

# Package ‘precrec’

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**Type** Package

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as.data.frame	<i>Convert a curves and points object to a data frame</i>
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---

### Description

The `as.data.frame` function converts an S3 object generated by `evalmod` to a data frame.

### Usage

```
## S3 method for class 'sscurves'
as.data.frame(x, row.names = NULL, optional = FALSE, raw_curves = NULL, ...)

## S3 method for class 'mscurves'
as.data.frame(x, row.names = NULL, optional = FALSE, raw_curves = NULL, ...)

## S3 method for class 'smcurves'
as.data.frame(x, row.names = NULL, optional = FALSE, raw_curves = NULL, ...)

## S3 method for class 'mmcurves'
as.data.frame(x, row.names = NULL, optional = FALSE, raw_curves = NULL, ...)

## S3 method for class 'sspoinst'
```

```

as.data.frame(x, row.names = NULL, optional = FALSE, raw_curves = NULL, ...)

## S3 method for class 'mspoints'
as.data.frame(x, row.names = NULL, optional = FALSE, raw_curves = NULL, ...)

## S3 method for class 'smpoints'
as.data.frame(x, row.names = NULL, optional = FALSE, raw_curves = NULL, ...)

## S3 method for class 'mmpoints'
as.data.frame(x, row.names = NULL, optional = FALSE, raw_curves = NULL, ...)

## S3 method for class 'aucroc'
as.data.frame(x, row.names = NULL, optional = FALSE, ...)

```

## Arguments

**x** An S3 object generated by [evalmod](#). The `as.data.frame` function takes one of the following S3 objects.

1. ROC and Precision-Recall curves (mode = "rocpr")

S3 object	# of models	# of test datasets
sscurves	single	single
mscurves	multiple	single
smcurves	single	multiple
mmcurves	multiple	multiple

2. Basic evaluation measures (mode = "basic")

S3 object	# of models	# of test datasets
sspoin	single	single
msspoin	multiple	single
smpoin	single	multiple
mmpoin	multiple	multiple

3. Fast AUC (ROC) calculation with the U statistic (mode = "aucroc")

S3 object	# of models	# of test datasets
aucroc	-	-

See the **Value** section of [evalmod](#) for more details.

**row.names** Not used by this method.

**optional** Not used by this method.

**raw\_curves** A Boolean value to specify whether raw curves are shown instead of the average curve. It is effective only when `raw_curves` is set to TRUE of the [evalmod](#) function.

**...** Not used by this method.

**Value**

The `as.data.frame` function returns a data frame.

**See Also**

[evalmod](#) for generating S3 objects with performance evaluation measures.

