Package 'dtametaTMB'

October 26, 2026

Title Diagnostic Test Accuracy Meta-Analysis using Template Model Builder

Version 0.1.4

Description Fits the hierarchical summary receiver operating characteristic (HSROC) model of Rutter and Gatsonis (2001) <doi:10.1002/sim.942>, the bivariate binomial-normal model of Reitsma et al. (2005) <doi:10.1016/j.jclinepi.2005.02.022>, the threshold-based bivariate time-to-event model of Hoyer et al. (2018) <doi:10.1002/jrsm.1273>, and the latent class extensions of Liu et al. (2015) <doi:10.1111/biom.12264> for diagnostic studies with an imperfect reference standard. Provides subgroup analyses, HSROC meta-regression, likelihood-ratio tests, summary ROC plots, and coupled forest plots.

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URL https://github.com/EBME-UWK/dtametaTMB

BugReports https://github.com/EBME-UWK/dtametaTMB/issues

Encoding UTF-8

Imports forestploter, glmmTMB, grid, survival, TMB

LinkingTo RcppEigen, TMB

Suggests knitr, quarto, testthat (>= 3.0.0)

Config/testthat/edition 3

Depends R (>= 3.5)

LazyData true

Config/roxygen2/version 8.1.0

VignetteBuilder quarto

NeedsCompilation yes

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Repository CRAN

Date/Publication 2026-10-26 08:20:02 UTC

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`anaemia` *Anaemia Synthetic Dataset*

Description

This is a synthetic dataset where haemoglobin was measured by a point-of-care device, with laboratory measurement acting as the reference standard. Lower values indicate disease (anaemia).

Usage

```
anaemia
```

Format

A data frame with 81 rows and 11 variables:

study Study identifier

threshold Haemoglobin in g/dL

TP Number of true positives

FN Number of false negatives

FP Number of false positives

TN Number of true negatives

D Number of diseased individuals

H Number of healthy individuals

sens Sensitivity

fpr False positive rate

testdirection Smaller values indicate disease (=less)

Source

Synthetic dataset.

---

anova.dtametaTMB *Likelihood Ratio Tests for Diagnostic Test Accuracy Models*

Description

Compare nested diagnostic test accuracy meta-analysis models using likelihood ratio tests (LRTs).

Usage

```
## S3 method for class 'Reitsma'
anova(object, ..., test = "Chisq")

## S3 method for class 'RutterGatsonis'
anova(object, ..., test = "Chisq")
```

Arguments

`object`	A fitted model object.
`...`	Additional fitted model objects to be compared.
`test`	Character string specifying the test to perform. Currently, only `"Chisq"` is supported.

Details

These methods compute likelihood ratio statistics from the fitted model log-likelihoods and compare models ordered by increasing numbers of estimated parameters. The test statistic is

$$-2(\ell_0 - \ell_1)$$

where ℓ_0 and ℓ_1 are the log-likelihoods of two nested models. Under standard regularity conditions, the statistic follows a chi-squared distribution with degrees of freedom equal to the difference in the numbers of estimated parameters.

The models supplied should be nested and fitted to the same dataset. Warnings are issued when models have identical numbers of parameters or when the log-likelihood decreases for a more complex model, suggesting that the nesting assumptions may be violated.

Value

An object of class `"anova"` inheriting from `"data.frame"` with the following columns:

Df Number of estimated parameters in the model.

logLik Model log-likelihood.

Df.diff Difference in parameters compared with the previous model.

Chisq Likelihood ratio chi-squared statistic.

Pr(>Chisq) P-value from the chi-squared test.

Caution for variance-component tests

The usual chi-squared reference distribution requires appropriate regularity conditions. In particular, these conditions may not hold when the null hypothesis constrains one or more random-effects variance components to zero, because variances are non-negative and zero lies on the boundary of the parameter space.

This issue can arise when comparing Reitsma models that constrain sigma2_A or sigma2_B, or Rutter-Gatsonis models that constrain sigma2_alpha or sigma2_theta. Tests involving multiple variance components constrained to zero may require additional care. In such cases, the asymptotic reference distribution may be a mixture of chi-squared distributions rather than a single chi-squared distribution. The appropriate distribution depends on the model and the constraints being tested.

The implementation uses the ordinary chi-squared reference distribution and does not apply a boundary-adjusted reference distribution. Therefore, the reported p-values may not be appropriately calibrated for tests of variance components on the boundary.

References

Self, S. G. and Liang, K. Y. (1987). Asymptotic properties of maximum likelihood estimators and likelihood ratio tests under nonstandard conditions. *Journal of the American Statistical Association*, 82, 605–610.

Stram, D. O. and Lee, J. W. (1994). Variance components testing in the longitudinal mixed effects model. *Biometrics*, 50, 1171–1177.

See Also

logLik(), anova()

---

anticcp *Anticcp Dataset*

Description

This is the anticcp dataset from Nishimura (2007) from a review of anti-cyclic citrullinated peptide antibody (anti-ccp) to diagnose rheumatoid arthritis.

Usage

```
anticcp
```

Format

A data frame with 37 rows and 7 variables:

study Study identifier

year Year of the study

TP Number of true positives

FP Number of false positives

FN Number of false negatives

TN Number of true negatives

generation First generation (CCP1) or second generation (CCP2) assay

Source

Nishimura, K. et al. (2007). *Meta-analysis: diagnostic accuracy of anti-cyclic citrullinated peptide antibody and rheumatoid factor for rheumatoid arthritis*. Annals of Internal Medicine, 146(11), 392-403. doi:10.7326/0003481914611200706050000008

`as_revman.dtametaTMB` *Export Model Results for RevMan*

Description

Converts fitted model objects (`Reitsma`, `ReitsmaSubgroup`, `RutterGatsonis`, `RutterGatsonisSubgroup`, `ReitsmaLCA`, `ReitsmaSubgroupLCA`, `RutterGatsonisLCA`, and `RutterGatsonisSubgroupLCA`) into a format suitable for manual entry into the Diagnostic Test Accuracy module of Review Manager (RevMan).

Usage

```
as_revman(x, ...)

## S3 method for class 'Reitsma'
as_revman(x, ...)

## S3 method for class 'RutterGatsonis'
as_revman(x, ...)

## S3 method for class 'ReitsmaSubgroup'
as_revman(x, ...)

## S3 method for class 'RutterGatsonisSubgroup'
as_revman(x, ...)

## S3 method for class 'ReitsmaLCA'
as_revman(x, ...)

## S3 method for class 'RutterGatsonisLCA'
as_revman(x, ...)

## S3 method for class 'ReitsmaSubgroupLCA'
as_revman(x, ...)

## S3 method for class 'RutterGatsonisSubgroupLCA'
as_revman(x, ...)

## S3 method for class 'ReitsmaSubgroupTMB'
as_revman(x, ...)

## S3 method for class 'ReitsmaTMB'
as_revman(x, ...)
```

Arguments

`x`	A fitted model object.

... Currently not used.

Value

A data frame with columns:

Subgroup Only returned for subgroup model objects.

Externally_Calculated_Parameters RevMan model/parameter types.

Parameter RevMan parameter name.

Estimate Parameter estimate.

The returned table contains the model parameters displayed by RevMan:

- `E(logitSe)`
- `E(logitSp)`
- `Var(logitSe)`
- `Var(logitSp)`
- `Cov(logits)`
- `Corr(logits)`
- `Lambda`
- `Theta`
- `beta`
- `Var(accuracy)`
- `Var(threshold)`
- `SE(E(logitSe))`
- `SE(E(logitSp))`
- `Cov(Es)`
- `Studies`

Note

For Rutter and Gatsonis models `SE(E(logitSe))`, `SE(E(logitSp))`, and `Cov(Es)` are not computed.

`coef.dtametaTMB` *Extract Model Coefficients*

Description

Returns the estimated model parameters.

Usage

```
## S3 method for class 'DTAmodel'
coef(object, ...)

## S3 method for class 'Reitsma'
coef(object, ...)

## S3 method for class 'ReitsmaSubgroup'
coef(object, ...)

## S3 method for class 'ReitsmaLCA'
coef(object, ...)

## S3 method for class 'ReitsmaSubgroupLCA'
coef(object, ...)

## S3 method for class 'ReitsmaSubgroupTMB'
coef(object, ...)

## S3 method for class 'ReitsmaTMB'
coef(object, ...)
```

Arguments

`object`	A fitted model object.
`...`	Not currently used.

Value

A named vector of parameter estimates.

Note

For `ReitsmaSubgroup` models, `coef()` returns parameter estimates from the cell-means parameterization rather than treatment-contrast coefficients.

See Also

`vcov.dtametaTMB()`

`dementia` *Dementia Dataset*

Description

This is the dementia dataset from Harrison et al. (2015) from a review of the Informant Questionnaire on Cognitive Decline in the Elderly (IQCODE) for the diagnosis of dementia within a secondary care setting.

Usage

```
dementia
```

Format

A data frame with 13 rows and 17 variables:

author Author of the study

year Year of the study

TP Number of true positives

FN Number of false negatives

FP Number of false positives

TN Number of true negatives

rob_PS Risk of bias: Patient selection

rob_IT Risk of bias: Index test

rob_RS Risk of bias: Reference standard

rob_FT Risk of bias: Flow and timing

ac_PS Applicability: Patient selection

ac_IT Applicability: Index test

ac_RS Applicability: Reference standard

Threshold.cat Threshold category

Country.cat Country category

IQCODE.cat Informant Questionnaire on Cognitive Decline in the Elderly category

reference.cat Reference category

Note

The data were taken as provided from the MetaBayesDTA application.

Source

Cerullo, E. et al. (2023). *MetaBayesDTA: codeless Bayesian meta-analysis of test accuracy, with or without a gold standard* BMC Medical Research Methodology 23(127). doi:10.1186/s12874-02301910y

Harrison, J. et al. (2015). *Informant Questionnaire on Cognitive Decline in the Elderly (IQCODE) for the diagnosis of dementia within a secondary care setting.*. Cochrane Database of Systematic Reviews 3. doi:10.1002/14651858.CD010772.pub2

`diabetes` *Diabetes Dataset*

Description

This is the diabetes dataset from the supplementary material in Hoyer (2018).

Usage

```
diabetes
```

Format

A data frame with 124 rows and 9 variables

study Study identifier

threshold Threshold HbA1c used to derive TP, FN, FP, TN

TP Number of true positives

TN Number of true negatives

FP Number of false positives

FN Number of false negatives

D Number of diseased individuals

H Number of healthy individuals

originally_published Whether the data threshold/row was used in the original publication (1=yes, 0=no)

Source

Hoyer, A., Hirt, S., Kuss, O. (2018). *Meta-analysis of full ROC curves using bivariate time-to-event models for interval-censored data*. Research Synthesis Methods, 9(1), 62-72. doi:10.1002/jrsm.1273

`dtametaTMB` *dtametaTMB: Diagnostic Test Accuracy Meta-Analysis using Template Model Builder*

Description

Functions for fitting diagnostic test accuracy (DTA) meta-analysis models using Template Model Builder (TMB).

Details

Implemented methods

- Reitsma model
- Rutter-Gatsonis HSROC model
- Hoyer multiple-threshold model
- Latent class analysis for studies with an imperfect reference standard

Main workflow

- fitReitsma() -> print() -> summary() -> plot() -> forest()
- fitReitsmaTMB() -> print() -> summary() -> plot() -> forest()
- fitReitsmaSubgroup() -> print() -> summary() -> plot() -> forest()
- fitReitsmaSubgroupTMB() -> print() -> summary() -> plot() -> forest()
- fitRutterGatsonis() -> print() -> summary() -> plot() -> forest()
- fitRutterGatsonisSubgroup() -> print() -> summary() -> plot() -> forest()
- fitHoyer() -> print() -> summary() -> plot() -> forest()
- fitReitsmaLCA() -> print() -> summary() -> plot() -> forest()
- fitReitsmaSubgroupLCA() -> print() -> summary() -> plot() -> forest()
- fitRutterGatsonisLCA() -> print() -> summary() -> plot() -> forest()
- fitRutterGatsonisSubgroupLCA() -> print() -> summary() -> plot() -> forest()

Included datasets

- anaemia
- anticcp
- diabetes
- dementia
- FENO
- pap
- RF
- schuetz
- tub

See the package vignettes for worked examples and model descriptions.

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See Also

Useful links:

- https://github.com/EBME-UWK/dtametaTMB
- Report bugs at https://github.com/EBME-UWK/dtametaTMB/issues

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FENO *FENO Dataset*

Description

This is the FENO dataset from Schneider (2017) from a review of fractional exhaled nitric oxide (FeNO) for diagnosis of asthma.

Usage

```
FENO
```

Format

A data frame with 150 rows and 7 variables:

study Study identifier

study_id Study identifier (numeric)

cutoff Threshold for FeNO measured in ppb

TP Number of true positives

FN Number of false negatives

FP Number of false positives

TN Number of true negatives

Note

The data are reproduced from the original source and the supplementary material accompanying the Cochrane Handbook. However, the study 'Schneider 2013' contains inconsistent diseased counts (TP + FN). To illustrate the Hoyer analysis in the vignette, we modify the TP counts in rows 118–120 from 39 to 38. Other corrections restoring internal consistency are also conceivable.

Source

Schneider, A. et al. (2017). *A novel statistical model for analyzing data of a systematic review generates optimal cutoff values for fractional exhaled nitric oxide for asthma diagnosis.* Journal of Clinical Epidemiology, 92, 69-78. doi:10.1016/j.jclinepi.2017.09.001

`fitHoyer` *Fit Threshold-Based Bivariate Time-to-Event Model (Hoyer)*

Description

This is a high-level wrapper that performs the full workflow for fitting the Hoyer AFT model:

1. Restructuring of threshold-based data into interval format
2. Estimation of initial parameter values
3. Model fitting via likelihood maximization

The input data must contain cumulative counts for true positives, false positives, false negatives, and true negatives at multiple thresholds within each study.

Usage

```
fitHoyer(
  data,
  TP,
  FP,
  FN,
  TN,
  study,
  threshold,
  smallest,
  largest,
  testdirection = c("greater", "less"),
  eval_threshold = NULL,
  conflevel = 0.95,
  dist = "loglogistic",
  verbose = FALSE,
  ...
)
```

Arguments

`data`	A data.frame containing study-level data.
`TP`	True positives (column name).
`FP`	False positives (column name).
`FN`	False negatives (column name).

TN	True negatives (column name).
study	Study identifier (column name).
threshold	The observed threshold value (column name). Must be positive and strictly increasing within each study.
smallest	Positive lower bound used to define the leftmost interval. Must be smaller than minimum threshold.
largest	Positive upper bound used to define the rightmost interval. Must be greater than maximum threshold.
testdirection	Direction of the test. Enter "greater" when larger test values indicate disease. Conversely, enter "less" when lower test values indicate disease (e.g. anaemia-type tests). Defaults to "greater".
eval_threshold	Optional numeric value or vector specifying the prediction grid threshold(s) at which sensitivity and specificity should be evaluated. If NULL (default), the median threshold from the original data is used.
conflevel	Confidence level for confidence intervals for sensitivities and specificities at the chosen thresholds. Defaults to 0.95.
dist	Character string specifying the parametric distribution for the AFT model. One of "weibull", "lognormal", or "loglogistic" (default).
verbose	Whether TMB optimization output should be printed (default: FALSE).
...	Additional arguments (unused).

Details

Fits the threshold-based bivariate accelerated failure time (AFT) model for diagnostic test accuracy (DTA) meta-analysis as described by Hoyer et al. (2018). The model is estimated using interval-censored likelihoods via Template Model Builder (TMB).

The function internally calls:

- restructure_data to convert cumulative counts into interval-censored data
- initHoyerAFT to estimate starting values
- fitHoyerAFT to fit the model

Missing values in the input data are removed prior to analysis. A message is issued listing the affected studies.

Value

An object of class "HoyerAFT" as returned by fitHoyerAFT, containing:

data Processed original data

restructured Interval-formatted data

fit Optimization output

sdreport TMB report object

sdreport2 Summary of reported parameters

sensspec Sensitivity and specificity estimates

Note

Requires a compiled TMB model named `"Hoyer"`.

References

Hoyer, A., Hirt, S., Kuss, O. (2018). Meta-analysis of full ROC curves using bivariate time-to-event models for interval-censored data. *Research Synthesis Methods*, 9(1), 62-72. doi:10.1002/jrsm.1273

Examples

```
data("diabetes")
fit <- fitHoyer(
  data = diabetes,
  TP = TP,
  FP = FP,
  FN = FN,
  TN = TN,
  study = study,
  threshold = threshold,
  testdirection = "greater",
  smallest = 2,
  largest = 10
)
summary(fit)
```

---

fitHoyerAFT *Fit Threshold-Based Bivariate Time-to-Event Model (HoyerAFT)*

Description

Fits a bivariate accelerated failure time (AFT) model for diagnostic test accuracy (DTA) data using interval-censored likelihoods as described in Hoyer et al. (2018). The model is estimated using Template Model Builder (TMB) with study-specific random effects.

Usage

```
fitHoyerAFT(
  data,
  init,
  conflevel = 0.95,
  eval_threshold = NULL,
  verbose = FALSE
)
```

Arguments

data	A list as produced by restructure_data, containing: **restructured** Interval-formatted data **original** Processed original data with derived quantities
init	A data frame of initial parameter values as produced by initHoyerAFT.
conflevel	Confidence level for confidence intervals for sensitivities and specificities at the chosen thresholds. Defaults to 0.95.
eval_threshold	Optional numeric value or vector specifying the prediction grid threshold(s) at which sensitivity and specificity should be evaluated. If NULL (default), the median threshold from the original data is used.
verbose	Whether TMB optimization output should be printed (default: FALSE).

Details

The model reports logit-survival quantities, which correspond to sensitivity and false positive rate for testdirection = "greater", and to false negative rate and specificity for testdirection = "less".

Model fitting is performed using nlminb, and uncertainty estimates are obtained via TMB::sdreport. Parameter transformations include log-scale parameters and Fisher's Z-transform for correlations.

Value

An object of class "HoyerAFT" containing:

data Processed original data

restructured Interval-formatted data

fit Optimization output from nlminb

sdreport TMB report object from sdreport

sdreport2 Summary of reported parameters

distcode Distribution code used in the model

sensspec Sensitivities and specificities at the chosen thresholds

Note

Requires a compiled TMB model named "Hoyer".

References

Hoyer, A., Hirt, S., Kuss, O. (2018). Meta-analysis of full ROC curves using bivariate time-to-event models for interval-censored data. *Research Synthesis Methods*, 9(1), 62-72. doi:10.1002/jrsm.1273

Examples

```
data("diabetes")
res <- restructure_data(
  data = diabetes,
  TP = TP,
  FP = FP,
  FN = FN,
  TN = TN,
  threshold = threshold,
  study = study,
  smallest = 2,
  largest = 10
)
init <- initHoyerAFT(res$restructured)
fit <- fitHoyerAFT(res, init)
summary(fit)
```

`fitReitsma` *Fit the Reitsma Model*

Description

Fits the Reitsma bivariate random-effects model for diagnostic test accuracy (DTA) meta-analysis using a binomial-normal likelihood via `glmmTMB`.

