Package ‘poth’

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Title Precision of Treatment Hierarchy (POTH)

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Depends R (>= 3.5.0)

Imports ggplot2, stringr, netmeta, MASS

Suggests mvtnorm

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Maintainer Augustine Wigle <`amhwigle@uwaterloo.ca`>

Description Calculate POTH for treatment hierarchies from frequentist and Bayesian network meta-analysis. POTH quantifies the certainty in a treatment hierarchy. Subset POTH, POTH residuals, and best k treatments POTH can also be calculated to improve interpretation of treatment hierarchies.

URL `https://github.com/augustinewigle/poth`

BugReports `https://github.com/augustinewigle/poth/issues`

Encoding UTF-8

LazyData true

RoxygenNote 7.3.2

NeedsCompilation no

Repository CRAN

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Contents

`poth-package` *poth: Brief overview of methods and general hints*

Description

R package **poth** allows to calculate the precision of treatment hierarchy (POTH) metric to quantify the uncertainty in a treatment hierarchy in network meta-analysis (Wigle et al., 2024).

Details

R package **poth** provides the following methods:

- Calculate the separation in ranking metric (`poth`)
- Conduct leave-one-out analysis (`loo.poth`)

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

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

The development version of **poth** is available on GitHub `https://github.com/augustinewigle/poth`.

Author(s)

Augustine Wigle <`amhwigle@uwaterloo.ca`>, Guido Schwarzer <`guido.schwarzer@uniklinik-freiburg.de`>

References

Wigle A, Béliveau A, Salanti G, Rücker G, Schwarzer G, Mavridis D, Nikolakopoulou A (2024): Precision of treatment hierarchy: A metric for quantifying uncertainty in treatment hierarchies in network meta-analysis. Preprint on arXiv, doi:10.48550/arXiv.2501.11596

See Also

Useful links:

- `https://github.com/augustinewigle/poth`
- Report bugs at `https://github.com/augustinewigle/poth/issues`

`bestk.poth` *Best k treatments method for precision of treatment hierarchy (POTH) metric*

Description

Best k treatments method for precision of treatment hierarchy (POTH) metric

Usage

```
## S3 method for class 'poth'
bestk(x, sort = TRUE, ...)

## S3 method for class 'bestk.poth'
print(x, digits = 3, legend = TRUE, ...)

bestk(x, ...)
```

Arguments

`x`	An R object of class `poth`.
`sort`	A logical indicating whether results should be sorted by decreasing ranking metric.
`...`	Additional arguments.
`digits`	Minimal number of significant digits, see `print.default`.
`legend`	A logical indicating whether a legend should be printed.

Value

A data frame with additional class `bestk.poth` and the following variables:

`trt`	Name of added treatment.
`rank`	Treatment rank (global).
`score`	Ranking metric (global).
`poth_bestk`	Best k treatments POTH.

Examples

```
library("netmeta")
data(Senn2013)
net1 <- netmeta(TE, seTE, treat1.long, treat2.long, studlab,
  data = Senn2013, sm = "MD", random = FALSE)

# Best k treatments method
bk1 <- bestk(poth(net1))
bk1
```

```
plot(bk1)
plot(bk1, labels = TRUE)
bk2 <- bestk(poth(net1), sort = FALSE)
bk2
plot(bk2)
plot(bk2, labels = TRUE)
```

---

loo.poth *Leave-one-out method for precision of treatment hierarchy (POTH) metric*

Description

Leave-one-out method for precision of treatment hierarchy (POTH) metric

Usage

```
## S3 method for class 'poth'
loo(x, ...)

loo(x, ...)

## S3 method for class 'loo.poth'
print(x, digits = 3, legend = TRUE, ...)
```

Arguments

`x`	An R object of class `poth`.
`...`	Additional arguments.
`digits`	Minimal number of significant digits, see `print.default`.
`legend`	A logical indicating whether a legend should be printed.

