

# Package ‘rmeta’

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**Description** Functions for simple fixed and random effects meta-analysis for two-sample comparisons and cumulative meta-analyses. Draws standard summary plots, funnel plots, and computes summaries and tests for association and heterogeneity

**Title** Meta-analysis

**License** GPL-2

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catheter

---

*Meta-analysis of antibacterial catheter coating*


---

### Description

Data on the effectiveness of silver sulfadiazine coating on venous catheters for preventing bacterial colonisation of the catheter and bloodstream infection

### Usage

```
data(catheter)
```

### Format

A data.frame with 8 variables giving information about 16 controlled trials of antibacterial-coated venous catheters

```
Name : Name of principal author
n.trt : number of coated catheters
n.ctrl : number of standard catheters
col.trt : number of coated catheters colonised
          by bacteria
col.ctrl : number of standard catheters colonised
          by bacteria
inf.trt : number of coated catheters resulting in
          bloodstream infection
inf.ctrl : number of standard catheters resulting in
          bloodstream infection
or : Odds ratio
```

### Source

Veenstra D et al (1998) "Efficacy of Antiseptic Impregnated Central Venous Catheters in Preventing Nosocomial Infections: A Meta-analysis" JAMA 281:261-267

### Examples

```
library(rmeta)
data(catheter)
a <- meta.MH(n.trt, n.ctrl, col.trt, col.ctrl, data=catheter,
             names=Name, subset=c(13,6,5,3,7,12,4,11,1,8,10,2))
b <- meta.DSL(n.trt, n.ctrl, col.trt, col.ctrl, data=catheter,
             names=Name, subset=c(13,6,5,3,7,12,4,11,1,8,10,2))
a
b
summary(a)
summary(b)
plot(a)
```

```
plot(b)
```

---

```
cochrane
```

*Data for Cochrane Collaboration logo*

---

## Description

Data from randomised trials before 1980 of corticosteroid therapy in premature labour and its effect on neonatal death.

## Usage

```
data(cochrane)
```

## Format

This data frame contains the following columns:

**name** Identifier for the study

**ev.trt** Number of deaths in the treated group

**n.trt** Number in the treated group

**ev.ctrl** Number of deaths in the control group

**n.ctrl** Number in the control group

## Details

This meta-analysis, if done, would likely have resulted in the treatment being widely used a decade earlier than it was, saving many lives. The graph is part of the logo of the Cochrane Collaboration, a group aiming to perform systematic reviews of the entire clinical trial literature.

## Source

<http://www.cochrane.org>

## Examples

```
data(cochrane)
steroid <- meta.MH(n.trt, n.ctrl, ev.trt, ev.ctrl,
                  names=name, data=cochrane)
plot(steroid, col=meta.colors("RoyalBlue"))
```

cummeta

*Cumulative meta-analysis of binary data***Description**

A cumulative meta-analysis plot shows how evidence has accumulated over time. The  $i$ th line in the cumulative meta-analysis plot is the summary produced by a meta-analysis of the first  $i$  trials.

**Usage**

```
cummeta(ntrt, nctrl, ptrt, pctrl, conf.level = 0.95, names = NULL, data=
NULL, subset = NULL, na.action = na.fail, method = c("meta.MH", "meta.DSL"), stati
cummeta.summaries(effects, stderrs, conf.level = 0.95, names = NULL, weights=NULL, da
## S3 method for class 'meta.cum':
plot(x, conf.level = NULL, colors = meta.colors(), xlab = NULL,
      summary.line = TRUE, summary.conf = FALSE, main="Cumulative meta-analysis", lwd
## S3 method for class 'meta.cum':
summary(object ,conf.level=NULL,...)
```

