Package: ROCnGO (via r-universe)

May 18, 2026

Title Fast Analysis of ROC Curves

Version 0.1.0.9000

Description A toolkit for analyzing classifier performance by using receiver operating characteristic (ROC) curves. Performance may be assessed on a single classifier or multiple ones simultaneously, making it suitable for comparisons. In addition, different metrics allow the evaluation of local performance when working within restricted ranges of sensitivity and specificity. For details on the different implementations, see McClish D. K. (1989) <doi:10.1177/0272989X8900900307>, Vivo J.-M., Franco M. and Vicari D. (2018) <doi:10.1007/S11634-017-0295-9>, Jiang Y., et al (1996) <doi:10.1148/radiology.201.3.8939225>, Franco M. and Vivo J.-M. (2021) <doi:10.3390/math9212826> and Carrington, André M., et al (2020) <doi:10.1186/s12911-019-1014-6>.

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RoxygenNote 7.3.3

Imports cli, dplyr, forcats, ggplot2, magrittr, purrr, rlang, stringr, SummarizedExperiment, tibble, tidyr

Suggests knitr, rmarkdown, testthat (>= 3.0.0)

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URL `https://pablopnc.github.io/ROCnGO/`, `https://github.com/pabloPNC/ROCnGO`

Depends R (>= 4.1.0)

LazyData true

BugReports `https://github.com/pabloPNC/ROCnGO/issues`

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Contents

`add_chance_line` *Show chance line in a ROC plot*

Description

Plot chance line in a ROC plot.

Usage

```
add_chance_line()
```

Value

A ggplot layer instance object.

Examples

```
plot_roc_curve(iris, response = Species, predictor = Sepal.Width) +
 add_chance_line()
```

`add_fpauc_partially_proper_lower_bound` *Add FpAUC lower bound to a ROC plot*

Description

Calculate and plot lower bound defined by FpAUC sensitivity index.

- `add_fpauc_lower_bound()` provides an upper level function which automatically calculates curve shape and plots a lower bound that better fits it.
- `add_fpauc_partially_proper_lower_bound()` and `add_fpauc_concave_lower_bound()` are lower level functions that enforce the plot of specific bounds.

First one plots lower bound when curve shape is partially proper (presents some kind of hook). Second one plots lower bound when curve shape is concave in the region of interest.

Usage

```
add_fpauc_partially_proper_lower_bound(
  data,
  response = NULL,
  predictor = NULL,
  threshold,
  .condition = NULL,
  .label = NULL
)

add_fpauc_concave_lower_bound(
  data,
  response = NULL,
  predictor = NULL,
  threshold,
  .condition = NULL,
  .label = NULL
)
```

```
add_fpauc_lower_bound(
  data,
  response = NULL,
  predictor = NULL,
  threshold,
  .condition = NULL,
  .label = NULL
)
```

Arguments

`data`	A data.frame or extension (e.g. a tibble) containing values for predictors and response variables.
`response`	A data variable which must be a factor, integer or character vector representing the prediction outcome on each observation (*Gold Standard*). If the variable presents more than two possible outcomes, classes or categories: • The outcome of interest (the one to be predicted) will remain distinct. • All other categories will be combined into a single category. New combined category represents the "absence" of the condition to predict. See `.condition` for more information.
`predictor`	A data variable which must be numeric, representing values of a classifier or predictor for each observation.
`threshold`	A number between 0 and 1, inclusive. This number represents the lower value of TPR for the region where to calculate and plot lower bound. Because of definition of `fp_auc()`, region upper bound will be established as 1.
`.condition`	A value from response that represents class, category or condition of interest which wants to be predicted. If `NULL`, condition of interest will be selected automatically depending on `response` type. Once the class of interest is selected, rest of them will be collapsed in a common category, representing the "absence" of the condition to be predicted. See `vignette("selecting-condition")` for further information on how automatic selection is performed and details on selecting the condition of interest.
`.label`	A string representing the name used in labels. If `NULL`, variable name from `predictor` will be used as label.

Value

A ggplot layer instance object.

Examples

```
# Add lower bound based on curve shape (Concave)
plot_roc_curve(iris, response = Species, predictor = Sepal.Width) +
  add_fpauc_lower_bound(
```

```
    data = iris,
    response = Species,
    predictor = Sepal.Width,
    threshold = 0.9
  )
```

---

add_fpr_threshold_line

Add a threshold line to a ROC plot

Description

Include a threshold line on an specified axis.

Usage

```
add_fpr_threshold_line(threshold)

add_tpr_threshold_line(threshold)

add_threshold_line(threshold, ratio = NULL)
```

Arguments

`threshold`	A number between 0 and 1, both inclusive, which represents the region bound where to calculate partial area under curve. If `ratio` = `"tpr"`, it represents lower bound of the TPR region, being its upper limit equal to 1. If `ratio` = `"fpr"`, it represents the upper bound of the FPR region, being its lower limit equal to 0.
`ratio`	Ratio in which to display threshold. • If `"tpr"` threshold will be displayed in TPR, y axis • If `"fpr"` it will be displayed in FPR, x axis.

Value

A ggplot layer instance object.

Examples

```
# Add two threshold line in TPR = 0.9 and FPR = 0.1
plot_roc_curve(iris, response = Species, predictor = Sepal.Width) +
 add_threshold_line(threshold = 0.9, ratio = "tpr") +
 add_threshold_line(threshold = 0.1, ratio = "fpr")
# Add threshold line in TPR = 0.9
plot_roc_curve(iris, response = Species, predictor = Sepal.Width) +
 add_tpr_threshold_line(threshold = 0.9)
```

```
# Add threshold line in FPR = 0.1
plot_roc_curve(iris, response = Species, predictor = Sepal.Width) +
 add_fpr_threshold_line(threshold = 0.1)
```

`add_partial_roc_curve` *Add a section of a ROC curve to an existing one*

Description

Add an specific region of a ROC curve to an existing ROC plot.

