Package ‘bamdit’

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Bayesian meta-analysis of diagnostic test data based on a scale mixtures bivariate random-effects model. This package was developed with the aim of simplifying the use of meta-analysis models that up to now have demanded great statistical expertise in Bayesian meta-analysis. The package implements a series of innovative statistical techniques including: the BSROC (Bayesian Summary ROC) curve, the BAUC (Bayesian AUC), predictive surfaces, the use of prior distributions that avoid boundary estimation problems of component of variance and correlation parameters, analysis of conflict of evidence and robust estimation of model parameters. In addition, the package comes with several published examples of meta-analysis that can be used for illustration or further research in this area.

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References

bsroc

Description

This function plots the observed data in the ROC (Receiving Operating Characteristics) space with the Bayesian SROC (Summary ROC) curve. The predictive curves are approximated using a parametric model.

Usage

bsroc(m, level = c(0.05, 0.5, 0.95), title = "Bayesian SROC Curve", fpr.x = seq(0.01, 0.95, 0.01), partial.AUC = TRUE, xlim.bsroc = c(0, 1), ylim.bsroc = c(0, 1), lower.auc = 0, upper.auc = 0.95, col.fill.points = "blue", results.bauc = TRUE, results.bsroc = FALSE, plot.post.bauc = FALSE, bins = 30, scale.size.area = 10)

Arguments

m The object generated by metadiag.
level Credibility levels of the predictive curve
title Optional parameter for setting a title in the plot.
fpr.x Grid of values where the conditional distribution is calculated.
partial.AUC Automatically calculate the AUC for the observed range of FPRs, default is TRUE.
xlim.bsroc Graphical limits of the x-axis for the BSROC curve plot.
ylim.bsroc Graphical limits of the y-axis for the BSROC curve plot.
lower.auc Lower limit of the AUC.
upper.auc Upper limit of the AUC.
col.fill.points Color used to fill points, default is blue.
results.bauc Print results of the Bayesian Area Under the Curve, default value is TRUE.
results.bsroc Print results of the Bayesian SROC curve, default value is FALSE.
plot.post.bauc The BSROC and the posterior of the BAUC are plotted in the same page, default is FALSE.
bins Histograms' bins.
scale.size.area Scale area for the plotted points, default = 10.
References


See Also

metadiag.

Examples

```r
## execute analysis
## Not run:
# Example: data from Glas et al. (2003)

data(glas)
glas.t <- glas[glas$marker == "Telomerase", 1:4]
glas.m1 <- metadiag(glas.t, re = "normal", link = "logit")
bsroc(glas.m1)
bsroc(glas.m1, plot.post.bauc = TRUE)

# Example: data from Scheidler et al. (1997)
# In this example the range of the observed FPR is less than 20%.
# Calculating the BSROC curve makes no sense! You will get a warning message!

data(mri)
mri.m <- metadiag(mri)
bsroc(mri.m)

## End(Not run)
```

ct

Diagnosis of appendicities with computer tomography scans

Description

This data frame corresponds to 51 clinical studies reporting the accuracy of computer tomography (CT) scans for the diagnosis of appendicities.

Format

A matrix with 51 rows and 17 columns. Each row represents study results, the columns are:

- `tp` number of true positives.
- `n1` number of patients with disease.
- `fp` number of false positives.
n2 number of patients without disease.

Author First author and year.

country Country: EU = 1, others/USA = 2.

hosp Type of hospital: 1 = university, 2 = others.

inclus Inclusion criteria: 1 = Suspected, 2 = appendectomy.

indfind Other CT findings included: 1 = no, 2 = yes.

design Study design: 1 = prospective, 2 = retrospective.

contr Contrast medium: 1 = no, 2 = yes.

localis Localisation: 1 = one area, 2 = more than one area.

child Children included: 1 = no, 2 = yes.

fup.na Followup: 0 = no, 1 = yes.

refer.na Valid reference: 0 = no, 1 = yes.

sample.na Sample: 0 = selected, 1= consecutive/random.

gender.na Gender, female: 0 = less than 50%; 1 = more than 50%.

