

# Package ‘raptools’

May 9, 2026

**Title** Risk Assessment Plot and Reclassification Metrics

**Version** 1.23.0

**Description** Assessing the comparative performance of two logistic regression models or results of such models or classification models. Discrimination metrics include Integrated Discrimination Improvement (IDI), Net Reclassification Improvement (NRI), and difference in Area Under the Curves (AUCs), Brier scores and Brier skill. Plots include Risk Assessment Plots, Decision curves and Calibration plots. Methods are described in Pickering and Endre (2012) <[doi:10.1373/clinchem.2011.167965](https://doi.org/10.1373/clinchem.2011.167965)> and Pencina et al. (2008) <[doi:10.1002/sim.2929](https://doi.org/10.1002/sim.2929)>.

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pracma, ggrepel

**License** GPL-3

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<https://researchverse.github.io/raptools/>

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anova_glm	<i>The function anova_glm() returns the Chi^2 and degrees of freedom for each variable &amp; the same was anova.rms() does from lrm() in the rms package.</i>
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### Description

The function anova\_glm() returns the Chi^2 and degrees of freedom for each variable & the same was anova.rms() does from lrm() in the rms package.

### Usage

```
anova_glm(f)
```

### Arguments

f                    A logistic regression fit created using glm (base package)

### Value

A data frame with Chi-Square values and degrees of freedom for each variable in the model, plus a TOTAL row summarizing the overall model statistics.

**Description**

The function CI.classNRI calculates the NRI statistics for reclassification of data already in classes with confidence intervals. Uses statistics.classNRI.

**Usage**

```
CI.classNRI(
  c1,
  c2,
  y,
  s1 = NULL,
  s2 = NULL,
  conf.level = 0.95,
  n.boot = 1000,
  dp = 3
)
```

**Arguments**

c1	Risk classes of the baseline model (ordinal)
c2	Risk classes of new model
y	Binary of outcome of interest. Must be 0 or 1.
s1	The savings or benefit when an event is reclassified to a higher group by the new model (positive numeric)
s2	The benefit when a non-event is reclassified to a lower group (positive numeric)
conf.level	The confidence interval expressed as a fraction of 1 (ie 0.95 is the 95% confidence interval )
n.boot	The number of "bootstraps" to use. Performance slows down with more bootstraps. For trialling result, use a low number (eg 2), for accuracy use a large number (eg 2000)
dp	The number of decimal places to display

**Value**

A list with the following elements:

**meta\_data** Some overall meta data - Confidence Interval, number of bootstraps, s1, s2

**Metrics** Point estimates of the statistical metrics.

**Each\_bootstrap\_metrics** Point estimates of the statistical metrics for each bootstrapped sample.

**Summary\_metrics** Point estimates with confidence intervals of the statistical metrics (e.g. Total, Events, Non-events, Prevalence, NRI, IDI, confusion matrices).

A matrix of metrics

**Description**

The CI.raplot function produces summary metrics for risk assessment. Outputs the NRI, IDI, weighted NRI and category Free NRI all for those with events and those without events. Also the AUCs of the two models and the comparison (DeLong) between AUCs. Output includes confidence intervals. Uses statistics.raplot. Displayed graphically by raplot.

**Usage**

```
CI.raplot(
  x1,
  x2 = NULL,
  y = NULL,
  t = NULL,
  NRI_return = FALSE,
  conf.level = 0.95,
  n.boot = 1000,
  dp = 3
)
```

**Arguments**

x1	Either a logistic regression fitted using glm (base package) or lrm (rms package) or calculated probabilities (eg through a logistic regression model) of the baseline model. Must be between 0 & 1
x2	Either a logistic regression fitted using glm (base package) or lrm (rms package) or calculated probabilities (eg through a logistic regression model) of the new (alternative) model. Must be between 0 & 1
y	Binary of outcome of interest. Must be 0 or 1 (if fitted models are provided this is extracted from the fit which for an rms fit must have x = TRUE, y = TRUE).
t	The risk threshold(s) for groups. eg t<-c(0,0.1,1) is a two group model with a threshold of 0.1 & t<-c(0,0.1,0.3,1) is a three group model with thresholds at 0.1 and 0.3.
NRI_return	If NRI statistics are required (default = FALSE).
conf.level	The confidence interval expressed as a fraction of 1 (ie 0.95 is the 95% confidence interval )
n.boot	The number of "bootstraps" to use. Performance slows down with more bootstraps. For trialling result, use a low number (eg 5), for accuracy use a large number (eg 2000)
dp	The number of decimal places to display

**Value**

A list with the following elements:

**meta\_data** A data.frame with thresholds, confidence interval, number of bootstraps, input data type and decimal places.