**Examples**

```
## Not run:
#####
### Single model & single test dataset
###

## Load a dataset with 10 positives and 10 negatives
data(P10N10)

## Generate an sscurve object that contains ROC and Precision-Recall curves
sscurves <- evalmod(scores = P10N10$scores, labels = P10N10$labels)

## Convert sscurves to a data frame
sscurves.df <- as.data.frame(sscurves)

## Show data frame
head(sscurves.df)

## Generate an sspoints object that contains basic evaluation measures
sspoints <- evalmod(
  mode = "basic", scores = P10N10$scores,
  labels = P10N10$labels
)
## Convert sspoints to a data frame
sspoints.df <- as.data.frame(sspoints)

## Show data frame
head(sspoints.df)

#####
### Multiple models & single test dataset
###

## Create sample datasets with 100 positives and 100 negatives
samps <- create_sim_samples(1, 100, 100, "all")
mdat <- mmdata(samps[["scores"]], samps[["labels"]],
  modnames = samps[["modnames"]]
)

## Generate an mscurve object that contains ROC and Precision-Recall curves
mscurves <- evalmod(mdat)

## Convert mscurves to a data frame
```

```
mscurves.df <- as.data.frame(mscurves)

## Show data frame
head(mscurves.df)

## Generate an mspoints object that contains basic evaluation measures
mspoints <- evalmod(mdat, mode = "basic")

## Convert mspoints to a data frame
mspoints.df <- as.data.frame(mspoints)

## Show data frame
head(mspoints.df)

#####
### Single model & multiple test datasets
###

## Create sample datasets with 100 positives and 100 negatives
samps <- create_sim_samples(10, 100, 100, "good_er")
mdat <- mmdata(samps[["scores"]], samps[["labels"]],
             modnames = samps[["modnames"]],
             dsids = samps[["dsids"]])
)

## Generate an smcurve object that contains ROC and Precision-Recall curves
smcurves <- evalmod(mdat, raw_curves = TRUE)

## Convert smcurves to a data frame
smcurves.df <- as.data.frame(smcurves)

## Show data frame
head(smcurves.df)

## Generate an smpoints object that contains basic evaluation measures
smpoints <- evalmod(mdat, mode = "basic")

## Convert smpoints to a data frame
smpoints.df <- as.data.frame(smpoints)

## Show data frame
head(smpoints.df)

#####
### Multiple models & multiple test datasets
###

## Create sample datasets with 100 positives and 100 negatives
samps <- create_sim_samples(10, 100, 100, "all")
mdat <- mmdata(samps[["scores"]], samps[["labels"]],
             modnames = samps[["modnames"]],
```

```

    dsids = samps[["dsids"]]
  )

  ## Generate an mscurve object that contains ROC and Precision-Recall curves
  mmcurves <- evalmod(mdat, raw_curves = TRUE)

  ## Convert mmcurves to a data frame
  mmcurves.df <- as.data.frame(mmcurves)

  ## Show data frame
  head(mmcurves.df)

  ## Generate an mmpoints object that contains basic evaluation measures
  mmpoints <- evalmod(mdat, mode = "basic")

  ## Convert mmpoints to a data frame
  mmpoints.df <- as.data.frame(mmpoints)

  ## Show data frame
  head(mmpoints.df)

#####
### N-fold cross validation datasets
###

  ## Load test data
  data(M2N50F5)

  ## Specify necessary columns to create mdat
  cvdat <- mmdata(
    nfold_df = M2N50F5, score_cols = c(1, 2),
    lab_col = 3, fold_col = 4,
    modnames = c("m1", "m2"), dsids = 1:5
  )

  ## Generate an mmcurve object that contains ROC and Precision-Recall curves
  cvcurves <- evalmod(cvdat)

  ## Convert mmcurves to a data frame
  cvcurves.df <- as.data.frame(cvcurves)

  ## Show data frame
  head(cvcurves.df)

  ## Generate an mmpoints object that contains basic evaluation measures
  cvpoints <- evalmod(cvdat, mode = "basic")

  ## Convert mmpoints to a data frame
  cvpoints.df <- as.data.frame(cvpoints)

  ## Show data frame
  head(cvpoints.df)

```

```
#####
### AUC with the U statistic
###

## mode = "aucroc"
data(P10N10)
uauc1 <- evalmod(
  scores = P10N10$scores, labels = P10N10$labels,
  mode = "aucroc"
)

# as.data.frame 'aucroc'
as.data.frame(uauc1)

## mode = "aucroc"
samps <- create_sim_samples(10, 100, 100, "all")
mdat <- mmdata(samps[["scores"]], samps[["labels"]],
  modnames = samps[["modnames"]],
  dsids = samps[["dsids"]]
)
uauc2 <- evalmod(mdat, mode = "aucroc")

# as.data.frame 'aucroc'
head(as.data.frame(uauc2))

## End(Not run)
```

---

auc

*Retrieve a data frame of AUC scores*


---

### Description

The auc function takes an S3 object generated by [evalmod](#) and retrieves a data frame with the Area Under the Curve (AUC) scores of ROC and Precision-Recall curves.

### Usage

```
auc(curves)

## S3 method for class 'aucs'
auc(curves)
```

### Arguments

**curves** An S3 object generated by [evalmod](#). The auc function accepts the following S3 objects.

S3 object	# of models	# of test datasets
sscurves	single	single
mcurves	multiple	single
smcurves	single	multiple
mmcurves	multiple	multiple

See the **Value** section of [evalmod](#) for more details.

## Value

The auc function returns a data frame with AUC scores.

## See Also

[evalmod](#) for generating S3 objects with performance evaluation measures. [pauc](#) for retrieving a dataset of pAUCs.

