Package ‘pROC’

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Title display and analyze ROC curves

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Description Tools for visualizing, smoothing and comparing receiver operating characteristic (ROC curves). (Partial) area under the curve (AUC) can be compared with statistical tests based on U-statistics or bootstrap. Confidence intervals can be computed for (p)AUC or ROC curves.

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URL http://expasy.org/tools/pROC/

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R topics documented:

`pROC-package` *pROC*

Description

Tools for visualizing, smoothing and comparing receiver operating characteristic (ROC curves). (Partial) area under the curve (AUC) can be compared with statistical tests based on U-statistics or bootstrap. Confidence intervals can be computed for (p)AUC or ROC curves.

Details

The basic unit of the pROC package is the `roc` function. It will build a ROC curve, smooth it if requested (if `smooth=TRUE`), compute the AUC (if `auc=TRUE`), the confidence interval (CI) if requested (if `ci=TRUE`) and plot the curve if requested (if `plot=TRUE`).

The `roc` function will call `smooth.roc`, `auc`, `ci` and `plot` as necessary. See these individual functions for the arguments that can be passed to them through `roc`. These function can be called separately.

Two paired ROC curves (that is `roc` objects with the same `response`) can be compared with the `roc.test` function.

Citation

If you use pROC in published research, please cite the following paper:

Xavier Robin, Natacha Turck, Alexandre Hainard, Natalia Tiberti, Frédérique Lisacek, Jean-Charles Sanchez and Markus Müller (2011). “pROC: an open-source package for R and S+ to analyze and compare ROC curves”. *BMC Bioinformatics*, **12**, p. 77. DOI: 10.1186/1471-2105-12-77

Type `citation("pROC")` for a BibTeX entry.

The authors would be glad to hear how pROC is employed. You are kindly encouraged to notify Xavier Robin <Xavier.Robin@unige.ch> about any work you publish.

Abbreviations

The following abbreviations are employed extensively in this package:

- ROC: receiver operating characteristic
- AUC: area under the ROC curve
- pAUC: partial area under the ROC curve
- CI: confidence interval
- SP: specificity
- SE: sensitivity

Functions

`roc`	Build a ROC curve
`are.paired`	Dertermine if two ROC curves are paired
`auc`	Compute the area under the ROC curve
`ci`	Compute confidence intervals of a ROC curve
`ci.auc`	Compute the CI of the AUC
`ci.se`	Compute the CI of sensitivities at given specificities
`ci.sp`	Compute the CI of specificities at given sensitivities
`ci.thresholds`	Compute the CI of specificity and sensitivity of thresholds
`coords`	Coordinates of a ROC curve
`lines.roc`	Add a ROC line to a ROC plot
`plot.ci`	Plot CIs
`plot`	Plot a ROC curve
`print`	Print a ROC curve object
`roc.test`	Compare the AUC of two correlated ROC curves
`smooth`	Smooth a ROC curve

Dataset

This package comes with a dataset of 141 patients with aneurysmal subarachnoid hemorrhage: `aSAH`.

Installing and using

To install this package, make sure you are connected to the internet and issue the following command in the R prompt:

```
install.pkgutils()
library(pkgutils)
install.packages("pROC")
```

To load the package in S+:

```
        library(pROC)
```

Author(s)

Xavier Robin, Natacha Turck, Jean-Charles Sanchez and Markus Müller

Maintainer: Xavier Robin <Xavier.Robin@unige.ch>

References

Tom Fawcett (2006) "An introduction to ROC analysis". *Pattern Recognition Letters* **27**, 861–874. DOI: 10.1016/j.patrec.2005.10.010

Xavier Robin, Natacha Turck, Alexandre Hainard, *et al.* (2011) "pROC: an open-source package for R and S+ to analyze and compare ROC curves". *BMC Bioinformatics*, **7**, 77. DOI: 10.1186/1471-2105-12-77

See Also

CRAN packages **ROCR**, **verification** or Bioconductor's **roc**.

Examples

```
data(aSAH)

# Build a ROC object and compute the AUC
roc(aSAH$outcome, aSAH$s100b)
roc(outcome ~ s100b, aSAH)

# Smooth ROC curve
roc(outcome ~ s100b, aSAH, smooth=TRUE)

# more options, CI and plotting
roc1 <- roc(aSAH$outcome,
            aSAH$s100b, percent=TRUE,
            # arguments for auc
            partial.auc=c(100, 90), partial.auc.correct=TRUE,
            partial.auc.focus="sens",
            # arguments for ci
            ci=TRUE, boot.n=100, ci.alpha=0.9, stratified=FALSE,
            # arguments for plot
            plot=TRUE, auc.polygon=TRUE, max.auc.polygon=TRUE, grid=TRUE,
            print.auc=TRUE, show.thres=TRUE)

# Add to an existing plot. Beware of 'percent' specification!
roc2 <- roc(aSAH$outcome, aSAH$wfns,
            plot=TRUE, add=TRUE, percent=roc1$percent)

## Confidence intervals ##

# CI of the AUC
ci(roc2)
```

```
## Not run:
# CI of the curve
sens.ci <- ci.se(roc1, specificities=seq(0, 100, 5))
plot(sens.ci, type="shape", col="lightblue")
plot(sens.ci, type="bars")

## End(Not run)

# need to re-add roc2 over the shape
plot(roc2, add=T)

## Not run:
# CI of thresholds
plot(ci.thresholds(roc2))

## End(Not run)


## Comparisons ##

# Test on the whole AUC
roc.test(roc1, roc2, reuse.auc=FALSE)

## Not run:
# Test on a portion of the whole AUC
roc.test(roc1, roc2, reuse.auc=FALSE, partial.auc=c(100, 90),
         partial.auc.focus="se", partial.auc.correct=TRUE)

# With modified bootstrap parameters
roc.test(roc1, roc2, reuse.auc=FALSE, partial.auc=c(100, 90),
         partial.auc.correct=TRUE, boot.n=1000, boot.stratified=FALSE)

## End(Not run)
```

`are.paired` *Are two ROC curves paired?*

Description

This function determines if two ROC curves can be paired.

Usage

```
are.paired(x, ...)
## S3 method for class 'auc'
are.paired(roc1, roc2, ...)
## S3 method for class 'smooth.roc'
are.paired(roc1, roc2, ...)
## S3 method for class 'roc'
```

```
are.paired(roc1, roc2, return.paired.rocs=FALSE,
  reuse.auc = TRUE, reuse.ci = FALSE, reuse.smooth=TRUE, ...)
```

Arguments

`x`	a roc object from the roc function (for roc.test.roc), an auc from the auc function (for roc.test.auc) a formula (for roc.test.formula) or a response vector (for roc.test.default).
`roc1, roc2`	the two ROC curves to compare. Either "roc", "auc" or "smooth.roc" objects (types can be mixed).
`return.paired.rocs`	if `TRUE` and the ROC curves can be paired, the two paired ROC curves with `NA`s removed will be returned.
`reuse.auc, reuse.ci, reuse.smooth`	if `return.paired.rocs=TRUE`, determines if `auc`, `ci` and `smooth.roc` should be re-computed (with the same parameters than the original ROC curves)
`...`	additionnal arguments for `are.paired.roc`. Ignored in `are.paired.roc`

Details

Two ROC curves are paired if they are built on two variables observed on the same sample.

In practice, the paired status is granted if the `response` vector of both ROC curves are identical. If the `responses` are different, this can be due to missing values differing between the curves. In this case, the function will strip all `NA`s in both curves and check for identity again.

It can raise false positives if the responses are identical but correspond to different patients.

Value

`TRUE` if `roc1` and `roc2` are paired, `FALSE` otherwise.

In addition, if `TRUE` and `return.paired.rocs=TRUE`, the following atributes are defined:

`roc1, roc2`	the two ROC curve with all `NA`s values removed in both curves.

See Also

`roc`, `roc.test`

Examples

```
data(aSAH)
aSAH.copy <- aSAH

# artificially insert NAs for demonstration purposes
aSAH.copy$outcome[42] <- NA
aSAH.copy$s100b[24] <- NA
aSAH.copy$ndka[1:10] <- NA

# Call roc() on the whole data
roc1 <- roc(aSAH.copy$outcome, aSAH.copy$s100b)
```

```
roc2 <- roc(aSAH.copy$outcome, aSAH.copy$ndka)
# are.paired can still find that the curves were paired
are.paired(roc1, roc2) # TRUE

# Removing the NAs manually before passing to roc() un-pairs the ROC curves
nas <- is.na(aSAH.copy$outcome) | is.na(aSAH.copy$ndka)
roc2b <- roc(aSAH.copy$outcome[!nas], aSAH.copy$ndka[!nas])
are.paired(roc1, roc2b) # FALSE

# Getting the two paired ROC curves with additional smoothing and ci options
roc2$ci <- ci(roc2)
paired <- are.paired(smooth(roc1), roc2, return.paired.rocs=TRUE, reuse.ci=TRUE)
paired.roc1 <- attr(paired, "roc1")
paired.roc2 <- attr(paired, "roc2")
```

`aSAH` *Subarachnoid hemorrhage data*

Description

This dataset summarizes several clinical and one laboratory variable of 113 patients with an aneurysmal subarachnoid hemorrhage.

Usage

```
aSAH
```

Format

A data.frame containing 113 observations of 7 variables.

Source

Natacha Turck, Laszlo Vutskits, Paola Sanchez-Pena, Xavier Robin, Alexandre Hainard, Marianne Gex-Fabry, Catherine Fouda, Hadiji Bassem, Markus Mueller, Frédérique Lisacek, Louis Puybasset and Jean-Charles Sanchez (2010) “A multiparameter panel method for outcome prediction following aneurysmal subarachnoid hemorrhage”. *Intensive Care Medicine* **36**(1), 107–115. DOI: 10.1007/s00134-009-1641-y.

See Also

Other examples can be found in all the documentation pages of this package: `roc`, `auc`, `ci`, `ci.auc`, `ci.se`, `ci.sp`, `ci.thresholds`, `coords`, `plot.ci`, `plot.roc`, `print.roc`, `roc.test` and `smooth`.

An example analysis with pROC is shown in:

Xavier Robin, Natacha Turck, Alexandre Hainard, *et al.* (2011) “pROC: an open-source package for R and S+ to analyze and compare ROC curves”. *BMC Bioinformatics*, **7**, 77. DOI: 10.1186/1471-2105-12-77

Examples

```
# load the dataset
data(aSAH)

# Gender, outcome and set
with(aSAH, table(gender, outcome))

# Age
with(aSAH, by(age, outcome, mean))
with(aSAH, by(age, outcome,
     function(x) sprintf("mean: %.1f (±%.1f), median: %.1f (%i-%i)",
                         mean(x), sd(x), median(x), min(x), max(x))))

# WFNS score
with(aSAH, table(wfns=ifelse(wfns<=2, "1-2", "3-4-5"), outcome))
```

`auc` *Compute the area under the ROC curve*

Description

This function computes the numeric value of area under the ROC curve (AUC) with the trapezoidal rule. Two syntaxes are possible: one object of class "roc", or either two vectors (response, predictor) or a formula (response~predictor) as in the `roc` function. By default, the total AUC is computed, but a portion of the ROC curve can be specified with `partial.auc`.

Usage

```
auc(x, ...)
## S3 method for class 'roc'
auc(roc, partial.auc=FALSE, partial.auc.focus=c("specificity",
"sensitivity"), partial.auc.correct=FALSE, ...)
## S3 method for class 'smooth.roc'
auc(smooth.roc, ...)
## S3 method for class 'formula'
auc(formula, data, ...)
## Default S3 method:
auc(response, predictor, ...)
```

Arguments

`x`	a roc object from the roc function (for auc.roc), a smoothed roc object from the smoothed.roc function (for auc.smooth.roc) a formula (for auc.formula) or a response vector (for auc.default).
`roc, smooth.roc`	a "roc" object from the `roc` function, or a "smooth.roc" object from the `smooth.roc` function.

`response, predictor`	arguments for the `roc` function.
`formula, data`	a formula (and possibly a data object) of type response~predictor for the `roc` function.
`partial.auc`	either `FALSE` (default: consider total area) or a numeric vector of length 2: boundaries of the AUC to consider in [0,1] (or [0,100] if percent is `TRUE`).
`partial.auc.focus`	if `partial.auc` is not `FALSE` and a partial AUC is computed, specifies if `partial.auc` specifies the bounds in terms of specificity (default) or sensitivity. Can be shortened to spec/sens or even sp/se. Ignored if `partial.auc=FALSE`.
`partial.auc.correct`	logical indicating if the correction of AUC must be applied in order to have a maximal AUC of 1.0 and a non-discriminant AUC of 0.5 whatever the `partial.auc` defined. Ignored if `partial.auc=FALSE`. Default: `FALSE`.
`...`	further arguments passed to or from other methods, especially arguments for `roc` when calling `auc.default` or `auc.formula`. Note that the `auc` argument of `roc` is not allowed. Unused in `auc.roc`.

Details

This function is typically called from `roc` when `auc=TRUE` (default). It is also used by `ci`. When it is called with two vectors (response, predictor) or a formula (response~predictor) arguments, the `roc` function is called and only the AUC is returned.