**Metrics** Point estimates of the statistical metrics (see function docs).

**Each\_bootstrap\_metrics** List of per-bootstrap metric results.

**Summary\_metrics** A table of summary metrics with confidence intervals (e.g. Total, Events, Non-events, NRI, IDI, AUCs, Brier scores, etc.).

**References**

Pencina, M. J., D'Agostino, R. B., & Vasan, R. S. (2008). Evaluating the added predictive ability of a new marker: From area under the ROC curve to reclassification and beyond. *Statistics in Medicine*, 27(2), 157-172. doi:10.1002/sim.2929

**Examples**

```
# Quick example with subset of data and fewer bootstraps
data(data_risk)
data_subset <- data_risk[1:100, ] # Use first 100 rows for speed
complete_cases <- complete.cases(data_subset)
data_clean <- data_subset[complete_cases, ]
y <- data_clean$outcome
x1 <- data_clean$baseline
x2 <- data_clean$new
t <- c(0, 0.19, 1)
output <- CI.raplot(x1, x2, y, t, conf.level = 0.95, n.boot = 10, dp = 2)
```

```
# Full dataset example with more bootstraps
data(data_risk)
complete_cases <- complete.cases(data_risk)
data_clean <- data_risk[complete_cases, ]
y <- data_clean$outcome
x1 <- data_clean$baseline
x2 <- data_clean$new
t <- c(0, 0.19, 1)
output <- CI.raplot(x1, x2, y, t, conf.level = 0.95, n.boot = 1000, dp = 2)
```

---

data\_class

*Simple data set with classifications*

---

**Description**

Example data for use with CI.classNRI

**Usage**

```
data_class
```

**Format**

data frame with 3 columns

**ref\_class** The class of the baseline model. Must be a factor

**new\_class** The class of the new model. Must be a factor

**Outcome** The outcome of interest (Low or High). Must be a factor

---

data_risk	<i>Simple data set with risk predictions</i>
-----------	--

---

**Description**

Example data for use with CI.raplot

**Usage**

```
data_risk
```

**Format**

data frame with 3 columns

**ref** The prediction from the baseline model

**new** The prediction from the new model

**outcome** The outcome of interest (0 or 1)

---

extractCI	<i>Extract confidence interval</i>
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---

**Description**

Extract a confidence in interval from the bootstrapped results. Used by CI.raplot

**Usage**

```
extractCI(results.boot, conf.level, n.boot, dp)
```

**Arguments**

results.boot	The matrix of n.boot metrics from within CI.raplot
conf.level	The confidence interval expressed between 0 & 1 (eg 95%CI is conf.level = 0.95)
n.boot	The number of bootstrapped samples
dp	the number of decimal places to report the point estimate and confidence interval

**Value**

A two column matrix with the metric name and statistic with a confidence interval

---

extract_NRI_CI	<i>Extract NRI confidence intervals</i>
----------------	---

---

**Description**

Extract a confidence in interval from the bootstrapped results. Used by CI.NRI

**Usage**

```
extract_NRI_CI(results.boot, conf.level, n.boot, dp)
```

**Arguments**

results.boot	The matrix of n.boot metrics from within CI.NRI
conf.level	The confidence interval expressed between 0 & 1 (eg 95%CI is conf.level = 0.95)
n.boot	The number of bootstrapped samples
dp	the number of decimal places to report the point estimate and confidence interval

**Value**

A two column matrix with the metric name and statistic with a confidence interval