**Arguments**

|              |   |
|--------------|---|
| ntrt         | Number of subjects in treated/exposed group   |
| nctrl        | Number of subjects in control group   |
| ptrt         | Number of events in treated/exposed group   |
| pctrl        | Number of events in control group   |
| effects      | Difference between control and treatment group                                      |
| stderrs      | Standard errors of effects  |
| weights      | Study weights (see <a href="#">meta.summaries</a> )                                 |
| names        | names or labels for studies   |
| data         | data frame to interpret variables   |
| subset       | subset of studies to include  |
| na.action    | How to handle missing values  |
| method       | Which meta-analysis method to use   |
| statistic    | "OR" for odds ratio or "RR" for relative risk.                                      |
| logscale     | The <code>effects</code> values are the logarithms of actual effects (for plotting) |
| x, object    | a <code>meta.cum</code> object  |
| ...          | other graphical arguments for <a href="#">metaplot</a>                              |
| conf.level   | Coverage for confidence intervals   |
| colors       | see <a href="#">meta.colors</a>   |
| xlab         | X-axis label  |
| summary.line | Plot a vertical line at the final summary value?                                    |
| summary.conf | Plot vertical lines at the final confidence interval limits?                        |
| main, lwd    | graphical parameters  |

**Value**

Object of class `meta.cum`.

**See Also**

[meta.MH](#), [meta.DSL](#)

**Examples**

```
data(cochrane)
steroid<-cummeta(n.trt,n.ctrl,ev.trt,ev.ctrl,names=name,data=cochrane,statistic="RR",method="random")
summary(steroid)
summary(steroid)
data(catheter)
b <- meta.DSL(n.trt, n.ctrl, col.trt, col.ctrl, data=catheter,
              names=Name, subset=c(13,6,5,3,12,4,11,1,8,10,2))
d <- cummeta.summaries(b$log, b$selogs, names=b$names,
                       method="random", logscale=TRUE)
plot(d,summary.conf=TRUE)
summary(d)
```

---

forestplot

*Forest plots*

---

**Description**

Draw a forest plot together with a table of text.

**Usage**

```
forestplot(labeltext, mean, lower, upper, align = NULL, is.summary =
FALSE, clip = c(-Inf, Inf), xlab = "", zero = 0, graphwidth = unit(2,
"inch"), col = meta.colors(), xlog = FALSE, xticks=NULL, boxsize=NULL,...)
```

**Arguments**

|                         |  |
|-------------------------|--|
| <code>labeltext</code>  | Matrix of strings or NAs for blank spaces  |
| <code>mean</code>       | Vector of centers of confidence intervals (or NAs for blank space)                 |
| <code>lower</code>      | Vector of lower ends of confidence intervals                                       |
| <code>upper</code>      | Vector of upper ends of confidence intervals                                       |
| <code>align</code>      | Vector giving alignment (l,r,c) for columns of table                               |
| <code>is.summary</code> | Vector of logicals. Summary lines have bold text and diamond confidence intervals. |
| <code>clip</code>       | Lower and upper limits for clipping confidence intervals to arrows                 |
| <code>xlab</code>       | x-axis label   |

|            |   |
|------------|---|
| zero       | x-axis coordinate for zero line   |
| graphwidth | Width of confidence interval graph  |
| col        | See <code>meta.colors</code>  |
| xlog       | If TRUE, x-axis tick marks are exponentiated  |
| xticks     | Optional user-specified x-axis tick marks. Specify <code>NULL</code> to use the defaults, <code>numeric(0)</code> to omit the x-axis. |
| boxsize    | Override the default box size based on precision  |
| ...        | Not used.   |

### Details

This function is more flexible than `metaplot` and the `plot` methods for meta-analysis objects, but requires more work by the user.

In particular, it allows for a table of text, and clips confidence intervals to arrows when they exceed specified limits.

### Value

None

### See Also

`metaplot`

### Examples

```
data(cochrane)
steroid <- meta.MH(n.trt, n.ctrl, ev.trt, ev.ctrl,
                  names=name, data=cochrane)

tabletext<-cbind(c("", "Study", steroid$names, NA, "Summary"),
                 c("Deaths", "(steroid)", cochrane$ev.trt, NA, NA),
                 c("Deaths", "(placebo)", cochrane$ev.ctrl, NA, NA),
                 c("", "OR", format(exp(steroid$logOR), digits=2), NA, format(exp(steroid$logMH),
)

m<- c(NA, NA, steroid$logOR, NA, steroid$logMH)
l<- m-c(NA, NA, steroid$selogOR, NA, steroid$selogMH) *2
u<- m+c(NA, NA, steroid$selogOR, NA, steroid$selogMH) *2
forestplot(tabletext, m, l, u, zero=0, is.summary=c(TRUE, TRUE, rep(FALSE, 8), TRUE),
           clip=c(log(0.1), log(2.5)), xlog=TRUE,
           col=meta.colors(box="royalblue", line="darkblue", summary="royalblue"))

forestplot(tabletext, m, l, u, zero=0, is.summary=c(TRUE, TRUE, rep(FALSE, 8), TRUE),
           clip=c(log(0.1), log(2.5)), xlog=TRUE, boxsize=0.75,
           col=meta.colors(box="royalblue", line="darkblue", summary="royalblue"))
```