Details

This data frame corresponds to 51 clinical studies reporting the accuracy of computer tomography (CT) scans for the diagnosis of appendicities.

Source

The data were obtained from


References


---

diabetes Systematic review which compares the accuracy of HbA1c vs FPG in diabetes

Description

This data frame contains results of diagnostic accuracy of 38 studies which reported comparison of sensitivity and specificity between HbA1c vs FPG in a population based screening for type 2 diabetes.
Format

A data frame with 38 rows and 9 columns. Each row represents study results, the columns are:

- **Study** Name of the first author.
- **TP\_HbA1c** Number of true positive cases for HbA1c.
- **FP\_HbA1c** Number of false positive cases for HbA1c.
- **FN\_HbA1c** Number of false negative cases for HbA1c.
- **TN\_HbA1c** Number of true negative cases for HbA1c.
- **TP\_FPG** Number of true positive cases for FPG.
- **FP\_FPG** Number of false positive cases for FPG.
- **FN\_FPG** Number of false negative cases for FPG.
- **TN\_FPG** Number of true negative cases for FPG.

Details

This data frame contains results of diagnostic accuracy of 38 studies which reported comparison of sensitivity and specificity between HbA1c vs FPG in a population-based screening for type 2 diabetes.

Source


---

**Description**

Ectopic pregnancy vs. all other pregnancies data Table III Mol et al. 1998

Format

A matrix with 21 rows and 8 columns. Each row represents study results, the columns are:

- **tp** number of true positives.
- **n1** number of patients with disease.
- **fp** number of false positives.
- **n2** number of patients without disease.
- **d1** Prospective vs. retrospective.
- **d2** Cohort vs. case-control
- **d3** Consecutive sampling patients series vs. non-consecutive.

Source

Table III Mol et al. 1998
**Description**

Outcome of individual studies evaluating urine markers

**Format**

A matrix with 46 rows and 7 columns. Each row represents study results, the columns are:

- **tp** number of true positives.
- **n1** number of patients with disease.
- **fp** number of false positives.
- **n2** number of patients without disease.
- **author** first author of the study.
- **cutoff** cutoff in U/ml.
- **marker** test method used in the study.

**Source**

The data were obtained from


**References**


---

**gould**

*Accuracy of Positron Emission Tomography for Diagnosis of Pulmonary Nodules and Mass Lesions*

**Description**

Data from a Meta-Analysis of Studies Quality of FDG-PET for Diagnosis of SPNs and Mass Lesions
Format

A matrix with 31 rows and 6 columns. Each row represents study results, the columns are:

- **tp** number of true positives.
- **n1** number of patients with disease.
- **fp** number of false positives.
- **n2** number of patients without disease.
- **author** first author of the study.
- **year** publication date.

Source

The data were obtained from


metadiag  
*Bayesian Meta-Analysis of diagnostic test data*

Description

This function performs a Bayesian meta-analysis of diagnostic test data by fitting a bivariate random effects model. The number of true positives and false positives are modeled with two conditional Binomial distributions and the random-effects are based on a bivariate scale mixture of Normals. Computations are done by calling JAGS (Just Another Gibbs Sampler) to perform MCMC (Markov Chain Monte Carlo) sampling and returning an object of the class *mcmc.list.*

Usage

```
metadiag(data, two.by.two = FALSE, re = "normal", re.model = "DS",
  link = "logit", mean.mu.D = 0, mean.mu.S = 0, sd.mu.D = 1,
  sd.mu.S = 1, sigma.D.upper = 10, sigma.S.upper = 10,
  mean.Fisher.rho = 0, sd.Fisher.rho = 1/sqrt(2), df = 4,
  df.estimate = FALSE, df.lower = 3, df.upper = 20,
  split.w = FALSE, n.1.new = 50, n.2.new = 50, nr.chains = 2,
  nr.iterations = 10000, nr.adapt = 1000, nr.burnin = 1000,
  nr.thin = 1, be.quiet = FALSE, r2jags = TRUE)
```
Arguments

data Either a data frame with at least 4 columns containing the true positives (tp), number of patients with disease (n1), false positives (fp), number of patients without disease (n2), or for two.by.two = TRUE a data frame where each line contains the diagnostic results as a two by two table, where the column names are: TP, FP, TN, FN.