## Examples

```
#####
### Single model & single test dataset
###

## Load a dataset with 10 positives and 10 negatives
data(P10N10)

## Generate an sscurve object that contains ROC and Precision-Recall curves
sscurves <- evalmod(scores = P10N10$scores, labels = P10N10$labels)

## Shows AUCs
auc(sscurves)

#####
### Multiple models & single test dataset
###

## Create sample datasets with 100 positives and 100 negatives
samps <- create_sim_samples(1, 100, 100, "all")
mdat <- mmdata(samps[["scores"]], samps[["labels"]],
  modnames = samps[["modnames"]]
)

## Generate an mscurve object that contains ROC and Precision-Recall curves
mcurves <- evalmod(mdat)

## Shows AUCs
auc(mcurves)

#####
### Single model & multiple test datasets
```



```
###

## Create sample datasets with 100 positives and 100 negatives
samps <- create_sim_samples(4, 100, 100, "good_er")
mdat <- mmdata(samps[["scores"]], samps[["labels"]],
  modnames = samps[["modnames"]],
  dsids = samps[["dsids"]]
)

## Generate an smcurve object that contains ROC and Precision-Recall curves
smcurves <- evalmod(mdat, raw_curves = TRUE)

## Get AUCs
sm_auc <- auc(smcurves)

## Shows AUCs
sm_auc

## Get AUCs of Precision-Recall
sm_auc_prc <- subset(sm_auc, curvetypes == "PRC")

## Shows AUCs
sm_auc_prc

#####
### Multiple models & multiple test datasets
###

## Create sample datasets with 100 positives and 100 negatives
samps <- create_sim_samples(4, 100, 100, "all")
mdat <- mmdata(samps[["scores"]], samps[["labels"]],
  modnames = samps[["modnames"]],
  dsids = samps[["dsids"]]
)

## Generate an mscurve object that contains ROC and Precision-Recall curves
mmcurves <- evalmod(mdat, raw_curves = TRUE)

## Get AUCs
mm_auc <- auc(mmcurves)

## Shows AUCs
mm_auc

## Get AUCs of Precision-Recall
mm_auc_prc <- subset(mm_auc, curvetypes == "PRC")

## Shows AUCs
mm_auc_prc
```

---

auc\_ci *Calculate CIs of ROC and precision-recall AUCs*

---

### Description

The `auc_ci` function takes an S3 object generated by `evalmod` and calculates CIs of AUCs when multiple data sets are specified.

### Usage

```
auc_ci(curves, alpha = NULL, dtype = NULL)

## S3 method for class 'aucs'
auc_ci(curves, alpha = 0.05, dtype = "normal")
```

### Arguments

`curves` An S3 object generated by `evalmod`. The `auc_ci` function accepts the following S3 objects.

S3 object	# of models	# of test datasets
<code>smcurves</code>	single	multiple
<code>mmcurves</code>	multiple	multiple

See the **Value** section of `evalmod` for more details.

`alpha` A numeric value of the significant level (default: 0.05)

`dtype` A string to specify the distribution used for CI calculation.

dtype	distribution
normal (default)	Normal distribution
z	Normal distribution
t	t-distribution

### Value

The `auc_ci` function returns a dataframe of AUC CIs.

### See Also

`evalmod` for generating S3 objects with performance evaluation measures. `auc` for retrieving a dataset of AUCs.

## Examples

```
#####
### Single model & multiple test datasets
###

## Create sample datasets with 100 positives and 100 negatives
samps <- create_sim_samples(4, 100, 100, "good_er")
mdat <- mmdata(samps[["scores"]], samps[["labels"]],
  modnames = samps[["modnames"]],
  dsids = samps[["dsids"]]
)

## Generate an smcurve object that contains ROC and Precision-Recall curves
smcurves <- evalmod(mdat)

## Calculate CI of AUCs
sm_auc_ci <- auc_ci(smcurves)

## Shows the result
sm_auc_ci

#####
### Multiple models & multiple test datasets
###

## Create sample datasets with 100 positives and 100 negatives
samps <- create_sim_samples(4, 100, 100, "all")
mdat <- mmdata(samps[["scores"]], samps[["labels"]],
  modnames = samps[["modnames"]],
  dsids = samps[["dsids"]]
)

## Generate an mscurve object that contains ROC and Precision-Recall curves
mmcurves <- evalmod(mdat)

## Calculate CI of AUCs
mm_auc_ci <- auc_ci(mmcurves)

## Shows the result
mm_auc_ci
```

---

 autoplot

*Plot performance evaluation measures with ggplot2*


---

## Description

The autoplot function plots performance evaluation measures by using **ggplot2** instead of the general R plot.