---

funnelplot

*Funnel plot for publication bias*


---

### Description

Plots the treatment difference for trials against the size of the trial (or other specified variable). Asymmetry in the plot often indicates publication bias. Generic, with methods for meta-analysis objects.

### Usage

```
funnelplot(x, ...)
## Default S3 method:
funnelplot(x, se, size=1/se, summ=NULL,
           xlab="Effect", ylab="Size", colors=meta.colors(),
           conf.level=0.95, plot.conf=FALSE,
           zero=NULL, mirror=FALSE, ...)
```

### Arguments

|            |  |
|------------|--|
| x          | Treatment difference                               |
| se         | Standard error of x                                |
| size       | Variable for the vertical axis                     |
| summ       | summary treatment difference                       |
| xlab       | x-axis label                                       |
| ylab       | y-axis label                                       |
| colors     | list of colors for components of the plot          |
| conf.level | For confidence interval plotting                   |
| plot.conf  | Plot confidence intervals instead of just points?  |
| zero       | location of a null hypothesis line                 |
| mirror     | Add points reflected around summ?                  |
| ...        | further arguments to be passed from or to methods. |

### Details

With the default value of `size` the plot should appear as a upwards-pointing funnel shape. Publication bias often causes one side of the funnel to be trimmed near the base. The `mirror` plot creates a symmetric funnel by reflecting the plot around the `summ` value. In the presence of publication bias the added points will separate from the real studies.

### Value

Used for its side-effect.

**Author(s)**

Thomas Lumley

**See Also**

[meta.DSL](#), [meta.MH](#), [meta.summaries](#), [metaplot](#)

**Examples**

```
data(catheter)
a <- meta.MH(n.trt, n.ctrl, col.trt, col.ctrl, data=catheter,
             names=Name, subset=c(13,6,5,3,7,12,4,11,1,8,10,2))
funnelplot(a$logOR, a$selogOR)
funnelplot(a$logOR, a$selogOR,
           plot.conf=TRUE, summ=a$logMH, mirror=TRUE)
funnelplot(a, plot.conf=TRUE)
```

---

meta.colors

*Control colours in meta-analysis plot*

---

**Description**

Wrapper function for specifying colours to meta-analysis plots

**Usage**

```
meta.colors(all.elements, box="black", lines="gray", summary="black",
            zero="lightgray", mirror="lightblue", text="black",
            axes="black", background=NA)
```

**Arguments**

|                           |   |
|---------------------------|---|
| <code>all.elements</code> | if present, overrides other arguments                       |
| <code>box</code>          | Colour of sample size box                                   |
| <code>lines</code>        | Colour of confidence intervals                              |
| <code>summary</code>      | Colour of summary estimate                                  |
| <code>zero</code>         | Colour of null hypothesis line                              |
| <code>mirror</code>       | Colour of reflected points (in <a href="#">funnelplot</a> ) |
| <code>text</code>         | Colour of labels  |
| <code>axes</code>         | Colour of x-axis and axis labels                            |
| <code>background</code>   | Background colour.  |

**Value**

a list of colors

**See Also**

[plot.meta.MH](#), [plot.meta.DSL](#), [plot.meta.summaries](#), [funnelplot](#), [metaplot](#)

**Examples**

```
data(cochrane)
steroid <- meta.MH(n.trt, n.ctrl, ev.trt, ev.ctrl,
                  names=name, data=cochrane)

## All black, for better photocopying
plot(steroid, col=meta.colors("black"))

## distinguish the summary
plot(steroid, colors=meta.colors(summary="forestgreen"))

data(catheter)
e <- meta.DSL(n.trt, n.ctrl, inf.trt, inf.ctrl, data=catheter,
              names=Name, subset=c(13,6,3,12,4,11,1,14,8,10,2))

## Truly awful colour scheme to illustrate flexibility
plot(e, colors=meta.colors(summary="green", lines=c("purple", "skyblue"),
                           box="red", zero="yellow", text=palette(), background="tomato",
                           axes="lightgreen"))

## Dark blue background popular for presentations.
plot(e, colors=meta.colors(summary="white", lines="#FFFFFF0",
                           box="#FFFF50", zero="grey90", text="white", background="darkblue",
                           axes="grey90"))
```