Usage

```
fitReitsma(data, TP, FP, FN, TN, study, constrain = NULL, conflevel = 0.95)
```

Arguments

`data`	A data.frame containing study-level data.
`TP`	True positives (column name).
`FP`	False positives (column name).
`FN`	False negatives (column name).
`TN`	True negatives (column name).
`study`	Study identifier (column name).
`constrain`	Optional character string specifying a simplified covariance structure for the Reitsma model. This can be useful for sparse data, small meta-analyses, or for reproducing simplified bivariate models described in the Cochrane Handbook for Diagnostic Test Accuracy Reviews. Allowed values are: `NULL` The standard unconstrained Reitsma model is fitted.

"sigma_AB" The covariance between logit-sensitivity and logit-specificity random effects is fixed at zero. Random effects remain independent.

"sigma2_A" The between-study variance of logit-sensitivity is fixed at zero. This also implies a zero covariance.

"sigma2_B" The between-study variance of logit-specificity is fixed at zero. This also implies a zero covariance.

"all" All random-effects variance and covariance parameters are fixed at zero, resulting in a fixed-effects model.

`conflevel` Confidence level for confidence intervals. Default is 0.95.

Value

A list of class "Reitsma" with components:

- `data`: the original data set with derived quantities
- `glmmTMB`: fitted model object.
- `estimates`: parameter estimates with SE.
- `vcov`: variance-covariance matrix.
- `sensspec`: sensitivity and specificity estimates.
- `LRDOR`: Diagnostic odds ratio and likelihood ratios.
- `RutterGatsonis_recovered`: Recovered parameters in the Rutter-Gatsonis (HSROC) parameterization.
- `constrain`: Random effects parameters fixed at zero.

References

Reitsma, J. B., et al. (2005). Bivariate analysis of sensitivity and specificity produces informative summary measures in diagnostic reviews. *Journal of Clinical Epidemiology*, 58(10), 982–990. doi:10.1016/j.jclinepi.2005.02.022

Rutter, C. M., & Gatsonis, C. A. (2001). A hierarchical regression approach to meta-analysis of diagnostic test accuracy evaluations. *Statistics in Medicine*, 20(19), 2865–2884. doi:10.1002/sim.942

Harbord, R. M., Deeks, J. J., Egger, M., Whiting, P., & Sterne, J. A. C. (2007). A unification of models for meta-analysis of diagnostic accuracy studies. *Biostatistics*, 8(2), 239–251. doi:10.1093/biostatistics/kxl004

Examples

```
data("anticcp")
fit <- fitReitsma(
  data = anticcp,
  TP = TP,
  FP = FP,
  FN = FN,
  TN = TN,
  study = study
)
summary(fit)
```

`fitReitsmaLCA` *Fit the Reitsma LCA Model*

Description

Fits the Reitsma latent class model for diagnostic test accuracy (DTA), allowing for an imperfect reference standard under conditional independence.

Usage

```
fitReitsmaLCA(
  data,
  y11,
  y10,
  y01,
  y00,
  study,
  conflevel = 0.95,
  constrain = NULL,
  verbose = FALSE
)
```

Arguments

`data`	A data.frame containing study-level data.
`y11`	Number testing positive with both index and reference tests (column name).
`y10`	Number testing positive with index test but negative with reference test (column name).
`y01`	Number testing negative with index test but positive with reference test (column name).
`y00`	Number testing negative with both index and reference tests (column name).
`study`	Study identifier (column name).
`conflevel`	Confidence level for confidence intervals. Default is 0.95.
`constrain`	Optional character string specifying a simplified covariance structure for the index test of the Reitsma LCA model. Allowed values are: `NULL` The standard unconstrained Reitsma model is fitted. `"sigma_AB.index"` The covariance between logit-sensitivity and logit-specificity random effects is fixed at zero. Random effects remain independent. `"sigma2_A.index"` The between-study variance of logit-sensitivity is fixed at zero. This also implies a zero covariance.

"sigma2_B.index" The between-study variance of logit-specificity is fixed at zero. This also implies a zero covariance.

"all" All random-effects variance and covariance parameters are fixed at zero, resulting in a fixed-effects model.

verbose Whether TMB optimization output should be printed (default: FALSE).

Value

A list of class "ReitsmaLCA" with components:

- data: the original data set with derived quantities.
- fit: Optimization result from nlminb.
- sdreport: TMB standard report.
- sdreport2: Summary of reported parameters.
- vcov: variance-covariance matrix of reported parameters.
- sensspec: sensitivity and specificity estimates.
- prevref: Estimated (average) prevalence and reference standard sensitivity/specificity with confidence intervals.
- LRDOR: Diagnostic odds ratio and likelihood ratios.
- RutterGatsonis_recovered: Recovered parameters in the Rutter-Gatsonis (HSROC) parameterization.
- constrain: Random effects parameters fixed at zero.

References

Liu, Y., Chen, Y., & Chu, H. (2015). A unification of models for meta-analysis of diagnostic accuracy studies without a gold standard. *Biometrics*, 71(2), 538-547. doi:10.1111/biom.12264

Reitsma, J. B., et al. (2005). Bivariate analysis of sensitivity and specificity produces informative summary measures in diagnostic reviews. *Journal of Clinical Epidemiology*, 58(10), 982–990. doi:10.1016/j.jclinepi.2005.02.022

Rutter, C. M., & Gatsonis, C. A. (2001). A hierarchical regression approach to meta-analysis of diagnostic test accuracy evaluations. *Statistics in Medicine*, 20(19), 2865–2884. doi:10.1002/sim.942

Harbord, R. M., Deeks, J. J., Egger, M., Whiting, P., & Sterne, J. A. C. (2007). A unification of models for meta-analysis of diagnostic accuracy studies. *Biostatistics*, 8(2), 239–251. doi:10.1093/biostatistics/kxl004

Examples

```
data("anticcp")
fit <- fitReitsmaLCA(
  data = anticcp,
  y11 = TP,
  y10 = FP,
  y01 = FN,
  y00 = TN,
  study = study
```

```
)
fit
summary(fit)
```

`fitReitsmaSubgroup` *Fit the Reitsma Subgroup Model*

Description

Fits the Reitsma bivariate random-effects model with a single categorical covariate for diagnostic test accuracy (DTA) meta-analysis using a binomial-normal likelihood via `glmmTMB`. The model is fitted twice, once using treatment-contrast coding with a reference subgroup and once using the cell-means parameterization.

Usage

```
fitReitsmaSubgroup(
  data,
  TP,
  FP,
  FN,
  TN,
  study,
  subgroup,
  constrain = NULL,
  sensspec_constrain = NULL,
  variances = c("common", "unequal"),
  conflevel = 0.95
)
```

Arguments

`data`	A data.frame containing study-level data.
`TP`	True positives (column name).
`FP`	False positives (column name).
`FN`	False negatives (column name).
`TN`	True negatives (column name).
`study`	Study identifier (column name).
`subgroup`	A single categorical study-level subgroup variable (column name).
`constrain`	Optional character string specifying a simplified covariance structure for the Reitsma model. This can be useful for sparse data, small meta-analyses, or for reproducing simplified bivariate models described in the Cochrane Handbook for Diagnostic Test Accuracy Reviews. Allowed values are:

`NULL` The standard unconstrained Reitsma model is fitted.

`"sigma_AB"` The covariance between logit-sensitivity and logit-specificity random effects is fixed at zero. Random effects remain independent.

`"sigma2_A"` The between-study variance of logit-sensitivity is fixed at zero. This also implies a zero covariance.

`"sigma2_B"` The between-study variance of logit-specificity is fixed at zero. This also implies a zero covariance.

`"all"` All random-effects variance and covariance parameters are fixed at zero, resulting in a fixed-effects model.

These random-effects simplifications are currently only available for `variances="common"`.

`sensspec_constrain`

Optional character vector specifying restrictions on subgroup-specific logit-sensitivity and/or logit-specificity parameters.

This can be useful for testing whether subgroup differences are present in sensitivity, specificity, or both.

Allowed values are:

`"sens"` Constrain all subgroup-specific logit-sensitivity parameters to be equal. Subgroup differences are therefore only allowed in logit-specificity.

`"spec"` Constrain all subgroup-specific logit-specificity parameters to be equal. Subgroup differences are therefore only allowed in logit-sensitivity.

Both constraints may be specified simultaneously, e.g. `sensspec_constrain = c("sens", "spec")`, which forces all subgroup-specific sensitivity and specificity parameters to be equal across subgroups.

If `NULL` (default), separate sensitivity and specificity parameters are estimated for each subgroup.

`variances` Whether the between-study random-effects variance-covariance matrix should be assumed to be `"common"` (default) or `"unequal"` across subgroups. If `"common"`, a single between-study variance-covariance matrix is estimated and shared across all subgroups. If `"unequal"`, subgroup-specific variance-covariance matrices are estimated.

`conflevel` Confidence level for confidence intervals. Default is 0.95.

Value

A list of class `"ReitsmaSubgroup"` with components:

- `data`: the original data set with derived quantities.
- `glmmTMB_mu`: fitted model object with cell means parameterization.
- `estimates_mu`: parameter estimates with SE with cell means parameterization.
- `vcov_mu`: variance-covariance matrix with cell means parameterization.
- `sensspec`: sensitivity and specificity estimates.
- `glmmTMB_nu`: fitted model object with dummy/reference-cell parameterization.
- `estimates_nu`: parameter estimates with SE with dummy/reference-cell parameterization.
- `vcov_nu`: variance-covariance matrix with dummy/reference-cell parameterization.

- `LRDOR`: Diagnostic odds ratios and likelihood ratios.
- `RutterGatsonis_recovered`: Recovered parameters in the Rutter-Gatsonis (HSROC) parameterization.
- `subgroups`: The subgroup levels used in the model fit.
- `constrain`: Random effects parameters fixed at zero.
- `sensspec_constrain`: Whether sensitivities/specificities are assumed common across subgroups.
- `variances`: Variance structure used in the fitted model.

References

Reitsma, J. B., et al. (2005). Bivariate analysis of sensitivity and specificity produces informative summary measures in diagnostic reviews. *Journal of Clinical Epidemiology*, 58(10), 982–990. doi:10.1016/j.jclinepi.2005.02.022

Rutter, C. M., & Gatsonis, C. A. (2001). A hierarchical regression approach to meta-analysis of diagnostic test accuracy evaluations. *Statistics in Medicine*, 20(19), 2865–2884. doi:10.1002/sim.942

Harbord, R. M., Deeks, J. J., Egger, M., Whiting, P., & Sterne, J. A. C. (2007). A unification of models for meta-analysis of diagnostic accuracy studies. *Biostatistics*, 8(2), 239–251. doi:10.1093/biostatistics/kxl004

Examples

```
data("anticcp")
fit <- fitReitsmaSubgroup(
  data = anticcp,
  TP = TP,
  FP = FP,
  FN = FN,
  TN = TN,
  study = study,
  subgroup = generation
)
fit
summary(fit)
```

`fitReitsmaSubgroupLCA` *Fit the Reitsma Subgroup LCA Model*

Description

Fits the Reitsma latent class model with a single categorical covariate, allowing for an imperfect reference standard under conditional independence.

Usage

```
fitReitsmaSubgroupLCA(
  data,
  y11,
  y10,
  y01,
  y00,
  study,
  subgroup,
  constrain = NULL,
  sensspec_constrain = NULL,
  variances = c("common", "unequal"),
  prev_variances = c("common", "unequal"),
  conflevel = 0.95,
  verbose = FALSE
)
```

Arguments

`data`	A data.frame containing study-level data.
`y11`	Number testing positive with both index and reference tests (column name).
`y10`	Number testing positive with index test but negative with reference test (column name).
`y01`	Number testing negative with index test but positive with reference test (column name).
`y00`	Number testing negative with both index and reference tests (column name).
`study`	Study identifier (column name).
`subgroup`	A single categorical study-level subgroup variable (column name).
`constrain`	Optional character string specifying a simplified covariance structure for the index test in the Reitsma LCA model.

Allowed values are:

`NULL` The standard unconstrained Reitsma model is fitted.

`"sigma_AB.index"` The covariance between logit-sensitivity and logit-specificity random effects is fixed at zero. Random effects remain independent.

`"sigma2_A.index"` The between-study variance of logit-sensitivity is fixed at zero. This also implies a zero covariance.

`"sigma2_B.index"` The between-study variance of logit-specificity is fixed at zero. This also implies a zero covariance.

`"all"` All random-effects variance and covariance parameters are fixed at zero, resulting in a fixed-effects model.

These random-effects simplifications are currently only available for `variances="common"`.

`sensspec_constrain`

Optional character vector specifying restrictions on subgroup-specific logit-sensitivity and/or logit-specificity parameters for the index test.

This can be useful for testing whether subgroup differences are present in sensitivity, specificity, or both.

Allowed values are:

`"sens"` Constrain all subgroup-specific logit-sensitivity parameters to be equal. Subgroup differences are therefore only allowed in logit-specificity.

`"spec"` Constrain all subgroup-specific logit-specificity parameters to be equal. Subgroup differences are therefore only allowed in logit-sensitivity.

Both constraints may be specified simultaneously, e.g. `sensspec_constrain = c("sens", "spec")`, which forces all subgroup-specific sensitivity and specificity parameters to be equal across subgroups.

If `NULL` (default), separate sensitivity and specificity parameters are estimated for each subgroup.

`variances` Whether the between-study random-effects variance-covariance matrix of the index test should be assumed to be `"common"` (default) or `"unequal"` across subgroups. If `"common"`, a single between-study variance-covariance matrix is estimated and shared across all subgroups. If `"unequal"`, subgroup-specific variance-covariance matrices are estimated.

`prev_variances` Whether the between-study random-effects variance for logit prevalence should be assumed to be `"common"` (default) or `"unequal"` across subgroups. If `"common"`, a single between-study variance is estimated and shared across all subgroups. If `"unequal"`, subgroup-specific variances are estimated.

`conflevel` Confidence level for confidence intervals. Default is 0.95.

`verbose` Whether TMB optimization output should be printed (default: FALSE).

Value

A list of class `"ReitsmaSubgroupLCA"` with components:

- `data`: the original data set with derived quantities.
- `fit`: Optimization result from `nlminb`.
- `sdreport`: TMB standard report.
- `sdreport2`: Summary of reported parameters.
- `vcov`: variance-covariance matrix of reported parameters.
- `sensspec`: sensitivity and specificity estimates.
- `prevref`: Estimated (average) prevalence and reference standard sensitivity/specificity with confidence intervals.
- `LRDOR`: Diagnostic odds ratio and likelihood ratios.
- `RutterGatsonis_recovered`: Recovered parameters in the Rutter-Gatsonis (HSROC) parameterization.
- `subgroups`: The subgroup levels used in the model fit.
- `constrain`: Random effects parameters fixed at zero.
- `sensspec_constrain`: Whether sensitivities/specificities are assumed common across subgroups.
- `variances`: Variance structure used in the fitted model.
- `prev_variances`: Prevalence variance structure used in the fitted model.

References

Liu, Y., Chen, Y., & Chu, H. (2015). A unification of models for meta-analysis of diagnostic accuracy studies without a gold standard. *Biometrics*, 71(2), 538-547. doi:10.1111/biom.12264

Reitsma, J. B., et al. (2005). Bivariate analysis of sensitivity and specificity produces informative summary measures in diagnostic reviews. *Journal of Clinical Epidemiology*, 58(10), 982–990. doi:10.1016/j.jclinepi.2005.02.022

Rutter, C. M., & Gatsonis, C. A. (2001). A hierarchical regression approach to meta-analysis of diagnostic test accuracy evaluations. *Statistics in Medicine*, 20(19), 2865–2884. doi:10.1002/sim.942

Harbord, R. M., Deeks, J. J., Egger, M., Whiting, P., & Sterne, J. A. C. (2007). A unification of models for meta-analysis of diagnostic accuracy studies. *Biostatistics*, 8(2), 239–251. doi:10.1093/biostatistics/kxl004

Examples

```
data("anticcp")
fit <- fitReitsmaSubgroupLCA(
  data = anticcp,
  y11 = TP,
  y10 = FP,
  y01 = FN,
  y00 = TN,
  study = study,
  subgroup = generation
)
fit
summary(fit)
```

`fitReitsmaSubgroupTMB` *Fit the Reitsma Subgroup TMB Model*

Description

Fits the Reitsma bivariate random-effects model with a single categorical covariate for diagnostic test accuracy (DTA) meta-analysis using a binomial-normal likelihood via a custom `TMB` template, which may offer improved numerical robustness in difficult or near-boundary cases.

Usage

```
fitReitsmaSubgroupTMB(
  data,
  TP,
  FP,
  FN,
  TN,
  study,
```

```
  subgroup,
  constrain = NULL,
  sensspec_constrain = NULL,
  variances = c("common", "unequal"),
  conflevel = 0.95,
  verbose = FALSE
)
```

Arguments

`data`	A data.frame containing study-level data.
`TP`	True positives (column name).
`FP`	False positives (column name).
`FN`	False negatives (column name).
`TN`	True negatives (column name).
`study`	Study identifier (column name).
`subgroup`	A single categorical study-level subgroup variable (column name).
`constrain`	Optional character string specifying a simplified covariance structure for the Reitsma model. This can be useful for sparse data, small meta-analyses, or for reproducing simplified bivariate models described in the Cochrane Handbook for Diagnostic Test Accuracy Reviews. Allowed values are: `NULL` The standard unconstrained Reitsma model is fitted. `"sigma_AB"` The covariance between logit-sensitivity and logit-specificity random effects is fixed at zero. Random effects remain independent. `"sigma2_A"` The between-study variance of logit-sensitivity is fixed at zero. This also implies a zero covariance. `"sigma2_B"` The between-study variance of logit-specificity is fixed at zero. This also implies a zero covariance. `"all"` All random-effects variance and covariance parameters are fixed at zero, resulting in a fixed-effects model. These random-effects simplifications are currently only available for `variances="common"`.
`sensspec_constrain`	Optional character vector specifying restrictions on subgroup-specific logit-sensitivity and/or logit-specificity parameters. This can be useful for testing whether subgroup differences are present in sensitivity, specificity, or both. Allowed values are: `"sens"` Constrain all subgroup-specific logit-sensitivity parameters to be equal. Subgroup differences are therefore only allowed in logit-specificity. `"spec"` Constrain all subgroup-specific logit-specificity parameters to be equal. Subgroup differences are therefore only allowed in logit-sensitivity.

	Both constraints may be specified simultaneously, e.g. `sensspec_constrain = c("sens", "spec")`, which forces all subgroup-specific sensitivity and specificity parameters to be equal across subgroups. If `NULL` (default), separate sensitivity and specificity parameters are estimated for each subgroup.
`variances`	Whether the between-study random-effects variance-covariance matrix should be assumed to be `"common"` (default) or `"unequal"` across subgroups. If `"common"`, a single between-study variance-covariance matrix is estimated and shared across all subgroups. If `"unequal"`, subgroup-specific variance-covariance matrices are estimated.
`conflevel`	Confidence level for confidence intervals. Default is 0.95.
`verbose`	Whether TMB optimization output should be printed (default: FALSE).

