Package 'netdose'

April 17, 2025

Title Dose-Response Network Meta-Analysis in a Frequentist Way

Version 0.6-0

Date 2025-04-14

Depends R (>= 4.4.0), netmeta (>= 3.1.1)

Imports MASS, Hmisc, meta, ggplot2, gridExtra, grid, Matrix

Maintainer Maria Petropoulou <maria.petropoulou@uniklinik-freiburg.de>

URL https://github.com/petropouloumaria/netdose

Description A set of functions providing the implementation of the network meta-
analysis model with dose-response relationships, predicted values of the fitted model and dose-
response plots in a frequentist way.

License GPL (>= 2)

Encoding UTF-8

RoxygenNote 7.3.2

NeedsCompilation no

LazyData true

Author Maria Petropoulou [aut, cre] (<https://orcid.org/0000-0002-7147-3644>),
Guido Schwarzer [aut] (<https://orcid.org/0000-0001-6214-9087>)

Repository CRAN

Date/Publication 2025-04-17 07:10:05 UTC

Contents

netdose-package	*netdose: Brief overview of measures and methodologies for detection of outlying and influential studies in network meta-analysis.*

Description

R package **netdose** provides methods and graphical tools to conduct the network meta-analysis with dose-response relationships in a frequentist way.

Details

R package **netdose** is a tool to conduct dose-response network meta-analysis a frequentist way (Petropoulou et al, 2025). The package can implement the dose-response network meta-analysis model (function (netdose)); calculate the predicted values of the dose-response network meta-analysis model (function (predict)); provide dose-response plots (function (plot.netdose)) (Petropoulou et al., 2025).

Type `help(package = "netdose")` for a listing of R functions available in **netdose**.

Type `citation("netdose")` on how to cite **NMAoutlier** in publications.

To report problems and bugs, please send an email to Dr. Maria Petropoulou <maria.petropoulou@uniklinik-freiburg.de>.

The development version of **netdose** is available on GitHub https://github.com/petropouloumaria/netdose.

Author(s)

Petropoulou Maria <maria.petropoulou@.uniklinik-freiburg.de>, Guido Schwarzer <guido.schwarzer@uniklinik-freiburg.de>

References

Petropoulou et al. (2025): Network meta-analysis with dose-response relationships.

See Also

Useful links:

- https://github.com/petropouloumaria/netdose

---

anesthesia *Anesthesia Dataset for Dose-Response Network Meta-Analysis*

Description

This dataset is a synthesis of randomized controlled studies investigating the effects of different agents for preventing vomiting within 24 h postoperatively in adults after general anaesthesia. Multicomponent interventions have been excluded from this subset to focus on single-agent interventions and their dose-response relationships.

Usage

anesthesia

Format

A data frame with the following columns:

agent1	Character vector indicating the name of the agent in arm 1.
agent2	Character vector indicating the name of the agent in arm 2.
agent3	Character vector indicating the name of the agent in arm 3.
agent4	Character vector indicating the name of the agent in arm 4.
agent5	Character vector indicating the name of the agent in arm 5.
event1	Integer vector for the number of participants who experienced vomiting in arm 1.
event2	Integer vector for the number of participants who experienced vomiting in arm 2.
event3	Integer vector for the number of participants who experienced vomiting in arm 3.
event4	Integer vector for the number of participants who experienced vomiting in arm 4.
event5	Integer vector for the number of participants who experienced vomiting in arm 5.
n1	Integer vector for the total number of participants in study arm 1.
n2	Integer vector for the total number of participants in study arm 2.
n3	Integer vector for the total number of participants in study arm 3.
n4	Integer vector for the total number of participants in study arm 4.
n5	Integer vector for the total number of participants in study arm 5.
dose1	Numeric vector specifying the dose level in arm 1.
dose2	Numeric vector specifying the dose level in arm 2.
dose3	Numeric vector specifying the dose level in arm 3.
dose4	Numeric vector specifying the dose level in arm 4.
dose5	Numeric vector specifying the dose level in arm 5.
studyid	Character vector with unique study identifiers.