Usage

```
add_partial_roc_curve(
  data,
  response = NULL,
  predictor = NULL,
  ratio,
  threshold,
  .condition = NULL,
  .label = NULL
)
```

Arguments

`data`	A data.frame or extension (e.g. a tibble) containing values for predictors and response variables.
`response`	A data variable which must be a factor, integer or character vector representing the prediction outcome on each observation (*Gold Standard*). If the variable presents more than two possible outcomes, classes or categories: • The outcome of interest (the one to be predicted) will remain distinct. • All other categories will be combined into a single category. New combined category represents the "absence" of the condition to predict. See `.condition` for more information.
`predictor`	A data variable which must be numeric, representing values of a classifier or predictor for each observation.
`ratio`	Ratio or axis where to apply calculations. • If `"tpr"`, only points within the specified region of TPR, y axis, will be considered for calculations. • If `"fpr"`, only points within the specified region of FPR, x axis, will be considered for calculations.
`threshold`	A number between 0 and 1, both inclusive, which represents the region bound where to calculate partial area under curve. If `ratio` = `"tpr"`, it represents lower bound of the TPR region, being its upper limit equal to 1.

	If `ratio = "fpr"`, it represents the upper bound of the FPR region, being its lower limit equal to 0.
`.condition`	A value from response that represents class, category or condition of interest which wants to be predicted. If `NULL`, condition of interest will be selected automatically depending on `response` type. Once the class of interest is selected, rest of them will be collapsed in a common category, representing the "absence" of the condition to be predicted. See `vignette("selecting-condition")` for further information on how automatic selection is performed and details on selecting the condition of interest.
`.label`	A string representing the name used in labels. If `NULL`, variable name from `predictor` will be used as label.

Value

A ggplot layer instance object.

Examples

```
plot_roc_curve(iris, response = Species, predictor = Sepal.Width) +
  add_partial_roc_curve(
    iris,
    response = Species,
    predictor = Sepal.Length,
    ratio = "tpr",
    threshold = 0.9
  )
```

`add_partial_roc_points` *Add points in a section of a ROC curve to an existing plot*

Description

Add points in a specific ROC region to an existing ROC plot.

Usage

```
add_partial_roc_points(
  data,
  response = NULL,
  predictor = NULL,
  ratio,
  threshold,
  .condition = NULL,
  .label = NULL
)
```

Arguments

`data`	A data.frame or extension (e.g. a tibble) containing values for predictors and response variables.
`response`	A data variable which must be a factor, integer or character vector representing the prediction outcome on each observation (*Gold Standard*). If the variable presents more than two possible outcomes, classes or categories: • The outcome of interest (the one to be predicted) will remain distinct. • All other categories will be combined into a single category. New combined category represents the "absence" of the condition to predict. See `.condition` for more information.
`predictor`	A data variable which must be numeric, representing values of a classifier or predictor for each observation.
`ratio`	Ratio or axis where to apply calculations. • If `"tpr"`, only points within the specified region of TPR, y axis, will be considered for calculations. • If `"fpr"`, only points within the specified region of FPR, x axis, will be considered for calculations.
`threshold`	A number between 0 and 1, both inclusive, which represents the region bound where to calculate partial area under curve. If `ratio = "tpr"`, it represents lower bound of the TPR region, being its upper limit equal to 1. If `ratio = "fpr"`, it represents the upper bound of the FPR region, being its lower limit equal to 0.
`.condition`	A value from response that represents class, category or condition of interest which wants to be predicted. If `NULL`, condition of interest will be selected automatically depending on `response` type. Once the class of interest is selected, rest of them will be collapsed in a common category, representing the "absence" of the condition to be predicted. See `vignette("selecting-condition")` for further information on how automatic selection is performed and details on selecting the condition of interest.
`.label`	A string representing the name used in labels. If `NULL`, variable name from `predictor` will be used as label.

Value

A ggplot layer instance object.

Examples

```
plot_roc_curve(iris, response = Species, predictor = Sepal.Width) +
  add_partial_roc_points(
    iris,
    response = Species,
    predictor = Sepal.Length,
```

```
    ratio = "tpr",
    threshold = 0.9
  )
```

`add_roc_curve` *Add a ROC curve plot to an existing one*

Description

Add a ROC curve to an existing ROC plot.

Usage

```
add_roc_curve(
  data,
  response = NULL,
  predictor = NULL,
  .condition = NULL,
  .label = NULL
)
```

Arguments

`data`	A data.frame or extension (e.g. a tibble) containing values for predictors and response variables.
`response`	A data variable which must be a factor, integer or character vector representing the prediction outcome on each observation (*Gold Standard*). If the variable presents more than two possible outcomes, classes or categories: • The outcome of interest (the one to be predicted) will remain distinct. • All other categories will be combined into a single category. New combined category represents the "absence" of the condition to predict. See `.condition` for more information.
`predictor`	A data variable which must be numeric, representing values of a classifier or predictor for each observation.
`.condition`	A value from response that represents class, category or condition of interest which wants to be predicted. If `NULL`, condition of interest will be selected automatically depending on `response` type. Once the class of interest is selected, rest of them will be collapsed in a common category, representing the "absence" of the condition to be predicted. See `vignette("selecting-condition")` for further information on how automatic selection is performed and details on selecting the condition of interest.
`.label`	A string representing the name used in labels. If `NULL`, variable name from `predictor` will be used as label.

Value

A ggplot layer instance object.

Examples

```
plot_roc_curve(iris, response = Species, predictor = Sepal.Width) +
 add_roc_curve(iris, response = Species, predictor = Sepal.Length)
```

`add_roc_points` *Add ROC points plot to an existing one*

Description

Add ROC points to an existing ROC plot.

Usage

```
add_roc_points(
  data,
  response = NULL,
  predictor = NULL,
  .condition = NULL,
  .label = NULL
)
```

Arguments

`data`	A data.frame or extension (e.g. a tibble) containing values for predictors and response variables.
`response`	A data variable which must be a factor, integer or character vector representing the prediction outcome on each observation (*Gold Standard*). If the variable presents more than two possible outcomes, classes or categories: • The outcome of interest (the one to be predicted) will remain distinct. • All other categories will be combined into a single category. New combined category represents the "absence" of the condition to predict. See `.condition` for more information.
`predictor`	A data variable which must be numeric, representing values of a classifier or predictor for each observation.
`.condition`	A value from response that represents class, category or condition of interest which wants to be predicted. If `NULL`, condition of interest will be selected automatically depending on `response` type. Once the class of interest is selected, rest of them will be collapsed in a common category, representing the "absence" of the condition to be predicted. See `vignette("selecting-condition")` for further information on how automatic selection is performed and details on selecting the condition of interest.

`.label`	A string representing the name used in labels. If `NULL`, variable name from `predictor` will be used as label.

Value

A ggplot layer instance object.

Examples

```
plot_roc_curve(iris, response = Species, predictor = Sepal.Width) +
 add_roc_points(iris, response = Species, predictor = Sepal.Length)
```

---

add_tpauc_concave_lower_bound
Add TpAUC lower bound to a ROC plot

Description

Calculate and plot lower bound defined by TpAUC specificity index.

