

Package ‘GeneticMediation’

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Type Package

Title Genetic Causal Mediation

Version 0.1.0

License GPL-3

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

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

R topics documented:

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|-------------|---------------------------|
| chr_numeric | <i>Chromosome Numeric</i> |
|-------------|---------------------------|

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 | <i>Clean Data</i> |
|------------|-------------------|

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 | <i>Data by Chromosome</i> |
|-------------|---------------------------|

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 | <i>SNP-Peak-Clinical Data Prep Helper</i> |
|---------------|---|

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 | <i>SNP-Peak-Gene Data Prep Helper</i> |
|---------------|---------------------------------------|

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 | <i>Last to First</i> |
|---------------|----------------------|

Description

Make the last column the first column in a dataframe

Usage

```
last_to_first(df)
```

Arguments

| | |
|----|-----------|
| df | dataframe |
|----|-----------|

| | |
|----|----------------------|
| lu | <i>Length Unique</i> |
|----|----------------------|

Description

Get the length of unique values in a vector

Usage

```
lu(x)
```

Arguments

| | |
|---|--------|
| x | vector |
|---|--------|

| | |
|-------------|--------------------|
| make_folder | <i>Make Folder</i> |
|-------------|--------------------|

Description

Make a folder only if the folder does not already exist

Usage

```
make_folder(path)
```

Arguments

| | |
|------|---------------------|
| path | path for new folder |
|------|---------------------|

| | |
|-----------|------------------------------|
| match_all | <i>Match All Chromosomes</i> |
|-----------|------------------------------|

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 | <i>Match Chromosome</i> |
|-----------|-------------------------|

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 | <i>SNP-Peak-Clinical Mediation Data Prep</i> |
|-------------|--|

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 |
| 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/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 |

| | |
|-------------|--|
| med_all_spc | <i>SNP-Peak-Clinical Mediation Table</i> |
|-------------|--|

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> |
|-------------|---|

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> |
|-------------|---|

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 | <i>SNP-Peak-Clinical Mediation Table</i> |
|---------------|--|

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> |
|---------------|--------------------------------------|

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 |

| | |
|---------------------|----------------------------|
| transpose_readcount | <i>Transpose Readcount</i> |
|---------------------|----------------------------|

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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