---

meta.DSL

*Random effects (DerSimonian-Laird) meta-analysis*

---

**Description**

Computes the individual odds ratios or relative risks, the summary, the random effects variance, and Woolf's test for heterogeneity. The `print` method gives the summary and test for heterogeneity; the `summary` method also gives all the individual odds ratios and confidence intervals. Studies with zero or infinite odds ratio are omitted, as their variance cannot be calculated sensibly.

The `plot` method draws a standard meta-analysis plot. The confidence interval for each study is given by a horizontal line, and the point estimate is given by a square whose height is inversely proportional to the standard error of the estimate. The summary odds ratio, if requested, is drawn as a diamond with horizontal limits at the confidence limits and width inversely proportional to its standard error.

**Usage**

```
meta.DSL(ntrt, nctrl, ptrt, pctrl, conf.level=0.95,
         names=NULL, data=NULL, subset=NULL, na.action=na.fail, statistic="OR")
```

```
## S3 method for class 'meta.DSL':
summary(object, conf.level=NULL, ...)
## S3 method for class 'meta.DSL':
plot(x, summary=TRUE, summlabel="Summary",
      conf.level=NULL, colors=meta.colors(), xlab=NULL,...)
```

### Arguments

|            |   |
|------------|---|
| ntrt       | Number of subjects in treated/exposed group   |
| nctrl      | Number of subjects in control group   |
| ptrt       | Number of events in treated/exposed group   |
| pctrl      | Number of events in control group   |
| conf.level | Coverage for confidence intervals   |
| names      | names or labels for studies   |
| data       | data frame to interpret variables   |
| subset     | subset of studies to include  |
| na.action  | a function which indicates what should happen when the data contain NAs. Defaults to <code>na.fail</code> . |
| statistic  | "OR" for odds ratio, "RR" for relative risk   |
| x, object  | a <code>meta.DSL</code> object  |
| summary    | Plot the summary odds ratio?  |
| summlabel  | Label for the summary odds ratio  |
| colors     | see <code>meta.colors</code>  |
| xlab       | x-axis label, default is based on <code>statistic</code>  |
| ...        | further arguments to be passed from or to methods.  |

### Value

An object of class `meta.DSL` with `print`, `plot`, `funnelplot` and `summary` methods.

### Author(s)

Thomas Lumley

### See Also

`plot`, `par`, `meta.MH`, `funnelplot`

### Examples

```
data(catheter)
b <- meta.DSL(n.trt, n.ctrl, col.trt, col.ctrl, data=catheter,
              names=Name, subset=c(13, 6, 5, 3, 7, 12, 4, 11, 1, 8, 10, 2))
b
summary(b)
```

```

plot(b)
e <- meta.DSL(n.trt, n.ctrl, inf.trt, inf.ctrl, data=catheter,
              names=Name, subset=c(13,6,3,12,4,11,1,14,8,10,2))
e
summary(e)
##tasteless
plot(e, colors=meta.colors(summary="green", lines="purple", box="orange"))

```

---

meta.MH

*Fixed effects (Mantel-Haenszel) meta-analysis*


---

## Description

Computes the individual odds ratio or relative risk, the Mantel-Haenszel summary, and Woolf's test for heterogeneity. The `print` method gives the summary and test for heterogeneity; the `summary` method also gives all the individual odds ratios and confidence intervals.

The `plot` method draws a standard meta-analysis plot. The confidence interval for each study is given by a horizontal line, and the point estimate is given by a square whose height is inversely proportional to the standard error of the estimate. The summary odds ratio, if requested, is drawn as a diamond with horizontal limits at the confidence limits and width inversely proportional to its standard error.