Details

The dataset includes data on several agents for preventing vomiting and their observed effects across multiple clinical randomized controlled trials. The outcome is the occurrence of vomiting within 24 hours after surgery. By excluding multicomponent interventions, this subset allows for a more precise evaluation of single-agent dose-response relationships.

The dataset is structured in a contrast-based format and includes the following variables:

- `agent1, agent2, agent3, agent4, agent5`: Names of the agents used in each study arm.
- `event1, event2, event3, event4, event5`: Number of participants who experienced vomiting within 24 hours postoperatively in each study arm.
- `n1, n2, n3, n4, n5`: Total number of participants in each study arm.
- `dose1, dose2, dose3, dose4, dose5`: Dose levels of the agents in each study arm.
- `studyid`: Unique identifier for the study.

This dataset is intended for use in dose-response network meta-analysis to explore the effects of single agents across various doses.

Source

The dataset is a subset of data derived from: Weibel S, Rücker G, Eberhart LHJ, et al. Drugs for preventing postoperative nausea and vomiting in adults after general anaesthesia: a network meta-analysis. Cochrane Database of Systematic Reviews. 2020;10(10):CD012859. Weibel S, Schaefer MS, Raj D, et al. Drugs for preventing postoperative nausea and vomiting in adults after general anaesthesia: an abridged Cochrane network meta-analysis. Anaesthesia. 2021;76:962-973.

Examples

```
data(anesthesia)
# Summarize the dataset
summary(anesthesia)
```

---

antidepressants   *Antidepressants Dataset for Dose-Response Network Meta-Analysis*

Description

This dataset is a synthesis of randomized controlled studies investigating the effects of antidepressant interventions for unipolar major depressive disorder.

Usage

```
antidepressants
```

Format

A data frame with the following columns:

drug	Character vector indicating the name of the antidepressant agent.
r	Integer vector for the number of participants who responded to treatment.
n	Integer vector for the total number of participants in the study arm.
dose	Numeric vector specifying the dose level of the antidepressant agent.
studyid	Character vector with unique study identifiers.

Details

The dataset includes data on several antidepressant agents and their observed effects across multiple clinical randomized controlled trials. The primary outcome is the response rate, defined as the proportion of patients achieving at least a 50

The dataset is structured in an arm-level format and includes the following variables:

- drug: Name of the antidepressant agent.
- r: Number of participants who responded to treatment.
- n: Total number of participants in the study arm.
- dose: Dose level of the antidepressant agent.
- studyid: Unique study identifier.

This dataset is intended for use in dose-response network meta-analysis to explore the effects of the several agents across various doses.

Source

The dataset is a subset of data derived from: Cipriani A et al. Comparative efficacy and acceptability of 21 antidepressant drugs for the acute treatment of adults with major depressive disorder: a systematic review and network meta-analysis. The Lancet. 2018;391:1357–1366.

Examples

```
data(antidepressants)
# Summarize the dataset
summary(antidepressants)
```

---

netdose   *Network meta-analysis with dose-response relationships*

Description

The 'netdose' function performs a dose-response network meta-analysis in a frequentist way. It accepts a dataset with study-level data, constructs a design matrix for the dose-response model, and computes treatment effects under common and/or random effects models. The function supports multiple dose-response relationship modeling approaches, including linear, exponential, quadratic, restricted cubic splines (rcs), and fractional polynomial methods (fp1).

Usage

```
netdose(
  TE,
  seTE,
  agent1,
  dose1,
```

```
        agent2,
        dose2,
        studlab,
        data = NULL,
        subset = NULL,
        n1 = NULL,
        n2 = NULL,
        event1 = NULL,
        event2 = NULL,
        sm,
        common = gs("common"),
        random = gs("random") | !is.null(tau.preset),
        tau.preset = NULL,
        method = "linear",
        param = NULL,
        reference.group,
        common.dose = NULL,
        level = gs("level.comb"),
        backtransf = gs("backtransf"),
        tol.multiarm = 0.001,
        tol.multiarm.se = NULL,
        details.chkmultiarm = FALSE,
        func.inverse = invmat,
        keepdata = gs("keepdata"),
        warn = TRUE,
        ...
    )
```

