Package: PAST (via r-universe)

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Type Package

Title Pathway Association Study Tool (PAST)

Version 1.30.0

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

Config/pak/sysreqs make libbz2-dev libicu-dev liblzma-dev libxml2-dev libssl-dev xz-utils zlib1g-dev

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`assign_chunk` *Assign SNPs in a chunk to genes*

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` *Assign SNPs to genes*

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 *Determine Linkage*

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

chunk	A chunk of data to parse
r_squared_cutoff	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

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Description

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

Usage

```
find_representative_SNP_gene_pairing(chunk)
```

Arguments

chunk	A chunk of gene assignments

Value

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

---

`load_GWAS_data` *Load GWAS data*

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 *Load Linkage Disequilibrium*

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 *Plot Rugplots for Selected Pathways*

Description

Plot Rugplots for Selected Pathways

Usage

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

Arguments

rugplots_data	The data to be plotted (returned from find_pathway_significance())
filter_type	The parameter to be used for filtering
filter_parameter	The cut-off value of the filtering parameter
mode	The mode used to create the data (increasing/decreasing)
output_directory	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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