

Package ‘fairmetrics’

May 8, 2026

Title Fairness Evaluation Metrics with Confidence Intervals for Binary Protected Attributes

Version 1.0.8

Description A collection of functions for computing fairness metrics for machine learning and statistical models, including confidence intervals for each metric. The package supports the evaluation of group-level fairness criterion commonly used in fairness research, particularly in health-care for binary protected attributes. It is based on the overview of fairness in machine learning written by Gao et al (2025) <[doi:10.1002/sim.70234](https://doi.org/10.1002/sim.70234)>.

Imports stats

License MIT + file LICENSE

Encoding UTF-8

RoxygenNote 7.3.2

Suggests dplyr, magrittr, corrplot, randomForest, pROC,
SpecsVerification, knitr, rmarkdown, testthat, kableExtra,
naniar

Config/testthat/edition 3

Depends R (>= 3.5.0)

LazyData true

URL <https://jianhuig.github.io/fairmetrics/>

VignetteBuilder knitr

NeedsCompilation no

Author Jianhui Gao [aut] (ORCID: <<https://orcid.org/0000-0003-0915-1473>>),
Benjamin Smith [aut, cre] (ORCID:
<<https://orcid.org/0009-0007-2206-0177>>),
Benson Chou [aut] (ORCID: <<https://orcid.org/0009-0007-0265-033X>>),
Jessica Gronsbell [aut] (ORCID:
<<https://orcid.org/0000-0002-5360-5869>>)

Maintainer Benjamin Smith <benyamin.smith@mail.utoronto.ca>

Repository CRAN

Date/Publication 2026-04-16 15:00:02 UTC

Contents

eval_acc_parity	2
eval_bs_parity	4
eval_cond_acc_equality	6
eval_eq_odds	8
eval_eq_opp	10
eval_neg_class_bal	12
eval_neg_pred_parity	13
eval_pos_class_bal	15
eval_pos_pred_parity	17
eval_pred_equality	19
eval_stats_parity	21
eval_treatment_equality	23
get_fairness_metrics	25
mimic	27
mimic_preprocessed	29

Index	30
--------------	-----------

eval_acc_parity	<i>Examine Accuracy Parity of a Model</i>
-----------------	---

Description

This function assesses *Accuracy Parity*, a fairness criterion that evaluates whether the overall accuracy of a predictive model is consistent across two groups defined by a binary protected attribute.

Usage

```
eval_acc_parity(
  data,
  outcome,
  group,
  probs,
  cutoff = 0.5,
  confint = TRUE,
  alpha = 0.05,
  bootstraps = 2500,
  digits = 2,
  message = TRUE
)
```

Arguments

data	Data frame containing the outcome, predicted outcome, and binary protected attribute
outcome	Name of the outcome variable

group	Name of the binary protected attribute. Must consist of only two groups.
probs	Predicted probabilities
cutoff	Cutoff value for the predicted probabilities
confint	Logical indicating whether to calculate confidence intervals
alpha	The 1 - significance level for the confidence interval, default is 0.05
bootstraps	Number of bootstraps to use for confidence intervals
digits	Number of digits to round the results to, default is 2
message	Logical; if TRUE (default), prints a textual summary of the fairness evaluation. Only works if confint is TRUE.

Value

A list containing the following elements:

- Accuracy for Group 1
- Accuracy for Group 2
- Difference in accuracy
- Ratio in accuracy If confidence intervals are computed (confint = TRUE):
- A vector of length 2 containing the lower and upper bounds of the 95% confidence interval for the difference in accuracy
- A vector of length 2 containing the lower and upper bounds of the 95% confidence interval for the ratio in accurac

See Also

[eval_cond_acc_equality](#)

Examples

```
library(fairmetrics)
library(dplyr)
library(magrittr)
library(randomForest)
data("mimic_preprocessed")
set.seed(123)
train_data <- mimic_preprocessed %>%
  dplyr::filter(dplyr::row_number() <= 700)
# Fit a random forest model
rf_model <- randomForest::randomForest(factor(day_28_flg) ~ ., data = train_data, ntree = 1000)
# Test the model on the remaining data
test_data <- mimic_preprocessed %>%
  dplyr::mutate(gender = ifelse(gender_num == 1, "Male", "Female")) %>%
  dplyr::filter(dplyr::row_number() > 700)

test_data$pred <- predict(rf_model, newdata = test_data, type = "prob")[, 2]

# Fairness evaluation
```

```

# We will use sex as the protected attribute and day_28_flg as the outcome.
# We choose threshold = 0.41 so that the overall FPR is around 5%.

# Evaluate Accuracy Parity
eval_acc_parity(
  data = test_data,
  outcome = "day_28_flg",
  group = "gender",
  probs = "pred",
  cutoff = 0.41
)

```

eval_bs_parity

Examine Brier Score Parity of a Model

Description

This function evaluates *Brier Score Parity*, a fairness measure that checks whether the Brier score (a measure of the calibration of probabilistic predictions) is similar across across two groups defined by a binary protected attribute. Brier score parity ensures that the model's predicted probabilities are equally well calibrated across subpopulations.

Usage

```

eval_bs_parity(
  data,
  outcome,
  group,
  probs,
  confint = TRUE,
  alpha = 0.05,
  bootstraps = 2500,
  digits = 2,
  message = TRUE
)

```

Arguments

data	Data frame containing the outcome, predicted outcome, and binary protected attribute
outcome	Name of the outcome variable
group	Name of the binary protected attribute. Must consist of only two groups.
probs	Predicted probabilities
confint	Logical indicating whether to calculate confidence intervals
alpha	The 1 - significance level for the confidence interval, default is 0.05

bootstraps	Number of bootstraps to use for confidence intervals
digits	Number of digits to round the results to, default is 2
message	Logical; if TRUE (default), prints a textual summary of the fairness evaluation. Only works if confint is TRUE.

