

# Package ‘metrica’

October 13, 2022

**Title** Prediction Performance Metrics

**Version** 2.0.1

**Date** 2022-07-07

**Description** A compilation of more than 80 functions designed to quantitatively and visually evaluate prediction performance of regression (continuous variables) and classification (categorical variables) of point-forecast models (e.g. APSIM, DSSAT, DNDC, supervised Machine Learning). For regression, it includes functions to generate plots (scatter, tiles, density, & Bland-Altman plot), and to estimate error metrics (e.g. MBE, MAE, RMSE), error decomposition (e.g. lack of accuracy-precision), model efficiency (e.g. NSE, E1, KGE), indices of agreement (e.g. d, RAC), goodness of fit (e.g. r, R2), adjusted correlation coefficients (e.g. CCC, dcorr), symmetric regression coefficients (intercept, slope), and mean absolute scaled error (MASE) for time series predictions. For classification (binomial and multinomial), it offers functions to generate and plot confusion matrices, and to estimate performance metrics such as accuracy, precision, recall, specificity, F-score, Cohen's Kappa, G-mean, and many more. For more details visit the vignettes <<https://adriancorrendo.github.io/metrica/>>.

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**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.2.0

**Depends** R (>= 2.10)

**Suggests** tidyverse, purrr, knitr, rmarkdown, apsimx, testthat (>= 3.0.0)

**Config/testthat/edition** 3

**Imports** stats, ggplot2, dplyr, rlang, tidyr, utils, DBI, RSQLite, ggpp, minerva, energy

**VignetteBuilder** knitr

**URL** <https://adriancorrendo.github.io/metrica/>

**BugReports** <https://github.com/adriancorrendo/metrica/issues>

**NeedsCompilation** no

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**Repository** CRAN

**Date/Publication** 2022-07-24 07:20:03 UTC

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AC *Ji and Gallo's Agreement Coefficient (AC)*

### Description

It estimates the agreement coefficient suggested by Ji & Gallo (2006) for a continuous predicted-observed dataset.

### Usage

```
AC(data = NULL, obs, pred, tidy = FALSE, na.rm = TRUE)
```

### Arguments

data	(Optional) argument to call an existing data frame containing the data.
obs	Vector with observed values (numeric).
pred	Vector with predicted values (numeric).
tidy	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
na.rm	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

### Details

The Ji and Gallo's AC measures general agreement, including both accuracy and precision. It is normalized, dimensionless, positively bounded (-infinity;1), and symmetric. For the formula and more details, see [online-documentation](#)

### Value

an object of class `numeric` within a `list` (if `tidy = FALSE`) or within a `data frame` (if `tidy = TRUE`).

### References

Ji & Gallo (2006). An agreement coefficient for image comparison. *Photogramm. Eng. Remote Sensing* 7, 823–833 [doi:10.14358/PERS.72.7.823](https://doi.org/10.14358/PERS.72.7.823)

## Examples

```
set.seed(1)
X <- rnorm(n = 100, mean = 0, sd = 10)
Y <- rnorm(n = 100, mean = 0, sd = 9)
df <- data.frame(obs = X, pred = Y)
AC(df, obs = X, pred = Y)
```

---

accuracy	<i>Accuracy</i>
----------	-----------------

---

## Description

It estimates the accuracy for a nominal/categorical predicted-observed dataset.

## Usage

```
accuracy(data = NULL, obs, pred, tidy = FALSE, na.rm = TRUE)
```

## Arguments

data	(Optional) argument to call an existing data frame containing the data.
obs	Vector with observed values (character   factor).
pred	Vector with predicted values (character   factor).
tidy	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list (default).
na.rm	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

## Details

Accuracy is the simplest and most popular classification metric in literature. It refers to a measure of the degree to which the predictions of a model matches the reality being modeled. The classification accuracy is calculated as the ratio between the number of correctly classified objects with respect to the total number of cases.

It is bounded between 0 and 1. The closer to 1 the better. Values towards zero indicate low accuracy of predictions. It can be also expressed as percentage if multiplied by 100. It is estimated at a global level (not at the class level).

Accuracy presents limitations to address classification quality under unbalanced classes, and it is not able to distinguish among misclassification distributions. For those cases, it is advised to apply other metrics such as balanced accuracy (baccu), F-score (fscore), Matthews Correlation Coefficient (mcc), or Cohen's Kappa Coefficient (cohen\_kappa).

Accuracy is directly related to the error\_rate, since  $accuracy = 1 - error\_rate$ .

For the formula and more details, see [online-documentation](#)

**Value**

an object of class `numeric` within a list (if `tidy = FALSE`) or within a data frame (if `tidy = TRUE`).

**References**

Sammut & Webb (2017). Accuracy. In: Sammut C., Webb G.I. (eds) *Encyclopedia of Machine Learning and Data Mining*. Springer, Boston, MA. doi:10.1007/9781489976871\_3

**See Also**

[balacc](#) [fscore](#) [mcc](#) [khat](#)

**Examples**

```
set.seed(123)
# Two-class
binomial_case <- data.frame(labels = sample(c("True", "False"), 100,
replace = TRUE), predictions = sample(c("True", "False"), 100, replace = TRUE))
# Multi-class
multinomial_case <- data.frame(labels = sample(c("Red", "Blue", "Green"), 100,
replace = TRUE), predictions = sample(c("Red", "Blue", "Green"), 100, replace = TRUE) )

# Get accuracy estimate for two-class case
accuracy(data = binomial_case, obs = labels, pred = predictions, tidy = TRUE)

# Get accuracy estimate for multi-class case
accuracy(data = multinomial_case, obs = labels, pred = predictions, tidy = TRUE)
```

---

agf

*Adjusted F-score*


---

**Description**

It estimates the Adjusted F-score for a nominal/categorical predicted-observed dataset.

**Usage**

```
agf(
  data = NULL,
  obs,
  pred,
  pos_level = 2,
  atom = FALSE,
  tidy = FALSE,
  na.rm = TRUE
)
```

## Arguments

<code>data</code>	(Optional) argument to call an existing data frame containing the data.
<code>obs</code>	Vector with observed values (character   factor).
<code>pred</code>	Vector with predicted values (character   factor).
<code>pos_level</code>	Integer, for binary cases, indicating the order (1 2) of the level corresponding to the positive. Generally, the positive level is the second (2) since following an alpha-numeric order, the most common pairs are (Negative   Positive), (0   1), (FALSE   TRUE). Default : 2.
<code>atom</code>	Logical operator (TRUE/FALSE) to decide if the estimate is made for each class (atom = TRUE) or at a global level (atom = FALSE); Default : FALSE. When dataset is "binomial" atom does not apply.
<code>tidy</code>	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
<code>na.rm</code>	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

## Details

The Adjusted F-score (or Adjusted F-measure) is an improvement over the F1-score especially when the data classes are imbalanced. This metric more properly accounts for the different misclassification costs across classes. It weights more the sensitivity (recall) metric than precision and gives strength to the false negative values. This index accounts for all elements of the original confusion matrix and provides more weight to patterns correctly classified in the minority class (positive).

It is bounded between 0 and 1. The closer to 1 the better. Values towards zero indicate low performance. For the formula and more details, see [online-documentation](#)

## Value

an object of class numeric within a list (if `tidy = FALSE`) or within a data frame (if `tidy = TRUE`).

## References

Maratea, A., Petrosino, A., Manzo, M. (2014). Adjusted-F measure and kernel scaling for imbalanced data learning. *Inf. Sci.* 257: 331-341. doi:10.1016/j.ins.2013.04.016

## Examples

```
set.seed(123)
# Two-class
binomial_case <- data.frame(labels = sample(c("True","False"), 100, replace = TRUE),
  predictions = sample(c("True","False"), 100, replace = TRUE))
# Multi-class
multinomial_case <- data.frame(labels = sample(c("Red","Blue", "Green"), 100, replace = TRUE),
  predictions = sample(c("Red","Blue", "Green"), 100, replace = TRUE) )
```

```
# Get F-score estimate for two-class case
agf(data = binomial_case, obs = labels, pred = predictions, tidy = TRUE)

# Get F-score estimate for each class for the multi-class case
agf(data = multinomial_case, obs = labels, pred = predictions, tidy = TRUE)

# Get F-score estimate for the multi-class case at a global level
agf(data = multinomial_case, obs = labels, pred = predictions, tidy = TRUE)
```

---

AUC\_roc

*Area Under the ROC Curve*


---

### Description

The AUC estimates the area under the receiver operator curve (ROC) for a nominal/categorical predicted-observed dataset using the Mann-Whitney U-statistic.

### Usage

```
AUC_roc(data = NULL, obs, pred, tidy = FALSE, na.rm = TRUE)
```

### Arguments

data	(Optional) argument to call an existing data frame containing the data.
obs	Vector with observed values (character   factor).
pred	Vector with predicted values (character   factor).
tidy	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list (default).
na.rm	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

### Details

The AUC tests whether positives are ranked higher than negatives. It is simply the area under the ROC curve.

The AUC estimation of this function follows the procedure described by Hand & Till (2001). The AUC\_roc estimated following the trapezoid approach is equivalent to the average between recall and specificity (Powers, 2011), which is equivalent to the balanced accuracy (balacc):

$$AUC_{ROC} = \frac{(recall - FPR + 1)}{2} = \frac{recall + specificity}{2} = 1 - \frac{FPR + FNR}{2}$$

Interpretation: the AUC is equivalent to the probability that a randomly case from a given class (positive for binary) will have a smaller estimated probability of belonging to another class (negative for binary) compared to a randomly chosen member of the another class.

Values: the AUC is bounded between 0 and 1. The closer to 1 the better. Values close to 0 indicate inaccurate predictions. An AUC = 0.5 suggests no discrimination ability between classes; 0.7 <



AUC < 0.8 is considered acceptable,  $0.8 < \text{AUC} < 0.9$  is considered excellent, and  $\text{AUC} > 0.9$  is outstanding (Mandrekar, 2010).

For the multiclass cases, the AUC is equivalent to the average of AUC of each class (Hand & Till, 2001).

Finally, the AUC is directly related to the Gini-index (a.k.a. G1) since  $\text{Gini} + 1 = 2 * \text{AUC}$ . (Hand & Till, 2001).

For the formula and more details, see [online-documentation](#)

## Value

an object of class `numeric` within a `list` (if `tidy = FALSE`) or within a `data frame` (if `tidy = TRUE`).

## References

Hanley, J.A., McNeil, J.A. (2017). The meaning and use of the area under a receiver operating characteristic (ROC) curve. *\_ Radiology* 143(1): 29-36\_ [doi:10.1148/radiology.143.1.7063747](#)

Hand, D.J., Till, R.J. (2001). A simple generalisation of the area under the ROC curve for multiple class classification problems. *\_ Machine Learning* 45: 171-186\_ [doi:10.1023/A:1010920819831](#)

Mandrekar, J.N. (2010). Receiver operating characteristic curve in diagnostic test assessment. *\_ J. Thoracic Oncology* 5(9): 1315-1316\_ [doi:10.1097/JTO.0b013e3181ec173d](#)

Powers, D.M.W. (2011). Evaluation: From Precision, Recall and F-Measure to ROC, Informedness, Markedness & Correlation. *Journal of Machine Learning Technologies* 2(1): 37-63. [doi:10.48550/arXiv.2010.16061](#)

## Examples

```
set.seed(123)
# Two-class
binomial_case <- data.frame(labels = sample(c("True","False"), 100,
replace = TRUE), predictions = sample(c("True","False"), 100, replace = TRUE))
# Multi-class
multinomial_case <- data.frame(labels = sample(c("Red","Blue", "Green"), 100,
replace = TRUE), predictions = sample(c("Red","Blue", "Green"), 100, replace = TRUE) )

# Get AUC estimate for two-class case
AUC_roc(data = binomial_case, obs = labels, pred = predictions, tidy = TRUE)

# Get AUC estimate for multi-class case
AUC_roc(data = multinomial_case, obs = labels, pred = predictions, tidy = TRUE)
```

---

B0_sma	<i>Intercept of standardized major axis regression (SMA).</i>
--------	---

---

### Description

It calculates the intercept (B0) for the bivariate linear relationship between predicted and observed values following the SMA regression.

### Usage

```
B0_sma(data = NULL, obs, pred, orientation = "PO", tidy = FALSE, na.rm = TRUE)
```

### Arguments

data	(Optional) argument to call an existing data frame containing the data.
obs	Vector with observed values (numeric).
pred	Vector with predicted values (numeric).
orientation	Argument of class string specifying the axis orientation, PO for predicted vs observed, and OP for observed vs predicted. Default is orientation = "PO".
tidy	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
na.rm	Logic argument to remove rows with missing values (NA). Default is na_rm = TRUE.

### Details

SMA is a symmetric linear regression (invariant results/interpretation to axis orientation) recommended to describe the bivariate scatter instead of OLS regression (classic linear model, which results vary with the axis orientation). For the formula and more details, see [online-documentation](#)

### Value

an object of class numeric within a list (if tidy = FALSE) or within a data frame (if tidy = TRUE).

### References

Warton et al. (2006). Bivariate line-fitting methods for allometry. *Biol. Rev. Camb. Philos. Soc.* 81, 259–291. doi:10.1002/15214036(200203)44:2<161::AIDBIMJ161>3.0.CO;2N

### Examples

```
set.seed(1)
X <- rnorm(n = 100, mean = 0, sd = 10)
Y <- rnorm(n = 100, mean = 0, sd = 9)
B0_sma(obs = X, pred = Y)
```

---

B1_sma	<i>Slope of standardized major axis regression (SMA).</i>
--------	---

---

### Description

It calculates the slope (B1) for the bivariate linear relationship between predicted and observed values following the SMA regression.

### Usage

```
B1_sma(data = NULL, obs, pred, tidy = FALSE, orientation = "PO", na.rm = TRUE)
```

### Arguments

data	(Optional) argument to call an existing data frame containing the data.
obs	Vector with observed values (numeric).
pred	Vector with predicted values (numeric).
tidy	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
orientation	Argument of class string specifying the axis orientation, PO for predicted vs observed, and OP for observed vs predicted. Default is orientation = "PO".
na.rm	Logic argument to remove rows with missing values (NA). Default is na_rm = TRUE.

### Details

SMA is a symmetric linear regression (invariant results/interpretation to axis orientation) recommended to describe the bivariate scatter instead of OLS regression (classic linear model, which results vary with the axis orientation). For the formula and more details, see [online-documentation](#)

### Value

an object of class numeric within a list (if tidy = FALSE) or within a data frame (if tidy = TRUE).

### References

Warton et al. (2006). Bivariate line-fitting methods for allometry. *Biol. Rev. Camb. Philos. Soc.* 81, 259–291. doi:10.1002/15214036(200203)44:2<161::AIDBIMJ161>3.0.CO;2N

### Examples

```
set.seed(1)
X <- rnorm(n = 100, mean = 0, sd = 10)
Y <- rnorm(n = 100, mean = 0, sd = 9)
B1_sma(obs = X, pred = Y)
```

---

balacc *Balanced Accuracy*

---

### Description

It estimates the balanced accuracy for a nominal/categorical predicted-observed dataset.

### Usage

```
balacc(data = NULL, obs, pred, pos_level = 2, tidy = FALSE, na.rm = TRUE)
```

### Arguments

data	(Optional) argument to call an existing data frame containing the data.
obs	Vector with observed values (character   factor).
pred	Vector with predicted values (character   factor).
pos_level	Integer, for binary cases, indicating the order (1 2) of the level corresponding to the positive. Generally, the positive level is the second (2) since following an alpha-numeric order, the most common pairs are (Negative   Positive), (0   1), (FALSE   TRUE). Default : 2.
tidy	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
na.rm	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

### Details

The balanced accuracy is the average between recall and specificity. It is particularly useful when the number of observation belonging to each class is despar or imbalanced, and when especial attention is given to the negative cases. It is bounded between 0 and 1. Values towards zero indicate low performance. The closer to 1 the better.

For the formula and more details, see [online-documentation](#)

### Value

an object of class numeric within a list (if tidy = FALSE) or within a data frame (if tidy = TRUE).

### References

García, V., Mollineda, R.A., Sánchez, J.S. (2009). Index of Balanced Accuracy: A Performance Measure for Skewed Class Distributions. *In: Araujo, H., Mendonça, A.M., Pinho, A.J., Torres, M.I. (eds) Pattern Recognition and Image Analysis. IbPRIA 2009. Lecture Notes in Computer Science, vol 5524. Springer-Verlag Berlin Heidelberg. doi:10.1007/9783642021725\_57*

## Examples

```

set.seed(123)
# Two-class
binomial_case <- data.frame(labels = sample(c("True","False"), 100, replace = TRUE),
  predictions = sample(c("True","False"), 100, replace = TRUE))
# Multi-class
multinomial_case <- data.frame(labels = sample(c("Red","Blue", "Green"), 100, replace = TRUE),
  predictions = sample(c("Red","Blue", "Green"), 100, replace = TRUE)  )

# Get balanced accuracy estimate for two-class case
balacc(data = binomial_case, obs = labels, pred = predictions, tidy = TRUE)

# Get balanced accuracy estimate for the multi-class case
balacc(data = multinomial_case, obs = labels, pred = predictions, tidy = TRUE)

```

---

barley	<i>Barley grain number</i>
--------	----------------------------

---

## Description

This example dataset is a set of APSIM simulations of barley grain number (x1000 grains per squared meter), which presents high accuracy but medium precision. The experimental trials come from 11 site-years in 2 countries (Australia, and New Zealand). These data correspond to the latest, up-to-date, documentation and validation of version number 2020.03.27.4956. Data available at: [doi:10.7910/DVN/EJS4M0](https://doi.org/10.7910/DVN/EJS4M0). Further details can be found at the official APSIM Next Generation website: <https://APSIMnextgeneration.netlify.app/modeldocumentation/>

## Usage

```
barley
```

## Format

This data frame has 69 rows and the following 2 columns:

**pred** predicted values

**obs** observed values

## Source

<https://github.com/adriancorrendo/metrica>

---

bland\_altman\_plot      *Bland-Altman plot*

---

### Description

It creates a scatter plot of the difference between observed and predicted values (obs-pred) vs. observed values.

