Package 'GeneticMediation'

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Type Package

Title Genetic Mediation

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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 conducting causal mediation analysis on data from the ROSMAP study and for cleaning, matching, and preparing the data for analysis.

Encoding UTF-8

LazyData true

RoxygenNote 7.1.0

Depends R (>= 3.6.0)

Imports BiocManager, data.table, IRanges, mediation, readr, stats

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`check_data` *Check Data*

Description

Checks if the data is in the data folder

Usage

```
check_data()
```

`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

`GeneticMediation` *GeneticMediation: A package for conducting causal mediation analysis on ROSMAP data*

Description

GeneticMediation provides methods for conducting causal mediation analysis on data from the ROSMAP study. It also provides methods for cleaning, matching, and preparing the data for analysis.

Author(s)

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See Also

Useful links:

- https://github.com/tydarnell/GeneticMediation
- https://tydarnell.github.io/GeneticMediation

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

lu *Length Unique*

Description

Get the length of unique values in a vector

Usage

```
lu(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

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, simulations)
```

Arguments

chr	chromosome name
gene_matches	list of peak-SNP matches for each gene
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_dat, match_row, simulations)
```

Arguments

med_dat	gene mediation data
match_row	row in match dataframe: col1 SNP, col2 Peak, col3 Gene
simulations	number of simulations to run

setup_folders *Setup Folders*

Description

Creates data, data/mediator, results folders

Usage

```
setup_folders()
```

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

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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