Value

A list containing the following elements:

- Brier Score for Group 1
- Brier Score for Group 2
- Difference in Brier Score
- Ratio in Brier Score If confidence intervals are computed (confint = TRUE):
- A vector of length 2 containing the lower and upper bounds of the 95% confidence interval for the difference in Brier Score
- A vector of length 2 containing the lower and upper bounds of the 95% confidence interval for the ratio in Brier Score

See Also

[eval_acc_parity](#), [eval_cond_acc_equality](#), [eval_pos_pred_parity](#), [eval_neg_pred_parity](#)

Examples

```
library(fairmetrics)
library(dplyr)
library(magrittr)
library(randomForest)
data("mimic_preprocessed")
set.seed(123)
train_data <- mimic_preprocessed %>%
  dplyr::filter(dplyr::row_number() <= 700)
# Fit a random forest model
rf_model <- randomForest::randomForest(factor(day_28_flg) ~ ., data = train_data, ntree = 1000)
# Test the model on the remaining data
test_data <- mimic_preprocessed %>%
  dplyr::mutate(gender = ifelse(gender_num == 1, "Male", "Female")) %>%
  dplyr::filter(dplyr::row_number() > 700)

test_data$pred <- predict(rf_model, newdata = test_data, type = "prob")[, 2]

# Fairness evaluation
# We will use sex as the protected attribute and day_28_flg as the outcome.

# Evaluate Brier Score Parity
eval_bs_parity(
  data = test_data,
  outcome = "day_28_flg",
  group = "gender",
  probs = "pred"
```

)

 eval_cond_acc_equality

Examine Conditional Use Accuracy Equality of a Model

Description

This function evaluates *Conditional Use Accuracy Equality*, a fairness criterion that requires predictive performance to be similar across across two groups - defined by a binary protected attribute - when a model makes positive or negative predictions.

Usage

```
eval_cond_acc_equality(
  data,
  outcome,
  group,
  probs,
  cutoff = 0.5,
  confint = TRUE,
  alpha = 0.05,
  bootstraps = 2500,
  digits = 2,
  message = TRUE
)
```

Arguments

data	Data frame containing the outcome, predicted outcome, and binary protected attribute
outcome	Name of the outcome variable, it must be binary
group	Name of the binary protected attribute. Must consist of only two groups.
probs	Name of the predicted outcome variable
cutoff	Threshold for the predicted outcome, default is 0.5
confint	Whether to compute 95% confidence interval, default is TRUE
alpha	The 1 - significance level for the confidence interval, default is 0.05
bootstraps	Number of bootstrap samples, default is 2500
digits	Number of digits to round the results to, default is 2
message	Logical; if TRUE (default), prints a textual summary of the fairness evaluation. Only works if confint is TRUE.

Value

A list containing the following elements:

- `PPV_Group1`: Positive Predictive Value for the first group
- `PPV_Group2`: Positive Predictive Value for the second group
- `PPV_Diff`: Difference in Positive Predictive Value
- `NPV_Group1`: Negative Predictive Value for the first group
- `NPV_Group2`: Negative Predictive Value for the second group
- `NPV_Diff`: Difference in Negative Predictive Value If confidence intervals are computed (`confint = TRUE`):
- `PPV_Diff_CI`: A vector of length 2 containing the lower and upper bounds of the 95% confidence interval for the difference in Positive Predictive Value
- `NPV_Diff_CI`: A vector of length 2 containing the lower and upper bounds of the 95% confidence interval for the difference in Negative Predictive Value

See Also

[eval_acc_parity](#)

Examples

```
library(fairmetrics)
library(dplyr)
library(magrittr)
library(randomForest)
data("mimic_preprocessed")
set.seed(123)
train_data <- mimic_preprocessed %>%
  dplyr::filter(dplyr::row_number() <= 700)
# Fit a random forest model
rf_model <- randomForest::randomForest(factor(day_28_flg) ~ ., data = train_data, ntree = 1000)
# Test the model on the remaining data
test_data <- mimic_preprocessed %>%
  dplyr::mutate(gender = ifelse(gender_num == 1, "Male", "Female")) %>%
  dplyr::filter(dplyr::row_number() > 700)

test_data$pred <- predict(rf_model, newdata = test_data, type = "prob")[, 2]

# Fairness evaluation
# We will use sex as the protected attribute and day_28_flg as the outcome.
# We choose threshold = 0.41 so that the overall FPR is around 5%.

# Evaluate Conditional Use Accuracy Equality
eval_cond_acc_equality(
  data = test_data,
  outcome = "day_28_flg",
  group = "gender",
  probs = "pred",
  cutoff = 0.41
```

)

eval_eq_odds

*Examine Equalized Odds of a Predictive Model***Description**

This function evaluates whether a predictive model satisfies the Equalized Odds criterion by comparing both False Negative Rates (FNR) and False Positive Rates (FPR) across two groups defined by a binary protected attribute. It reports the rate for each group, their differences, ratios, and bootstrap-based confidence regions. A Bonferroni-corrected union test is used to test whether the model violates the Equalized Odds criterion.

Usage

```
eval_eq_odds(
  data,
  outcome,
  group,
  probs,
  cutoff = 0.5,
  confint = TRUE,
  bootstraps = 2500,
  alpha = 0.05,
  digits = 2,
  message = TRUE
)
```

Arguments

data	A data frame containing the true binary outcomes, predicted probabilities, and binary protected attribute.
outcome	A string specifying the name of the binary outcome variable in data.
group	Name of the binary protected attribute. Must consist of only two groups.
probs	A string specifying the name of the variable containing predicted probabilities or risk scores.
cutoff	A numeric value used to threshold predicted probabilities into binary predictions; defaults to 0.5.
confint	Whether to compute 95% confidence interval, default is TRUE.
bootstraps	An integer specifying the number of bootstrap resamples for constructing confidence intervals; vdefaults to 2500.
alpha	Significance level for the (1 - alpha) confidence interval; defaults to 0.05.
digits	Number of decimal places to round numeric results; defaults to 2.
message	Logical; if TRUE (default), prints a textual summary of the fairness evaluation. Only works if confint is TRUE.