### Usage

```
bland_altman_plot(
  data = NULL,
  obs,
  pred,
  shape_type = NULL,
  shape_size = NULL,
  shape_color = NULL,
  zeroline_type = NULL,
  zeroline_size = NULL,
  zeroline_color = NULL,
  limitsline_type = NULL,
  limitsline_size = NULL,
  limitsline_color = NULL,
  na.rm = TRUE
)
```

### Arguments

data	(Optional) argument to call an existing data frame containing the data.
obs	Vector with observed values (numeric).
pred	Vector with predicted values (numeric).
shape_type	number indicating the shape type for the data points.
shape_size	number indicating the shape size for the data points.
shape_color	string indicating the shape color for the data points.
zeroline_type	string or integer indicating the zero line-type.
zeroline_size	number indicating the zero line size.
zeroline_color	string indicating the zero line color.
limitsline_type	string or integer indicating the limits (+/- 1.96*SD) line-type.
limitsline_size	number indicating the limits (+/- 1.96*SD) line size.
limitsline_color	string indicating the limits (+/- 1.96*SD) line color.
na.rm	Logic argument to remove rows with missing values

## Details

For more details, see [online-documentation](#)

## Value

an object of class `ggplot`.

## References

Bland & Altman (1986). Statistical methods for assessing agreement between two methods of clinical measurement *The Lancet* 327(8476), 307-310 doi:[10.1016/S01406736\(86\)908378](https://doi.org/10.1016/S01406736(86)908378)

## See Also

[ggplot](#), [geom\\_point](#), [aes](#)

## Examples

```
X <- rnorm(n = 100, mean = 0, sd = 10)
Y <- rnorm(n = 100, mean = 0, sd = 10)
bland_altman_plot(obs = X, pred = Y)
```

---

bmi

*Bookmaker Informedness*

---

## Description

It estimates the Bookmaker Informedness (a.k.a. Youden's J-index) for a nominal/categorical predicted-observed dataset.

## Usage

```
bmi(  
  data = NULL,  
  obs,  
  pred,  
  pos_level = 2,  
  atom = FALSE,  
  tidy = FALSE,  
  na.rm = TRUE  
)
```

## Arguments

<code>data</code>	(Optional) argument to call an existing data frame containing the data.
<code>obs</code>	Vector with observed values (character   factor).
<code>pred</code>	Vector with predicted values (character   factor).
<code>pos_level</code>	Integer, for binary cases, indicating the order (1 2) of the level corresponding to the positive. Generally, the positive level is the second (2) since following an alpha-numeric order, the most common pairs are (Negative   Positive), (0   1), (FALSE   TRUE). Default : 2.
<code>atom</code>	Logical operator (TRUE/FALSE) to decide if the estimate is made for each class (atom = TRUE) or at a global level (atom = FALSE); Default : FALSE. When dataset is "binomial" atom does not apply.
<code>tidy</code>	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
<code>na.rm</code>	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

## Details

The Bookmaker Informedness (or Youden's J index) it is a suitable metric when the number of cases for each class is uneven.

The general formula applied to both binary and multiclass cases is:

$$bmi = recall + specificity - 1$$

It is bounded between 0 and 1. The closer to 1 the better. Values towards zero indicate low performance. For the formula and more details, see [online-documentation](#)

## Value

an object of class `numeric` within a list (if `tidy = FALSE`) or within a data frame (if `tidy = TRUE`).

## References

Youden, W.J. (1950). Index for rating diagnostic tests. . *Cancer* 3: 32-35. doi:10.1002/1097-0142(1950)3:1<32::AIDCNCR2820030106>3.0.CO;23

## Examples

```
set.seed(123)
# Two-class
binomial_case <- data.frame(labels = sample(c("True","False"), 100, replace = TRUE),
  predictions = sample(c("True","False"), 100, replace = TRUE))
# Multi-class
multinomial_case <- data.frame(labels = sample(c("Red","Blue", "Green"), 100, replace = TRUE),
  predictions = sample(c("Red","Blue", "Green"), 100, replace = TRUE) )

# Get Informedness estimate for two-class case
```



```

bmi(data = binomial_case, obs = labels, pred = predictions, tidy = TRUE)

# Get Informedness estimate for each class for the multi-class case
bmi(data = multinomial_case, obs = labels, pred = predictions, tidy = TRUE)

# Get Informedness estimate for the multi-class case at a global level
bmi(data = multinomial_case, obs = labels, pred = predictions, tidy = TRUE)

```

---

CCC

*Concordance correlation coefficient (CCC)*


---

### Description

It estimates the Concordance Correlation Coefficient (CCC) for a continuous predicted-observed dataset.

### Usage

```
CCC(data = NULL, obs, pred, tidy = FALSE, na.rm = TRUE)
```

### Arguments

<code>data</code>	(Optional) argument to call an existing data frame containing the data.
<code>obs</code>	Vector with observed values (numeric).
<code>pred</code>	Vector with predicted values (numeric).
<code>tidy</code>	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
<code>na.rm</code>	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

### Details

The CCC it is a normalized coefficient that tests general agreement. It presents both precision ( $r$ ) and accuracy ( $X_a$ ) components. It is positively bounded to 1. The closer to 1 the better. Values towards zero indicate low correlation between observations and predictions. Negative values would indicate a negative relationship between predicted and observed. For the formula and more details, see [online-documentation](#)

### Value

an object of class `numeric` within a list (if `tidy = FALSE`) or within a data frame (if `tidy = TRUE`).

### References

Lin (1989). A concordance correlation coefficient to evaluate reproducibility. *Biometrics* 45 (1), 255–268. [doi:10.2307/2532051](https://doi.org/10.2307/2532051)

## Examples

```
set.seed(1)
X <- rnorm(n = 100, mean = 0, sd = 10)
Y <- X + rnorm(n=100, mean = 0, sd = 3)
CCC(obs = X, pred = Y)
```

---

chickpea

*Chickpea dry mass*

---

## Description

This example dataset is a set of APSIM simulations of chickpea aboveground dry mass (kg per hectare), which exhibits low accuracy and medium-low precision as it represents a model still under development. The experimental trials come from 7 site-years in 3 countries (Australia, India, and New Zealand). These data correspond to the latest, up-to-date, documentation and validation of version number 2020.03.27.4956. Data available at: [doi:10.7910/DVN/EJS4M0](https://doi.org/10.7910/DVN/EJS4M0). Further details can be found at the official APSIM Next Generation website: <https://apsimnextgeneration.netlify.app/modeldocumentation/>

## Usage

chickpea

## Format

This data frame has 39 rows and the following 2 columns:

**pred** predicted values

**obs** observed values

## Source

<https://github.com/adriancorrendo/metrica>

---

confusion_matrix	<i>Confusion Matrix</i>
------------------	-------------------------

---

### Description

It creates a confusion matrix table or plot displaying the agreement between the observed and the predicted classes by the model.

### Usage

```
confusion_matrix(
  data = NULL,
  obs,
  pred,
  plot = FALSE,
  unit = "count",
  colors = c(low = NULL, high = NULL),
  print_metrics = FALSE,
  metrics_list = c("accuracy", "precision", "recall"),
  position_metrics = "top",
  na.rm = TRUE
)
```

### Arguments

<code>data</code>	(Optional) argument to call an existing data frame containing the data.
<code>obs</code>	Vector with observed values (character or factor).
<code>pred</code>	Vector with predicted values (character or factor).
<code>plot</code>	Logical operator (TRUE/FALSE) that controls the output as a data.frame (plot = FALSE) or as a plot of type ggplot (plot = TRUE), Default: FALSE
<code>unit</code>	String (text) indicating the type of unit ("count" or "proportion") to show in the confusion matrix, Default: 'count'
<code>colors</code>	Vector or list with two colors indicating how to paint the gradient between "low" and "high", Default: c(low = NULL, high = NULL) uses the standard blue gradient of ggplot2.
<code>print_metrics</code>	boolean TRUE/FALSE to embed metrics in the plot. Default is FALSE.
<code>metrics_list</code>	vector or list of selected metrics to print on the plot. Default: c("accuracy", "precision", "recall").
<code>position_metrics</code>	string specifying the position to print the performance metrics_list. Options are "top" (as a subtitle) or "bottom" (as a caption). Default: "bottom".
<code>na.rm</code>	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

## Details

A confusion matrix is a method for summarizing the predictive performance of a classification algorithm. It is particularly useful if you have an unbalanced number of observations belonging to each class or if you have a multinomial dataset (more than two classes in your dataset). A confusion matrix can give you a good hint about the types of errors that your model is making. See [online-documentation](#)

## Value

An object of class `data.frame` when `plot = FALSE`, or of type `ggplot` when `plot = TRUE`.

## References

Ting K.M. (2017). Confusion Matrix. In: Sammut C., Webb G.I. (eds) *Encyclopedia of Machine Learning and Data Mining*. Springer, Boston, MA. doi:10.1007/9781489976871\_50

## See Also

[eval\\_tidy](#), [defusing-advanced select](#)

## Examples

```
set.seed(183)
# Two-class
binomial_case <- data.frame(labels = sample(c("True","False"), 100, replace = TRUE),
  predictions = sample(c("True","False"), 100, replace = TRUE))
# Multi-class
multinomial_case <- data.frame(labels = sample(c("Red","Blue", "Green"), 100,
  replace = TRUE), predictions = sample(c("Red","Blue", "Green"), 100, replace = TRUE))

# Plot two-class confusion matrix
confusion_matrix(data = binomial_case, obs = labels, pred = predictions,
  plot = TRUE, colors = c(low="pink" , high="steelblue"), unit = "count")

# Plot multi-class confusion matrix
confusion_matrix(data = multinomial_case, obs = labels, pred = predictions,
  plot = TRUE, colors = c(low="#f9dbbd" , high="#735d78"), unit = "count")
```

## Description

It estimates the Critical Success Index (a.k.a. threat score, Jaccard Index) for a nominal/categorical predicted-observed dataset.

**Usage**

```
csi(
  data = NULL,
  obs,
  pred,
  pos_level = 2,
  atom = FALSE,
  tidy = FALSE,
  na.rm = TRUE
)
```

**Arguments**

<code>data</code>	(Optional) argument to call an existing data frame containing the data.
<code>obs</code>	Vector with observed values (character   factor).
<code>pred</code>	Vector with predicted values (character   factor).
<code>pos_level</code>	Integer, for binary cases, indicating the order (1 2) of the level corresponding to the positive. Generally, the positive level is the second (2) since following an alpha-numeric order, the most common pairs are (Negative   Positive), (0   1), (FALSE   TRUE). Default : 2.
<code>atom</code>	Logical operator (TRUE/FALSE) to decide if the estimate is made for each class (atom = TRUE) or at a global level (atom = FALSE); Default : FALSE. When dataset is "binomial" atom does not apply.
<code>tidy</code>	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
<code>na.rm</code>	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

**Details**

The `csi` is also known as the threat score or the Jaccard Index. It is a metric especially useful for binary classification tasks, representing the proportion of true positive (TP) cases with respect to the sum of predicted positive (PP = TP + FP) and true negative (TN) cases.

$$csi = \frac{TP}{TP+TN+FP}$$

It is bounded between 0 and 1. The closer to 1 the better the classification performance, while zero represents the worst result.

It has been extensively used in meteorology (NOOA) as a verification measure of categorical forecast performance equal to the total number of correct event forecast (hits = TP) divided by the total number of event forecasts plus the number of misses (hits + false alarms + misses = TP + FP + TN). However, the `csi` has been criticized for not representing an unbiased measure of forecast skill (Schaefer, 1990).

For the formula and more details, see [online-documentation](#)

**Value**

an object of class `numeric` within a `list` (if `tidy = FALSE`) or within a `data frame` (if `tidy = TRUE`).

## References

NOOA. Forecast Verification Glossary. *Space Weather Prediction Center, NOAA*. <https://www.swpc.noaa.gov/sites/default/files/images/u30/Forecast%20Verification%20Glossary.pdf>

Schaefer, J.T. (1990). The critical success index as an indicator of warning skill. *Weather and Forecasting* 5(4): 570-575. doi:10.1175/15200434(1990)005<0570:TCSIAA>2.0.CO;2

## Examples

```
set.seed(123)
# Two-class
binomial_case <- data.frame(labels = sample(c("True", "False"), 100, replace = TRUE),
  predictions = sample(c("True", "False"), 100, replace = TRUE))
# Get csi estimate for two-class case
csi(data = binomial_case, obs = labels, pred = predictions)
```

---

d *Willmott's Index of Agreement (d)*

---

## Description

It estimates the Willmott's index of agreement (d) for a continuous predicted-observed dataset.

## Usage

```
d(data = NULL, obs, pred, tidy = FALSE, na.rm = TRUE)
```

## Arguments

data	(Optional) argument to call an existing data frame containing the data.
obs	Vector with observed values (numeric).
pred	Vector with predicted values (numeric).
tidy	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
na.rm	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

## Details

The d index it is a normalized, dimensionless metric that tests general agreement. It measures both accuracy and precision using squared residuals. It is bounded between 0 and 1. The disadvantage is that d is an asymmetric index, that is, dependent to what is orientation of predicted and observed values. For the formula and more details, see [online-documentation](#)

**Value**

an object of class `numeric` within a `list` (if `tidy = FALSE`) or within a `data frame` (if `tidy = TRUE`).

**References**

Willmott (1981). On the validation of models. *Phys. Geogr. 2*, 184–194. doi:10.1080/02723646.1981.10642213

**Examples**

```
set.seed(1)
X <- rnorm(n = 100, mean = 0, sd = 10)
Y <- rnorm(n = 100, mean = 0, sd = 9)
d(obs = X, pred = Y)
```

---

d1	<i>Modified Index of Agreement (d1).</i>
----	--

---

**Description**

It estimates the modified index of agreement (d1) using absolute differences following Willmott et al. (1985).

**Usage**

```
d1(data = NULL, obs, pred, tidy = FALSE, na.rm = TRUE)
```

**Arguments**

<code>data</code>	(Optional) argument to call an existing data frame containing the data.
<code>obs</code>	Vector with observed values (numeric).
<code>pred</code>	Vector with predicted values (numeric).
<code>tidy</code>	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a <code>data.frame</code> , FALSE returns a <code>list</code> ; Default : FALSE.
<code>na.rm</code>	Logic argument to remove rows with missing values (NA). Default is <code>na.rm = TRUE</code> .

**Details**

Similar to `d`, the `d1` index it is a normalized, dimensionless metric that tests general agreement. The difference with `d`, is that `d1` uses absolute residuals instead of squared residuals. It is bounded between 0 and 1. The disadvantage is that `d` is an asymmetric index, that is, dependent to the orientation of predicted and observed values. For the formula and more details, see [online-documentation](#)

**Value**

an object of class `numeric` within a list (if `tidy = FALSE`) or within a data frame (if `tidy = TRUE`).

**References**

Willmott et al. (1985). Statistics for the evaluation and comparison of models. *J. Geophys. Res.* 90, 8995. doi:[10.1029/jc090ic05p08995](https://doi.org/10.1029/jc090ic05p08995)

**Examples**

```
set.seed(1)
X <- rnorm(n = 100, mean = 0, sd = 10)
Y <- rnorm(n = 100, mean = 0, sd = 9)
d1(obs = X, pred = Y)
```

---

<code>d1r</code>	<i>Refined Index of Agreement (d1).</i>
------------------	---

---

**Description**

It estimates the refined index of agreement (`d1r`) following Willmott et al. (2012).

**Usage**

```
d1r(data = NULL, obs, pred, tidy = FALSE, na.rm = TRUE)
```

**Arguments**

<code>data</code>	(Optional) argument to call an existing data frame containing the data.
<code>obs</code>	Vector with observed values (numeric).
<code>pred</code>	Vector with predicted values (numeric).
<code>tidy</code>	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
<code>na.rm</code>	Logic argument to remove rows with missing values (NA). Default is <code>na.rm = TRUE</code> .

**Details**

Similar to `d`, and `d1`, the `d1r` index it is a normalized, dimensionless metric that tests general agreement. The difference is that `d1r` modifies the denominator of the formula (potential error), normalizing the mean absolute error (numerator) by two-times the mean absolute deviation of observed values. It is bounded between 0 and 1. The disadvantage is that `d1r` is an asymmetric index, that is, dependent to the orientation of predicted and observed values. For the formula and more details, see [online-documentation](#)



**Value**

an object of class `numeric` within a `list` (if `tidy = FALSE`) or within a `data frame` (if `tidy = TRUE`).

**References**

Willmott et al. (2012). A refined index of model performance. *Int. J. Climatol.* 32, 2088–2094. doi:10.1002/joc.2419

**Examples**

```
set.seed(1)
X <- rnorm(n = 100, mean = 0, sd = 10)
Y <- rnorm(n = 100, mean = 0, sd = 9)
d1r(obs = X, pred = Y)
```

---

dcorr	<i>Distance Correlation</i>
-------	-----------------------------

---

**Description**

It estimates the Distance Correlation coefficient (`dcorr`) for a continuous predicted-observed dataset.

**Usage**

```
dcorr(data = NULL, obs, pred, tidy = FALSE, na.rm = TRUE)
```

**Arguments**

<code>data</code>	(Optional) argument to call an existing data frame containing the data.
<code>obs</code>	Vector with observed values (numeric).
<code>pred</code>	Vector with predicted values (numeric).
<code>tidy</code>	logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a <code>data.frame</code> , FALSE returns a <code>list</code> (default).
<code>na.rm</code>	Logic argument to remove rows with missing values (NA). Default is <code>na.rm = TRUE</code> .

**Details**

The **dcorr** function is a wrapper for the `dcor` function from the **energy**-package. See Rizzo & Szekely (2022). The distance correlation (`dcorr`) coefficient is a novel measure of dependence between random vectors introduced by Szekely et al. (2007).

The `dcorr` is characterized for being symmetric, which is relevant for the predicted-observed case (PO).

For all distributions with finite first moments, distance correlation  $\mathcal{R}$  generalizes the idea of correlation in two fundamental ways:

- (1)  $\mathcal{R}(P, O)$  is defined for  $P$  and  $O$  in arbitrary dimension.
- (2)  $\mathcal{R}(P, O) = 0$  characterizes independence of  $P$  and  $O$ .

Distance correlation satisfies  $0 \leq \mathcal{R} \leq 1$ , and  $\mathcal{R} = 0$  only if  $P$  and  $O$  are independent. Distance covariance  $\mathcal{V}$  provides a new approach to the problem of testing the joint independence of random vectors. The formal definitions of the population coefficients  $\mathcal{V}$  and  $\mathcal{R}$  are given in Szekely et al. (2007).

The empirical distance correlation  $\mathcal{R}_n(\mathbf{P}, \mathbf{O})$  is the square root of

$$\mathcal{R}_n^2(\mathbf{P}, \mathbf{O}) = \frac{\mathcal{V}_n^2(\mathbf{P}, \mathbf{O})}{\sqrt{\mathcal{V}_n^2(\mathbf{P})\mathcal{V}_n^2(\mathbf{O})}}.$$

For the formula and more details, see [online-documentation](#) and the [energy-package](#)

### Value

an object of class `numeric` within a `list` (if `tidy = FALSE`) or within a `data frame` (if `tidy = TRUE`).