## Description

ggcalibrate plots the stats::predicted events against the actual event rate

## Usage

```
ggcalibrate(  
  x1,  
  x2 = NULL,  
  y = NULL,  
  n_knots = 5,  
  ci_level = 0.95,  
  smooth_method = "loess",  
  smooth_span = 0.75  
)
```

## Arguments

x1	Either a logistic regression fitted using glm (base package) or lrm (rms package) or calculated probabilities (eg through a logistic regression model) of the baseline model. Must be between 0 & 1
x2	Either a logistic regression fitted using glm (base package) or lrm (rms package) or calculated probabilities (eg through a logistic regression model) of the new (alternative) model. Must be between 0 & 1
y	Binary of outcome of interest. Must be 0 or 1 (if fitted models are provided this is extracted from the fit which for an rms fit must have x = TRUE, y = TRUE).
n_knots	The curves are made by fitting a restricted cubic spline (rms package). The default 5-knots is usually enough.
ci_level	Confidence interval of the curve (default = 0.95).
smooth_method	Smoothing method for geom_smooth. Options: "loess", "lm", "glm", "gam". Default is "loess"
smooth_span	Span parameter for loess smoothing, controls the degree of smoothing (default = 0.75). Lower values = less smooth

## Value

a ggplot

## Examples

```
# Quick example with subset of data
data(data_risk)
data_subset <- data_risk[1:100, ] # Use first 100 rows for speed
complete_cases <- complete.cases(data_subset)
data_clean <- data_subset[complete_cases, ]
y <- data_clean$outcome
x1 <- data_clean$baseline
x2 <- data_clean$new
output <- ggcalibrate(x1, x2, y, n_knots = 3, ci_level = 0.95)

# Full dataset example
data(data_risk)
complete_cases <- complete.cases(data_risk)
data_clean <- data_risk[complete_cases, ]
y <- data_clean$outcome
x1 <- data_clean$baseline
x2 <- data_clean$new
output <- ggcalibrate(x1, x2, y, n_knots = 5, ci_level = 0.95)
```

---

ggcalibrate\_original *The Original Calibration plot*

---

## Description

ggcalibrate\_original plots the stats::predicted events against the actual event rate using the "old" form.

## Usage

```
ggcalibrate_original(
  x1,
  x2 = NULL,
  y = NULL,
  n_cut = 5,
  cut_type = c("interval", "number", "width"),
  include_margin = FALSE
)
```

## Arguments

- |    |  |
|----|--|
| x1 | Either a logistic regression fitted using glm (base package) or lrm (rms package) or calculated probabilities (eg through a logistic regression model) of the baseline model. Must be between 0 & 1          |
| x2 | Either a logistic regression fitted using glm (base package) or lrm (rms package) or calculated probabilities (eg through a logistic regression model) of the new (alternative) model. Must be between 0 & 1 |

<code>y</code>	Binary of outcome of interest. Must be 0 or 1 (if fitted models are provided this is extracted from the fit which for an rms fit must have <code>x = TRUE</code> , <code>y = TRUE</code> ).
<code>n_cut</code>	An integer indicating either the number of intervals of the same width, the number of intervals of the same number of subjects, or the width (as a percentage) of the intervals.
<code>cut_type</code>	One of three strings: "interval", "number", or "width". - "interval": uses <code>cut_interval()</code> to get <code>n_cut</code> intervals of approximately equal width. - "number": uses <code>cut_number()</code> to get <code>n_cut</code> intervals with approximately equal counts. - "width": uses <code>cut_width()</code> to get intervals of a fixed width (approximately $100/n\_cut$ ).
<code>include_margin</code>	TRUE for including producing a bar plot of the counts of in each of the intervals. Default is FALSE. Note if the output is saved to <code>my_graphs</code> then using the library <code>gridExtra</code> the function <code>grid.arrange(graphs\$g, graphs\$g_marg, nrow = 2, heights = c(2,1))</code> will produce a plot with both the calibration plot and the marginal plot.

