

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>

Author Ty Darnell [aut, cre]

Maintainer Ty Darnell <tydarnell@gmail.com>

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)

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

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check_data	<i>Check Data</i>
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Description

Checks if the data is in the data folder

Usage

```
check_data()
```

chr_numeric	<i>Chromosome Numeric</i>
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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
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clean_data	<i>Clean Data</i>
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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	<i>Combine Data SNP-Peak-Clinical</i>
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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	<i>Combine Data SNP-Peak-Gene</i>
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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
-----	-----------------

last_to_first	<i>Last to First</i>
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Description

Make the last column the first column in a dataframe

Usage

```
last_to_first(df)
```

Arguments

df	dataframe
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lu	<i>Length Unique</i>
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Description

Get the length of unique values in a vector

Usage

```
lu(x)
```

Arguments

x	vector
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make_folder	<i>Make Folder</i>
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Description

Make a folder only if the folder does not already exist

Usage

```
make_folder(path)
```

Arguments

path	folder path
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match_all	<i>Match SNPs Peaks All Chromosomes</i>
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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	<i>Match SNPs and Peaks</i>
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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	<i>SNP-Peak-Clinical Mediation Data Prep</i>
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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	<i>SNP-Peak-Gene Mediation Data Prep</i>
-------------	--

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	<i>SNP-Peak-Clinical Mediation Table</i>
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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	<i>SNP-Peak-Clinical Mediation Table Chromosome</i>
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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	<i>SNP-Peak-Gene Mediation Table Chromosome</i>
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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	<i>SNP-Peak-Clinical Mediation Table</i>
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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	<i>SNP-Peak-Gene Mediation Table</i>
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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	<i>Merge CSV</i>
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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	<i>Setup Folders</i>
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Description

Creates data, data/mediator, results folders

Usage

```
setup_folders()
```

snp_peak_bychr	<i>SNPs and Peaks by Chromosome</i>
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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	<i>Sum Zero</i>
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Description

Get names of columns that have a sum of zero

Usage

```
sum_zero(df)
```

Arguments

df	dataframe
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transpose_readcount	<i>Transpose Readcount</i>
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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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