### References

Szekely, G.J., Rizzo, M.L., and Bakirov, N.K. (2007). *Measuring and testing dependence by correlation of distances*. *Annals of Statistics*, Vol. 35(6): 2769-2794. [doi:10.1214/009053607000000505](https://doi.org/10.1214/009053607000000505).

Rizzo, M., and Szekely, G. (2022). `energy`: E-Statistics: Multivariate Inference via the Energy of Data. *R package version 1.7-10*. <https://CRAN.R-project.org/package=energy>.

### See Also

[eval\\_tidy](#), [defusing-advanced dcor](#), [energy](#)

### Examples

```
set.seed(1)
P <- rnorm(n = 100, mean = 0, sd = 10)
O <- P + rnorm(n=100, mean = 0, sd = 3)
dcorr(obs = P, pred = O)
```

---

deltap	<i>deltaP or Markedness</i>
--------	-----------------------------

---

### Description

deltap estimates the Markedness or deltaP for a nominal/categorical predicted-observed dataset.

### Usage

```
deltap(
  data = NULL,
  obs,
  pred,
  pos_level = 2,
  atom = FALSE,
  tidy = FALSE,
  na.rm = TRUE
)
```

### Arguments

<code>data</code>	(Optional) argument to call an existing data frame containing the data.
<code>obs</code>	Vector with observed values (character   factor).
<code>pred</code>	Vector with predicted values (character   factor).
<code>pos_level</code>	Integer, for binary cases, indicating the order (1 2) of the level corresponding to the positive. Generally, the positive level is the second (2) since following an alpha-numeric order, the most common pairs are (Negative   Positive), (0   1), (FALSE   TRUE). Default : 2.
<code>atom</code>	Logical operator (TRUE/FALSE) to decide if the estimate is made for each class (atom = TRUE) or at a global level (atom = FALSE); Default : FALSE. When dataset is "binomial" atom does not apply.
<code>tidy</code>	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
<code>na.rm</code>	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

### Details

The deltap is also known as the markedness. It is a metric that quantifies the probability that a condition is marked by the predictor with respect to a random chance (Powers, 2011).

The deltap is related to precision (or positive predictive values -ppv-) and its inverse (the negative predictive value -npv-) as follows:

$$deltap = PPV + NPV - 1 = precision + npv - 1$$

The higher the deltap the better the classification performance.

For the formula and more details, see [online-documentation](#)

**Value**

an object of class `numeric` within a list (if `tidy = FALSE`) or within a data frame (if `tidy = TRUE`).

**References**

Powers, D.M.W. (2011). Evaluation: From Precision, Recall and F-Measure to ROC, Informedness, Markedness & Correlation. *Journal of Machine Learning Technologies* 2(1): 37–63. doi:10.48550/arXiv.2010.16061

**Examples**

```
set.seed(123)
# Two-class
binomial_case <- data.frame(labels = sample(c("True", "False"), 100, replace = TRUE),
  predictions = sample(c("True", "False"), 100, replace = TRUE))
# Get deltap estimate for two-class case
deltap(data = binomial_case, obs = labels, pred = predictions)
```

---

density\_plot

*Density plot of predicted and observed values*

---

**Description**

It draws a density area plot of predictions and observations with alternative axis orientation (P vs. O; O vs. P).

**Usage**

```
density_plot(
  data = NULL,
  obs,
  pred,
  n = 10,
  colors = c(low = NULL, high = NULL),
  orientation = "PO",
  print_metrics = FALSE,
  metrics_list = NULL,
  position_metrics = c(x = NULL, y = NULL),
  print_eq = TRUE,
  position_eq = c(x = NULL, y = NULL),
  eq_color = NULL,
  regline_type = NULL,
  regline_size = NULL,
  regline_color = NULL,
```

```

    na.rm = TRUE
  )

```

### Arguments

data	(Optional) argument to call an existing data frame containing the data.
obs	Vector with observed values (numeric).
pred	Vector with predicted values (numeric).
n	Argument of class numeric specifying the number of data points in each group.
colors	Vector or list with two colors '(low, high)' to paint the density gradient.
orientation	Argument of class string specifying the axis orientation, PO for predicted vs observed, and OP for observed vs predicted. Default is orientation = "PO".
print_metrics	boolean TRUE/FALSE to embed metrics in the plot. Default is FALSE.
metrics_list	vector or list of selected metrics to print on the plot.
position_metrics	vector or list with '(x,y)' coordinates to locate the metrics_table into the plot. Default : c(x = min(obs), y = 1.05*max(pred)).
print_eq	boolean TRUE/FALSE to embed metrics in the plot. Default is FALSE.
position_eq	vector or list with '(x,y)' coordinates to locate the SMA equation into the plot. Default : c(x = 0.70 max(x), y = 1.25*min(y)).
eq_color	string indicating the color of the SMA-regression text.
regline_type	string or integer indicating the SMA-regression line-type.
regline_size	number indicating the SMA-regression line size.
regline_color	string indicating the SMA-regression line color.
na.rm	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

### Details

It creates a density plot of predicted vs. observed values. The plot also includes the 1:1 line (solid line) and the linear regression line (dashed line). By default, it places the observed on the x-axis and the predicted on the y-axis (orientation = "PO"). This can be inverted by changing the argument orientation = "OP". For more details, see [online-documentation](#)

### Value

Object of class ggplot.

### See Also

[ggplot](#), [geom\\_point](#), [aes](#)

**Examples**

```
X <- rnorm(n = 100, mean = 0, sd = 10)
Y <- rnorm(n = 100, mean = 0, sd = 10)
density_plot(obs = X, pred = Y)
```

---

E1	<i>Absolute Model Efficiency (E1)</i>
----	---------------------------------------

---

**Description**

It estimates the E1 model efficiency using absolute differences.

**Usage**

```
E1(data = NULL, obs, pred, tidy = FALSE, na.rm = TRUE)
```

**Arguments**

data	(Optional) argument to call an existing data frame containing the data.
obs	Vector with observed values (numeric).
pred	Vector with predicted values (numeric).
tidy	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
na.rm	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

**Details**

The E1 is a type of model efficiency that modifies the Nash-Sutcliffe model efficiency by using absolute residuals instead of squared residuals. The E1 is used to overcome the NSE over-sensitivity to extreme values caused by the used of squared residuals. For the formula and more details, see [online-documentation](#)

**Value**

an object of class numeric within a list (if tidy = FALSE) or within a data frame (if tidy = TRUE).

**References**

Legates & McCabe (1999). Evaluating the use of “goodness-of-fit” measures in hydrologic and hydroclimatic model validation. *Water Resour. Res.* [doi:10.1029/1998WR900018](https://doi.org/10.1029/1998WR900018)

## Examples

```
set.seed(1)
X <- rnorm(n = 100, mean = 0, sd = 10)
Y <- rnorm(n = 100, mean = 0, sd = 9)
E1(obs = X, pred = Y)
```

---

Erel	<i>Relative Model Efficiency (Erel)</i>
------	---

---

## Description

It estimates the Erel model efficiency using differences to observations.

## Usage

```
Erel(data = NULL, obs, pred, tidy = FALSE, na.rm = TRUE)
```

## Arguments

data	(Optional) argument to call an existing data frame containing the data.
obs	Vector with observed values (numeric).
pred	Vector with predicted values (numeric).
tidy	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
na.rm	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

## Details

The Erel model efficiency normalizes both residuals (numerator) and observed deviations (denominator) by observed values before squaring them. Compared to the NSE, the Erel is suggested as more sensitive to systematic over- or under-predictions. For the formula and more details, see [online-documentation](#)

## Value

an object of class numeric within a list (if tidy = FALSE) or within a data frame (if tidy = TRUE).

## References

Krause et al. (2005). Comparison of different efficiency criteria for hydrological model assessment. *Adv. Geosci.* 5, 89–97. [doi:10.5194/adgeo5892005](https://doi.org/10.5194/adgeo5892005)

## Examples

```
set.seed(1)
X <- rnorm(n = 100, mean = 0, sd = 10)
Y <- rnorm(n = 100, mean = 0, sd = 9)
Erel(obs = X, pred = Y)
```

---

error_rate	<i>Error rate</i>
------------	-------------------

---

## Description

It estimates the error rate for a nominal/categorical predicted-observed dataset.

## Usage

```
error_rate(data = NULL, obs, pred, tidy = FALSE, na.rm = TRUE)
```

## Arguments

data	(Optional) argument to call an existing data frame containing the data.
obs	Vector with observed values (character   factor).
pred	Vector with predicted values (character   factor).
tidy	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list (default).
na.rm	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

## Details

The error rate represents the opposite of accuracy, referring to a measure of the degree to which the predictions miss-classify the reality. The classification error\_rate is calculated as the ratio between the number of incorrectly classified objects with respect to the total number of objects. It is bounded between 0 and 1. The closer to 1 the worse. Values towards zero indicate low error\_rate of predictions. It can be also expressed as percentage if multiplied by 100. It is estimated at a global level (not at the class level). The error rate is directly related to the accuracy, since  $\text{error\_rate} = 1 - \text{accuracy}$ . For the formula and more details, see [online-documentation](#)

## Value

an object of class `numeric` within a list (if `tidy = FALSE`) or within a data frame (if `tidy = TRUE`).

## References

(2017) Accuracy. In: Sammut C., Webb G.I. (eds) *Encyclopedia of Machine Learning and Data Mining* Springer, Boston, MA. doi:10.1007/9781489976871\_3



## Examples

```
set.seed(123)
# Two-class
binomial_case <- data.frame(labels = sample(c("True","False"), 100,
replace = TRUE), predictions = sample(c("True","False"), 100, replace = TRUE))
# Multi-class
multinomial_case <- data.frame(labels = sample(c("Red","Blue", "Green"), 100,
replace = TRUE), predictions = sample(c("Red","Blue", "Green"), 100, replace = TRUE) )

# Get error_rate estimate for two-class case
error_rate(data = binomial_case, obs = labels, pred = predictions, tidy = TRUE)

# Get error_rate estimate for multi-class case
error_rate(data = multinomial_case, obs = labels, pred = predictions, tidy = TRUE)
```

fmi

*Fowlkes-Mallows Index*

## Description

It estimates the Fowlkes-Mallows Index for a nominal/categorical predicted-observed dataset.

## Usage

```
fmi(data = NULL, obs, pred, pos_level = 2, tidy = FALSE, na.rm = TRUE)
```

## Arguments

data	(Optional) argument to call an existing data frame containing the data.
obs	Vector with observed values (character   factor).
pred	Vector with predicted values (character   factor).
pos_level	Integer, for binary cases, indicating the order (1 2) of the level corresponding to the positive. Generally, the positive level is the second (2) since following an alpha-numeric order, the most common pairs are (Negative   Positive), (0   1), (FALSE   TRUE). Default : 2.
tidy	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
na.rm	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

## Details

The fmi has gained popularity within the machine learning community to summarize into a single value the confusion matrix of a binary classification. It is particularly useful when the number of observations belonging to each class is uneven or imbalanced. It is characterized for being symmetric (i.e. no class has more relevance than the other). It is bounded between -1 and 1. The closer to 1 the better the classification performance.

The fmi is only available for the evaluation of binary cases (two classes). For multiclass cases, fmi will produce a NA and display a warning.

For the formula and more details, see [online-documentation](#)

## Value

an object of class `numeric` within a `list` (if `tidy = FALSE`) or within a `data frame` (if `tidy = TRUE`).

## References

Fowlkes, Edward B; Mallows, Colin L (1983). A method for comparing two hierarchical clusterings. *Journal of the American Statistical Association*. 78 (383): 553–569. doi:10.1080/01621459.1983.10478008

## Examples

```
set.seed(123)
# Two-class
binomial_case <- data.frame(labels = sample(c("True", "False"), 100, replace = TRUE),
  predictions = sample(c("True", "False"), 100, replace = TRUE))
# Get fmi estimate for two-class case
fmi(data = binomial_case, obs = labels, pred = predictions)
```

---

fscore

*F-score*

---

## Description

It estimates the F-score for a nominal/categorical predicted-observed dataset.

## Usage

```
fscore(
  data = NULL,
  obs,
  pred,
  B = 1,
  pos_level = 2,
  atom = FALSE,
```

```

  tidy = FALSE,
  na.rm = TRUE
)
```

### Arguments

<code>data</code>	(Optional) argument to call an existing data frame containing the data.
<code>obs</code>	Vector with observed values (character   factor).
<code>pred</code>	Vector with predicted values (character   factor).
<code>B</code>	Numeric value indicating the weight (a.k.a. B or beta) to be applied to the relationship between recall and precision. $B < 1$ weights more precision than recall. $B > 1$ gives B times more importance to recall than precision. Default: 1.
<code>pos_level</code>	Integer, for binary cases, indicating the order (1 2) of the level corresponding to the positive. Generally, the positive level is the second (2) since following an alpha-numeric order, the most common pairs are (Negative   Positive), (0   1), (FALSE   TRUE). Default : 2.
<code>atom</code>	Logical operator (TRUE/FALSE) to decide if the estimate is made for each class (atom = TRUE) or at a global level (atom = FALSE); Default : FALSE. When dataset is "binomial" atom does not apply.
<code>tidy</code>	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
<code>na.rm</code>	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

### Details

The F-score (or F-measure) it is a more robust metric than the classic accuracy, especially when the number of cases for each class is uneven. It represents the harmonic mean of precision and recall. Thus, to achieve high values of F-score it is necessary to have both high precision and high recall.

The universal version of F-score employs a coefficient B, by which we can tune the precision-recall ratio. Values of  $B > 1$  give more weight to recall, and  $B < 1$  give more weight to precision.

For binomial/binary cases,  $fscore = TP / (TP + 0.5*(FP + FN))$

The generalized formula applied to multiclass cases is:

$$f score = \frac{(1+B^2)*(precision*recall)}{((B^2*precision)+recall)}$$

It is bounded between 0 and 1. The closer to 1 the better. Values towards zero indicate low performance. For the formula and more details, see [online-documentation](#)

### Value

an object of class `numeric` within a `list` (if `tidy = FALSE`) or within a `data frame` (if `tidy = TRUE`).

## References

Goutte, C., Gaussier, E. (2005). A Probabilistic Interpretation of Precision, Recall and F-Score, with Implication for Evaluation. In: *D.E. Losada and J.M. Fernandez-Luna (Eds.): ECIR 2005 . Advances in Information Retrieval LNCS 3408, pp. 345–359, 2. Springer-Verlag Berlin Heidelberg.* doi:10.1007/9783540318651\_25

## Examples

```
set.seed(123)
# Two-class
binomial_case <- data.frame(labels = sample(c("True","False"), 100, replace = TRUE),
  predictions = sample(c("True","False"), 100, replace = TRUE))
# Multi-class
multinomial_case <- data.frame(labels = sample(c("Red","Blue", "Green"), 100, replace = TRUE),
  predictions = sample(c("Red","Blue", "Green"), 100, replace = TRUE)  )

# Get F-score estimate for two-class case
fscore(data = binomial_case, obs = labels, pred = predictions, tidy = TRUE)

# Get F-score estimate for each class for the multi-class case
fscore(data = multinomial_case, obs = labels, pred = predictions, tidy = TRUE)

# Get F-score estimate for the multi-class case at a global level
fscore(data = multinomial_case, obs = labels, pred = predictions, tidy = TRUE)
```

---

gmean

*Geometric Mean*

---

## Description

It estimates the Geometric Mean score for a nominal/categorical predicted-observed dataset.

## Usage

```
gmean(
  data = NULL,
  obs,
  pred,
  pos_level = 2,
  atom = FALSE,
  tidy = FALSE,
  na.rm = TRUE
)
```

**Arguments**

<code>data</code>	(Optional) argument to call an existing data frame containing the data.
<code>obs</code>	Vector with observed values (character   factor).
<code>pred</code>	Vector with predicted values (character   factor).
<code>pos_level</code>	Integer, for binary cases, indicating the order (1 2) of the level corresponding to the positive. Generally, the positive level is the second (2) since following an alpha-numeric order, the most common pairs are (Negative   Positive), (0   1), (FALSE   TRUE). Default : 2.
<code>atom</code>	Logical operator (TRUE/FALSE) to decide if the estimate is made for each class (atom = TRUE) or at a global level (atom = FALSE); Default : FALSE. When dataset is "binomial" atom does not apply.
<code>tidy</code>	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
<code>na.rm</code>	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

**Details**

The `gmean` is a metric especially useful for imbalanced classes because it measures the balance between the classification performance on both major (over-represented) as well as on minor (under-represented) classes. As stated above, it is particularly useful when the number of observations belonging to each class is uneven.

The `gmean` score is equivalent to the square-root of the product of specificity and recall (a.k.a. sensitivity).

$$gmean = \sqrt{recall * specificity}$$

It is bounded between 0 and 1. The closer to 1 the better the classification performance, while zero represents the worst.

For the formula and more details, see [online-documentation](#)

**Value**

an object of class `numeric` within a `list` (if `tidy = FALSE`) or within a `data frame` (if `tidy = TRUE`).

**References**

De Diego, I.M., Redondo, A.R., Fernández, R.R., Navarro, J., Moguerza, J.M. (2022). General Performance Score for classification problems. *\_ Appl. Intell. (2022)\_* [doi:10.1007/s10489021-030417](https://doi.org/10.1007/s10489021-030417)

**Examples**

```
set.seed(123)
# Two-class
binomial_case <- data.frame(labels = sample(c("True", "False"), 100, replace = TRUE),
```

```

predictions = sample(c("True","False"), 100, replace = TRUE))
# Get gmean estimate for two-class case
gmean(data = binomial_case, obs = labels, pred = predictions)

```

---

import\_apsim\_db

---

*Import SQLite databases generated by APSIM NextGen*


---

## Description

Imports data from SQLite databases (\*.db) applied by APSIM Next Generation. It reads one file at a time.

## Usage

```
import_apsim_db(filename = "", folder = ".", value = "report", simplify = TRUE)
```

## Arguments

filename	file name including the file extension (*.db), as a string ("").
folder	source folder/directory containing the file, as a string ("").
value	either 'report', 'all' (list) or user-defined for a specific report.
simplify	if TRUE will attempt to simplify multiple reports into a single data.frame. If FALSE it will return a list. Default: TRUE.

## Value

An object of class data.frame, but it depends on the argument 'value' above

## Note

This function was adapted from apsimx package (Miguez, 2022). For reference, we recommend to check and use the function apsimx::read\_apsimx() as an alternative. Source: <https://github.com/femiguez/apsimx> by F. Miguez.