Value

A data frame summarizing group disparities in both FNR and FPR with the following columns:

- **Metric:** The reported metrics ("FNR; FPR").
- **Group1:** Estimated FNR and FPR for the first group.
- **Group2:** Estimated FNR and FPR for the second group.
- **Difference:** Differences in FNR and FPR, computed as Group1 - Group2.
- **95% CR:** Bonferroni-adjusted confidence regions for the differences.
- **Ratio:** Ratios in FNR and FPR, computed as Group1 / Group2.
- **95% CR:** Bonferroni-adjusted confidence regions for the ratios.

Examples

```
library(fairmetrics)
library(dplyr)
library(magrittr)
library(randomForest)
data("mimic_preprocessed")
set.seed(123)
train_data <- mimic_preprocessed %>%
  dplyr::filter(dplyr::row_number() <= 700)
# Fit a random forest model
rf_model <- randomForest::randomForest(factor(day_28_flg) ~ .,
  data = train_data, ntree = 1000
)
# Test the model on the remaining data
test_data <- mimic_preprocessed %>%
  dplyr::mutate(gender = ifelse(gender_num == 1, "Male", "Female")) %>%
  dplyr::filter(dplyr::row_number() > 700)

test_data$pred <- predict(rf_model, newdata = test_data, type = "prob")[, 2]

# Fairness evaluation
# We will use sex as the protected attribute and day_28_flg as the outcome.
# We choose threshold = 0.41 so that the overall FPR is around 5%.

# Evaluate Equalized Odds
eval_eq_odds(
  data = test_data,
  outcome = "day_28_flg",
  group = "gender",
  probs = "pred",
  cutoff = 0.41
)
```

 eval_eq_opp

Evaluate Equal Opportunity Compliance of a Predictive Model

Description

This function evaluates the fairness of a predictive model with respect to the Equal Opportunity criterion, which requires that the False Negative Rate (FNR) be comparable across groups defined by a binary protected attribute. The function quantifies disparities in FNR between two groups and provides both the absolute difference and ratio, along with confidence intervals obtained via bootstrapping.

Usage

```
eval_eq_opp(
  data,
  outcome,
  group,
  probs,
  cutoff = 0.5,
  confint = TRUE,
  bootstraps = 2500,
  alpha = 0.05,
  digits = 2,
  message = TRUE
)
```

Arguments

data	A data frame containing the true binary outcomes, predicted probabilities, and binary protected attribute.
outcome	A string specifying the name of the binary outcome variable in data.
group	group Name of the binary protected attribute. Must consist of only two groups.
probs	A string specifying the name of the variable containing predicted probabilities or risk scores.
cutoff	A numeric value used to threshold predicted probabilities into binary decisions; defaults to 0.5.
confint	Whether to compute 95% confidence interval, default is TRUE.
bootstraps	An integer specifying the number of bootstrap resamples for constructing confidence intervals; defaults to 2500.
alpha	Significance level for constructing the (1 - alpha) confidence interval; defaults to 0.05.
digits	Integer indicating the number of decimal places to round results to; defaults to 2.
message	Logical; if TRUE (default), prints a textual summary of the fairness evaluation. Only works if confint is TRUE.

Value

A data frame summarizing FNR-based group disparity metrics with the following columns:

- Metric A label indicating the reported fairness criterion.
- Group1 Estimated FNR and FPR for the first group.
- Group2 Estimated FNR and FPR for the second group.
- Difference The difference in FNR between the two groups, computed as the FNR of Group1 minus the FNR of Group2.
- 1-alpha% Diff CI The (1 - alpha) confidence interval for the FNR difference.
- Ratio The ratio of FNRs between Group1 and Group2, computed as FNR for Group1 divided by FNR for Group2.
- 1-alpha% Ratio CI The corresponding confidence interval for the FNR ratio.

Examples

```
library(fairmetrics)
library(dplyr)
library(magrittr)
library(randomForest)
data("mimic_preprocessed")
set.seed(123)
train_data <- mimic_preprocessed %>%
  dplyr::filter(dplyr::row_number() <= 700)
# Fit a random forest model
rf_model <- randomForest::randomForest(factor(day_28_flg) ~ .,
  data =
    train_data, ntree = 1000
)
# Test the model on the remaining data
test_data <- mimic_preprocessed %>%
  dplyr::mutate(gender = ifelse(gender_num == 1, "Male", "Female")) %>%
  dplyr::filter(dplyr::row_number() > 700)

test_data$pred <- predict(rf_model, newdata = test_data, type = "prob")[, 2]

# Fairness evaluation
# We will use sex as the protected attribute and day_28_flg as the outcome.
# We choose threshold = 0.41 so that the overall FPR is around 5%.

# Evaluate Equal Opportunity Compliance
eval_eq_opp(
  data = test_data,
  outcome = "day_28_flg",
  group = "gender",
  probs = "pred",
  cutoff = 0.41
)
```

eval_neg_class_bal *Examine Balance for Negative Class of a Model*

Description

This function evaluates *Balance for the Negative Class*, a fairness criterion that checks whether the model assigns similar predicted probabilities among individuals whose true outcome is negative (i.e. $Y = 0$) across groups defined by a binary protected attribute.

