

Package ‘EvidenceSynthesis’

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Type Package

Title An R Package for Combining Evidence from Multiple Sources

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Description Routines for combining evidence and diagnostics across multiple sources, such as multiple data sites in a distributed study. This includes functions for performing meta-analysis and forest plots.

Imports ggplot2 (>= 2.0.0),
gridExtra,
meta,
EmpiricalCalibration

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URL <https://github.com/OHDSI/EvidenceSynthesis>

BugReports <https://github.com/OHDSI/EvidenceSynthesis/issues>

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R topics documented:

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| EvidenceSynthesis | <i>EvidenceSynthesis</i> |
|-------------------|--------------------------|

Description

EvidenceSynthesis

plotCovariateBalances *Plot covariate balances*

Description

plotCovariateBalances plots the covariate balance before and after matching for multiple data sources.

Usage

```
plotCovariateBalances(balances, labels, threshold = 0,
  beforeLabel = "Before matching", afterLabel = "After matching",
  fileName = NULL)
```

Arguments

| | |
|-------------|--|
| balances | A list of covariate balance objects as created using the computeCovariateBalance function in the CohortMethod package. Each balance object is expected to be a data.frame with at least these two columns: beforeMatchingStdDiff and afterMatchingStdDiff. |
| labels | A vector containing the labels for the various sources. |
| threshold | Show a threshold value for the standardized difference. |
| beforeLabel | Label for before matching / stratification / trimming. |
| afterLabel | Label for after matching / stratification / trimming. |
| fileName | Name of the file where the plot should be saved, for example 'plot.png'. See the function ggsave in the ggplot2 package for supported file formats. |

Details

Creates a plot showing the covariate balance before and after matching. Balance distributions are displayed as box plots combined with scatterplots.

Value

A Ggplot object. Use the ggsave function to save to file.

Examples

```
# Some example data:
balance1 <- data.frame(beforeMatchingStdDiff = rnorm(1000, 0.1, 0.1),
  afterMatchingStdDiff = rnorm(1000, 0.0, 0.01))
balance2 <- data.frame(beforeMatchingStdDiff = rnorm(1000, 0.2, 0.1),
  afterMatchingStdDiff = rnorm(1000, 0.0, 0.05))
balance3 <- data.frame(beforeMatchingStdDiff = rnorm(1000, 0.0, 0.1),
  afterMatchingStdDiff = rnorm(1000, 0.0, 0.03))
plotCovariateBalances(balances = list(balance1, balance2, balance3),
  labels = c("Site A", "Site B", "Site C"))
```

| | |
|--------------------|--|
| plotEmpiricalNulls | <i>Plot empirical null distributions</i> |
|--------------------|--|

Description

plotEmpiricalNulls plots the empirical null distribution for multiple data sources.

Usage

```
plotEmpiricalNulls(logRr, seLogRr, labels, xLabel = "Relative risk",
  limits = c(0.1, 10), showCis = TRUE, fileName = NULL)
```

Arguments

| | |
|----------|---|
| logRr | A numeric vector of effect estimates for the negative controls on the log scale. |
| seLogRr | The standard error of the log of the effect estimates. Hint: often the standard error = $(\log(\text{lower bound 95 percent confidence interval}) - \log(\text{effect estimate})) / qnorm(0.025)$. |
| labels | A vector containing the labels for the various sources. Should be of equal length as logRr and seLogRr. |
| xLabel | The label on the x-axis: the name of the effect estimate. |
| limits | The limits of the effect size axis. |
| showCis | Show the 95 percent confidence intervals on the null distribution and distribution parameter estimates? |
| fileName | Name of the file where the plot should be saved, for example 'plot.png'. See the function ggsave in the ggplot2 package for supported file formats. |

Details

Creates a plot showing the empirical null distributions. Distributions are shown as mean plus minus one standard deviation, as well as a distribution plot.

Value

A Ggplot object. Use the ggsave function to save to file.

Examples

```
# Some example data:
site1 <- EmpiricalCalibration::simulateControls(n = 50, mean = 0, sd = 0.1, trueLogRr = 0)
site1$label <- "Site 1"
site2 <- EmpiricalCalibration::simulateControls(n = 50, mean = 0.1, sd = 0.2, trueLogRr = 0)
site2$label <- "Site 2"
site3 <- EmpiricalCalibration::simulateControls(n = 50, mean = 0.15, sd = 0.25, trueLogRr = 0)
site3$label <- "Site 3"
sites <- rbind(site1, site2, site3)

plotEmpiricalNulls(logRr = sites$logRr,
  seLogRr = sites$seLogRr,
  labels = sites$label)
```

plotMetaAnalysisForest

Perform a meta-analysis and create a forest plot

Description

plotMetaAnalysisForest performs a meta-analysis and creates a forest plot of effect size estimates.