- `add_tpauc_lower_bound()` provides a upper level function which automatically calculates curve shape and plots a lower bound that better fits it.

Additionally, several lower level functions are provided to plot specific lower bounds:

- `add_tpauc_concave_lower_bound()`. Plot lower bound corresponding to a ROC curve with concave shape in selected region.
- `add_tpauc_partially_proper_lower_bound`. Plot lower bound corresponding to a ROC curve with partially proper (presence of some hook) in selected region.
- `add_tpauc_under_chance_lower_bound`. Plot lower bound corresponding to a ROC curve with a hook under chance line in selected region.

Usage

```
add_tpauc_concave_lower_bound(
  data,
  response = NULL,
  predictor = NULL,
  lower_threshold,
  upper_threshold,
  .condition = NULL,
  .label = NULL
)

add_tpauc_partially_proper_lower_bound(
  data,
  response = NULL,
  predictor = NULL,
```

```
  lower_threshold,
  upper_threshold,
  .condition = NULL,
  .label = NULL
)

add_tpauc_under_chance_lower_bound(
  data,
  response = NULL,
  predictor = NULL,
  lower_threshold,
  upper_threshold,
  .condition = NULL,
  .label = NULL
)

add_tpauc_lower_bound(
  data,
  response = NULL,
  predictor = NULL,
  lower_threshold,
  upper_threshold,
  .condition = NULL,
  .label = NULL
)
```

Arguments

`data` A data.frame or extension (e.g. a tibble) containing values for predictors and response variables.

`response` A data variable which must be a factor, integer or character vector representing the prediction outcome on each observation (*Gold Standard*).

If the variable presents more than two possible outcomes, classes or categories:

- The outcome of interest (the one to be predicted) will remain distinct.
- All other categories will be combined into a single category.

New combined category represents the "absence" of the condition to predict. See `.condition` for more information.

`predictor` A data variable which must be numeric, representing values of a classifier or predictor for each observation.

`lower_threshold`, `upper_threshold`

Two numbers between 0 and 1, inclusive. These numbers represent lower and upper values of FPR region where to calculate and plot lower bound.

`.condition` A value from response that represents class, category or condition of interest which wants to be predicted.

If `NULL`, condition of interest will be selected automatically depending on `response` type.

	Once the class of interest is selected, rest of them will be collapsed in a common category, representing the "absence" of the condition to be predicted. See `vignette("selecting-condition")` for further information on how automatic selection is performed and details on selecting the condition of interest.
`.label`	A string representing the name used in labels. If `NULL`, variable name from `predictor` will be used as label.

Value

A ggplot layer instance object.

Examples

```
plot_roc_curve(iris, response = Species, predictor = Sepal.Width) +
  add_tpauc_lower_bound(
    data = iris,
    response = Species,
    predictor = Sepal.Width,
    upper_threshold =  0.1,
    lower_threshold = 0
  )
```

`auc` *Calculate area under ROC curve*

Description

Calculates area under curve (AUC) of a predictor's ROC curve.

Usage

```
auc(data = NULL, response, predictor, .condition = NULL)
```

Arguments

`data`	A data.frame or extension (e.g. a tibble) containing values for predictors and response variables.
`response`	A data variable which must be a factor, integer or character vector representing the prediction outcome on each observation (*Gold Standard*). If the variable presents more than two possible outcomes, classes or categories: • The outcome of interest (the one to be predicted) will remain distinct. • All other categories will be combined into a single category. New combined category represents the "absence" of the condition to predict. See `.condition` for more information.
`predictor`	A data variable which must be numeric, representing values of a classifier or predictor for each observation.

`.condition`	A value from response that represents class, category or condition of interest which wants to be predicted. If `NULL`, condition of interest will be selected automatically depending on `response` type. Once the class of interest is selected, rest of them will be collapsed in a common category, representing the "absence" of the condition to be predicted. See `vignette("selecting-condition")` for further information on how automatic selection is performed and details on selecting the condition of interest.

Value

A numerical value representing the area under ROC curve.

Examples

```
# Calc AUC of Sepal.Width as a classifier of setosa species
auc(iris, Species, Sepal.Width)
# Change class to predict to virginica
auc(iris, Species, Sepal.Width, .condition = "virginica")
```

`calc_curve_shape` *Calculate curve shape over an specific region*

Description

`calc_curve_shape()` calculates ROC curve shape over a specified region.

Usage

```
calc_curve_shape(
  data = NULL,
  response = NULL,
  predictor = NULL,
  lower_threshold,
  upper_threshold,
  ratio,
  .condition = NULL
)
```

Arguments

`data`	A data.frame or extension (e.g. a tibble) containing values for predictors and response variables.
`response`	A data variable which must be a factor, integer or character vector representing the prediction outcome on each observation (*Gold Standard*). If the variable presents more than two possible outcomes, classes or categories: • The outcome of interest (the one to be predicted) will remain distinct.

	• All other categories will be combined into a single category. New combined category represents the "absence" of the condition to predict. See `.condition` for more information.
`predictor`	A data variable which must be numeric, representing values of a classifier or predictor for each observation.
`lower_threshold, upper_threshold`	Two numbers between 0 and 1, inclusive. These numbers represent lower and upper bounds of the region where to apply calculations.
`ratio`	Ratio or axis where to apply calculations. • If `"tpr"`, only points within the specified region of TPR, y axis, will be considered for calculations. • If `"fpr"`, only points within the specified region of FPR, x axis, will be considered for calculations.
`.condition`	A value from response that represents class, category or condition of interest which wants to be predicted. If `NULL`, condition of interest will be selected automatically depending on `response` type. Once the class of interest is selected, rest of them will be collapsed in a common category, representing the "absence" of the condition to be predicted. See `vignette("selecting-condition")` for further information on how automatic selection is performed and details on selecting the condition of interest.

Value

A string indicating ROC curve shape in the specified region. Result can take any of the following values:

- `"Concave"`. ROC curve is concave over the entire specified region.
- `"Partially proper"`. ROC curve loses concavity at some point of the specified region.
- `"Hook under chance"`. ROC curve loses concavity at some point of the region and it lies below chance line.