two.by.two If TRUE indicates that the diagnostic results are given as: TP, FP, TN, FN.

re Random effects distribution for the resulting model. Possible values are normal for bivariate random effects and sm for scale mixtures.

re.model If re.model = "DS" indicates that the sum and differences of TPR and FPR are modeled as random effects and re.model = "SeSp" indicates that the Sensitivity and Specificity are modeled as random effects. The default value is re.model = "DS".

link The link function used in the model. Possible values are logit, cloglog probit.

mean.mu.D prior Mean of D, default value is 0.

mean.mu.S prior Mean of S, default value is 0.

sd.mu.D prior Standard deviation of D, default value is 1 (the prior of mu.D is a logistic distribution).

sd.mu.S prior Standard deviation of S, default value is 1 (the prior of mu.S is a logistic distribution).

sigma.D.upper Upper bound of the uniform prior of sigma.D, default value is 10.

sigma.S.upper Upper bound of the uniform prior of sigma.S, default value is 10.

mean.Fisher.rho Mean of rho in the Fisher scale default value is 0.

sd.Fisher.rho Standard deviation of rho in the Fisher scale, default value is 1/sqrt(2).

df If de.estimate = FALSE, then df is the degrees of freedom for the scale mixture distribution, default value is 4.

df.lower Lower bound of the prior of df. The default value is 3.

df.upper Upper bound of the prior of df. The default value is 30.

split.w Split the w parameter in two independent weights one for each random effect. The default value is FALSE.

n.1.new Number of patients with disease in a predictive study default is 50.

n.2.new Number of patients with non-disease in a predictive study default is 50.

nr.chains Number of chains for the MCMC computations, default 5.

nr.iterations Number of iterations after adapting the MCMC, default is 10000. Some models may need more iterations.

nr.adapt Number of iterations in the adaptation process, default is 1000. Some models may need more iterations during adaptation.

nr.burnin Number of iterations discarded for burnin period, default is 1000. Some models may need a longer burnin period.
nr.thin  Thinning rate, it must be a positive integer, the default value 1.

be.qiet  Do not print warning message if the model does not adapt default value is FALSE. If you are not sure about the adaptation period choose be.qiet=TRUE.

r2jags  Which interface is used to link R to JAGS (rjags and R2jags) default value is R2Jags TRUE.

Details

Installation of JAGS: It is important to note that R 3.3.0 introduced a major change in the use of toolchain for Windows. This new toolchain is incompatible with older packages written in C++. As a consequence, if the installed version of JAGS does not match the R installation, then the rjags package will spontaneously crash. Therefore, if a user works with R version >= 3.3.0, then JAGS must be installed with the installation program JAGS-4.2.0-Rtools33.exe. For users who continue using R 3.2.4 or an earlier version, the installation program for JAGS is the default installer JAGS-4.2.0.exe.

Value

This function returns an object of the class metadiag. This object contains the MCMC output of each parameter and hyper-parameter in the model, the data frame used for fitting the model, the link function, type of random effects distribution and the splitting information for conflict of evidence analysis.

The results of the object of the class metadiag can be extracted with R2jags or with rjags. In addition a summary, a print and a plot functions are implemented for this type of object.