Value

A data frame with additional class `loo.poth` and the following variables:

`trt`	Treatment names.
`rank`	Treatment rank (global).
`score`	Ranking metric (global).
`poth_loo`	Leave-one-out POTH.
`resid`	Residuals (global POTH minus leave-one-out POTH.
`ratio`	Ratio of residual devided by absolute sum of residuals.

Examples

```
library("netmeta")
data(smokingcessation)
p1 <- pairwise(list(treat1, treat2, treat3),
  event = list(event1, event2, event3), n = list(n1, n2, n3),
  data = smokingcessation, sm = "OR")
net1 <- netmeta(p1, random = FALSE)

# Leave-one-out method
loo1 <- loo(poth(net1))
loo1
```

`plot.bestk.poth` *Plot best k treatments precision of treatment hierarchy (POTH) values*

Description

Plot best k treatments precision of treatment hierarchy (POTH) values

Usage

```
## S3 method for class 'bestk.poth'
plot(x, labels = FALSE, nchar.trts = 4, digits = 3, ...)
```

Arguments

`x`	R object of class `bestk.poth`.
`labels`	A logical indicating whether treatment names should be shown in the plot.
`nchar.trts`	Number of characters to keep for each treatment name if labels = TRUE.
`digits`	Minimal number of significant digits for best k treatments POTH, see `print.default`.
`...`	Additional arguments (ignored).

Details

Plot results of best k treatments method for precision of treatment hierarchy (POTH) metric (Wigle et al., 2024).

Value

A ggplot2 object.

Author(s)

Augustine Wigle <`amhwigle@uwaterloo.ca`>, Guido Schwarzer <`guido.schwarzer@uniklinik-freiburg.de`>

References

Wigle A, Béliveau A, Salanti G, Rücker G, Schwarzer G, Mavridis D, Nikolakopoulou A (2024): Precision of treatment hierarchy: A metric for quantifying uncertainty in treatment hierarchies in network meta-analysis. Preprint on arXiv, doi:10.48550/arXiv.2501.11596

Examples

```
library("netmeta")
data(Senn2013)
net1 <- netmeta(TE, seTE, treat1.long, treat2.long, studlab,
  data = Senn2013, sm = "MD", random = FALSE)

# Best k treatments method
bk1 <- bestk(poth(net1))
bk1
plot(bk1)
plot(bk1, labels = TRUE)
bk2 <- bestk(poth(net1), sort = FALSE)
bk2
plot(bk2)
plot(bk2, labels = TRUE)
```

`plot.loo.poth` *Plot results of leave-one-out method*

Description

Plot results of leave-one-out method for precision of treatment hierarchy (POTH) metric

Usage

```
## S3 method for class 'loo.poth'
plot(x, labels = TRUE, digits = 3, ...)
```

Arguments

`x`	R object of class `poth`.
`labels`	A logical indicating whether treatment names should be shown in the plot.
`digits`	Minimal number of significant digits for global POTH, see `print.default`.
`...`	Additional arguments (ignored).

Details

Plot results of leave-one-out method for precision of treatment hierarchy (POTH) metric (Wigle et al., 2024).

Value

A ggplot2 object.

Author(s)

Augustine Wigle <`amhwigle@uwaterloo.ca`>, Guido Schwarzer <`guido.schwarzer@uniklinik-freiburg.de`>

References

Wigle A, Béliveau A, Salanti G, Rücker G, Schwarzer G, Mavridis D, Nikolakopoulou A (2024): Precision of treatment hierarchy: A metric for quantifying uncertainty in treatment hierarchies in network meta-analysis. Preprint on arXiv, doi:10.48550/arXiv.2501.11596

Examples

```
library("netmeta")
data(smokingcessation)
p1 <- pairwise(list(treat1, treat2, treat3),
  event = list(event1, event2, event3), n = list(n1, n2, n3),
  data = smokingcessation, sm = "OR")
net1 <- netmeta(p1, random = FALSE)

# Leave-one-out method
loo1 <- loo(poth(net1))
loo1
plot(loo1)


data(Senn2013)
net2 <- netmeta(TE, seTE, treat1.long, treat2.long, studlab,
                data = Senn2013, sm = "MD", random = FALSE)

# Leave-one-out method (without sorting by ranking metric)
loo2 <- loo(poth(net2), sort = FALSE)
loo2
plot(loo2)
```