Examples

```
# Calc ROC curve shape of Sepal.Width as a classifier of setosa species
# in TPR = (0.9, 1)
calc_curve_shape(iris, Species, Sepal.Width, 0.9, 1, "tpr")
# Change class to virginica
calc_curve_shape(iris, Species, Sepal.Width, 0.9, 1, "tpr", .condition = "virginica")
```

`calc_partial_roc_points` *Calculate ROC curve partial points*

Description

Calculates a series pairs of (FPR, TPR) which correspond to ROC curve points in a specified region.

Usage

```
calc_partial_roc_points(
  data = NULL,
  response = NULL,
  predictor = NULL,
  lower_threshold,
  upper_threshold,
  ratio,
  .condition = NULL
)
```

Arguments

`data`	A data.frame or extension (e.g. a tibble) containing values for predictors and response variables.
`response`	A data variable which must be a factor, integer or character vector representing the prediction outcome on each observation (*Gold Standard*). If the variable presents more than two possible outcomes, classes or categories: • The outcome of interest (the one to be predicted) will remain distinct. • All other categories will be combined into a single category. New combined category represents the "absence" of the condition to predict. See `.condition` for more information.
`predictor`	A data variable which must be numeric, representing values of a classifier or predictor for each observation.
`lower_threshold`, `upper_threshold`	Two numbers between 0 and 1, inclusive. These numbers represent lower and upper bounds of the region where to apply calculations.
`ratio`	Ratio or axis where to apply calculations. • If `"tpr"`, only points within the specified region of TPR, y axis, will be considered for calculations. • If `"fpr"`, only points within the specified region of FPR, x axis, will be considered for calculations.
`.condition`	A value from response that represents class, category or condition of interest which wants to be predicted.

If `NULL`, condition of interest will be selected automatically depending on `response` type.

Once the class of interest is selected, rest of them will be collapsed in a common category, representing the "absence" of the condition to be predicted.

See `vignette("selecting-condition")` for further information on how automatic selection is performed and details on selecting the condition of interest.

Value

A tibble with two columns:

- "tpr". Containing "true positive ratio", or y, values of points within the specified region.
- "fpr". Containing "false positive ratio", or x, values of points within the specified region.

Examples

```
# Calc ROC points of Sepal.Width as a classifier of setosa species
# in TPR = (0.9, 1)
calc_partial_roc_points(
 iris,
 response = Species,
 predictor = Sepal.Width,
 lower_threshold = 0.9,
 upper_threshold = 1,
 ratio = "tpr"
)

# Change class to virginica
calc_partial_roc_points(
 iris,
 response = Species,
 predictor = Sepal.Width,
 lower_threshold = 0.9,
 upper_threshold = 1,
 ratio = "tpr",
 .condition = "virginica"
)
```

`concordance_indexes` *Concordance indexes*

Description

Concordance derived indexes allow calculation and explanation of area under ROC curve in a specific region. They use a dual perspective since they consider both TPR and FPR ranges which enclose the region of interest.

`cp_auc()` applies *concordan partial area under curve* (CpAUC), while `ncp_auc()` applies its normalized version by dividing by the total area.

Usage

```
cp_auc(
  data = NULL,
  response,
  predictor,
  lower_threshold,
  upper_threshold,
  ratio,
  .condition = NULL
)

ncp_auc(
  data = NULL,
  response,
  predictor,
  lower_threshold,
  upper_threshold,
  ratio,
  .condition = NULL
)
```

Arguments

`data`	A data.frame or extension (e.g. a tibble) containing values for predictors and response variables.
`response`	A data variable which must be a factor, integer or character vector representing the prediction outcome on each observation (*Gold Standard*). If the variable presents more than two possible outcomes, classes or categories: • The outcome of interest (the one to be predicted) will remain distinct. • All other categories will be combined into a single category. New combined category represents the "absence" of the condition to predict. See `.condition` for more information.
`predictor`	A data variable which must be numeric, representing values of a classifier or predictor for each observation.
`lower_threshold`, `upper_threshold`	Two numbers between 0 and 1, inclusive. These numbers represent lower and upper bounds of the region where to apply calculations.
`ratio`	Ratio or axis where to apply calculations. • If `"tpr"`, only points within the specified region of TPR, y axis, will be considered for calculations. • If `"fpr"`, only points within the specified region of FPR, x axis, will be considered for calculations.
`.condition`	A value from response that represents class, category or condition of interest which wants to be predicted. If `NULL`, condition of interest will be selected automatically depending on `response` type.

Once the class of interest is selected, rest of them will be collapsed in a common category, representing the "absence" of the condition to be predicted.

See `vignette("selecting-condition")` for further information on how automatic selection is performed and details on selecting the condition of interest.

Value

A numeric value representing index score for the partial area under ROC curve.

References

Carrington, André M., et al. A new concordant partial AUC and partial c statistic for imbalanced data in the evaluation of machine learning algorithms. *BMC medical informatics and decision making* 20 (2020): 1-12.

Examples

```
# Calculate cp_auc of Sepal.Width as a classifier of setosa especies in
# FPR = (0, 0.1)
cp_auc(
  iris,
  response = Species,
  predictor = Sepal.Width,
  lower_threshold = 0,
  upper_threshold = 0.1,
  ratio = "fpr"
)
# Calculate ncp_auc of Sepal.Width as a classifier of setosa especies in
# FPR = (0, 0.1)
ncp_auc(
  iris,
  response = Species,
  predictor = Sepal.Width,
  lower_threshold = 0,
  upper_threshold = 0.1,
  ratio = "fpr"
)
```

`hide_legend` *Hide legend in a ROC plot*

Description

Hide legend showing name of ploted classifiers and bounds in a ROC curve plot.

Usage

```
hide_legend()
```

Value

A ggplot theme object.

`npauc_lower_bounds` *Add NpAUC lower bound to a ROC plot*

Description

Calculate and plot lower bound defined by NpAUC specificity index.

- `add_npauc_normalized_lower_bound()` allows to plot normalized lower bound, which is used to formally calculate NpAUC.
- `add_npauc_lower_bound()` is a lower level function providing a way to plot lower bound previous to normalization.

Usage

```
add_npauc_lower_bound(
  data,
  response = NULL,
  predictor = NULL,
  threshold,
  .condition = NULL,
  .label = NULL
)

add_npauc_normalized_lower_bound(
  data,
  response = NULL,
  predictor = NULL,
  threshold,
  .condition = NULL,
  .label = NULL
)
```

Arguments

`data` A data.frame or extension (e.g. a tibble) containing values for predictors and response variables.

`response` A data variable which must be a factor, integer or character vector representing the prediction outcome on each observation (*Gold Standard*).

