Package 'GeneticMediation'

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Type Package

Title Genetic Mediation

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<pre>URL https://github.com/tydarnell/GeneticMediation</pre>									
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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.									
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chr_numeric									
clean_data									
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make_folder									
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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

Index

```
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

 ${\tt combine_data_spc} \qquad \qquad {\tt Combine\ Data\ SNP-Peak-Clinical}$

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 3

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)

Maintainer: Ty Darnell <tydarnell@gmail.com>

See Also

Useful links:

• https://github.com/tydarnell/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

4 match_all

lu

Length Unique

Description

Get the length of unique values in a vector

Usage

lu(x)

Arguments

Х

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 5

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

6 med_chr_spc

med_all_spc	SNP-Peak-Clinical Mediation Table
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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 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 7

med_chr_spg	SNP-Peak-Gene Mediation Table Chromosome
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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

8 sum_zero

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

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 9

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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