## Usage

```

meta.MH(ntrt, nctrl, ptrt, pctrl, conf.level=0.95,
        names=NULL, data=NULL, subset=NULL, na.action = na.fail, statistic="OR")
## S3 method for class 'meta.MH':
summary(object, conf.level=NULL, ...)
## S3 method for class 'meta.MH':
plot(x, summary=TRUE, summlabel="Summary",
     conf.level=NULL, colors=meta.colors(), xlab=NULL, ...)

```

## Arguments

|                        |   |
|------------------------|---|
| <code>ntrt</code>      | Number of subjects in treated/exposed group   |
| <code>nctrl</code>     | Number of subjects in control group   |
| <code>ptrt</code>      | Number of events in treated/exposed group   |
| <code>pctrl</code>     | Number of events in control group   |
| <code>names</code>     | names or labels for studies   |
| <code>data</code>      | data frame to interpret variables   |
| <code>subset</code>    | subset of studies to include  |
| <code>na.action</code> | a function which indicates what should happen when the data contain NAs. Defaults to <code>na.fail</code> . |
| <code>statistic</code> | "OR" for odds ratio, "RR" for relative risk   |
| <code>x, object</code> | a <code>meta.MH</code> object   |

|                         |  |
|-------------------------|--|
| <code>summary</code>    | Plot the summary odds ratio?                             |
| <code>summlabel</code>  | Label for the summary odds ratio                         |
| <code>conf.level</code> | Coverage for confidence intervals                        |
| <code>colors</code>     | see <code>meta.colors</code>                             |
| <code>xlab</code>       | x-axis label, default is based on <code>statistic</code> |
| <code>...</code>        | further arguments to be passed to or from methods.       |

**Value**

An object of class `meta.MH` with `print`, `plot`, `funnelplot` and `summary` methods.

**Note**

There are at least two other ways to do a fixed effects meta-analysis of binary data. Peto's method is a computationally simpler approximation to the Mantel-Haenszel approach. It is also possible to weight the individual odds ratios according to their estimated variances. The Mantel-Haenszel method is superior if there are trials with small numbers of events (less than 5 or so in either group)

**Author(s)**

Thomas Lumley

**See Also**

`plot`, `par`, `meta.DSL`, `funnelplot`

**Examples**

```
data(catheter)
a <- meta.MH(n.trt, n.ctrl, col.trt, col.ctrl, data=catheter,
             names=Name, subset=c(13,6,5,3,7,12,4,11,1,8,10,2))
a
summary(a)
plot(a)
d <- meta.MH(n.trt, n.ctrl, inf.trt, inf.ctrl, data=catheter,
             names=Name, subset=c(13,6,3,12,4,11,1,14,8,10,2))
d
summary(d)
## plot with par("fg")
plot(d, colors=meta.colors(NULL))
```

---

meta.summaries      *Meta-analysis based on effect estimates*

---

## Description

Computes a summary estimate and confidence interval from a collection of treatment effect estimates and standard errors. Allows fixed or random effects, optional quality weights.

## Usage

```
meta.summaries(d, se, method=c("fixed", "random"), weights=NULL,
               logscale=FALSE, names=NULL, data=NULL,
               conf.level=0.95, subset=NULL, na.action=na.fail)
## S3 method for class 'meta.summaries':
summary(object, conf.level=NULL, ...)
## S3 method for class 'meta.summaries':
plot(x, summary=TRUE, summlabel="Summary",
      conf.level=NULL, colors=meta.colors(),
      xlab=NULL, logscale=NULL, ...)
```

## Arguments

|            |   |
|------------|---|
| d          | Effect estimates  |
| se         | standard errors for d   |
| method     | Standard errors and default weights from fixed or random-effects?   |
| weights    | Optional weights (eg quality weights)   |
| logscale   | Effect is on a log scale? (for plotting)  |
| names      | labels for the separate studies   |
| data       | optional data frame to find variables in  |
| conf.level | level for confidence intervals  |
| subset     | Which studies to use  |
| na.action  | a function which indicates what should happen when the data contain NAs. Defaults to <code>na.fail</code> . |
| x, object  | a <code>meta.summaries</code> object  |
| summary    | Plot the summary odds ratio?  |
| summlabel  | Label for the summary odds ratio  |
| colors     | see <code>meta.colors</code>  |
| xlab       | label for the effect estimate axis.   |
| ...        | further arguments to be passed to or from methods.  |

**Details**

The summary estimate is a weighted average. If `weights` are specified they are used, otherwise the reciprocal of the estimated variance is used.