Usage

```
eval_neg_class_bal(
  data,
  outcome,
  group,
  probs,
  confint = TRUE,
  alpha = 0.05,
  bootstraps = 2500,
  digits = 2,
  message = TRUE
)
```

Arguments

data	Data frame containing the outcome, predicted outcome, and binary protected attribute
outcome	Name of the outcome variable
group	Name of the protected attribute. Must consist of only two groups.
probs	Predicted probabilities
confint	Logical indicating whether to calculate confidence intervals
alpha	The 1 - significance level for the confidence interval, default is 0.05
bootstraps	Number of bootstraps to use for confidence intervals
digits	Number of digits to round the results to, default is 2
message	Logical; if TRUE (default), prints a textual summary of the fairness evaluation. Only works if confint is TRUE.

Value

A list containing the following elements:

- Average predicted probability for Group 1
- Average predicted probability for Group 2
- Difference in average predicted probability

- Ratio in average predicted probability If confidence intervals are computed (confint = TRUE):
- A vector of length 2 containing the lower and upper bounds of the 95% confidence interval for the difference in average predicted probability
- A vector of length 2 containing the lower and upper bounds of the 95% confidence interval for the ratio in average predicted probability

See Also

[eval_neg_class_bal](#)

Examples

```
library(fairmetrics)
library(dplyr)
library(magrittr)
library(randomForest)
data("mimic_preprocessed")
set.seed(123)
train_data <- mimic_preprocessed %>%
  dplyr::filter(dplyr::row_number() <= 700)
# Fit a random forest model
rf_model <- randomForest::randomForest(factor(day_28_flg) ~ ., data = train_data, ntree = 1000)
# Test the model on the remaining data
test_data <- mimic_preprocessed %>%
  dplyr::mutate(gender = ifelse(gender_num == 1, "Male", "Female")) %>%
  dplyr::filter(dplyr::row_number() > 700)

test_data$pred <- predict(rf_model, newdata = test_data, type = "prob")[, 2]

# Fairness evaluation
# We will use sex as the protected attribute and day_28_flg as the outcome.

# Evaluate Balance for Negative Class
eval_neg_class_bal(
  data = test_data,
  outcome = "day_28_flg",
  group = "gender",
  probs = "pred"
)
```

eval_neg_pred_parity *Examine Negative Predictive Parity of a Model*

Description

This function evaluates *negative predictive predictive parity*, a key fairness criterion that compares the *Negative Predictive Value (NPV)* between groups defined by a binary protected attribute. In other words, it assesses whether, among individuals predicted to be negative, the probability of being truly negative is equal across subgroups.

Usage

```
eval_neg_pred_parity(
  data,
  outcome,
  group,
  probs,
  cutoff = 0.5,
  confint = TRUE,
  bootstraps = 2500,
  alpha = 0.05,
  digits = 2,
  message = TRUE
)
```

Arguments

data	Data frame containing the outcome, predicted outcome, and protected attribute
outcome	Name of the outcome variable, it must be binary
group	Name of the protected attribute. Must consist of only two groups.
probs	Name of the predicted outcome variable
cutoff	Threshold for the predicted outcome, default is 0.5
confint	Whether to compute 95% confidence interval, default is TRUE
bootstraps	Number of bootstrap samples, default is 2500
alpha	The 1 - significance level for the confidence interval, default is 0.05
digits	Number of digits to round the results to, default is 2
message	Logical; if TRUE (default), prints a textual summary of the fairness evaluation. Only works if confint is TRUE.

Value

A list containing the following elements:

- NPV_Group1: Negative Predictive Value for the first group
- NPV_Group2: Negative Predictive Value for the second group
- NPV_Diff: Difference in Negative Predictive Value
- NPV_Ratio: Ratio in Negative Predictive Value If confidence intervals are computed (confint = TRUE):
- NPV_Diff_CI: A vector of length 2 containing the lower and upper bounds of the 95% confidence interval for the difference in Negative Predictive Value
- NPV_Ratio_CI: A vector of length 2 containing the lower and upper bounds of the 95% confidence interval for the ratio in Negative Predictive Value

See Also

[eval_pos_pred_parity](#)

Examples

```

library(fairmetrics)
library(dplyr)
library(magrittr)
library(randomForest)
data("mimic_preprocessed")
set.seed(123)
train_data <- mimic_preprocessed %>%
  dplyr::filter(dplyr::row_number() <= 700)
# Fit a random forest model
rf_model <- randomForest::randomForest(factor(day_28_flg) ~ ., data = train_data, ntree = 1000)
# Test the model on the remaining data
test_data <- mimic_preprocessed %>%
  dplyr::mutate(gender = ifelse(gender_num == 1, "Male", "Female")) %>%
  dplyr::filter(dplyr::row_number() > 700)

test_data$pred <- predict(rf_model, newdata = test_data, type = "prob")[, 2]

# Fairness evaluation
# We will use sex as the protected attribute and day_28_flg as the outcome.
# We choose threshold = 0.41 so that the overall FPR is around 5%.

# Evaluate Negative Predictive Parity
eval_neg_pred_parity(
  data = test_data,
  outcome = "day_28_flg",
  group = "gender",
  probs = "pred",
  cutoff = 0.41
)

```

eval_pos_class_bal *Examine Balance for the Positive Class of a Model*

Description

This function evaluates *Balance for the Positive Class*, a fairness criterion that checks whether the model assigns similar predicted probabilities among individuals whose true outcome is positive (i.e. $Y = 1$) across groups defined by a binary protected attribute.