Value

A list of class `"ReitsmaSubgroupTMB"` with components:

- `data`: the original data set with derived quantities
- `fit`: Optimization result from `nlminb`.
- `sdreport`: TMB standard report.
- `sdreport2`: Summary of reported parameters.
- `vcov`: variance-covariance matrix of reported parameters.
- `sensspec`: sensitivity and specificity estimates.
- `LRDOR`: Diagnostic odds ratios and likelihood ratios.
- `RutterGatsonis_recovered`: Recovered parameters in the Rutter-Gatsonis (HSROC) parameterization.
- `subgroups`: The subgroup levels used in the model fit.
- `constrain`: Random effects parameters fixed at zero.
- `sensspec_constrain`: Whether sensitivities/specificities are assumed common across subgroups.
- `variances`: Variance structure used in the fitted model.

References

Reitsma, J. B., et al. (2005). Bivariate analysis of sensitivity and specificity produces informative summary measures in diagnostic reviews. *Journal of Clinical Epidemiology*, 58(10), 982–990. doi:10.1016/j.jclinepi.2005.02.022

Rutter, C. M., & Gatsonis, C. A. (2001). A hierarchical regression approach to meta-analysis of diagnostic test accuracy evaluations. *Statistics in Medicine*, 20(19), 2865–2884. doi:10.1002/sim.942

Harbord, R. M., Deeks, J. J., Egger, M., Whiting, P., & Sterne, J. A. C. (2007). A unification of models for meta-analysis of diagnostic accuracy studies. *Biostatistics*, 8(2), 239–251. doi:10.1093/biostatistics/kxl004

Examples

```
data("anticcp")
fit <- fitReitsmaSubgroupTMB(
  data = anticcp,
  TP = TP,
  FP = FP,
  FN = FN,
  TN = TN,
  study = study,
  subgroup = generation
)
fit
summary(fit)
```

`fitReitsmaTMB` *Fit the Reitsma TMB Model*

Description

Fits the Reitsma bivariate random-effects model for diagnostic test accuracy (DTA) meta-analysis using a binomial-normal likelihood via a custom `TMB` template, which may offer improved numerical robustness in difficult or near-boundary cases.

Usage

```
fitReitsmaTMB(
  data,
  TP,
  FP,
  FN,
  TN,
  study,
  constrain = NULL,
  conflevel = 0.95,
  verbose = FALSE
)
```

Arguments

`data`	A data.frame containing study-level data.
`TP`	True positives (column name).
`FP`	False positives (column name).
`FN`	False negatives (column name).
`TN`	True negatives (column name).

study	Study identifier (column name).
constrain	Optional character string specifying a simplified covariance structure for the Reitsma model. This can be useful for sparse data, small meta-analyses, or for reproducing simplified bivariate models described in the Cochrane Handbook for Diagnostic Test Accuracy Reviews. Allowed values are: NULL The standard unconstrained Reitsma model is fitted. "sigma_AB" The covariance between logit-sensitivity and logit-specificity random effects is fixed at zero. Random effects remain independent. "sigma2_A" The between-study variance of logit-sensitivity is fixed at zero. This also implies a zero covariance. "sigma2_B" The between-study variance of logit-specificity is fixed at zero. This also implies a zero covariance. "all" All random-effects variance and covariance parameters are fixed at zero, resulting in a fixed-effects model.
conflevel	Confidence level for confidence intervals. Default is 0.95.
verbose	Whether TMB optimization output should be printed (default: FALSE).

Value

A list of class "ReitsmaTMB" with components:

- data: the original data set with derived quantities
- fit: Optimization result from nlminb.
- sdreport: TMB standard report.
- sdreport2: Summary of reported parameters.
- vcov: variance-covariance matrix of reported parameters.
- sensspec: sensitivity and specificity estimates.
- LRDOR: Diagnostic odds ratio and likelihood ratios.
- RutterGatsonis_recovered: Recovered parameters in the Rutter-Gatsonis (HSROC) parameterization.
- constrain: Random effects parameters fixed at zero.

References

Reitsma, J. B., et al. (2005). Bivariate analysis of sensitivity and specificity produces informative summary measures in diagnostic reviews. *Journal of Clinical Epidemiology*, 58(10), 982–990. doi:10.1016/j.jclinepi.2005.02.022

Rutter, C. M., & Gatsonis, C. A. (2001). A hierarchical regression approach to meta-analysis of diagnostic test accuracy evaluations. *Statistics in Medicine*, 20(19), 2865–2884. doi:10.1002/sim.942

Harbord, R. M., Deeks, J. J., Egger, M., Whiting, P., & Sterne, J. A. C. (2007). A unification of models for meta-analysis of diagnostic accuracy studies. *Biostatistics*, 8(2), 239–251. doi:10.1093/biostatistics/kxl004

Examples

```
data("anticcp")
fit <- fitReitsmaTMB(
  data = anticcp,
  TP = TP,
  FP = FP,
  FN = FN,
  TN = TN,
  study = study
)
summary(fit)
```

`fitRutterGatsonis` *Fit the Rutter and Gatsonis (HSROC) Model*

Description

Fits the hierarchical summary receiver operating characteristic (HSROC) model as proposed by Rutter and Gatsonis for meta-analysis of diagnostic test accuracy (DTA) studies using Template Model Builder (TMB).

Usage

```
fitRutterGatsonis(
  data,
  TP,
  FP,
  FN,
  TN,
  study,
  conflevel = 0.95,
  constrain = NULL,
  spec = NULL,
  verbose = FALSE
)
```

Arguments

`data`	A data.frame containing study-level data.
`TP`	True positives (column name).
`FP`	False positives (column name).
`FN`	False negatives (column name).
`TN`	True negatives (column name).
`study`	Study identifier (column name).

`conflevel` Confidence level for confidence intervals. Default is 0.95.

`constrain` Optional character vector specifying model parameters that should be fixed at zero during estimation.

This can be useful for sparse data, small meta-analyses, or for reproducing simplified HSROC models described in the Cochrane Handbook for Diagnostic Test Accuracy Reviews.

Allowed values are:

"sigma2_alpha" Fix the between-study variance of the HSROC accuracy random effect at zero.

"sigma2_theta" Fix the between-study variance of the HSROC threshold random effect at zero.

"shape" Fix the HSROC shape parameter (beta) at zero, resulting in a symmetric summary ROC curve.

Multiple constraints may be specified simultaneously, e.g. `constrain = c("sigma2_alpha", "shape")`.

If `NULL` (default), the unconstrained HSROC model is fitted.

`spec` Optional specificity value at which sensitivity is estimated. If `NULL`, the median observed specificity is used as a proxy.

`verbose` Whether TMB optimization output should be printed (default: FALSE).

Details

The function internally transforms the data into long format and fits the model via maximum likelihood using TMB. Random effects are included for study-specific accuracy and threshold parameters.

Reitsma parameterization is recovered from the fitted HSROC parameters.

The `constrain` argument allows simplified HSROC models to be fitted by fixing selected parameters at zero. These constrained models may improve numerical stability in sparse datasets and can be used to reproduce several simplified models presented in the Cochrane Handbook for Diagnostic Test Accuracy Reviews.

Constraints are imposed using parameter mapping within Template Model Builder (TMB), so constrained parameters are excluded from numerical optimization and treated as fixed constants.

Value

An object of class `"RutterGatsonis"` containing:

data Processed input data with derived quantities.

fit Optimization result from `nlminb`.

sdreport TMB standard report.

sdreport2 Summary of reported parameters.

sensspec Estimated sensitivity at given specificity with confidence intervals.

Reitsma_recovered Recovered parameters in the Reitsma parameterization.

constrain Parameters fixed at zero.

Note

Requires a compiled TMB model named "RutterGatsonis".

References

Reitsma, J. B., et al. (2005). Bivariate analysis of sensitivity and specificity produces informative summary measures in diagnostic reviews. *Journal of Clinical Epidemiology*, 58(10), 982–990. doi:10.1016/j.jclinepi.2005.02.022

Rutter, C. M., & Gatsonis, C. A. (2001). A hierarchical regression approach to meta-analysis of diagnostic test accuracy evaluations. *Statistics in Medicine*, 20(19), 2865–2884. doi:10.1002/sim.942

Harbord, R. M., Deeks, J. J., Egger, M., Whiting, P., & Sterne, J. A. C. (2007). A unification of models for meta-analysis of diagnostic accuracy studies. *Biostatistics*, 8(2), 239–251. doi:10.1093/biostatistics/kxl004

Examples

```
data("RF")
fit <- fitRutterGatsonis(
  data = RF,
  TP = TP,
  FP = FP,
  FN = FN,
  TN = TN,
  study = study
)
summary(fit)
```

`fitRutterGatsonisLCA` *Fit the Rutter and Gatsonis LCA Model*

Description

Fits the Rutter and Gatsonis latent class model for diagnostic test accuracy (DTA), allowing for an imperfect reference standard under conditional independence.

Usage

```
fitRutterGatsonisLCA(
  data,
  y11,
  y10,
  y01,
  y00,
  study,
  conflevel = 0.95,
  constrain = NULL,
```

```
  spec = NULL,
  verbose = FALSE
)
```

Arguments

`data`	A data.frame containing study-level data.
`y11`	Number testing positive with both index and reference tests (column name).
`y10`	Number testing positive with index test but negative with reference test (column name).
`y01`	Number testing negative with index test but positive with reference test (column name).
`y00`	Number testing negative with both index and reference tests (column name).
`study`	Study identifier (column name).
`conflevel`	Confidence level for confidence intervals. Default is 0.95.
`constrain`	Optional character vector specifying model parameters of the index test that should be fixed at zero during estimation. Allowed values are: **"sigma2_alpha"** Fix the between-study variance of the HSROC accuracy random effect at zero. **"sigma2_theta"** Fix the between-study variance of the HSROC threshold random effect at zero. **"shape"** Fix the HSROC shape parameter (beta) at zero, resulting in a symmetric summary ROC curve. Multiple constraints may be specified simultaneously, e.g. `constrain = c("sigma2_alpha", "shape")`. If `NULL` (default), the unconstrained HSROC LCA model is fitted.
`spec`	Optional specificity value at which sensitivity is estimated. If `NULL`, a specificity of 0.8 is used as a proxy.
`verbose`	Whether TMB optimization output should be printed (default: FALSE).

Value

An object of class `"RutterGatsonisLCA"` containing:

data Processed input data with derived quantities.

fit Optimization result from `nlminb`.

sdreport TMB standard report.

sdreport2 Summary of reported parameters.

sensspec Estimated index test sensitivity at given specificity with confidence intervals.

prevref Estimated (average) prevalence and reference standard sensitivity/specificity with confidence intervals.

Reitsma_recovered Recovered parameters in the Reitsma parameterization.

constrain Parameters fixed at zero.

References

Liu, Y., Chen, Y., & Chu, H. (2015). A unification of models for meta-analysis of diagnostic accuracy studies without a gold standard. *Biometrics*, 71(2), 538-547. doi:10.1111/biom.12264

Reitsma, J. B., et al. (2005). Bivariate analysis of sensitivity and specificity produces informative summary measures in diagnostic reviews. *Journal of Clinical Epidemiology*, 58(10), 982–990. doi:10.1016/j.jclinepi.2005.02.022

Rutter, C. M., & Gatsonis, C. A. (2001). A hierarchical regression approach to meta-analysis of diagnostic test accuracy evaluations. *Statistics in Medicine*, 20(19), 2865–2884. doi:10.1002/sim.942

Harbord, R. M., Deeks, J. J., Egger, M., Whiting, P., & Sterne, J. A. C. (2007). A unification of models for meta-analysis of diagnostic accuracy studies. *Biostatistics*, 8(2), 239–251. doi:10.1093/biostatistics/kxl004

Examples

```
data("anticcp")
fit <- fitRutterGatsonisLCA(
  data = anticcp,
  y11 = TP,
  y10 = FP,
  y01 = FN,
  y00 = TN,
  study = study
)
fit
summary(fit)
```

`fitRutterGatsonisReg` *Fit the Rutter and Gatsonis Regression Model*

Description

Fits a general HSROC meta-regression model using user-supplied design matrices for estimation and prediction.

Usage

```
fitRutterGatsonisReg(
  data,
  TP,
  FP,
  FN,
  TN,
  study,
  Z,
  Z_pred = NULL,
```

```
  map = NULL,
  init = NULL,
  spec = NULL,
  conflevel = 0.95,
  verbose = FALSE
)
```

Arguments

data	A data.frame containing study-level data.
TP	True positives (column name).
FP	False positives (column name).
FN	False negatives (column name).
TN	True negatives (column name).
study	Study identifier (column name).
Z	Design matrix containing covariate values for model fitting. The current implementation is intended primarily for study-level covariates. In the long-format representation, this typically means that each study is represented by two consecutive rows with identical covariate values. The number of rows of Z must equal twice the number of studies.
Z_pred	Prediction design matrix used to obtain covariate-specific parameter estimates and SROC curves. Each row defines a covariate pattern at which predictions are evaluated. The number of columns of Z_pred must equal the number of columns of Z. If NULL (default), a single row of zeros is used. For meaningful predictions, users will typically want to specify Z_pred explicitly.
map	Optional named list of parameter mappings passed to MakeADFun. Parameter mapping allows selected model parameters to be fixed or constrained during estimation. This can be useful for fitting simplified HSROC models, imposing equality constraints, or reproducing model specifications described in the literature. Each component of map should be a factor vector with the same length as the corresponding parameter. Parameters assigned NA levels are fixed at their initial values supplied via the init argument, whereas parameters sharing the same factor level are estimated as equal. This is an advanced feature intended primarily for users familiar with Template Model Builder (TMB). If NULL (default), all model parameters are estimated freely. Example map = list(shape_coef=factor(c(1, rep(NA, ncol(Z) - 1)))).
init	Optional list of initial parameter values. If NULL (default), all fixed and random effects are initialized to zero. Advanced users may provide a named list containing: **accuracy_coef** Initial values for the accuracy regression coefficients. **threshold_coef** Initial values for the threshold regression coefficients. **shape_coef** Initial values for the shape regression coefficients.

log_sigma_alpha Initial value for the log standard deviation of the accuracy random effects.

log_sigma_theta Initial value for the log standard deviation of the threshold random effects.

alpha Initial values for the study-specific accuracy random effects.

theta Initial values for the study-specific threshold random effects.

The lengths of `accuracy_coef`, `threshold_coef`, and `shape_coef` must equal the number of columns in `Z`. The lengths of `alpha` and `theta` must equal the number of studies.

`spec` Optional specificity value or vector of specificity values at which sensitivity is evaluated for each covariate pattern specified in `Z_pred`. If `NULL`, the median observed specificity is used.

`conflevel` Confidence level for confidence intervals. Default is `0.95`.

`verbose` Logical indicating whether TMB optimization output should be printed (default: `FALSE`).

Details

This function is intended for advanced users who wish to specify design matrices directly. The user is responsible for constructing appropriate design matrices, choosing prediction covariate patterns through `Z_pred`, and interpreting or visualizing the resulting regression model.

By default, all fixed and random effects are initialized at zero. For difficult optimization problems, user-supplied starting values may be provided through the `init` argument.

The fitted model estimates covariate effects on the HSROC accuracy, threshold, and optionally shape parameters. Predicted sensitivities are obtained by evaluating the resulting SROC curve(s) at the specificity value(s) supplied through `spec` and the covariate patterns defined by `Z_pred`.

Value

An object of class `"RutterGatsonisReg"` containing:

data Processed input data with derived quantities.

fit Optimization result returned by `nlminb`.

sdreport TMB standard report object.

sdreport2 Summary of reported model parameters and derived quantities.

sensspec Estimated sensitivities at the specified specificity value(s), including confidence intervals.

Note

Requires a compiled TMB model named `"RutterGatsonisReg"`.

References

Reitsma, J. B., Glas, A. S., Rutjes, A. W. S., Scholten, R. J. P. M., Bossuyt, P. M., & Zwinderman, A. H. (2005). Bivariate analysis of sensitivity and specificity produces informative summary

measures in diagnostic reviews. *Journal of Clinical Epidemiology*, 58(10), 982–990. doi:10.1016/j.jclinepi.2005.02.022

Rutter, C. M., & Gatsonis, C. A. (2001). A hierarchical regression approach to meta-analysis of diagnostic test accuracy evaluations. *Statistics in Medicine*, 20(19), 2865–2884. doi:10.1002/sim.942

Harbord, R. M., Deeks, J. J., Egger, M., Whiting, P., & Sterne, J. A. C. (2007). A unification of models for meta-analysis of diagnostic accuracy studies. *Biostatistics*, 8(2), 239–251. doi:10.1093/biostatistics/kxl004

Examples

```
data("RF")
RF2        <- RF[RF$method %in% c("LA","ELISA","Nephelometry"),]
RF2$method <- factor(RF2$method,levels=c("LA","ELISA","Nephelometry"))
Z <- model.matrix(~ method, data = RF2)
Z <- Z[rep(seq_len(nrow(Z)), each = 2), , drop = FALSE]
Z_pred <- matrix(c(1,0,0,1,1,0,1,0,1),ncol=3,nrow=3,byrow=TRUE)

fit <- fitRutterGatsonisReg(
  data = RF2,
  TP = TP,
  FP = FP,
  FN = FN,
  TN = TN,
  study = study,
  Z = Z,
  Z_pred = Z_pred
)

summary(fit)
```

---

fitRutterGatsonisSubgroup

Fit the Rutter and Gatsonis Subgroup Model

Description

The function fits an HSROC model with a single categorical study-level covariate (subgroup).

Usage

```
fitRutterGatsonisSubgroup(
  data,
  TP,
  FP,
  FN,
  TN,
  study,
```

```
  subgroup,
  constrain = NULL,
  spec = NULL,
  conflevel = 0.95,
  verbose = FALSE
)
```

Arguments

data	A data.frame containing study-level data.
TP	True positives (column name).
FP	False positives (column name).
FN	False negatives (column name).
TN	True negatives (column name).
study	Study identifier (column name).
subgroup	A single categorical study-level subgroup variable (column name).
constrain	Optional character vector specifying model parameters that should be constrained during estimation. This can be useful for sparse data, small meta-analyses, or for reproducing simplified HSROC models described in the Cochrane Handbook for Diagnostic Test Accuracy Reviews. Allowed values are: **"sigma2_alpha"** Fix the between-study variance of the HSROC accuracy random effect at zero. **"sigma2_theta"** Fix the between-study variance of the HSROC threshold random effect at zero. **"accuracy"** No subgroup effect on accuracy. **"threshold"** No subgroup effect on threshold. **"shape"** No subgroup effect on shape. **"shape_zero"** All shape parameters (beta's) are fixed at zero. Multiple constraints may be specified simultaneously, e.g. `constrain = c("sigma2_alpha", "shape")`. `shape_zero` overrides `shape`. If `NULL` (default), the unconstrained HSROC model is fitted.
spec	Optional specificity value or vector of specificity values at which sensitivity is estimated. If `NULL`, the median observed specificity is used as a proxy.
conflevel	Confidence level for confidence intervals. Default is 0.95.
verbose	Whether TMB optimization output should be printed (default: FALSE).

Details

The function fits an HSROC model with a single categorical study-level covariate (subgroup). Separate subgroup effects are estimated for the accuracy and threshold parameters. Optionally, subgroup-specific effects can also be estimated for the shape parameter.

The fitted model returns subgroup-specific summary sensitivity estimates evaluated at user-specified specificity values. If `spec = NULL`, the median observed specificity is used as a proxy.

This function is intended as a convenient wrapper for subgroup analyses with a single categorical covariate and provides output suitable for dedicated `summary()`, `plot()`, and `forest()` methods.