## References

Miguez, F. (2022) apsimx: Inspect, Read, Edit and Run 'APSIM' "Next Generation" and 'APSIM' Classic. *R package version 2.3.1*, <https://CRAN.R-project.org/package=apsimx>

## Examples

```
## See [documentation](https://adriancorrendo.github.io/metrica/index.html)
```

---

import_apsim_out	<i>import_apsim_out</i>
------------------	-------------------------

---

**Description**

Function to import \*.out files generated by APSIM Classic.

**Usage**

```
import_apsim_out(filepath)
```

**Arguments**

filepath      Argument to specify the location path to the \*.out file.

**Details**

This function will generate a data frame object from an APSIM Classic \*.out file.

**Value**

Element of class data.frame.

**Note**

Note: It imports one file at a time.

**Examples**

```
## See [documentation](https://adriancorrendo.github.io/metrica/index.html)
```

---

iqRMSE	<i>Inter-Quartile Root Mean Squared Error</i>
--------	---

---

**Description**

It estimates the IqRMSE for a continuous predicted-observed dataset.

**Usage**

```
iqRMSE(data = NULL, obs, pred, tidy = FALSE, na.rm = TRUE)
```

**Arguments**

<code>data</code>	(Optional) argument to call an existing data frame containing the data.
<code>obs</code>	Vector with observed values (numeric).
<code>pred</code>	Vector with predicted values (numeric).
<code>tidy</code>	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
<code>na.rm</code>	Logic argument to remove rows with missing values (NA). Default is <code>na.rm = TRUE</code> .

**Details**

The `iqRMSE` normalizes the RMSE by the length of the inter-quartile range of observations (percentiles 25th to 75th). As an error metric, the lower the values the better. For the formula and more details, see [online-documentation](#)

**Value**

an object of class `numeric` within a `list` (if `tidy = FALSE`) or within a `data frame` (if `tidy = TRUE`).

**Examples**

```
set.seed(1)
X <- rnorm(n = 100, mean = 0, sd = 10)
Y <- X + rnorm(n=100, mean = 0, sd = 3)
iqRMSE(obs = X, pred = Y)
```

---

KGE

*Kling-Gupta Model Efficiency (KGE).*

---

**Description**

It estimates the KGE for a predicted-observed dataset.

**Usage**

```
KGE(data = NULL, obs, pred, tidy = FALSE, na.rm = TRUE)
```



**Arguments**

data	(Optional) argument to call an existing data frame containing the data.
obs	Vector with observed values (numeric).
pred	Vector with predicted values (numeric).
tidy	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
na.rm	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

**Details**

The KGE is a normalized, dimensionless, model efficiency that measures general agreement. It presents accuracy, precision, and consistency components. It is symmetric (invariant to predicted observed orientation). It is positively bounded up to 1. The closer to 1 the better. For the formula and more details, see [online-documentation](#)

**Value**

an object of class `numeric` within a `list` (if `tidy = FALSE`) or within a `data frame` (if `tidy = TRUE`).

**References**

Kling et al. (2012). Runoff conditions in the upper Danube basin under an ensemble of climate change scenarios. *Journal of Hydrology* 424-425, 264-277. [doi:10.1016/j.jhydrol.2012.01.011](https://doi.org/10.1016/j.jhydrol.2012.01.011)

**Examples**

```
set.seed(1)
X <- rnorm(n = 100, mean = 0, sd = 10)
Y <- rnorm(n = 100, mean = 0, sd = 9)
KGE(obs = X, pred = Y)
```

---

khat

*K-hat (Cohen's Kappa Coefficient)*


---

**Description**

It estimates the Cohen's Kappa Coefficient for a nominal/categorical predicted-observed dataset.

**Usage**

```
khat(data = NULL, obs, pred, pos_level = 2, tidy = FALSE, na.rm = TRUE)
```

**Arguments**

data	(Optional) argument to call an existing data frame containing the data.
obs	Vector with observed values (character   factor).
pred	Vector with predicted values (character   factor).
pos_level	Integer, for binary cases, indicating the order (1 2) of the level corresponding to the positive. Generally, the positive level is the second (2) since following an alpha-numeric order, the most common pairs are (Negative   Positive), (0   1), (FALSE   TRUE). Default : 2.
tidy	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
na.rm	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

**Details**

The Cohen's Kappa Coefficient is the accuracy normalized by the possibility of agreement by chance. Thus, it is considered a more robust agreement measure than simply the accuracy. The kappa coefficient was originally described for evaluating agreement of classification between different "raters" (inter-rater reliability).

It is positively bounded to 1, but it is not negatively bounded. The closer to 1 the better as Kappa assumes its theoretical maximum value of 1 (perfect agreement) only when both observed and predicted values are equally distributed across the classes (i.e. identical row and column sums). Thus, the lower the kappa the lower the prediction quality.

For the formula and more details, see [online-documentation](#)

**Value**

an object of class `numeric` within a `list` (if `tidy = FALSE`) or within a `data frame` (if `tidy = TRUE`).

**References**

Cohen, J. (1960). A coefficient of agreement for nominal scales. *Journal of Educational and Psychological Measurement* 20 (1): 37-46. [doi:10.1177/001316446002000104](https://doi.org/10.1177/001316446002000104)

**Examples**

```
set.seed(123)
# Two-class
binomial_case <- data.frame(labels = sample(c("True","False"), 100, replace = TRUE),
  predictions = sample(c("True","False"), 100, replace = TRUE))
# Multi-class
multinomial_case <- data.frame(labels = sample(c("Red","Blue", "Green"), 100,
  replace = TRUE), predictions = sample(c("Red","Blue", "Green"), 100, replace = TRUE))

# Get Cohen's Kappa Coefficient estimate for two-class case
khat(data = binomial_case, obs = labels, pred = predictions, tidy = TRUE)
```

```
# Get Cohen's Kappa Coefficient estimate for each class for the multi-class case
khat(data = multinomial_case, obs = labels, pred = predictions, tidy = TRUE)

# Get Cohen's Kappa Coefficient estimate for the multi-class case at a global level
khat(data = multinomial_case, obs = labels, pred = predictions, tidy = TRUE)
```

---

lambda	<i>Duveiller's Agreement Coefficient</i>
--------	--

---

### Description

It estimates the agreement coefficient (lambda) suggested by Duveiller et al. (2016) for a continuous predicted-observed dataset.

### Usage

```
lambda(data = NULL, obs, pred, tidy = FALSE, na.rm = TRUE)
```

### Arguments

data	(Optional) argument to call an existing data frame containing the data.
obs	Vector with observed values (numeric).
pred	Vector with predicted values (numeric).
tidy	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
na.rm	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

### Details

lambda measures both accuracy and precision. It is normalized, dimensionless, bounded (-1;1), and symmetric (invariant to predicted-observed orientation). lambda is equivalent to CCC when r is greater or equal to 0. The closer to 1 the better. Values towards zero indicate low correlation between observations and predictions. Negative values would indicate a negative relationship between predicted and observed. For the formula and more details, see [online-documentation](#)

### Value

an object of class numeric within a list (if tidy = FALSE) or within a data frame (if tidy = TRUE).

### References

Duveiller et al. (2016). Revisiting the concept of a symmetric index of agreement for continuous datasets. *Sci. Rep.* 6, 1-14. doi:10.1038/srep19401

## Examples

```
set.seed(1)
X <- rnorm(n = 100, mean = 0, sd = 10)
Y <- rnorm(n = 100, mean = 0, sd = 9)
lambda(obs = X, pred = Y)
```

---

land_cover	<i>Binary Land Cover Data</i>
------------	-------------------------------

---

## Description

This example dataset was obtained in 2022 over a small region in Kansas, using visual interpretation. The predicted values were the result of a Random Forest classification, with a 70/30 % split. Values equal to 1 are associated to vegetation, and values equal to 0 are other type of land cover.

## Usage

```
land_cover
```

## Format

This data frame has 284 rows and the following 2 columns:

**predicted** predicted values

**actual** observed values

## Source

<https://github.com/adriancorrendo/metrica>

---

LCS	<i>Lack of Correlation (LCS)</i>
-----	----------------------------------

---

## Description

It estimates the lack of correlation (LCS) component of the Mean Squared Error (MSE) proposed by Kobayashi & Salam (2000).

## Usage

```
LCS(data = NULL, obs, pred, tidy = FALSE, na.rm = TRUE)
```

**Arguments**

data	(Optional) argument to call an existing data frame containing the data.
obs	Vector with observed values (numeric).
pred	Vector with predicted values (numeric).
tidy	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
na.rm	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

**Details**

The LCS represents the random component of the prediction error following Kobayashi & Salam (2000). The lower the value the less contribution to the MSE. However, it needs to be compared to MSE as its benchmark. For the formula and more details, see [online-documentation](#)

**Value**

an object of class `numeric` within a `list` (if `tidy = FALSE`) or within a `data frame` (if `tidy = TRUE`).

**References**

Kobayashi & Salam (2000). Comparing simulated and measured values using mean squared deviation and its components. *Agron. J.* 92, 345–352. doi:10.2134/agronj2000.922345x

**Examples**

```
set.seed(1)
X <- rnorm(n = 100, mean = 0, sd = 10)
Y <- X + rnorm(n=100, mean = 0, sd = 3)
LCS(obs = X, pred = Y)
```

---

likelihood\_ratios      *Likelihood Ratios (Classification)*

---

**Description**

It estimates the positive likelihood ratio `posLr`, negative likelihood ratio `negLr`, and diagnostic odds ratio `dor` for a nominal/categorical predicted-observed dataset.

**Usage**

```
posLr(
  data = NULL,
  obs,
  pred,
  pos_level = 2,
  atom = FALSE,
  tidy = FALSE,
  na.rm = TRUE
)
```

```
negLr(
  data = NULL,
  obs,
  pred,
  pos_level = 2,
  atom = FALSE,
  tidy = FALSE,
  na.rm = TRUE
)
```

```
dor(
  data = NULL,
  obs,
  pred,
  pos_level = 2,
  atom = FALSE,
  tidy = FALSE,
  na.rm = TRUE
)
```

**Arguments**

<code>data</code>	(Optional) argument to call an existing data frame containing the data.
<code>obs</code>	Vector with observed values (character   factor).
<code>pred</code>	Vector with predicted values (character   factor).
<code>pos_level</code>	Integer, for binary cases, indicating the order (1 2) of the level corresponding to the positive. Generally, the positive level is the second (2) since following an alpha-numeric order, the most common pairs are (Negative   Positive), (0   1), (FALSE   TRUE). Default : 2.
<code>atom</code>	Logical operator (TRUE/FALSE) to decide if the estimate is made for each class (atom = TRUE) or at a global level (atom = FALSE); Default : FALSE. When dataset is "binomial" atom does not apply.
<code>tidy</code>	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
<code>na.rm</code>	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

## Details

The likelihood ratios are metrics designed to assess the expectations of classification tasks. They are highly related to recall (sensitivity or true positive rate) and specificity (selectivity or true negative rate).

For a multiclass case, positive and negative results are class-wise. We can either hit the actual class, or the actual non-class. For example, a classification may have 3 potential results: cat, dog, or fish. Thus, when the actual value is dog, the only true positive is dog, but we can obtain a true negative either by classifying it as a cat or a fish. The posLr, negLr, and dor estimates are the mean across all classes.

The positive likelihood ratio (posLr) measures the odds of obtaining a positive prediction in cases that are actual positives.

The negative likelihood ratio (negLr) relates the odds of obtaining a negative prediction for actual non-negatives relative to the probability of actual negative cases obtaining a negative prediction result.

Finally, the diagnostic odds ratio (dor) measures the effectiveness of classification. It represents the odds of a positive prediction result in actual (observed) positive cases with respect to the odds of a positive prediction for the actual negative cases.

The ratios are define as follows:

$$posLr = \frac{recall}{1+specificity} = \frac{TPR}{FPR}$$

$$negLr = \frac{1-recall}{specificity} = \frac{FNR}{TNR}$$

$$dor = \frac{posLr}{negLr}$$

For more details, see [online-documentation](#)

## Value

an object of class numeric within a list (if tidy = FALSE) or within a data frame (if tidy = TRUE).

## References

GlasaJeroen, A.S., Lijmer, G., Prins, M.H., Bonsel, G.J., Bossuyta, P.M.M. (2009). The diagnostic odds ratio: a single indicator of test performance. *Journal of Clinical Epidemiology* 56(11): 1129-1135. doi:10.1016/S08954356(03)00177X

## Examples

```
set.seed(123)
# Two-class
binomial_case <- data.frame(labels = sample(c("True","False"), 100, replace = TRUE),
  predictions = sample(c("True","False"), 100, replace = TRUE))
# Multi-class
multinomial_case <- data.frame(labels = sample(c("Red","Blue", "Green"), 100, replace = TRUE),
  predictions = sample(c("Red","Blue", "Green"), 100, replace = TRUE) )

# Get posLr, negLr, and dor for a two-class case
```

```
posLr(data = binomial_case, obs = labels, pred = predictions, tidy = TRUE)
negLr(data = binomial_case, obs = labels, pred = predictions, tidy = TRUE)
dor(data = binomial_case, obs = labels, pred = predictions, tidy = TRUE)
```

---

MAE

*Mean Absolute Error (MAE)*


---

### Description

It estimates the MAE for a continuous predicted-observed dataset.

### Usage

```
MAE(data = NULL, obs, pred, tidy = FALSE, na.rm = TRUE)
```

### Arguments

<code>data</code>	(Optional) argument to call an existing data frame containing the data.
<code>obs</code>	Vector with observed values (numeric).
<code>pred</code>	Vector with predicted values (numeric).
<code>tidy</code>	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
<code>na.rm</code>	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

### Details

The MAE measures both lack of accuracy and precision in absolute scale. It keeps the same units than the response variable. It is less sensitive to outliers than the MSE or RMSE. The lower the better. For the formula and more details, see [online-documentation](#)

### Value

an object of class `numeric` within a `list` (if `tidy = FALSE`) or within a `data frame` (if `tidy = TRUE`).

### References

Willmott & Matsuura (2005). Advantages of the mean absolute error (MAE) over the root mean square error (RMSE) in assessing average model performance. *Clim. Res.* 30, 79–82. [doi:10.3354/cr030079](#)



## Examples

```
set.seed(1)
X <- rnorm(n = 100, mean = 0, sd = 10)
Y <- X + rnorm(n=100, mean = 0, sd = 3)
MAE(obs = X, pred = Y)
```

---

maize\_phenology

*Multi Class Phenology*

---

## Description

This example data set includes maize phenology classes collected in Kansas during the 2018 growing season. The predicted values were obtained using a Random Forest classifier with a 70/30 split. The dataset includes 16 phenology stages from VT to R6. For more information please visit [doi:10.3390/rs14030469](https://doi.org/10.3390/rs14030469).

## Usage

```
maize_phenology
```

## Format

This data frame has 103 rows and the following 2 columns:

**predicted** predicted values

**actual** observed values

## Source

<https://github.com/adriancorrendo/metrica>

---

MAPE

*Mean Absolute Percentage Error (MAPE)*

---

## Description

It estimates the MAPE of a continuous predicted-observed dataset.

## Usage

```
MAPE(data = NULL, obs, pred, tidy = FALSE, na.rm = TRUE)
```

**Arguments**

<code>data</code>	(optional) argument to call an existing data frame containing the data.
<code>obs</code>	Vector with observed values (numeric).
<code>pred</code>	Vector with predicted values (numeric).
<code>tidy</code>	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
<code>na.rm</code>	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

**Details**

The MAPE is expressed in percentage units (independent scale), which it makes easy to explain and to compare performance across models with different response variables. MAPE is asymmetric (sensitive to axis orientation). The lower the better. As main disadvantage, MAPE produces infinite or undefined values for zero or close-to-zero observed values. For the formula and more details, see [online-documentation](#)

**Value**

an object of class `numeric` within a `list` (if `tidy = FALSE`) or within a `data frame` (if `tidy = TRUE`).

**References**

Kim & Kim (2016). A new metric of absolute percentage error for intermittent demand forecast. *Int. J. Forecast.* 32, 669-679. [doi:10.1016/j.ijforecast.2015.12.003](https://doi.org/10.1016/j.ijforecast.2015.12.003)

**Examples**

```
set.seed(1)
X <- rnorm(n = 100, mean = 0, sd = 10)
Y <- X + rnorm(n=100, mean = 0, sd = 3)
MAPE(obs = X, pred = Y)
```

---

MASE

*Mean Absolute Scaled Error (MASE)*

---

**Description**

It estimates the mean absolute error using the naive-error approach for a continuous predicted-observed dataset.

**Usage**

```
MASE(
  data = NULL,
  obs,
  pred,
  time = NULL,
  naive_step = 1,
  oob_mae = NULL,
  tidy = FALSE,
  na.rm = TRUE
)
```

**Arguments**

<code>data</code>	(Required) argument to call an existing data frame containing the data.
<code>obs</code>	Vector with observed values (numeric).
<code>pred</code>	Vector with predicted values (numeric).
<code>time</code>	(Optional) String with the "name" of the vector containing the time variable to sort observations. "Optional" to ensure an appropriate MASE estimation. Default: NULL, assumes observations are already sorted by time.
<code>naive_step</code>	A positive number specifying how many observed values to recall back in time when computing the naive expectation. Default = 1
<code>oob_mae</code>	A numeric value indicating the out-of-bag (out-of-sample) MAE. By default, an <i>in-sample</i> MAE is calculated using the naive forecast method. See Hyndman & Koehler (2006). Default : NULL.
<code>tidy</code>	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
<code>na.rm</code>	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

**Details**

The MASE is especially well suited for time series predictions. It can be used to compare forecast methods on a single series and also to compare forecast accuracy between series.

This metric never gives an infinite or undefined values (unless all observations over time are exactly the same!).

By default, the MASE scales the error based on *in-sample* MAE from the naive forecast method (random walk). The in-sample MAE is used in the denominator because it is always available and it effectively scales the errors. Since it is based on absolute error, it is less sensitive to outliers compared to the classic MSE.

$$MASE = \frac{1}{n} \left( \frac{|O_i - P_i|}{\frac{1}{T-1} \sum_{t=2}^T |O_t - O_{t-1}|} \right)$$

If available, users may use and out-of-bag error from an independent dataset, which can be specified with the `oob_mae` arg. and will replace the denominator into the MASE equation.

MASE measures total error (i.e. both lack of accuracy and precision.). The lower the MASE below 1, the better the prediction quality. MASE = indicates no difference between the model and the naive forecast (or oob predictions). MASE > 1 indicate poor performance.

For the formula and more details, see [online-documentation](#)

### Value

an object of class `numeric` within a `list` (if `tidy = FALSE`) or within a `data frame` (if `tidy = TRUE`).