Usage

```

eval_pos_class_bal(
  data,
  outcome,
  group,
  probs,
  confint = TRUE,

```

```

alpha = 0.05,
bootstraps = 2500,
digits = 2,
message = TRUE
)

```

Arguments

data	Data frame containing the outcome, predicted outcome, and binary protected attribute
outcome	Name of the outcome variable
group	Name of the protected attribute. Must consist of only two groups.
probs	Predicted probabilities
confint	Logical indicating whether to calculate confidence intervals
alpha	The 1 - significance level for the confidence interval, default is 0.05
bootstraps	Number of bootstraps to use for confidence intervals
digits	Number of digits to round the results to, default is 2
message	Logical; if TRUE (default), prints a textual summary of the fairness evaluation. Only works if confint is TRUE.

Value

A list containing the following elements:

- Average predicted probability for Group 1
- Average predicted probability for Group 2
- Difference in average predicted probability
- Ratio in average predicted probability If confidence intervals are computed (confint = TRUE):
- A vector of length 2 containing the lower and upper bounds of the 95% confidence interval for the difference in average predicted probability
- A vector of length 2 containing the lower and upper bounds of the 95% confidence interval for the ratio in average predicted probability

See Also

[eval_neg_class_bal](#)

Examples

```

library(fairmetrics)
library(dplyr)
library(magrittr)
library(randomForest)
data("mimic_preprocessed")
set.seed(123)
train_data <- mimic_preprocessed %>%

```

```
dplyr::filter(dplyr::row_number() <= 700)
# Fit a random forest model
rf_model <- randomForest::randomForest(factor(day_28_flg) ~ ., data = train_data, ntree = 1000)
# Test the model on the remaining data
test_data <- mimic_preprocessed %>%
  dplyr::mutate(gender = ifelse(gender_num == 1, "Male", "Female")) %>%
  dplyr::filter(dplyr::row_number() > 700)

test_data$pred <- predict(rf_model, newdata = test_data, type = "prob")[, 2]

# Fairness evaluation
# We will use sex as the protected attribute and day_28_flg as the outcome.

# Evaluate Balance for Positive Class
eval_pos_class_bal(
  data = test_data,
  outcome = "day_28_flg",
  group = "gender",
  probs = "pred"
)
```

eval_pos_pred_parity *Examine Positive Predictive Parity of a Model*

Description

This function evaluates *positive predictive parity*, a key fairness criterion that compares the *Positive Predictive Value (PPV)* between groups defined by a binary protected attribute. In other words, it assesses whether, among individuals predicted to be positive, the probability of being truly positive is equal across subgroups.

Usage

```
eval_pos_pred_parity(
  data,
  outcome,
  group,
  probs,
  cutoff = 0.5,
  confint = TRUE,
  bootstraps = 2500,
  alpha = 0.05,
  digits = 2,
  message = TRUE
)
```

Arguments

data	Data frame containing the outcome, predicted outcome, and binary protected attribute
outcome	Name of the outcome variable, it must be binary
group	Name of the protected attribute. Must consist of only two groups.
probs	Name of the predicted outcome variable
cutoff	Threshold for the predicted outcome, default is 0.5
confint	Whether to compute 95% confidence interval, default is TRUE
bootstraps	Number of bootstrap samples, default is 2500
alpha	The 1 - significance level for the confidence interval, default is 0.05
digits	Number of digits to round the results to, default is 2
message	Logical; if TRUE (default), prints a textual summary of the fairness evaluation. Only works if confint is TRUE.

Value

A list containing the following elements:

- PPV_Group1: Positive Predictive Value for the first group
- PPV_Group2: Positive Predictive Value for the second group
- PPV_Diff: Difference in Positive Predictive Value
- PPV_Ratio: Ratio in Positive Predictive Value If confidence intervals are computed (confint = TRUE):
- PPV_Diff_CI: A vector of length 2 containing the lower and upper bounds of the 95% confidence interval for the difference in Positive Predictive Value
- PPV_Ratio_CI: A vector of length 2 containing the lower and upper bounds of the 95% confidence interval for the ratio in Positive Predictive Value

See Also

[eval_neg_pred_parity](#)

Examples

```
library(fairmetrics)
library(dplyr)
library(magrittr)
library(randomForest)
data("mimic_preprocessed")
set.seed(123)
train_data <- mimic_preprocessed %>%
  dplyr::filter(dplyr::row_number() <= 700)
# Fit a random forest model
rf_model <- randomForest::randomForest(factor(day_28_flg) ~ ., data = train_data, ntree = 1000)
# Test the model on the remaining data
test_data <- mimic_preprocessed %>%
```

```
dplyr::mutate(gender = ifelse(gender_num == 1, "Male", "Female")) %>%
dplyr::filter(dplyr::row_number() > 700)

test_data$pred <- predict(rf_model, newdata = test_data, type = "prob")[, 2]

# Fairness evaluation
# We will use sex as the protected attribute and day_28_flg as the outcome.
# We choose threshold = 0.41 so that the overall FPR is around 5%.

# Evaluate Positive Predictive Parity
eval_pos_pred_parity(
  data = test_data,
  outcome = "day_28_flg",
  group = "gender",
  probs = "pred",
  cutoff = 0.41
)
```

eval_pred_equality *Examine Predictive Equality of a Model*

Description

This function evaluates predictive equality, a fairness metric that compares the False Positive Rate (FPR) between groups defined by a binary protected attribute. It assesses whether individuals from different groups are equally likely to be incorrectly flagged as positive when they are, in fact, negative.

Usage

```
eval_pred_equality(
  data,
  outcome,
  group,
  probs,
  cutoff = 0.5,
  confint = TRUE,
  alpha = 0.05,
  bootstraps = 2500,
  digits = 2,
  message = TRUE
)
```

Arguments

data Data frame containing the outcome, predicted outcome, and binary protected attribute

outcome	Name of the outcome variable, it must be binary
group	Name of the protected attribute. Must consist of only two groups.
probs	Name of the predicted outcome variable
cutoff	Threshold for the predicted outcome, default is 0.5
confint	Whether to compute 95% confidence interval, default is TRUE
alpha	The 1 - significance level for the confidence interval, default is 0.05
bootstraps	Number of bootstrap samples, default is 2500
digits	Number of digits to round the results to, default is 2
message	Logical; if TRUE (default), prints a textual summary of the fairness evaluation. Only works if confint is TRUE.