If the variable presents more than two possible outcomes, classes or categories:

- The outcome of interest (the one to be predicted) will remain distinct.
- All other categories will be combined into a single category.

New combined category represents the "absence" of the condition to predict. See `.condition` for more information.

`predictor`	A data variable which must be numeric, representing values of a classifier or predictor for each observation.
`threshold`	A number between 0 and 1, inclusive. This number represents the lower value of TPR for the region where to calculate and plot lower bound. Because of definition of `np_auc()`, region upper bound will be established as 1.
`.condition`	A value from response that represents class, category or condition of interest which wants to be predicted. If `NULL`, condition of interest will be selected automatically depending on `response` type. Once the class of interest is selected, rest of them will be collapsed in a common category, representing the "absence" of the condition to be predicted. See `vignette("selecting-condition")` for further information on how automatic selection is performed and details on selecting the condition of interest.
`.label`	A string representing the name used in labels. If `NULL`, variable name from `predictor` will be used as label.

Value

A ggplot layer instance object.

Examples

```
plot_roc_curve(iris, response = Species, predictor = Sepal.Width) +
  add_npauc_lower_bound(
    iris,
    response = Species,
    predictor = Sepal.Width,
    threshold = 0.9
  )
```

`pauc` *Calculate partial area under curve*

Description

Calculates area under curve curve in an specific TPR or FPR region.

Usage

```
pauc(
  data = NULL,
  response,
  predictor,
  ratio,
  lower_threshold,
  upper_threshold,
  .condition = NULL
)
```

Arguments

`data`	A data.frame or extension (e.g. a tibble) containing values for predictors and response variables.
`response`	A data variable which must be a factor, integer or character vector representing the prediction outcome on each observation (*Gold Standard*). If the variable presents more than two possible outcomes, classes or categories: • The outcome of interest (the one to be predicted) will remain distinct. • All other categories will be combined into a single category. New combined category represents the "absence" of the condition to predict. See `.condition` for more information.
`predictor`	A data variable which must be numeric, representing values of a classifier or predictor for each observation.
`ratio`	Ratio or axis where to apply calculations. • If `"tpr"`, only points within the specified region of TPR, y axis, will be considered for calculations. • If `"fpr"`, only points within the specified region of FPR, x axis, will be considered for calculations.
`lower_threshold, upper_threshold`	Two numbers between 0 and 1, inclusive. These numbers represent lower and upper bounds of the region where to apply calculations.
`.condition`	A value from response that represents class, category or condition of interest which wants to be predicted. If `NULL`, condition of interest will be selected automatically depending on `response` type. Once the class of interest is selected, rest of them will be collapsed in a common category, representing the "absence" of the condition to be predicted. See `vignette("selecting-condition")` for further information on how automatic selection is performed and details on selecting the condition of interest.

Value

A numeric value representing the area under ROC curve in the specified region.

Examples

```
# Calculate pauc of Sepal.Width as a classifier of setosa species in
# in TPR = (0.9, 1)
pauc(
  iris,
  response = Species,
  predictor = Sepal.Width,
  ratio = "tpr",
  lower_threshold = 0.9,
  upper_threshold = 1
)
# Calculate pauc of Sepal.Width as a classifier of setosa species in
```

```
# in FPR = (0, 0.1)
pauc(
  iris,
  response = Species,
  predictor = Sepal.Width,
  ratio = "fpr",
  lower_threshold = 0,
  upper_threshold = 0.1
)
```

---

plot_partial_roc_curve

Plot a section of a classifier ROC curve

Description

Create a curve plot using points in an specific region of ROC curve.

Usage

```
plot_partial_roc_curve(
  data,
  response = NULL,
  predictor = NULL,
  ratio,
  threshold,
  .condition = NULL,
  .label = NULL
)
```

Arguments

`data`	A data.frame or extension (e.g. a tibble) containing values for predictors and response variables.
`response`	A data variable which must be a factor, integer or character vector representing the prediction outcome on each observation (*Gold Standard*). If the variable presents more than two possible outcomes, classes or categories: • The outcome of interest (the one to be predicted) will remain distinct. • All other categories will be combined into a single category. New combined category represents the "absence" of the condition to predict. See `.condition` for more information.
`predictor`	A data variable which must be numeric, representing values of a classifier or predictor for each observation.
`ratio`	Ratio or axis where to apply calculations. • If `"tpr"`, only points within the specified region of TPR, y axis, will be considered for calculations.

	• If `"fpr"`, only points within the specified region of FPR, x axis, will be considered for calculations.
`threshold`	A number between 0 and 1, both inclusive, which represents the region bound where to calculate partial area under curve. If `ratio = "tpr"`, it represents lower bound of the TPR region, being its upper limit equal to 1. If `ratio = "fpr"`, it represents the upper bound of the FPR region, being its lower limit equal to 0.
`.condition`	A value from response that represents class, category or condition of interest which wants to be predicted. If `NULL`, condition of interest will be selected automatically depending on `response` type. Once the class of interest is selected, rest of them will be collapsed in a common category, representing the "absence" of the condition to be predicted. See `vignette("selecting-condition")` for further information on how automatic selection is performed and details on selecting the condition of interest.
`.label`	A string representing the name used in labels. If `NULL`, variable name from `predictor` will be used as label.

Value

A ggplot object.

Examples

```
plot_partial_roc_curve(
 iris,
 response = Species,
 predictor = Sepal.Width,
 ratio = "tpr",
 threshold = 0.9
)
```

`plot_partial_roc_points`

Plot points in a region of a ROC curve

Description

Create an scatter plot using points in an specific region of ROC curve.

Usage

```
plot_partial_roc_points(
  data,
  response = NULL,
  predictor = NULL,
  ratio,
  threshold,
  .condition = NULL,
  .label = NULL
)
```

Arguments

`data`	A data.frame or extension (e.g. a tibble) containing values for predictors and response variables.
`response`	A data variable which must be a factor, integer or character vector representing the prediction outcome on each observation (*Gold Standard*). If the variable presents more than two possible outcomes, classes or categories: • The outcome of interest (the one to be predicted) will remain distinct. • All other categories will be combined into a single category. New combined category represents the "absence" of the condition to predict. See `.condition` for more information.
`predictor`	A data variable which must be numeric, representing values of a classifier or predictor for each observation.
`ratio`	Ratio or axis where to apply calculations. • If `"tpr"`, only points within the specified region of TPR, y axis, will be considered for calculations. • If `"fpr"`, only points within the specified region of FPR, x axis, will be considered for calculations.
`threshold`	A number between 0 and 1, both inclusive, which represents the region bound where to calculate partial area under curve. If `ratio` = `"tpr"`, it represents lower bound of the TPR region, being its upper limit equal to 1. If `ratio` = `"fpr"`, it represents the upper bound of the FPR region, being its lower limit equal to 0.
`.condition`	A value from response that represents class, category or condition of interest which wants to be predicted. If `NULL`, condition of interest will be selected automatically depending on `response` type. Once the class of interest is selected, rest of them will be collapsed in a common category, representing the "absence" of the condition to be predicted. See `vignette("selecting-condition")` for further information on how automatic selection is performed and details on selecting the condition of interest.
`.label`	A string representing the name used in labels. If `NULL`, variable name from `predictor` will be used as label.

