified.
keyword	The keyword is used when specific trait is of interest. If keyword is specified, only the SNPs associated to the trait are used for analyses. Otherwise, all traits will be analyzed.
rankby	Traits could be ranked by either p-value or adds.ratio based on the enrichment level of trait-associated SNPs in genomic intervals.
test.method	Several hypothesis testing options are provided: binomial(binomial test),fisher(Fisher's exact test),chisq(Chi-squared test),chisq(nonparametric test). Default is binomial(binomial test)
alternative	Indicate the alternative hypothesis. If greater, test if the genomic intervals are enriched in trait-associated SNPs than background. If less, test if the genomic intervals are depleted in trait-associated SNPs than background. If two.sided, test if there is difference between the enrichment of trait-associated SNPs in genomic intervals and in background.
ntimes	The number of shuffling time for one batch. See nbatch.
nbatch	The number of batches. The product of ntimes and nbatch is the total number of shuffling time.
trait.threshold	Test traits with number of SNPs more than the threshold.
traitclass.threshold	Test trait class with number of SNPs more than the threshold.
pvalue	SNPs with p-value less than this threshold are used for analyses.

Details

Return a list that contains three data frames. One data frame tb.all contains the results of enrichment analyses for all trait-associated SNPs in genomic intervals. Another data frame tb1 contains the results of enrichment analyses for each trait-associated SNPs in genomic intervals separately. Another data frame tb2 contains the results of enrichment analyses for each trait-class-associated SNPs in genomic intervals separately.

Value

The data frame tb1 has columns,

Trait	Name of trait

p.value	P-value calculated from hypothesis testing
q.value	Adjusted p-value from multiple testing using FDR correction
odds.ratio	Odds ratio calculated based on number of trait-associated SNPs in genomic intervals, number of trait-associated SNPs across whole genome, genomic intervals size (bps) and genome size (bps)
taSNP.hits	Number of trait-associated SNPs in genomic intervals
taSNP.num	Number of SNPs for specific trait

Author(s)

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See Also

print.traseR

Examples

```
data(taSNP)
data(Tcell)
x=traseR(snpdb=taSNP,region=Tcell)
print(x)
```

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