Arguments

TE	Estimate of treatment effect, i.e. difference between first and second treatment (e.g. log odds ratio, mean difference, or log hazard ratio). Or an R object created with [pairwise]().
seTE	Standard error of treatment estimate.
agent1	Agents corresponding to the first treatment in each comparison.
dose1	Doses for the first treatment in each comparison.
agent2	Agents corresponding to the second treatment in each comparison.
dose2	Doses for the second treatment in each comparison.
studlab	An optional - but important! - vector with study labels.
data	An optional data frame containing the study information.
subset	An optional vector specifying a subset of studies to be used. The default is 'NULL'.
n1	Numeric. Optional. Sample sizes for the first treatment in each comparison.
n2	Numeric. Optional. Sample sizes for the second treatment in each comparison.
event1	Numeric. Optional. Number of events for the first treatment in each comparison.

event2	Numeric. Optional. Number of events for the second treatment in each comparison.
sm	A character string indicating underlying summary measure, e.g., $″RD″$, $″RR″$, $″OR″$, $″ASD″$, $″HR″$, $″MD″$, $″SMD″$, or $″ROM″$.
common	A logical indicating whether a common effects dose-response network meta-analysis should be conducted. The default is 'TRUE'.
random	A logical indicating whether a random effects dose-response network meta-analysis should be conducted. The default is 'TRUE'.
tau.preset	An optional value for the square-root of the between-study variance τ^2.
method	An optional character string specifying the method to be used for the dose-response relationship. Either, "linear", "exponential", "quadratic", "rcs", "fp1", or "fp2", can be abbreviated (see Details).
param	A numeric vector specifying the parameters for some dose-response functions (see Details).
reference.group	Reference agent (first agent with dose 0 is used if argument is missing).
common.dose	A named vector with the common dose for each agent in the network (see Examples). The median dose is used for each agent if this argument is not provided.
level	The level used to calculate confidence intervals for individual comparisons.
backtransf	A logical indicating whether results should be back transformed in printouts and forest plots. If backtransf = TRUE, results for sm = $″OR″$ are presented as odds ratios rather than log odds ratios, for example.
tol.multiarm	A numeric for the tolerance for consistency of treatment estimates in multi-arm studies which are consistent by design.
tol.multiarm.se	A numeric for the tolerance for consistency of standard errors in multi-arm studies which are consistent by design. This check is not conducted if the argument is NULL.
details.chkmultiarm	A logical indicating whether treatment estimates and / or variances of multi-arm studies with inconsistent results or negative multi-arm variances should be printed.
func.inverse	R function used to calculate the pseudoinverse of the Laplacian matrix L.
keepdata	A logical indicating whether original data(set) should be kept in netdose object.
warn	A logical indicating whether warnings should be printed (e.g., if studies are excluded from network meta-analysis due to zero standard errors).
...	Additional arguments (to catch deprecated arguments).

Details

The dose-response network meta-analysis (DR-NMA) has been implemented by modelling different dose-response functions, as described by Mandema et al. 2005 and Mawdsley et al. 2016 and by using restricted cubic splines (Hamza et al. 2020) in Bayesian framework.

The function `netdose` conducts a dose-response network meta-analysis with a variety of dose-response functions (such as the linear, exponential, fractional polynomials and restricted cubic splines) in a frequentist way as described in Petropoulou et al. (2025).

The following dose-response functions are available:

- Linear dose-response relationship (method = "linear")
- Exponential dose-response relationship (method = "exponential")
- Quadratic polynomial dose-response relationship (method = "quadratic")
- Restricted cubic splines (method = "rcs")
- Fractional polynomial (order 1) (method = "fp1")
- Fractional polynomial (order 2) (method = "fp2")

By default, a linear dose-response relationship is assumed.

The parameters for the selected dose-response function can be specified using argument `param`: a numeric vector specifying the percentiles to set the knots for the restricted cubic splines (default: knots at the 10th, 50th, and 90th percentile), a single numeric specifying the power of the fractional polynomial with order 1 (default: -0.5), or a numeric vector of length 2 specifying the first and second power of a fractional polynomial with order 2 (default: -0.5 and -0.5). The input for argument `param` is ignored for a linear, exponential or quadratic polynomial dose-response relationship.