Value

A ggplot object.

Examples

```
plot_partial_roc_points(
 iris,
 response = Species,
 predictor = Sepal.Width,
 ratio = "tpr",
 threshold = 0.9
)
```

`plot_roc_curve` *Plot a classifier ROC curve*

Description

Create a curve plot using ROC curve points.

Usage

```
plot_roc_curve(
  data,
  response = NULL,
  predictor = NULL,
  .condition = NULL,
  .label = NULL
)
```

Arguments

`data` A data.frame or extension (e.g. a tibble) containing values for predictors and response variables.

`response` A data variable which must be a factor, integer or character vector representing the prediction outcome on each observation (*Gold Standard*).

If the variable presents more than two possible outcomes, classes or categories:

- The outcome of interest (the one to be predicted) will remain distinct.
- All other categories will be combined into a single category.

New combined category represents the "absence" of the condition to predict. See `.condition` for more information.

`predictor` A data variable which must be numeric, representing values of a classifier or predictor for each observation.

`.condition`	A value from response that represents class, category or condition of interest which wants to be predicted. If `NULL`, condition of interest will be selected automatically depending on `response` type. Once the class of interest is selected, rest of them will be collapsed in a common category, representing the "absence" of the condition to be predicted. See `vignette("selecting-condition")` for further information on how automatic selection is performed and details on selecting the condition of interest.
`.label`	A string representing the name used in labels. If `NULL`, variable name from `predictor` will be used as label.

Value

A ggplot object.

Examples

```
plot_roc_curve(iris, response = Species, predictor = Sepal.Width)
```

`plot_roc_points` *Plot classifier points of a ROC curve*

Description

Create an scatter plot using ROC curve points.

Usage

```
plot_roc_points(
  data,
  response = NULL,
  predictor = NULL,
  .condition = NULL,
  .label = NULL
)
```

Arguments

`data`	A data.frame or extension (e.g. a tibble) containing values for predictors and response variables.
`response`	A data variable which must be a factor, integer or character vector representing the prediction outcome on each observation (*Gold Standard*). If the variable presents more than two possible outcomes, classes or categories: • The outcome of interest (the one to be predicted) will remain distinct. • All other categories will be combined into a single category.

	New combined category represents the "absence" of the condition to predict. See `.condition` for more information.
`predictor`	A data variable which must be numeric, representing values of a classifier or predictor for each observation.
`.condition`	A value from response that represents class, category or condition of interest which wants to be predicted. If `NULL`, condition of interest will be selected automatically depending on `response` type. Once the class of interest is selected, rest of them will be collapsed in a common category, representing the "absence" of the condition to be predicted. See `vignette("selecting-condition")` for further information on how automatic selection is performed and details on selecting the condition of interest.
`.label`	A string representing the name used in labels. If `NULL`, variable name from `predictor` will be used as label.

Value

A ggplot object.

Examples

```
plot_roc_points(iris, response = Species, predictor = Sepal.Width)
```

`prost` *Prostate cancer gene expression data*

Description

This dataset contains gene expression levels obtained from healthy and diseased tissue samples from patients with prostate cancer. The data includes the expression values for each selected gene, as well as clinical variables derived from the direct observation of the tissue samples.

Usage

```
prost
```

Format

A tibble with 554 observations and 2654 variables:

ENSG... Gene expression levels. Column names correspond to the measured gene identifier.

gleason_score Score derived from tissue observation, which indicates disease severity and progression.

disease Categorical variable indicating whether the sample comes from diseased ("1") or healthy ("0") tissue.

prognostic Categorical variable indicating whether a poor ("1") or a good ("0") prognosis is expected for the patient. Diseased cases in the dataset are assumed to have a poor prognosis when their Gleason score is equal to or above 8. Non-diseased cases are labelled as "Normal".

Details

Gene identifiers used in columns (e.g. `ENSG00000113924`, `ENSG00000109182`, ...) correspond to Ensembl gene identifiers.

Gene expression values are reported as *Transcript Per Million* (TPM).

Source

Raw data obtained from The Cancer Genome Atlas (TCGA) through the Genomic Data Commons Data Portal (`https://portal.gdc.cancer.gov/`). Data have been preprocessed and curated by the authors (e.g., gene selection and variable creation, etc.) to create the final dataset.

The data shown here are in whole or part based upon data generated by the TCGA Research Network: `https://www.cancer.gov/tcga`.

`roc_points` *Calculate ROC curve points*

Description

Calculates a series pairs of (FPR, TPR) which correspond to points displayed by ROC curve. "false positive ratio" will be represented on x axis, while "true positive ratio" on y one.

Usage

```
roc_points(data = NULL, response, predictor, .condition = NULL)
```

Arguments

`data`	A data.frame or extension (e.g. a tibble) containing values for predictors and response variables.
`response`	A data variable which must be a factor, integer or character vector representing the prediction outcome on each observation (*Gold Standard*). If the variable presents more than two possible outcomes, classes or categories: • The outcome of interest (the one to be predicted) will remain distinct. • All other categories will be combined into a single category. New combined category represents the "absence" of the condition to predict. See `.condition` for more information.
`predictor`	A data variable which must be numeric, representing values of a classifier or predictor for each observation.
`.condition`	A value from response that represents class, category or condition of interest which wants to be predicted. If `NULL`, condition of interest will be selected automatically depending on `response` type. Once the class of interest is selected, rest of them will be collapsed in a common category, representing the "absence" of the condition to be predicted. See `vignette("selecting-condition")` for further information on how automatic selection is performed and details on selecting the condition of interest.

Value

A tibble with two columns:

- "tpr". Containing values for "true positive ratio", or y axis.
- "fpr". Containing values for "false positive ratio", or x axis.

