

Package ‘PAST’

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Type Package

Title Pathway Association Study Tool (PAST)

Version 1.27.0

Description PAST takes GWAS output and assigns SNPs to genes, uses those genes to find pathways associated with the genes, and plots pathways based on significance. Implements methods for reading GWAS input data, finding genes associated with SNPs, calculating enrichment score and significance of pathways, and plotting pathways.

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Encoding UTF-8

Depends R (>= 4.0)

Imports stats, utils, dplyr, rlang, iterators, parallel, foreach,
doParallel, qvalue, rtracklayer, ggplot2, GenomicRanges,
S4Vectors

Suggests knitr, rmarkdown

VignetteBuilder knitr

RoxygenNote 7.1.0

URL <https://github.com/IGBB/past>

BugReports <https://github.com/IGBB/past/issues>

biocViews Pathways, GeneSetEnrichment

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assign_chunk	<i>Assign SNPs in a chunk to genes</i>
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Description

Assign SNPs in a chunk to genes

Usage

assign_chunk(gff, chunk, window)

Arguments

- | | |
|--------|--|
| gff | The GFF data for the chromosome being parsed |
| chunk | The dataframe containing SNP data |
| window | The search window around the SNPs |

Value

tagSNPs labeled with gene names

assign_SNPs_to_genes	<i>Assign SNPs to genes</i>
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Description

Assign SNPs to genes

Usage

```
assign_SNPs_to_genes(
  gwas_data,
  LD,
  gff_file,
  filter_type,
  window,
  r_squared_cutoff,
  num_cores
)
```

Arguments

gwas_data	Merged association and effects data from merge_data()
LD	Linkage disequilibrium data from parse_LD()
gff_file	The path to a GFF file
window	The search window for genes around the SNP
r_squared_cutoff	The R ² value used to determine SNP significance
num_cores	The number of cores to use in parallelizing PAST

Value

A dataframe of genes from the SNP data

Examples

```
example("load_GWAS_data")
example("load_LD")
demo_genes_file = system.file("extdata", "genes.gff",
  package = "PAST", mustWork = TRUE)
filter_type = c("gene")
genes <- assign_SNPs_to_genes(gwas_data, LD, demo_genes_file, filter_type, 1000, 0.8, 2)
```

determine_linkage	<i>Determine Linkage</i>
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Description

Determine Linkage

Usage

```
determine_linkage(chunk, r_squared_cutoff)
```

Arguments

chunk A chunk of data to be processed
 r_squared_cutoff The R^2 value to check against

Value

Either the first unlinked SNP or a set of linked SNPs

find_pathway_significance
Find Pathway Significance

Description

Find Pathway Significance

Usage

```
find_pathway_significance(  
  genes,  
  pathways_file,  
  gene_number_cutoff = 5,  
  mode,  
  sample_size = 1000,  
  num_cores  
)
```

Arguments

genes Genes from assign_SNPs_to_genes()
 pathways_file A file containing the pathway IDs, their names, and the genes in the pathway
 gene_number_cutoff A cut-off for the minimum number of genes in a pathway
 mode increasing/decreasing
 sample_size How many times to sample the effects data during random sampling
 num_cores The number of cores to use in parallelizing PAST

Value

Rugplots data

Examples

```
example("assign_SNPs_to_genes")
demo_pathways_file = system.file("extdata", "pathways.txt.xz",
  package = "PAST", mustWork = TRUE)
rugplots_data <- find_pathway_significance(genes, demo_pathways_file, 5,
  "increasing", 1000, 2)
```

`find_representative_SNP`*Find representative SNP for a chunk of SNPs*

Description

Find representative SNP for a chunk of SNPs

Usage

```
find_representative_SNP(chunk, r_squared_cutoff)
```

Arguments

<code>chunk</code>	A chunk of data to parse
<code>r_squared_cutoff</code>	The R^2 value to check against when counting SNPs

Value

A single SNP representing the whole chunk

`find_representative_SNP_gene_pairing`*Find the SNP-gene assignment that represents SNPs assigned to a gene*

Description

Find the SNP-gene assignment that represents SNPs assigned to a gene

Usage

```
find_representative_SNP_gene_pairing(chunk)
```

Arguments

<code>chunk</code>	A chunk of gene assignments
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Value

A single SNP-gene assignment representing all SNPS assigned to the same gene to a gene

load_GWAS_data	<i>Load GWAS data</i>
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Description

Load GWAS data

Usage

```
load_GWAS_data(  
  association_file,  
  effects_file,  
  association_columns = c("Trait", "Marker", "Locus", "Site", "p", "marker_R2"),  
  effects_columns = c("Trait", "Marker", "Locus", "Site", "Effect")  
)
```

Arguments

- association_file The association file
- effects_file The effects file
- association_columns The names of the columns in your association data for Trait, Marker, Chromosome, Site, F, p, and marker_Rsquared
- effects_columns The names of the columns in your effects data for Trait, Marker, Chromosome, Site, and effect

Value

The association data and the effects data merged into a dataframe with one row for each SNP

Examples

```
demo_association_file = system.file("extdata", "association.txt.xz",  
  package = "PAST", mustWork = TRUE)  
demo_effects_file = system.file("extdata", "effects.txt.xz",  
  package = "PAST", mustWork = TRUE)  
gwas_data <- load_GWAS_data(demo_association_file, demo_effects_file)
```

load_LD	<i>Load Linkage Disequilibrium</i>
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Description

Load Linkage Disequilibrium

Usage

```
load_LD(  
  LD_file,  
  LD_columns = c("Locus1", "Position1", "Site1", "Position2", "Site2", "Dist_bp",  
                 "R.2")  
)
```

Arguments

LD_file	The file containing linkage disequilibrium data
LD_columns	The names of the columns in your linkage disequilibrium data for the chromosome of the first SNP, the position of the first SNP, the site of the first SNP, the chromosome of the second SNP, the position of the second SNP, the site of the second SNP, the distance between the two SNPs, and the R.2

Value

The linkage disequilibrium data in a list containing dataframes for each chromosome.

Examples

```
demo_LD_file = system.file("extdata", "LD.txt.xz",  
  package = "PAST", mustWork = TRUE)  
LD <- load_LD(demo_LD_file)
```

plot_pathways	<i>Plot Rugplots for Selected Pathways</i>
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Description

Plot Rugplots for Selected Pathways

Usage

```
plot_pathways(  
  rugplots_data,  
  filter_type,  
  filter_parameter,  
  mode,  
  output_directory  
)
```

Arguments

<code>rugplots_data</code>	The data to be plotted (returned from <code>find_pathway_significance()</code>)
<code>filter_type</code>	The parameter to be used for filtering
<code>filter_parameter</code>	The cut-off value of the filtering parameter
<code>mode</code>	The mode used to create the data (increasing/decreasing)
<code>output_directory</code>	An existing directory to save results in

Value

Does not return a value

Examples

```
example("find_pathway_significance")  
plot_pathways(rugplots_data, "pvalue", "0.03", "decreasing", tempdir())
```


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