Value

An object of class `netdose`; a list containing the following components:

`studlab`	Study labels.
`agent1`	Label/Agents corresponding to the first treatment in each comparison..
`agent2`	Label/Agents corresponding to the second treatment in each comparison..
`dose1`	Doses for the first treatment in each comparison.
`dose2`	Doses for the second treatment in each comparison.
`treat1`	Label/First treatment in each comparison.
`treat2`	Label/Second treatment in each comparison.
`TE`	Estimate of treatment effect, i.e. difference between first and second treatment.
`seTE`	Standard error of treatment estimate.
`seTE.adj.common`, `seTE.adj.random`	
	Standard error of treatment estimate, adjusted for multi-arm studies.
`k`	Total number of studies.
`m`	Total number of pairwise comparisons.
`a`	Total number of agents.
`n`	Total number of treatments.
`trts`	Treatments included in the dataset in alphabetic order.
`agents`	Agents included in dose-response network meta-analysis in alphabetic order.
`inactive`	Identifier for the reference group or inactive treatment.
`common.dose`	Common dose value used in the analysis, if specified.

#' **Common/Random effects model results:**

TE.common, TE.random

>Matrix with overall treatment effects estimated by the dose-response (common and random effects) model.

seTE.common, seTE.random

>Matrix with standard errors estimated by the dose-response (common and random effects) model.

lower.common, upper.common, lower.random, upper.random

>Matrices with lower and upper confidence interval limits estimated by the dose-response (common and random effects) model.

statistic.common, pval.common, statistic.random, pval.random

>Matrices with z-values and p-values for test of overall effect estimated by the dose-response (common and random effects) model.

TE.drnma.common

>A vector of dose-response effects (common and random effects model).

seTE.drnma.common, seTE.drnma.random

>A vector with corresponding standard errors (common and random effects model).

lower.drnma.common, lower.drnma.random

>A vector with lower confidence limits for dose-response treatment estimates (common and random effects model).

upper.drnma.common, upper.drnma.random

>A vector with upper confidence limits for dose-response treatment estimates (common and random effects model).

statistic.drnma.common, statistic.drnma.random

>A vector with z-values for the overall dose-response effects (common and random effects model).

pval.drnma.common, pval.drnma.random

>A vector with p-values for the overall dose-response effects (common and random effects model).

Heterogeneity and goodness-of-fit statistics:

Q.dose	Overall heterogeneity / inconsistency statistic for dose-response network meta-analysis.
df.Q.dose	Degrees of freedom for test of heterogeneity / inconsistency for dose-response network meta-analysis.
pval.Q.dose	P-value for test of heterogeneity / inconsistency for dose-response network meta-analysis.
tau	Square-root of between-study variance with DerSimonian and Laird method for dose-response network meta-analysis.
tauml	Square-root of between-study variance with Maximum likelihood method for dose-response network meta-analysis.
I2, lower.I2, upper.I2	
	I-squared, lower and upper confidence limits.
Q.standard	Overall heterogeneity / inconsistency statistic (standard model).

df.Q.standard	Degrees of freedom for test of heterogeneity / inconsistency (standard model).
pval.Q.standard	
	P-value for test of heterogeneity / inconsistency (standard model).
Q.diff	Test statistic for difference in goodness of fit between standard and dose-response model.
df.Q.diff	Degrees of freedom for difference in goodness of fit between standard and dose-response model.
pval.Q.diff	P-value for difference in goodness of fit between standard and additive model.
Xd	Design matrix for dose-response network meta-analysis.
sm	Summary measure used in the analysis.
level	Level used to calculate confidence intervals for individual comparisons.
common	A logical indicating whether a common effects dose-response network meta-analysis should be conducted.
random	A logical indicating whether a random effects dose-response network meta-analysis should be conducted.
method	Method used for the dose-response relationship.
reference.group	
	Reference agent.
Q.to.df.ratio	Q to df ratio, i.e, Q.dose/df.Q.dose.
func.inverse	Function used to calculate the pseudoinverse of the Laplacian matrix L.
backtransf	A logical indicating whether results should be back transformed in printouts and forest plots.
data	Data frame containing the study information.

