

Package ‘miniMeta’

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Type Package

Title Web Application to Run Meta-Analyses

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Imports shiny, shinyjs, shinyWidgets, colourpicker, rhandsontable,
metafor, markdown, WriteXLS, readxl, jsonlite, grDevices,
methods, stats

Depends meta (>= 7.0-0), R (>= 4.0.0)

Description Shiny web application to run meta-analyses.

Essentially a graphical front-end to package 'meta' for R.

Can be useful as an educational tool, and for quickly
analyzing and sharing meta-analyses.

Provides output to quickly fill in GRADE (Grading of
Recommendations, Assessment, Development and Evaluations)
Summary-of-Findings tables.

Importantly, it allows further processing of the results
inside R, in case more specific analyses are needed.

License GPL (>= 2)

Encoding UTF-8

LazyData true

RoxygenNote 7.3.1

Suggests knitr, rmarkdown

VignetteBuilder knitr

URL <https://github.com/thlytras/miniMeta>

BugReports <https://github.com/thlytras/miniMeta/issues>

NeedsCompilation no

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analysisOptions	<i>Get analytical options from miniMeta object</i>
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Description

This function returns the analytical options stored in a miniMeta object, as a named list of arguments, for further processing.

Usage

```
analysisOptions(x, data = FALSE)
```

Arguments

x	An object of class miniMeta
data	If TRUE, the data associated with the meta-analysis are included in the return value. This allows you for example to run: <code>do.call(metabin, analysisOptions(x, data=TRUE))</code> or <code>do.call(metagen, analysisOptions(x, data=TRUE))</code> (depending on the contents of x), in order to re-run the meta-analysis.

Value

A named list of arguments corresponding to the arguments of `metagen` or `metabin`.

Examples

```
analysisOptions(example_miniMeta_rct)
```

as.source	<i>Return miniMeta analysis as source code</i>
-----------	--

Description

Returns an entire miniMeta analysis in an R source code format. This provides a basis for further processing the results exported from miniMeta, using R code, in order to perform more elaborate or more specific analyses.

Usage

```
as.source(x)
```

Arguments

x An object of class miniMeta

Value

A character vector of length one, containing R code that loads the data, runs the meta-analysis, and plots a forest plot. You can save this in a text file using [writeLines](#).

Examples

```
fname <- tempfile("my_analysis", fileext = ".R")
fname
# Writes the miniMeta analysis to an R script
writeLines(as.source(example_miniMeta_rct), fname)
```

example_analyses	<i>Example miniMeta analyses</i>
------------------	----------------------------------

Description

These are example miniMeta meta-analyses, with study data taken from [Lytras et al, 2014](#). Object `example_miniMeta_rct` contains a meta-analysis of Randomized Controlled Trials (RCTs), and `example_miniMeta_obs` a meta-analysis of observational studies.

Usage

```
example_miniMeta_obs
```

```
example_miniMeta_rct
```

Format

Objects of class miniMeta

An object of class miniMeta (inherits from list) of length 4.

An object of class miniMeta (inherits from list) of length 4.

References

Lytras T, Nikolopoulos G, Bonovas S. World J Gastroenterol 2014;20(7):1858-70 ([PubMed](#))

forest.miniMeta	<i>Forest plot for miniMeta objects</i>
-----------------	---

Description

Draws a forest plot for a miniMeta object using the options stored in the object

Usage

```
## S3 method for class 'miniMeta'
forest(x, ...)
```

Arguments

x	An object of class miniMeta
...	Further arguments passed to or from other methods

Examples

```
forest(example_miniMeta_obs)
```

is.miniMeta	<i>Is this a miniMeta object?</i>
-------------	-----------------------------------

Description

This function checks whether this is a valid miniMeta object

Usage

```
is.miniMeta(x)
```

Arguments

x	An object of class miniMeta
---	-----------------------------

Value

TRUE if it is a valid miniMeta object, FALSE if it is not.

Examples

```
is.miniMeta(example_miniMeta_obs) # returns TRUE  
is.miniMeta(example_miniMeta_rct) # returns TRUE
```

`is.miniMeta.obs` *Is this a miniMeta object for observational studies?*

Description

This function checks whether this is a valid miniMeta object holding a a meta-analysis of observational studies.

Usage

```
is.miniMeta.obs(x)
```

Arguments

x An object of class miniMeta

Value

TRUE if it is a valid miniMeta object holding a meta-analysis of observational studies, FALSE if it is not.

Examples

```
is.miniMeta.obs(example_miniMeta_obs) # returns TRUE  
is.miniMeta.obs(example_miniMeta_rct) # returns FALSE
```

<code>is.miniMeta.rct</code>	<i>Is this a miniMeta object for RCTs?</i>
------------------------------	--

Description

This function checks whether this is a valid miniMeta object holding a meta-analysis of Randomized Controlled Trials (RCTs).

Usage

```
is.miniMeta.rct(x)
```

Arguments

x	An object of class miniMeta
---	-----------------------------

Value

TRUE if it is a valid miniMeta object holding a meta-analysis of Randomized Controlled Trials (RCTs), FALSE if it is not.