Usage

```
plotMetaAnalysisForest(logRr, logLb95Ci, logUb95Ci, labels,
  xLabel = "Relative risk", limits = c(0.1, 10), hakn = TRUE,
  fileName = NULL)
```

Arguments

| | |
|-----------|---|
| logRr | A numeric vector of effect estimates on the log scale. |
| logLb95Ci | The lower bound of the 95 percent confidence interval on the log scale. |
| logUb95Ci | The upper bound of the 95 percent confidence interval on the log scale. |
| labels | A vector containing the labels for the various estimates. |
| xLabel | The label on the x-axis: the name of the effect estimate. |
| limits | The limits of the effect size axis. |
| hakn | A logical indicating whether method by Hartung and Knapp should be used to adjust test statistics and confidence intervals. |
| fileName | Name of the file where the plot should be saved, for example 'plot.png'. See the function ggsave in the ggplot2 package for supported file formats. |

Details

Creates a forest plot of effect size estimates, and includes a meta-analysis estimate using a random effects model. The DerSimonian-Laird estimate (1986) is used.

Value

A Ggplot object. Use the ggsave function to save to file.

References

DerSimonian R, Laird N (1986), Meta-analysis in clinical trials. Controlled Clinical Trials, 7, 177-188.

Examples

```
plotMetaAnalysisForest(logRr = c(0, 0.2, -0.2, 0, 0.2, -0.2),
  logLb95Ci = c(-0.2, -0.2, -0.6, -0.2, -0.2, -0.6),
  logUb95Ci = c(0.2, 0.6, 0.2, 0.2, 0.6, 0.2),
  labels = c("Site A", "Site B", "Site C", "Site D", "Site E", "Site F"))
```

| | |
|----------------|---|
| plotPreparedPs | <i>Plot the propensity score distribution</i> |
|----------------|---|

Description

Plot the propensity score distribution

Usage

```
plotPreparedPs(preparedPsPlots, labels, treatmentLabel = "Target",
               comparatorLabel = "Comparator", fileName = NULL)
```

Arguments

| | |
|-----------------|---|
| preparedPsPlots | A list of prepared propensity score data as created by the preparePsPlot function. |
| labels | A vector containing the labels for the various sources. |
| treatmentLabel | A label to us for the treated cohort. |
| comparatorLabel | A label to us for the comparator cohort. |
| fileName | Name of the file where the plot should be saved, for example 'plot.png'. See the function ggsave in the ggplot2 package for supported file formats. |

Value

A ggplot object. Use the [ggsave](#) function to save to file in a different format.

Examples

```
treatment <- rep(0:1, each = 100)
propensityScore <- c(rnorm(100, mean = 0.4, sd = 0.25), rnorm(100, mean = 0.6, sd = 0.25))
data <- data.frame(treatment = treatment, propensityScore = propensityScore)
data <- data[data$propensityScore > 0 & data$propensityScore < 1, ]
preparedPlot <- preparePsPlot(data)
# Just reusing the same data three times for demonstration purposes:
preparedPsPlots <- list(preparedPlot, preparedPlot, preparedPlot)
labels <- c("Data site A", "Data site B", "Data site C")
```

| | |
|---------------|--|
| preparePsPlot | <i>Prepare to plot the propensity score distribution</i> |
|---------------|--|

Description

`preparePsPlot` prepares to plot the propensity (or preference) score distribution. It computes the distribution, so the output does not contain person-level data.

Usage

```
preparePsPlot(data, unfilteredData = NULL, scale = "preference")
```

Arguments

| | |
|----------------|---|
| data | A data frame with at least the two columns described below |
| unfilteredData | To be used when computing preference scores on data from which subjects have already been removed, e.g. through trimming and/or matching. This data frame should have the same structure as data. |
| scale | The scale of the graph. Two scales are supported: <code>scale = 'propensity'</code> or <code>scale = 'preference'</code> . The preference score scale is defined by Walker et al (2013). |

Details

The data frame should have at least the following two columns:

| | | |
|-----------------|-----------|--|
| treatment | (integer) | Column indicating whether the person is in the treated (1) or comparator (0) group |
| propensityScore | (numeric) | Propensity score |

Value

A data frame describing the propensity score (or preference score) distribution at 100 equally-spaced points.

References

Walker AM, Patrick AR, Lauer MS, Hornbrook MC, Marin MG, Platt R, Roger VL, Stang P, and Schneeweiss S. (2013) A tool for assessing the feasibility of comparative effectiveness research, *Comparative Effective Research*, 3, 11-20

Examples

```
treatment <- rep(0:1, each = 100)
propensityScore <- c(rnorm(100, mean = 0.4, sd = 0.25), rnorm(100, mean = 0.6, sd = 0.25))
data <- data.frame(treatment = treatment, propensityScore = propensityScore)
data <- data[data$propensityScore > 0 & data$propensityScore < 1, ]
preparedPlot <- preparePsPlot(data)
```

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