Author(s)

Maria Petropoulou <maria.petropoulou@uniklinik-freiburg.de>, Guido Schwarzer <guido.schwarzer@uniklinik-freiburg.de>

References

Mandema JW, Cox EJ (2005): Therapeutic benefit of eletriptan compared to sumatriptan for the acute relief of migraine pain–results of a model-based meta-analysis that accounts for encapsulation. *Cephalalgia*, **25**, 715-725

Mawdsley D, Bennetts M, Dias S, Boucher M, Welton N (2016): Model-Based Network Meta-Analysis: A Framework for Evidence Synthesis of Clinical Trial Data. *PT Pharmacometrics & Systems Pharmacology*, **5**, 393-401

Hamza T, Furukawa TA, Orsin N, Cipriani A, Iglesias C, Salanti G (2022): A dose-effect network meta-analysis model: an application in antidepressants. *Statistical Methods in Medical Research*

Petropoulou et al. (2025): Network meta-analysis with dose-response relationships.

Examples

```
# Load anesthesia data
data(anesthesia)

# Use a subset of 5 studies
anesthesia_subset <- subset(anesthesia, study %in% unique(anesthesia$study)[1:5])

# Prepare data for DR-NMA
dat <- meta::pairwise(
  agent = list(agent1, agent2, agent3),
  event = list(event1, event2, event3),
  n = list(n1, n2, n3),
  dose = list(dose1, dose2, dose3),
  data = anesthesia_subset,
  studlab = study,
  append = FALSE,
  sm = "RR"
)

# Perform DR-NMA with a linear dose-response function
dr1 <- netdose(
  TE, seTE, agent1, dose1, agent2,
  dose2, studlab,
  data = dat
)


# DR-NMA with FP1 dose-response function with p = -0.5
FP1 <- netdose(TE, seTE, agent1, dose1, agent2,
  dose2, studlab,
  data = dat,
  method = "fp1"
)

# DR-NMA with FP1 dose-response function with p = 0.5
FP1_p0.5 <- netdose(TE, seTE, agent1, dose1, agent2,
  dose2, studlab,
  data = dat,
  method = "fp1", param = 0.5
)


# DR-NMA with RCS dose-response function with knots at 10th, 50th and 90th percentiles
dr_rcs <- netdose(TE, seTE, agent1, dose1, agent2,
  dose2, studlab,
  data = dat,
  method = "rcs"
)

# DR-NMA with RCS dose-response function with knots at 25th, 50th and 100th percentiles
dr_rcs2 <- netdose(TE, seTE, agent1, dose1, agent2,
  dose2, studlab,
```

```
  data = dat,
  method = "rcs", p = c(0.25, 0.50, 1),
)
```

---

plot.netdose   *Dose-response curve plot*

Description

Generates a dose-response plot based on the results of a dose-response network meta-analysis (DR-NMA). The plot visualizes predicted dose-response curves alongside observed responses for easy interpretation of model outputs.

Usage

```
## S3 method for class 'netdose'
plot(
  x,
  pooled = if (x$random) "random" else "common",
  only.direct = TRUE,
  col.direct = if (only.direct) "black" else "green",
  col.indirect = "red",
  agents = NULL,
  same.ylim = TRUE,
  ylim = NULL,
  benchmark.threshold = 0.01,
  plateau.threshold = 1e-04,
  ...
)
```

Arguments

x	An object of class netdose (mandatory).
pooled	A character string indicating whether results for the common ("common") or random effects model ("random") should be plotted. Abbreviations are allowed. Defaults to "random" if the input object specifies a random effects model; otherwise, defaults to "common".
only.direct	A logical value indicating whether only the study results of direct comparisons with the reference agent for the observed data should be shown in the plot. Defaults to TRUE.
col.direct	The color used for points representing direct comparisons. By default, "black" when only.direct = TRUE; otherwise, "green".
col.indirect	The color used for points representing indirect comparisons. Defaults to "red".

agents   Optional character vector specifying which agents to include in the plot. If NULL, all agents will be plotted.