By default, the total area under the curve is computed, but you can specify a partial AUC with the `partial.auc` argument. It specifies the bounds of specificity or sensitivity (depending on `partial.auc.focus`) between which the AUC will be computed. As it specifies specificities or sensitivities, you must adapt it accordingly to the 'percent' specification (see details in `roc`).

`partial.auc.focus` is ignored if `partial.auc=FALSE` (default). If a partial AUC is computed, `partial.auc.focus` specifies if the bounds specified in `partial.auc` must be interpreted as sensitivity or specificity. Any other value will produce an error.

`partial.auc.correct` is ignored if `partial.auc=FALSE` (default). If `TRUE`, the correction by McClish will be applied:

$$\frac{1 + \frac{auc - min}{max - min}}{2}$$

where min is the value of the non-discriminant AUC in the region and max is the maximum possible AUC in the region. With this correction, the AUC will be 0.5 if non discriminant and 1.0 if maximal, whatever the region defined. Fully compatible with `percent`.

There is no difference in the computation of the area under a smoothed ROC curve.

Value

The numeric AUC value, of class "auc", in fraction of the area in percent if `percent=TRUE`, with the following attributes:

`partial.auc`	if the AUC is full (FALSE) or partial (and in this case the bounds), as defined in argument.
`partial.auc.focus`	only for a partial AUC, if the bound specifies the sensitivity or specificity, as defined in argument.
`partial.auc.correct`	only for a partial AUC, was it corrected? As defined in argument.
`percent`	whether the AUC is given in percent or fraction.
`roc`	the original ROC curve, as a "roc" object.

References

Tom Fawcett (2006) "An introduction to ROC analysis". *Pattern Recognition Letters* **27**, 861–874. DOI: 10.1016/j.patrec.2005.10.010.

Donna Katzman McClish (1989) "Analyzing a Portion of the ROC Curve". *Medical Decision Making* **9**(3), 190–195. DOI: 10.1177/0272989X8900900307

Xavier Robin, Natacha Turck, Alexandre Hainard, *et al.* (2011) "pROC: an open-source package for R and S+ to analyze and compare ROC curves". *BMC Bioinformatics*, **7**, 77. DOI: 10.1186/1471-2105-12-77

See Also

`roc`, `ci.auc`

Examples

```
data(aSAH)

# Syntax (response, predictor):
auc(aSAH$outcome, aSAH$s100b)

# With a roc object:
rocobj <- roc(aSAH$outcome, aSAH$s100b)
# Full AUC:
auc(rocobj)
# Partial AUC:
auc(rocobj, partial.auc=c(1, .8), partial.auc.focus="se", partial.auc.correct=TRUE)

# Alternatively, you can get the AUC directly from roc():
roc(aSAH$outcome, aSAH$s100b)$auc
roc(aSAH$outcome, aSAH$s100b,
    partial.auc=c(1, .8), partial.auc.focus="se",
    partial.auc.correct=TRUE)$auc
```

`ci` *Compute the confidence interval of a ROC curve*

Description

This function computes the confidence interval (CI) of a ROC curve. The `of` argument controls the type of CI that will be computed. By default, the 95% CI are computed with 2000 stratified bootstrap replicates.

Usage

```
ci(x, ...)
## S3 method for class 'roc'
ci(roc, of = c("auc", "thresholds", "sp", "se"), ...)
## S3 method for class 'smooth.roc'
ci(smooth.roc, of = c("auc", "sp", "se"), ...)
## S3 method for class 'formula'
ci(formula, data, ...)
## Default S3 method:
ci(response, predictor, ...)
```

Arguments

`x`	a roc object from the roc function (for ci.roc), a formula (for ci.formula) or a response vector (for ci.default).
`roc, smooth.roc`	a "roc" object from the `roc` function, or a "smooth.roc" object from the `smooth.roc` function.
`response, predictor`	arguments for the `roc` function.
`formula, data`	a formula (and possibly a data object) of type response~predictor for the `roc` function.
`of`	The type of confidence interval. One of "auc", "thresholds", "sp" or "se". Note that confidence interval on "thresholds" are not available for smoothed ROC curves.
`...`	further arguments passed to or from other methods, especially `auc`, `roc`, and the specific `ci` functions `ci.auc`, `ci.se`, `ci.sp` and `ci.thresholds`.

Details

`ci.formula` and `ci.default` are convenience methods that build the ROC curve (with the `roc` function) before calling `ci.roc`. You can pass them arguments for both `roc` and `ci.roc`. Simply use `ci` that will dispatch to the correct method.

This function is typically called from `roc` when `ci=TRUE` (not by default). Depending on the `of` argument, the specific `ci` functions `ci.auc`, `ci.thresholds`, `ci.sp` or `ci.se` are called.

Value

The return value of the specific `ci` functions `ci.auc`, `ci.thresholds`, `ci.sp` or `ci.se`, depending on the `of` argument.

References

Xavier Robin, Natacha Turck, Alexandre Hainard, *et al.* (2011) “pROC: an open-source package for R and S+ to analyze and compare ROC curves”. *BMC Bioinformatics*, **7**, 77. DOI: 10.1186/1471-2105-12-77.

See Also

`roc`, `auc`, `ci.auc`, `ci.thresholds`, `ci.sp`, `ci.se`

Examples

```
data(aSAH)

# Syntax (response, predictor):
ci(aSAH$outcome, aSAH$s100b)

# With a roc object:
rocobj <- roc(aSAH$outcome, aSAH$s100b)

# Of an AUC
ci(rocobj)
ci(rocobj, of="auc")
# this is strictly equivalent to:
ci.auc(rocobj)

# Of thresholds, sp, se...
## Not run:
ci(rocobj, of="thresholds")
ci(rocobj, of="thresholds", thresholds=0.51)
ci(rocobj, of="thresholds", thresholds="all")
ci(rocobj, of="sp", sensitivities=c(.95, .9, .85))
ci(rocobj, of="se")

## End(Not run)

# Alternatively, you can get the CI directly from roc():
rocobj <- roc(aSAH$outcome, aSAH$s100b, ci=TRUE, of="auc")
rocobj$ci
```

`ci.auc` *Compute the confidence interval of the AUC*

Description

This function computes the confidence interval (CI) of an area under the curve (AUC). By default, the 95% CI is computed with 2000 stratified bootstrap replicates.

Usage

```
ci.auc(x, ...)
## S3 method for class 'roc'
ci.auc(roc, conf.level=0.95, method=c("delong",
"bootstrap"), boot.n = 2000, boot.stratified = TRUE, reuse.auc=TRUE,
...)
## S3 method for class 'smooth.roc'
ci.auc(smooth.roc, conf.level=0.95, boot.n=2000,
boot.stratified=TRUE, reuse.auc=TRUE, ...)
## S3 method for class 'auc'
ci.auc(auc, ...)
## S3 method for class 'formula'
ci.auc(formula, data, ...)
## Default S3 method:
ci.auc(response, predictor, ...)
```

Arguments

`x`	a roc object from the `roc` or `smooth.roc` functions (for `ci.auc.roc` or `ci.auc.smooth.roc`), a formula (for `ci.auc.formula`) or a response vector (for `ci.auc.default`).
`roc, smooth.roc`	a “roc” object from the `roc` function, or a “smooth.roc” object from the `smooth.roc` function.
`auc`	an “auc” object from the `auc` function.
`response, predictor`	arguments for the `roc` function.
`formula, data`	a formula (and possibly a data object) of type response~predictor for the `roc` function.
`conf.level`	the width of the confidence interval as [0,1], never in percent. Default: 0.95, resulting in a 95% CI.
`method`	the method to use, either “delong” or “bootstrap”. The first letter is sufficient. If omitted, the appropriate method is selected as explained in details.
`boot.n`	the number of bootstrap replicates. Default: 2000.
`boot.stratified`	should the bootstrap be stratified (default, same number of cases/controls in each replicate than in the original sample) or not.
`reuse.auc`	if `TRUE` (default) and the “roc” object contains an “auc” field, re-use these specifications for the test. If false, use optional `...` arguments to `auc`. See details.

`...`	further arguments passed to or from other methods, especially arguments for `roc` and `roc.test.roc` when calling `roc.test.default` or `roc.test.formula`. Arguments for `auc` if applicable.

Details

This function computes the CI of an AUC. Two methods are available: “delong” and “bootstrap” with the parameters defined in “roc$auc” to compute a CI. When it is called with two vectors (response, predictor) or a formula (response~predictor) arguments, the `roc` function is called to build the ROC curve first.

Default is to use “delong” method except for comparison of partial AUC and smoothed curves, where `bootstrap` is used. Using “delong” for partial AUC and smoothed ROCs is not supported in pROC (with smoothed ROCs, `method` is ignored, otherwise for pAUC a warning is produced and “bootstrap” is employed instead).

With `method="bootstrap"`, the function calls `auc` `boot.n` times, according to the method described by Carpenter and Bithell (2000). `boot.n` bootstrap replicates are drawn. Stratification of bootstrap can be controlled with `boot.stratified`. In stratified bootstrap, each replicate contains the same number of cases and controls than the original sample. Stratification is especially useful if one group has only little observations, or if groups are not balanced. Higher numbers of `boot.n` will give a more precise estimate of the CI, but take more time to compute. 2000 is recommanded by Carpenter and Bithell.

For smoothed ROC curves, smoothing is performed again at each bootstrap replicate with the parameters originally provided. If a density smoothing was performed with user-provided `density.cases` or `density.controls` the bootstrap cannot be performed and an error is issued.

With `method="delong"`, the variance of the AUC is computed as defined by DeLong *et al.* (1988) and the CI is deduced with `qnorm`.

Value

A numeric vector of length 3 and class “ci.auc”, with the lower bound, the median and the upper bound of the CI, and the following attributes:

`conf.level`	the width of the CI, in fraction.
`boot.n`	the number of bootstrap replicates.
`boot.stratified`	whether or not the bootstrapping was stratified.
`auc`	an object of class “auc” stored for reference about the compued AUC details (partial, percent, ...)

The `aucs` item is not included in this list since version 1.2 for consistency reasons.

AUC specification

The comparison of the CI needs a specification of the AUC. This allows to compute the CI for full or partial AUCs. The specification is defined by:

1. the “auc” field in the “roc” object if `reuse.auc` is set to `TRUE` (default). It is naturally inherited from any call to `roc` and fits most cases.

2. passing the specification to `auc` with . . . (arguments `partial.auc`, `partial.auc.correct` and `partial.auc.focus`). In this case, you must ensure either that the `roc` object do not contain an `auc` field (if you called `roc` with `auc=FALSE`), or set `reuse.auc=FALSE`.

If `reuse.auc=FALSE` the `auc` function will always be called with `...` to determine the specification, even if the "roc" object do contain an `auc` field.

As well if the "roc" object do not contain an `auc` field, the `auc` function will always be called with `...` to determine the specification.

Warning: if the roc object passed to ci contains an `auc` field and `reuse.auc=TRUE`, auc is not called and arguments such as `partial.auc` are silently ignored.

Warnings

If `method="delong"` and the AUC specification specifies a partial AUC, the warning "Using DeLong's test for partial AUC is not supported. Using bootstrap test instead." is issued. The `method` argument is ignored and "bootstrap" is used instead.

If `boot.stratified=FALSE` and the sample has a large imbalance between cases and controls, it could happen that one or more of the replicates contains no case or control observation, or that there are not enough points for smoothing, producing a `NA` area. The warning "NA value(s) produced during bootstrap were ignored." will be issued and the observation will be ignored. If you have a large imbalance in your sample, it could be safer to keep `boot.stratified=TRUE`.

Errors

If `density.cases` and `density.controls` were provided for smoothing, the error "Cannot compute the statistic on ROC curves smoothed with density.controls and density.cases." is issued.

References

Elisabeth R. DeLong, David M. DeLong and Daniel L. Clarke-Pearson (1988) "Comparing the areas under two or more correlated receiver operating characteristic curves: a nonparametric approach". *Biometrics* **44**, 837–845.

James Carpenter and John Bithell (2000) "Bootstrap condence intervals: when, which, what? A practical guide for medical statisticians". *Statistics in Medicine* **19**, 1141–1164.

Xavier Robin, Natacha Turck, Alexandre Hainard, *et al.* (2011) "pROC: an open-source package for R and S+ to analyze and compare ROC curves". *BMC Bioinformatics*, **7**, 77. DOI: 10.1186/1471-2105-12-77

See Also

`roc`, `auc`, `ci`

Examples

```
data(aSAH)

# Syntax (response, predictor):
ci.auc(aSAH$outcome, aSAH$s100b)
```

```
# With a roc object:
rocobj <- roc(aSAH$outcome, aSAH$s100b)
# default values
ci.auc(rocobj)
ci(rocobj)
ci(auc(rocobj))
ci(rocobj$auc)
ci(rocobj$auc, method="delong")

# Partial AUC and customized bootstrap:
ci.auc(aSAH$outcome, aSAH$s100b,
       boot.n=100, conf.level=0.9, stratified=FALSE, partial.auc=c(1, .8),
       partial.auc.focus="se", partial.auc.correct=TRUE)

# Note that the following will NOT give a CI of the partial AUC:
ci.auc(rocobj, boot.n=500, conf.level=0.9, stratified=FALSE,
       partial.auc=c(1, .8), partial.auc.focus="se", partial.auc.correct=TRUE)
# This is because rocobj$auc is not a partial AUC.
## Not run:
# You can overcome this problem with reuse.auc:
ci.auc(rocobj, boot.n=500, conf.level=0.9, stratified=FALSE,
       partial.auc=c(1, .8), partial.auc.focus="se", partial.auc.correct=TRUE,
       reuse.auc=FALSE)

## End(Not run)

# Alternatively, you can get the CI directly from roc():
rocobj <- roc(aSAH$outcome, aSAH$s100b, ci=TRUE, of="auc")
rocobj$ci

## Not run:
# On a smoothed ROC, the CI is re-computed automatically
smooth(rocobj)
# Or you can compute a new one:
ci.auc(smooth(rocobj, method="density", reuse.ci=FALSE), boot.n=100)

## End(Not run)
```

`ci.se` *Compute the confidence interval of sensitivities at given specificities*

Description

This function computes the confidence interval (CI) of the sensitivity at the given specificity points. By default, the 95% CI are computed with 2000 stratified bootstrap replicates.