Value

An object of class `"RutterGatsonisSubgroup"` containing:

data Processed input data with derived quantities.

fit Optimization result from `nlminb`.

sdreport TMB standard report.

sdreport2 Summary of reported subgroup-specific parameters.

sensspec Estimated subgroup-specific sensitivities at the given specificity value(s), with confidence intervals.

constrain Constraints on parameters applied during model fitting.

subgroups The subgroup levels used in the model fit.

Note

Requires a compiled TMB model named `"RutterGatsonisReg"`.

References

Reitsma, J. B., et al. (2005). Bivariate analysis of sensitivity and specificity produces informative summary measures in diagnostic reviews. *Journal of Clinical Epidemiology*, 58(10), 982–990. doi:10.1016/j.jclinepi.2005.02.022

Rutter, C. M., & Gatsonis, C. A. (2001). A hierarchical regression approach to meta-analysis of diagnostic test accuracy evaluations. *Statistics in Medicine*, 20(19), 2865–2884. doi:10.1002/sim.942

Harbord, R. M., Deeks, J. J., Egger, M., Whiting, P., & Sterne, J. A. C. (2007). A unification of models for meta-analysis of diagnostic accuracy studies. *Biostatistics*, 8(2), 239–251. doi:10.1093/biostatistics/kxl004

Examples

```
data("RF")
fit <- fitRutterGatsonisSubgroup(
  data = RF,
  TP = TP,
  FP = FP,
  FN = FN,
  TN = TN,
  study = study,
  subgroup = method
)
summary(fit)
```

`fitRutterGatsonisSubgroupLCA` *Fit the Rutter and Gatsonis Subgroup LCA Model*

Description

The function fits an HSROC model with a single categorical study-level covariate (subgroup), allowing for an imperfect reference standard assuming conditional independence.

Usage

```
fitRutterGatsonisSubgroupLCA(
  data,
  y11,
  y10,
  y01,
  y00,
  study,
  subgroup,
  constrain = NULL,
  prev_variances = c("common", "unequal"),
  spec = NULL,
  conflevel = 0.95,
  verbose = FALSE
)
```

Arguments

`data`	A data.frame containing study-level data.
`y11`	Number testing positive with both index and reference tests (column name).
`y10`	Number testing positive with index test but negative with reference test (column name).
`y01`	Number testing negative with index test but positive with reference test (column name).
`y00`	Number testing negative with both index and reference tests (column name).
`study`	Study identifier (column name).
`subgroup`	A single categorical study-level subgroup variable (column name).
`constrain`	Optional character vector specifying model parameters that should be constrained during estimation. Allowed values are: **"sigma2_alpha"** Fix the between-study variance of the HSROC accuracy random effect at zero. **"sigma2_theta"** Fix the between-study variance of the HSROC threshold random effect at zero.

"accuracy" No subgroup effect on accuracy.

"threshold" No subgroup effect on threshold.

"shape" No subgroup effect on shape.

"shape_zero" All shape parameters (beta's) are fixed at zero.

Multiple constraints may be specified simultaneously, e.g. `constrain = c("sigma2_alpha", "shape")`.

`shape_zero` overrides `shape`.

If `NULL` (default), the unconstrained HSROC model is fitted.

`prev_variances` Whether the between-study random-effects variance for logit prevalence should be assumed to be `"common"` (default) or `"unequal"` across subgroups. If `"common"`, a single between-study variance is estimated and shared across all subgroups. If `"unequal"`, subgroup-specific variances are estimated.

`spec` Optional specificity value at which sensitivity is estimated. If `NULL`, a specificity of 0.8 is used as a proxy.

`conflevel` Confidence level for confidence intervals. Default is 0.95.

`verbose` Whether TMB optimization output should be printed (default: FALSE).

Value

An object of class `"RutterGatsonisSubgroupLCA"` containing:

data Processed input data with derived quantities.

fit Optimization result from `nlminb`.

sdreport TMB standard report.

sdreport2 Summary of reported subgroup-specific parameters.

sensspec Estimated subgroup-specific index test sensitivities at the given specificity value(s), with confidence intervals.

prevref Estimated (average) prevalence and reference standard sensitivity/specificity with confidence intervals.

constrain Constraints on parameters applied during model fitting.

subgroups The subgroup levels used in the model fit.

prev_variances Prevalence variance structure used in the fitted model.

Note

Requires a compiled TMB model named `"RutterGatsonisSubgroupLCA"`.

References

Liu, Y., Chen, Y., & Chu, H. (2015). A unification of models for meta-analysis of diagnostic accuracy studies without a gold standard. *Biometrics*, 71(2), 538-547. doi:10.1111/biom.12264

Reitsma, J. B., et al. (2005). Bivariate analysis of sensitivity and specificity produces informative summary measures in diagnostic reviews. *Journal of Clinical Epidemiology*, 58(10), 982–990. doi:10.1016/j.jclinepi.2005.02.022

Rutter, C. M., & Gatsonis, C. A. (2001). A hierarchical regression approach to meta-analysis of diagnostic test accuracy evaluations. *Statistics in Medicine*, 20(19), 2865–2884. doi:10.1002/sim.942

Harbord, R. M., Deeks, J. J., Egger, M., Whiting, P., & Sterne, J. A. C. (2007). A unification of models for meta-analysis of diagnostic accuracy studies. *Biostatistics*, 8(2), 239–251. doi:10.1093/biostatistics/kxl004

Examples

```
data("schuetz")
fit <- fitRutterGatsonisSubgroupLCA(
  data = schuetz,
  y11 = TP,
  y10 = FP,
  y01 = FN,
  y00 = TN,
  study = study,
  subgroup = test
)
fit
summary(fit)
```

`forest` *Coupled Forest Plot*

Description

Produces coupled forest plots.

Usage

```
forest(x, ...)
```

Arguments

`x`	Object
`...`	Additional arguments

Value

Invisibly returns a `forestploter` object. Users may further modify the plot using `forestploter` functions before printing or exporting.

forest.HoyerAFT *Coupled Forest Plot for Diagnostic Test Accuracy Meta-Analysis*

Description

Provides coupled forest plots of sensitivities and specificities with Clopper-Pearson confidence limits.

Usage

```
## S3 method for class 'HoyerAFT'
forest(x, conflevel = 0.95, ...)
```

Arguments

x	Object of class "HoyerAFT"
conflevel	Confidence level for confidence intervals. Default is 0.95.
...	Additional graphical arguments (not currently in use)

Value

Invisibly returns a forestploter object. Users may further modify the plot using forestploter functions before printing or exporting.

forest.Reitsma *Coupled Forest Plot for Diagnostic Test Accuracy Meta-Analysis*

Description

Provides coupled forest plots of sensitivities and specificities with Clopper-Pearson confidence limits.

Usage

```
## S3 method for class 'Reitsma'
forest(x, conflevel = 0.95, ...)
```

Arguments

x	Object of class "Reitsma"
conflevel	Confidence level for confidence intervals. Default is 0.95.
...	Additional graphical arguments (not currently in use)

Value

Invisibly returns a forestploter object. Users may further modify the plot using forestploter functions before printing or exporting.

forest.ReitsmaLCA *Coupled Forest Plot for Latent Class Diagnostic Test Accuracy Meta-Analysis*

Description

Study-specific sensitivities and specificities are empirical Bayes estimates derived from the fitted latent class model. Confidence intervals are based on the conditional posterior variance of the study-specific random effects obtained from the TMB Laplace approximation.

Usage

```
## S3 method for class 'ReitsmaLCA'
forest(x, conflevel = 0.95, ...)
```

Arguments

x	Object of class "ReitsmaLCA"
conflevel	Confidence level for confidence intervals. Default is 0.95.
...	Additional graphical arguments (not currently in use)

Value

Invisibly returns a forestploter object. Users may further modify the plot using forestploter functions before printing or exporting.

forest.ReitsmaSubgroup *Coupled Forest Plot for Diagnostic Test Accuracy Meta-Analysis*

Description

Provides coupled forest plots of sensitivities and specificities with Clopper-Pearson confidence limits.

Usage

```
## S3 method for class 'ReitsmaSubgroup'
forest(
  x,
  conflevel = 0.95,
  subgroup_label = "Subgroup",
  order = c("study", "subgroup"),
  ...
)
```

Arguments

x	Object of class "ReitsmaSubgroup"
conflevel	Confidence level for confidence intervals. Default is 0.95.
subgroup_label	Column name for the subgroup. Defaults to "Subgroup".
order	Specifies the ordering of studies in the forest plot. Can be "study" (default), which orders observations by study identifier and then subgroup, or "subgroup", which orders observations by subgroup and then study identifier.
...	Additional graphical arguments (not currently in use)

Value

Invisibly returns a forestploter object. Users may further modify the plot using forestploter functions before printing or exporting.

---

forest.ReitsmaSubgroupLCA

Coupled Forest Plot for Latent Class Diagnostic Test Accuracy Meta-Analysis

---

Description

Study-specific sensitivities and specificities are empirical Bayes estimates derived from the fitted latent class model. Confidence intervals are based on the conditional posterior variance of the study-specific random effects obtained from the TMB Laplace approximation.

Usage

```
## S3 method for class 'ReitsmaSubgroupLCA'
forest(
  x,
  conflevel = 0.95,
  subgroup_label = "Subgroup",
  order = c("study", "subgroup"),
  ...
)
```

Arguments

x	Object of class "ReitsmaSubgroupLCA"
conflevel	Confidence level for confidence intervals. Default is 0.95.
subgroup_label	Column name for the subgroup. Defaults to "Subgroup".
order	Specifies the ordering of studies in the forest plot. Can be "study" (default), which orders observations by study identifier and then subgroup, or "subgroup", which orders observations by subgroup and then study identifier.
...	Additional graphical arguments (not currently in use)

Value

Invisibly returns a `forestploter` object. Users may further modify the plot using `forestploter` functions before printing or exporting.

`forest.ReitsmaSubgroupTMB` *Coupled Forest Plot for Diagnostic Test Accuracy Meta-Analysis*

Description

Provides coupled forest plots of sensitivities and specificities with Clopper-Pearson confidence limits.

Usage

```
## S3 method for class 'ReitsmaSubgroupTMB'
forest(
  x,
  conflevel = 0.95,
  subgroup_label = "Subgroup",
  order = c("study", "subgroup"),
  ...
)
```

Arguments

`x`	Object of class `"ReitsmaSubgroupTMB"`
`conflevel`	Confidence level for confidence intervals. Default is 0.95.
`subgroup_label`	Column name for the subgroup. Defaults to `"Subgroup"`.
`order`	Specifies the ordering of studies in the forest plot. Can be `"study"` (default), which orders observations by study identifier and then subgroup, or `"subgroup"`, which orders observations by subgroup and then study identifier.
`...`	Additional graphical arguments (not currently in use)

Value

Invisibly returns a `forestploter` object. Users may further modify the plot using `forestploter` functions before printing or exporting.

forest.RutterGatsonis *Coupled Forest Plot for Diagnostic Test Accuracy Meta-Analysis*

Description

Provides coupled forest plots of sensitivities and specificities with Clopper-Pearson confidence limits.

Usage

```
## S3 method for class 'RutterGatsonis'
forest(x, conflevel = 0.95, ...)
```

Arguments

x	Object of class "RutterGatsonis"
conflevel	Confidence level for confidence intervals. Default is 0.95.
...	Additional graphical arguments (not currently in use)

Value

Invisibly returns a forestploter object. Users may further modify the plot using forestploter functions before printing or exporting.

forest.RutterGatsonisLCA *Coupled Forest Plot for Latent Class Diagnostic Test Accuracy Meta-Analysis*

Description

Study-specific sensitivities and specificities are empirical Bayes estimates derived from the fitted latent class model. Confidence intervals are based on the conditional posterior variance of the study-specific random effects obtained from the TMB Laplace approximation.

Usage

```
## S3 method for class 'RutterGatsonisLCA'
forest(x, conflevel = 0.95, ...)
```

Arguments

x	Object of class "RutterGatsonisLCA"
conflevel	Confidence level for confidence intervals. Default is 0.95.
...	Additional graphical arguments (not currently in use)

Value

Invisibly returns a `forestploter` object. Users may further modify the plot using `forestploter` functions before printing or exporting.

`forest.RutterGatsonisSubgroup` *Coupled Forest Plot for Diagnostic Test Accuracy Meta-Analysis*

Description

Provides coupled forest plots of sensitivities and specificities with Clopper-Pearson confidence limits.

Usage

```
## S3 method for class 'RutterGatsonisSubgroup'
forest(
  x,
  conflevel = 0.95,
  subgroup_label = "Subgroup",
  order = c("study", "subgroup"),
  ...
)
```

Arguments

`x`	Object of class `"RutterGatsonisSubgroup"`
`conflevel`	Confidence level for confidence intervals. Default is 0.95.
`subgroup_label`	Column name for the subgroup. Defaults to `"Subgroup"`.
`order`	Specifies the ordering of studies in the forest plot. Can be `"study"` (default), which orders observations by study identifier and then subgroup, or `"subgroup"`, which orders observations by subgroup and then study identifier.
`...`	Additional graphical arguments (not currently in use)

Value

Invisibly returns a `forestploter` object. Users may further modify the plot using `forestploter` functions before printing or exporting.

forest.RutterGatsonisSubgroupLCA *Coupled Forest Plot for Latent Class Diagnostic Test Accuracy Meta-Analysis*

Description

Study-specific sensitivities and specificities are empirical Bayes estimates derived from the fitted latent class model. Confidence intervals are based on the conditional posterior variance of the study-specific random effects obtained from the TMB Laplace approximation.

Usage

```
## S3 method for class 'RutterGatsonisSubgroupLCA'
forest(
  x,
  conflevel = 0.95,
  subgroup_label = "Subgroup",
  order = c("study", "subgroup"),
  ...
)
```

Arguments

x	Object of class "RutterGatsonisSubgroupLCA"
conflevel	Confidence level for confidence intervals. Default is 0.95.
subgroup_label	Column name for the subgroup. Defaults to "Subgroup".
order	Specifies the ordering of studies in the forest plot. Can be "study" (default), which orders observations by study identifier and then subgroup, or "subgroup", which orders observations by subgroup and then study identifier.
...	Additional graphical arguments (not currently in use)

Value

Invisibly returns a forestploter object. Users may further modify the plot using forestploter functions before printing or exporting.

`initHoyerAFT` *Compute Initial Parameter Values for HoyerAFT Models*

Description

Computes initial values for the threshold-based bivariate time-to-event model of Hoyer et al. (2018).

Usage

```
initHoyerAFT(restructured, dist = "loglogistic")
```

Arguments

`restructured`	A data frame in interval format as produced by `restructure_data` (specifically the `restructured` component of its output). Must contain the columns: **study** Study identifier **lowerB** Lower interval bound **upperB** Upper interval bound **events0** Non-diseased counts within interval **events1** Diseased counts within interval **ctype** Censoring type (1 = left, 2 = interval, 3 = right) **lcutmean** Midpoint of log-threshold interval
`dist`	Character string specifying the parametric distribution used in the survival regression models. Must be one of: `"weibull"`, `"lognormal"`, or `"loglogistic"`. Default is `"loglogistic"`.

Details

The function fits separate intercept-only parametric survival models for diseased and non-diseased groups using weighted interval-censored likelihoods. It further derives initial estimates of between-study variability based on study-specific weighted averages of log-thresholds.

To ensure compatibility with `survival::survreg`, interval bounds are modified as follows:

- Left-censored intervals (`ctype = 1`) are assigned a small positive lower bound.
- Right-censored intervals (`ctype = 3`) are assigned an infinite upper bound.

Value

A single-row data frame containing initial parameter values:

beta0_init Intercept for non-diseased group

lambda0_init Scale parameter for non-diseased group

beta1_init Intercept for diseased group

lambda1_init Scale parameter for diseased group

su0_init Standard deviation of random effects (non-diseased)

su1_init Standard deviation of random effects (diseased)

coru0u1_init Correlation between random effects

distcode Numeric code for the distribution (1 = Weibull, 2 = lognormal, 3 = loglogistic)

References

Hoyer, A., Hirt, S., Kuss, O. (2018). Meta-analysis of full ROC curves using bivariate time-to-event models for interval-censored data. *Research Synthesis Methods*, 9(1), 62-72. doi:10.1002/jrsm.1273

Examples

```
data("diabetes")
res <- restructure_data(
  data = diabetes,
  TP = TP,
  FP = FP,
  FN = FN,
  TN = TN,
  threshold = threshold,
  study = study,
  smallest = 2,
  largest = 10
)
init <- initHoyerAFT(res$restructured)
```

---

logLik.dtametaTMB *Extract Log-Likelihood from Diagnostic Test Accuracy Models*

Description

Returns the maximized log-likelihood for a fitted diagnostic test accuracy meta-analysis model. The returned value is an object of class `"logLik"` and includes the number of estimated parameters (`df`) and the number of observations used in model fitting (`nobs`).

Usage

```
## S3 method for class 'DTAmodel'
logLik(object, ...)

## S3 method for class 'HoyerAFT'
logLik(object, ...)

## S3 method for class 'Reitsma'
logLik(object, ...)
```

```
## S3 method for class 'ReitsmaSubgroup'
logLik(object, ...)

## S3 method for class 'ReitsmaLCA'
logLik(object, ...)

## S3 method for class 'ReitsmaSubgroupLCA'
logLik(object, ...)

## S3 method for class 'ReitsmaSubgroupTMB'
logLik(object, ...)

## S3 method for class 'ReitsmaTMB'
logLik(object, ...)
```

Arguments

object	A fitted model object.
...	Not used.

Value

An object of class "logLik".

See Also

anova.dtametaTMB()

---

pap *Pap Dataset*

Description

This is the pap dataset from Fahey et al. (1995) from a meta-analysis comparing Papanicolaou (Pap) test results with histology for the diagnosis of cervical cancer.

Usage

```
pap
```

Format

A data frame with 59 rows and 6 variables:

id Study identifier

type Test taken during screening (SC) or follow-up (FU)

y11 Number testing positive with both tests

y10 Number testing positive with index test but negative with reference test

y01 Number testing negative with index test but positive with reference test

y00 Number testing negative with both tests

Note

The data set was reconstructed from the SAS code in the supplementary material from Liu et al. (2015).

Source

Liu, Y., Chen, Y., & Chu, H. (2015). *A unification of models for meta-analysis of diagnostic accuracy studies without a gold standard.* Biometrics, 71(2), 538-547. doi:10.1111/biom.12264

Fahey, M., Irwig, L., & Macaskill, P. (1995). *Meta-analysis of pap test accuracy*. American Journal of Epidemiology, 141(7), 680-689. doi:10.1093/oxfordjournals.aje.a117485

---

plot.HoyerAFT *Plot Results from a HoyerAFT Model*

Description

Produces a hierarchical summary receiver operating characteristic (HSROC) plot from a fitted HoyerAFT model. The plot shows study-level sensitivity and specificity estimates together with the meta-analytic HSROC curve derived from the fitted model.