**Usage**

```
## S3 method for class 'sscurves'
autoplot(object, curvetype = c("ROC", "PRC"), ...)

## S3 method for class 'mscurves'
autoplot(object, curvetype = c("ROC", "PRC"), ...)

## S3 method for class 'smcurves'
autoplot(object, curvetype = c("ROC", "PRC"), ...)

## S3 method for class 'mmcurves'
autoplot(object, curvetype = c("ROC", "PRC"), ...)

## S3 method for class 'sspoinst'
autoplot(object, curvetype = .get_metric_names("basic"), ...)

## S3 method for class 'mspoinst'
autoplot(object, curvetype = .get_metric_names("basic"), ...)

## S3 method for class 'smpoinst'
autoplot(object, curvetype = .get_metric_names("basic"), ...)

## S3 method for class 'mmpoinst'
autoplot(object, curvetype = .get_metric_names("basic"), ...)
```

**Arguments**

**object** An S3 object generated by [evalmod](#). The autoplot function accepts the following S3 objects for two different modes, "rocprc" and "basic".

1. ROC and Precision-Recall curves (mode = "rocprc")

S3 object	# of models	# of test datasets
sscurves	single	single
mscurves	multiple	single
smcurves	single	multiple
mmcurves	multiple	multiple

2. Basic evaluation measures (mode = "basic")

S3 object	# of models	# of test datasets
sspoinst	single	single
mspoinst	multiple	single
smpoinst	single	multiple
mmpoinst	multiple	multiple

See the **Value** section of [evalmod](#) for more details.

**curvetype** A character vector with the following curve types.

1. ROC and Precision-Recall curves (mode = "rocprc")

curvetype	description
ROC	ROC curve
PRC	Precision-Recall curve

Multiple curvetype can be combined, such as `c("ROC", "PRC")`.

2. Basic evaluation measures (mode = "basic")

curvetype	description
error	Normalized ranks vs. error rate
accuracy	Normalized ranks vs. accuracy
specificity	Normalized ranks vs. specificity
sensitivity	Normalized ranks vs. sensitivity
precision	Normalized ranks vs. precision
mcc	Normalized ranks vs. Matthews correlation coefficient
fscore	Normalized ranks vs. F-score

Multiple curvetype can be combined, such as `c("precision", "sensitivity")`.

...

Following additional arguments can be specified.

**type** A character to specify the line type as follows.

"l" lines

"p" points

"b" both lines and points

**show\_cb** A Boolean value to specify whether point-wise confidence bounds are drawn. It is effective only when `calc_avg` of the `evalmod` function is set to TRUE.

**raw\_curves** A Boolean value to specify whether raw curves are shown instead of the average curve. It is effective only when `raw_curves` of the `evalmod` function is set to TRUE.

**show\_legend** A Boolean value to specify whether the legend is shown.

**ret\_grob** A logical value to indicate whether `autoplot` returns a grob object. The grob object is internally generated by `arrangeGrob`. The `grid.draw` function takes a grob object and shows a plot. It is effective only when a multiple-panel plot is generated, for example, when `curvetype` is `c("ROC", "PRC")`.

**reduce\_points** A Boolean value to decide whether the points should be reduced when `mode = "rocprc"`. The points are reduced according to `x_bins` of the `evalmod` function. The default values is TRUE.

## Value

The `autoplot` function returns a `ggplot` object for a single-panel plot and a frame-grob object for a multiple-panel plot.

## See Also

`evalmod` for generating an S3 object. `fortify` for converting a curves and points object to a data frame. `plot` for plotting the equivalent curves with the general R plot.