Usage

```
ci.se(x, ...)
## S3 method for class 'roc'
```

```
ci.se(roc, specificities = seq(0, 1, .1) * ifelse(roc$percent,
100, 1), conf.level=0.95, boot.n=2000, boot.stratified=TRUE, ...)
## S3 method for class 'smooth.roc'
ci.se(smooth.roc, specificities = seq(0, 1, .1) *
ifelse(smooth.roc$percent, 100, 1), conf.level=0.95, boot.n=2000,
boot.stratified=TRUE, ...)
## S3 method for class 'formula'
ci.se(formula, data, ...)
## Default S3 method:
ci.se(response, predictor, ...)
```

Arguments

`x`	a roc object from the `roc` or `smooth.roc` functions (for `ci.se.roc` or `ci.se.smooth.roc`), a formula (for `ci.se.formula`) or a response vector (for `ci.se.default`).
`roc, smooth.roc`	a "roc" object from the `roc` function, or a "smooth.roc" object from the `smooth.roc` function.
`response, predictor`	arguments for the `roc` function.
`formula, data`	a formula (and possibly a data object) of type response~predictor for the `roc` function.
`specificities`	on which specificities to evaluate the CI.
`conf.level`	the width of the confidence interval as [0,1], never in percent. Default: 0.95, resulting in a 95% CI.
`boot.n`	the number of bootstrap replicates. Default: 2000.
`boot.stratified`	should the bootstrap be stratified (default, same number of cases/controls in each replicate than in the original sample) or not.
`...`	further arguments passed to or from other methods, especially arguments for `roc` and `ci.se.roc` when calling `ci.se.default` or `ci.se.formula`.

Details

`ci.se.formula` and `ci.se.default` are convenience methods that build the ROC curve (with the `roc` function) before calling `ci.se.roc`. You can pass them arguments for both `roc` and `ci.se.roc`. Simply use `ci.se` that will dispatch to the correct method.

The `ci.se.roc` function creates `boot.n` bootstrap replicate of the ROC curve, and evaluates the sensitivity at specificities given by the `specificities` argument. Then it computes the confidence interval as the percentiles given by `conf.level`.

Stratification of bootstrap can be controlled with `boot.stratified`. In stratified bootstrap, each replicate contains the same number of cases and controls than the original sample. Stratification is especially useful if one group has only little observations, or if groups are not balanced. Higher numbers of `boot.n` will give a more precise estimate of the CI, but take more time to compute. 2000 is recommanded by Carpenter and Bithell.

For smoothed ROC curves, smoothing is performed again at each bootstrap replicate with the parameters originally provided. If a density smoothing was performed with user-provided `density.cases` or `density.controls` the bootstrap cannot be performed and an error is issued.

Value

A matrix of CI for the given sensitivities. Row (names) are the specificities, the first column the lower bound, the 2nd column the median and the 3rd column the upper bound.

Additionally, the list has the following attributes:

`conf.level`	the width of the CI, in fraction.
`boot.n`	the number of bootstrap replicates.
`boot.stratified`	whether or not the bootstrapping was stratified.
`specificities`	the specificities as given in argument.
`roc`	the object of class "roc" that was used to compute the CI.

Warnings

If `boot.stratified=FALSE` and the sample has a large imbalance between cases and controls, it could happen that one or more of the replicates contains no case or control observation, or that there are not enough points for smoothing, producing a `NA` area. The warning "NA value(s) produced during bootstrap were ignored." will be issued and the observation will be ignored. If you have a large imbalance in your sample, it could be safer to keep `boot.stratified=TRUE`.

Errors

If `density.cases` and `density.controls` were provided for smoothing, the error "Cannot compute the statistic on ROC curves smoothed with density.controls and density.cases." is issued.

References

Tom Fawcett (2006) "An introduction to ROC analysis". *Pattern Recognition Letters* **27**, 861–874. DOI: 10.1016/j.patrec.2005.10.010.

James Carpenter and John Bithell (2000) "Bootstrap condence intervals: when, which, what? A practical guide for medical statisticians". *Statistics in Medicine* **19**, 1141–1164.

Xavier Robin, Natacha Turck, Alexandre Hainard, *et al.* (2011) "pROC: an open-source package for R and S+ to analyze and compare ROC curves". *BMC Bioinformatics*, **7**, 77. DOI: 10.1186/1471-2105-12-77

See Also

`roc`, `ci`, `ci.sp`, `plot.ci`

Examples

```
data(aSAH)

## Not run:
# Syntax (response, predictor):
ci.se(aSAH$outcome, aSAH$s100b)

# With a roc object:
rocobj <- roc(aSAH$outcome, aSAH$s100b)
ci.se(rocobj)

# Customized bootstrap and specific specificities:
ci.se(rocobj, c(.95, .9, .85), boot.n=500, conf.level=0.9, stratified=FALSE)

## End(Not run)

# Alternatively, you can get the CI directly from roc():
rocobj <- roc(aSAH$outcome,
              aSAH$s100b, ci=TRUE, of="se", boot.n=100)
rocobj$ci

# Plotting the CI
plot(rocobj)
plot(rocobj$ci)

## Not run:
# On a smoothed ROC, the CI is re-computed automatically
smooth(rocobj)
# Or you can compute a new one:
ci.se(smooth(rocobj, method="density", reuse.ci=FALSE), boot.n=100)

## End(Not run)
```

`ci.sp` *Compute the confidence interval of specificities at given sensitivities*

Description

This function computes the confidence interval (CI) of the specificity at the given sensitivity points. By default, the 95% CI are computed with 2000 stratified bootstrap replicates.

Usage

```
ci.sp(x, ...)
## S3 method for class 'roc'
ci.sp(roc, sensitivities = seq(0, 1, .1) * ifelse(roc$percent,
100, 1), conf.level=0.95, boot.n=2000, boot.stratified=TRUE, ...)
## S3 method for class 'smooth.roc'
ci.sp(smooth.roc, sensitivities = seq(0, 1, .1) *
ifelse(smooth.roc$percent, 100, 1), conf.level=0.95, boot.n=2000,
boot.stratified=TRUE, ...)
## S3 method for class 'formula'
ci.sp(formula, data, ...)
## Default S3 method:
ci.sp(response, predictor, ...)
```

Arguments

`x`	a roc object from the `roc` or `smooth.roc` functions (for `ci.sp.roc` or `ci.sp.smooth.roc`), a formula (for `ci.sp.formula`) or a response vector (for `ci.sp.default`).
`roc, smooth.roc`	a "roc" object from the `roc` function, or a "smooth.roc" object from the `smooth.roc` function.
`response, predictor`	arguments for the `roc` function.
`formula, data`	a formula (and possibly a data object) of type response~predictor for the `roc` function.
`sensitivities`	on which sensitivities to evaluate the CI.
`conf.level`	the width of the confidence interval as [0,1], never in percent. Default: 0.95, resulting in a 95% CI.
`boot.n`	the number of bootstrap replicates. Default: 2000.
`boot.stratified`	should the bootstrap be stratified (default, same number of cases/controls in each replicate than in the original sample) or not.
`...`	further arguments passed to or from other methods, especially arguments for `roc` and `ci.sp.roc` when calling `ci.sp.default` or `ci.sp.formula`.

Details

`ci.sp.formula` and `ci.sp.default` are convenience methods that build the ROC curve (with the `roc` function) before calling `ci.sp.roc`. You can pass them arguments for both `roc` and `ci.sp.roc`. Simply use `ci.sp` that will dispatch to the correct method.

The `ci.sp.roc` function creates `boot.n` bootstrap replicate of the ROC curve, and evaluates the specificity at sensitivities given by the `sensitivities` argument. Then it computes the confidence interval as the percentiles given by `conf.level`.

Stratification of bootstrap can be controlled with `boot.stratified`. In stratified bootstrap, each replicate contains the same number of cases and controls than the original sample. Stratification is especially useful if one group has only little observations, or if groups are not balanced. Higher numbers of `boot.n` will give a more precise estimate of the CI, but take more time to compute. 2000 is recommanded by Carpenter and Bithell.

For smoothed ROC curves, smoothing is performed again at each bootstrap replicate with the parameters originally provided. If a density smoothing was performed with user-provided `density.cases` or `density.controls` the bootstrap cannot be performed and an error is issued.

Value

A matrix of CI for the given specificities. Row (names) are the sensitivities, the first column the lower bound, the 2nd column the median and the 3rd column the upper bound.

Additionally, the list has the following attributes:

`conf.level`	the width of the CI, in fraction.
`boot.n`	the number of bootstrap replicates.
`boot.stratified`	whether or not the bootstrapping was stratified.
`sensitivities`	the sensitivities as given in argument.
`roc`	the object of class "roc" that was used to compute the CI.

Warnings

If `boot.stratified=FALSE` and the sample has a large imbalance between cases and controls, it could happen that one or more of the replicates contains no case or control observation, or that there are not enough points for smoothing, producing a `NA` area. The warning "NA value(s) produced during bootstrap were ignored." will be issued and the observation will be ignored. If you have a large imbalance in your sample, it could be safer to keep `boot.stratified=TRUE`.

Errors

If `density.cases` and `density.controls` were provided for smoothing, the error "Cannot compute the statistic on ROC curves smoothed with density.controls and density.cases." is issued.

References

Tom Fawcett (2006) "An introduction to ROC analysis". *Pattern Recognition Letters* **27**, 861–874. DOI: 10.1016/j.patrec.2005.10.010.

James Carpenter and John Bithell (2000) "Bootstrap condence intervals: when, which, what? A practical guide for medical statisticians". *Statistics in Medicine* **19**, 1141–1164.

Xavier Robin, Natacha Turck, Alexandre Hainard, *et al.* (2011) "pROC: an open-source package for R and S+ to analyze and compare ROC curves". *BMC Bioinformatics*, **7**, 77. DOI: 10.1186/1471-2105-12-77

See Also

`roc`, `ci`, `ci.se`, `plot.ci`

Examples

```
data(aSAH)

## Not run:
# Syntax (response, predictor):
ci.sp(aSAH$outcome, aSAH$s100b)
```

```
# With a roc object:
rocobj <- roc(aSAH$outcome, aSAH$s100b)
ci.sp(rocobj)

# Customized bootstrap and specific specificities:
ci.sp(rocobj, c(.95, .9, .85), boot.n=500, conf.level=0.9, stratified=FALSE)

## End(Not run)

# Alternatively, you can get the CI directly from roc():
rocobj <- roc(aSAH$outcome,
              aSAH$s100b, ci=TRUE, of="sp", boot.n=100)
rocobj$ci

# Plotting the CI
plot(rocobj)
plot(rocobj$ci)

## Not run:
# On a smoothed ROC, the CI is re-computed automatically
smooth(rocobj)
# Or you can compute a new one:
ci.sp(smooth(rocobj, method="density", reuse.ci=FALSE), boot.n=100)

## End(Not run)
```

`ci.thresholds` *Compute the confidence interval of thresholds*

Description

This function computes the confidence interval (CI) of the sensitivity and specificity of the thresholds given in argument. By default, the 95% CI are computed with 2000 stratified bootstrap replicates.

Usage

```
ci.thresholds(x, ...)
## S3 method for class 'roc'
ci.thresholds(roc, conf.level=0.95, boot.n=2000,
boot.stratified=TRUE, thresholds = "local maximas", ...)
## S3 method for class 'smooth.roc'
ci.thresholds(smooth.roc, ...)
## S3 method for class 'formula'
ci.thresholds(formula, data, ...)
## Default S3 method:
ci.thresholds(response, predictor, ...)
```

Arguments

`x`	a roc object from the roc function (for ci.thresholds.roc), a formula (for ci.thresholds.formula) or a response vector (for ci.thresholds.default).
`roc`	a "roc" object from the `roc` function.
`smooth.roc`	not available for smoothed ROC curves, available only to catch the error and provide a clear error message.
`response, predictor`	arguments for the `roc` function.
`formula, data`	a formula (and possibly a data object) of type response~predictor for the `roc` function.
`conf.level`	the width of the confidence interval as [0,1], never in percent. Default: 0.95, resulting in a 95% CI.
`boot.n`	the number of bootstrap replicates. Default: 2000.
`boot.stratified`	should the bootstrap be stratified (default, same number of cases/controls in each replicate than in the original sample) or not.
`thresholds`	on which thresholds to evaluate the CI. Either the numeric values of the thresholds, a logical vector (as index of `roc$thresholds`) or a character "all", "local maximas" or "best".
`...`	further arguments passed to or from other methods, especially arguments for `roc` and `ci.thresholds.roc` when calling `ci.thresholds.default` or `ci.thresholds.formula`.