same.ylim   Logical; if TRUE, all plots will have the same y-axis limits. Default is FALSE.

ylim   Optional numeric vector of length 2 specifying the y-axis limits. If NULL, limits are determined automatically (or based on "same.ylim" if TRUE).

benchmark.threshold

         Numeric; benchmark response level (e.g., 0.1 for 10 percent). Used to compute Benchmark Dose Lower Confidence Limit (BMDL).

plateau.threshold

         Numeric; threshold for identifying the plateau in the dose-response curve. Defines the minimum absolute change in predicted response between adjacent dose levels, below which the response is considered stable (i.e., plateau has been reached). Used to calculate the Maximum Effective Dose (MED). Default: 0.0001.

...   Additional arguments. Currently ignored, but included for potential future extensions or compatibility with generic plotting functions.

Details

The function plots the dose-response curve alongside the observed responses: - The vertical axis represents the dose range, which is defined from 0 to the maximum observed dose, with 100 evenly spaced points generated within this range. - The horizontal axis represents the predicted response values, calculated using the predict.netdose function.

The plot includes shaded confidence intervals for the predicted dose-response curve. Observed responses are overlaid for comparison, differentiated into direct and indirect comparisons with customizable colors.

The function also optionally displays the Benchmark Dose (BMD) and the Benchmark Dose Lower Confidence Limit (BMDL), based on a user-defined benchmark response threshold (e.g., 0.01 for 10 percent increase).

If the model indicates that the predicted response stabilizes beyond a certain dose level, the function estimates and plots the Maximum Effective Dose (MED) — the smallest dose beyond which the predicted response increases less than a given threshold (controlled via plateau.threshold). MED is shown only if it occurs after the BMDL, ensuring biological and statistical coherence.

Value

No return value, called for side effects (generates a plot).

Author(s)

Maria Petropoulou <maria.petropoulou@uniklinik-freiburg.de>, Guido Schwarzer <guido.schwarzer@uniklinik-freiburg.de>

Examples

```
# Load anesthesia data
data(anesthesia)
```

```
# Use a subset of 5 studies
anesthesia_subset <- subset(anesthesia, study %in% unique(anesthesia$study)[1:5])

# Prepare data for DR-NMA
dat <- meta::pairwise(
  agent = list(agent1, agent2, agent3),
  event = list(event1, event2, event3),
  n = list(n1, n2, n3),
  dose = list(dose1, dose2, dose3),
  data = anesthesia_subset,
  studlab = study,
  append = FALSE,
  sm = "RR"
)


# DR-NMA with linear dose-response function
dr1 <- netdose(TE, seTE, agent1, dose1, agent2,
  dose2, studlab,
  data = dat
)

# Dose-response plot
plot(dr1)
```

| predict.netdose | *Predicted values for dose-response network meta-analysis* |

Description

This function provides the predicted values based on the results of dose-response network meta-analysis.

Usage

```
## S3 method for class 'netdose'
predict(object, agent1 = NULL, dose1 = NULL, agent2 = NULL, dose2 = NULL, ...)
```

Arguments

object   An object of class netdose (mandatory).

agent1   An optional character string specifying the first agent to be used for the prediction. By default, all agents are used.

dose1   An optional numeric vector specifying custom doses for the prediction. By default, the doses are set to the common observed doses as defined in the data.

agent2   An optional character string specifying the second agent to be used for the prediction. By default, the reference agent is used.

dose2	An optional numeric vector specifying the dose for the second agent. By default the common dose of the second agent is used.
...	Additional arguments (ignored).

Details

The predict.netdose function calculates predicted effects for specified doses of one or more agents, based on a dose-response network meta-analysis. It supports both linear and non-linear dose-response relationships, accommodating various modeling methods including linear, exponential, fractional polynomials, restricted cubic splines (RCS), and quadratic relationships. This function is particularly useful for exploring comparative effectiveness at specific dose levels of the agents, facilitating the interpretation of complex dose-response relationships in a network meta-analysis setting. By allowing predictions for multiple combinations of agents and doses, it offers flexibility in evaluating hypothetical scenarios or estimating effects for doses outside the directly observed range (where extrapolation is appropriate).