The estimated variance is the square of `se` for a `fixed` analysis. For a random analysis a heterogeneity variance is estimated and added.

The variance of a weighted average is a weighted average of the estimated variances using the squares of the weights. This is the square of the summary standard error.

With the default weights these are the standard fixed and random effects calculations.

**Value**

An object of class `meta.summaries`, which has `print`, `plot`, `summary` and `funnelplot` methods.

**Author(s)**

Thomas Lumley

**See Also**

[meta.DSL](#), [meta.MH](#), [funnelplot](#), [metaplot](#)

**Examples**

```
data(catheter)
b <- meta.DSL(n.trt, n.ctrl, col.trt, col.ctrl, data=catheter,
             names=Name, subset=c(13,6,5,3,12,4,11,1,8,10,2))
d <- meta.summaries(b$logos, b$selogs, names=b$names,
                  method="random", logscale=TRUE)
```

---

metaplot

*Meta-analysis plot (forest plot)*

---

**Description**

Plot confidence intervals with boxes indicating the sample size/precision and optionally a diamond indicating a summary confidence interval. This function is usually called by `plot` methods for meta-analysis objects.

**Usage**

```
metaplot(mn, se, nn=NULL, labels=NULL, conf.level=0.95,
         xlab="Odds ratio", ylab="Study Reference", xlim=NULL,
         summn=NULL, sumse=NULL, sumnn=NULL, summlabel="Summary",
         logeffect=FALSE, lwd=2, boxsize=1,
         zero=as.numeric(logeffect), colors=meta.colors(),
         xaxt="s", logticks=TRUE, ...)
```

**Arguments**

|                         |  |
|-------------------------|--|
| <code>mn</code>         | point estimates from studies   |
| <code>se</code>         | standard errors of <code>mn</code>   |
| <code>nn</code>         | precision: box ares is proportional to this. $1/se^2$ is the default                             |
| <code>labels</code>     | labels for each interval   |
| <code>conf.level</code> | Confidence level for confidence intervals  |
| <code>xlab</code>       | label for the point estimate axis  |
| <code>ylab</code>       | label for the axis indexing the different studies  |
| <code>xlim</code>       | the range for the x axis.  |
| <code>summn</code>      | summary estimate   |
| <code>sumse</code>      | standard error of summary estimate   |
| <code>sumnn</code>      | precision of summary estimate  |
| <code>summlabel</code>  | label for summary estimate   |
| <code>logeffect</code>  | TRUE to display on a log scale   |
| <code>lwd</code>        | line width   |
| <code>boxsize</code>    | Scale factor for box size  |
| <code>zero</code>       | "Null" effect value  |
| <code>xaxt</code>       | use "n" for no x-axis (to add a customised one)  |
| <code>logticks</code>   | if TRUE and <code>logscale</code> , have tick values approximately equally spaced on a log scale |
| <code>colors</code>     | see <code>meta.colors</code>   |
| <code>...</code>        | Other graphical parameters   |

**Value**

This function is used for its side-effect.

**See Also**

`forestplot` for more flexible plots  
`plot.meta.DSL`, `plot.meta.MH`, `plot.meta.summaries`

**Examples**

```
data(catheter)
a <- meta.MH(n.trt, n.ctrl, col.trt, col.ctrl, data=catheter,
             names=Name, subset=c(13,6,5,3,7,12,4,11,1,8,10,2))
metaplot(a$logOR, a$selogOR, nn=a$selogOR^-2, a$names,
         summn=a$logMH, sumse=a$selogMH, sumnn=a$selogMH^-2,
         logeffect=TRUE)
metaplot(a$logOR, a$selogOR, nn=a$selogOR^-2, a$names,
         summn=a$logMH, sumse=a$selogMH, sumnn=a$selogMH^-2,
         logeffect=TRUE, logticks=FALSE)
```

```
## angry fruit salad
metaplot(a$logOR, a$selogOR, nn=a$selogOR^-2, a$names,
         summn=a$logMH, sumse=a$selogMH, sumnn=a$selogMH^-2,
         logeffect=TRUE, colors=meta.colors(box="magenta",
         lines="blue", zero="red", summary="orange",
         text="forestgreen"))
```

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