Details

`ci.thresholds.formula` and `ci.thresholds.default` are convenience methods that build the ROC curve (with the `roc` function) before calling `ci.thresholds.roc`. You can pass them arguments for both `roc` and `ci.thresholds.roc`. Simply use `ci.thresholds` that will dispatch to the correct method.

This function creates `boot.n` bootstrap replicate of the ROC curve, and evaluates the sensitivity and specificity at thresholds given by the `thresholds` argument. Then it computes the confidence interval as the percentiles given by `conf.level`.

Stratification of bootstrap can be controlled with `boot.stratified`. In stratified bootstrap, each replicate contains the same number of cases and controls than the original sample. Stratification is especially useful if one group has only little observations, or if groups are not balanced. Higher numbers of `boot.n` will give a more precise estimate of the CI, but take more time to compute. 2000 is recommanded by Carpenter and Bithell.

Value

A list of length 2 and class "ci.thresholds", with the confidence intervals of the CI and the following items:

`specificity`	a matrix of CI for the specificity. Row (names) are the thresholds, the first column the lower bound, the 2nd column the median and the 3rd column the upper bound.

`sensitivity`	same than specificity.

Additionally, the list has the following attributes:

`conf.level`	the width of the CI, in fraction.
`boot.n`	the number of bootstrap replicates.
`boot.stratified`	whether or not the bootstrapping was stratified.
`thresholds`	the thresholds, as given in argument.
`roc`	the object of class "roc" that was used to compute the CI.

Warnings

If `boot.stratified=FALSE` and the sample has a large imbalance between cases and controls, it could happen that one or more of the replicates contains no case or control observation, or that there are not enough points for smoothing, producing a `NA` area. The warning "NA value(s) produced during bootstrap were ignored." will be issued and the observation will be ignored. If you have a large imbalance in your sample, it could be safer to keep `boot.stratified=TRUE`.

References

Tom Fawcett (2006) "An introduction to ROC analysis". *Pattern Recognition Letters* **27**, 861–874. DOI: 10.1016/j.patrec.2005.10.010.

James Carpenter and John Bithell (2000) "Bootstrap condence intervals: when, which, what? A practical guide for medical statisticians". *Statistics in Medicine* **19**, 1141–1164.

Xavier Robin, Natacha Turck, Alexandre Hainard, *et al.* (2011) "pROC: an open-source package for R and S+ to analyze and compare ROC curves". *BMC Bioinformatics*, **7**, 77. DOI: 10.1186/1471-2105-12-77

See Also

`roc`, `ci`

Examples

```
data(aSAH)

## Not run:
# Syntax (response, predictor):
ci.thresholds(aSAH$outcome, aSAH$s100b)

# With a roc object:
rocobj <- roc(aSAH$outcome, aSAH$s100b)
ci.thresholds(rocobj)

# Customized bootstrap and specific thresholds:
ci.thresholds(aSAH$outcome, aSAH$s100b,
              boot.n=500, conf.level=0.9, stratified=FALSE,
              thresholds=c(0.5, 1, 2))
```

```
## End(Not run)

# Alternatively, you can get the CI directly from roc():
rocobj <- roc(aSAH$outcome,
              aSAH$s100b, ci=TRUE, of="thresholds")
rocobj$ci

# Plotting the CI
plot(rocobj)
plot(rocobj$ci)
```

`coords` *Coordinates of a ROC curve*

Description

This function returns the coordinates of the ROC curve at the specified point.

Usage

```
coords(...)
## S3 method for class 'roc'
coords(roc, x, input=c("threshold", "specificity",
"sensitivity"), ret=c("threshold", "specificity", "sensitivity"),
as.list=FALSE, best.method=c("youden", "closest.topleft"),
best.weights=c(1, 0.5), ...)
## S3 method for class 'smooth.roc'
coords(smooth.roc, x, input=c("specificity",
"sensitivity"), ret=c("specificity", "sensitivity"), as.list=FALSE,
best.method=c("youden", "closest.topleft"), best.weights=c(1, 0.5), ...)
```

Arguments

`roc, smooth.roc`	a “roc” object from the `roc` function, or a “smooth.roc” object from the `smooth.roc` function.
`x`	the coordinates to look for. Numeric (if so, their meaning is defined by the `input` argument) or one of “all” (all the points of the ROC curve), “local maximas” (the local maximas of the ROC curve) or “best” (the point with the best sum of sensitivity and specificity).
`input`	If `x` is numeric, the kind of input coordinate (x). One of “threshold”, “specificity” or “sensitivity”. Can be shortenend (for example to “thr”, “sens” and “spec”, or even to “t”, “se” and “sp”). Note that “threshold” is not allowed in `coords.smooth.roc`, and that the argument is ignored when `x` is a character.
`ret`	The coordinates to return. One or more of “threshold”, “specificity” or “sensitivity”. Can be shortenend (for example to “thr”, “sens” and “spec”, or even to “t”, “se” and “sp”). Note that “threshold” is not allowed in `coords.smooth.roc`.

`as.list`	If the returned object must be a list. If `FALSE` (default), a named numeric vector is returned.
`best.method`	if `x="best"`, the method to determine the best threshold. See details in the 'Best thresholds' section.
`best.weights`	if `x="best"`, the weights to determine the best threshold. See details in the 'Best thresholds' section.
`...`	further arguments passed to or from other methods. Ignored.

Details

This function takes a "roc" or "smooth.roc" object as first argument, on which the coordinates will be determined. The coordinates are defined by the `x` and `input` arguments. "threshold" coordinates cannot be determined in a smoothed ROC.

If `input="threshold"`, the coordinates for the threshold are reported, even if the exact threshold do not define the ROC curve. The following convenience characters are allowed: "all", "local maximas" and "best". They will return all the thresholds, only the thresholds defining local maximas (upper angles of the ROC curve), or only the threshold(s) corresponding to the best sum of sensitivity + specificity respectively. Note that "best" can return more than one threshold. If `x` is a character, the coordinates are limited to the thresholds within the partial AUC if it has been defined, and not necessarily to the whole curve.

For `input="specificity"` and `input="sensitivity"`, the function checks if the specificity or sensitivity is one of the points of the ROC curve (in `roc$sensitivities` or `roc$specificities`). More than one point may match (in *step* curves), then only the upper-left-most point coordinates are returned. Otherwise, the specificity and specificity of the point is interpolated and `NA` is returned as threshold.

The coords function in this package is a generic, but it might be superseded by functions in other packages such as **colorspace** or **spatstat** if they are loaded after **pROC**. In this case, call the `coords.roc` or `coords.smooth.roc` functions directly.

Value

Depending on the length of `x` and `as.list` argument.

	length(x) == 1	length(x) > 1
`as.list=TRUE`	a list of the length of, in the order of, and named after, `ret`.	a list of the length of, and na
`as.list=FALSE`	a numeric vector of the length of, in the order of, and named after, `ret`.	a numeric matrix with one ro

In all cases if `input="specificity"` or `input="sensitivity"` and interpolation was required, threshold is returned as `NA`.

Note that if giving a character as `x` ("all", "local maximas" or "best"), you cannot predict the dimension of the return value, so be prepared to receive either a numeric vector or a matrix (if `as.list=FALSE`) or either a list of numeric or a list of lists (if `as.list=TRUE`). Even "best" may return more than one value (for example if the ROC curve is below the identity line, both extreme points).

`coords` may also return `NULL` when there a partial area is defined but no point of the ROC curve falls within the region.

Best thresholds

If `x="best"`, the `best.method` argument controls how the optimal threshold is determined.

"youden" The Youden index is employed. The optimal cut-off is the threshold that maximizes the distance to the identity (diagonal) line. Can be shortened to "y".

The optimality criterion is:

$$max(sensitivities + specificities)$$

"closest.topleft" The optimal threshold is the point closest to the top-left part of the plot with perfect sensitivity or specificity. Can be shortened to "c" or "t".

The optimality criterion is:

$$min((1 - sensitivities)^2 + (1 - specificities)^2)$$

In addition, weights can be supplied if false positive and false negative predictions are not equivalent: a numeric vector of length 2 to the `best.weights` argument. The indices define

1. the cost of of a false negative classification
2. the prevalence, or the proportion of cases in the total population ($\frac{n_{cases}}{n_{controls}+n_{cases}}$).

The optimality criteria are modified as proposed by Perkins and Schisterman:

"youden"

$$max(sensitivities + r * specificities)$$

"closest.topleft"

$$min((1 - sensitivities)^2 + r * (1 - specificities)^2)$$

with

$$r = \frac{1 - prevalence}{cost * prevalence}$$

By default, prevalence is 0.5 and cost is 1 so that no weight is applied in effect.

Note that several thresholds might be equally optimal.

References

Neil J. Perkins, Enrique F. Schisterman (2006) "The Inconsistency of "Optimal" Cutpoints Obtained using Two Criteria based on the Receiver Operating Characteristic Curve". *American Journal of Epidemiology* **163**(7), 670–675. DOI: 10.1093/aje/kwj063

Xavier Robin, Natacha Turck, Alexandre Hainard, *et al.* (2011) "pROC: an open-source package for R and S+ to analyze and compare ROC curves". *BMC Bioinformatics*, **7**, 77. DOI: 10.1186/1471-2105-12-77

See Also

roc

Examples

```
data(aSAH)

# Print a roc object:
rocobj <- roc(aSAH$outcome, aSAH$s100b)

coords(rocobj, 0.55)
coords(rocobj, 0.9, "specificity", as.list=TRUE)
coords(rocobj, 0.5, "se", ret="se")
# fully qualified but identical:
coords(roc=rocobj, x=0.5, input="sensitivity", ret="sensitivity")

# Same in percent
rocobj <- roc(aSAH$outcome, aSAH$s100b,
              percent=TRUE)

coords(rocobj, 0.55)
coords(rocobj, 90, "specificity", as.list=TRUE)
coords(rocobj, x=50, input="sensitivity", ret=c("sen", "spec"))

# Get the sensitivities for all thresholds
sensitivities <- coords(rocobj, rocobj$thresholds, "thr", "se")
# This is equivalent to taking sensitivities from rocobj directly
stopifnot(all.equal(as.vector(rocobj$sensitivities), as.vector(sensitivities)))
# You could also write:
sensitivities <- coords(rocobj, "all", ret="se")
stopifnot(all.equal(as.vector(rocobj$sensitivities), as.vector(sensitivities)))

# Get the best threshold
coords(rocobj, "b", ret="t")

# Get the best threshold according to different methods
rocobj <- roc(aSAH$outcome, aSAH$ndka, percent=TRUE)
coords(rocobj, "b", ret="t", best.method="youden") # default
coords(rocobj, "b", ret="t", best.method="closest.topleft")
# and with different weights
coords(rocobj, "b", ret="t", best.method="youden", best.weights=c(50, 0.2))
coords(rocobj, "b", ret="t", best.method="closest.topleft", best.weights=c(5, 0.2))
# and plot them
plot(rocobj, print.thres="best", print.thres.best.method="youden")
plot(rocobj, print.thres="best", print.thres.best.method="closest.topleft")
plot(rocobj, print.thres="best", print.thres.best.method="youden",
                                 print.thres.best.weights=c(50, 0.2))
plot(rocobj, print.thres="best", print.thres.best.method="closest.topleft",
                                 print.thres.best.weights=c(5, 0.2))
```

`lines.roc` *Add a ROC line to a ROC plot*

Description

This convenience function adds a ROC line to a ROC curve.

Usage

```
## S3 method for class 'roc'
lines(x, ...)
## S3 method for class 'smooth.roc'
lines(x, ...)
## S3 method for class 'roc'
lines.roc(x, lwd=3, ...)
## S3 method for class 'formula'
lines.roc(x, data, ...)
## Default S3 method:
lines.roc(x, predictor, ...)
## S3 method for class 'smooth.roc'
lines.roc(x, ...)
```

Arguments

`x`	a roc object from the roc function (for plot.roc.roc), a formula (for plot.roc.formula) or a response vector (for plot.roc.default).
`predictor, data`	arguments for the roc function.
`lwd`	line width (see `par`).
`...`	graphical parameters for `lines`, and especially `type` (see `plot.default`) and arguments for `par` such as `col` (color), `lty` (line type) or line characteristics `lend`, `ljoin` and `lmitre`.

Details

The `lines.roc` function just adds a ROC curve to an existing plot with basic styling options. To plot more details such as the AUC value or confidence interval, see the `add=TRUE` argument to `plot.roc`.

Value

This function returns a list of class "roc" invisibly. See `roc` for more details.

See Also

`roc`, `plot.roc`

Examples

```
data(aSAH)

rocobj <- plot.roc(aSAH$outcome, aSAH$s100b, type="n")
lines(rocobj, type="b", pch=16, col="blue")

# Without using 'lines':
rocobj <- plot.roc(aSAH$outcome, aSAH$s100b, type="b", pch=16, col="blue")
```

---

plot.ci *Plot confidence intervals*

Description

This function adds confidence intervals to a ROC curve plot, either as bars or as a confidence shape.