Examples

```
# Calc ROC points of Sepal.Width as a classifier of setosa species
roc_points(iris, Species, Sepal.Width)
# Change class to predict to virginica
roc_points(iris, Species, Sepal.Width, .condition = "virginica")
```

`sensitivity_indexes` *Sensitivity indexes*

Description

Sensitivity indexes provide different ways of calculating area under ROC curve in a specific TPR region. Two different approaches to calculate this area are available:

- `fp_auc()` applies *fitted partial area under curve* index (FpAUC). This one calculates area under curve adjusting to points defined by the curve in the selected region.
- `np_auc()` applies *normalized partial area under curve* index (NpAUC), which calculates area under curve over the whole specified region.

Usage

```
fp_auc(data = NULL, response, predictor, lower_tpr, .condition = NULL)

np_auc(data, response, predictor, lower_tpr, .condition = NULL)
```

Arguments

`data`	A data.frame or extension (e.g. a tibble) containing values for predictors and response variables.
`response`	A data variable which must be a factor, integer or character vector representing the prediction outcome on each observation (*Gold Standard*). If the variable presents more than two possible outcomes, classes or categories: • The outcome of interest (the one to be predicted) will remain distinct. • All other categories will be combined into a single category. New combined category represents the "absence" of the condition to predict. See `.condition` for more information.
`predictor`	A data variable which must be numeric, representing values of a classifier or predictor for each observation.

`lower_tpr`	A numeric value between 0 and 1, inclusive, which represents lower value of TPR for the region where to calculate the partial area under curve. Because of definition of sensitivity indexes, upper bound of the region will be established as 1.
`.condition`	A value from response that represents class, category or condition of interest which wants to be predicted. If `NULL`, condition of interest will be selected automatically depending on `response` type. Once the class of interest is selected, rest of them will be collapsed in a common category, representing the "absence" of the condition to be predicted. See `vignette("selecting-condition")` for further information on how automatic selection is performed and details on selecting the condition of interest.

Value

A numeric value representing the index score for the partial area under ROC curve.

References

Franco M. y Vivo J.-M. Evaluating the Performances of Biomarkers over a Restricted Domain of High Sensitivity. *Mathematics* 9, 2826 (2021).

Jiang Y., Metz C. E. y Nishikawa R. M. A receiver operating characteristic partial area index for highly sensitive diagnostic tests. *Radiology* 201, 745-750 (1996).

Examples

```
# Calculate fp_auc of Sepal.Width as a classifier of setosa species
# in TPR = (0.9, 1)
fp_auc(iris, response = Species, predictor = Sepal.Width, lower_tpr = 0.9)
# Calculate np_auc of Sepal.Width as a classifier of setosa species
# in TPR = (0.9, 1)
np_auc(iris, response = Species, predictor = Sepal.Width, lower_tpr = 0.9)
```

`sp_auc` *Specificity indexes*

Description

Specificity indexes provide different ways of calculating area under ROC curve in a specific FPR region. Two different approaches to calculate this area are available:

- `tp_auc()` applies *tighter partial area under curve* index (SpAUC). This one calculates area under curve adjusting to points defined by the curve in the selected region.
- `sp_auc()` applies *standardized partial area under curve* index (TpAUC), which calculates area under curve over the whole specified region.

Usage

```
sp_auc(
  data = NULL,
  response,
  predictor,
  lower_fpr,
  upper_fpr,
  .condition = NULL,
  .invalid = FALSE
)

tp_auc(
  data = NULL,
  response,
  predictor,
  lower_fpr,
  upper_fpr,
  .condition = NULL
)
```

Arguments

`data`	A data.frame or extension (e.g. a tibble) containing values for predictors and response variables.
`response`	A data variable which must be a factor, integer or character vector representing the prediction outcome on each observation (*Gold Standard*). If the variable presents more than two possible outcomes, classes or categories: • The outcome of interest (the one to be predicted) will remain distinct. • All other categories will be combined into a single category. New combined category represents the "absence" of the condition to predict. See `.condition` for more information.
`predictor`	A data variable which must be numeric, representing values of a classifier or predictor for each observation.
`lower_fpr`, `upper_fpr`	Two numbers between 0 and 1, inclusive. These numbers represent lower and upper values of FPR region where to calculate partial area under curve.
`.condition`	A value from response that represents class, category or condition of interest which wants to be predicted. If `NULL`, condition of interest will be selected automatically depending on `response` type. Once the class of interest is selected, rest of them will be collapsed in a common category, representing the "absence" of the condition to be predicted. See `vignette("selecting-condition")` for further information on how automatic selection is performed and details on selecting the condition of interest.
`.invalid`	If `FALSE`, the default, `sp_auc()` will return `NA` when ROC curve does not fit theoretical bounds and index cannot be applied. If `TRUE`, function will force the calculation and return a value despite probably being incorrect.

Value

A numeric value representing the index score for the partial area under ROC curve.

References

McClish D. K. Analyzing a Portion of the ROC Curve. *Medical Decision Making* 9, 190-195 (1989).

Vivo J.-M., Franco M. y Vicari D. Rethinking an ROC partial area index for evaluating the classification performance at a high specificity range. *Advances in Data Analysis and Classification* 12, 683-704 (2018).

Examples

```
# Calculate sp_auc of Sepal.Width as a classifier of setosa species
# in FPR = (0.9, 1)
sp_auc(
 iris,
 response = Species,
 predictor = Sepal.Width,
 lower_fpr = 0,
 upper_fpr = 0.1
)
# Calculate tp_auc of Sepal.Width as a classifier of setosa species
 # in FPR = (0.9, 1)
tp_auc(
 iris,
 response = Species,
 predictor = Sepal.Width,
 lower_fpr = 0,
 upper_fpr = 0.1
)
```

`spauc_lower_bounds` *Add SpAUC lower bound to a ROC plot*

Description

Calculate and plot lower bound defined by SpAUC specificity index.

Usage

```
add_spauc_lower_bound(
  data,
  response = NULL,
  predictor = NULL,
  lower_threshold,
  upper_threshold,
  .condition = NULL,
```

```
  .label = NULL
)
```

Arguments

`data`	A data.frame or extension (e.g. a tibble) containing values for predictors and response variables.
`response`	A data variable which must be a factor, integer or character vector representing the prediction outcome on each observation (*Gold Standard*). If the variable presents more than two possible outcomes, classes or categories: • The outcome of interest (the one to be predicted) will remain distinct. • All other categories will be combined into a single category. New combined category represents the "absence" of the condition to predict. See `.condition` for more information.
`predictor`	A data variable which must be numeric, representing values of a classifier or predictor for each observation.
`lower_threshold`, `upper_threshold`	Two numbers between 0 and 1, inclusive. These numbers represent lower and upper bounds of the region where to apply calculations.
`.condition`	A value from response that represents class, category or condition of interest which wants to be predicted. If `NULL`, condition of interest will be selected automatically depending on `response` type. Once the class of interest is selected, rest of them will be collapsed in a common category, representing the "absence" of the condition to be predicted. See `vignette("selecting-condition")` for further information on how automatic selection is performed and details on selecting the condition of interest.
`.label`	A string representing the name used in labels. If `NULL`, variable name from `predictor` will be used as label.