Value

A list containing the following elements:

- FPR_Group1: False Positive Rate for the first group
- FPR_Group2: False Positive Rate for the second group
- FPR_Diff: Difference in False Positive Rate
- FPR_Ratio: Ratio in False Positive Rate If confidence intervals are computed (confint = TRUE):
- FPR_Diff_CI: A vector of length 2 containing the lower and upper bounds of the 95% confidence interval for the difference in False Positive Rate
- FPR_Ratio_CI: A vector of length 2 containing the lower and upper bounds of the 95% confidence interval for the ratio in False Positive Rate

See Also

[eval_pos_pred_parity](#), [eval_neg_pred_parity](#), [eval_stats_parity](#)

Examples

```
library(fairmetrics)
library(dplyr)
library(magrittr)
library(randomForest)
data("mimic_preprocessed")
set.seed(123)
train_data <- mimic_preprocessed %>%
  dplyr::filter(dplyr::row_number() <= 700)
# Fit a random forest model
rf_model <- randomForest::randomForest(factor(day_28_flg) ~ ., data = train_data, ntree = 1000)
# Test the model on the remaining data
test_data <- mimic_preprocessed %>%
  dplyr::mutate(gender = ifelse(gender_num == 1, "Male", "Female")) %>%
  dplyr::filter(dplyr::row_number() > 700)

test_data$pred <- predict(rf_model, newdata = test_data, type = "prob")[, 2]
```

```
# Fairness evaluation
# We will use sex as the protectedR attribute and day_28_flg as the outcome.
# We choose threshold = 0.41 so that the overall FPR is around 5%.

# Evaluate Predictive Equality
eval_pred_equality(
  data = test_data,
  outcome = "day_28_flg",
  group = "gender",
  probs = "pred",
  cutoff = 0.41
)
```

eval_stats_parity *Examine Statistical Parity of a Model*

Description

This function assesses *statistical parity* - also known as *demographic parity* - in the predictions of a binary classifier across two groups defined by a protected attribute. Statistical parity compares the rate at which different groups receive a positive prediction, irrespective of the true outcome. It reports the Positive Prediction Rate (PPR) for each group, their differences, ratios, and bootstrap-based confidence regions.

Usage

```
eval_stats_parity(
  data,
  outcome,
  group,
  probs,
  cutoff = 0.5,
  confint = TRUE,
  bootstraps = 2500,
  alpha = 0.05,
  digits = 2,
  message = TRUE
)
```

Arguments

data	Data frame containing the outcome, predicted outcome, and protected attribute
outcome	Name of the outcome variable, it must be binary
group	Name of the protected attribute. Must consist of only two groups.
probs	Name of the predicted outcome variable

cutoff	Threshold for the predicted outcome, default is 0.5
confint	Whether to compute 95% confidence interval, default is TRUE
bootstraps	Number of bootstrap samples, default is 2500
alpha	The 1 - significance level for the confidence interval, default is 0.05
digits	Number of digits to round the results to, default is 2
message	Logical; if TRUE (default), prints a textual summary of the fairness evaluation. Only works if confint is TRUE.

Value

A list containing the following elements:

- PPR_Group1: Positive Prediction Rate for the first group
- PPR_Group2: Positive Prediction Rate for the second group
- PPR_Diff: Difference in Positive Prediction Rate
- PPR_Ratio: The ratio in Positive Prediction Rate between the two groups. If confidence intervals are computed (confint = TRUE):
- PPR_Diff_CI: A vector of length 2 containing the lower and upper bounds of the 95% confidence interval for the difference in Positive Prediction Rate
- PPR_Ratio_CI: A vector of length 2 containing the lower and upper bounds of the 95% confidence interval for the ratio in Positive Prediction Rate

Examples

```
library(fairmetrics)
library(dplyr)
library(magrittr)
library(randomForest)
data("mimic_preprocessed")
set.seed(123)
train_data <- mimic_preprocessed %>%
  dplyr::filter(dplyr::row_number() <= 700)
# Fit a random forest model
rf_model <- randomForest::randomForest(factor(day_28_flg) ~ ., data = train_data, ntree = 1000)
# Test the model on the remaining data
test_data <- mimic_preprocessed %>%
  dplyr::mutate(gender = ifelse(gender_num == 1, "Male", "Female")) %>%
  dplyr::filter(dplyr::row_number() > 700)

test_data$pred <- predict(rf_model, newdata = test_data, type = "prob")[, 2]

# Fairness evaluation
# We will use sex as the protected attribute and day_28_flg as the outcome.
# We choose threshold = 0.41 so that the overall FPR is around 5%.

# Evaluate Statistical Parity
eval_stats_parity(
  data = test_data,
```

```
outcome = "day_28_flg",
group = "gender",
probs = "pred",
cutoff = 0.41
)
```

eval_treatment_equality

Examine Treatment Equality of a Model

Description

This function evaluates *Treatment Equality*, a fairness criterion that assesses whether the ratio of false negatives to false positives is similar across groups defined by a binary protected attribute. Treatment Equality ensures that the model does not disproportionately favor or disadvantage any group in terms of the relative frequency of missed detections (false negatives) versus false alarms (false positives).