Usage

```
## S3 method for class 'ci.thresholds'
plot(x, length=.01*ifelse(attr(x,
  "roc")$percent, 100, 1), col=par("fg"), ...)
## S3 method for class 'ci.sp'
plot(x, type=c("bars", "shape"), length=.01*ifelse(attr(x,
"roc")$percent, 100, 1), col=ifelse(type=="bars", par("fg"),
"gainsboro"), no.roc=FALSE, ...)
## S3 method for class 'ci.se'
plot(x, type=c("bars", "shape"), length=.01*ifelse(attr(x,
"roc")$percent, 100, 1), col=ifelse(type=="bars", par("fg"),
"gainsboro"), no.roc=FALSE, ...)
```

Arguments

`x`	a confidence interval object from the functions `ci.thresholds`, `ci.se` or `ci.sp`.
`type`	type of plot, “bars” or “shape”. Can be shortened to “b” or “s”. “shape” is only available for `ci.se` and `ci.sp`, not for `ci.thresholds`.
`length`	the length (as plot coordinates) of the bar ticks. Only if `type="bars"`.
`no.roc`	if `FALSE`, the ROC line is re-added over the shape. Otherwise if `TRUE`, only the shape is plotted. Ignored if `type="bars"`
`col`	color of the bars or shape.
`...`	further arguments for `segments` (if `type="bars"`) or `polygon` (if `type="shape"`).

Details

This function adds confidence intervals to a ROC curve plot, either as bars or as a confidence shape, depending on the state of the `type` argument. The shape is plotted over the ROC curve, so that the curve is re-plotted unless `no.roc=TRUE`.

Value

This function returns the confidence interval object invisibly.

Warnings

With `type="shape"`, the warning "Low definition shape" is issued when the shape is defined by less than 15 confidence intervals. In such a case, the shape is not well defined and the ROC curve could pass outside the shape. To get a better shape, increase the number of intervals, for example with:

```
plot(ci.sp(rocobj, sensitivities=seq(0, 1, .01)), type="shape")
```

References

Xavier Robin, Natacha Turck, Alexandre Hainard, *et al.* (2011) "pROC: an open-source package for R and S+ to analyze and compare ROC curves". *BMC Bioinformatics*, **7**, 77. DOI: 10.1186/1471-2105-12-77

See Also

`plot.roc`, `ci.thresholds`, `ci.sp`, `ci.se`

Examples

```
data(aSAH)
## Not run:
# Start a ROC plot
rocobj <- plot.roc(aSAH$outcome, aSAH$s100b)
plot(rocobj)
# Thresholds
ci.thresolds.obj <- ci.thresholds(rocobj)
plot(ci.thresolds.obj)
# Specificities
plot(rocobj) # restart a new plot
ci.sp.obj <- ci.sp(rocobj, boot.n=500)
plot(ci.sp.obj)
# Sensitivities
plot(rocobj) # restart a new plot
ci.se.obj <- ci(rocobj, of="se", boot.n=500)
plot(ci.se.obj)

# Plotting a shape. We need more
ci.sp.obj <- ci.sp(rocobj, sensitivities=seq(0, 1, .01), boot.n=100)
plot(rocobj) # restart a new plot
plot(ci.sp.obj, type="shape", col="blue")
```

```
# Direct syntax (response, predictor):
plot.roc(aSAH$outcome, aSAH$s100b,
         ci=TRUE, of="thresholds")

## End(Not run)
```

`plot.roc` *Plot a ROC curve*

Description

This function plots a ROC curve. It can accept many arguments to tweak the appearance of the plot. Two syntaxes are possible: one object of class "roc", or either two vectors (response, predictor) or a formula (response~predictor) as in the `roc` function.

Usage

```
## S3 method for class 'roc'
plot(x, ...)
## S3 method for class 'smooth.roc'
plot(x, ...)
## S3 method for class 'roc'
plot.roc(x, add=FALSE, reuse.auc=TRUE,
# Generic arguments for par:
xlim=if(x$percent){c(100, 0)} else{c(1, 0)},
ylim=if(x$percent){c(0, 100)} else{c(0, 1)},
xlab=ifelse(x$percent, "Specificity (%)", "Specificity"),
ylab=ifelse(x$percent, "Sensitivity (%)", "Sensitivity"),
width=8.5,
height=8.5,
# col, lty and lwd for the ROC line only
col=par("col"),
lty=par("lty"),
lwd=3,
type="l",
# Identity line
identity=!add,
identity.col="darkgrey",
identity.lty=1,
identity.lwd=1,
# Print the thresholds on the plot
print.thres=FALSE,
print.thres.pch=16,
print.thres.col="black",
print.thres.pattern=ifelse(x$percent, "%.1f (%.1f%%, %.1f%%)", "%.3f (%.3f, %.3f)")
print.thres.cex=par("cex"),
print.thres.pattern.cex=print.thres.cex,
# Print the AUC on the plot
print.auc=FALSE,
print.auc.pattern=NULL,
print.auc.x=ifelse(x$percent, 50, .5),
print.auc.y=ifelse(x$percent, 50, .5),
print.auc.col=col,
print.auc.cex=par("cex"),
# Grid
grid=FALSE,
grid.v={if(is.logical(grid) && grid[1]==TRUE){seq(0, 1, 0.1) * ifelse(x$percent, 10
grid.h={if (length(grid) == 1) {grid.v} else if (is.logical(grid) && grid[2]==TRUE)
grid.lty=2,
grid.lwd=1,
grid.col="#DDDDDD",
# Polygon for the AUC
auc.polygon=FALSE,
auc.polygon.col="gainsboro",
auc.polygon.lty=par("lty"),
auc.polygon.border="#000000",
auc.polygon.density=-1,
auc.polygon.angle=45,
# Polygon for the maximal AUC possible
max.auc.polygon=FALSE,
max.auc.polygon.col="#EEEEEE",
max.auc.polygon.lty=par("lty"),
max.auc.polygon.border="#000000",
max.auc.polygon.density=-1,
max.auc.polygon.angle=45,
# Confidence interval
ci=!is.null(x$ci),
ci.type=c("bars", "shape", "no"),
ci.col=ifelse(ci.type=="bars", par("fg"), "gainsboro"),
...)
## S3 method for class 'formula'
plot.roc(x, data, ...)
## Default S3 method:
plot.roc(x, predictor, ...)
## S3 method for class 'smooth.roc'
plot.roc(x, ...)
```

Arguments

`x`	a roc object from the roc function (for plot.roc.roc), a formula (for plot.roc.formula) or a response vector (for plot.roc.default).
`predictor, data`	arguments for the roc function.

`add`	if TRUE, the ROC curve will be added to an existing plot. If FALSE (default), a new plot will be created.
`reuse.auc`	if `TRUE` (default) and the "roc" object contains an "auc" field, re-use these specifications for the test. See details.
`xlim, ylim, xlab, ylab`	Generic arguments for the plot. See plot and plot.window for more details.
`width, height`	If no device is open, specify the dimensions of the plot. Further arguments can be passed to `graphsheet` in `...`.
`col,lty, lwd`	color, line type and line width for the ROC curve. See par for more details.
`type`	type of plotting as in `plot`.
`identity`	logical: whether or not the identity line (no discrimination line) must be displayed. Default: only on new plots.
`identity.col, identity.lty, identity.lwd`	color, line type and line width for the identity line. Used only if identity=TRUE. See par for more details.
`print.thres`	Should a selected set of thresholds be displayed on the ROC curve? `FALSE`, `NULL` or "no": no threshold is displayed. `TRUE` or "best": the threshold with the highest sum sensitivity + specificity is plotted (this might be more than one threshold). "all": all the points of the ROC curve. "local maximas": all the local maximas. Numeric vector: direct definition of the thresholds to display. Note that on a smoothed ROC curve, only "best" is supported.
`print.thres.pch, print.thres.col, print.thres.cex`	the plotting character (pch), color (col) and character expansion factor (cex) parameters for the printing of the thresholds. See points and par for more details.
`print.thres.pattern`	the text pattern for the thresholds, as a sprintf format. Three numerics are passed to sprintf: threshold, specificity, sensitivity.
`print.thres.pattern.cex`	the character expansion factor (cex) for the threshold text pattern. See par for more details.
`print.auc`	boolean. Should the numeric value of AUC be printed on the plot?
`print.auc.pattern`	the text pattern for the AUC, as a sprintf format. If NULL, a reasonable value is computed that takes partial AUC, CI and percent into account. If the CI of the AUC was computed, three numerics are passed to sprintf: AUC, lower CI bound, higher CI bound. Otherwise, only AUC is passed.
`print.auc.x, print.auc.y`	x and y position for the printing of the AUC.
`print.auc.cex, print.auc.col`	character expansion factor and color for the printing of the AUC. See par for more details.
`grid`	boolean or numeric vector of length 1 or 2. Should a background grid be added to the plot? Numeric: show a grid with the specified interval between each line; Logical: show the grid or not. Length 1: same values are taken for horizontal and

vertical lines. Length 2: grid value for vertical (grid[1]) and horizontal (grid[2]). Note that these values are used to compute grid.v and grid.h. Therefore if you specify a grid.h and grid.v, it will be ignored.

`grid.v, grid.h`
: numeric. The x and y values at which a vertical or horizontal line (respectively) must be drawn. NULL if no line must be added.

`grid.lty, grid.lwd, grid.col`
: the line type (lty), line width (lwd) and color (col) of the lines of the grid. See par for more details. Note that you can pass vectors of length 2, in which case it specifies the vertical (1) and horizontal (2) lines.

`auc.polygon` boolean. Whether or not to display the area as a polygon.

`auc.polygon.col, auc.polygon.lty, auc.polygon.border, auc.polygon.density, auc.poly`
: color (col), line type (lty), border, density and angle for the AdUC polygon. See `polygon` and `par` for more details.

`max.auc.polygon`
: boolean. Whether or not to display the maximal possible area as a polygon.

`max.auc.polygon.col, max.auc.polygon.lty, max.auc.polygon.border, max.auc.polygon.d`
: color (col), line type (lty), border, density and angle for the maximum AUC polygon. See `polygon` and `par` for more details.

`ci` boolean. Should we plot the confidence intervals?

`ci.type, ci.col`
: `type` and `col` arguments for `plot.ci`. The special value “no” disables the plotting of confidence intervals.

`...` further arguments passed to or from other methods, especially arguments for `roc` and `plot.roc.roc` when calling `plot.roc.default` or `plot.roc.formula`. Note that the `plot` argument for `roc` is not allowed. Arguments for `auc` and graphical functions `plot`, `abline`, `points`, `text` and `plot.ci` if applicable.

Details

This function is typically called from `roc` when plot=TRUE (not by default). `plot.roc.formula` and `plot.roc.default` are convenience methods that build the ROC curve (with the `roc` function) before calling `plot.roc.roc`. You can pass them arguments for both `roc` and `plot.roc.roc`. Simply use `plot.roc` that will dispatch to the correct method.

The plotting is done in the following order:

1. A new plot is created if `add=FALSE`. If no graphical device is opened, a new graphsheet is started with margins set to make the plot square. Otherwise the plot will have the proportions defined by the device previously opened.
2. The grid is added if `grid.v` and `grid.h` are not NULL.
3. The maximal AUC polygon is added if `max.auc.polygon=TRUE`.
4. The CI shape is added if `ci=TRUE`, `ci.type="shape"` and `x$ci` isn't a “ci.auc”.
5. The AUC polygon is added if `auc.polygon=TRUE`.
6. The identity line if `identity=TRUE`.

7. The actual ROC line is added.
8. The CI bars are added if `ci=TRUE`, `ci.type="bars"` and `x$ci` isn't a "ci.auc".
9. The selected thresholds are printed if `print.thres` is `TRUE` or numeric.
10. The AUC is printed if `print.auc=TRUE`.

Value

This function returns a list of class "roc" invisibly. See roc for more details.

AUC specification

For `print.auc`, `auc.polygon` and `max.auc.polygon` arguments, an AUC specification is required. By default, the total AUC is plotted, but you may want a partial AUCs. The specification is defined by:

1. the "auc" field in the "roc" object if `reuse.auc` is set to `TRUE` (default). It is naturally inherited from any call to `roc` and fits most cases.
2. passing the specification to `auc` with . . . (arguments `partial.auc`, `partial.auc.correct` and `partial.auc.focus`). In this case, you must ensure either that the `roc` object do not contain an `auc` field (if you called `roc` with `auc=FALSE`), or set `reuse.auc=FALSE`.

If `reuse.auc=FALSE` the `auc` function will always be called with `...` to determine the specification, even if the "roc" object do contain an `auc` field.

As well if the "roc" object do not contain an `auc` field, the `auc` function will always be called with `...` to determine the specification.

Warning: if the roc object passed to plot.roc contains an `auc` field and `reuse.auc=TRUE`, auc is not called and arguments such as `partial.auc` are silently ignored.

