Package 'GeneticMediation'

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Type Package

Title An R Package for Causal Mediation Analysis of ROSMAP Data

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License GPL-3

URL https://github.com/tydarnell/GeneticMediation,
https://tydarnell.github.io/GeneticMediation

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Description Provides methods for cleaning and processing data from the ROSMAP study
and preparing it for causal mediation analysis

Encoding UTF-8

LazyData true

RoxygenNote 7.1.0

Depends R (>= 3.6.0)

biocViews

Imports data.table,
IRanges,
mediation,
purrr,
readr,
stats,
utils

Suggests dplyr,
knitr,
magrittr,
rmarkdown,
testthat,
tibble,
tidyselect

VignetteBuilder knitr

R **topics documented:**

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check_data   *Check Data*

Description

Checks if the data is in the data folder

Usage

```
check_data()
```

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chr_numeric *Chromosome Numeric*

Description

Convert chromosome names from character to numeric. Useful when sorting a dataframe by chromosome number.

Usage

```
chr_numeric(Chr)
```

Arguments

Chr   a character column or vector of chromosome names

---

clean_data *Clean Data*

Description

Clean snp.info, peak.info data and save as data/chipseq.RData

Usage

```
clean_data(snp.path, peak.path)
```

Arguments

snp.path   path to SNP information dataframe

peak.path   path to Peak annotation dataframe

---

combine_data_spc *Combine Data SNP-Peak-Clinical*

Description

SNP-Peak-Clinical data: combine projid, SNPs, PCs, membership, age, gender, peaks, and outcome data for a chromosome

Usage

```
combine_data_spc(chr)
```

Arguments

chr   chromosome name

---

combine_data_spg   *Combine Data SNP-Peak-Gene*

Description

SNP-Peak-Gene Data: combine projid, SNPs, PCs, membership, age, gender, peaks, gene and outcome data for a chromosome.

Usage

```
combine_data_spg(chr)
```

Arguments

chr   chromosome name

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last_to_first   *Last to First*

Description

Make the last column the first column in a dataframe

Usage

```
last_to_first(df)
```

Arguments

df   dataframe

---

lenu   *Length Unique*

Description

Get the length of unique values in a vector

Usage

```
lenu(x)
```

Arguments

x   vector

---

make_folder *Make Folder*

Description

Make a folder only if the folder does not already exist

Usage

```
make_folder(path)
```

Arguments

path   folder path

---

match_all *Match SNPs Peaks All Chromosomes*

Description

Match SNPs and Peaks in all chromosomes and return dataframe of matches

Usage

```
match_all(snp.info, peak.info, chrs)
```

Arguments

snp.info   SNP information

peak.info   Peak information

chrs   character vector of chromosome names

---

match_snp_peak *Match SNPs and Peaks*

Description

Match SNPs and Peaks in a chromosome

Usage

```
match_snp_peak(snp.info, peak.info)
```

Arguments

snp.info   SNP information for chr

peak.info   Peak information chr

---

med.res_spc   *SNP-Peak-Clinical Mediation Data Prep*

Description

Prepare a chromosome of SNP-Peak-Clinical data for mediation analysis and save as "data/spc.res/res_chr.RData"

Usage

```
med.res_spc(chr, all_matches)
```

Arguments

chr	chromosome name
all_matches	dataframe of SNP-Peak matches for all chromosomes

---

med.res_spg   *SNP-Peak-Gene Mediation Data Prep*

Description

Prepare a chromosome SNP-Peak-Gene data for mediation analysis data and save as "data/spg.res/res_chr.RData"

Usage

```
med.res_spg(chr, med.data, matches, mediator.path)
```

Arguments

chr	chromosome name
med.data	gene mediation data
matches	SNP-Peak-Gene matches dataframe

---

mediation_spg   *Mediation SNP-Peak-Gene*

Description

Mediation analysis one SNP-Peak-Gene match

Usage

```
mediation_spg(med.res.data, match_row, simulations = 1000)
```

Arguments

med.res.data	gene mediation data
match_row	row in match dataframe: col1 SNP, col2 Peak, col3 Gene
simulations	number of simulations, 1000 by default

---

med_all_spc *SNP-Peak-Clinical Mediation Table*

Description

Create a table of SNP-Peak-Clinical mediation results for all chromosomes

Usage

```
med_all_spc(chrs, covar, simulations)
```

Arguments

chrs character vector of chromosome names

covar covariates string, each covariate separated by +

simulations number of simulations to run

---

med_chr_spc *SNP-Peak-Clinical Mediation Table Chromosome*

Description

Create SNP-Peak-Clinical mediation table for SNP-Peak matches in a chromosome

Usage

```
med_chr_spc(matches, med.res.data, covar, simulations)
```

Arguments

matches SNP-Peak matches dataframe for a chromosome

med.res.data mediation data

covar covariates string, separate covariates with +

simulations number of simulations to run

---

med_chr_spg   *SNP-Peak-Gene Mediation Table Chromosome*

Description

Create a SNP-Peak-Gene mediation table for a chromosome

Usage

```
med_chr_spg(chr, gene_matches, covar, simulations)
```

Arguments

chr	chromosome name
gene_matches	list of peak-SNP matches for each gene
covar	covariates string, separate covariates with +
simulations	number of simulations to run

---

med_table_spc   *SNP-Peak-Clinical Mediation Table*

Description

Create SNP-Peak-Clinical mediation table for a SNP-Peak match

Usage

```
med_table_spc(med.res.data, match_row, covar, simulations)
```

Arguments

med.res.data	mediation data
match_row	row in match dataframe, should have 2 columns
covar	covariates character variable, separate covariates with +
simulations	number of simulations to run

---

med_table_spg   *SNP-Peak-Gene Mediation Table*

Description

Create a mediation table for one SNP-Peak-Gene match

Usage

```
med_table_spg(med.res.data, match_row, covar, simulations)
```

Arguments

med.res.data	gene mediation data
match_row	row in match dataframe: col1 SNP, col2 Peak, col3 Gene
covar	covariates character variable, separate covariates with +
simulations	number of simulations to run

---

merge_csv   *Merge CSV*

Description

merge multiple csv files into a single dataframe

Usage

```
merge_csv(path)
```

Arguments

path	path to folder containing csv files

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setup_folders   *Setup Folders*

Description

Creates data, data/mediator, results folders

Usage

```
setup_folders()
```

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sig_chr_spg	*Significant SNP-Peak-Gene*

Description

Returns summary of mediation results for a chr with significant results

Usage

```
sig_chr_spg(chr)
```

Arguments

chr	chromosome name

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snp_peak_bychr	*SNPs and Peaks by Chromosome*

Description

save snp.info, peak.info for each chromosome as "data/chipseq/chipseq_chr.RData"

Usage

```
snp_peak_bychr(chrs, snps, peaks)
```

Arguments

chrs	Character vector of chromosomes names
snps	SNP information dataframe
peaks	Peak information dataframe

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sum_zero	*Sum Zero*

Description

Get names of columns that have a sum of zero

Usage

```
sum_zero(df)
```

Arguments

df	dataframe

transpose_readcount *Transpose Readcount*

Description

Read in and transpose ChIP-seq Readcount dataframe and match project id

Usage

```
transpose_readcount(readcount.path)
```

Arguments

readcount.path   ChIP-seq readcount dataframe file path

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