Usage

```
eval_treatment_equality(
  data,
  outcome,
  group,
  probs,
  cutoff = 0.5,
  confint = TRUE,
  alpha = 0.05,
  bootstraps = 2500,
  digits = 2,
  message = TRUE
)
```

Arguments

data	Data frame containing the outcome, predicted outcome, and binary protected attribute
outcome	Name of the outcome variable
group	group Name of the binary protected attribute. Must consist of only two groups.
probs	Predicted probabilities
cutoff	Cutoff value for the predicted probabilities
confint	Logical indicating whether to calculate confidence intervals
alpha	The 1 - significance level for the confidence interval, default is 0.05
bootstraps	Number of bootstraps to use for confidence intervals

digits	Number of digits to round the results to, default is 2
message	Logical; if TRUE (default), prints a textual summary of the fairness evaluation. Only works if confint is TRUE.

Value

A list containing the following elements:

- False Negative / False Positive ratio for Group 1
- False Negative / False Positive ratio for Group 2
- Difference in False Negative / False Positive ratio
- Ratio in False Negative / False Positive ratio If confidence intervals are computed (confint = TRUE):
- A vector of length 2 containing the lower and upper bounds of the 95% confidence interval for the difference in False Negative / False Positive ratio
- A vector of length 2 containing the lower and upper bounds of the 95% confidence interval for the ratio in False Negative / False Positive ratio

See Also

[eval_acc_parity](#), [eval_bs_parity](#), [eval_pos_pred_parity](#), [eval_neg_pred_parity](#)

Examples

```
library(fairmetrics)
library(dplyr)
library(magrittr)
library(randomForest)
# Data for tests
data("mimic_preprocessed")
set.seed(123)
train_data <- mimic_preprocessed %>%
  dplyr::filter(dplyr::row_number() <= 700)
# Fit a random forest model
rf_model <- randomForest::randomForest(factor(day_28_flg) ~ ., data = train_data, ntree = 1000)
# Test the model on the remaining data
test_data <- mimic_preprocessed %>%
  dplyr::mutate(gender = ifelse(gender_num == 1, "Male", "Female")) %>%
  dplyr::filter(dplyr::row_number() > 700)

test_data$pred <- predict(rf_model, newdata = test_data, type = "prob")[, 2]

# Fairness evaluation
# We will use sex as the protected attribute and day_28_flg as the outcome.

# Evaluate Treatment Equality
eval_treatment_equality(
  data = test_data,
  outcome = "day_28_flg",
  group = "gender",
```

```
    probs = "pred",
    cutoff = 0.41,
    confint = TRUE,
    alpha = 0.05,
    bootstraps = 2500,
    digits = 2,
    message = FALSE
  )
```

get_fairness_metrics *Compute Fairness Metrics for Binary Classification*

Description

Computes a comprehensive set of fairness metrics for binary classification models, disaggregated by a binary protected attribute. The function also computes corresponding performance metrics used in the fairness calculations.

Usage

```
get_fairness_metrics(
  data,
  outcome,
  group,
  probs,
  confint = TRUE,
  cutoff = 0.5,
  bootstraps = 2500,
  alpha = 0.05,
  digits = 2
)
```

Arguments

data	A data frame containing the outcome, group, and predicted probabilities.
outcome	The name of the column containing the true binary outcome.
group	The name of the column representing the binary protected attribute (e.g., race, gender).
probs	The name of the column with predicted probabilities.
confint	Logical indicating whether to calculate confidence intervals.
cutoff	Numeric threshold for classification. Default is 0.5.
bootstraps	Number of bootstrap samples. Default is 2500.
alpha	Significance level for confidence intervals. Default is 0.05.
digits	Number of digits to round the metrics to. Default is 2.

Details

The results are returned as a list of two data frames:

- **performance**: Contains performance metrics (e.g., TPR, FPR, PPV) by group.
- **fairness**: Contains group-level fairness metrics (e.g., disparities or ratios), confidence intervals (if specified).

Fairness Metrics Included::

- **Statistical Parity**: Difference in positive prediction rates across groups.
- **Equal Opportunity**: Difference in true positive rates (TPR) across groups.
- **Predictive Equality**: Difference in false positive rates (FPR) across groups.
- **Balance for Positive Class**: Checks whether the predicted probability distributions for positive outcomes are similar across groups.
- **Balance for Negative Class**: Same as above, but for negative outcomes.
- **Positive Predictive Parity**: Difference in positive predictive values (precision) across groups.
- **Negative Predictive Parity**: Difference in negative predictive values across groups.
- **Brier Score Parity**: Difference in Brier scores across groups.
- **Overall Accuracy Parity**: Difference in overall accuracy across groups.
- **Treatment Equality**: Ratio of false negatives to false positives across groups.

NOTE: Statistical inference from bootstrapped confidence intervals should be interpreted with caution. A confidence interval crossing 0 (for differences) or 1 (for ratios) means the evidence is inconclusive rather than proving absence of unfairness. Apparent violations may reflect sampling variability rather than systematic bias. Always complement these results with domain knowledge, sensitivity analyses, and additional fairness diagnostics before drawing strong conclusions about a specific fairness assessment.

Value

A dataframe containing fairness assessments, the performance metrics they use and the evaluated results for each (binary) group (specified by the group parameter) along with the difference and ratio between them. If `conf_int` is set to `TRUE`, then the estimated $(1-\alpha)*100\%$ bootstrap confidence intervals are returned as well.

