Package 'MetABEL'

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Type Package

Title Meta-analysis of genome-wide SNP association results

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Depends R (>= 2.5.1)

Suggests GenABEL

Description A package for meta-analysis of genome-wide association
scans between quantitative or binary traits and SNPs

License GPL (>= 2)

NeedsCompilation no

Repository CRAN

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R topics documented:

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forestplot   *Function to draw meta-analysis forest plots*

Description

This function creates forest plots from meta-analysis data.

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Usage

```
forestplot(estimate, se, labels = paste("Study", c(1:length(estimate))),
  CI = 0.95, xexp = FALSE, xlab = expression(beta), ylab = "", ...)
```

Arguments

estimate	Vector of effect estimates
se	Vector of standard errors
labels	Vector of labels for the individual studies (default: Study 1, Study 2, etc.)
CI	Confidence interval (default: 0.95)
xexp	Whether the effect values are to be depicted on an exponential scale (default: FALSE)
xlab	Label for the horizontal axis (default: β)
ylab	Label for the horizontal axis (default: empty)
...	Arguments passed to the plot function, e.g. main="My plot"

Author(s)

Yurii Aulchenko, Lennart C. Karssen

Examples

```
beta <- c(0.16, 0.091, 0.072, -0.03)
se   <- c(0.07, 0.042, 0.048, 0.12)
forestplot(beta, se, main="Example plot")
```

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metagwa.files	*Meta-analysis of a series of results from GWA scans*

Description

Performes meta-analysis of results of multiple GWA studies stored in files.

Usage

```
metagwa.files(dir = ".", pops, extens, maf = 5, call = 0.95,
  phwe = 1e-08, precorrect = TRUE, correct.pooled = FALSE)
```

Arguments

`dir`	Path to directory containing files with GWA results
`pops`	A vector specifying study names, which make the first part of the file names
`extens`	Fixed extension to the file name
`maf`	Filter threshold for the absolute number/frequency of minor allele. If the parameter is < 1, this MAF threshold is used for filtering before meta-analysis; if this parameter is >1, n*MAF – absolute number of the minor allele copies – is used
`call`	Filter threshold for SNP call rate
`phwe`	Filter threshold for SNP P-value for HWE
`precorrect`	Should GC be applied to the original data before pooling
`correct.pooled`	Whether to apply Genomic Control correction to the study named "POOLED"

Details

The function looks for files named "POPSextens" in the directory "dir", reads them and pool consecutively using `metagwa.tables` function.

The source files should contain a number of variables, such as allelic coding, code for the effective allele, etc. Please refer to the formetascore function of GenABEL package for details.

When the file is not available for the first population, or there are non-unique population names, the function stops with an error message.

If there are no files corresponding to next populations, these are skipped in analysis with a warning message (see details in the description of returned values).

Value

Results are dumped to file named "POOLEDextens" in the directory "dir". Additionally, a list is returned with elements

`analysed.pops`	list of populations successfully analysed

Author(s)

Yurii Aulchenko

See Also

`metagwa.tables`

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metagwa.tables   *Pairwise meta-analysis of results from GWA scans*

Description

Performes meta-analysis of results of two individual GWA studies

Usage

```
metagwa.tables(data.x, data.y, name.x = ”P1”, name.y = ”P2”,
  precorrect = TRUE, correct.pooled = FALSE)
```

Arguments

data.x	First data frame with GWA data
data.y	Second data frame with GWA data
name.x	First study name
name.y	Second study name
precorrect	Should GC be applied to the original data before pooling
correct.pooled	Whether to apply Genomic Control correction to the study named "POOLED"

Details

Original data frames should contain a number of variables, such as allelic coding, code for the effective allele, etc. Please refer to the formetascore function of the GenABEL package for details.

Value

A data frame containing summary statistics and essential details of the individual studies

Author(s)

Yurii Aulchenko

See Also

metagwa.files

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