### References

Hyndman, R.J., Koehler, A.B. (2006). Another look at measures of forecast accuracy. *\_ Int. J. Forecast\_* [doi:10.3354/cr030079](https://doi.org/10.3354/cr030079)

### Examples

```
set.seed(1)
# Create a fake dataset
X <- rnorm(n = 100, mean = 8, sd = 10)
Y <- rnorm(n = 100, mean = 8.2, sd = 15)
Z <- seq(1, 100, by = 1)

time_data <- as.data.frame(list("observed" = X, "predicted" = Y, "time" = Z))

MASE(data = time_data, obs = observed, pred = predicted, time = time)
```

---

MBE

*Mean Bias Error (MBE)*

---

### Description

It estimates the MBE for a continuous predicted-observed dataset.

### Usage

```
MBE(data = NULL, obs, pred, tidy = FALSE, na.rm = TRUE)
```

### Arguments

<code>data</code>	(Optional) argument to call an existing data frame containing the data.
<code>obs</code>	Vector with observed values (numeric).
<code>pred</code>	Vector with predicted values (numeric).
<code>tidy</code>	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a <code>data.frame</code> , FALSE returns a <code>list</code> ; Default : FALSE.
<code>na.rm</code>	Logic argument to remove rows with missing values (NA). Default is <code>na.rm = TRUE</code> .

## Details

The MBE is one of the most widely used error metrics. It presents the same units than the response variable, and it is unbounded. It can be simply estimated as the difference between the means of predictions and observations. The closer to zero the better. Negative values indicate overestimation. Positive values indicate general underestimation. The disadvantages are that it is only sensitive to additional bias, so the MBE may mask a poor performance if overestimation and underestimation co-exist (a type of proportional bias). For the formula and more details, see [online-documentation](#)

## Value

an object of class `numeric` within a `list` (if `tidy = FALSE`) or within a `data frame` (if `tidy = TRUE`).

## Examples

```
set.seed(1)
X <- rnorm(n = 100, mean = 0, sd = 10)
Y <- X + rnorm(n=100, mean = 0, sd = 3)
MBE(obs = X, pred = Y)
```

---

mcc

*Matthews Correlation Coefficient*


---

## Description

It estimates the `mcc` for a nominal/categorical predicted-observed dataset.

## Usage

```
mcc(data = NULL, obs, pred, pos_level = 2, tidy = FALSE, na.rm = TRUE)
```

## Arguments

<code>data</code>	(Optional) argument to call an existing data frame containing the data.
<code>obs</code>	Vector with observed values (character   factor).
<code>pred</code>	Vector with predicted values (character   factor).
<code>pos_level</code>	Integer, for binary cases, indicating the order (1 2) of the level corresponding to the positive. Generally, the positive level is the second (2) since following an alpha-numeric order, the most common pairs are (Negative   Positive), (0   1), (FALSE   TRUE). Default : 2.
<code>tidy</code>	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a <code>data.frame</code> , FALSE returns a <code>list</code> ; Default : FALSE.
<code>na.rm</code>	Logic argument to remove rows with missing values (NA). Default is <code>na.rm = TRUE</code> .

## Details

The mcc it is also known as the phi-coefficient. It has gained popularity within the machine learning community to summarize into a single value the confusion matrix of a binary classification.

It is particularly useful when the number of observations belonging to each class is uneven or imbalanced. It is characterized for being symmetric (i.e. no class has more relevance than the other). It is bounded between -1 and 1. The closer to 1 the better the classification performance.

For the formula and more details, see [online-documentation](#)

## Value

an object of class `numeric` within a `list` (if `tidy = FALSE`) or within a `data frame` (if `tidy = TRUE`).

## References

Chicco, D., Jurman, G. (2020) The advantages of the Matthews correlation coefficient (MCC) over F1 score and accuracy in binary classification evaluation. *BMC Genomics* 21, 6 (2020). [doi:10.1186/s1286401964137](https://doi.org/10.1186/s1286401964137)

## Examples

```
set.seed(123)
# Two-class
binomial_case <- data.frame(labels = sample(c("True","False"), 100, replace = TRUE),
  predictions = sample(c("True","False"), 100, replace = TRUE))

# Get mcc estimate for two-class case
mcc(data = binomial_case, obs = labels, pred = predictions, tidy = TRUE)
```

---

metrics\_summary

*Prediction Performance Summary*

---

## Description

It estimates a group of metrics characterizing the prediction performance for a continuous (regression) or categorical (classification) predicted-observed dataset. By default, it calculates all available metrics for either regression or classification.

## Usage

```
metrics_summary(
  data = NULL,
  obs,
  pred,
  type = NULL,
```

```

    metrics_list = NULL,
    orientation = "PO",
    pos_level = 2,
    na.rm = TRUE
  )

```

### Arguments

data	argument to call an existing data frame containing the data (optional).
obs	vector with observed values (numeric).
pred	vector with predicted values (numeric).
type	argument of class string specifying the type of model. For continuous variables use <i>type = 'regression'</i> . For categorical variables use <i>type = 'classification'</i> .
metrics_list	vector or list of specific selected metrics. Default is NULL, which will estimate all metrics available for either regression or classification.
orientation	argument of class string specifying the axis orientation to estimate slope(B1) and intercept(B0). It only applies when type = "regression". "PO" is for predicted vs observed, and "OP" for observed vs predicted. Default is orientation = "PO".
pos_level	(for classification only). Integer, for binary cases, indicating the order (1 2) of the level corresponding to the positive. Generally, the positive level is the second (2) since following an alpha-numeric order, the most common pairs are (Negative   Positive), (0   1), (FALSE   TRUE). Default : 2.
na.rm	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

### Details

The user can choose to calculate a single metric, or to calculate all metrics at once. This function creates a data.frame with all (or selected) metrics in the *metrica*-package. If looking for specific metrics, the user can pass a list of desired metrics using the argument "metrics\_list" (e.g. `metrics_list = c("R2", "MAE", "RMSE", "RSR", "NSE", "KGE")`). For the entire list of available metrics with formula, see [online-documentation](#)

### Value

an object of class `data.frame` containing all (or selected) metrics.

### Examples

```

# Continuous variable (regression)
X <- rnorm(n = 100, mean = 0, sd = 10)
Y <- rnorm(n = 100, mean = 0, sd = 10)
regression_case <- data.frame(obs = X, pred = Y)

# Get a metrics summary for a regression problem
metrics_summary(regression_case, obs = X, pred = Y, type = "regression")

```

```
# Categorical variable (classification)
binomial_case <- data.frame(labels = sample(c("True","False"), 100,
replace = TRUE), predictions = sample(c("True","False"), 100, replace = TRUE))

#' # Get a metrics summary for a regression problem
metrics_summary(binomial_case, obs = labels, pred = predictions,
type = "classification")
```

MIC

*Maximal Information Coefficient***Description**

It estimates the Maximal Information Coefficient (MIC) for a continuous predicted-observed dataset.

**Usage**

```
MIC(data = NULL, obs, pred, tidy = FALSE, na.rm = TRUE)
```

**Arguments**

<code>data</code>	(Optional) argument to call an existing data frame containing the data.
<code>obs</code>	Vector with observed values (numeric).
<code>pred</code>	Vector with predicted values (numeric).
<code>tidy</code>	logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list (default).
<code>na.rm</code>	Logic argument to remove rows with missing values (NA). Default is <code>na.rm = TRUE</code> .

**Details**

The **MIC** function is a wrapper for the `mine_stat` function of the **minerva**-package, a collection of Maximal Information-Based Nonparametric statistics (MINE). See Reshef et al. (2011).

For the predicted-observed case (PO), the **MIC** is defined as follows:

$$\text{MIC}(D) = \max_{PO < B(n)} M(D)_{X,Y} = \max_{PO < B(n)} \frac{I^*(D, P, O)}{\log(\min P, O)},$$

where  $B(n) = n^\alpha$  is the search-grid size,  $I^*(D, P, O)$  is the maximum mutual information over all grids  $P$ -by- $O$ , of the distribution induced by  $D$  on a grid having  $P$  and  $O$  bins (where the probability mass on a cell of the grid is the fraction of points of  $D$  falling in that cell). Albanese et al. (2013).

For the formula and more details, see [online-documentation](#)

**Value**

an object of class `numeric` within a `list` (if `tidy = FALSE`) or within a `data frame` (if `tidy = TRUE`).



## References

Reshef, D., Reshef, Y., Finucane, H., Grossman, S., McVean, G., Turnbaugh, P., Lander, R., Mitzenmacher, M., and Sabeti, P. (2011). Detecting novel associations in large datasets. *Science* 334, 6062. doi:10.1126/science.1205438.

Albanese, D., M. Filosi, R. Visintainer, S. Riccadonna, G. Jurman, C. Furlanello. minerva and minepy: a C engine for the MINE suite and its R, Python and MATLAB wrappers. *Bioinformatics* (2013) 29(3):407-408. doi:10.1093/bioinformatics/bts707.

## See Also

[eval\\_tidy](#), [defusing-advanced\\_mine\\_stat](#)

## Examples

```
set.seed(1)
X <- rnorm(n = 100, mean = 0, sd = 10)
Y <- X + rnorm(n=100, mean = 0, sd = 3)
MIC(obs = X, pred = Y)
```

---

MLA

*Mean Lack of Accuracy (MLA)*

---

## Description

It estimates the MLA, the systematic error component to the Mean Squared Error (MSE), for a continuous predicted-observed dataset following Correndo et al. (2021).

## Usage

```
MLA(data = NULL, obs, pred, tidy = FALSE, na.rm = TRUE)
```

## Arguments

data	(Optional) argument to call an existing data frame containing the data.
obs	Vector with observed values (numeric).
pred	Vector with predicted values (numeric).
tidy	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
na.rm	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

**Details**

The MLA represents the systematic (bias) component of the MSE. It is obtained via a symmetric decomposition of the MSE (invariant to predicted-observed orientation) using a symmetric regression line. The MLA is equal to the sum of systematic differences divided by the sample size (n). The greater the value the greater the bias of the predictions. For the formula and more details, see [online-documentation](#)

**Value**

an object of class `numeric` within a `list` (if `tidy = FALSE`) or within a `data frame` (if `tidy = TRUE`).

**References**

Correndo et al. (2021). Revisiting linear regression to test agreement in continuous predicted-observed datasets. *Agric. Syst.* 192, 103194. doi:10.1016/j.agsy.2021.103194

**Examples**

```
set.seed(1)
X <- rnorm(n = 100, mean = 0, sd = 10)
Y <- X + rnorm(n=100, mean = 0, sd = 3)
MLA(obs = X, pred = Y)
```

---

MLP

---

*Mean Lack of Precision (MLP)*


---

**Description**

It estimates the MLP, the unsystematic error component to the Mean Squared Error (MSE), for a continuous predicted-observed dataset following Correndo et al. (2021).

**Usage**

```
MLP(data = NULL, obs, pred, tidy = FALSE, na.rm = TRUE)
```

**Arguments**

<code>data</code>	(Optional) argument to call an existing data frame containing the data.
<code>obs</code>	Vector with observed values (numeric).
<code>pred</code>	Vector with predicted values (numeric).
<code>tidy</code>	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a <code>data.frame</code> , FALSE returns a <code>list</code> ; Default : FALSE.
<code>na.rm</code>	Logic argument to remove rows with missing values (NA). Default is <code>na.rm = TRUE</code> .

## Details

The MLP represents the unsystematic (random) component of the MSE. It is obtained via a symmetric decomposition of the MSE (invariant to predicted-observed orientation) using a symmetric regression line. The MLP is equal to the sum of unsystematic differences divided by the sample size (n). The greater the value the greater the random noise of the predictions. For the formula and more details, see [online-documentation](#)

## Value

an object of class `numeric` within a `list` (if `tidy = FALSE`) or within a `data frame` (if `tidy = TRUE`).

## References

Correndo et al. (2021). Revisiting linear regression to test agreement in continuous predicted-observed datasets. *Agric. Syst.* 192, 103194. doi:10.1016/j.agsy.2021.103194

## Examples

```
set.seed(1)
X <- rnorm(n = 100, mean = 0, sd = 10)
Y <- X + rnorm(n=100, mean = 0, sd = 3)
MLP(obs = X, pred = Y)
```

---

MSE	<i>Mean Squared Error (MSE)</i>
-----	---------------------------------

---

## Description

It estimates the MSE for a continuous predicted-observed dataset.

## Usage

```
MSE(data = NULL, obs, pred, tidy = FALSE, na.rm = TRUE)
```

## Arguments

<code>data</code>	(Optional) argument to call an existing data frame containing the data.
<code>obs</code>	Vector with observed values (numeric).
<code>pred</code>	Vector with predicted values (numeric).
<code>tidy</code>	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a <code>data.frame</code> , FALSE returns a <code>list</code> ; Default : FALSE.
<code>na.rm</code>	Logic argument to remove rows with missing values (NA). Default is <code>na.rm = TRUE</code> .

## Details

The MSE, also known as MSD, measures general agreement, as includes both variance (lack of precision) and bias (lack of accuracy). The MSE of predictions could be decomposed following a variety of approaches (e.g. Willmott et al. 1981; Correndo et al. 2021). Its calculation is simple, the sum of squared differences between predictions and observations divided by the sample size (n). The greater the value the worse the predicted performance. Unfortunately, the units of MSE do not have a direct interpretation. For a more direct interpretation, the square root of MSE (RMSE) has the same units as the variable of interest. For the formula and more details, see [online-documentation](#)

## Value

an object of class `numeric` within a `list` (if `tidy = FALSE`) or within a `data frame` (if `tidy = TRUE`).

## References

- Willmott (1981). On the validation of models. *Phys. Geogr.* 2, 184–194. doi:10.1080/02723646.1981.10642213
- Correndo et al. (2021). Revisiting linear regression to test agreement in continuous predicted-observed datasets. *Agric. Syst.* 192, 103194. doi:10.1016/j.agry.2021.103194

## Examples

```
set.seed(1)
X <- rnorm(n = 100, mean = 0, sd = 10)
Y <- rnorm(n = 100, mean = 0, sd = 9)
MSE(obs = X, pred = Y)
```

---

npv

*Negative Predictive Value*

---

## Description

npv estimates the npv (a.k.a. positive predictive value -PPV-) for a nominal/categorical predicted-observed dataset.

FOR estimates the false omission rate, which is the complement of the negative predictive value for a nominal/categorical predicted-observed dataset.

## Usage

```
npv(
  data = NULL,
  obs,
  pred,
  atom = FALSE,
  pos_level = 2,
```

```

  tidy = FALSE,
  na.rm = TRUE
)

FOR(
  data = NULL,
  obs,
  pred,
  atom = FALSE,
  pos_level = 2,
  tidy = FALSE,
  na.rm = TRUE
)

```

### Arguments

data	(Optional) argument to call an existing data frame containing the data.
obs	Vector with observed values (character   factor).
pred	Vector with predicted values (character   factor).
atom	Logical operator (TRUE/FALSE) to decide if the estimate is made for each class (atom = TRUE) or at a global level (atom = FALSE); Default : FALSE.
pos_level	Integer, for binary cases, indicating the order (1 2) of the level corresponding to the positive. Generally, the positive level is the second (2) since following an alpha-numeric order, the most common pairs are (Negative   Positive), (0   1), (FALSE   TRUE). Default : 2.
tidy	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
na.rm	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

### Details

The npv is a non-normalized coefficient that represents the ratio between the correctly predicted cases (or true positive -TP- for binary cases) to the total predicted observations for a given class (or total predicted positive -PP- for binary cases) or at overall level.

For binomial cases,  $npv = \frac{TP}{PP} = \frac{TP}{TP+FP}$

The npv metric is bounded between 0 and 1. The closer to 1 the better. Values towards zero indicate low npv of predictions. It can be estimated for each particular class or at a global level.

The false omission rate (FOR) represents the proportion of false negatives with respect to the number of negative predictions (PN).

For binomial cases,  $FOR = 1 - npv = \frac{FN}{PN} = \frac{FN}{TN+FN}$

The npv metric is bounded between 0 and 1. The closer to 1 the better. Values towards zero indicate low npv of predictions.

For the formula and more details, see [online-documentation](#)

**Value**

an object of class numeric within a list (if `tidy = FALSE`) or within a data frame (if `tidy = TRUE`).

**References**

Wang H., Zheng H. (2013). Negative Predictive Value. *In: Dubitzky W., Wolkenhauer O., Cho KH., Yokota H. (eds) Encyclopedia of Systems Biology.* \_ Springer, New York, NY. [doi:10.1007/9781441998637\\_234](https://doi.org/10.1007/9781441998637_234)

Trevethan, R. (2017). *Sensitivity, Specificity, and Predictive Values: Foundations, Pliabilities, and Pitfalls* \_ in Research and Practice. *Front. Public Health* 5:307\_ [doi:10.3389/fpubh.2017.00307](https://doi.org/10.3389/fpubh.2017.00307)

**Examples**

```
set.seed(123)
# Two-class
binomial_case <- data.frame(labels = sample(c("True","False"), 100,
replace = TRUE), predictions = sample(c("True","False"), 100, replace = TRUE))
# Multi-class
multinomial_case <- data.frame(labels = sample(c("Red","Blue", "Green"), 100,
replace = TRUE), predictions = sample(c("Red","Blue", "Green"), 100, replace = TRUE))

# Get npv estimate for two-class case
npv(data = binomial_case, obs = labels, pred = predictions, tidy = TRUE)

# Get fdr estimate for two-class case
FDR(data = binomial_case, obs = labels, pred = predictions, tidy = TRUE)

# Get npv estimate for each class for the multi-class case
npv(data = multinomial_case, obs = labels, pred = predictions, tidy = TRUE, atom = TRUE)

# Get npv estimate for the multi-class case at a global level
npv(data = multinomial_case, obs = labels, pred = predictions, tidy = TRUE, atom = TRUE)
```

---

NSE

*Nash-Sutcliffe Model Efficiency (NSE)*


---

**Description**

It estimates the model efficiency suggested by Nash & Sutcliffe (1970) for a continuous predicted-observed dataset.

**Usage**

```
NSE(data = NULL, obs, pred, tidy = FALSE, na.rm = TRUE)
```

**Arguments**

<code>data</code>	(Optional) argument to call an existing data frame containing the data.
<code>obs</code>	Vector with observed values (numeric).
<code>pred</code>	Vector with predicted values (numeric).
<code>tidy</code>	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
<code>na.rm</code>	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

**Details**

The NSE measures general agreement. It is normalized (by the variance of the observations) and dimensionless. It is calculated using the absolute squared differences between the predictions and observations, which has been suggested as an issue due to over-sensitivity to outliers. It goes from -infinity to 1. The closer to 1 the better the prediction performance. For the formula and more details, see [online-documentation](#)

**Value**

an object of class `numeric` within a `list` (if `tidy = FALSE`) or within a `data frame` (if `tidy = TRUE`).