**Value**

a list of one or two ggplots

**Examples**

```
# Quick example with subset of data
data(data_risk)
data_subset <- data_risk[1:100, ] # Use first 100 rows for speed
complete_cases <- complete.cases(data_subset)
data_clean <- data_subset[complete_cases, ]
y <- data_clean$outcome
x1 <- data_clean$baseline
x2 <- data_clean$new
output <- ggcalibrate_original(
  x1, x2, y,
  n_cut = 3, cut_type = "interval",
  include_margin = FALSE
)
```

```
# Full dataset example
data(data_risk)
complete_cases <- complete.cases(data_risk)
data_clean <- data_risk[complete_cases, ]
y <- data_clean$outcome
x1 <- data_clean$baseline
x2 <- data_clean$new
output <- ggcalibrate_original(
  x1, x2, y,
  n_cut = 5, cut_type = "interval",
  include_margin = FALSE
)
```

---

ggcontribute	<i>The Contribution plot</i>
--------------	------------------------------

---

**Description**

ggcontribute plots the contribution of each variable to the model

**Usage**

```
ggcontribute(x1, x2 = NULL, option_flag = c("chi2", "percent"))
```

**Arguments**

x1	Either a logistic regression fitted using glm (base package) or lrm (rms package) of the baseline model.
x2	Either a logistic regression fitted using glm (base package) or lrm (rms package) of the new (alternative) model.
option_flag	A flag to choose if the relative percentage of the Chi2-degrees of freedom are plotted.

**Value**

A ggplot object displaying the contribution of each variable to the model(s) using either Chi-square minus degrees of freedom or relative percentage contribution. If two models are provided, arrows show the change in contribution between models.

---

ggdecision	<i>The Decision curve</i>
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---

**Description**

ggdecision plots decision curves to assess the net benefit at different thresholds

ggdecision plots decision curves to assess the net benefit at different thresholds

**Usage**

```
ggdecision(
  x1,
  x2 = NULL,
  y = NULL,
  show_smooth = TRUE,
  smooth_method = "loess",
  smooth_span = 0.75,
  smooth_se = FALSE
)
```

```
ggdecision(
  x1,
  x2 = NULL,
  y = NULL,
  show_smooth = TRUE,
  smooth_method = "loess",
  smooth_span = 0.75,
  smooth_se = FALSE
)
```

### Arguments

x1	Either a logistic regression fitted using glm (base package) or lrm (rms package) or calculated probabilities (eg through a logistic regression model) of the baseline model. Must be between 0 & 1
x2	Either a logistic regression fitted using glm (base package) or lrm (rms package) or calculated probabilities (eg through a logistic regression model) of the new (alternative) model. Must be between 0 & 1
y	Binary of outcome of interest. Must be 0 or 1 (if fitted models are provided this is extracted from the fit which for an rms fit must have x = TRUE, y = TRUE).
show_smooth	Logical, whether to display smoothed curves (default = TRUE)
smooth_method	Smoothing method for geom_smooth. Options: "loess", "lm", "glm", "gam". Default is "loess"
smooth_span	Span parameter for loess smoothing, controls the degree of smoothing (default = 0.75). Lower values = less smooth
smooth_se	Logical, whether to display confidence interval around smooth (default = FALSE)

### Value

a ggplot  
a ggplot

### References

Vickers AJ, van Calster B, Steyerberg EW. A simple, step-by-step guide to interpreting decision curve analysis. *Diagn Progn Res* 2019;3(1):18. 2. Zhang Z, Rousson V, Lee W-C, et al. Decision curve analysis: a technical note. *Ann Transl Med* 2018;6(15):308-308.

Vickers AJ, van Calster B, Steyerberg EW. A simple, step-by-step guide to interpreting decision curve analysis. *Diagn Progn Res* 2019;3(1):18. 2. Zhang Z, Rousson V, Lee W-C, et al. Decision curve analysis: a technical note. *Ann Transl Med* 2018;6(15):308-308.