References


Examples

```r
## Not run:

# Example: data from Glas et al. (2003)..............................
library(bamdit)
data("glas")
glas.t <- glas[glas$marker == "Telomerase", 1:4]

# Simple visualization ...

plotdata(glas.t, two.by.two = FALSE)  # Data frame
# Data is given as: (tp, n1, fp, n2)
```
I produced a data frame as: 

```r
summary(glas.m1, digit=3)
```

```
plot(glas.m1, level = c(0.5, 0.75, 0.95), parametric.smooth = TRUE)  # Parametric curve
```

```
plot(glas.m1, level = c(0.5, 0.75, 0.95), parametric.smooth = FALSE)  # Non-parametric curve
```

```
library(dplyr)
glas.t %>%
  metadiag(re = "normal", re.model = "SeSp") %>%
  plot(parametric.smooth = FALSE, color.pred.points = "red")
```

```
library(ggplot2)
library(GGally)
library(R2jags)
attach.jags(glas.m1)
ggpairs(hyper.post, title = "Hyper-Posterior", lower = list(continuous = "density") # contour plots )
```

```
# Visualization of posteriors of hyper-parameters
```

```
# List of different statistical models:
```
# 1) Different link functions: logit, cloglog and probit

# 2) Different parametrization of random effects in the link scale:
#     DS = "differences of TPR and FPR"
#     SeSp = "Sensitivity and Specificity"

# 3) Different random effects distributions:
#     "normal" or "sm = scale mixtures".

# 4) For the scale mixture random effects:
#     split.w = TRUE => "split the weights".

# 5) For the scale mixture random effects:
#     df.estimate = TRUE => "estimate the degrees of freedom".

# 6) For the scale mixture random effects:
#     df.estimate = TRUE => "estimate the degrees of freedom".

# 7) For the scale mixture random effects:
#     df = 4 => "fix the degrees of freedom to a particular value".
#     Note that df = 1 fits a Cauchy bivariate distribution to the random effects.

# logit-normal-DS
m <- metadiag(glas.t, re = "normal", re.model = "DS", link = "logit")
summary(m)
plot(m)

# cloglog-normal-DS
summary(metadiag(glas.t, re = "normal", re.model = "DS", link = "cloglog"))

# probit-normal-DS
summary(metadiag(glas.t, re = "normal", re.model = "DS", link = "probit"))
# logit-normal-Sept
summary(metadiag(glas.t, re = "normal", re.model = "SeSp", link = "logit"))

# cloglog-normal-SeSp
summary(metadiag(glas.t, re = "normal", re.model = "SeSp", link = "cloglog"))
# probit-normal-SeSp
summary(metadiag(glas.t, re = "normal", re.model = "SeSp", link = "probit"))

# logit-sm-DS
summary(metadiag(glas.t, re = "sm", re.model = "DS", link = "logit", df = 1))

# cloglog-sm-DS
summary(metadiag(glas.t, re = "sm", re.model = "DS", link = "cloglog", df = 1))
plot(m, parametric.smooth = FALSE)

# probit-sm-DS
summary(metadiag(glas.t, re = "sm", re.model = "DS", link = "probit", df = 1))
plot(m, parametric.smooth = FALSE)

# logit-sm-SeSp
summary(metadiag(glas.t, re = "sm", re.model = "SeSp", link = "logit", df = 1))
plot(m, parametric.smooth = FALSE, level = c(0.5, 0.9))

# cloglog-sm-SeSp
summary(m<-metadiag(glas.t, re = "sm", re.model = "SeSp", link = "cloglog", df = 1))
plot(m, parametric.smooth = FALSE, level = c(0.5, 0.9))

# probit-sm-SeSp
summary(m<-metadiag(glas.t, re = "sm", re.model = "SeSp", link = "probit", df = 1))
plot(m, parametric.smooth = FALSE, level = c(0.5, 0.9))

# logit-sm-DS
summary(m<-metadiag(glas.t, re = "sm", re.model = "DS", link = "logit",
  df.estimate = TRUE))
plot(m, parametric.smooth = FALSE, level = c(0.5, 0.9))

# cloglog-sm-DS
summary(m<-metadiag(glas.t, re = "sm", re.model = "DS", link = "cloglog",
  df.estimate = TRUE))
plot(m, parametric.smooth = FALSE, level = c(0.5, 0.9))