`plot.refdist` *Plot reference distribution for given network*

Description

Plot a histogram of simulated reference distribution for POTH

Usage

```
## S3 method for class 'refdist'
plot(x, observed = TRUE, probability = FALSE, ...)
```

Arguments

`x`	R object of class `refdist`.
`observed`	A logical indicating whether a line with the observed POTH should be drawn in the plot.
`probability`	A logical indicating whether the probability of a POTH greater than the observed POTH should be printed in the legend. This argument is ignored if `observed = FALSE`.
`...`	Additional arguments (ignored).

Details

Plots a histogram of the simulated POTH values from the reference distribution. (Wigle et al., 2024).

Value

A ggplot2 object.

Author(s)

Augustine Wigle `<amhwigle@uwaterloo.ca>`, Guido Schwarzer `<guido.schwarzer@uniklinik-freiburg.de>`

References

Wigle A, Béliveau A, Salanti G, Rücker G, Schwarzer G, Mavridis D, Nikolakopoulou A (2024): Precision of treatment hierarchy: A metric for quantifying uncertainty in treatment hierarchies in network meta-analysis. Preprint on arXiv, doi:10.48550/arXiv.2501.11596

Examples

```
library("netmeta")
data(smokingcessation)
p1 <- pairwise(list(treat1, treat2, treat3),
  event = list(event1, event2, event3), n = list(n1, n2, n3),
  data = smokingcessation, sm = "OR")
net1 <- netmeta(p1, random = FALSE)

# Reference distribution
dist1 <- refdist(net1, pooled = "common", nsim = 2)
plot(dist1, observed = FALSE)

data(Senn2013)
net2 <- netmeta(TE, seTE, treat1.long, treat2.long, studlab,
                data = Senn2013, sm = "MD", random = FALSE)

# Reference distribution
dist2 <- refdist(net2, pooled = "common", nsim = 25)
plot(dist2, probability = TRUE)
```

`poth` *Calculate precision of treatment hierarchy (POTH) metric*

Description

Precision of treatment hierarchy (POTH) is a metric to quantify the uncertainty in a treatment hierarchy in network meta-analysis

Usage

```
poth(x, se = NULL, small.values, pooled, trts = NULL)

## S3 method for class 'poth'
print(x, sort = TRUE, digits = 3, ...)

## S3 method for class 'poth'
summary(object, ...)

## S3 method for class 'summary.poth'
print(x, sort = TRUE, digits = 3, ...)
```

Arguments

`x`	Mandatory argument with suitable information on the treatment hierarchy (see Details).
`se`	Matrix of estimated standard errors for relative effects.
`small.values`	A character string specifying whether small outcome values indicate a beneficial (`"desirable"`) or harmful (`"undesirable"`) effect, can be abbreviated.
`pooled`	A character string indicating whether the treatment hierarchy is based on a common or random effects model. Either `"common"` or `"random"`, can be abbreviated.
`trts`	An optional vector with treatment names. Must match the order of treatments provided for argument `x`.
`sort`	A logical indicating whether printout should be sorted by decreasing ranking metric.
`digits`	Minimal number of significant digits, see `print.default`.
`...`	Additional arguments (ignored).
`object`	An object of class `summary.poth`.

Details

This function calculates the precision of treatment hierarchy (POTH) metric to quantify the uncertainty in a treatment hierarchy in network meta-analysis (Wigle et al., 2024).

