

# Package: mccf1 (via r-universe)

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**Title** Creates the MCC-F1 Curve and Calculates the MCC-F1 Metric and the Best Threshold

**Version** 1.1

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**Depends** R (>= 3.3.3), ggplot2

**Imports** ROCR

**Description** The MCC-F1 analysis is a method to evaluate the performance of binary classifications. The MCC-F1 curve is more reliable than the Receiver Operating Characteristic (ROC) curve and the Precision-Recall (PR) curve under imbalanced ground truth. The MCC-F1 analysis also provides the MCC-F1 metric that integrates classifier performance over varying thresholds, and the best threshold of binary classification.

**License** GPL (>= 2)

**URL** <https://bitbucket.org/hoffmanlab/mccf1/>

**BugReports** <https://stackoverflow.com/questions/tagged/mccf1>

**RoxygenNote** 6.0.1

**NeedsCompilation** no

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**Repository** <https://cranhaven.r-universe.dev>

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autoplot.mccf1	<i>Plot the MCC-F1 curve</i>
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### Description

‘autoplot.mccf1()’ plots the MCC-F1 curve using ggplot2.

### Usage

```
## S3 method for class 'mccf1'
autoplot(object, xlab = "F1 score", ylab = "normalized MCC",
  ...)
```

### Arguments

object	S3 object of class "mccf1" from the ‘mccf1()’
xlab, ylab	x- and y- axis annotation (default: "F1 score","normalized MCC")
...	further arguments passed to and from method ‘ggplot()’

### Value

the ggplots object

### Examples

```
response <- c(rep(1, 1000), rep(0, 10000))
predictor <- c(rbeta(300, 12, 2), rbeta(700, 3, 4), rbeta(10000, 2, 3))
autoplot(mccf1(response, predictor))
```

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mccf1	<i>Perform MCCF1 analysis</i>
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**Description**

'mccf1()' performs MCC (Matthews correlation coefficient)-F1 analysis for paired vectors of binary response classes and fractional prediction scores representing the performance of a binary classification task.

**Usage**

```
mccf1(response, predictor)
```

**Arguments**

response	numeric vector representing ground truth classes (0 or 1).
predictor	numeric vector representing prediction scores (in the range [0,1]).

**Value**

S3 object of class "mccf1", a list with the following members: 'thresholds': vector of doubles describing the thresholds; 'normalized\_mcc': vector of doubles representing normalized MCC for each threshold; 'f1': vector of doubles representing F1 for each threshold.

**Examples**

```
response <- c(rep(1L, 1000L), rep(0L, 10000L))
set.seed(2017)
predictor <- c(rbeta(300L, 12, 2), rbeta(700L, 3, 4), rbeta(10000L, 2, 3))
x <- mccf1(response, predictor)
head(x$thresholds)
# [1] Inf 0.9935354 0.9931493 0.9930786 0.9925507 0.9900520
head(x$normalized_mcc)
# [1] NaN 0.5150763 0.5213220 0.5261152 0.5301566 0.5337177
head(x$f1)
# [1] NaN 0.001998002 0.003992016 0.005982054 0.007968127 0.009950249
```

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summary.mccf1	<i>Summarize the the performance of a binary classification using MCC-F1 metric and the best threshold</i>
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**Description**

'summary.mccf1()' calculates the MCC-F1 metric and the best threshold for a binary classification.

**Usage**

```
## S3 method for class 'mccf1'  
summary(object, digits, bins = 100, ...)
```

**Arguments**

object	S3 object of class "mccf1" object resulting from the function 'mccf1()'
digits	integer, used for number formatting with <a href="#">signif</a>
bins	integer, representing number of bins used to divide up the range of normalized MCC when calculating the MCC-F1 metric (default = 100L)
...	other arguments ignored (for compatibility with generic)

**Value**

data.frame that shows the MCC-F1 metric (in the range [0,1]) and the best threshold (in the range [0,1])

**Examples**

```
response <- c(rep(1L, 1000L), rep(0L, 10000L))  
set.seed(2017)  
predictor <- c(rbeta(300L, 12, 2), rbeta(700L, 3, 4), rbeta(10000L, 2, 3))  
## Not run: summary(mccf1(response, predictor))  
# mccf1_metric best_threshold  
# 0.3508904 0.786905  
summary(mccf1(response, predictor), bins = 50)  
# mccf1_metric best_threshold  
# 0.3432971 0.786905  
## Not run: summary(mccf1(response, predictor), digits = 3)  
# mccf1_metric best_threshold  
# 0.351 0.787
```

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