# probit-sm-DS
summary(m<-metadiag(glas.t, re = "sm", re.model = "DS", link = "probit",
  df.estimate = TRUE))
plot(m, parametric.smooth = FALSE, level = c(0.5, 0.9))

# logit-sm-SeSp-DS
summary(m<-metadiag(glas.t, re = "sm", re.model = "SeSp", link = "probit",
  df.estimate = TRUE))
plot(m, parametric.smooth = FALSE, level = c(0.5, 0.9))

# cloglog-sm-SeSp-DS
summary(m<-metadiag(glas.t, re = "sm", re.model = "SeSp", link = "cloglog",
  df.estimate = TRUE))
plot(m, parametric.smooth = FALSE, level = c(0.5, 0.9))

# probit-sm-SeSp-DS
summary(m<-metadiag(glas.t, re = "sm", re.model = "SeSp", link = "probit",
  df.estimate = TRUE))
plot(m, parametric.smooth = FALSE, level = c(0.5, 0.9))

# split.w .................................................................

# logit-sm-DS
summary(m <- metadiag(glas.t, re = "sm", re.model = "DS", link = "logit", split.w = TRUE, df = 10))
plot(m)

# cloglog-sm-DS
summary(m<metadiag(glas.t, re = "sm", re.model = "DS", link = "cloglog", split.w = TRUE, df = 4))
plot(m)

# probit-sm-DS
summary(m<-metadiag(glas.t, re = "sm", re.model = "DS", link = "probit", split.w = TRUE, df = 4))
plot(m, parametric.smooth = FALSE)
# logit-sm-SeSp
summary(m<metadiag(glas.t, re = "sm", re.model = "SeSp", link = "logit", split.w = TRUE, df = 1))
plot(m, parametric.smooth = FALSE, level = c(0.5, 0.9))
plot(m)

# cloglog-sm-SeSp
summary(m<metadiag(glas.t, re = "sm", re.model = "SeSp", link = "cloglog", split.w = TRUE, df = 1))
plot(m, parametric.smooth = FALSE, level = c(0.5, 0.9))
plot(m)

# probit-sm-SeSp
summary(m<metadiag(glas.t, re = "sm", re.model = "SeSp", link = "probit", split.w = TRUE, df = 1))
plot(m, parametric.smooth = FALSE, level = c(0.5, 0.9))
plot(m)

# logit-sm-DS-df
summary(m<metadiag(glas.t, re = "sm", re.model = "DS", link = "logit", split.w = TRUE, df.estimate = TRUE))
plot(m, parametric.smooth = FALSE, level = c(0.5, 0.9))
plot(m)

# cloglog-sm-DS-df
summary(m<metadiag(glas.t, re = "sm", re.model = "DS", link = "cloglog", split.w = TRUE, df.estimate = TRUE))
plot(m, parametric.smooth = FALSE, level = c(0.5, 0.9))
plot(m)

# probit-sm-DS-df
summary(m<metadiag(glas.t, re = "sm", re.model = "DS", link = "probit", split.w = TRUE, df.estimate = TRUE))
plot(m, parametric.smooth = FALSE, level = c(0.5, 0.9))
plot(m)

# logit-sm-SeSp-df
summary(m<metadiag(glas.t, re = "sm", re.model = "SeSp", link = "probit", split.w = TRUE, df.estimate = TRUE))
plot(m, parametric.smooth = FALSE, level = c(0.5, 0.9))
plot(m)

# cloglog-sm-SeSp-df
summary(m<metadiag(glas.t, re = "sm", re.model = "SeSp", link = "cloglog", split.w = TRUE, df.estimate = TRUE))
plot(m, parametric.smooth = FALSE, level = c(0.5, 0.9))
plot(m)

# probit-sm-SeSp-df
summary(m<metadiag(glas.t, re = "sm", re.model = "SeSp", link = "probit", split.w = TRUE, df.estimate = TRUE))
plot(m, parametric.smooth = FALSE, level = c(0.5, 0.9))
plot(m)
**Description**