Argument `x` providing information on the treatment hierarchy is the only mandatory argument. The following input formats can be provided:

1. vector representing a ranking metric, i.e., SUCRAs or P-scores,
2. square matrix with the probabilities for each possible rank (with treatments in rows and ranks in columns),
3. MCMC samples (with samples in rows and treatments in columns),
4. relative effect matrix,
5. R object created with `netmeta`, `netrank`, or `rankogram` object from R package **netmeta**.

Argument `se` must be provided if argument `x` is a matrix with relative effects. Otherwise, argument `se` is ignored.

Argument `small.values` must be provided if argument `x` contains MCMC samples, relative effects, or is an object created with `netmeta`. This argument can be provided for an R object created with `netrank` or `rankogram` and is ignored otherwise.

For a `netmeta`, `netrank`, or `rankogram` object, argument `pooled` is by default equal to "random" if only the random effects model was considered in the analysis.

Argument `trts` is ignored for `netmeta`, `netrank`, and `rankogram` objects.

Value

An object of class `poth` with corresponding `print` function. The object is a list containing the following components:

`poth`	Separation in ranking metric.
`ranking`	A named numeric vector with rankings, i.e., SUCRAs or P-scores.
`ranking.matrix`	A square matrix with the probabilities for each possible rank (if information is available).
`pooled`	As defined above.

Author(s)

Augustine Wigle <`amhwigle@uwaterloo.ca`>, Guido Schwarzer <`guido.schwarzer@uniklinik-freiburg.de`>

References

Wigle A, Béliveau A, Salanti G, Rücker G, Schwarzer G, Mavridis D, Nikolakopoulou A (2024): Precision of treatment hierarchy: A metric for quantifying uncertainty in treatment hierarchies in network meta-analysis. Preprint on arXiv, doi:10.48550/arXiv.2501.11596

Examples

```
library("netmeta")
data(smokingcessation)
p1 <- pairwise(list(treat1, treat2, treat3),
  event = list(event1, event2, event3), n = list(n1, n2, n3),
  data = smokingcessation, sm = "OR")
net1 <- netmeta(p1, random = FALSE)

# Calculate probabilities for each possible rank
set.seed(1909) # make results reproducible
```

```
rg1 <- rankogram(net1)
rg1

# Calculate POTH
s1 <- poth(rg1)
s1

# Also print probabilities for each possible rank
summary(s1)

# Use SUCRAs to calculate POTH
nr1 <- netrank(rg1)
nr1
poth(nr1)
poth(nr1$ranking.common)

data(Senn2013)
net2 <- netmeta(TE, seTE, treat1.long, treat2.long, studlab,
                data = Senn2013, sm = "MD", random = FALSE)

# Use P-scores to calculate POTH
nr2 <- netrank(net2)
nr2
poth(nr2)
```

`pscores` *Calculate P-scores from a set of relative effects and standard errors*

Description

Calculate P-scores from a set of relative effects and standard errors

Usage

```
pscores(TE, seTE, small.values = "desirable", trts = NULL)
```

Arguments

`TE`	Matrix of relative effects
`seTE`	Matrix of estimated standard errors for relative effects
`small.values`	A character string specifying whether small outcome values indicate a beneficial (`"desirable"`) or harmful (`"undesirable"`) effect, can be abbreviated.
`trts`	optional; vector of treatment names matching order in TE and sds

Value

named vector of P-scores

`rankMCMC` *Calculate a ranking probabilities matrix from MCMC samples*

Description

Calculate a ranking probabilities matrix from MCMC samples

Usage

```
rankMCMC(x, small.values = "desirable", trts = NULL)
```

Arguments

`x`	a matrix or data.frame of MCMC samples, where rows are MCMC samples and columns are relative effects (relative to anchor) for treatments. must have column names that are the name of each treatment.
`small.values`	A character string specifying whether small outcome values indicate a beneficial (`"desirable"`) or harmful (`"undesirable"`) effect, can be abbreviated.
`trts`	character vector of treatment names, optional if samples has column names

Value

A matrix of ranking probabilities where rows are treatments and columns are ranks

---

`refdist` *Generate reference distribution for POTH for a given network structure*