**References**

Nash & Sutcliffe (1970). River flow forecasting through conceptual models part I - A discussion of principles. *J. Hydrol.* 10(3), 292-290. doi:10.1016/00221694(70)902556

**Examples**

```
set.seed(1)
X <- rnorm(n = 100, mean = 0, sd = 10)
Y <- rnorm(n = 100, mean = 0, sd = 9)
NSE(obs = X, pred = Y)
```

---

PAB

*Percentage Additive Bias (PAB)*


---

**Description**

It estimates the contribution of the proportional bias to the Mean Squared Error (MSE) following Correndo et al. (2021).

**Usage**

```
PAB(data = NULL, obs, pred, tidy = FALSE, na.rm = TRUE)
```

**Arguments**

<code>data</code>	(Optional) argument to call an existing data frame containing the data.
<code>obs</code>	Vector with observed values (numeric).
<code>pred</code>	Vector with predicted values (numeric).
<code>tidy</code>	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
<code>na.rm</code>	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

**Details**

The PAB represents contribution of additive bias () component of the MSE. The  $PAB = 100 * ((mO - mP)^2 / MSE)$ , where  $mO$ , and  $mP$  represent the mean of observations and predictions, respectively. The greater the value the greater the contribution of additive bias to the prediction error. For the formula and more details, see [online-documentation](#)

**Value**

an object of class `numeric` within a `list` (if `tidy = FALSE`) or within a `data frame` (if `tidy = TRUE`).

**References**

Correndo et al. (2021). Revisiting linear regression to test agreement in continuous predicted-observed datasets. *Agric. Syst.* 192, 103194. doi:10.1016/j.agsy.2021.103194

**Examples**

```
set.seed(1)
X <- rnorm(n = 100, mean = 0, sd = 10)
Y <- X + rnorm(n=100, mean = 0, sd = 3)
PAB(obs = X, pred = Y)
```

---

PBE

*Percentage Bias Error (PBE).*


---

**Description**

It estimates the PBE for a continuous predicted-observed dataset following Gupta et al. (1999).

**Usage**

```
PBE(data = NULL, obs, pred, tidy = FALSE, na.rm = TRUE)
```



**Arguments**

data	(Optional) argument to call an existing data frame containing the data.
obs	Vector with observed values (numeric).
pred	Vector with predicted values (numeric).
tidy	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
na.rm	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

**Details**

The PBE (%) is useful to identify systematic over or under predictions. It is an unbounded metric. The closer to zero the bias of predictions. Negative values indicate overestimation, while positive values indicate underestimation. For the formula and more details, see [online-documentation](#)

**Value**

an object of class numeric within a list (if tidy = FALSE) or within a data frame (if tidy = TRUE).

**References**

Gupta et al. (1999). Status of automatic calibration for hydrologic models: Comparison with multi-level expert calibration. *J. Hydrologic Eng.* 4(2): 135-143. doi:10.1061/(ASCE)10840699(1999)4:2(135)

**Examples**

```
set.seed(1)
X <- rnorm(n = 100, mean = 0, sd = 10)
Y <- X + rnorm(n=100, mean = 0, sd = 3)
PBE(obs = X, pred = Y)
```

---

 PLA

---

*Percentage Lack of Accuracy (PLA)*


---

**Description**

It estimates the PLA, the contribution of the systematic error to the Mean Squared Error (MSE) for a continuous predicted-observed dataset following Correndo et al. (2021).

**Usage**

```
PLA(data = NULL, obs, pred, tidy = FALSE, na.rm = TRUE)
```

**Arguments**

<code>data</code>	(Optional) argument to call an existing data frame containing the data.
<code>obs</code>	Vector with observed values (numeric).
<code>pred</code>	Vector with predicted values (numeric).
<code>tidy</code>	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
<code>na.rm</code>	Logic argument to remove rows with missing values (NA). Default is <code>na.rm = TRUE</code> .

**Details**

The PLA (% , 0-100) represents the contribution of the Mean Lack of Accuracy (MLA), the systematic (bias) component of the MSE. It is obtained via a symmetric decomposition of the MSE (invariant to predicted-observed orientation). The PLA can be further segregated into percentage additive bias (PAB) and percentage proportional bias (PPB). The greater the value the greater the contribution of systematic error to the MSE. For the formula and more details, see [online-documentation](#)

**Value**

an object of class `numeric` within a `list` (if `tidy = FALSE`) or within a `data frame` (if `tidy = TRUE`).

**References**

Correndo et al. (2021). Revisiting linear regression to test agreement in continuous predicted-observed datasets. *Agric. Syst.* 192, 103194. doi:10.1016/j.agsy.2021.103194

**Examples**

```
set.seed(1)
X <- rnorm(n = 100, mean = 0, sd = 10)
Y <- X + rnorm(n=100, mean = 0, sd = 3)
PLA(obs = X, pred = Y)
```

---

 PLP

---

*Percentage Lack of Precision (PLP)*


---

**Description**

It estimates the PLP, the contribution of the unsystematic error to the Mean Squared Error (MSE) for a continuous predicted-observed dataset following Correndo et al. (2021).

**Usage**

```
PLP(data = NULL, obs, pred, tidy = FALSE, na.rm = TRUE)
```

**Arguments**

<code>data</code>	(Optional) argument to call an existing data frame containing the data.
<code>obs</code>	Vector with observed values (numeric).
<code>pred</code>	Vector with predicted values (numeric).
<code>tidy</code>	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
<code>na.rm</code>	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

**Details**

The PLP (% , 0-100) represents the contribution of the Mean Lack of Precision (MLP), the unsystematic (random) component of the MSE. It is obtained via a symmetric decomposition of the MSE (invariant to predicted-observed orientation). The greater the value the greater the contribution of unsystematic error to the MSE. For the formula and more details, see [online-documentation](#)

**Value**

an object of class numeric within a list (if `tidy = FALSE`) or within a data frame (if `tidy = TRUE`).

**References**

Correndo et al. (2021). Revisiting linear regression to test agreement in continuous predicted-observed datasets. *Agric. Syst.* 192, 103194. doi:10.1016/j.agry.2021.103194

**Examples**

```
set.seed(1)
X <- rnorm(n = 100, mean = 0, sd = 10)
Y <- X + rnorm(n=100, mean = 0, sd = 3)
PLP(obs = X, pred = Y)
```

---

 PPB

---

*Percentage Proportional Bias (PPB)*


---

**Description**

It estimates the contribution of the proportional bias to the Mean Squared Error (MSE) following Correndo et al. (2021).

**Usage**

```
PPB(data = NULL, obs, pred, tidy = FALSE, na.rm = TRUE)
```

**Arguments**

<code>data</code>	(Optional) argument to call an existing data frame containing the data.
<code>obs</code>	Vector with observed values (numeric).
<code>pred</code>	Vector with predicted values (numeric).
<code>tidy</code>	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
<code>na.rm</code>	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

**Details**

The PPB (%) measures the contribution of proportional bias to the MSE. The  $PPB = 100 * ((sO - sP)^2 / MSE)$ , where  $sO$ , and  $sP$  are the sample variances of observations and predictions, respectively. The greater the value the greater the contribution of proportional bias to the prediction error. For the formula and more details, see [online-documentation](#)

**Value**

an object of class `numeric` within a `list` (if `tidy = FALSE`) or within a `data frame` (if `tidy = TRUE`).

**References**

Correndo et al. (2021). Revisiting linear regression to test agreement in continuous predicted-observed datasets. *Agric. Syst.* 192, 103194. doi:10.1016/j.agsy.2021.103194

**Examples**

```
set.seed(1)
X <- rnorm(n = 100, mean = 0, sd = 10)
Y <- X + rnorm(n=100, mean = 0, sd = 3)
PPB(obs = X, pred = Y)
```

---

```
precision
```

```
Precision
```

---

**Description**

`precision` estimates the precision (a.k.a. positive predictive value -PPV-) for a nominal/categorical predicted-observed dataset.

`FDR` estimates the complement of precision (a.k.a. positive predictive value -PPV-) for a nominal/categorical predicted-observed dataset.

**Usage**

```
precision(
  data = NULL,
  obs,
  pred,
  tidy = FALSE,
  atom = FALSE,
  na.rm = TRUE,
  pos_level = 2
)
```

```
FDR(
  data = NULL,
  obs,
  pred,
  atom = FALSE,
  pos_level = 2,
  tidy = FALSE,
  na.rm = TRUE
)
```

**Arguments**

data	(Optional) argument to call an existing data frame containing the data.
obs	Vector with observed values (character   factor).
pred	Vector with predicted values (character   factor).
tidy	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
atom	Logical operator (TRUE/FALSE) to decide if the estimate is made for each class (atom = TRUE) or at a global level (atom = FALSE); Default : FALSE.
na.rm	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.
pos_level	Integer, for binary cases, indicating the order (1 2) of the level corresponding to the positive. Generally, the positive level is the second (2) since following an alpha-numeric order, the most common pairs are (Negative   Positive), (0   1), (FALSE   TRUE). Default : 2.

**Details**

The precision is a non-normalized coefficient that represents the ratio between the correctly predicted cases (or true positive -TP- for binary cases) to the total predicted observations for a given class (or total predicted positive -PP- for binary cases) or at overall level.

For binomial cases,  $precision = \frac{TP}{PP} = \frac{TP}{TP+FP}$

The precision metric is bounded between 0 and 1. The closer to 1 the better. Values towards zero indicate low precision of predictions. It can be estimated for each particular class or at a global level.

The false detection rate or false discovery rate (FDR) represents the proportion of false positives with respect to the total number of cases predicted as positive.

For binomial cases,  $FDR = 1 - precision = \frac{FP}{PP} = \frac{FP}{TP+FP}$

The precision metric is bounded between 0 and 1. The closer to 1 the better. Values towards zero indicate low precision of predictions.

For the formula and more details, see [online-documentation](#)

### Value

an object of class numeric within a list (if tidy = FALSE) or within a data frame (if tidy = TRUE).

### References

Ting K.M. (2017) Precision and Recall. In: *Sammut C., Webb G.I. (eds) Encyclopedia of Machine Learning and Data Mining. Springer, Boston, MA. doi:10.1007/9781489976871\_659*

### Examples

```
set.seed(123)
# Two-class
binomial_case <- data.frame(labels = sample(c("True","False"), 100,
replace = TRUE), predictions = sample(c("True","False"), 100, replace = TRUE))
# Multi-class
multinomial_case <- data.frame(labels = sample(c("Red","Blue", "Green"), 100,
replace = TRUE), predictions = sample(c("Red", "Blue", "Green"), 100, replace = TRUE))

# Get precision estimate for two-class case
precision(data = binomial_case, obs = labels, pred = predictions, tidy = TRUE)

# Get FDR estimate for two-class case
FDR(data = binomial_case, obs = labels, pred = predictions, tidy = TRUE)

# Get precision estimate for each class for the multi-class case
precision(data = multinomial_case, obs = labels, pred = predictions, tidy = TRUE, atom = TRUE)

# Get precision estimate for the multi-class case at a global level
precision(data = multinomial_case, obs = labels, pred = predictions, tidy = TRUE, atom = TRUE)
```

---

```
prevalence
```

```
Prevalence
```

---

### Description

preval estimates the prevalence of positive cases for a nominal/categorical predicted-observed dataset.

preval\_t estimates the prevalence threshold for a binary predicted-observed dataset.

**Usage**

```
preval(
  data = NULL,
  obs,
  pred,
  atom = FALSE,
  pos_level = 2,
  tidy = FALSE,
  na.rm = TRUE
)

preval_t(
  data = NULL,
  obs,
  pred,
  atom = FALSE,
  pos_level = 2,
  tidy = FALSE,
  na.rm = TRUE
)
```

**Arguments**

<code>data</code>	(Optional) argument to call an existing data frame containing the data.
<code>obs</code>	Vector with observed values (character   factor).
<code>pred</code>	Vector with predicted values (character   factor).
<code>atom</code>	Logical operator (TRUE/FALSE) to decide if the estimate is made for each class (atom = TRUE) or at a global level (atom = FALSE); Default : FALSE.
<code>pos_level</code>	Integer, for binary cases, indicating the order (1 2) of the level corresponding to the positive. Generally, the positive level is the second (2) since following an alpha-numeric order, the most common pairs are (Negative   Positive), (0   1), (FALSE   TRUE). Default : 2.
<code>tidy</code>	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
<code>na.rm</code>	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

**Details**

The prevalence measures the overall proportion of actual positives with respect to the total number of observations. Currently, it is defined for binary cases only.

The general formula is:

$$preval = \frac{positive}{positive+negative}$$

The prevalence threshold represents an point on the ROC curve (function of sensitivity (recall) and specificity) below which the precision (or PPV) dramatically drops.

$$preval_t = \frac{\sqrt{TPR * FPR} - FPR}{TPR - FPR}$$

It is bounded between 0 and 1. The closer to 1 the better. Values towards zero indicate low performance. For the formula and more details, see [online-documentation](#)

### Value

an object of class numeric within a list (if tidy = FALSE) or within a data frame (if tidy = TRUE).

### References

Freeman, E.A., Moisen, G.G. (2008). A comparison of the performance of threshold criteria for binary classification in terms of predicted prevalence and kappa. . *Ecol. Modell.* 217(1-2): 45-58. [doi:10.1016/j.ecolmodel.2008.05.015](#)

Balayla, J. (2020). Prevalence threshold and the geometry of screening curves. *\_Plos one*, 15(10):e0240215, [\\_doi:10.1371/journal.pone.0240215](#)

### Examples

```
set.seed(123)
# Two-class
binomial_case <- data.frame(labels = sample(c("True", "False"), 100, replace = TRUE),
  predictions = sample(c("True", "False"), 100, replace = TRUE))
# Multi-class
multinomial_case <- data.frame(labels = sample(c("Red", "Blue", "Green"), 100, replace = TRUE),
  predictions = sample(c("Red", "Blue", "Green"), 100, replace = TRUE) )

# Get prevalence estimate for two-class case
preval(data = binomial_case, obs = labels, pred = predictions, tidy = TRUE)

# Get prevalence estimate for each class for the multi-class case
preval(data = multinomial_case, obs = labels, pred = predictions, atom = TRUE)
```

---

 r

---

*Sample Correlation Coefficient (r)*


---

### Description

It estimates the Pearson's coefficient of correlation (r) for a continuous predicted-observed dataset.

### Usage

```
r(data = NULL, obs, pred, tidy = FALSE, na.rm = TRUE)
```



**Arguments**

data	(Optional) argument to call an existing data frame containing the data.
obs	Vector with observed values (numeric).
pred	Vector with predicted values (numeric).
tidy	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
na.rm	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

**Details**

The  $r$  coefficient measures the strength of linear relationship between two variables. It only accounts for precision, but it is not sensitive to lack of prediction accuracy. It is a normalized, dimensionless coefficient, that ranges between -1 to 1. It is expected that predicted and observed values will show  $0 < r < 1$ . It is also known as the Pearson Product Moment Correlation, among other names. For the formula and more details, see [online-documentation](#)

**Value**

an object of class `numeric` within a `list` (if `tidy = FALSE`) or within a `data frame` (if `tidy = TRUE`).

**References**

Kirch (2008) Pearson's Correlation Coefficient. In: Kirch W. (eds) *Encyclopedia of Public Health*. Springer, Dordrecht. doi:[10.1007/9781402056147\\_2569](https://doi.org/10.1007/9781402056147_2569)

**Examples**

```
set.seed(1)
X <- rnorm(n = 100, mean = 0, sd = 10)
Y <- X + rnorm(n=100, mean = 0, sd = 3)
r(obs = X, pred = Y)
```

---

R2

*Coefficient of determination (R2).*


---

**Description**

It estimates the R2 for a continuous predicted-observed dataset.

**Usage**

```
R2(data = NULL, obs, pred, tidy = FALSE, na.rm = TRUE)
```

**Arguments**

<code>data</code>	(Optional) argument to call an existing data frame containing the data.
<code>obs</code>	Vector with observed values (numeric).
<code>pred</code>	Vector with predicted values (numeric).
<code>tidy</code>	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
<code>na.rm</code>	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

**Details**

The R2 is one of the most widely used metrics evaluating models performance. R2 is appropriate to estimate the strength of linear association between two variables. It is positively bounded to 1, but it may produce negative values. The closer to 1 the better linear association between predictions and observations. However, R2 presents a major flaw for prediction performance evaluation: it is not sensitive to lack of accuracy (additive or proportional bias). Thus, R2 only measures precision, but it does not account for accuracy of the predictions. For the formula and more details, see [online-documentation](#)

**Value**

an object of class `numeric` within a `list` (if `tidy = FALSE`) or within a `data frame` (if `tidy = TRUE`).

**References**

Yang et al. (2014). An evaluation of the statistical methods for testing the performance of crop models with observed data. *Agric. Syst.* 127, 81-89. doi:10.1016/j.agsy.2014.01.008

**Examples**

```
set.seed(1)
X <- rnorm(n = 100, mean = 0, sd = 10)
Y <- X + rnorm(n=100, mean = 0, sd = 3)
R2(obs = X, pred = Y)
```

---

RAC

---

*Robinson's Agreement Coefficient (RAC).*


---

**Description**

It estimates the agreement coefficient suggested by Robinson (1957; 1959) for a continuous predicted-observed dataset.

**Usage**

```
RAC(data = NULL, obs, pred, tidy = FALSE, na.rm = TRUE)
```

**Arguments**

<code>data</code>	(Optional) argument to call an existing data frame containing the data.
<code>obs</code>	Vector with observed values (numeric).
<code>pred</code>	Vector with predicted values (numeric).
<code>tidy</code>	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
<code>na.rm</code>	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

**Details**

The RAC measures both accuracy and precision (general agreement). It is normalized, dimensionless, bounded (0 to 1), and symmetric (invariant to predicted-observed orientation). For the formula and more details, see [online-documentation](#)

**Value**

an object of class `numeric` within a `list` (if `tidy = FALSE`) or within a `data frame` (if `tidy = TRUE`).

**References**

Robinson (1957). The statistical measurement of agreement. *Am. Sociol. Rev.* 22(1), 17-25  
[doi:10.2307/2088760](#)

Robinson (1959). The geometric interpretation of agreement. *Am. Sociol. Rev.* 24(3), 338-345  
[doi:10.2307/2089382](#)

**Examples**

```
set.seed(1)
X <- rnorm(n = 100, mean = 0, sd = 10)
Y <- X + rnorm(n=100, mean = 0, sd = 3)
RAC(obs = X, pred = Y)
```

---

RAE *Relative Absolute Error (RAE)*

---

### Description

It estimates the RAC for a continuous predicted-observed dataset.