Diagnosis of lymph node metastasis with magnetic resonance imaging

**Format**

A matrix with 10 rows and 4 columns. Each row represents study results, the columns are:

- **tp**: true positives
- **n1**: number of patients with disease
- **fp**: false positives
- **n2**: number of patients without disease

**Source**


**References**


**Description**

This function plots the observe data in the ROC (Receiving Operating Characteristics) space with the posterior predictive contours. The predictive curves are approximated using a non-parametric smoother or with a parametric model. For the parametric model the current implementation supports only a logistic link function. The marginal posterior predictive distributions are plotted outside the ROC space.
Usage

```r
## S3 method for class 'metadiag'
plot(x, parametric.smooth = TRUE, level = c(0.5, 0.75, 0.95), limits.x = c(0, 1), limits.y = c(0, 1), kde2d.n = 25, color.line = "red", title = paste("Posterior Predictive Contours (50%, 75% and 95%)"), marginals = TRUE, bin.hist = 30, color.hist = "lightblue", S = 500, color.pred.points = "lightblue", color.data.points = "blue", ...)```

Arguments

- `x`: The object generated by the metadiag function.
- `parametric.smooth`: Indicates if the predictive curve is a parametric or non-parametric.
- `level`: Credibility levels of the predictive curve. If parametric.smooth = FALSE, then the probability levels are estimated from the nonparametric surface.
- `limits.x`: Numeric vector of length 2 specifying the x-axis limits. The default value is c(0, 1).
- `limits.y`: Numeric vector of length 2 specifying the x-axis limits. The default value is c(0, 1).
- `kde2d.n`: The number of grid points in each direction for the non-parametric density estimation. Can be scalar or a length-2 inter vector.
- `color.line`: Color of the predictive contour line.
- `title`: Optional parameter for setting a title in the plot.
- `marginals`: Plot the posterior marginal predictive histograms.
- `bin.hist`: Number of bins of the marginal histograms.
- `color.hist`: Color of the histograms.
- `S`: Number of predictive rates to be plotted.
- `color.pred.points`: Color of the posterior predictive rates.
- `color.data.points`: Color of the data points.
- `...`: Further arguments.

See Also

`metadiag`

Examples

```r
## Not run:
```
library(bamdit)
data("glas")
glas.t <- glas[glas$marker == "Telomerase", 1:4]
glas.m1 <- metadiag(glas.t,  # Data frame
  re = "normal",  # Random effects distribution
  re.model = "DS",  # Random effects on D and S
  link = "logit",  # Link function
  sd.Fisher.rho = 1.7, # Prior standard deviation of correlation
  nr.burnin = 1000, # Iterations for burnin
  nr.iterations = 10000, # Total iterations
  nr.chains = 2,  # Number of chains
  r2jags = TRUE)  # Use r2jags as interface to jags

plot(glas.m1,  # Fitted model
  level = c(0.5, 0.75, 0.95), # Credibility levels
  parametric.smooth = TRUE)  # Parametric curve

# Plot results: based on a non-parametric smoother of the posterior predictive rates .......

plot(glas.m1,  # Fitted model
  level = c(0.5, 0.75, 0.95), # Credibility levels
  parametric.smooth = FALSE)  # Non-parametric curve

# Using the pipe command in the package dplyr and changing some colors .......

library(dplyr)
glas.t %>%
  metadiag(re = "normal", re.model = "SeSp") %>%
  plot(parametric.smooth = FALSE,
       S = 100,
       color.data.points = "green",
       color.pred.points = "blue",
       color.line = "black")

## End(Not run)

plotcompare

---

Description

This function compares the predictive posterior surfaces of two fitted models.

Usage

plotcompare(m1, m2, level = 0.95,
            title = paste("Comparative Predictive Posterior Contours"),
m1.name = "Model.1", m2.name = "Model.2", group = NULL,
limits.x = c(0, 1), limits.y = c(0, 1), group.colors = c("blue",
"red"))

**Arguments**

m1 A model fitted to the data. This is an object generated by the metadiag function.
m2 A second model fitted to the data. This is an object generated by the metadiag function.
level Credibility level of the predictive curves.
title The title of the plot.
m1.name Label of the model 1.
m2.name Label of the model 2.
group An optional argument, which is a variable name indicating a group factor. This argument is used to compare results from two subgroups.
limits.x A vector with the limits of the horizontal axis.
limits.y A vector with the limits of the vertical axis.
group.colors A character vector with two color names.

**See Also**

metadiag.

**Examples**