## Examples

```
## Not run:

## Load libraries
library(ggplot2)
library(grid)

#####
### Single model & single test dataset
###

## Load a dataset with 10 positives and 10 negatives
data(P10N10)

## Generate an sscurve object that contains ROC and Precision-Recall curves
sscurves <- evalmod(scores = P10N10$scores, labels = P10N10$labels)

## Plot both ROC and Precision-Recall curves
autoplot(sscurves)

## Reduced/Full supporting points
sampss <- create_sim_samples(1, 50000, 50000)
evalss <- evalmod(scores = sampss$scores, labels = sampss$labels)

# Reduced supporting point
system.time(autoplot(evalss))

# Full supporting points
system.time(autoplot(evalss, reduce_points = FALSE))

## Get a grob object for multiple plots
pp1 <- autoplot(sscurves, ret_grob = TRUE)
plot.new()
grid.draw(pp1)

## A ROC curve
autoplot(sscurves, curvetype = "ROC")

## A Precision-Recall curve
autoplot(sscurves, curvetype = "PRC")

## Generate an sspoints object that contains basic evaluation measures
sspoints <- evalmod(
  mode = "basic", scores = P10N10$scores,
  labels = P10N10$labels
)

## Normalized ranks vs. basic evaluation measures
autoplot(sspoints)

## Normalized ranks vs. precision
autoplot(sspoints, curvetype = "precision")
```

```
#####
### Multiple models & single test dataset
###

## Create sample datasets with 100 positives and 100 negatives
samps <- create_sim_samples(1, 100, 100, "all")
mdat <- mmdata(samps[["scores"]], samps[["labels"]],
  modnames = samps[["modnames"]]
)

## Generate an mscurve object that contains ROC and Precision-Recall curves
mscurves <- evalmod(mdat)

## ROC and Precision-Recall curves
autoplot(mscurves)

## Reduced/Full supporting points
sampsms <- create_sim_samples(5, 50000, 50000)
evalms <- evalmod(scores = sampsms$scores, labels = sampsms$labels)

# Reduced supporting point
system.time(autoplot(evalms))

# Full supporting points
system.time(autoplot(evalms, reduce_points = FALSE))

## Hide the legend
autoplot(mscurves, show_legend = FALSE)

## Generate an mspoints object that contains basic evaluation measures
mspoints <- evalmod(mdat, mode = "basic")

## Normalized ranks vs. basic evaluation measures
autoplot(mspoints)

## Hide the legend
autoplot(mspoints, show_legend = FALSE)

#####
### Single model & multiple test datasets
###

## Create sample datasets with 100 positives and 100 negatives
samps <- create_sim_samples(10, 100, 100, "good_er")
mdat <- mmdata(samps[["scores"]], samps[["labels"]],
  modnames = samps[["modnames"]],
  dsids = samps[["dsids"]]
)

## Generate an smcurve object that contains ROC and Precision-Recall curves
```

```

smcurves <- evalmod(mdat, raw_curves = TRUE)

## Average ROC and Precision-Recall curves
autoplot(smcurves, raw_curves = FALSE)

## Hide confidence bounds
autoplot(smcurves, raw_curves = FALSE, show_cb = FALSE)

## Raw ROC and Precision-Recall curves
autoplot(smcurves, raw_curves = TRUE, show_cb = FALSE)

## Reduced/Full supporting points
sampsm <- create_sim_samples(4, 5000, 5000)
mdatsm <- mmdata(sampsm$scores, sampsm$labels, expd_first = "dsids")
evalsm <- evalmod(mdatsm, raw_curves = TRUE)

# Reduced supporting point
system.time(autoplot(evalsm, raw_curves = TRUE))

# Full supporting points
system.time(autoplot(evalsm, raw_curves = TRUE, reduce_points = FALSE))

## Generate an smpoints object that contains basic evaluation measures
smpoints <- evalmod(mdat, mode = "basic")

## Normalized ranks vs. average basic evaluation measures
autoplot(smpoints)

#####
### Multiple models & multiple test datasets
###

## Create sample datasets with 100 positives and 100 negatives
samps <- create_sim_samples(10, 100, 100, "all")
mdat <- mmdata(samps[["scores"]], samps[["labels"]],
  modnames = samps[["modnames"]],
  dsids = samps[["dsids"]]
)

## Generate an mscurve object that contains ROC and Precision-Recall curves
mmcurves <- evalmod(mdat, raw_curves = TRUE)

## Average ROC and Precision-Recall curves
autoplot(mmcurves, raw_curves = FALSE)

## Show confidence bounds
autoplot(mmcurves, raw_curves = FALSE, show_cb = TRUE)

## Raw ROC and Precision-Recall curves
autoplot(mmcurves, raw_curves = TRUE)

## Reduced/Full supporting points