Usage

```
## S3 method for class 'HoyerAFT'
plot(
  x,
 symbol = c("rectangle", "ellipse", "diamond", "triangle", "cross", "plus", "star"),
  scale = 0.02,
  size = c("equal", "sampsize", "se", "sampsize_revman", "se_revman"),
  HSROC = TRUE,
  thresholdrange = NULL,
  main = "Diagnostic Test Accuracy Meta-Analysis",
  studyCI = FALSE,
  conflevel = 0.95,
  studylabels = FALSE,
  legend = TRUE,
  ...
)
```

Arguments

x	An object of class "HoyerAFT" as returned by fitHoyerAFT. Must contain: **data** Original processed data including sensitivity (sens) and false positive rate (fpr) **sdreport2** Summary of model parameters **distcode** Distribution code (1 = Weibull, 2 = lognormal, 3 = loglogistic)
symbol	Character string specifying the symbol used for study-level estimates. One of "rectangle", "ellipse", "diamond", "triangle", "cross", "plus", or "star". The default is "rectangle".
scale	Numeric scaling factor controlling study-symbol dimensions. The default is 0.02. Values below or above the default decrease or increase all symbol dimensions proportionally. Relative adjustments can be specified directly, for example, scale = 0.02 * 0.3 produces marker dimensions equal to 30 percent of the default.
size	Character string controlling display of study-level point estimates: **"equal"** All studies shown with equal size. **"sampsize"** Horizontal and vertical symbol dimensions are proportional to the relative numbers of non-diseased and diseased participants, respectively. **"se"** Horizontal and vertical symbol dimensions are proportional to normalized approximate inverse standard errors of observed logit specificity and logit sensitivity, respectively. **"sampsize_revman"** RevMan-style sample-size scaling. Horizontal and vertical symbol dimensions are based on the square roots of the numbers of non-diseased and diseased participants, respectively. A common analysis-specific scaling constant is chosen so that the average larger dimension measure across studies equals nine before adding the fixed baseline dimension. **"se_revman"** RevMan-style inverse-standard-error scaling. Horizontal and vertical symbol dimensions are based on approximate inverse standard errors of observed logit specificity and logit sensitivity, respectively. A common analysis-specific scaling constant is chosen so that the average larger dimension measure across studies equals nine before adding the fixed baseline dimension.
HSROC	if TRUE, the HSROC curve is added to the plot. Default is TRUE.
thresholdrange	A numeric vector of length 2 giving the range of threshold over which sensitivities and specificities are predicted. If NULL (default), then the minimum and maximum thresholds from the data are used.
main	Character string giving the main title of the plot. Defaults to "Diagnostic Test Accuracy Meta-Analysis".
studyCI	Whether study-level confidence intervals should be displayed for the observed sensitivity and specificity estimates. Defaults to FALSE.
conflevel	Confidence level for the study-level confidence intervals. Default is 0.95.
studylabels	Whether study identifiers should be displayed next to the study-level estimates. Defaults to FALSE.
legend	Whether a legend should be displayed. Default is TRUE.
...	Additional graphical arguments (currently unused).

Details

The plot includes:

- Study-specific sensitivity and false positive rate estimates
- Symbols representing study observations, with dimensions determined by the selected graphical sizing method.
- Lines connecting thresholds within studies
- A meta-analytic HSROC curve based on the fitted AFT model

The HSROC curve is constructed using the estimated model parameters and depends on the specified distribution:

- Weibull
- Lognormal
- Loglogistic

The plot is constructed on the ROC scale with sensitivity on the y-axis and specificity on the x-axis (displayed as 1 - false positive rate on a reversed axis).

Value

No return value. Called for its side effect of producing a plot.

See Also

`fitHoyerAFT` `fitHoyer`

`plot.Reitsma` *Plot Results from a Reitsma Model*

Description

Produces a summary ROC plot for objects of class `"Reitsma"` obtained from `fitReitsma`. The plot displays study-level estimates of sensitivity and specificity, the summary operating point, and corresponding confidence and prediction regions. Optionally, the HSROC (hierarchical summary ROC) curve can be overlaid.

Usage

```
## S3 method for class 'Reitsma'
plot(
  x,
 symbol = c("rectangle", "ellipse", "diamond", "triangle", "cross", "plus", "star"),
  scale = 0.02,
 size = c("fisher", "fisher_revman", "equal", "sampsize", "se", "sampsize_revman",
    "se_revman"),
  main = "Diagnostic Test Accuracy Meta-Analysis",
```

```
  HSROC = FALSE,
  specrange = c(0.7, 0.995),
  conflevel = 0.95,
  predlevel = 0.95,
  studyCI = FALSE,
  studylabels = FALSE,
  legend = TRUE,
  ...
)
```

Arguments

x	An object of class "Reitsma", as returned by fitReitsma.
symbol	Character string specifying the symbol used for study-level estimates. One of "rectangle", "ellipse", "diamond", "triangle", "cross", "plus", or "star". The default is "rectangle".
scale	Numeric scaling factor controlling study-symbol dimensions. The default is 0.02. Values below or above the default decrease or increase all symbol dimensions proportionally. Relative adjustments can be specified directly, for example, scale = 0.02 * 0.3 produces marker dimensions equal to 30 percent of the default.
size	Character string controlling display of study-level point estimates:

"fisher" Size proportional to a decomposition of Fisher's Information matrix. Default.

"fisher_revman" Horizontal and vertical symbol dimensions are based on the same per-study percentage contributions to the logit sensitivity and logit specificity Fisher information as size = "fisher". These percentages are then converted to graphical dimensions using the same RevMan-style normalization applied under "sampsize_revman" and "se_revman".

"equal" All studies shown with equal size.

"sampsize" Horizontal and vertical symbol dimensions are proportional to the relative numbers of non-diseased and diseased participants, respectively.

"se" Horizontal and vertical symbol dimensions are proportional to normalized approximate inverse standard errors of observed logit specificity and logit sensitivity, respectively.

"sampsize_revman" RevMan-style sample-size scaling. Horizontal and vertical symbol dimensions are based on the square roots of the numbers of non-diseased and diseased participants, respectively. A common analysis-specific scaling constant is chosen so that the average larger dimension measure across studies equals nine before adding the fixed baseline dimension.

"se_revman" RevMan-style inverse-standard-error scaling. Horizontal and vertical symbol dimensions are based on approximate inverse standard errors of observed logit specificity and logit sensitivity, respectively. A common analysis-specific scaling constant is chosen so that the average larger dimension measure across studies equals nine before adding the fixed baseline dimension.

main	Character string giving the main title of the plot. Defaults to "Diagnostic Test Accuracy Meta-Analysis".
HSROC	if TRUE, the HSROC curve is added to the plot. Default is FALSE.
specrange	A numeric vector of length 2 giving the range of specificities over which the HSROC curve is plotted. Defaults to c(0.7, 0.995).
conflevel	Confidence level for the confidence region. Default is 0.95.
predlevel	Confidence level for the prediction region. Default is 0.95.
studyCI	Whether study-level confidence intervals should be displayed for the observed sensitivity and specificity estimates. Defaults to FALSE.
studylabels	Whether study identifiers should be displayed next to the study-level estimates. Defaults to FALSE.
legend	Whether a legend should be displayed. Default is TRUE.
...	Additional graphical arguments passed to plotting functions.

Details

The plot is constructed on the ROC scale with sensitivity on the y-axis and specificity on the x-axis (displayed as 1 - false positive rate on a reversed axis).

Study-specific estimates are shown using the selected symbol (rectangles by default), where the size reflects approximate study weights derived from the Fisher information matrix (default).

The following elements are displayed:

- Study-level sensitivity and specificity estimates
- Summary (pooled) estimate
- confidence region around the summary point
- prediction region reflecting between-study variability
- Optional HSROC curve (if HSROC = TRUE)

Confidence and prediction regions are derived using the delta method based on the estimated variance-covariance structure of the model.

Value

No return value. Called for its side effect of producing a plot.

References

Freeman, S. C., Kerby, C. R., Patel, A., Cooper, N. J., Quinn, T., & Sutton, A. J. (2019). Development of an interactive web-based tool to conduct and interrogate meta-analysis of diagnostic test accuracy studies: MetaDTA. *BMC Medical Research Methodology*, 19, 81. doi:10.1186/s12874-0190724x

Harbord, R. M., Deeks, J. J., Egger, M., Whiting, P., & Sterne, J. A. C. (2007). A unification of models for meta-analysis of diagnostic accuracy studies. *Biostatistics*, 8(2), 239–251. doi:10.1093/biostatistics/kxl004

Riley, R. D., Ensor, J., Jackson, D., & Burke, D. L. (2018). Deriving percentage study weights in multi-parameter meta-analysis models: with application to meta-regression, network meta-analysis and one-stage individual participant data models. *Statistical Methods in Medical Research*, 27(10), 2885–2905. doi:10.1177/0962280216688033

See Also

`fitReitsma`

`plot.ReitsmaLCA` *Plot Results from a Reitsma LCA Model*

Description

Produces a summary ROC plot for objects of class `"ReitsmaLCA"` obtained from `fitReitsmaLCA`. Study-specific sensitivities and specificities are empirical Bayes estimates derived from the fitted latent class model.

Usage

```
## S3 method for class 'ReitsmaLCA'
plot(
  x,
 symbol = c("rectangle", "ellipse", "diamond", "triangle", "cross", "plus", "star"),
  scale = 0.02,
  size = c("eb", "equal", "sampsize", "eb_revman", "sampsize_revman"),
  main = "Diagnostic Test Accuracy Meta-Analysis",
  HSROC = FALSE,
  specrange = c(0.7, 0.995),
  conflevel = 0.95,
  predlevel = 0.95,
  studyCI = FALSE,
  studylabels = FALSE,
  legend = TRUE,
  ...
)
```

Arguments

`x`	An object of class `"ReitsmaLCA"`, as returned by `fitReitsmaLCA`.
`symbol`	Character string specifying the symbol used for study-level estimates. One of `"rectangle"`, `"ellipse"`, `"diamond"`, `"triangle"`, `"cross"`, `"plus"`, or `"star"`. The default is `"rectangle"`.
`scale`	Numeric scaling factor controlling study-symbol dimensions. The default is `0.02`. Values below or above the default decrease or increase all symbol dimensions proportionally. Relative adjustments can be specified directly, for example, `scale = 0.02 * 0.3` produces marker dimensions equal to 30 percent of the default.

`size` Character string controlling display of study-level point estimates:

- `"eb"` Horizontal and vertical symbol dimensions are proportional to normalized inverse posterior standard errors of the study-specific empirical Bayes logit-specificity and logit-sensitivity estimates, respectively.
- `"equal"` All studies are shown with equal size.
- `"sampsize"` Horizontal and vertical symbol dimensions are both proportional to relative total study sample size. The same dimension measure is used horizontally and vertically because true disease status is latent.
- `"eb_revman"` RevMan-style graphical scaling applied to the inverse conditional posterior standard errors of the study-specific empirical Bayes logit-specificity and logit-sensitivity estimates. A common analysis-specific scaling constant is chosen so that the average larger dimension measure across studies equals nine before adding the fixed baseline dimension. This is an analogous graphical extension for latent-class models and is not an original Cochrane latent-class weighting method.
- `"sampsize_revman"` RevMan-style graphical scaling based on total study sample size. The same transformed total-sample-size measure is used horizontally and vertically.

`main` Character string giving the main title of the plot. Defaults to `"Diagnostic Test Accuracy Meta-Analysis"`.

`HSROC` if `TRUE`, the HSROC curve is added to the plot. Default is `FALSE`.

`specrange` A numeric vector of length 2 giving the range of specificities over which the HSROC curve is plotted. Defaults to `c(0.7, 0.995)`.

`conflevel` Confidence level for the confidence region. Default is `0.95`.

`predlevel` Confidence level for the prediction region. Default is `0.95`.

`studyCI` Whether study-level confidence intervals should be displayed for the observed sensitivity and specificity estimates. Defaults to `FALSE`.

`studylabels` Whether study identifiers should be displayed next to the study-level estimates. Defaults to `FALSE`.

`legend` Whether a legend should be displayed. Default is `TRUE`.

`...` Additional graphical arguments passed to plotting functions.

Details

The plot is constructed on the ROC scale with sensitivity on the y-axis and specificity on the x-axis (displayed as 1 - false positive rate on a reversed axis).

Study-specific estimates are shown using the selected symbol (rectangles by default).

The following elements are displayed:

- Study-level sensitivity and specificity estimates (Empirical Bayes Estimates)
- Summary (pooled) estimate
- confidence region around the summary point
- prediction region reflecting between-study variability
- Optional HSROC curve (if `HSROC = TRUE`)

Confidence and prediction regions are derived using the delta method based on the estimated variance-covariance structure of the model.

Value

No return value. Called for its side effect of producing a plot.

References

Liu, Y., Chen, Y., & Chu, H. (2015). A unification of models for meta-analysis of diagnostic accuracy studies without a gold standard. *Biometrics*, 71(2), 538-547. doi:10.1111/biom.12264

Freeman, S. C., Kerby, C. R., Patel, A., Cooper, N. J., Quinn, T., & Sutton, A. J. (2019). Development of an interactive web-based tool to conduct and interrogate meta-analysis of diagnostic test accuracy studies: MetaDTA. *BMC Medical Research Methodology*, 19, 81. doi:10.1186/s12874-0190724x

Harbord, R. M., Deeks, J. J., Egger, M., Whiting, P., & Sterne, J. A. C. (2007). A unification of models for meta-analysis of diagnostic accuracy studies. *Biostatistics*, 8(2), 239–251. doi:10.1093/biostatistics/kxl004

See Also

`fitReitsmaLCA`

`plot.ReitsmaSubgroup` *Plot Results from a Reitsma Subgroup Model*

Description

Produces a summary ROC plot for objects of class `"ReitsmaSubgroup"` obtained from `fitReitsmaSubgroup`. The plot displays study-level estimates of sensitivity and specificity, the summary operating point, and corresponding confidence and prediction regions. Optionally, the HSROC (hierarchical summary ROC) curve can be overlaid.

Usage

```
## S3 method for class 'ReitsmaSubgroup'
plot(
  x,
  symbol = NULL,
  scale = 0.02,
 size = c("equal", "fisher", "fisher_revman", "sampsize", "se", "sampsize_revman",
    "se_revman"),
  main = "Diagnostic Test Accuracy Meta-Analysis",
  col = NULL,
  nudge_legend = -0.4,
  HSROC = FALSE,
  specrange = c(0.7, 0.995),
```

```
  conflevel = 0.95,
  predlevel = 0.95,
  connectstudies = FALSE,
  studyCI = FALSE,
  studylabels = FALSE,
  legend = TRUE,
  ...
)
```

Arguments

x	An object of class "ReitsmaSubgroup", as returned by fitReitsmaSubgroup.
symbol	Character vector specifying the symbols used for study-level estimates of the subgroups. One can choose "rectangle", "ellipse", "diamond", "triangle", "cross", "plus", or "star". If NULL, symbols are generated automatically.
scale	Numeric scaling factor controlling study-symbol dimensions. The default is 0.02. Values below or above the default decrease or increase all symbol dimensions proportionally. Relative adjustments can be specified directly, for example, scale = 0.02 * 0.3 produces marker dimensions equal to 30 percent of the default.
size	Character string controlling display of study-level point estimates:

"fisher" Study-symbol dimensions represent percentage contributions to the estimated logit sensitivity and logit specificity of the study's own subgroup. Weights sum to 100 separately within each subgroup and outcome dimension. If sensspec_constrain is used in fitReitsmaSubgroup to constrain logit sensitivity and/or logit specificity to a common value across subgroups, weights for the constrained outcome dimension(s) instead sum to 100 across all studies and subgroups combined, reflecting that all studies then inform a single shared parameter.

"fisher_revman" Horizontal and vertical symbol dimensions are based on the same per-study percentage contributions to the logit sensitivity and logit specificity Fisher information as size = "fisher". These percentages are then converted to graphical dimensions using the same RevMan-style normalization applied under "sampsize_revman" and "se_revman".

"equal" All studies shown with equal size. Default.

"sampsize" Horizontal and vertical symbol dimensions are proportional to the relative numbers of non-diseased and diseased participants, respectively.

"se" Horizontal and vertical symbol dimensions are proportional to normalized approximate inverse standard errors of observed logit specificity and logit sensitivity, respectively.

"sampsize_revman" RevMan-style sample-size scaling. Horizontal and vertical symbol dimensions are based on the square roots of the numbers of non-diseased and diseased participants, respectively. A common analysis-specific scaling constant is chosen so that the average larger dimension measure across studies equals nine before adding the fixed baseline dimension.

"se_revman" RevMan-style inverse-standard-error scaling. Horizontal and vertical symbol dimensions are based on approximate inverse standard errors

of observed logit specificity and logit sensitivity, respectively. A common analysis-specific scaling constant is chosen so that the average larger dimension measure across studies equals nine before adding the fixed baseline dimension.

main	Character string giving the main title of the plot. Defaults to "Diagnostic Test Accuracy Meta-Analysis".
col	Vector of colours used for subgroup-specific HSROC curves, study-level point estimates, summary points, confidence and prediction region. If NULL, colours are generated automatically.
nudge_legend	Numeric horizontal offset for the subgroup legend. More negative values move the legend further right, outside the plotting area. Values closer to zero move it closer to the panel. Default is -0.4.
HSROC	if TRUE, the HSROC curve is added to the plot. Default is FALSE.
specrange	A numeric vector of length 2 giving the range of specificities over which the HSROC curve is plotted. Defaults to c(0.7, 0.995).
conflevel	Confidence level for the confidence region. Default is 0.95.
predlevel	Confidence level for the prediction region. Default is 0.95.
connectstudies	Whether the point estimates of two subgroups within the same study should be connected. Defaults to FALSE.
studyCI	Whether study-level confidence intervals should be displayed for the observed sensitivity and specificity estimates. Defaults to FALSE.
studylabels	Whether study identifiers should be displayed next to the study-level estimates. Defaults to FALSE.
legend	Whether a legend should be displayed. Default is TRUE.
...	Additional graphical arguments passed to plotting functions.

Details

The plot is constructed on the ROC scale with sensitivity on the y-axis and specificity on the x-axis (displayed as 1 - false positive rate on a reversed axis).

Study-specific estimates are shown with subgroup-specific symbols and colours.

The following elements are displayed:

- Study-level sensitivity and specificity estimates
- Summary (pooled) estimate
- confidence region around the summary point
- prediction region reflecting between-study variability
- Optional HSROC curve (if HSROC = TRUE)

Confidence and prediction regions are derived using the delta method based on the estimated variance-covariance structure of the model.

Value

No return value. Called for its side effect of producing a plot.

References

Freeman, S. C., Kerby, C. R., Patel, A., Cooper, N. J., Quinn, T., & Sutton, A. J. (2019). Development of an interactive web-based tool to conduct and interrogate meta-analysis of diagnostic test accuracy studies: MetaDTA. *BMC Medical Research Methodology*, 19, 81. doi:10.1186/s12874-0190724x

Harbord, R. M., Deeks, J. J., Egger, M., Whiting, P., & Sterne, J. A. C. (2007). A unification of models for meta-analysis of diagnostic accuracy studies. *Biostatistics*, 8(2), 239–251. doi:10.1093/biostatistics/kxl004

Riley, R. D., Ensor, J., Jackson, D., & Burke, D. L. (2018). Deriving percentage study weights in multi-parameter meta-analysis models: with application to meta-regression, network meta-analysis and one-stage individual participant data models. *Statistical Methods in Medical Research*, 27(10), 2885–2905. doi:10.1177/0962280216688033

See Also

`fitReitsmaSubgroup`

`plot.ReitsmaSubgroupLCA` *Plot Results from a Reitsma Subgroup LCA Model*

Description

Produces a summary ROC plot for objects of class `"ReitsmaSubgroupLCA"` obtained from `fitReitsmaSubgroupLCA`. Study-specific sensitivities and specificities are empirical Bayes estimates derived from the fitted latent class model.