```r
## execute analysis
## Not run:

# Comparing results from two models same data
data(glas)
glas.t <- glas[glas$marker == "Telomerase", 1:4]
glas.m1 <- metadiag(glas.t)
glas.m2 <- metadiag(glas.t, re = "sm")
plotcompare(m1 = glas.m1, m2 = glas.m2)

# Comparing results from two models fitted to two subgroups of data:
# studies with retrospective design and studies with prospective design
data("ct")
ct$design = factor(ct$design, labels = c("Prospective", "Retrospective"))
ml.ct <- metadiag(ct[ct$design == "Prospective", ])
m2.ct <- metadiag(ct[ct$design == "Retrospective", ])
plotcompare(ml.ct, m2.ct, m1.name = "Retrospective design",
m2.name = "Prospective design", group = "design",
```
plotdata

Basic function to plot the data of meta-analysis of diagnostic test

Description

This function plots the true positive rates vs the false positive rates of each study included in the meta-analysis. Study results are displayed by circles, the diameter of each circle is proportional to the sample size of the study (or table). If subgroups are displayed each group is represented by different colours. This function use the package ggplot2.

Usage

plotdata(data, two.by.two = FALSE, group = NULL, x.lo = 0, x.up = 1, y.lo = 0, y.up = 1, alpha.p = 0.7, max.size = 15)

Arguments

data
  Either a data frame with at least 4 columns containing the true positives (tp), number of patients with disease (n1), false positives (fp), number of patients without disease (n2), or for two.by.two = TRUE a data frame where each line contains the diagnostic results as a two by two table, where the column names are: TP, FP, TN, FN.
two.by.two
  If TRUE indicates that the diagnostic results are given as: TP, FP, TN, FN.
group
  a variable name indicating a group factor
x.lo
  lower limit of the x-axis
x.up
  upper limit of the x-axis
y.lo
  lower limit of the y-axis
y.up
  upper limit of the y-axis
alpha.p
  transparency of the points
max.size
  scale parameter of the maximum size

Examples

## execute analysis
## Not run:

data(ct)
ct$design <- with(ct, factor(design,
labels = c("Prospective", "Retrospective"))

plotdata(ct, # Data frame
group = "design", # Grouping variable
y.lo = 0.75, # Lower limit of y-axis
x.up = 0.75, # Upper limit of x-axis
alpha.p = 0.5, # Transparency of the balls
max.size = 5) # Scale the circles

## End(Not run)

plotsesp() plot the posterior densities for Se and Sp

Description

plotsesp() plot the posterior densities for Se and Sp

Usage

plotsesp(m, binwidth.p = 0.03, CI.level = 0.95)

Arguments

m The object generated by the metdiag function.
binwidth.p Histograms binwidth, default is 0.03.
CI.level Level of the posterior interval default is 0.95.

See Also

metadiag.

Examples

## execute analysis
## Not run:
data(ep)
m1.ep <- metadiag(ep[,1:4])

plotsesp(m = m1.ep)

## End(Not run)
plotw

Plot for the conflict of evidence parameters w1 and w2

Description
Conflict of evidence plot: this plot displays the posterior distribution of the study’s weights w1 and w1. These weights indicate potential conflict of evidence of the studies. The weight w1 indicates deviations with respect to the specificity and w2 to the sensitivity.

Usage
plotw(m, group = NULL,
     title = "Posterior quantiles (25%, 50%, 75%)",
     group.colors = c("blue", "red"))

Arguments
m The object generated by metadiag. The model object must be fitted with the options: re = "sm" and split.w = TRUE.

group An optional argument which is a variable name indicating a group factor. If set, then the plot is colored by groups.
title The title of the plot.
group.colors A character vector with two color names.

See Also
metadiag.

Examples
## execute analysis
## Not run:
data(ep)
ep$design = factor(ep$d1.labels = c("prospective", "retrospective"))
m.ep <- metadiag(ep, re = "sm", re.model = "SeSp",
                 split.w = TRUE,
                 df.estimate = TRUE)

plotw(m.ep)
#Relationship between conflict and study design
plotw(m.ep, group = "design")

## End(Not run)
**print.metadiag**  
*Generic print function for metadiag object in bamdit*

### Description

Generic print function for metadiag object in bamdit

### Usage

