Package 'GeneticMediation'

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Title Genetic Causal Mediation
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License GPL-3
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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
Imports data.table, IRanges, mediation, readr, stats
<pre>URL https://tydarnell.github.io/GeneticMediation/</pre>
R topics documented:
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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

data_by_chr

Data by Chromosome

Description

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

Usage

```
data_by_chr(chrs, snps, peaks)
```

Arguments

chrs Character vector of chromosomes names

snps SNP information dataframe peaks Peak information dataframe

data_prep_spc 3

data_prep_spc

SNP-Peak-Clinical Data Prep Helper

Description

Helper function for SNP-Peak-Clinical mediation data. Combine projid, SNPs, PCs, membership, age, gender, peaks, and outcome data for a chromosome

Usage

```
data_prep_spc(chr)
```

Arguments

chr

chromosome name

data_prep_spg

SNP-Peak-Gene Data Prep Helper

Description

Helper function for SNP-Peak-Gene data prep. Combine projid, SNPs, PCs, membership, age, gender, peaks, gene and outcome data for a chromosome.

Usage

```
data_prep_spg(chr)
```

Arguments

chr

chromosome name

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

path for new folder

match_all

Match All Chromosomes

Description

Match SNPs and Peaks in all chromosomes, save as "data/matches.csv"

Usage

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

Arguments

snp.info SNP information peak.info Peak information

chrs character vector of chromosome names

match_chr 5

match_chr Match Chromosome

Description

Match Peaks and SNPs in a chromosome

Usage

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

Arguments

snp.info SNP information peak.info Peak information

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/med.res/res_chr.RData"

Usage

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

Arguments

chr chromosome name

 $\verb| all_matches| & data frame of SNP-Peak matches for all chromosomes| \\$

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/gene.res/res_chr.RData"

Usage

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

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
IIIEU_all_Spc	SIVI -I EUK-CHINGUI MEGIGION IUDIE

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

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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 transpose_readcount

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

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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