Usage

```
## S3 method for class 'ReitsmaSubgroupLCA'
plot(
  x,
  symbol = NULL,
  scale = 0.02,
  size = c("eb", "equal", "sampsize", "eb_revman", "sampsize_revman"),
  main = "Diagnostic Test Accuracy Meta-Analysis",
  col = NULL,
  nudge_legend = -0.4,
  HSROC = FALSE,
  specrange = c(0.7, 0.995),
  conflevel = 0.95,
  predlevel = 0.95,
  connectstudies = FALSE,
  studyCI = FALSE,
  studylabels = FALSE,
  legend = TRUE,
```

```
  ...
)
```

Arguments

x	An object of class "ReitsmaSubgroupLCA", as returned by fitReitsmaSubgroupLCA.
symbol	Character vector specifying the symbols used for study-level estimates of the subgroups. One can choose "rectangle", "ellipse", "diamond", "triangle", "cross", "plus", or "star". If NULL, symbols are generated automatically.
scale	Numeric scaling factor controlling study-symbol dimensions. The default is 0.02. Values below or above the default decrease or increase all symbol dimensions proportionally. Relative adjustments can be specified directly, for example, scale = 0.02 * 0.3 produces marker dimensions equal to 30 percent of the default.
size	Character string controlling display of study-level point estimates: "eb" Horizontal and vertical symbol dimensions are proportional to normalized inverse posterior standard errors of the study-specific empirical Bayes logit-specificity and logit-sensitivity estimates, respectively. "equal" All studies are shown with equal size. "sampsize" Horizontal and vertical symbol dimensions are both proportional to relative total study sample size. The same dimension measure is used horizontally and vertically because true disease status is latent. "eb_revman" RevMan-style graphical scaling applied to the inverse conditional posterior standard errors of the study-specific empirical Bayes logit-specificity and logit-sensitivity estimates. A common analysis-specific scaling constant is chosen so that the average larger dimension measure across studies equals nine before adding the fixed baseline dimension. This is an analogous graphical extension for latent-class models and is not an original Cochrane latent-class weighting method. "sampsize_revman" RevMan-style graphical scaling based on total study sample size. The same transformed total-sample-size measure is used horizontally and vertically.
main	Character string giving the main title of the plot. Defaults to "Diagnostic Test Accuracy Meta-Analysis".
col	Vector of colours used for subgroup-specific HSROC curves, study-level point estimates, summary points, confidence and prediction region. If NULL, colours are generated automatically.
nudge_legend	Numeric horizontal offset for the subgroup legend. More negative values move the legend further right, outside the plotting area. Values closer to zero move it closer to the panel. Default is -0.4.
HSROC	if TRUE, the HSROC curve is added to the plot. Default is FALSE.
specrange	A numeric vector of length 2 giving the range of specificities over which the HSROC curve is plotted. Defaults to c(0.7, 0.995).
conflevel	Confidence level for the confidence region. Default is 0.95.
predlevel	Confidence level for the prediction region. Default is 0.95.

`connectstudies`	Whether the point estimates of two subgroups within the same study should be connected. Defaults to `FALSE`.
`studyCI`	Whether study-level confidence intervals should be displayed for the observed sensitivity and specificity estimates. Defaults to `FALSE`.
`studylabels`	Whether study identifiers should be displayed next to the study-level estimates. Defaults to `FALSE`.
`legend`	Whether a legend should be displayed. Default is `TRUE`.
`...`	Additional graphical arguments passed to plotting functions.

Details

The plot is constructed on the ROC scale with sensitivity on the y-axis and specificity on the x-axis (displayed as 1 - false positive rate on a reversed axis).

Study-specific estimates are shown with subgroup-specific symbols and colours.

The following elements are displayed:

- Study-level sensitivity and specificity estimates
- Summary (pooled) estimate
- confidence region around the summary point
- prediction region reflecting between-study variability
- Optional HSROC curve (if `HSROC = TRUE`)

Confidence and prediction regions are derived using the delta method based on the estimated variance-covariance structure of the model.

Value

No return value. Called for its side effect of producing a plot.

References

Liu, Y., Chen, Y., & Chu, H. (2015). A unification of models for meta-analysis of diagnostic accuracy studies without a gold standard. *Biometrics*, 71(2), 538-547. doi:10.1111/biom.12264

Freeman, S. C., Kerby, C. R., Patel, A., Cooper, N. J., Quinn, T., & Sutton, A. J. (2019). Development of an interactive web-based tool to conduct and interrogate meta-analysis of diagnostic test accuracy studies: MetaDTA. *BMC Medical Research Methodology*, 19, 81. doi:10.1186/s12874-0190724x

Harbord, R. M., Deeks, J. J., Egger, M., Whiting, P., & Sterne, J. A. C. (2007). A unification of models for meta-analysis of diagnostic accuracy studies. *Biostatistics*, 8(2), 239–251. doi:10.1093/biostatistics/kxl004

See Also

`fitReitsmaSubgroupLCA`

plot.ReitsmaSubgroupTMB

Plot Results from a Reitsma Subgroup TMB Model

Description

Produces a summary ROC plot for objects of class "ReitsmaSubgroupTMB" obtained from fitReitsmaSubgroupTMB. The plot displays study-level estimates of sensitivity and specificity, the summary operating point, and corresponding confidence and prediction regions. Optionally, the HSROC (hierarchical summary ROC) curve can be overlaid.

Usage

```
## S3 method for class 'ReitsmaSubgroupTMB'
plot(
  x,
  symbol = NULL,
  scale = 0.02,
 size = c("equal", "fisher", "fisher_revman", "sampsize", "se", "sampsize_revman",
    "se_revman"),
  main = "Diagnostic Test Accuracy Meta-Analysis",
  col = NULL,
  nudge_legend = -0.4,
  HSROC = FALSE,
  specrange = c(0.7, 0.995),
  conflevel = 0.95,
  predlevel = 0.95,
  connectstudies = FALSE,
  studyCI = FALSE,
  studylabels = FALSE,
  legend = TRUE,
  ...
)
```

Arguments

x	An object of class "ReitsmaSubgroupTMB", as returned by fitReitsmaSubgroupTMB.
symbol	Character vector specifying the symbols used for study-level estimates of the subgroups. One can choose "rectangle", "ellipse", "diamond", "triangle", "cross", "plus", or "star". If NULL, symbols are generated automatically.
scale	Numeric scaling factor controlling study-symbol dimensions. The default is 0.02. Values below or above the default decrease or increase all symbol dimensions proportionally. Relative adjustments can be specified directly, for example, scale = 0.02 * 0.3 produces marker dimensions equal to 30 percent of the default.
size	Character string controlling display of study-level point estimates:

"fisher" Study-symbol dimensions represent percentage contributions to the estimated logit sensitivity and logit specificity of the study's own subgroup. Weights sum to 100 separately within each subgroup and outcome dimension. If `sensspec_constrain` is used in `fitReitsmaSubgroupTMB` to constrain logit sensitivity and/or logit specificity to a common value across subgroups, weights for the constrained outcome dimension(s) instead sum to 100 across all studies and subgroups combined, reflecting that all studies then inform a single shared parameter.

"fisher_revman" Horizontal and vertical symbol dimensions are based on the same per-study percentage contributions to the logit sensitivity and logit specificity Fisher information as `size = "fisher"`. These percentages are then converted to graphical dimensions using the same RevMan-style normalization applied under `"sampsize_revman"` and `"se_revman"`.

"equal" All studies shown with equal size. Default.

"sampsize" Horizontal and vertical symbol dimensions are proportional to the relative numbers of non-diseased and diseased participants, respectively.

"se" Horizontal and vertical symbol dimensions are proportional to normalized approximate inverse standard errors of observed logit specificity and logit sensitivity, respectively.

"sampsize_revman" RevMan-style sample-size scaling. Horizontal and vertical symbol dimensions are based on the square roots of the numbers of non-diseased and diseased participants, respectively. A common analysis-specific scaling constant is chosen so that the average larger dimension measure across studies equals nine before adding the fixed baseline dimension.

"se_revman" RevMan-style inverse-standard-error scaling. Horizontal and vertical symbol dimensions are based on approximate inverse standard errors of observed logit specificity and logit sensitivity, respectively. A common analysis-specific scaling constant is chosen so that the average larger dimension measure across studies equals nine before adding the fixed baseline dimension.

`main` Character string giving the main title of the plot. Defaults to `"Diagnostic Test Accuracy Meta-Analysis"`.

`col` Vector of colours used for subgroup-specific HSROC curves, study-level symbols, summary points, confidence and prediction region. If `NULL`, colours are generated automatically.

`nudge_legend` Numeric horizontal offset for the subgroup legend. More negative values move the legend further right, outside the plotting area. Values closer to zero move it closer to the panel. Default is `-0.4`.

`HSROC` if `TRUE`, the HSROC curve is added to the plot. Default is `FALSE`.

`specrange` A numeric vector of length 2 giving the range of specificities over which the HSROC curve is plotted. Defaults to `c(0.7, 0.995)`.

`conflevel` Confidence level for the confidence region. Default is `0.95`.

`predlevel` Confidence level for the prediction region. Default is `0.95`.

`connectstudies` Whether the point estimates of two subgroups within the same study should be connected. Defaults to `FALSE`.

`studyCI`	Whether study-level confidence intervals should be displayed for the observed sensitivity and specificity estimates. Defaults to `FALSE`.
`studylabels`	Whether study identifiers should be displayed next to the study-level estimates. Defaults to `FALSE`.
`legend`	Whether a legend should be displayed. Default is `TRUE`.
`...`	Additional graphical arguments passed to plotting functions.

Details

The plot is constructed on the ROC scale with sensitivity on the y-axis and specificity on the x-axis (displayed as 1 - false positive rate on a reversed axis).

Study-specific estimates are shown with study-specific symbols and colours.

The following elements are displayed:

- Study-level sensitivity and specificity estimates
- Summary (pooled) estimate
- confidence region around the summary point
- prediction region reflecting between-study variability
- Optional HSROC curve (if `HSROC = TRUE`)

Confidence and prediction regions are derived using the delta method based on the estimated variance-covariance structure of the model.

Value

No return value. Called for its side effect of producing a plot.

References

Harbord, R. M., Deeks, J. J., Egger, M., Whiting, P., & Sterne, J. A. C. (2007). A unification of models for meta-analysis of diagnostic accuracy studies. *Biostatistics*, 8(2), 239–251. doi:10.1093/biostatistics/kxl004

See Also

`fitReitsmaSubgroupTMB`

plot.ReitsmaTMB *Plot Results from a ReitsmaTMB Model*

Description

Produces a summary ROC plot for objects of class "ReitsmaTMB" obtained from fitReitsmaTMB. The plot displays study-level estimates of sensitivity and specificity, the summary operating point, and corresponding confidence and prediction regions. Optionally, the HSROC (hierarchical summary ROC) curve can be overlaid.

Usage

```
## S3 method for class 'ReitsmaTMB'
plot(
  x,
 symbol = c("rectangle", "ellipse", "diamond", "triangle", "cross", "plus", "star"),
  scale = 0.02,
 size = c("fisher", "fisher_revman", "equal", "sampsize", "se", "sampsize_revman",
    "se_revman"),
  main = "Diagnostic Test Accuracy Meta-Analysis",
  HSROC = FALSE,
  specrange = c(0.7, 0.995),
  conflevel = 0.95,
  predlevel = 0.95,
  studyCI = FALSE,
  studylabels = FALSE,
  legend = TRUE,
  ...
)
```

Arguments

x	An object of class "ReitsmaTMB", as returned by fitReitsmaTMB.
symbol	Character string specifying the symbol used for study-level estimates. One of "rectangle", "ellipse", "diamond", "triangle", "cross", "plus", or "star". The default is "rectangle".
scale	Numeric scaling factor controlling study-symbol dimensions. The default is 0.02. Values below or above the default decrease or increase all symbol dimensions proportionally. Relative adjustments can be specified directly, for example, scale = 0.02 * 0.3 produces marker dimensions equal to 30 percent of the default.
size	Character string controlling display of study-level point estimates:
	"fisher" Size proportional to a decomposition of Fisher's Information matrix. Default.

"fisher_revman" Horizontal and vertical symbol dimensions are based on the same per-study percentage contributions to the logit sensitivity and logit specificity Fisher information as `size = "fisher"`. These percentages are then converted to graphical dimensions using the same RevMan-style normalization applied under `"sampsize_revman"` and `"se_revman"`.

"equal" All studies shown with equal size.

"sampsize" Horizontal and vertical symbol dimensions are proportional to the relative numbers of non-diseased and diseased participants, respectively.

"se" Horizontal and vertical symbol dimensions are proportional to normalized approximate inverse standard errors of observed logit specificity and logit sensitivity, respectively.

"sampsize_revman" RevMan-style sample-size scaling. Horizontal and vertical symbol dimensions are based on the square roots of the numbers of non-diseased and diseased participants, respectively. A common analysis-specific scaling constant is chosen so that the average larger dimension measure across studies equals nine before adding the fixed baseline dimension.

"se_revman" RevMan-style inverse-standard-error scaling. Horizontal and vertical symbol dimensions are based on approximate inverse standard errors of observed logit specificity and logit sensitivity, respectively. A common analysis-specific scaling constant is chosen so that the average larger dimension measure across studies equals nine before adding the fixed baseline dimension.

`main` Character string giving the main title of the plot. Defaults to `"Diagnostic Test Accuracy Meta-Analysis"`.

`HSROC` If `TRUE`, the HSROC curve is added to the plot. Default is `FALSE`.

`specrange` A numeric vector of length 2 giving the range of specificities over which the HSROC curve is plotted. Defaults to `c(0.7, 0.995)`.

`conflevel` Confidence level for the confidence region. Default is `0.95`.

`predlevel` Confidence level for the prediction region. Default is `0.95`.

`studyCI` Whether study-level confidence intervals should be displayed for the observed sensitivity and specificity estimates. Defaults to `FALSE`.

`studylabels` Whether study identifiers should be displayed next to the study-level estimates. Defaults to `FALSE`.

`legend` Whether a legend should be displayed. Default is `TRUE`.

`...` Additional graphical arguments passed to plotting functions.

Details

The plot is constructed on the ROC scale with sensitivity on the y-axis and specificity on the x-axis (displayed as 1 - false positive rate on a reversed axis).

Study-specific estimates are shown using the selected symbol (rectangles by default).

The following elements are displayed:

- Study-level sensitivity and specificity estimates
- Summary (pooled) estimate

- confidence region around the summary point
- prediction region reflecting between-study variability
- Optional HSROC curve (if `HSROC = TRUE`)

Confidence and prediction regions are derived using the delta method based on the estimated variance-covariance structure of the model.

Value

No return value. Called for its side effect of producing a plot.

References

Freeman, S. C., Kerby, C. R., Patel, A., Cooper, N. J., Quinn, T., & Sutton, A. J. (2019). Development of an interactive web-based tool to conduct and interrogate meta-analysis of diagnostic test accuracy studies: MetaDTA. *BMC Medical Research Methodology*, 19, 81. doi:10.1186/s12874-0190724x

Harbord, R. M., Deeks, J. J., Egger, M., Whiting, P., & Sterne, J. A. C. (2007). A unification of models for meta-analysis of diagnostic accuracy studies. *Biostatistics*, 8(2), 239–251. doi:10.1093/biostatistics/kxl004

See Also

`fitReitsmaTMB`

---

plot.RutterGatsonis *Plot Results from a Rutter and Gatsonis Model*

Description

Produces a summary ROC plot for objects of class `"RutterGatsonis"` obtained from `fitRutterGatsonis`. The plot displays study-level estimates of sensitivity and specificity and the HSROC (hierarchical summary ROC).

Usage

```
## S3 method for class 'RutterGatsonis'
plot(
  x,
 symbol = c("rectangle", "ellipse", "diamond", "triangle", "cross", "plus", "star"),
  scale = 0.02,
 size = c("fisher", "fisher_revman", "equal", "sampsize", "se", "sampsize_revman",
    "se_revman"),
  specrange = c(0.7, 0.995),
  main = "Diagnostic Test Accuracy Meta-Analysis",
  HSROC = TRUE,
  conflevel = 0.95,
```

```
  studyCI = FALSE,
  studylabels = FALSE,
  legend = TRUE,
  ...
)
```

Arguments

x	An object of class "RutterGatsonis", as returned by fitRutterGatsonis.
symbol	Character string specifying the symbol used for study-level estimates. One of "rectangle", "ellipse", "diamond", "triangle", "cross", "plus", or "star". The default is "rectangle".
scale	Numeric scaling factor controlling study-symbol dimensions. The default is 0.02. Values below or above the default decrease or increase all symbol dimensions proportionally. Relative adjustments can be specified directly, for example, scale = 0.02 * 0.3 produces marker dimensions equal to 30 percent of the default.
size	Character string controlling display of study-level point estimates: **"fisher"** Size proportional to a decomposition of Fisher's Information matrix with respect to the recovered pooled logit sensitivity and specificity. Default. **"fisher_revman"** Horizontal and vertical symbol dimensions are based on the same per-study percentage contributions to the logit sensitivity and logit specificity Fisher information as size = "fisher". These percentages are then converted to graphical dimensions using the same RevMan-style normalization applied under "sampsize_revman" and "se_revman". **"equal"** All studies shown with equal size. **"sampsize"** Horizontal and vertical symbol dimensions are proportional to the relative numbers of non-diseased and diseased participants, respectively. **"se"** Horizontal and vertical symbol dimensions are proportional to normalized approximate inverse standard errors of observed logit specificity and logit sensitivity, respectively. **"sampsize_revman"** RevMan-style sample-size scaling. Horizontal and vertical symbol dimensions are based on the square roots of the numbers of non-diseased and diseased participants, respectively. A common analysis-specific scaling constant is chosen so that the average larger dimension measure across studies equals nine before adding the fixed baseline dimension. **"se_revman"** RevMan-style inverse-standard-error scaling. Horizontal and vertical symbol dimensions are based on approximate inverse standard errors of observed logit specificity and logit sensitivity, respectively. A common analysis-specific scaling constant is chosen so that the average larger dimension measure across studies equals nine before adding the fixed baseline dimension.
specrange	A numeric vector of length 2 giving the range of specificities over which the HSROC curve is plotted. Defaults to c(0.7, 0.995).
main	Character string giving the main title of the plot. Defaults to "Diagnostic Test Accuracy Meta-Analysis".

HSROC	if TRUE, the HSROC curve is added to the plot. Default is TRUE.
conflevel	Confidence level for the study-level confidence intervals. Default is 0.95.
studyCI	Whether study-level confidence intervals should be displayed for the observed sensitivity and specificity estimates. Defaults to FALSE.
studylabels	Whether study identifiers should be displayed next to the study-level estimates. Defaults to FALSE.
legend	Whether a legend should be displayed. Default is TRUE.
...	Additional graphical arguments passed to plotting functions.