```r
## S3 method for class 'metadiag'
print(x, digits = 3, ...)
```

### Arguments

- `x` The object generated by the function metadiag.
- `digits` The number of significant digits printed. The default value is 3.
- `...` ...

---

**rapt**  
*Systematic reviews of clinical decision tools for acute abdominal pain*

### Description

This data frame corresponds to 13 clinical studies reporting the accuracy of doctors added with decision tools.

### Format

A data frame with 13 rows and 13 columns. Each row represents study results, the columns are:

- **Author** Name of the first author and year of publication
- **tp.dr** Number of true positive cases for unadded doctors.
- **fp.dr** Number of false positive cases for unadded doctors.
- **fn.dr** Number of false negative cases for unadded doctors.
- **tn.dr** Number of true negative cases for unadded doctors.
- **tp.tools** Number of true positive cases for doctors with decision tools.
- **fp.tools** Number of false positive cases for doctors with decision tools.
- **fn.tools** Number of false negative cases for doctors with decision tools.
- **tn.tools** Number of true negative cases for doctors with decision tools.
- **tool** Diagnostic tool.
- **n.dr** Total number of cases for unadded doctors.
- **n.tools** Total number of cases for doctors with decision tools.
- **design** Study design.
Details

This data frame contains results of diagnostic accuracy of 13 studies which reported comparison of sensitivity and specificity between doctors using diagnostic tools vs doctors without decision tools.

Source


References


<table>
<thead>
<tr>
<th>safdar05</th>
<th>Diagnosis of Intravascular Device-Related Bloodstream Infection</th>
</tr>
</thead>
</table>

Description

Outcome of individual studies evaluating intravascular device-related bloodstream infection.

Format

A matrix with 78 rows and 8 columns. Each row represents study results, the columns are:

- **tp**: number of true positives.
- **n1**: number of patients with disease.
- **fp**: number of false positives.
- **n2**: number of patients without disease.
- **author**: first author of the study.
- **year**: publication date.
- **technique**: diagnostic technique used in the study.
- **duration**: duration of catheterization: short term or long term or both.

Source

The data were obtained from


Description
This data frame summarizes the tables 1-3 of Scheidler et al. 1997.

Format
A matrix with 46 rows and 7 columns. Each row represents study results, the columns are:
- **tp** true positives.
- **n1** number of patients with disease.
- **fp** false positives.
- **n2** number of patients without disease.
- **author** first author of the study.
- **year** publication date.
- **test** test method used in the study.

Source
The data were obtained from

References

Generic summary function for metadiag object in bamdit

Description
Generic summary function for metadiag object in bamdit

Usage
```r
## S3 method for class 'metadiag'
summary(object, digits = 3, intervals = c(0.025,
   0.5, 0.975), ...)
```
**Arguments**

- **object**
  The object generated by the `metadiag` function.

- **digits**
  The number of significant digits printed. The default value is 3.

- **intervals**
  A numeric vector of probabilities with values in $[0, 1]$. The default value is `intervals = c(0.025, 0.5, 0.975)`.
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