References

Xavier Robin, Natacha Turck, Alexandre Hainard, *et al.* (2011) "pROC: an open-source package for R and S+ to analyze and compare ROC curves". *BMC Bioinformatics*, **7**, 77. DOI: 10.1186/1471-2105-12-77

See Also

`roc`, `auc`, `ci`

Examples

```
data(aSAH)

# Syntax (response, predictor):
plot.roc(aSAH$outcome, aSAH$s100b)

# With a roc object:
rocobj <- roc(aSAH$outcome, aSAH$s100b)
# identical:
plot(rocobj)
```

```
plot.roc(rocobj)

# Add a smoothed ROC:
plot.roc(smooth(rocobj), add=TRUE, col="blue")
legend(.6, .4, legend=c("Empirical", "Smoothed"),
       col=c(par("fg"), "blue"), lwd=2)

# With more options:
plot(rocobj, print.auc=TRUE, auc.polygon=TRUE, grid=c(0.1, 0.2),
     grid.col=c("green", "red"), max.auc.polygon=TRUE,
     auc.polygon.col="blue", print.thres=TRUE)

# To plot a different partial AUC, we need to ignore the existing value
# with reuse.auc=FALSE:
plot(rocobj, print.auc=TRUE, auc.polygon=TRUE, partial.auc=c(1, 0.8),
     partial.auc.focus="se", grid=c(0.1, 0.2), grid.col=c("green", "red"),
     max.auc.polygon=TRUE, auc.polygon.col="blue", print.thres=TRUE,
     reuse.auc=FALSE)

# Add a line to the previous plot:
plot.roc(aSAH$outcome, aSAH$wfns, add=TRUE)

# Alternatively, you can get the plot directly from roc():
roc(aSAH$outcome, aSAH$s100b, plot=TRUE)
```

`print` *Print a ROC curve object*

Description

This function prints a ROC curve, AUC or CI object and return it invisibly.

Usage

```
## S3 method for class 'roc'
print(x, digits=max(3, getOption("digits") - 3), call=TRUE, ...)
## S3 method for class 'smooth.roc'
print(x, digits=max(3, getOption("digits") - 3),
call=TRUE, ...)
## S3 method for class 'auc'
print(x, digits=max(3, getOption("digits") - 3), ...)
## S3 method for class 'ci.auc'
print(x, digits=max(3, getOption("digits") - 3), ...)
## S3 method for class 'ci.thresholds'
print(x, digits=max(3, getOption("digits") - 3), ...)
## S3 method for class 'ci.se'
print(x, digits=max(3, getOption("digits") - 3), ...)
## S3 method for class 'ci.sp'
print(x, digits=max(3, getOption("digits") - 3), ...)
```

Arguments

`x`	a roc, auc or ci object, from the roc, auc or ci functions respectively.
`call`	if the call is printed.
`digits`	the number of significant figures to print. See signif for more details.
`...`	further arguments passed to or from other methods. In particular, `print.roc` calls `print.auc` and the `print.ci` variants internally, and a `digits` argument is propagated. Not used in print.auc and print.ci variants.

Value

These functions return the object they were passed invisibly.

See Also

`roc`, `auc`, `ci`, `coords`

Examples

```
data(aSAH)

# Print a roc object:
rocobj <- roc(aSAH$outcome, aSAH$s100b)
print(rocobj)

# Print a smoothed roc object
print(smooth(rocobj))

# implicit printing
 roc(aSAH$outcome, aSAH$s100b)

# Print an auc and a ci object, from the ROC object or calling
# the dedicated function:
print(rocobj$auc)
print(ci(rocobj))
```

`roc` *Build a ROC curve*

Description

This is the main function of the pROC package. It builds a ROC curve and returns a “roc” object, a list of class “roc”. This object can be `print`ed, `plot`ted, or passed to the functions `auc`, `ci`, `smooth.roc` and `coords`. Additionally, two `roc` objects can be compared with `roc.test`.

Usage

```
roc(x, ...)
## S3 method for class 'formula'
roc(formula, data, ...)
## Default S3 method:
roc(response, predictor,
levels=getFunction("levels")(as.factor(response)), percent=FALSE, na.rm=TRUE,
direction=c("auto", "<", ">"), smooth=FALSE, auc=TRUE, ci=FALSE,
plot=FALSE, smooth.method="binormal", ci.method=NULL, density=NULL, ...)
```

Arguments

`x`	a formula (for roc.formula) or a response vector (for roc.default).
`response`	a factor, numeric or character vector of responses, typically encoded with 0 (controls) and 1 (cases). The object. Only two classes can be used in a ROC curve. If the vector contains more than two unique values, or if their order could be ambiguous, use `levels` to specify which values must be used as control and case value.
`predictor`	a numeric vector, containing the value of each observation. An ordered factor is coerced to a numeric.
`formula`	a formula of the type `response~predictor`.
`data`	a matrix or data.frame containing the variables in the formula. See `model.frame` for more details.
`levels`	the value of the response for controls and cases respectively. By default, the first two values of `levels(as.factor(response))` are taken, and the remaining levels are ignored. It usually captures two-class factor data correctly, but will frequently fail for other data types (response factor with more than 2 levels, or for example if your response is coded "controls" and "cases", the levels will be inverted) and must then be precised here. If your data is coded as `0` and `1` with `0` being the controls, you can safely omit this argument.
`percent`	if the sensitivities, specificities and AUC must be given in percent (`TRUE`) or in fraction (`FALSE`, default).
`na.rm`	if `TRUE`, the `NA` values will be removed.
`direction`	in which direction to make the comparison? "auto" (default): automatically define in which group the median is higher and take the direction accordingly. ">": if the predictor values for the control group are higher than the values of the case group. ">": contrary.
`smooth`	if TRUE, the ROC curve is passed to `smooth` to be smoothed.
`auc`	compute the area under the curve (AUC)? If `TRUE` (default), additional arguments can be passed to `auc`.
`ci`	compute the confidence interval (CI)? If `TRUE` (default), additional arguments can be passed to `ci`.
`plot`	plot the ROC curve? If `TRUE`, additional arguments can be passed to `plot.roc`.

`smooth.method, ci.method`
: in `roc.formula` and `roc.default`, the `method` arguments to `smooth.roc` (if `smooth=TRUE`) and `of="auc"`) must be passed as `smooth.method` and `ci.method` to avoid confusions.

`density`
: `density` argument passed to `smooth.roc`.

`...`
: further arguments passed to or from other methods, and especially:

- `auc`: `partial.auc`, `partial.auc.focus`, `partial.auc.correct`.
- `ci`: `of`, `conf.level`, `boot.n`, `boot.stratified`
- `ci.auc`:, `reuse.auc`, `method`
- `ci.thresholds`: `thresholds`
- `ci.sp`: `sensitivities`
- `ci.se`: `specificities`
- `plot.roc`: `add`, `col` and most other arguments to the `plot.roc` function. See `plot.roc` directly for more details.
- `smooth`: `method`, `n`, and all other arguments. See `smooth` for more details.

Details

This function's main job is to build a ROC object. See the "Value" section to this page for more details. Before returning, it will call (in this order) the `smooth.roc`, `auc`, `ci` and `plot.roc` functions if `smooth` `auc`, `ci` and `plot.roc` (respectively) arguments are set to TRUE. By default, only `auc` is called.

Data can be provided as `response, predictor`, where the predictor is the numeric (or ordered) level of the evaluated signal, and the response encodes the observation class (control or case). The `level` argument specifies which response level must be taken as controls (first value of `level`) or cases (second). It can safely be ignored when the response is encoded as `0` and `1`, but it will frequently fail otherwise. By default, the first two values of `levels(as.factor(response))` are taken, and the remaining levels are ignored. This means that if your response is coded "control" and "case", the levels will be inverted.

Specifications for `auc`, `ci` and `plot.roc` are not kept if `auc`, `ci` or `plot` are set to `FALSE`. Especially, in the following case:

```
myRoc <- roc(..., auc.polygon=TRUE, grid=TRUE, plot=FALSE)
plot(myRoc)
```

the plot will not have the AUC polygon nor the grid. Similarly, when comparing "roc" objects, the following is not possible:

```
roc1 <- roc(..., partial.auc=c(1, 0.8), auc=FALSE)
roc2 <- roc(..., partial.auc=c(1, 0.8), auc=FALSE)
roc.test(roc1, roc2)
```

This will produce a test on the full AUC, not the partial AUC. To make a comparison on the partial AUC, you must repeat the specifications when calling `roc.test`:

```
    roc.test(roc1, roc2, partial.auc=c(1, 0.8))
```

Note that if `roc` was called with `auc=TRUE`, the latter syntax will not allow redefining the AUC specifications. You must use `reuse.auc=FALSE` for that.

Value

If the data contained any `NA` value, `NA` is returned. Otherwise, if `smooth=FALSE`, a list of class "roc" with the following fields:

`auc`	if called with `auc=TRUE`, a numeric of class "auc" as defined in `auc`.
`ci`	if called with `ci=TRUE`, a numeric of class "ci" as defined in `ci`.
`response`	the response vector as passed in argument. If `NA` values were removed, a `na.action` attribute similar to `na.omit` stores the row numbers.
`predictor`	the predictor vector converted to numeric as used to build the ROC curve. If `NA` values were removed, a `na.action` attribute similar to `na.omit` stores the row numbers.
`original.predictor`	the predictor vector as passed in argument.
`levels`	the levels of the response as defined in argument.
`controls`	the predictor values for the control observations.
`cases`	the predictor values for the cases.
`percent`	if the sensitivities, specificities and AUC are reported in percent, as defined in argument.
`direction`	the direction of the comparison, as defined in argument.
`sensitivities`	the sensitivities defining the ROC curve.
`specificities`	the specificities defining the ROC curve.
`thresholds`	the thresholds at which the sensitivities and specificities were computed.
`call`	how the function was called. See `match.call` for more details.

If `smooth=TRUE` a list of class "smooth.roc" as returned by `smooth`, with or without additional elements `auc` and `ci` (according to the call).

Errors

If no control or case observation exist for the given levels of response, no ROC curve can be built and an error is triggered with message "No control observation" or "No case observation".

If the predictor is not a numeric or ordered, as defined by `as.numeric` or `as.ordered`, the message "Predictor must be numeric or ordered" is returned.

The message "No valid data provided" is issued when the data wasn't properly passed. Remember you need both `response` and `predictor` of the same (not null) length, or bot `controls` and `cases`. Combinations such as `predictor` and `cases` are not valid and will trigger this error.

References

Tom Fawcett (2006) “An introduction to ROC analysis”. *Pattern Recognition Letters* **27**, 861–874. DOI: 10.1016/j.patrec.2005.10.010

Xavier Robin, Natacha Turck, Alexandre Hainard, *et al.* (2011) “pROC: an open-source package for R and S+ to analyze and compare ROC curves”. *BMC Bioinformatics*, **7**, 77. DOI: 10.1186/1471-2105-12-77

See Also

auc, ci, plot.roc, print.roc, roc.test

Examples

```
data(aSAH)

# Basic example
roc(aSAH$outcome, aSAH$s100b,
    levels=c("Good", "Poor"))
# As levels aSAH$outcome == c("Good", "Poor"),
# this is equivalent to:
roc(aSAH$outcome, aSAH$s100b)
# In some cases, ignoring levels could lead to unexpected results
# Equivalent syntaxes:
roc(outcome ~ s100b, aSAH)
roc(aSAH$outcome ~ aSAH$s100b)
with(aSAH, roc(outcome, s100b))
with(aSAH, roc(outcome ~ s100b))

# With a formula:
roc(outcome ~ s100b, data=aSAH)

# Inverted the levels: "Poor" are now controls and "Good" cases:
roc(aSAH$outcome, aSAH$s100b,
    levels=c("Poor", "Good"))

# The result was exactly the same because of direction="auto".
# The following will give an AUC < 0.5:
roc(aSAH$outcome, aSAH$s100b,
    levels=c("Poor", "Good"), direction="<")

# If we prefer counting in percent:
roc(aSAH$outcome, aSAH$s100b, percent=TRUE)

# Plot and CI (see plot.roc and ci for more options):
roc(aSAH$outcome, aSAH$s100b,
    percent=TRUE, plot=TRUE, ci=TRUE)

# Smoothed ROC curve
roc(aSAH$outcome, aSAH$s100b, smooth=TRUE)
# this is not identical to
smooth(roc(aSAH$outcome, aSAH$s100b))
```

```
# because in the latter case, the returned object contains no AUC
```

---

roc.test *Compare the AUC of two correlated ROC curves*

Description

This function compares the AUC or partial AUC of two correlated (or paired) ROC curves. Several syntaxes are available: two object of class roc (which must have the same response data, but can be AUC or smoothed ROC), or either three vectors (response, predictor1, predictor2) or a response vector and a matrix or data.frame with two columns (predictors).