Examples

```
library(fairmetrics)
library(dplyr)
library(randomForest)
library(magrittr)
data("mimic_preprocessed")
set.seed(123)
train_data <- mimic_preprocessed %>%
  dplyr::filter(dplyr::row_number() <= 700)
# Fit a random forest model
rf_model <- randomForest::randomForest(factor(day_28_flg) ~ ., data = train_data, ntree = 1000)
# Test the model on the remaining data
test_data <- mimic_preprocessed %>%
  dplyr::mutate(gender = ifelse(gender_num == 1, "Male", "Female"))%>%
```

```

dplyr::filter(dplyr::row_number() > 700)

test_data$pred <- predict(rf_model, newdata = test_data, type = "prob")[, 2]

# Fairness evaluation
# We will use sex as the protected attribute and day_28_flg as the outcome.
# We choose threshold = 0.41 so that the overall FPR is around 5%.

# Get Fairness Metrics
get_fairness_metrics(
  data = test_data,
  outcome = "day_28_flg",
  group = "gender",
  probs = "pred",
  confint = TRUE,
  cutoff = 0.41,
  alpha = 0.05
)

```

mimic

Clinical data from the MIMIC-II database for a case study on indwelling arterial catheters

Description

The Indwelling Arterial Catheter Clinical dataset contains clinical data for 1776 patients from the MIMIC-II clinical database. It was the basis for the article: Hsu DJ, et al. The association between indwelling arterial catheters and mortality in hemodynamically stable patients with respiratory failure: A propensity score analysis. *Chest*, 148(6):1470–1476, Aug. 2015. This dataset was also used by Raffa et al. in Chapter 5 "Data Analysis" of the forthcoming book: *Secondary Analysis of Electronic Health Records*, published by Springer in 2016.

Usage

```
mimic
```

Format

A data frame with 1776 rows and 46 variables:

```

aline_flg Integer, indicates if IAC was used (1 = yes, 0 = no)
icu_los_day Double, length of stay in ICU (days)
hospital_los_day Integer, length of stay in hospital (days)
age Double, age at baseline (years)
gender_num Integer, patient gender (1 = male; 0 = female)

```

weight_first Double, first weight (kg)
bmi Double, patient BMI
sapsi_first Integer, first SAPS I score
sofa_first Integer, first SOFA score
service_unit Character, type of service unit (FICU, MICU, SICU)
service_num Integer, service as a numeric value (0 = MICU or FICU, 1 = SICU)
day_icu_intime Character, day of week of ICU admission
day_icu_intime_num Integer, day of week of ICU admission (numeric)
hour_icu_intime Integer, hour of ICU admission (24hr clock)
hosp_exp_flg Integer, death in hospital (1 = yes, 0 = no)
icu_exp_flg Integer, death in ICU (1 = yes, 0 = no)
day_28_flg Integer, death within 28 days (1 = yes, 0 = no)
mort_day_censored Double, day post ICU admission of censoring or death (days)
censor_flg Integer, censored or death (0 = death, 1 = censored)
sepsis_flg Integer, sepsis present (0 = no, 1 = yes)
chf_flg Integer, congestive heart failure (0 = no, 1 = yes)
afib_flg Integer, atrial fibrillation (0 = no, 1 = yes)
renal_flg Integer, chronic renal disease (0 = no, 1 = yes)
liver_flg Integer, liver disease (0 = no, 1 = yes)
copd_flg Integer, chronic obstructive pulmonary disease (0 = no, 1 = yes)
cad_flg Integer, coronary artery disease (0 = no, 1 = yes)
stroke_flg Integer, stroke (0 = no, 1 = yes)
mal_flg Integer, malignancy (0 = no, 1 = yes)
resp_flg Integer, respiratory disease (non-COPD) (0 = no, 1 = yes)
map_1st Double, mean arterial pressure (mmHg)
hr_1st Integer, heart rate
temp_1st Double, temperature (F)
spo2_1st Integer, S_pO₂ (percent)
abg_count Integer, arterial blood gas count (number of tests)
wbc_first Double, first white blood cell count (K/uL)
hgb_first Double, first hemoglobin (g/dL)
platelet_first Integer, first platelets (K/u)
sodium_first Integer, first sodium (mEq/L)
potassium_first Double, first potassium (mEq/L)
tco2_first Double, first bicarbonate (mEq/L)
chloride_first Integer, first chloride (mEq/L)
bun_first Integer, first blood urea nitrogen (mg/dL)
creatinine_first Double, first creatinine (mg/dL)
po2_first Integer, first PaO₂ (mmHg)
pco2_first Integer, first PaCO₂ (mmHg)
iv_day_1 Double, input fluids by IV on day 1 (mL)

Source

<https://physionet.org/content/mimic2-iaccd/1.0/>

mimic_preprocessed *Preprocessed Clinical Data from the MIMIC-II Database*

Description

This version of the mimic dataset has been cleaned by removing columns with more than 10% missing data, imputing remaining missing values with the median, and dropping columns highly correlated with the outcome. It is designed for use in fairness-aware machine learning tasks and streamlined analysis.

Usage

mimic_preprocessed

Format

A data frame with fewer variables than the original due to preprocessing. Number of rows: 1776.

Source

<https://physionet.org/content/mimic2-iaccd/1.0/>

See Also

[mimic](#)

Index

* datasets

mimic, [27](#)

mimic_preprocessed, [29](#)

eval_acc_parity, [2](#), [5](#), [7](#), [24](#)

eval_bs_parity, [4](#), [24](#)

eval_cond_acc_equality, [3](#), [5](#), [6](#)

eval_eq_odds, [8](#)

eval_eq_opp, [10](#)

eval_neg_class_bal, [12](#), [13](#), [16](#)

eval_neg_pred_parity, [5](#), [13](#), [18](#), [20](#), [24](#)

eval_pos_class_bal, [15](#)

eval_pos_pred_parity, [5](#), [14](#), [17](#), [20](#), [24](#)

eval_pred_equality, [19](#)

eval_stats_parity, [20](#), [21](#)

eval_treatment_equality, [23](#)

get_fairness_metrics, [25](#)

mimic, [27](#), [29](#)

mimic_preprocessed, [29](#)