```



```

sampmm <- create_sim_samples(4, 5000, 5000)
mdatmm <- mmdata(sampmm$scores, sampmm$labels,
  modnames = c("m1", "m2"),
  dsids = c(1, 2), expd_first = "modnames"
)
evalmm <- evalmod(mdatmm, raw_curves = TRUE)

# Reduced supporting point
system.time(autoplot(evalmm, raw_curves = TRUE))

# Full supporting points
system.time(autoplot(evalmm, raw_curves = TRUE, reduce_points = FALSE))

## Generate an mmpoints object that contains basic evaluation measures
mmpoints <- evalmod(mdat, mode = "basic")

## Normalized ranks vs. average basic evaluation measures
autoplot(mmpoints)

#####
### N-fold cross validation datasets
###

## Load test data
data(M2N50F5)

## Specify necessary columns to create mdat
cvdat <- mmdata(
  nfold_df = M2N50F5, score_cols = c(1, 2),
  lab_col = 3, fold_col = 4,
  modnames = c("m1", "m2"), dsids = 1:5
)

## Generate an mmcurve object that contains ROC and Precision-Recall curves
cvcurves <- evalmod(cvdat)

## Average ROC and Precision-Recall curves
autoplot(cvcurves)

## Show confidence bounds
autoplot(cvcurves, show_cb = TRUE)

## Generate an mmpoints object that contains basic evaluation measures
cvpoints <- evalmod(cvdat, mode = "basic")

## Normalized ranks vs. average basic evaluation measures
autoplot(cvpoints)

## End(Not run)

```

---

**B1000***Balanced data with 1000 positives and 1000 negatives.*

---

**Description**

A list contains labels and scores of five different performance levels. All scores were randomly generated.

**Usage**

```
data(B1000)
```

**Format**

A list with 8 items.

**np** number of positives: 1000

**nn** number of negatives: 1000

**labels** labels of observed data

**random\_scores** scores of a random performance level

**poor\_er\_scores** scores of a poor early retrieval level

**good\_er\_scores** scores of a good early retrieval level

**excel\_scores** scores of an excellent level

**perf\_scores** scores of the perfect level

---

**B500***Balanced data with 500 positives and 500 negatives.*

---

**Description**

A list contains labels and scores of five different performance levels. All scores were randomly generated.

**Usage**

```
data(B500)
```

**Format**

A list with 8 items.

**np** number of positives: 500

**nn** number of negatives: 500

**labels** labels of observed data

**random\_scores** scores of a random performance level

**poor\_er\_scores** scores of a poor early retrieval level

**good\_er\_scores** scores of a good early retrieval level

**excel\_scores** scores of an excellent level

**perf\_scores** scores of the perfect level

---

create\_sim\_samples      *Create random samples for simulations*

---

**Description**

The create\_sim\_samples function generates random samples with different performance levels.

**Usage**

```
create_sim_samples(n_repeat, np, nn, score_names = "random")
```

**Arguments**

n_repeat	The number of iterations to make samples.
np	The number of positives in a sample.
nn	The number of negatives in a sample.
score_names	A character vector for the names of the following performance levels. <b>"random"</b> Random <b>"poor_er"</b> Poor early retrieval <b>"good_er"</b> Good early retrieval <b>"excel"</b> Excellent <b>"perf"</b> Perfect <b>"all"</b> All of the above

**Value**

The create\_sim\_samples function returns a list with the following items.

- scores: a list of numeric vectors
- labels: an integer vector
- modnames: a character vector of the model names
- dsids: a character vector of the dataset IDs

**See Also**

[mmdata](#) for formatting input data. [evalmod](#) for calculation evaluation measures.