Usage

```
roc.test(x, ...)
## S3 method for class 'roc'
roc.test(roc1, roc2, method=c("delong", "bootstrap",
"venkatraman", "sensitivity", "specificity"), sensitivity = NULL,
specificity = NULL, alternative = c("two.sided", "less", "greater"),
paired=NULL, reuse.auc=TRUE, boot.n=2000, boot.stratified=TRUE,
ties.method="first", progress=getOption("pROCProgress")$name, ...)
## S3 method for class 'auc'
roc.test(roc1, roc2, ...)
## S3 method for class 'smooth.roc'
roc.test(roc1, roc2, ...)
## S3 method for class 'formula'
roc.test(formula, data, ...)
## Default S3 method:
roc.test(response, predictor1, predictor2=NULL,
na.rm=TRUE, method=NULL, ...)
```

Arguments

`x`	a roc object from the roc function (for roc.test.roc), an auc from the auc function (for roc.test.auc) a formula (for roc.test.formula) or a response vector (for roc.test.default).
`roc1, roc2`	the two ROC curves to compare. Either “roc”, “auc” or “smooth.roc” objects (types can be mixed as long as the original ROC curve are paired).
`response`	a vector or factor, as for the roc function.
`predictor1`	a numeric or ordered vector as for the roc function, or a matrix or data.frame with predictors two colums.
`predictor2`	only if predictor1 was a vector, the second predictor as a numeric vector.
`formula`	a formula of the type response~predictor1+predictor2.
`data`	a matrix or data.frame containing the variables in the formula. See `model.frame` for more details.

`na.rm`	if `TRUE`, the observations with `NA` values will be removed.
`method`	the method to use, either "delong", "bootstrap" or "venkatraman". The first letter is sufficient. If omitted, the appropriate method is selected as explained in details.
`sensitivity, specificity`	if `method="sensitivity"` or `method="specificity"`, the respective level where the test must be assessed as a numeric of length 1.
`alternative`	specifies the alternative hypothesis. Either of "two.sided", "less" or "greater". The first letter is sufficient. Default: "two.sided". Only "two.sided" is available with `method="venkatraman"`.
`paired`	a logical indicating whether you want a paired roc.test. If `NULL`, the paired status will be auto-detected by `are.paired`. If `TRUE` but the paired status cannot be assessed by `are.paired` will produce an error.
`reuse.auc`	if `TRUE` (default) and the "roc" objects contain an "auc" field, re-use these specifications for the test. See details.
`boot.n`	for `method="bootstrap"` and `method="venkatraman"` only: the number of bootstrap replicates or permutations. Default: *2000*.
`boot.stratified`	for `method="bootstrap"` only: should the bootstrap be stratified (same number of cases/controls in each replicate than in the original sample) or not. Ignored with `method="venkatraman"`. Default: *TRUE*.
`ties.method`	for `method="venkatraman"` only: argument for `rank` specifying how ties are handled. Defaults to "first" as described in the paper.
`progress`	the name of progress bar to display. Typically "none", "win", "tk" or "text" (see the `name` argument to `create_progress_bar` for more information), but a list as returned by `create_progress_bar` is also accepted. See also the "Progress bars" section of this package's documentation.
`...`	further arguments passed to or from other methods, especially arguments for `roc` and `roc.test.roc` when calling `roc.test.default` or `roc.test.formula`. Arguments for `auc`, and `txtProgressBar` (only `char` and `style`) if applicable.

Details

This function compares two ROC curves. It is typically called with the two roc objects to compare. `roc.test.default` is provided as a convenience method and creates two roc objects before calling `roc.test.roc`.

Three methods are available: "delong", "bootstrap" and "venkatraman" (see "Computational details" section below). "delong" and "bootstrap" are tests over the AUC whereas "venkatraman" compares the the ROC curves themselves. "delong" and "bootstrap" are available as both paired and unpaired tests, whereas "venkatraman" is only paired yet.

Default is to use "delong" method except for comparison of partial AUC, smoothed curves and curves with different `direction`, where `bootstrap` is used. Using "delong" for partial AUC and smoothed ROCs is not supported in pROC (a warning is produced and "bootstrap" is employed instead). It is spurious to use "delong" for `roc` with different `direction` (a warning is issued but the spurious comparison is enforced). “venkatraman”’s test cannot be employed to compare smoothed ROC curves. Additionally, partial AUC specifications are ignored (with a warning), and comparison of ROC curves with different `direction` should be used with care (a warning is produced as well).

If `alternative="two.sided"`, a two-sided test for difference in AUC is performed. If `alternative="less"`, the alternative is that the AUC of roc1 is smaller than the AUC of roc2. For `method="venkatraman"`, only “two.sided” test is available.

If the `paired` argument is not provided, the `are.paired` function is employed to detect the paired status of the ROC curves. It will test if the original `response` is identical between the two ROC curves (this is always the case if the call is made with `roc.test.default`). This detection is unlikely to raise false positives, but this possibility cannot be excluded entierly. It would require equal sample sizes and `response` values and order in both ROC curves. If it happens to you, use `paired=FALSE`. If you know the ROC curves are paired you can pass `paired=TRUE`. However this is useless as it will be tested anyway.

For smoothed ROC curves, smoothing is performed again at each bootstrap replicate with the parameters originally provided. If a density smoothing was performed with user-provided `density.cases` or `density.controls` the bootstrap cannot be performed and an error is issued.

Value

A list of class "htest" with following content:

`p.value`	the p-value of the test.
`statistic`	the value of the Z (`method="delong"`) or D (`method="bootstrap"`) statistics.
`alternative`	the alternative hypothesis.
`method`	the character string “DeLong’s test for two correlated ROC curves” (if `method="delong"`) or “Bootstrap test for two correlated ROC curves” (if `method="bootstrap"`).
`null.value`	the expected value of the statistic under the null hypothesis, that is 0.
`estimate`	the AUC in the two ROC curves.
`data.name`	the names of the data that was used.
`parameter`	for `method="bootstrap"` only: the values of the `boot.n` and `boot.stratified` arguments.

AUC specification

The comparison of the AUC of the ROC curves needs a specification of the AUC. The specification is defined by:

1. the “auc” field in the “roc” objects if `reuse.auc` is set to `TRUE` (default)
2. passing the specification to `auc` with . . . (arguments `partial.auc`, `partial.auc.correct` and `partial.auc.focus`). In this case, you must ensure either that the `roc` object do not contain an `auc` field (if you called `roc` with `auc=FALSE`), or set `reuse.auc=FALSE`.

If `reuse.auc=FALSE` the `auc` function will always be called with `...` to determine the specification, even if the “roc” objects do contain an `auc` field.

As well if the "roc" objects do not contain an `auc` field, the `auc` function will always be called with `...` to determine the specification.

The AUC specification is ignored in the Venkatraman test.

Warning: if the roc object passed to roc.test contains an `auc` field and `reuse.auc=TRUE`, auc is not called and arguments such as `partial.auc` are silently ignored.

Computation details

With `method="bootstrap"`, the processing is done as follow:

1. `boot.n` bootstrap replicates are drawn from the data. If `boot.stratified` is *TRUE*, each replicate contains exactly the same number of controls and cases than the original sample, otherwise if *FALSE* the numbers can vary.
2. for each bootstrap replicate, the AUC of the two ROC curves are computed and the difference is stored.
3. The following formula is used:

$$D = \frac{AUC1 - AUC2}{s}$$

   where s is the standard deviation of the bootstrap differences and AUC1 and AUC2 the AUC of the two (original) ROC curves.
4. *D* is then compared to the normal distribution, according to the value of `alternative`.

With `method="delong"`, the processing is done as described in DeLong *et al.* (1988) for paired ROC curves. Only comparison of two ROC curves is implemented. The method has been extended for unpaired ROC curves where the p-value is computed with an unpaired t-test with unequal sample size and unequal variance.

With `method="venkatraman"`, the processing is done as described in Venkatraman and Begg (1996) (for paired ROC curves) and Venkatraman (2000) (for unpaired ROC curves) with `boot.n` permutation of sample ranks (with ties breaking). For consistency reasons, the same argument `boot.n` as in bootstrap defines the number of permutations to execute, even though no bootstrap is performed.

For `method="specificity"`, the test assesses if the sensitivity of the ROC curves are different at the level of specificity given by the `specificity` argument, which must be a numeric of length 1. Bootstrap is employed as with `method="bootstrap"` and `boot.n` and `boot.stratified` are available. This is identical to the test proposed by Pepe *et al.* (2009). The `method="sensitivity"` is very similar, but assesses if the specificity of the ROC curves are different at the level of sensitivity given by the `sensitivity` argument.

Warnings

If "auc" specifications are different in both roc objects, the warning "Different AUC specifications in the ROC curves. Enforcing the inconsistency, but unexpected results may be produced." is issued. Unexpected results may be produced.

If one or both ROC curves are "smooth.roc" objects with different smoothing specifications, the warning "Different smoothing parameters in the ROC curves. Enforcing the inconsistency, but unexpected results may be produced." is issued. This warning can be benign, especially if ROC curves were generated with `roc(..., smooth=TRUE)` with different arguments to other functions (such as plot), or if you really want to compare two ROC curves smoothed differently.

If `method="delong"` and the AUC specification specifies a partial AUC, the warning “Using DeLong’s test for partial AUC is not supported. Using bootstrap test instead.” is issued. The `method` argument is ignored and “bootstrap” is used instead.

If `method="delong"` and the ROC curve is smoothed, the warning “Using DeLong’s test for smoothed ROCs is not supported. Using bootstrap test instead.” is issued. The `method` argument is ignored and “bootstrap” is used instead.

If `method="venkatraman"`, and the AUC specification specifies a partial AUC, the AUC specification is ignored with the warning “Partial AUC is ignored in Venkatraman’s test.”.

If `method="venkatraman"`, and `alternative` is “less” or “greater”, the warning “Only two-sided tests are available for Venkatraman. Performing two-sided test instead.” is produced and a two tailed test is performed.

Both DeLong and Venkatraman’s test ignores the direction of the ROC curve so that if two ROC curves have a different differ in the value of `direction`, the warning “(DeLong|Venkatraman)’s test should not be applied to ROC curves with different directions.” is printed. However, the spurious test is enforced.

If `boot.stratified=FALSE` and the sample has a large imbalance between cases and controls, it could happen that one or more of the replicates contains no case or control observation, or that there are not enough points for smoothing, producing a `NA` area. The warning “NA value(s) produced during bootstrap were ignored.” will be issued and the observation will be ignored. If you have a large imbalance in your sample, it could be safer to keep `boot.stratified=TRUE`.

Errors

Both Delong and Bootstrap tests work only on paired data. This assumption is enforced by the verification that the `responses` of `roc1` and `roc2` are identical. If they are found different, and the difference cannot be explained by missing values, the error “The ROC test is defined only on paired ROC curves” is produced.

An error will also occur if you give a `predictor2` when `predictor1` is a `matrix` or a `data.frame`, if `predictor1` has more than two columns, or if you do not give a `predictor2` when `predictor1` is a vector.

If `density.cases` and `density.controls` were provided for smoothing, the error “Cannot compute the statistic on ROC curves smoothed with density.controls and density.cases.” is issued.

If `method="venkatraman"` and one of the ROC curves is smoothed, the error “Using Venkatraman’s test for smoothed ROCs is not supported.” is produced.

With `method="specificity"`, the error “Argument ’specificity’ must be numeric of length 1 for a specificity test.” is given unless the specificity argument is specified as a numeric of length 1. The “Argument ’sensitivity’ must be numeric of length 1 for a sensitivity test.” message is given for `method="sensitivity"` under similar conditions.

Acknowledgements

We would like to thank E. S. Venkatraman and Colin B. Begg for their support in the implementation of their test.

References

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James A. Hanley and Barbara J. McNeil (1982) "The meaning and use of the area under a receiver operating characteristic (ROC) curve". *Radiology* **143**, 29–36.

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See Also

roc

Examples

```
data(aSAH)

# Basic example with 2 roc objects
roc1 <- roc(aSAH$outcome, aSAH$s100b)
roc2 <- roc(aSAH$outcome, aSAH$wfns)
roc.test(roc1, roc2)

## Not run:
# The latter used Delong's test. To use bootstrap test:
roc.test(roc1, roc2, method="bootstrap")
# Increase boot.n for a more precise p-value:
roc.test(roc1, roc2, method="bootstrap", boot.n=10000)

## End(Not run)

# Alternative syntaxes
roc.test(aSAH$outcome, aSAH$s100b, aSAH$wfns)
roc.test(aSAH$outcome, data.frame(aSAH$s100b, aSAH$wfns))

# If we had a good a priori reason to think that wfns gives a
# better classification than s100b (in other words, AUC of roc1
# should be lower than AUC of roc2):
```

```
roc.test(roc1, roc2, alternative="less")

## Not run:
# Comparison can be done on smoothed ROCs
# Smoothing is re-done at each iteration, and execution is slow
roc.test(smooth(roc1), smooth(roc2))
# or:
roc.test(aSAH$outcome, aSAH$s100b, aSAH$wfns, smooth=TRUE,
smooth.method="density", boot.n=100)

## End(Not run)
# or from an AUC (no smoothing)
roc.test(auc(roc1), roc2)

## Not run:
# Comparison of partial AUC:
roc3 <- roc(aSAH$outcome, aSAH$s100b, partial.auc=c(1, 0.8), partial.auc.focus="se")
roc4 <- roc(aSAH$outcome, aSAH$wfns, partial.auc=c(1, 0.8), partial.auc.focus="se")
roc.test(roc3, roc4)
# This is strictly equivalent to:
roc.test(roc3, roc4, method="bootstrap")

# Alternatively, we could re-use roc1 and roc2 to get the same result:
roc.test(roc1, roc2, reuse.auc=FALSE, partial.auc=c(1, 0.8), partial.auc.focus="se")

# Comparison on specificity and sensitivity
roc.test(roc1, roc2, method="specificity", specificity=0.9)
roc.test(roc1, roc2, method="sensitivity", sensitivity=0.9)

## End(Not run)

# Spurious use of DeLong's test with different direction:
roc5 <- roc(aSAH$outcome, aSAH$s100b, direction="<")
roc6 <- roc(aSAH$outcome, aSAH$s100b, direction=">")
roc.test(roc5, roc6, method="delong")

## Not run:
# Comparisons of the ROC curves
roc.test(roc1, roc2, method="venkatraman")

## End(Not run)

# Unpaired tests
roc7 <- roc(aSAH$outcome, aSAH$s100b)
# artificially create an roc8 unpaired with roc7
roc8 <- roc(aSAH$outcome[1:100], aSAH$s100b[1:100])
## Not run:
roc.test(roc7, roc8, paired=FALSE, method="delong")
roc.test(roc7, roc8, paired=FALSE, method="bootstrap")
roc.test(roc7, roc8, paired=FALSE, method="venkatraman")
roc.test(roc7, roc8, paired=FALSE, method="specificity", specificity=0.9)

## End(Not run)
```

smooth.roc *Smooth a ROC curve*

Description

This function smoothes a ROC curve of numeric predictor. By default, a binormal smoothing is performed, but density or custom smoothings are supported.