Description

Generate reference distribution for POTH for a given network structure

Usage

```
refdist(x, d, pooled, nsim = 25, verbose = TRUE)

## S3 method for class 'refdist'
print(x, ...)

## S3 method for class 'refdist'
summary(object, ...)
```

Arguments

`x`	A `netmeta` object.
`d`	A vector of the desired relative effects, must be in the same order as `x$trts`.
`pooled`	A character string indicating whether the treatment hierarchy is based on a common or random effects model. Either `"common"` or `"random"`, can be abbreviated.
`nsim`	Number of samples from reference distribution.
`verbose`	A logical indicating whether progress information should be printed.
`...`	Additional arguments passed on to print or summary function.
`object`	A `refdist` object.

Details

By default, argument `pooled` is equal to "random" if only the random effects model was considered in the network meta-analysis `x`. Otherwise, argument `pooled` is equal to "common".

If argument `d` is missing, the respective relative effects are taken to be all 0.

Value

A vector of POTH values.

See Also

`netmeta`

Examples

```
library("netmeta")
data(Senn2013)
net1 <- netmeta(TE, seTE, treat1.long, treat2.long, studlab,
  data = Senn2013,
  sm = "MD")

# POTH (based on common effects model)
poth(net1)

# Sample POTH values from reference distribution (common effects model)
set.seed(1909)
poths <- refdist(net1)
summary(poths)

# POTH (based on random effects model)
poth(net1, pooled = "random")

# Sample POTH values from reference distribution (common effect model)
poths.r <- refdist(net1, pooled = "random")
summary(poths.r)
```

`subset.poth` *Calculate the local POTH for a subset of treatments*

Description

Calculate the local POTH for a subset of treatments

Usage

```
## S3 method for class 'poth'
subset(x, subset, top, bottom, ...)
```

Arguments

`x`	An object of class `poth`.
`subset`	A character vector of treatment names to consider as the set of competing treatments.
`top`	A single integer to define the number of treatments with the largest ranking metric to consider in subset.
`bottom`	A single integer to define the number of treatments with the smallest ranking metric to consider in subset.
`...`	Additional arguments (ignored).

Value

An R object of class `poth`.

Examples

```
library("netmeta")
data(smokingcessation)
p1 <- pairwise(list(treat1, treat2, treat3),
  event = list(event1, event2, event3), n = list(n1, n2, n3),
  data = smokingcessation, sm = "OR")
net1 <- netmeta(p1, random = FALSE)

# Use P-scores to calculate local POTH for treatments "A" and "C"
subset(poth(net1), subset = c("A", "C"))

# Use P-scores to calculate local POTH for first three treatments
subset(poth(net1), top = 3)

# Use P-scores to calculate local POTH for first three treatments
subset(poth(net1), bottom = 3)
```

Xu2018 *Safety of Immune Checkpoint Inhibitors in Cancer*

Description

Data from a network meta-analysis on immune checkpoint inhibitors (ICIs) to assess the safety of ICI drugs as cancer treatment (Xu et al., 2018).

Format

A data frame with the following columns:

studyID	study id
treatment	treatment name
adverse	number of adverse events
n	group sample size

Details

Data were obtained from Rosenberger et al. (2021), who re-analysed the data. There are seven treatments and 23 studies. The outcome of interest is the number of treatment-related adverse events, so smaller values indicate a safer treatment.

Source

Rosenberger, K.J., Duan, R., Chen, Y. et al. (2021): Predictive P-score for treatment ranking in Bayesian network meta-analysis. *BMC Med Res Methodol* **21**, 213. doi:10.1186/s12874021013975

See Also

`netmeta`

Examples

```
data(Xu2018)
head(Xu2018)

library("netmeta")
pw <- pairwise(treat = treatment, event = adverse, n = n,
  studlab = studyID, data = Xu2018, sm = "OR")
#
net <- netmeta(pw, small.values = "desirable", method.tau = "REML",
  common = FALSE)
#
poth(net)
```

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