Details

The plot is constructed on the ROC scale with sensitivity on the y-axis and specificity on the x-axis (displayed as 1 - false positive rate on a reversed axis).

Study-specific estimates are shown using the selected symbol (rectangles by default).

The following elements are displayed:

- Study-level sensitivity and specificity estimates
- HSROC curve

Value

No return value. Called for its side effect of producing a plot.

References

Freeman, S. C., Kerby, C. R., Patel, A., Cooper, N. J., Quinn, T., & Sutton, A. J. (2019). Development of an interactive web-based tool to conduct and interrogate meta-analysis of diagnostic test accuracy studies: MetaDTA. *BMC Medical Research Methodology*, 19, 81. doi:10.1186/s12874-0190724x

See Also

fitRutterGatsonis

---

plot.RutterGatsonisLCA

Plot Results from a Rutter and Gatsonis LCA Model

Description

Produces a summary ROC plot for objects of class "RutterGatsonisLCA" obtained from fitRutterGatsonisLCA. Study-specific sensitivities and specificities are empirical Bayes estimates derived from the fitted latent class model.

Usage

```
## S3 method for class 'RutterGatsonisLCA'
plot(
  x,
 symbol = c("rectangle", "ellipse", "diamond", "triangle", "cross", "plus", "star"),
  scale = 0.02,
  size = c("eb", "equal", "sampsize", "eb_revman", "sampsize_revman"),
  specrange = c(0.7, 0.995),
  main = "Diagnostic Test Accuracy Meta-Analysis",
  HSROC = TRUE,
  studyCI = FALSE,
  conflevel = 0.95,
  studylabels = FALSE,
  legend = TRUE,
  ...
)
```

Arguments

x	An object of class "RutterGatsonisLCA", as returned by fitRutterGatsonisLCA.
symbol	Character string specifying the symbol used for study-level estimates. One of "rectangle", "ellipse", "diamond", "triangle", "cross", "plus", or "star". The default is "rectangle".
scale	Numeric scaling factor controlling study-symbol dimensions. The default is 0.02. Values below or above the default decrease or increase all symbol dimensions proportionally. Relative adjustments can be specified directly, for example, scale = 0.02 * 0.3 produces marker dimensions equal to 30 percent of the default.
size	Character string controlling display of study-level point estimates: "eb" Horizontal and vertical symbol dimensions are proportional to normalized inverse posterior standard errors of the study-specific empirical Bayes logit-specificity and logit-sensitivity estimates, respectively. "equal" All studies are shown with equal size. "sampsize" Horizontal and vertical symbol dimensions are both proportional to relative total study sample size. The same dimension measure is used horizontally and vertically because true disease status is latent. "eb_revman" RevMan-style graphical scaling applied to the inverse conditional posterior standard errors of the study-specific empirical Bayes logit-specificity and logit-sensitivity estimates. A common analysis-specific scaling constant is chosen so that the average larger dimension measure across studies equals nine before adding the fixed baseline dimension. This is an analogous graphical extension for latent-class models and is not an original Cochrane latent-class weighting method. "sampsize_revman" RevMan-style graphical scaling based on total study sample size. The same transformed total-sample-size measure is used horizontally and vertically.

specrange	A numeric vector of length 2 giving the range of specificities over which the HSROC curve is plotted. Defaults to c(0.7, 0.995).
main	Character string giving the main title of the plot. Defaults to "Diagnostic Test Accuracy Meta-Analysis".
HSROC	if TRUE, the HSROC curve is added to the plot. Default is TRUE.
studyCI	Whether study-level confidence intervals should be displayed for the observed sensitivity and specificity estimates. Defaults to FALSE.
conflevel	Confidence level for the study-level confidence intervals. Default is 0.95.
studylabels	Whether study identifiers should be displayed next to the study-level estimates. Defaults to FALSE.
legend	Whether a legend should be displayed. Default is TRUE.
...	Additional graphical arguments passed to plotting functions.

Details

The plot is constructed on the ROC scale with sensitivity on the y-axis and specificity on the x-axis (displayed as 1 - false positive rate on a reversed axis).

Study-specific estimates are shown using the selected symbol (rectangles by default).

The following elements are displayed:

- Study-level sensitivity and specificity estimates
- HSROC curve

Value

No return value. Called for its side effect of producing a plot.

References

Liu, Y., Chen, Y., & Chu, H. (2015). A unification of models for meta-analysis of diagnostic accuracy studies without a gold standard. *Biometrics*, 71(2), 538-547. doi:10.1111/biom.12264

Freeman, S. C., Kerby, C. R., Patel, A., Cooper, N. J., Quinn, T., & Sutton, A. J. (2019). Development of an interactive web-based tool to conduct and interrogate meta-analysis of diagnostic test accuracy studies: MetaDTA. *BMC Medical Research Methodology*, 19, 81. doi:10.1186/s12874-0190724x

See Also

fitRutterGatsonisLCA

plot.RutterGatsonisSubgroup *Plot Results from a Rutter and Gatsonis Subgroup Model*

Description

Produces summary ROC plots for objects of class "RutterGatsonisSubgroup" obtained from fitRutterGatsonisSubgroup. The plot displays study-level estimates of sensitivity and specificity, stratified by subgroup, together with subgroup-specific HSROC (hierarchical summary ROC) curves.

Usage

```
## S3 method for class 'RutterGatsonisSubgroup'
plot(
  x,
  symbol = NULL,
  scale = 0.02,
 size = c("equal", "fisher", "fisher_revman", "sampsize", "se", "sampsize_revman",
    "se_revman"),
  nudge_legend = -0.4,
  specrange = c(0.7, 0.995),
  col = NULL,
  main = "Diagnostic Test Accuracy Meta-Analysis",
  HSROC = TRUE,
  connectstudies = FALSE,
  studyCI = FALSE,
  conflevel = 0.95,
  studylabels = FALSE,
  legend = TRUE,
  ...
)
```

Arguments

x	An object of class "RutterGatsonisSubgroup", as returned by fitRutterGatsonisSubgroup.
symbol	Character vector specifying the symbols used for study-level estimates of the subgroups. One can choose "rectangle", "ellipse", "diamond", "triangle", "cross", "plus", or "star". If NULL, symbols are generated automatically.
scale	Numeric scaling factor controlling study-symbol dimensions. The default is 0.02. Values below or above the default decrease or increase all symbol dimensions proportionally. Relative adjustments can be specified directly, for example, scale = 0.02 * 0.3 produces marker dimensions equal to 30 percent of the default.
size	Character string controlling display of study-level point estimates:
	"equal" All studies shown with equal size. Default.

"fisher" Displays parameter-specific percentage study contributions to the recovered subgroup-specific pooled logit sensitivity and logit specificity. Fisher sizing is available when HSROC accuracy and threshold parameters are subgroup-specific.

"fisher_revman" Horizontal and vertical symbol dimensions are based on the same per-study percentage contributions to the logit sensitivity and logit specificity Fisher information as `size = "fisher"`. These percentages are then converted to graphical dimensions using the same RevMan-style normalization applied under `"sampsize_revman"` and `"se_revman"`.

"sampsize" Horizontal and vertical symbol dimensions are proportional to the relative numbers of non-diseased and diseased participants, respectively.

"se" Horizontal and vertical symbol dimensions are proportional to normalized approximate inverse standard errors of observed logit specificity and logit sensitivity, respectively.

"sampsize_revman" RevMan-style sample-size scaling. Horizontal and vertical symbol dimensions are based on the square roots of the numbers of non-diseased and diseased participants, respectively. A common analysis-specific scaling constant is chosen so that the average larger dimension measure across studies equals nine before adding the fixed baseline dimension.

"se_revman" RevMan-style inverse-standard-error scaling. Horizontal and vertical symbol dimensions are based on approximate inverse standard errors of observed logit specificity and logit sensitivity, respectively. A common analysis-specific scaling constant is chosen so that the average larger dimension measure across studies equals nine before adding the fixed baseline dimension.

`nudge_legend` Numeric horizontal offset for the subgroup legend. More negative values move the legend further right, outside the plotting area. Values closer to zero move it closer to the panel. Default is `-0.4`.

`specrange` A numeric vector of length 2 giving the range of specificities over which the HSROC curve is plotted. Defaults to `c(0.7, 0.995)`.

`col` Vector of colours used for subgroup-specific HSROC curves and study-level point estimates. If `NULL`, colours are generated automatically.

`main` Character string giving the main title of the plot. Defaults to `"Diagnostic Test Accuracy Meta-Analysis"`.

`HSROC` if `TRUE`, the HSROC curve is added to the plot. Default is `TRUE`.

`connectstudies` Whether the point estimates of two subgroups within the same study should be connected. Defaults to `FALSE`.

`studyCI` Whether study-level confidence intervals should be displayed for the observed sensitivity and specificity estimates. Defaults to `FALSE`.

`conflevel` Confidence level for the study-level confidence intervals. Default is `0.95`.

`studylabels` Whether study identifiers should be displayed next to the study-level estimates. Defaults to `FALSE`.

`legend` Whether a legend should be displayed. Default is `TRUE`.

`...` Additional graphical arguments passed to plotting functions.

Details

The plot is constructed on the ROC scale with sensitivity on the y-axis and specificity on the x-axis (displayed as 1 - false positive rate on a reversed axis).

Study-specific estimates are shown with subgroup-specific symbols and colours.

The following elements are displayed:

- Study-level sensitivity and specificity estimates by subgroup
- Subgroup-specific HSROC curves
- A legend identifying the subgroups

Value

No return value. Called for its side effect of producing a plot.

References

Freeman, S. C., Kerby, C. R., Patel, A., Cooper, N. J., Quinn, T., & Sutton, A. J. (2019). Development of an interactive web-based tool to conduct and interrogate meta-analysis of diagnostic test accuracy studies: MetaDTA. *BMC Medical Research Methodology*, 19, 81. doi:10.1186/s12874-0190724x

See Also

`fitRutterGatsonisSubgroup`

`plot.RutterGatsonisSubgroupLCA`

Plot Results from a Rutter and Gatsonis Subgroup LCA Model

Description

Produces summary ROC plots for objects of class `"RutterGatsonisSubgroupLCA"` obtained from `fitRutterGatsonisSubgroupLCA`. The plot displays study-level estimates of sensitivity and specificity (empirical Bayes estimates), stratified by subgroup, together with subgroup-specific HSROC (hierarchical summary ROC) curves.

Usage

```
## S3 method for class 'RutterGatsonisSubgroupLCA'
plot(
  x,
  symbol = NULL,
  scale = 0.02,
  size = c("eb", "equal", "sampsize", "eb_revman", "sampsize_revman"),
  nudge_legend = -0.4,
  specrange = c(0.7, 0.995),
```

```
  col = NULL,
  main = "Diagnostic Test Accuracy Meta-Analysis",
  HSROC = TRUE,
  connectstudies = FALSE,
  studyCI = FALSE,
  conflevel = 0.95,
  studylabels = FALSE,
  legend = TRUE,
  ...
)
```

Arguments

x	An object of class "RutterGatsonisSubgroupLCA", as returned by fitRutterGatsonisSubgroupLCA.
symbol	Character vector specifying the symbols used for study-level estimates of the subgroups. One can choose "rectangle", "ellipse", "diamond", "triangle", "cross", "plus", or "star". If NULL, symbols are generated automatically.
scale	Numeric scaling factor controlling study-symbol dimensions. The default is 0.02. Values below or above the default decrease or increase all symbol dimensions proportionally. Relative adjustments can be specified directly, for example, scale = 0.02 * 0.3 produces marker dimensions equal to 30 percent of the default.
size	Character string controlling display of study-level point estimates: "eb" Horizontal and vertical symbol dimensions are proportional to normalized inverse posterior standard errors of the study-specific empirical Bayes logit-specificity and logit-sensitivity estimates, respectively. "equal" All studies are shown with equal size. "sampsize" Horizontal and vertical symbol dimensions are both proportional to relative total study sample size. The same dimension measure is used horizontally and vertically because true disease status is latent. "eb_revman" RevMan-style graphical scaling applied to the inverse conditional posterior standard errors of the study-specific empirical Bayes logit-specificity and logit-sensitivity estimates. A common analysis-specific scaling constant is chosen so that the average larger dimension measure across studies equals nine before adding the fixed baseline dimension. This is an analogous graphical extension for latent-class models and is not an original Cochrane latent-class weighting method. "sampsize_revman" RevMan-style graphical scaling based on total study sample size. The same transformed total-sample-size measure is used horizontally and vertically.
nudge_legend	Numeric horizontal offset for the subgroup legend. More negative values move the legend further right, outside the plotting area. Values closer to zero move it closer to the panel. Default is -0.4.
specrange	A numeric vector of length 2 giving the range of specificities over which the HSROC curve is plotted. Defaults to c(0.7, 0.995).
col	Vector of colours used for subgroup-specific HSROC curves and study-level point estimates. If NULL, colours are generated automatically.

main	Character string giving the main title of the plot. Defaults to "Diagnostic Test Accuracy Meta-Analysis".
HSROC	if TRUE, the HSROC curve is added to the plot. Default is TRUE.
connectstudies	Whether the point estimates of two subgroups within the same study should be connected. Defaults to FALSE.
studyCI	Whether study-level confidence intervals should be displayed for the observed sensitivity and specificity estimates. Defaults to FALSE.
conflevel	Confidence level for the study-level confidence intervals. Default is 0.95.
studylabels	Whether study identifiers should be displayed next to the study-level estimates. Defaults to FALSE.
legend	Whether a legend should be displayed. Default is TRUE.
...	Additional graphical arguments passed to plotting functions.

Details

The plot is constructed on the ROC scale with sensitivity on the y-axis and specificity on the x-axis (displayed as 1 - false positive rate on a reversed axis).

Study-specific estimates are shown with subgroup-specific symbols and colours.

The following elements are displayed:

- Study-level sensitivity and specificity estimates by subgroup
- Subgroup-specific HSROC curves
- A legend identifying the subgroups

Value

No return value. Called for its side effect of producing a plot.

References

Liu, Y., Chen, Y., & Chu, H. (2015). A unification of models for meta-analysis of diagnostic accuracy studies without a gold standard. *Biometrics*, 71(2), 538-547. doi:10.1111/biom.12264

Freeman, S. C., Kerby, C. R., Patel, A., Cooper, N. J., Quinn, T., & Sutton, A. J. (2019). Development of an interactive web-based tool to conduct and interrogate meta-analysis of diagnostic test accuracy studies: MetaDTA. *BMC Medical Research Methodology*, 19, 81. doi:10.1186/s12874-0190724x

Harbord, R. M., Deeks, J. J., Egger, M., Whiting, P., & Sterne, J. A. C. (2007). A unification of models for meta-analysis of diagnostic accuracy studies. *Biostatistics*, 8(2), 239–251. doi:10.1093/biostatistics/kxl004

See Also

fitRutterGatsonisSubgroupLCA

print.HoyerAFT *Print Method for HoyerAFT Objects*

Description

Displays a concise summary of a fitted Hoyer AFT model, including distribution, number of studies, convergence status, and likelihood-based fit statistics.

Usage

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

Arguments

x	An object of class "HoyerAFT".
...	Further arguments (unused).

Value

Invisibly returns the input object.

See Also

summary.HoyerAFT

print.Reitsma *Print Method for Reitsma Objects*

Description

Displays a concise summary of a fitted Reitsma diagnostic test accuracy model, including number of studies, convergence status and likelihood-based fit statistics.

Usage

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

Arguments

x	An object of class "Reitsma".
...	Additional arguments (unused).

Value

Invisibly returns the input object.

See Also

summary.Reitsma

---

print.ReitsmaLCA *Print Method for ReitsmaLCA Objects*

Description

Displays a concise summary of a fitted Reitsma LCA model, including number of studies, convergence status, and likelihood-based fit statistics.

Usage

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

Arguments

x	An object of class "ReitsmaLCA".
...	Additional arguments (unused).

Value

Invisibly returns the input object.

See Also

summary.ReitsmaLCA

---

print.ReitsmaSubgroup *Print Method for ReitsmaSubgroup Objects*

Description

Displays a concise summary of a fitted Reitsma Subgroup diagnostic test accuracy model, including number of studies, convergence status, and likelihood-based fit statistics.

Usage

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

Arguments

x	An object of class "ReitsmaSubgroup".
...	Additional arguments (unused).

Value

Invisibly returns the input object.

See Also

summary.ReitsmaSubgroup

---

print.ReitsmaSubgroupLCA *Print Method for ReitsmaSubgroupLCA Objects*

Description

Displays a concise summary of a fitted ReitsmaSubgroupLCA model, including number of studies, convergence status, and likelihood-based fit statistics.

Usage

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

Arguments

x	An object of class "ReitsmaSubgroupLCA".
...	Additional arguments (unused).

Value

Invisibly returns the input object.

See Also

summary.ReitsmaSubgroupLCA

print.ReitsmaSubgroupTMB *Print Method for ReitsmaSubgroupTMB Objects*

Description

Displays a concise summary of a fitted ReitsmaSubgroupTMB diagnostic test accuracy model, including number of studies, convergence status and likelihood-based fit statistics.

Usage

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

Arguments

x	An object of class "ReitsmaSubgroupTMB".
...	Additional arguments (unused).

Value

Invisibly returns the input object.

See Also

summary.ReitsmaSubgroupTMB

print.ReitsmaTMB *Print Method for ReitsmaTMB Objects*

Description

Displays a concise summary of a fitted ReitsmaTMB diagnostic test accuracy model, including number of studies, convergence status and likelihood-based fit statistics.

Usage

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

Arguments

x	An object of class "ReitsmaTMB".
...	Additional arguments (unused).

Value

Invisibly returns the input object.

See Also

summary.ReitsmaTMB

---

print.RutterGatsonis *Print Method for RutterGatsonis Objects*

Description

Displays a concise summary of a fitted HSROC model, including number of studies, convergence status, and likelihood-based fit statistics.

Usage

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

Arguments

x	An object of class "RutterGatsonis".
...	Additional arguments (unused).

Value

Invisibly returns the input object.

See Also

summary.RutterGatsonis

---

print.RutterGatsonisLCA *Print Method for RutterGatsonisLCA Objects*

Description

Displays a concise summary of a fitted HSROC LCA model, including number of studies, convergence status, and likelihood-based fit statistics.

Usage

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

Arguments

x	An object of class "RutterGatsonisLCA".
...	Additional arguments (unused).

Value

Invisibly returns the input object.

See Also

summary.RutterGatsonisLCA

---

print.RutterGatsonisReg

Print Method for RutterGatsonisReg Objects

Description

Displays a concise summary of a fitted HSROC model, including number of studies, convergence status, and likelihood-based fit statistics.

Usage

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

Arguments

x	An object of class "RutterGatsonisReg".
...	Additional arguments (unused).

Value

Invisibly returns the input object.

See Also

summary.RutterGatsonisReg

print.RutterGatsonisSubgroup *Print Method for RutterGatsonisSubgroup Objects*

Description

Displays a concise summary of a fitted HSROC model, including number of studies, convergence status, and likelihood-based fit statistics.

Usage

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

Arguments

x	An object of class "RutterGatsonisSubgroup".
...	Additional arguments (unused).

Value

Invisibly returns the input object.

See Also

summary.RutterGatsonisSubgroup

print.RutterGatsonisSubgroupLCA *Print Method for RutterGatsonisSubgroupLCA Objects*

Description

Displays a concise summary of a fitted RutterGatsonisSubgroupLCA model, including number of studies, convergence status, and likelihood-based fit statistics.