Usage

```
smooth(x, ...)
## Default S3 method:
smooth(x, ...)
## S3 method for class 'roc'
smooth(roc,
method=c("binormal", "density", "fitdistr"), n=512, bandwidth = "nrd",
density=NULL, density.controls=density, density.cases=density,
reuse.auc=TRUE, reuse.ci=FALSE, ...)
## S3 method for class 'smooth.roc'
smooth(smooth.roc, ...)
```

Arguments

`x` a roc object from the roc function (for smooth.roc), or a vector (for the regular (s+ default) smooth function).

`roc, smooth.roc`
a "roc" object from the `roc` function, or a "smooth.roc" object from the `smooth.roc` function.

`method` "binormal", "density", "fitdistr", or a function returning a list of smoothed sensitivities and specificities.

`n` the number of equally spaced points where the smoothed curve will be calculated.

`bandwidth` if `method="density"` and `density.controls` and `density.cases` are not provided, `bandwidth` is passed as `width` to `density` to determine the bandwidth of the density Can be a character string ("nrd", "hb", "ucv", "bcv" or "sj", but any name matching a function prefixed with "bandwidth." is supported) or a numeric value, as described in `density`. Defaults to "nrd".

`density, density.controls, density.cases`
if `method="density"`, a numeric value of density (over the y axis) or a function returning a density (such as `density`. If `method="fitdistr"`, one of "normal" (default), "exponential", "log-normal" (same as "lognormal") or "uniform", stating the shape of the underlying distribution. If the value is different for control and case observations, `density.controls` and `density.cases` can be employed instead, otherwise `density` will be propagated to both `density.controls` and `density.cases`.

`reuse.auc, reuse.ci`
: if `TRUE` (default for reuse.auc) and the "roc" objects contain "auc" or "ci" fields, re-use these specifications to regenerate `auc` or `ci` on the smoothed ROC curve with the original parameters. If `FALSE`, the object returned will not contain "auc" or "ci" fields. It is currently not possible to redefine `auc` and `ci` options directly: you need to call `auc` or `ci` later for that.

`...`
: further arguments passed to or from other methods, and especially to `density` (only `cut` and `window`, plus `kernel` and `adjust` for compatibility with R). Also passed to to `method` if it is a function.

Details

If `method="binormal"`, a linear model is fitted to the quantiles of the sensitivities and specificities. Smoothed sensitivities and specificities are then generated from this model on `n` points. This simple approach was found to work well for most ROC curves, but it may produce hooked smooths in some situations (see in Hanley (1988)).

With `method="density"`, the `density` function is employed to generate a smooth kernel density of the control and case observations as described by Zhou *et al.* (1997), unless `density.controls` or `density.cases` are provided directly. Otherwise, `bandwidth` can be given to specify a bandwidth to use with `density`. It can be a numeric value or a character string ("nrd", "hb", "ucv", "bcv" or "sj", but any name matching a function prefixed with "bandwidth." is supported). In the case of a character string, the whole predictor data is employed to determine the numeric value to use on both controls and cases. Note that the `width` argument to `density` is here called `bandwidth` to avoid clashes with the `width` argument to `plot.roc`. Depending on your data, it might be a good idea to specify the `window` argument for `density`. By default, "gaussian" is used, but "cosine", "3gaussian", "rectangular" and "triangular" are supported. As all the window kernels are symetrical, it might help to normalize the data first (that is, before calling `roc`), for example with quantile normalization:

```
norm.x <- qnorm(rank(x)/(length(x)+1))
smooth(roc(response, norm.x, ...), ...)
```

Additionally, `density` can be a function which must return either a numeric vector of densities over the y axis or a list with a "y" item like the `density` function. It must accept the following input:

```
density.fun(x, n, from, to, width, window, ...)
```

It is important to honour `n`, `from` and `to` in order to have the densities evaluated on the same points for controls and cases. Failing to do so and returning densities of different length will produce an error. It is also a good idea to use a constant smoothing parameter (such as `width`) especially when controls and cases have a different number of observations, to avoid producing smoother or rougher densities.

If `method="fitdistr"`, a function similar to the `fitdistr` function from the **MASS** package is employed to fit parameters for the density function `density`. The density function are fitted separately in control (`density.controls`) and case observations (`density.cases`).

`density` can be one of the character values “normal” (default), “exponential”, “log-normal” or “uniform”. No `start` parameter is supported, unlike `fitdistr` in the **MASS** package.

Finally, `method` can also be a function. It must return a list with exactly 2 elements named “sensitivities” and “specificities”, which must be numeric vectors between 0 and 1 or 100 (depending on the `percent` argument to `roc`). It is passed all the arguments to the `smooth` function.

`smooth.default` forces the usage of the default `smooth` function, so that other code relying on smooth should continue to function normally.

Smoothed ROC curves can be passed to smooth again. In this case, the smoothing is not re-applied on the smoothed ROC curve but the original “roc” object will be re-used.

Value

A list of class “smooth.roc” with the following fields:

`sensitivities`	the smoothed sensitivities defining the ROC curve.
`specificities`	the smoothed specificities defining the ROC curve.
`percent`	if the sensitivities, specificities and AUC are reported in percent, as defined in argument.
`direction`	the direction of the comparison, as defined in argument.
`thresholds`	the thresholds at which the sensitivities and specificities were computed.
`call`	how the function was called. See `match.call` for more details.
`smoothing.args`	a list of the arguments used for the smoothing. Will serve to apply the smoothing again in further bootstrap operations.
`fit.controls, fit.cases`	a list similar to a result of **MASS**’s `fitdistr` function for controls and cases, but with only “estimate”, and an additional “densfun” item indicating the density function, if possible as character.
`auc`	if the original ROC curve contained an AUC, it is computed again on the smoothed ROC.
`ci`	if the original ROC curve contained a CI, it is computed again on the smoothed ROC.

Additionally, the original `roc` object is stored as a “roc” attribute.

Errors

If `method` is a function, the return values will be checked thoroughly for validity (list with two numeric elements of the same length named “sensitivities” and “specificities” with values in the range of possible values for sensitivities and specificities).

The message “The ’density function must return a numeric vector or a list with a ’y’ item.” will be displayed if the `density` function did not return a valid output. The message “Length of ’density.controls’ and ’density.cases’ differ.” will be displayed if the returned value differ in length.

Binormal smoothing cannot smooth ROC curve defined by only one point. Any such attempt will fail with the error "ROC curve not smoothable (not enough points).". It will also fail if the points are poorly distributed and no model can be fit. In such a case, the error from 'lm' is printed within the message.

If the smooth ROC curve was generated by `roc` with `density.controls` and `density.cases` numeric arguments, it cannot be smoothed and the error "Cannot smooth a ROC curve generated directly with numeric 'density.controls' and 'density.cases'." is produced.

All three smoothing methods require a numeric `predictor`. If the ROC curve to smooth was generated with an ordered factor smoothing cannot be applied and the message "Only ROC curves of numeric predictors can be smoothed." is displayed.

References

James E. Hanley (1988) "The robustness of the "binormal" assumptions used in fitting ROC curves". *Medical Decision Making* **8**, 197–203.

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See Also

`roc`

Examples

```
data(aSAH)

## Basic example

rocobj <- roc(aSAH$outcome, aSAH$s100b)
smooth(rocobj)
# or directly with roc()
roc(aSAH$outcome, aSAH$s100b, smooth=TRUE)

# plotting
plot(rocobj)
rs <- smooth(rocobj, method="binormal")
plot(rs, add=TRUE, col="green")
rs2 <- smooth(rocobj, method="density")
plot(rs2, add=TRUE, col="blue")
rs3 <- smooth(rocobj, method="fitdistr", density="lognormal")
plot(rs3, add=TRUE, col="magenta")
legend(.6, .4, legend=c("Empirical", "Binormal", "Density", "Log-normal"),
       col=c("black", "green", "blue", "magenta"), lwd=2)

## Advanced smoothing
```

```
# different distibutions for controls and cases:
smooth(rocobj, method="fitdistr", density.controls="normal", density.cases="lognormal")

# with densities
width <- bandwidth.nrd(rocobj$predictor)
density.controls <- density(rocobj$controls, from=min(rocobj$predictor) - 3 * width,
                            to=max(rocobj$predictor) + 3*width, width=width, window="gaussia
density.cases <- density(rocobj$cases, from=min(rocobj$predictor) - 3 * width,
                            to=max(rocobj$predictor) + 3*width, width=width, window="gaussia
smooth(rocobj, method="density", density.controls=density.controls$y,
       density.cases=density.cases$y)
# which is roughly what is done by a simple:
smooth(rocobj, method="density")


## Smoothing artificial ROC curves

# two normals
roc.norm <- roc(rep(c(0, 1), each=1000),
                c(rnorm(1000), rnorm(1000)+1), plot=TRUE)
plot(smooth(roc.norm), col="green", lwd=1, add=TRUE)
plot(smooth(roc.norm, method="density"), col="red", lwd=1, add=TRUE)
plot(smooth(roc.norm, method="fitdistr"), col="blue", lwd=1, add=TRUE)
legend(.6, .4, legend=c("empirical", "binormal", "density",, "fitdistr"),
       col=c(par("fg"), "green", "red", "blue"), lwd=c(2, 1, 1, 1, 1))

# deviation from the normality
roc.norm.exp <- roc(rep(c(0, 1), each=1000),
                    c(rnorm(1000), rexp(1000)), plot=TRUE)
plot(smooth(roc.norm.exp), col="green", lwd=1, add=TRUE)
plot(smooth(roc.norm.exp, method="density"), col="red", lwd=1, add=TRUE)
# Wrong fitdistr: normality assumed by default
plot(smooth(roc.norm.exp, method="fitdistr"), col="blue", lwd=1, add=TRUE)
# Correct fitdistr
plot(smooth(roc.norm.exp, method="fitdistr", density.controls="normal",
            density.cases="exponential"), col="purple", lwd=1, add=TRUE)
legend(.6, .4, legend=c("empirical", "binormal", "density",
                        "wrong fitdistr", "correct fitdistr"),
       col=c(par("fg"), "green", "red", "blue", "purple"), lwd=c(2, 1, 1, 1, 1))


# large deviation from the normality
roc.unif.exp <- roc(rep(c(0, 1), each=1000),
                    c(runif(1000, -1, 1), rexp(1000)), plot=TRUE)
plot(smooth(roc.unif.exp), col="green", lwd=1, add=TRUE)
plot(smooth(roc.unif.exp, method="density"), col="red", lwd=1, add=TRUE)
# Wrong fitdistr: normality assumed by default
plot(smooth(roc.unif.exp, method="fitdistr"), col="blue", lwd=1, add=TRUE)
# Correct fitdistr
plot(smooth(roc.unif.exp, method="fitdistr", density.controls="uniform",
            density.cases="exponential"), col="purple", lwd=1, add=TRUE)
legend(.6, .4, legend=c("empirical", "binormal", "density", "density ucv",
                        "wrong fitdistr", "correct fitdistr"),
       col=c(par("fg"), "green", "red", "magenta", "blue", "purple"),
lwd=c(2, 1, 1, 1, 1))

# 2 uniform distributions with a custom density function
unif.density <- function(x, n, from, to, bw, kernel, ...) {
  smooth.x <- seq(from=from, to=to, length.out=n)
  smooth.y <- dunif(smooth.x, min=min(x), max=max(x))
  return(smooth.y)
}
roc.unif <- roc(rep(c(0, 1), each=1000),
                c(runif(1000, -1, 1), runif(1000, 0, 2)), plot=TRUE)
s <- smooth(roc.unif, method="density", density=unif.density)
plot(roc.unif)
plot(s, add=TRUE, col="grey")

## Not run:
# you can bootstrap a ROC curve smoothed with a density function:
ci(s, boot.n=100)

## End(Not run)
```

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