**Examples**

```
#####
### Create a set of samples with 10 positives and 10 negatives
### for the random performance level
###
samps1 <- create_sim_samples(1, 10, 10, "random")

## Show the list structure
str(samps1)

#####
### Create two sets of samples with 10 positives and 20 negatives
### for the random and the poor early retrieval performance levels
###
samps2 <- create_sim_samples(2, 10, 20, c("random", "poor_er"))

## Show the list structure
str(samps2)

#####
### Create 3 sets of samples with 5 positives and 5 negatives
### for all 5 levels
###
samps3 <- create_sim_samples(3, 5, 5, "all")

## Show the list structure
str(samps3)
```

---

evalmod

*Evaluate models and calculate performance evaluation measures*

---

**Description**

The `evalmod` function calculates ROC and Precision-Recall curves for specified prediction scores and binary labels. It also calculate several basic performance evaluation measures, such as accuracy, error rate, and precision, by specifying mode as "basic".

**Usage**

```
evalmod(
  mdat,
  mode = NULL,
```

```

scores = NULL,
labels = NULL,
modnames = NULL,
dsids = NULL,
posclass = NULL,
na_worst = TRUE,
ties_method = "equiv",
calc_avg = TRUE,
cb_alpha = 0.05,
raw_curves = FALSE,
x_bins = 1000,
interpolate = TRUE,
...
)

```

### Arguments

mdat	<p>An S3 object created by the <code>mmdata</code> function. It contains formatted scores and labels. The <code>evalmod</code> function ignores the following arguments when <code>mdat</code> is specified.</p> <ul style="list-style-type: none"> <li>• scores</li> <li>• labels</li> <li>• modnames</li> <li>• dsids</li> <li>• posclass</li> <li>• na_worst</li> <li>• ties_method</li> </ul> <p>These arguments are internally passed to the <code>mmdata</code> function when <code>mdat</code> is unspecified. In that case, both <code>scores</code> and <code>labels</code> must be at least specified.</p>
mode	<p>A string that specifies the types of evaluation measures that the <code>evalmod</code> function calculates.</p> <p><b>"rocpre"</b> ROC and Precision-Recall curves  <b>"prcroc"</b> Same as above  <b>"basic"</b> Normalized ranks vs. accuracy, error rate, specificity, sensitivity, precision, Matthews correlation coefficient, and F-score.  <b>"aucroc"</b> Fast AUC(ROC) calculation with the U statistic</p>
scores	<p>A numeric dataset of predicted scores. It can be a vector, a matrix, an array, a data frame, or a list. The <code>join_scores</code> function can be useful to make scores with multiple datasets.</p>
labels	<p>A numeric, character, logical, or factor dataset of observed labels. It can be a vector, a matrix, an array, a data frame, or a list. The <code>join_labels</code> function can be useful to make labels with multiple datasets.</p>
modnames	<p>A character vector for the names of the models. The <code>evalmod</code> function automatically generates default names as "m1", "m2", "m3", and so on when it is NULL.</p>