Examples

```
is.miniMeta.rct(example_miniMeta_obs) # returns FALSE  
is.miniMeta.rct(example_miniMeta_rct) # returns TRUE
```

<code>miniMeta</code>	<i>Launch miniMeta in your browser</i>
-----------------------	--

Description

This function launches miniMeta in your browser

Usage

```
miniMeta()
```

Examples

```
## Not run:  
miniMeta()  
  
## End(Not run)
```

parseArguments	<i>Parse arguments from a comma-separated list</i>
----------------	--

Description

Read a comma-separated list of arguments (as a character string), parse them, and return as a named R list. This function is used in `miniMeta` to parse arguments for `forest.meta()` when given as a string.

Usage

```
parseArguments(x)
```

Arguments

x	A character vector (of length one) containing the arguments. All should be named.
---	---

Value

A named list of arguments, or an object of class "try-error" on failure.

Examples

```
parseArguments('col.diamond="red", sm="RR", common=FALSE')
```

plotOptions	<i>Get forest plot options from miniMeta object</i>
-------------	---

Description

This function returns the forest plot options stored in a `miniMeta` object, as a named list of arguments, for further processing. This allows finer control than directly plotting using the `forest.miniMeta` method. See the example below.

Usage

```
plotOptions(x)
```

Arguments

x	An object of class <code>miniMeta</code>
---	--

Value

A named list of arguments corresponding to the arguments of `forest.meta`.

Examples

```
## Not run:
# Extract the plot options from the miniMeta object
plot_opts <- plotOptions(example_miniMeta_obs)
# Call directly the forest.meta method, with all plot options
do.call(forest, c(x=list(example_miniMeta_obs$meta), plot_opts))

# Equivalently, call the forest.miniMeta method directly
forest(example_miniMeta_obs)

## End(Not run)
```

sampleSizeBin

Sample size calculator for binary outcomes

Description

Calculates sample size for a trial with a binomial outcome, for a given power and false positive rate.

Usage

```
sampleSizeBin(cer, RRR = 25, ier = NULL, a = 0.05, b = 0.2, K = 1)
```

Arguments

cer	Control group event rate, a value between 0 and 1. All should be named.
RRR	Relative Risk Reduction (%) in the intervention group.
ier	Intervention group event rate, a value between 0 and 1. If NULL, it is calculated from RRR. If non-NULL, the value of this argument is used and RRR is ignored.
a	False positive rate (alpha). Defaults to 0.05 (5%).
b	False negative rate (beta). Defaults to 0.2. Power is one minus beta; thus the default is 80% power.
K	Ratio of intervention group size to control group size. Defaults to 1, meaning both groups have the same size. Set to infinity (Inf) in order to calculate sample size for a <i>single-group study</i> , see details below.

Value

An integer vector of length 2, with the sample sizes for the control and intervention groups.

If $K=Inf$, then the sample size calculation is not for a study with two groups, but for a single-group study in which a fixed known population event rate is assumed. In that case, argument `cer` represents the population event rate, and `ier` the study event rate that it we anticipate. And the return value is a single value, i.e. the sample size of the study.

Examples

```
# Sample size for a trial with 40% control event rate and 1:1 randomization,
# aiming to show a Relative Risk Reduction of 30% with 80% power.
sampleSizeBin(0.4, RRR=30)

# Sample size for a single-group study aiming to show an event rate of 20%
# against a population event rate of 10%, with 90% power.
sampleSizeBin(0.1, ier=0.2, b=0.1, K=Inf)
```

sampleSizeCont

*Sample size calculator for continuous outcomes***Description**

Calculates sample size for a trial with a continuous outcome, for a given power and false positive rate.

Usage

```
sampleSizeCont(Dm, SD, a = 0.05, b = 0.2, K = 1)
```

Arguments

Dm	Anticipated absolute difference in means between the two groups (intervention and control).
SD	Anticipated standard deviation for the outcome.
a	False positive rate (alpha). Defaults to 0.05 (5%).
b	False negative rate (beta). Defaults to 0.2. Power is one minus beta; thus the default is 80% power.
K	Ratio of intervention group size to control group size. Defaults to 1, meaning both groups have the same size. Set to infinity (Inf) in order to calculate sample size for a <i>single-group study</i> , see details below.

Value

An integer vector of length 2, with the sample sizes for the control and intervention groups.

If $K=Inf$, then the sample size calculation is not for a study with two groups, but for a single-group study in which we try to show a difference from a fixed known population mean. In that case, argument Dm represents the absolute difference between the study mean and population mean, rather than the difference in means between two groups. And the return value is a single value, i.e. the sample size of the study.

Examples

```
# Sample size for a trial with 2:1 randomization, aiming to show a mean
# difference of 2 for a continuous outcome with a standard deviation of 3,
# with 90% power.
sampleSizeCont(2, 3, b=0.1, K=2)

# Similar for a single-group study aiming to show a difference of 2 against
# a known population mean.
sampleSizeCont(2, 3, b=0.1, K=Inf)
```

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