Details

SpAUC presents some limitations regarding its lower bound. Lower bound defined by this index cannot be applied to sections where ROC curve is defined under chance line.

`add_spauc_lower_bound()` doesn't make any check to ensure the index can be safely applied. Consequently, it allows to enforce the representation even though SpAUC cound't be calculated in the region.

Value

A ggplot layer instance object.

Examples

```
plot_roc_curve(iris, response = Species, predictor = Sepal.Width) +
  add_spauc_lower_bound(
    iris,
    response = Species,
    predictor = Sepal.Width,
    lower_threshold = 0,
    upper_threshold = 0.1
  )
```

`sumexp_to_df` *Transform data in a SummarizedExperiment to a data.frame*

Description

Transforms a SummarizedExperiment into a data.frame which can be used as input for other functions.

Usage

```
sumexp_to_df(se, .n = NULL)
```

Arguments

`se`	A SummarizedExperiment object.
`.n`	An integer or string, representing the index or name of the assay to use. Same as `i` in `SummarizedExperiment::assay()` function. By default, function combines every assay in `se` argument.

Value

A data.frame created from combining assays and colData in a SummarizedExperiment.

`summarize_dataset` *Summarize classifiers performance in a dataset*

Description

Calculate a series of metrics describing global and local performance for selected classifiers in a dataset.

Usage

```
summarize_dataset(
  data,
  predictors = NULL,
  response,
  ratio,
  threshold,
  .condition = NULL,
  .progress = FALSE
)
```

Arguments

`data`	A data.frame or extension (e.g. a tibble) containing values for predictors and response variables.
`predictors`	A vector of numeric data variables which represents the different classifiers or predictors in data to be summarized. If `NULL`and by default, `predictors` will match all numeric variables in `data` with the exception of `response`, given that it has a numeric type.
`response`	A data variable which must be a factor, integer or character vector representing the prediction outcome on each observation (*Gold Standard*). If the variable presents more than two possible outcomes, classes or categories: • The outcome of interest (the one to be predicted) will remain distinct. • All other categories will be combined into a single category. New combined category represents the "absence" of the condition to predict. See `.condition` for more information.
`ratio`	Ratio or axis where to apply calculations. • If `"tpr"`, only points within the specified region of TPR, y axis, will be considered for calculations. • If `"fpr"`, only points within the specified region of FPR, x axis, will be considered for calculations.
`threshold`	A number between 0 and 1, both inclusive, which represents the region bound where to calculate partial area under curve. If `ratio` = `"tpr"`, it represents lower bound of the TPR region, being its upper limit equal to 1. If `ratio` = `"fpr"`, it represents the upper bound of the FPR region, being its lower limit equal to 0.
`.condition`	A value from response that represents class, category or condition of interest which wants to be predicted. If `NULL`, condition of interest will be selected automatically depending on `response` type. Once the class of interest is selected, rest of them will be collapsed in a common category, representing the "absence" of the condition to be predicted. See `vignette("selecting-condition")` for further information on how automatic selection is performed and details on selecting the condition of interest.
`.progress`	If `TRUE`, show progress of calculations.

Value

A list with different elements:

- Performance metrics for each of evaluated classifiers.
- Overall description of performance metrics in the dataset.

Examples

```
summarize_dataset(iris, response = Species, ratio = "tpr", threshold = 0.9)
```

`summarize_predictor` *Summarize classifier performance*

Description

Calculates a series of metrics describing global and local classifier performance.

Usage

```
summarize_predictor(
  data = NULL,
  predictor,
  response,
  ratio,
  threshold,
  .condition = NULL
)
```

Arguments

`data`	A data.frame or extension (e.g. a tibble) containing values for predictors and response variables.
`predictor`	A data variable which must be numeric, representing values of a classifier or predictor for each observation.
`response`	A data variable which must be a factor, integer or character vector representing the prediction outcome on each observation (*Gold Standard*). If the variable presents more than two possible outcomes, classes or categories: • The outcome of interest (the one to be predicted) will remain distinct. • All other categories will be combined into a single category. New combined category represents the "absence" of the condition to predict. See `.condition` for more information.
`ratio`	Ratio or axis where to apply calculations. • If `"tpr"`, only points within the specified region of TPR, y axis, will be considered for calculations.

- If `"fpr"`, only points within the specified region of FPR, x axis, will be considered for calculations.

`threshold`	A number between 0 and 1, both inclusive, which represents the region bound where to calculate partial area under curve. If `ratio = "tpr"`, it represents lower bound of the TPR region, being its upper limit equal to 1. If `ratio = "fpr"`, it represents the upper bound of the FPR region, being its lower limit equal to 0.
`.condition`	A value from response that represents class, category or condition of interest which wants to be predicted. If `NULL`, condition of interest will be selected automatically depending on `response` type. Once the class of interest is selected, rest of them will be collapsed in a common category, representing the "absence" of the condition to be predicted. See `vignette("selecting-condition")` for further information on how automatic selection is performed and details on selecting the condition of interest.

Value

A single row tibble with different predictor with following metrics as columns:

- Area under curve (AUC) as a metric of global performance.
- Partial are under curve (pAUC) as a metric of local performance.
- Indexes derived from pAUC, depending on the selected ratio. Sensitivity indexes will be used for TPR and specificity indexes for FPR.
- Curve shape in the specified region.

Examples

```
# Summarize Sepal.Width as a classifier of setosa species
# and local performance in TPR (0.9, 1)
summarize_predictor(
 data = iris,
 predictor = Sepal.Width,
 response = Species,
 ratio = "tpr",
 threshold = 0.9
)
# Summarize Sepal.Width as a classifier of setosa species
# and local performance in FPR (0, 0.1)
summarize_predictor(
 data = iris,
 predictor = Sepal.Width,
 response = Species,
 ratio = "fpr",
 threshold = 0.1
)
```

Index