Usage

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

Arguments

x	An object of class "RutterGatsonisSubgroupLCA".
...	Additional arguments (unused).

Value

Invisibly returns the input object.

See Also

summary.RutterGatsonisSubgroupLCA

---

print.summary.DTAmodel

Print a Diagnostic Test Accuracy Model Summary

Description

Prints summary objects returned by summary() methods for diagnostic test accuracy models.

Usage

```
## S3 method for class 'summary.DTAmodel'
print(x, digits = max(8L, getOption("digits") - 8L), ...)

## S3 method for class 'summary.HoyerAFT'
print(x, digits = max(8L, getOption("digits") - 8L), ...)

## S3 method for class 'summary.Reitsma'
print(x, digits = max(8L, getOption("digits") - 8L), ...)

## S3 method for class 'summary.ReitsmaTMB'
print(x, digits = max(8L, getOption("digits") - 8L), ...)

## S3 method for class 'summary.ReitsmaLCA'
print(x, digits = max(8L, getOption("digits") - 8L), ...)

## S3 method for class 'summary.ReitsmaSubgroup'
print(x, digits = max(8L, getOption("digits") - 8L), ...)

## S3 method for class 'summary.ReitsmaSubgroupTMB'
print(x, digits = max(8L, getOption("digits") - 8L), ...)

## S3 method for class 'summary.ReitsmaSubgroupLCA'
print(x, digits = max(8L, getOption("digits") - 8L), ...)

## S3 method for class 'summary.RutterGatsonis'
print(x, digits = max(8L, getOption("digits") - 8L), ...)

## S3 method for class 'summary.RutterGatsonisReg'
print(x, digits = max(8L, getOption("digits") - 8L), ...)
```

```
## S3 method for class 'summary.RutterGatsonisLCA'
print(x, digits = max(8L, getOption("digits") - 8L), ...)

## S3 method for class 'summary.RutterGatsonisSubgroup'
print(x, digits = max(8L, getOption("digits") - 8L), ...)

## S3 method for class 'summary.RutterGatsonisSubgroupLCA'
print(x, digits = max(8L, getOption("digits") - 8L), ...)
```

Arguments

x	A summary object inheriting from "summary.DTAmodel".
digits	Number of significant digits used for printing.
...	Additional arguments passed to printing methods.

Value

Invisibly returns x.

---

restructure_data *Construct Interval Data for Threshold-Based Bivariate Time-to-Event Models*

Description

Transforms study-level diagnostic test accuracy (DTA) data with multiple thresholds into interval-censored format suitable for likelihood-based modelling (Hoyer et al., 2018).

Usage

```
restructure_data(
  data,
  TP,
  FP,
  FN,
  TN,
  threshold,
  study,
  smallest,
  largest,
  testdirection = c("greater", "less")
)
```

Arguments

data	A data.frame containing study-level data.
TP	True positives (column name).
FP	False positives (column name).
FN	False negatives (column name).
TN	True negatives (column name).
threshold	The observed threshold value (column name). Must be positive and strictly increasing within each study.
study	Study identifier (column name).
smallest	Positive lower bound used to define the leftmost interval. Must be smaller than minimum threshold.
largest	Positive upper bound used to define the rightmost interval. Must be greater than maximum threshold.
testdirection	Direction of the test. Enter "greater" when larger test values indicate disease. Conversely, enter "less" when lower test values indicate disease (e.g. anaemia-type tests). Defaults to "greater".

Details

The function constructs:

- A left-censored interval (below the first threshold)
- Intermediate intervals between adjacent thresholds
- A right-censored interval (above the last threshold)

Event counts are derived from cumulative counts to represent the number of observations falling within each interval for diseased and non-diseased groups. Therefore, input counts must be cumulative over increasing thresholds within each study.

The function first validates that counts are numeric, non-negative integers and that threshold values are positive.

Within each study, total numbers of diseased (n1) and non-diseased (n0) individuals are required to be constant across thresholds. Intermediate interval counts are computed as differences between cumulative counts.

The log-scale midpoint (lcutmean) is provided to support initialization of random effects in subsequent Hoyer AFT models.

For testdirection = "greater", the function assumes that sensitivity decreases and specificity increases with increasing thresholds. For testdirection = "less", the reverse monotonicity is required. Internally, the function standardizes the definition of a positive test result so that it always corresponds to values above the threshold. For testdirection = "less", this is achieved by relabeling the observed counts. This does not affect the resulting sensitivity, specificity, or ROC curve, but ensures compatibility with the model formulation.

Value

A list with two components:

restructured A data frame with one row per constructed interval containing:

- **study** Study identifier
- **TP, TN, n1, n0** Original counts carried forward
- **threshold** Threshold associated with the interval
- **lowerB** Lower interval bound (NA for left-censored)
- **upperB** Upper interval bound (NA for right-censored)
- **events1** Number of diseased observations in the interval
- **events0** Number of non-diseased observations in the interval
- **ctype** Censoring type (1 = left, 2 = interval, 3 = right)
- **lcutmean** Midpoint of log-thresholds defining the interval

original The processed original data including (derived) quantities:

- **n1** Total number of diseased individuals (TP + FN)
- **n0** Total number of non-diseased individuals (TN + FP)
- **sens** Sensitivity (TP / n1)
- **spec** Specificity (TN / n0)
- **fpr** False positive rate (FP / n0)
- **testdirection** As specified by `testdirection`

References

Hoyer, A., Hirt, S., Kuss, O. (2018). Meta-analysis of full ROC curves using bivariate time-to-event models for interval-censored data. *Research Synthesis Methods*, 9(1), 62-72. doi:10.1002/jrsm.1273

Examples

```
data("diabetes")
res <- restructure_data(
  data = diabetes,
  TP = TP,
  FP = FP,
  FN = FN,
  TN = TN,
  threshold = threshold,
  study = study,
  smallest = 2,
  largest = 10
)
```

RF *RF Dataset*

Description

This is the RF dataset from Nishimura (2007) from a review of rheumatoid factor (RF) to diagnose rheumatoid arthritis.

Usage

```
RF
```

Format

A data frame with 50 rows and 8 variables:

study Study identifier

year Year of the study

TP Number of true positives

FP Number of false positives

FN Number of false negatives

TN Number of true negatives

cutoff Threshold used in U/mL for test positivity

method Different methods used to perform the test

Source

Nishimura, K. et al. (2007). *Meta-analysis: diagnostic accuracy of anti-cyclic citrullinated peptide antibody and rheumatoid factor for rheumatoid arthritis*. Annals of Internal Medicine, 146(11), 392-403. doi:10.7326/0003481914611200706050000008

schuetz *Schuetz Dataset*

Description

This is the schuetz dataset from Schuetz (2010) from a meta-analysis of non-invasive coronary angiography using computer tomography (CT) versus magnetic resonance imaging (MRI)

Usage

```
schuetz
```

Format

A data frame with 108 rows and 7 variables:

test Which test was used, CT or MRI

study Study identifier

TP Number of true positives

FP Number of false positives

FN Number of false negatives

TN Number of true negatives

indirect whether the comparison is indirect (=1) or direct (=0)

Source

Schuetz, K., et al. (2010). *Meta-analysis: noninvasive coronary angiography using computer tomography versus magnetic resonance imaging.* Annals of Internal Medicine, 152(3), 167-177. doi:10.7326/0003481915232010020200008

---

summary.HoyerAFT *Summary Method for HoyerAFT Objects*

Description

Extracts and returns the summary information stored in a fitted `HoyerAFT` model object.

Usage

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

Arguments

`object`	An object of class `"HoyerAFT"`, typically the result of a call to `fitHoyerAFT`.
`...`	Additional arguments (currently unused).

Details

This method is part of the standard S3 `summary()` generic and provides access to summary statistics computed from the fitted model, as stored in the `sdreport2` and `sensspec` component of the object.

Value

A list of class `"summary.HoyerAFT"` with two data frames containing summary statistics derived from the fitted model.

- `sdreport2`: Parameter estimates with standard errors as returned from TMB reported parameters.
- `sensspec`: Estimated sensitivity and specificity with confidence intervals at the specified thresholds.

See Also

fitHoyer fitHoyerAFT

---

summary.Reitsma *Summary Method for Reitsma Objects*

Description

Extracts key results from an object of class "Reitsma", including parameter estimates, sensitivity and specificity summaries, and recovered HSROC parameters from the Rutter–Gatsonis parameterization.

Usage

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

Arguments

object	An object of class "Reitsma" as returned by fitReitsma.
...	Additional arguments (currently ignored).

Value

A list of class "summary.Reitsma" with the following components:

- estimates: Parameter estimates with standard errors.
- sensspec: Estimated sensitivity and specificity with confidence intervals.
- RutterGatsonis_recovered: Recovered parameters in the Rutter-Gatsonis (HSROC) parameterization.

See Also

fitReitsma

summary.ReitsmaLCA *Summary Method for ReitsmaLCA Objects*

Description

Extracts key results from an object of class "ReitsmaLCA", including parameter estimates, sensitivity and specificity summaries, and recovered HSROC parameters from the Rutter–Gatsonis parameterization.

Usage

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

Arguments

object	An object of class "ReitsmaLCA" as returned by fitReitsmaLCA.
...	Additional arguments (currently ignored).

Value

A list of class "summary.ReitsmaLCA" with the following components:

- estimates: Parameter estimates with standard errors.
- sensspec: Estimated sensitivity and specificity with confidence intervals.
- prevref: Estimated (average) prevalence and reference standard sensitivity/specificity with confidence intervals.
- RutterGatsonis_recovered: Recovered parameters in the Rutter-Gatsonis (HSROC) parameterization.

See Also

fitReitsmaLCA

summary.ReitsmaSubgroup *Summary Method for ReitsmaSubgroup Objects*

Description

Extracts key results from an object of class "ReitsmaSubgroup", including parameter estimates, sensitivity and specificity summaries, and recovered HSROC parameters from the Rutter–Gatsonis parameterization.

Usage

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

Arguments

object	An object of class "ReitsmaSubgroup" as returned by fitReitsmaSubgroup.
...	Additional arguments (currently ignored).

Value

A list of class "summary.ReitsmaSubgroup" with the following components:

- estimates: Parameter estimates with standard errors.
- sensspec: Estimated sensitivity and specificity with confidence intervals.
- RutterGatsonis_recovered: Recovered parameters in the Rutter-Gatsonis (HSROC) parameterization.
- subgroups Subgroup names.

See Also

fitReitsmaSubgroup

---

summary.ReitsmaSubgroupLCA

Summary Method for ReitsmaSubgroupLCA Objects

Description

Extracts key results from an object of class "ReitsmaSubgroupLCA", including parameter estimates, sensitivity and specificity summaries, and recovered HSROC parameters from the Rutter–Gatsonis parameterization.

Usage

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

Arguments

object	An object of class "ReitsmaSubgroupLCA" as returned by fitReitsmaSubgroupLCA.
...	Additional arguments (currently ignored).

Value

A list of class "summary.ReitsmaSubgroupLCA" with the following components:

- estimates: Parameter estimates with standard errors.
- sensspec: Estimated sensitivity and specificity with confidence intervals.
- prevref: Estimated (average) prevalence and reference standard sensitivity/specificity with confidence intervals.
- RutterGatsonis_recovered: Recovered parameters in the Rutter-Gatsonis (HSROC) parameterization.

See Also

fitReitsmaSubgroupLCA

---

summary.ReitsmaSubgroupTMB

Summary Method for ReitsmaSubgroupTMB Objects

Description

Extracts key results from an object of class "ReitsmaSubgroupTMB", including parameter estimates, sensitivity and specificity summaries, and recovered HSROC parameters from the Rutter–Gatsonis parameterization.

Usage

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

Arguments

object	An object of class "ReitsmaSubgroupTMB" as returned by fitReitsmaSubgroupTMB.
...	Additional arguments (currently ignored).

Value

A list of class "summary.ReitsmaSubgroupTMB" with the following components:

- estimates: Parameter estimates with standard errors.
- sensspec: Estimated sensitivity and specificity with confidence intervals.
- RutterGatsonis_recovered: Recovered parameters in the Rutter-Gatsonis (HSROC) parameterization.
- subgroups Subgroup names.

See Also

fitReitsmaSubgroupTMB

summary.ReitsmaTMB *Summary Method for ReitsmaTMB Objects*

Description

Extracts key results from an object of class "ReitsmaTMB", including parameter estimates, sensitivity and specificity summaries, and recovered HSROC parameters from the Rutter–Gatsonis parameterization.

Usage

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

Arguments

object	An object of class "ReitsmaTMB" as returned by fitReitsmaTMB.
...	Additional arguments (currently ignored).

Value

A list of class "summary.ReitsmaTMB" with the following components:

- estimates: Parameter estimates with standard errors.
- sensspec: Estimated sensitivity and specificity with confidence intervals.
- RutterGatsonis_recovered: Recovered parameters in the Rutter-Gatsonis (HSROC) parameterization.

See Also

fitReitsmaTMB

summary.RutterGatsonis *Summary Method for RutterGatsonis Objects*

Description

This method extracts key components from a fitted HSROC model object returned by fitRutterGatsonis. It returns parameter estimates, sensitivity/specificity summaries, and the recovered Reitsma parameterization.

Usage

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

Arguments

object	An object of class "RutterGatsonis" as returned by fitRutterGatsonis.
...	Additional arguments (currently unused).

Details

Provides a concise summary of a fitted "RutterGatsonis" model.

Value

A list of class "summary.RutterGatsonis" containing the following components:

- estimates Parameter estimates with standard errors as returned from TMB reported parameters.
- sensspec Estimated sensitivity at the specified specificity, including confidence intervals.
- Reitsma_recovered Recovered parameters in the Reitsma parameterization.

See Also

fitRutterGatsonis

---

summary.RutterGatsonisLCA *Summary Method for RutterGatsonisLCA Objects*

Description

This method extracts key components from a fitted HSROC model object returned by fitRutterGatsonisLCA. It returns parameter estimates, sensitivity/specificity summaries, and the recovered Reitsma parameterization.

Usage

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

Arguments

object	An object of class "RutterGatsonisLCA" as returned by fitRutterGatsonisLCA.
...	Additional arguments (currently unused).

Details

Provides a concise summary of a fitted "RutterGatsonisLCA" model.

Value

A list of class "summary.RutterGatsonisLCA" containing the following components:

- estimates: Parameter estimates with standard errors as returned from TMB reported parameters.
- sensspec: Estimated index test sensitivity at the specified specificity, including confidence intervals.
- prevref: Estimated (average) prevalence and reference standard sensitivity/specificity with confidence intervals.
- Reitsma_recovered: Recovered parameters in the Reitsma parameterization.

See Also

fitRutterGatsonisLCA

---

summary.RutterGatsonisReg

Summary Method for RutterGatsonisReg Objects

Description

This method extracts key components from a fitted HSROC model object returned by fitRutterGatsonisReg. It returns parameter estimates, sensitivity/specificity summaries.

Usage

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

Arguments

object	An object of class "RutterGatsonisReg" as returned by fitRutterGatsonisReg.
...	Additional arguments (currently unused).

Details

Provides a concise summary of a fitted "RutterGatsonisReg" model.

Value

A list of class "summary.RutterGatsonisReg" containing the following components:

- estimates Parameter estimates with standard errors as returned from TMB reported parameters.
- sensspec Estimated sensitivity at the specified specificity, including confidence intervals.

See Also

fitRutterGatsonisReg

summary.RutterGatsonisSubgroup
Summary Method for RutterGatsonisSubgroup Objects

Description

This method extracts key components from a fitted HSROC model object returned by fitRutterGatsonisSubgroup. It returns parameter estimates and sensitivity/specificity summaries.

Usage

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

Arguments

object	An object of class "RutterGatsonisSubgroup" as returned by fitRutterGatsonisSubgroup.
...	Additional arguments (currently unused).

Details

Provides a concise summary of a fitted "RutterGatsonisSubgroup" model.

Value

A list of class "summary.RutterGatsonisSubgroup" containing the following components:

- estimates Parameter estimates with standard errors as returned from TMB reported parameters.
- sensspec Estimated sensitivity at the specified specificity, including confidence intervals.
- Reitsma_recovered Recovered parameters in the Reitsma parameterization.
- subgroups Subgroup names.

See Also

fitRutterGatsonisSubgroup

summary.RutterGatsonisSubgroupLCA *Summary Method for RutterGatsonisSubgroupLCA Objects*

Description

Extracts key results from an object of class "RutterGatsonisSubgroupLCA", including parameter estimates, sensitivity and specificity summaries, and recovered HSROC parameters from the Rutter–Gatsonis parameterization.

Usage

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

Arguments

object	An object of class "RutterGatsonisSubgroupLCA" as returned by fitRutterGatsonisSubgroupLCA.
...	Additional arguments (currently ignored).

Value

A list of class "summary.RutterGatsonisSubgroupLCA" with the following components:

- estimates: Parameter estimates with standard errors.
- sensspec: Estimated index test sensitivity at the specified specificity, including confidence intervals.
- prevref: Estimated (average) prevalence and reference standard sensitivity/specificity with confidence intervals.
- Reitsma_recovered: Recovered parameters in the Reitsma parameterization.

See Also

fitRutterGatsonisSubgroupLCA

tub *Tub Dataset*

Description

This is the tub dataset from Kohli et al. (2018) from a meta-analysis examining the accuracy of the GeneXpert test for tuberculosis meningitis. In each study the index test was GeneXpert and the (imperfect) reference standard was culture.

Usage

```
tub
```

Format

A data frame with 29 rows and 5 variables:

id Study identifier

y11 Number testing positive with both tests

y10 Number testing positive with index test but negative with reference test

y01 Number testing negative with index test but positive with reference test

y00 Number testing negative with both tests

Note

The dataset was taken from the supplementary material of the Cochrane Handbook for Systematic Reviews of Diagnostic Test Accuracy Studies.

Source

Deeks, J. J., Bossuyt, P. M., Leeflang, M. M., & Takwoingi, Y. (editors) (2023). *Cochrane Handbook for Systematic Reviews of Diagnostic Test Accuracy.* Version 2.0 (updated July 2023). Cochrane.

Kohli, M. et al. (2018). *Xpert MTB/RIF assay for extrapulmonary tuberculosis and rifampicin resistance*. Cochrane Database of Systematic Reviews 2018, 8, CD012768. doi:10.1002/14651858.CD012768.pub2

---

vcov.dtametaTMB *Extract Variance-Covariance Matrix*

Description

Returns the variance-covariance matrix of the estimated model parameters.

Usage

```
## S3 method for class 'DTAmodel'
vcov(object, ...)

## S3 method for class 'Reitsma'
vcov(object, ...)

## S3 method for class 'ReitsmaSubgroup'
vcov(object, ...)

## S3 method for class 'ReitsmaLCA'
vcov(object, ...)

## S3 method for class 'ReitsmaSubgroupLCA'
vcov(object, ...)
```

Arguments

`object`	A fitted model object.
`...`	Not currently used.

Value

A variance-covariance matrix corresponding to the parameters returned by `coef()`.

Note

For `ReitsmaSubgroup` models, the returned variance-covariance matrix corresponds to the cell-means parameterization returned by `coef()`.

See Also

`coef.dtametaTMB()`

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