**Description**

ggprerec plots Precision (PPV) v Recall (Sensitivity)

**Usage**

```
ggprerec(
  x1,
  x2 = NULL,
  y = NULL,
  show_smooth = TRUE,
  smooth_method = "loess",
  smooth_span = 0.75,
  smooth_se = FALSE
)
```

**Arguments**

x1	Either a logistic regression fitted using glm (base package) or lrm (rms package) or alculated probabilities (eg through a logistic regression model) of the baseline model. Must be between 0 & 1
x2	Either a logistic regression fitted using glm (base package) or lrm (rms package) or calculated probabilities (eg through a logistic regression model) of the new (alternative) model. Must be between 0 & 1
y	Binary of outcome of interest. Must be 0 or 1 (if fitted models are provided this is extracted from the fit which for an rms fit must have x = TRUE, y = TRUE).
show_smooth	Logical, whether to display smoothed curves (default = TRUE)
smooth_method	Smoothing method for geom_smooth. Options: "loess", "lm", "glm", "gam". Default is "loess"
smooth_span	Span parameter for loess smoothing, controls the degree of smoothing (default = 0.75). Lower values = less smooth
smooth_se	Logical, whether to display confidence interval around smooth (default = FALSE)

**Value**

A ggplot object displaying the precision-recall curve(s) with recall (sensitivity) on the x-axis and precision (positive predictive value) on the y-axis. If two models are provided, both curves are shown for comparison.

---

`ggrap`*The Risk Assessment Plot*

---

**Description**

The function `ggrap()` plots the Sensitivity and 1-Specificity curves against the calculated risk for the baseline (reference) and newmodels, thus graphically displaying the IDIs for those with and without the events. These plots can aid interpretation of the NRI and IDI metrics.

**Usage**

```
ggrap(x1, x2 = NULL, y = NULL)
```

```
ggrap(x1, x2 = NULL, y = NULL)
```

**Arguments**

<code>x1</code>	Either a logistic regression fitted using <code>glm</code> (base package) or <code>lrm</code> (rms package) or alculated probabilities (eg through a logistic regression model) of the baseline model. Must be between 0 & 1
<code>x2</code>	Either a logistic regression fitted using <code>glm</code> (base package) or <code>lrm</code> (rms package) or calculated probabilities (eg through a logistic regression model) of the new (alternative) model. Must be between 0 & 1
<code>y</code>	Binary of outcome of interest. Must be 0 or 1 (if fitted models are provided this is extracted from the fit which for an rms fit must have <code>x = TRUE</code> , <code>y = TRUE</code> ).

**Value**

a `ggplot`

a `ggplot`

**References**

The Risk Assessment Plot in this form was described by Pickering, J. W., & Endre, Z. H. (2012). New Metrics for Assessing Diagnostic Potential of Candidate Biomarkers. *Clinical Journal of the American Society of Nephrology*, 7, 1355–1364. doi:10.2215/CJN.09590911

The Risk Assessment Plot in this form was described by Pickering, J. W., & Endre, Z. H. (2012). New Metrics for Assessing Diagnostic Potential of Candidate Biomarkers. *Clinical Journal of the American Society of Nephrology*, 7, 1355–1364. doi:10.2215/CJN.09590911

ggroc

*The ROC plot***Description**

ggroc plots Sensitivity v 1-Specificity

**Usage**

```
ggroc(
  x1,
  x2 = NULL,
  y = NULL,
  carrington_line = FALSE,
  costs = c(0, 0, 1, 1),
  label_number = NULL
)
```

**Arguments**

x1	Either a logistic regression fitted using glm (base package) or lrm (rms package) or calculated probabilities (eg through a logistic regression model) of the baseline model. Must be between 0 & 1
x2	Either a logistic regression fitted using glm (base package) or lrm (rms package) or calculated probabilities (eg through a logistic regression model) of the new (alternative) model. Must be between 0 & 1
y	Binary of outcome of interest. Must be 0 or 1 (if fitted models are provided this is extracted from the fit which for an rms fit must have x = TRUE, y = TRUE).
carrington_line	The Useful Area is from the roc down to this line. It depends on prevalence and the costs of FP, FN, TP, TN. Default is FALSE. See Carrington et al.
costs	Numeric vectors costs = c(cFP, cFN, cTP, cTN). The costs of FP, FN, TP, TN. Default, c(0,0,1,1), is for there to be no costs for the FP & FN and identical costs for TN and TP. See Carrington et al.
label_number	The number of points on the curve to label. The default has no labels.