### Usage

```
RAE(data = NULL, obs, pred, tidy = FALSE, na.rm = TRUE)
```

### Arguments

data	(Optional) argument to call an existing data frame containing the data.
obs	Vector with observed values (numeric).
pred	Vector with predicted values (numeric).
tidy	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
na.rm	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

### Details

The RAE normalizes the Mean Absolute Error (MAE) with respect to the total absolute error. It is calculated as the ratio between the sum of absolute residuals (error of predictions with respect to observations) and the sum of absolute errors of observations with respect to its mean. It presents its lower bound at 0 (perfect fit), and has no upper bound. It can be used to compare models using different units. For the formula and more details, see [online-documentation](#)

### Value

an object of class `numeric` within a `list` (if `tidy = FALSE`) or within a `data frame` (if `tidy = TRUE`).

### Examples

```
set.seed(1)
X <- rnorm(n = 100, mean = 0, sd = 10)
Y <- X + rnorm(n=100, mean = 0, sd = 3)
RAE(obs = X, pred = Y)
```

recall

*Recall | Sensitivity***Description**

recall estimates the recall (a.k.a. sensitivity or true positive rate -TPR-) for a nominal/categorical predicted-observed dataset.

FNR estimates false negative rate (or false alarm, or fall-out) for a nominal/categorical predicted-observed dataset.

**Usage**

```
recall(
  data = NULL,
  obs,
  pred,
  atom = FALSE,
  pos_level = 2,
  tidy = FALSE,
  na.rm = TRUE
)
```

```
FNR(
  data = NULL,
  obs,
  pred,
  atom = FALSE,
  pos_level = 2,
  tidy = FALSE,
  na.rm = TRUE
)
```

**Arguments**

data	(Optional) argument to call an existing data frame containing the data.
obs	Vector with observed values (character   factor).
pred	Vector with predicted values (character   factor).
atom	Logical operator (TRUE/FALSE) to decide if the estimate is made for each class (atom = TRUE) or at a global level (atom = FALSE); Default : FALSE. When dataset is "binomial" atom does not apply.
pos_level	Integer, for binary cases, indicating the order (1 2) of the level corresponding to the positive. Generally, the positive level is the second (2) since following an alpha-numeric order, the most common pairs are (Negative   Positive), (0   1), (FALSE   TRUE). Default : 2.

tidy	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
na.rm	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

### Details

The recall (a.k.a. sensitivity or true positive rate -TPR-) is a non-normalized coefficient that represents the ratio between the correctly predicted cases (true positives -TP-) to the total number of actual observations that belong to a given class (actual positives -P-).

$$\text{For binomial cases, } recall = \frac{TP}{P} = \frac{TP}{TP+FN}$$

The recall metric is bounded between 0 and 1. The closer to 1 the better. Values towards zero indicate low performance. It can be either estimated for each particular class or at a global level.

The false negative rate (or false alarm, or fall-out) is the complement of the recall, representing the ratio between the number of false negatives (FN) to the actual number of positives (P). The FNR formula is:

$$FNR = 1 - recall = 1 - TPR = \frac{FN}{P}$$

The fpr is bounded between 0 and 1. The closer to 0 the better. Low performance is indicated with fpr > 0.5.

For the formula and more details, see [online-documentation](#)

### Value

an object of class numeric within a list (if tidy = FALSE) or within a data frame (if tidy = TRUE).

### References

Ting K.M. (2017) Precision and Recall. In: *Sammur C., Webb G.I. (eds) Encyclopedia of Machine Learning and Data Mining*. Springer, Boston, MA. doi:10.1007/9781489976871\_659

Ting K.M. (2017). Sensitivity. In: *Sammur C., Webb G.I. (eds) Encyclopedia of Machine Learning and Data Mining*. Springer, Boston, MA. doi:10.1007/9781489976871\_751

Trevethan, R. (2017). *Sensitivity, Specificity, and Predictive Values: Foundations, Plabilities, and Pitfalls* \_ in Research and Practice. Front. Public Health 5:307\_ doi:10.3389/fpubh.2017.00307

### Examples

```
set.seed(123)
# Two-class
binomial_case <- data.frame(labels = sample(c("True","False"), 100,
replace = TRUE), predictions = sample(c("True","False"), 100, replace = TRUE))

# Multi-class
multinomial_case <- data.frame(labels = sample(c("Red","Blue", "Green"), 100,
replace = TRUE), predictions = sample(c("Red","Blue", "Green"), 100, replace = TRUE))
```

```
# Get recall estimate for two-class case at global level
recall(data = binomial_case, obs = labels, pred = predictions, tidy = TRUE)

# Get FNR estimate for two-class case at global level
FNR(data = binomial_case, obs = labels, pred = predictions, tidy = TRUE)

# Get recall estimate for each class for the multi-class case at global level
recall(data = multinomial_case, obs = labels, pred = predictions, tidy = TRUE,
atom = FALSE)

# Get recall estimate for the multi-class case at a class-level
recall(data = multinomial_case, obs = labels, pred = predictions, tidy = TRUE,
atom = TRUE)
```

---

RMAE

*Relative Mean Absolute Error (RMAE)*

---

### Description

It estimates the RMAE for a continuous predicted-observed dataset.

### Usage

```
RMAE(data = NULL, obs, pred, tidy = FALSE, na.rm = TRUE)
```

### Arguments

data	(Optional) argument to call an existing data frame containing the data.
obs	Vector with observed values (numeric).
pred	Vector with predicted values (numeric).
tidy	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
na.rm	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

### Details

The RMAE normalizes the Mean Absolute Error (MAE) by the mean of observations. The closer to zero the lower the prediction error. For the formula and more details, see [online-documentation](#)

### Value

an object of class numeric within a list (if tidy = FALSE) or within a data frame (if tidy = TRUE).

## Examples

```
set.seed(1)
X <- rnorm(n = 100, mean = 0, sd = 10)
Y <- X + rnorm(n=100, mean = 0, sd = 3)
RMAE(obs = X, pred = Y)
```

---

RMLA

*Root Mean Lack of Accuracy (RMLA)*


---

## Description

It estimates the RMLA, the square root of the systematic error component to the Mean Squared Error (MSE), for a continuous predicted-observed dataset following Correndo et al. (2021).

## Usage

```
RMLA(data = NULL, obs, pred, tidy = FALSE, na.rm = TRUE)
```

## Arguments

<code>data</code>	(Optional) argument to call an existing data frame containing the data.
<code>obs</code>	Vector with observed values (numeric).
<code>pred</code>	Vector with predicted values (numeric).
<code>tidy</code>	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
<code>na.rm</code>	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

## Details

The RMLA represents the systematic (bias) component of the MSE expressed into the original variable units. It is obtained via a symmetric decomposition of the MSE (invariant to predicted-observed orientation) using a symmetric regression line (SMA). The RMLA is equal to the square-root of the sum of systematic differences divided by the sample size (n). The greater the value the greater the bias of the predictions. For the formula and more details, see [online-documentation](#)

## Value

an object of class `numeric` within a `list` (if `tidy = FALSE`) or within a `data frame` (if `tidy = TRUE`).

## References

Correndo et al. (2021). Revisiting linear regression to test agreement in continuous predicted-observed datasets. *Agric. Syst.* 192, 103194. doi:10.1016/j.agry.2021.103194



**Examples**

```
set.seed(1)
X <- rnorm(n = 100, mean = 0, sd = 10)
Y <- X + rnorm(n=100, mean = 0, sd = 3)
RMLA(obs = X, pred = Y)
```

RMLP

*Root Mean Lack of Precision (RMLP)***Description**

It estimates the RMLP, the square root of the unsystematic error component to the Mean Squared Error (MSE), for a continuous predicted-observed dataset following Correndo et al. (2021).

**Usage**

```
RMLP(data = NULL, obs, pred, tidy = FALSE, na.rm = TRUE)
```

**Arguments**

<code>data</code>	(Optional) argument to call an existing data frame containing the data.
<code>obs</code>	Vector with observed values (numeric).
<code>pred</code>	Vector with predicted values (numeric).
<code>tidy</code>	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
<code>na.rm</code>	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

**Details**

The RMLP represents the unsystematic (random) component of the MSE expressed on the original variables units  $\sqrt{MLP}$ . It is obtained via a symmetric decomposition of the MSE (invariant to predicted-observed orientation) using a symmetric regression line (SMA). The RMLP is equal to the square-root of the sum of unsystematic differences divided by the sample size (n). The greater the value the greater the random noise of the predictions. For the formula and more details, see [online-documentation](#)

**Value**

an object of class `numeric` within a list (if `tidy = FALSE`) or within a data frame (if `tidy = TRUE`).

**References**

Correndo et al. (2021). Revisiting linear regression to test agreement in continuous predicted-observed datasets. *Agric. Syst.* 192, 103194. doi:10.1016/j.agry.2021.103194

## Examples

```
set.seed(1)
X <- rnorm(n = 100, mean = 0, sd = 10)
Y <- X + rnorm(n=100, mean = 0, sd = 3)
RMLP(obs = X, pred = Y)
```

---

RMSE

*Root Mean Squared Error (RMSE)*

---

## Description

It estimates the RMSE for a continuous predicted-observed dataset.

## Usage

```
RMSE(data = NULL, obs, pred, tidy = FALSE, na.rm = TRUE)
```

## Arguments

<code>data</code>	(Optional) argument to call an existing data frame containing the data.
<code>obs</code>	Vector with observed values (numeric).
<code>pred</code>	Vector with predicted values (numeric).
<code>tidy</code>	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
<code>na.rm</code>	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

## Details

The RMSE is one of the most widely used error metrics in literature to evaluate prediction performance. It measures general agreement, being sensitive to both lack of precision and lack of accuracy. It is simply the square root of the Mean Squared Error (MSE). Thus, it presents the same units as the variable of interest, facilitating the interpretation. It goes from 0 to infinity. The lower the value the better the prediction performance. Its counterpart is being very sensitive to outliers. For the formula and more details, see [online-documentation](#)

## Value

an object of class `numeric` within a `list` (if `tidy = FALSE`) or within a `data frame` (if `tidy = TRUE`).

## Examples

```
set.seed(1)
X <- rnorm(n = 100, mean = 0, sd = 10)
Y <- X + rnorm(n=100, mean = 0, sd = 3)
RMSE(obs = X, pred = Y)
```

---

RRMSE

*Relative Root Mean Squared Error (RMSE)*

---

## Description

It estimates the RRMSE for a continuous predicted-observed dataset.

## Usage

```
RRMSE(data = NULL, obs, pred, tidy = FALSE, na.rm = TRUE)
```

## Arguments

data	(Optional) argument to call an existing data frame containing the data.
obs	Vector with observed values (numeric).
pred	Vector with predicted values (numeric).
tidy	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
na.rm	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

## Details

The RRMSE (%) normalizes the Root Mean Squared Error (RMSE) by the mean of observations. It goes from 0 to infinity. The lower the better the prediction performance. In literature, it can be also found as NRMSE (normalized root mean squared error). However, here we use RRMSE since several other alternatives to "normalize" the RMSE exist (e.g., RSR, iqRMSE). For the formula and more details, see [online-documentation](#)

## Value

an object of class numeric within a list (if tidy = FALSE) or within a data frame (if tidy = TRUE).

**Examples**

```
set.seed(1)
X <- rnorm(n = 100, mean = 0, sd = 10)
Y <- X + rnorm(n=100, mean = 0, sd = 3)
RRMSE(obs = X, pred = Y)
```

---

RSE *Relative Squared Error (RSE)*

---

**Description**

It estimates the RSE for a continuous predicted-observer dataset.

**Usage**

```
RSE(data = NULL, obs, pred, tidy = FALSE, na.rm = TRUE)
```

**Arguments**

data	(Optional) argument to call an existing data frame containing the data.
obs	Vector with observed values (numeric).
pred	Vector with predicted values (numeric).
tidy	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
na.rm	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

**Details**

The RSE is the ratio between the residual sum of squares (RSS, error of predictions with respect to observations) and the total sum of squares (TSS, error of observations with respect to its mean). RSE is dimensionless, so it can be used to compared models with different units. For the formula and more details, see [online-documentation](#)

**Value**

an object of class `numeric` within a list (if `tidy = FALSE`) or within a data frame (if `tidy = TRUE`).

**Examples**

```
set.seed(1)
X <- rnorm(n = 100, mean = 0, sd = 10)
Y <- X + rnorm(n=100, mean = 0, sd = 3)
RSE(obs = X, pred = Y)
```

---

RSR *Root Mean Standard Deviation Ratio (RSR)*

---

### Description

It estimates the MSE normalized by the standard deviation of observed values following Moriasi et al. (2007).

### Usage

```
RSR(data = NULL, obs, pred, tidy = FALSE, na.rm = TRUE)
```

### Arguments

<code>data</code>	(Optional) argument to call an existing data frame containing the data.
<code>obs</code>	Vector with observed values (numeric).
<code>pred</code>	Vector with predicted values (numeric).
<code>tidy</code>	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
<code>na.rm</code>	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

### Details

The RSR normalizes the Root Mean Squared Error (RMSE) using the standard deviation of observed values. It goes from a optimal value of 0 to infinity. Based on RSR, Moriasi et al. (2007) indicates performance ratings as: i) very-good (0-0.50), ii) good (0.50-0.60), iii) satisfactory (0.60-0.70), or iv) unsatisfactory (>0.70). For the formula and more details, see [online-documentation](#)

### Value

an object of class `numeric` within a `list` (if `tidy = FALSE`) or within a `data frame` (if `tidy = TRUE`).

### References

Moriasi et al. (2007). Model Evaluation Guidelines for Systematic Quantification of Accuracy in Watershed Simulations. *Trans. ASABE* 50, 885–900. doi:10.13031/2013.23153

### Examples

```
set.seed(1)
X <- rnorm(n = 100, mean = 0, sd = 10)
Y <- X + rnorm(n=100, mean = 0, sd = 3)
RSR(obs = X, pred = Y)
```

---

RSS

*Residual Sum of Squares (RSS)*

---

### Description

It estimates the RSS for a continuous predicted-observed dataset.

### Usage

```
RSS(data = NULL, obs, pred, tidy = FALSE, na.rm = TRUE)
```

### Arguments

<code>data</code>	(Optional) argument to call an existing data frame containing the data.
<code>obs</code>	Vector with observed values (numeric).
<code>pred</code>	Vector with predicted values (numeric).
<code>tidy</code>	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
<code>na.rm</code>	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

### Details

The RSS is the sum of the squared differences between predictions and observations. It represents the base of many error metrics using squared scale such as the Mean Squared Error (MSE). For the formula and more details, see [online-documentation](#)

### Value

an object of class numeric within a list (if tidy = FALSE) or within a data frame (if tidy = TRUE).

### Examples

```
set.seed(1)
X <- rnorm(n = 100, mean = 0, sd = 10)
Y <- X + rnorm(n=100, mean = 0, sd = 3)
RSS(obs = X, pred = Y)
```

---

SB *Squared bias (SB)*

---

### Description

It estimates the SB component of the Mean Squared Error (MSE) proposed by Kobayashi & Salam (2000).

### Usage

```
SB(data = NULL, obs, pred, tidy = FALSE, na.rm = TRUE)
```

### Arguments

data	(Optional) argument to call an existing data frame containing the data.
obs	Vector with observed values (numeric).
pred	Vector with predicted values (numeric).
tidy	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
na.rm	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

### Details

The SB represents the additive bias component of the prediction error following Kobayashi & Salam (2000). It is in square units of the variable of interest, so it does not have a direct interpretation. The lower the value the less contribution to the MSE. However, it needs to be compared to MSE as its benchmark. For the formula and more details, see [online-documentation](#)

### Value

an object of class `numeric` within a `list` (if `tidy = FALSE`) or within a `data frame` (if `tidy = TRUE`).

### References

Kobayashi & Salam (2000). Comparing simulated and measured values using mean squared deviation and its components. *Agron. J.* 92, 345–352. doi:10.2134/agronj2000.922345x

### Examples

```
set.seed(1)
X <- rnorm(n = 100, mean = 0, sd = 10)
Y <- rnorm(n = 100, mean = 0, sd = 9)
SB(obs = X, pred = Y)
```

---

scatter_plot	<i>Scatter plot of predicted and observed values</i>
--------------	--

---

### Description

It draws a scatter plot of predictions and observations with alternative axis orientation (P vs. O; O vs. P).

### Usage

```
scatter_plot(
  data = NULL,
  obs,
  pred,
  orientation = "PO",
  print_metrics = FALSE,
  metrics_list = NULL,
  position_metrics = c(x = NULL, y = NULL),
  print_eq = TRUE,
  position_eq = c(x = NULL, y = NULL),
  eq_color = NULL,
  shape_type = NULL,
  shape_size = NULL,
  shape_color = NULL,
  regline_type = NULL,
  regline_size = NULL,
  regline_color = NULL,
  na.rm = TRUE
)
```

### Arguments

<code>data</code>	(Optional) argument to call an existing data frame with the data.
<code>obs</code>	Vector with observed values (numeric).
<code>pred</code>	Vector with predicted values (numeric).
<code>orientation</code>	Argument of class string specifying the axis orientation, PO for predicted vs observed, and OP for observed vs predicted. Default is orientation = "PO".
<code>print_metrics</code>	boolean TRUE/FALSE to embed metrics in the plot. Default is FALSE.
<code>metrics_list</code>	vector or list of selected metrics to print on the plot.
<code>position_metrics</code>	vector or list with '(x,y)' coordinates to locate the metrics_table into the plot. Default : c(x = min(obs), y = 1.05*max(pred)).
<code>print_eq</code>	boolean TRUE/FALSE to embed metrics in the plot. Default is FALSE.
<code>position_eq</code>	vector or list with '(x,y)' coordinates to locate the SMA equation into the plot. Default : c(x = 0.70 max(x), y = 1.25*min(y)).



<code>eq_color</code>	string indicating the color of the SMA-regression text.
<code>shape_type</code>	integer indicating the shape type for the data points.
<code>shape_size</code>	number indicating the shape size for the data points.
<code>shape_color</code>	string indicating the shape color for the data points.
<code>regline_type</code>	string or integer indicating the SMA-regression line-type.
<code>regline_size</code>	number indicating the SMA-regression line size.
<code>regline_color</code>	string indicating the SMA-regression line color.
<code>na.rm</code>	Logic argument to remove rows with missing values (NA). Default is <code>na.rm = TRUE</code> .

### Details

It creates a scatter plot of predicted vs. observed values. The plot also includes the 1:1 line (solid line) and the linear regression line (dashed line). By default, it places the observed on the x-axis and the predicted on the y-axis (orientation = "PO"). This can be inverted by changing the argument orientation = "OP". For more details, see [online-documentation](#)

### Value

an object of class `ggplot`.