Value

A data frame with additional class `predict.netdose` containing the following variables:

agent1, dose1, agent2, dose2	As defined above
pred	A numeric vector with the predicted effects
se.pred	A numeric vector with standard errors of the predicted effects
lower	A numeric vector specifying the lower bounds of the predicted values
upper	A numeric vector specifying the upper bounds of the predicted values

Author(s)

Maria Petropoulou <maria.petropoulou@uniklinik-freiburg.de>, Guido Schwarzer <guido.schwarzer@uniklinik-freiburg.de>

References

Petropoulou et al. (2025): Network meta-analysis with dose-response relationships.

Examples

```
# Load anesthesia data
data(anesthesia)

# Use a subset of 5 studies
anesthesia_subset <- subset(anesthesia, study %in% unique(anesthesia$study)[1:5])

# Prepare data for DR-NMA
dat <- meta::pairwise(
  agent = list(agent1, agent2, agent3),
  event = list(event1, event2, event3),
  n = list(n1, n2, n3),
```

```
  dose = list(dose1, dose2, dose3),
  data = anesthesia_subset,
  studlab = study,
  append = FALSE,
  sm = "RR"
)


# Perform DR-NMA with a linear dose-response function
dr1 <- netdose(
  TE, seTE, agent1, dose1, agent2,
  dose2, studlab,
  data = dat
)

# Predicted values
pred1 <- predict(dr1)
```

---

print.netdose   *Print method for objects of class* netdose

Description

Displays a summary of the dose-response network meta-analysis results stored in a netdose object.

Usage

```
## S3 method for class 'netdose'
print(
  x,
  common = x$common,
  random = x$random,
  backtransf = x$backtransf,
  digits = gs("digits"),
  digits.stat = gs("digits.stat"),
  digits.pval = gs("digits.pval"),
  digits.pval.Q = max(gs("digits.pval.Q"), 2),
  digits.Q = gs("digits.Q"),
  digits.tau2 = gs("digits.tau2"),
  digits.tau = gs("digits.tau"),
  digits.I2 = gs("digits.I2"),
  scientific.pval = gs("scientific.pval"),
  big.mark = gs("big.mark"),
  text.tau2 = gs("text.tau2"),
  text.tau = gs("text.tau"),
  text.I2 = gs("text.I2"),
  ...
)
```

Arguments

x	An object of class `netdose`.
common	A logical indicating whether results from the common effects model should be printed.
random	A logical indicating whether results from the random effects model should be printed.
backtransf	A logical indicating whether printed results should be back transformed. If `backtransf = TRUE`, results for `sm = "OR"` are printed as odds ratios rather than log odds ratios, for example.
digits	Minimal number of significant digits to be used in output.
digits.stat	Number of decimal places for test statistics.
digits.pval	Number of decimal places for p-values.
digits.pval.Q	Number of decimal places for Q-test p-value.
digits.Q	Number of decimal places for Q statistic.
digits.tau2	Number of decimal places for tau-squared.
digits.tau	Number of decimal places for tau.
digits.I2	Number of decimal places for I-squared.
scientific.pval	
	A logical indicating whether p-values should be printed in scientific notation.
big.mark	A character used as thousands separator.
text.tau2	A character string used to label tau-squared in the output.
text.tau	A character string used to label tau in the output.
text.I2	A character string used to label I-squared in the output.
...	Additional arguments (ignored).

Value

The input object is printed to the console. No return value.

---

print.predict.netdose   *Print method for objects of class predict*

Description

Print method for objects of class predict

Usage

```
## S3 method for class 'predict.netdose'
print(
  x,
  backtransf = attr(x, "backtransf"),
  digits = gs("digits"),
  big.mark = gs("big.mark"),
  ...
)
```

Arguments

x	An object of class `predict.netdose`.
backtransf	A logical indicating whether printed results should be back transformed. If `backtransf=TRUE`, results for `sm="OR"` are printed as odds ratios rather than log odds ratios, for example.
digits	Minimal number of significant digits, see `print.default`.
big.mark	A character used as thousands separator.
...	Additional arguments (ignored).

Value

The input object is printed to the console. No return value.

Index