**Value**

A ggplot object displaying the ROC curve(s) with sensitivity on the y-axis and 1-specificity on the x-axis. If two models are provided, both curves are shown for comparison.

**References**

Carrington AM, Fieguth PW, Mayr F, James ND, Holzinger A, Pickering JW, et al. The ROC Diagonal is not Layperson's Chance: a New Baseline Shows the Useful Area. Machine Learning and Knowledge Extraction. Vienna, Austria: Springer; 2022. pp. 100-113. Available: [10.1007/978-3-031-14463-9\\_7](https://doi.org/10.1007/978-3-031-14463-9_7).

---

meta.rap	<i>List meta data</i>
----------	-----------------------

---

**Description**

Display the meta data

**Usage**

```
meta.rap(1)
```

**Arguments**

1	List returned from CI.raplot
---	------------------------------

**Value**

A tibble

---

statistics.classNRI	<i>Reclassification metrics with classes (ordinals) as inputs</i>
---------------------	---

---

**Description**

The function statistics.classNRI calculates the NRI metrics for reclassification of data already in classes. For use by CI.classNRI.

**Usage**

```
statistics.classNRI(c1, c2, y, s1 = NULL, s2 = NULL)
```

**Arguments**

c1	Risk class of Reference model (ordinal factor).
c2	Risk class of New model (ordinal factor)
y	Binary of outcome of interest. Must be 0 or 1.
s1	The savings or benefit when an event is reclassified to a higher group by the new model. i.e instead of counting as 1 an event classified to a higher group, it is counted as s1.
s2	The benefit when a non-event is reclassified to a lower group. i.e instead of counting as 1 an event classified to a lower group, it is counted as s2.

**Value**

A matrix of metrics for use within CI.classNRI

**Examples**

```
# Quick example
data(data_class)
data_subset <- data_class[1:100, ] # Use first 100 rows for speed
y <- data_subset$outcome
c1 <- data_subset$base_class
c2 <- data_subset$new_class
output <- statistics.classNRI(c1, c2, y)
```

```
# Full dataset example
data(data_class)
y <- data_class$outcome
c1 <- data_class$base_class
c2 <- data_class$new_class
output <- statistics.classNRI(c1, c2, y)
```

---

statistics.raplot      *Statistical metrics*

---

**Description**

The function `statistics.raplot` calculates the reclassification metrics. Used by `CI.raplot`.

**Usage**

```
statistics.raplot(x1, x2, y, t = NULL, NRI_return = FALSE)
```

**Arguments**

<code>x1</code>	Either a logistic regression fitted using <code>glm</code> (base package) or <code>lrm</code> (rms package) or calculated probabilities (eg through a logistic regression model) of the baseline model. Must be between 0 & 1
<code>x2</code>	Either a logistic regression fitted using <code>glm</code> (base package) or <code>lrm</code> (rms package) or calculated probabilities (eg through a logistic regression model) of the new (alternative) model. Must be between 0 & 1
<code>y</code>	Binary of outcome of interest. Must be 0 or 1 (if fitted models are provided this is extracted from the fit which for an rms fit must have <code>x = TRUE</code> , <code>y = TRUE</code> ).
<code>t</code>	The risk threshold(s) for groups. eg <code>t&lt;-c(0,0.1,1)</code> is a two group scenario with a threshold of 0.1 & <code>t&lt;-c(0,0.1,0.3,1)</code> is a three group scenario with thresholds at 0.1 and 0.3. Nb. If no <code>t</code> is provided it defaults to a single threshold at the prevalence of the cohort.
<code>NRI_return</code>	Flag to return NRI metrics, default is <code>FALSE</code> .

**Value**

A matrix of metrics for use within `CI.raplot`

---

`summary.rap`*List risk assessment metrics*

---

**Description**

Display the summary metrics

**Usage**

```
## S3 method for class 'rap'  
summary(1)
```

**Arguments**

1                   List returned from CI.raplot

**Value**

A tibble

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