### See Also

[ggplot](#), [geom\\_point](#), [aes](#)

### Examples

```
X <- rnorm(n = 100, mean = 0, sd = 10)
Y <- rnorm(n = 100, mean = 0, sd = 10)
scatter_plot(obs = X, pre = Y)
```

---

SDSD

*Squared difference between standard deviations (SDSD)*

---

### Description

It estimates the SDSD component of the Mean Squared Error (MSE) proposed by Kobayashi & Salam (2000).

### Usage

```
SDSD(data = NULL, obs, pred, tidy = FALSE, na.rm = TRUE)
```

**Arguments**

<code>data</code>	(Optional) argument to call an existing data frame containing the data.
<code>obs</code>	Vector with observed values (numeric).
<code>pred</code>	Vector with predicted values (numeric).
<code>tidy</code>	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
<code>na.rm</code>	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

**Details**

The SDSD represents the proportional bias component of the prediction error following Kobayashi & Salam (2000). It is in square units of the variable of interest, so it does not have a direct interpretation. The lower the value the less contribution to the MSE. However, it needs to be compared to MSE as its benchmark. For the formula and more details, see [online-documentation](#)

**Value**

an object of class `numeric` within a `list` (if `tidy = FALSE`) or within a `data frame` (if `tidy = TRUE`).

**References**

Kobayashi & Salam (2000). Comparing simulated and measured values using mean squared deviation and its components. *Agron. J.* 92, 345–352. doi:10.2134/agronj2000.922345x

**Examples**

```
set.seed(1)
X <- rnorm(n = 100, mean = 0, sd = 10)
Y <- X + rnorm(n=100, mean = 0, sd = 3)
SDSD(obs = X, pred = Y)
```

---

SMAPE

*Symmetric Mean Absolute Percentage Error (SMAPE).*


---

**Description**

It estimates the SMAPE for a continuous predicted-observed dataset.

**Usage**

```
SMAPE(data = NULL, obs, pred, tidy = FALSE, na.rm = TRUE)
```

**Arguments**

data	(Optional) argument to call an existing data frame containing the data.
obs	Vector with observed values (numeric).
pred	Vector with predicted values (numeric).
tidy	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
na.rm	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

**Details**

The SMAPE (%) is a normalized, dimensionless, and bounded (0% to 200%). It is a modification of the MAPE where the denominator is half of the sum of absolute differences between observations and predictions. This modification solves the problem of MAPE of producing negative or undefined values. For the formula and more details, see [online-documentation](#)

**Value**

an object of class `numeric` within a `list` (if `tidy = FALSE`) or within a `data frame` (if `tidy = TRUE`).

**References**

Makridakis (1993). Accuracy measures: theoretical and practical concerns. *Int. J. Forecast.* 9, 527-529. doi:[10.1016/01692070\(93\)900793](https://doi.org/10.1016/01692070(93)900793)

**Examples**

```
set.seed(1)
X <- rnorm(n = 100, mean = 0, sd = 10)
Y <- X + rnorm(n=100, mean = 0, sd = 3)
SMAPE(obs = X, pred = Y)
```

---

sorghum

*Sorghum grain number*


---

**Description**

This example dataset is a set of APSIM simulations of sorghum grain number (x1000 grains per squared meter), which exhibits both low accuracy and low precision as it represents a model still under development. The experimental trials come from 6 site-years in 1 country (Australia). These data correspond to the latest, up-to-date, documentation and validation of version number 2020.03.27.4956. Data available at: [doi:10.7910/DVN/EJS4M0](https://doi.org/10.7910/DVN/EJS4M0). Further details can be found at the official APSIM Next Generation website: <https://APSIMnextgeneration.netlify.app/modeldocumentation/>

**Usage**

sorghum

**Format**

This data frame has 36 rows and the following 2 columns:

**pred** predicted values

**obs** observed values

**Source**

<https://github.com/adriancorrendo/metrica>

---

specificity	<i>Specificity</i>
-------------	--------------------

---

**Description**

specificity estimates the specificity (a.k.a. selectivity, or true negative rate -TNR-) for a nominal/categorical predicted-observed dataset.

FPR estimates the false positive rate (a.k.a fall-out or false alarm) for a nominal/categorical predicted-observed dataset.

**Usage**

```
specificity(  
  data = NULL,  
  obs,  
  pred,  
  atom = FALSE,  
  pos_level = 2,  
  tidy = FALSE,  
  na.rm = TRUE  
)
```

```
FPR(  
  data = NULL,  
  obs,  
  pred,  
  atom = FALSE,  
  pos_level = 2,  
  tidy = FALSE,  
  na.rm = TRUE  
)
```

**Arguments**

data	(Optional) argument to call an existing data frame containing the data.
obs	Vector with observed values (character   factor).
pred	Vector with predicted values (character   factor).
atom	Logical operator (TRUE/FALSE) to decide if the estimate is made for each class (atom = TRUE) or at a global level (atom = FALSE); Default : FALSE. When dataset is "binomial" atom does not apply.
pos_level	Integer, for binary cases, indicating the order (1 2) of the level corresponding to the positive. Generally, the positive level is the second (2) since following an alpha-numeric order, the most common pairs are (Negative   Positive), (0   1), (FALSE   TRUE). Default : 2.
tidy	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
na.rm	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

**Details**

The specificity (or selectivity, or true negative rate-TNR-) is a non-normalized coefficient that represents the ratio between the correctly negative predicted cases (or true negative -TN- for binary cases) to the total number of actual observations not belonging to a given class (actual negatives -N- for binary cases).

For binomial cases,  $specificity = \frac{TN}{N} = \frac{TN}{TN+FP}$

The specificity metric is bounded between 0 and 1. The closer to 1 the better. Values towards zero indicate low performance. For multinomial cases, it can be either estimated for each particular class or at a global level.

The false positive rate (or false alarm, or fall-out) is the complement of the specificity, representing the ratio between the number of false positives (FP) to the actual number of negatives (N). The FPR formula is:

$$FPR = 1 - specificity = 1 - TNR = \frac{FP}{N}$$

The FPR is bounded between 0 and 1. The closer to 0 the better. Low performance is indicated with  $FPR > 0.5$ .

For the formula and more details, see [online-documentation](#)

**Value**

an object of class numeric within a list (if tidy = FALSE) or within a data frame (if tidy = TRUE).

**References**

- Ting K.M. (2017) Sensitivity and Specificity. In: Sammut C., Webb G.I. (eds) *Encyclopedia of Machine Learning and Data Mining*. Springer, Boston, MA. doi:10.1007/9780387301648\_752
- Trevethan, R. (2017). *Sensitivity, Specificity, and Predictive Values: Foundations, Plabilities, and Pitfalls* \_ in Research and Practice. Front. Public Health 5:307\_ doi:10.3389/fpubh.2017.00307

**Examples**

```

set.seed(123)
# Two-class
binomial_case <- data.frame(labels = sample(c("True","False"), 100,
replace = TRUE), predictions = sample(c("True","False"), 100, replace = TRUE))
# Multi-class
multinomial_case <- data.frame(labels = sample(c("Red","Blue", "Green"), 100,
replace = TRUE), predictions = sample(c("Red","Blue", "Green"), 100, replace = TRUE)  )

# Get specificity and FPR estimates for two-class case
specificity(data = binomial_case, obs = labels, pred = predictions, tidy = TRUE)
FPR(data = binomial_case, obs = labels, pred = predictions, tidy = TRUE)

# Get specificity estimate for each class for the multi-class case
specificity(data = multinomial_case, obs = labels, pred = predictions, tidy = TRUE)

# Get specificity estimate for the multi-class case at a global level
specificity(data = multinomial_case, obs = labels, pred = predictions, tidy = TRUE)

```

---

tiles\_plot

*Tiles plot of predicted and observed values*


---

**Description**

It draws a tiles plot of predictions and observations with alternative axis orientation (P vs. O; O vs. P).

**Usage**

```

tiles_plot(
  data = NULL,
  obs,
  pred,
  bins = 10,
  colors = c(low = NULL, high = NULL),
  orientation = "PO",
  print_metrics = FALSE,
  metrics_list = NULL,
  position_metrics = c(x = NULL, y = NULL),
  print_eq = TRUE,
  position_eq = c(x = NULL, y = NULL),
  eq_color = NULL,
  regline_type = NULL,
  regline_size = NULL,
  regline_color = NULL,
  na.rm = TRUE
)

```

**Arguments**

data	(Optional) argument to call an existing data frame containing the data.
obs	Vector with observed values (numeric).
pred	Vector with predicted values (numeric).
bins	Argument of class numeric specifying the number of bins to create the tiles.
colors	Vector or list with two colors '(low, high)' to paint the density gradient.
orientation	Argument of class string specifying the axis orientation, PO for predicted vs observed, and OP for observed vs predicted. Default is orientation = "PO".
print_metrics	boolean TRUE/FALSE to embed metrics in the plot. Default is FALSE.
metrics_list	vector or list of selected metrics to print on the plot.
position_metrics	vector or list with '(x,y)' coordinates to locate the metrics_table into the plot. Default : c(x = min(obs), y = 1.05*max(pred)).
print_eq	boolean TRUE/FALSE to embed metrics in the plot. Default is FALSE.
position_eq	vector or list with '(x,y)' coordinates to locate the SMA equation into the plot. Default : c(x = 0.70 max(x), y = 1.25*min(y)).
eq_color	string indicating the color of the SMA-regression text.
regline_type	string or integer indicating the SMA-regression line-type.
regline_size	number indicating the SMA-regression line size.
regline_color	string indicating the SMA-regression line color.
na.rm	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

**Details**

It creates a tiles plot of predicted vs. observed values. The plot also includes the 1:1 line (solid line) and the linear regression line (dashed line). By default, it places the observed on the x-axis and the predicted on the y-axis (orientation = "PO"). This can be inverted by changing the argument orientation = "OP". For more details, see [online-documentation](#)

**Value**

Object of class ggplot.

**See Also**

[ggplot](#), [geom\\_point](#), [aes](#)

**Examples**

```
X <- rnorm(n = 100, mean = 0, sd = 10)
Y <- rnorm(n = 100, mean = 0, sd = 10)
tiles_plot(obs = X, pred = Y)
```

---

TSS	<i>Total Sum of Squares (TSS)</i>
-----	-----------------------------------

---

### Description

It estimates the TSS for observed vector.

### Usage

```
TSS(data = NULL, obs, tidy = FALSE, na.rm = TRUE)
```

### Arguments

<code>data</code>	(Optional) argument to call an existing data frame containing the data.
<code>obs</code>	Vector with observed values (numeric).
<code>tidy</code>	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
<code>na.rm</code>	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

### Details

The TSS sum of the squared differences between the observations and its mean. It is used as a reference error, for example, to estimate explained variance. For the formula and more details, see [online-documentation](#)

### Value

an object of class `numeric` within a `list` (if `tidy = FALSE`) or within a `data frame` (if `tidy = TRUE`).

### Examples

```
set.seed(1)
X <- rnorm(n = 100, mean = 0, sd = 10)
Y <- X + rnorm(n=100, mean = 0, sd = 3)
TSS(obs = X)
```



---

Ub *Mean Bias Error Proportion (Ub)*

---

**Description**

It estimates the Ub component from the sum of squares decomposition described by Smith & Rose (1995).

**Usage**

```
Ub(data = NULL, obs, pred, tidy = FALSE, na.rm = TRUE)
```

**Arguments**

data	(Optional) argument to call an existing data frame containing the data.
obs	Vector with observed values (numeric).
pred	Vector with predicted values (numeric).
tidy	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
na.rm	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

**Details**

The Ub estimates the proportion of the total sum of squares related to the mean bias following the sum of squares decomposition suggested by Smith and Rose (1995) also known as Theil's partial inequalities. For the formula and more details, see [online-documentation](#)

**Value**

an object of class `numeric` within a `list` (if `tidy = FALSE`) or within a `data frame` (if `tidy = TRUE`).

**References**

Smith & Rose (1995). Model goodness-of-fit analysis using regression and related techniques. *Ecol. Model.* 77, 49–64. [doi:10.1016/03043800\(93\)E0074D](https://doi.org/10.1016/03043800(93)E0074D)

**Examples**

```
set.seed(1)
X <- rnorm(n = 100, mean = 0, sd = 10)
Y <- X + rnorm(n=100, mean = 0, sd = 3)
Ub(obs = X, pred = Y)
```

---

Uc *Lack of Consistency (Uc)*

---

### Description

It estimates the Uc component from the sum of squares decomposition described by Smith & Rose (1995).

### Usage

```
Uc(data = NULL, obs, pred, tidy = FALSE, na.rm = TRUE)
```

### Arguments

data	(Optional) argument to call an existing data frame containing the data.
obs	Vector with observed values (numeric).
pred	Vector with predicted values (numeric).
tidy	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
na.rm	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

### Details

The Uc estimates the proportion of the total sum of squares related to the lack of consistency (proportional bias) following the sum of squares decomposition suggested by Smith and Rose (1995) also known as Theil's partial inequalities. For the formula and more details, see [online-documentation](#)

### Value

an object of class `numeric` within a list (if `tidy = FALSE`) or within a data frame (if `tidy = TRUE`).

### References

Smith & Rose (1995). Model goodness-of-fit analysis using regression and related techniques. *Ecol. Model.* 77, 49–64. doi:10.1016/03043800(93)E0074D

### Examples

```
set.seed(1)
X <- rnorm(n = 100, mean = 0, sd = 10)
Y <- X + rnorm(n=100, mean = 0, sd = 3)
Uc(obs = X, pred = Y)
```

---

Ue *Lack of Consistency (Ue)*

---

### Description

It estimates the Ue component from the sum of squares decomposition described by Smith & Rose (1995).

### Usage

```
Ue(data = NULL, obs, pred, tidy = FALSE, na.rm = TRUE)
```

### Arguments

data	(Optional) argument to call an existing data frame containing the data.
obs	Vector with observed values (numeric).
pred	Vector with predicted values (numeric).
tidy	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
na.rm	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

### Value

an object of class `numeric` within a `list` (if `tidy = FALSE`) or within a `data frame` (if `tidy = TRUE`). The Ue estimates the proportion of the total sum of squares related to the random error (unsystematic error or variance) following the sum of squares decomposition suggested by Smith and Rose (1995) also known as Theil's partial inequalities. For the formula and more details, see [online-documentation](#)

### References

Smith & Rose (1995). Model goodness-of-fit analysis using regression and related techniques. *Ecol. Model.* 77, 49–64. doi:10.1016/03043800(93)E0074D

### Examples

```
set.seed(1)
X <- rnorm(n = 100, mean = 0, sd = 10)
Y <- X + rnorm(n=100, mean = 0, sd = 3)
Ue(obs = X, pred = Y)
```

---

uSD *Uncorrected Standard Deviation*

---

### Description

It estimates the (uSD) of observed or predicted values.

### Usage

```
uSD(data = NULL, x, tidy = FALSE, na.rm = TRUE)
```

### Arguments

data	(Optional) argument to call an existing data frame containing the data.
x	Vector with numeric observed or predicted values.
tidy	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
na.rm	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

### Details

The uSD is the sample, uncorrected standard deviation. The square root of the mean of sum of squared differences between vector values with respect to their mean. It is uncorrected because it is divided by the sample size (n), not n-1. For the formula and more details, see [online-documentation](#)

### Value

an object of class numeric within a list (if tidy = FALSE) or within a data frame (if tidy = TRUE).

### Examples

```
set.seed(1)
X <- rnorm(n = 100, mean = 0, sd = 10)
uSD(x = X)
```

---

var_u	<i>Uncorrected Variance (var_u)</i>
-------	-------------------------------------

---

### Description

It estimates the var\_u of observed or predicted values.

### Usage

```
var_u(data = NULL, x, tidy = FALSE, na.rm = TRUE)
```

### Arguments

data	(Optional) argument to call an existing data frame containing the data.
x	Vector with numeric elements.
tidy	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
na.rm	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

### Details

The var\_u is the sample, uncorrected variance. It is calculated as the mean of sum of squared differences between values of an x and its mean, divided by the sample size (n). It is uncorrected because it is divided by n, and by not n-1 (traditional variance). For the formula and more details, see [online-documentation](#)

### Value

an object of class numeric within a list (if tidy = FALSE) or within a data frame (if tidy = TRUE).

### Examples

```
set.seed(1)
X <- rnorm(n = 100, mean = 0, sd = 10)
var_u(x = X)
```

---

wheat	<i>Wheat grain nitrogen</i>
-------	-----------------------------

---

### Description

This example dataset is a set of APSIM simulations of wheat grain N (grams per squared meter), which presents both high accuracy and high precision. The experimental trials come from 11 site-years in 4 countries (Australia, Ethiopia, New Zealand, and Turkey). These data correspond to the latest, up-to-date, documentation and validation of version number 2020.03.27.4956. Data available at: [doi:10.7910/DVN/EJS4M0](https://doi.org/10.7910/DVN/EJS4M0). Further details can be found at the official APSIM Next Generation website: <https://APSIMnextgeneration.netlify.app/modeldocumentation/>

### Usage

wheat

### Format

This data frame has 137 rows and the following 2 columns:

**pred** predicted values

**obs** observed values

### Source

<https://github.com/adriancorrendo/metrica>

---

Xa	<i>Accuracy Component (Xa) of CCC</i>
----	---------------------------------------

---

### Description

It estimates the Xa component for the calculation of the Concordance Correlation Coefficient (CCC) following Lin (1989).

### Usage

```
Xa(data = NULL, obs, pred, tidy = FALSE, na.rm = TRUE)
```

### Arguments

data	(Optional) argument to call an existing data frame containing the data.
obs	Vector with observed values (numeric).
pred	Vector with predicted values (numeric).
tidy	Logical operator (TRUE/FALSE) to decide the type of return. TRUE returns a data.frame, FALSE returns a list; Default : FALSE.
na.rm	Logic argument to remove rows with missing values (NA). Default is na.rm = TRUE.

**Details**

The Xa measures accuracy of prediction. It goes from 0 (completely inaccurate) to 1 (perfectly accurate). It is used to adjust the precision measured by the correlation coefficient ( $r$ ) in order to evaluate agreement through the CCC. For the formula and more details, see [online-documentation](#)

**Value**

an object of class `numeric` within a `list` (if `tidy = FALSE`) or within a `data frame` (if `tidy = TRUE`).

**References**

Lin (1989). A concordance correlation coefficient to evaluate reproducibility. *Biometrics* 45 (1), 255–268. [doi:10.2307/2532051](https://doi.org/10.2307/2532051)

**Examples**

```
set.seed(1)
X <- rnorm(n = 100, mean = 0, sd = 10)
Y <- X + rnorm(n=100, mean = 0, sd = 3)
Xa(obs = X, pred = Y)
```

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