<code>dsids</code>	A numeric vector for test dataset IDs. The <code>evalmod</code> function automatically generates the default ID as 1 when it is NULL.
<code>posclass</code>	A scalar value to specify the label of positives in labels. It must be the same data type as labels. For example, <code>posclass = -1</code> changes the positive label from 1 to -1 when labels contains 1 and -1. The positive label will be automatically detected when <code>posclass</code> is NULL.
<code>na_worst</code>	A Boolean value for controlling the treatment of NAs in scores. <b>TRUE</b> All NAs are treated as the worst scores <b>FALSE</b> All NAs are treated as the best scores
<code>ties_method</code>	A string for controlling ties in scores. <b>"equiv"</b> Ties are equivalently ranked <b>"first"</b> Ties are ranked in an increasing order as appeared <b>"random"</b> Ties are ranked in random order
<code>calc_avg</code>	A logical value to specify whether average curves should be calculated. It is effective only when <code>dsids</code> contains multiple dataset IDs. For instance, the function calculates the average for the model "m1" when <code>modnames</code> is <code>c("m1", "m1", "m1")</code> and <code>dsids</code> is <code>c(1, 2, 3)</code> . The calculation points are defined by <code>x_bins</code> .
<code>cb_alpha</code>	A numeric value with range [0, 1] to specify the alpha value of the point-wise confidence bounds calculation. It is effective only when <code>calc_avg</code> is set to TRUE. For example, it should be 0.05 for the 95% confidence level. The calculation points are defined by <code>x_bins</code> .
<code>raw_curves</code>	A logical value to specify whether all raw curves should be discarded after the average curves are calculated. It is effective only when <code>calc_avg</code> is set to TRUE.
<code>x_bins</code>	An integer value to specify the number of minimum bins on the x-axis. It is then used to define supporting points. For instance, the x-values of the supporting points will be <code>c(0, 0.5, 1)</code> and <code>c(0, 0.25, 0.5, 0.75, 1)</code> when <code>x_bins = 2</code> and <code>x_bins = 4</code> , respectively. All corresponding y-values of the supporting points are calculated. <code>x_bins</code> is effective only when <code>mode</code> is set to <code>rocprc</code> or <code>prcroc</code> .
<code>interpolate</code>	A Boolean value to specify whether or not interpolation of ROC and precision-recall curves are performed. <code>x_bins</code> and <code>calc_avg</code> are ignored and when <code>x_bins</code> is set to FALSE. <code>interpolate</code> is effective only when <code>mode</code> is set to <code>rocprc</code> or <code>prcroc</code> .
<code>...</code>	These additional arguments are passed to <code>mmdata</code> for data preparation.

## Value

The `evalmod` function returns an S3 object that contains performance evaluation measures. The number of models and the number of datasets can be controlled by `modnames` and `dsids`. For example, the number of models is "single" and the number of test datasets is "multiple" when `modnames = c("m1", "m1", "m1")` and `dsids = c(1, 2, 3)` are specified.

Different S3 objects have different default behaviors of S3 generics, such as `plot`, `autoplot`, and `fortify`.

1. The `evalmod` function returns one of the following S3 objects when mode is "prcroc". The objects contain ROC and Precision-Recall curves.

S3 object	# of models	# of test datasets
sscurves	single	single
mcurves	multiple	single
smcurves	single	multiple
mmcurves	multiple	multiple

2. The `evalmod` function returns one of the following S3 objects when mode is "basic". They contain five different basic evaluation measures; error rate, accuracy, specificity, sensitivity, and precision.

S3 object	# of models	# of test datasets
sspoin	single	single
msspoin	multiple	single
smsspoin	single	multiple
mmsspoin	multiple	multiple

3. The `evalmod` function returns the `aucroc` S3 object when mode is "aucroc", which can be used with `'print'` and `'as.data.frame'`.

### See Also

`plot` for plotting curves with the general R plot. `autoplot` and `fortify` for plotting curves with `ggplot2`. `mmdata` for formatting input data. `join_scores` and `join_labels` for formatting scores and labels with multiple datasets. `format_nfold` for creating n-fold cross validation dataset from data frame. `create_sim_samples` for generating random samples for simulations.

### Examples

```
#####
### Single model & single test dataset
###

## Load a dataset with 10 positives and 10 negatives
data(P10N10)

## Generate an sscurve object that contains ROC and Precision-Recall curves
sscurves <- evalmod(scores = P10N10$scores, labels = P10N10$labels)
sscurves

## Generate an sspoints object that contains basic evaluation measures
sspoin <- evalmod(
  mode = "basic", scores = P10N10$scores,
  labels = P10N10$labels
)
sspoin

#####
```

```

### Multiple models & single test dataset
###

## Create sample datasets with 100 positives and 100 negatives
samps <- create_sim_samples(1, 100, 100, "all")
mdat <- mmdata(samps[["scores"]], samps[["labels"]],
  modnames = samps[["modnames"]]
)

## Generate an mscurve object that contains ROC and Precision-Recall curves
mscurves <- evalmod(mdat)
mscurves

## Generate an mspoints object that contains basic evaluation measures
mspoints <- evalmod(mdat, mode = "basic")
mspoints

#####
### Single model & multiple test datasets
###

## Create sample datasets with 100 positives and 100 negatives
samps <- create_sim_samples(4, 100, 100, "good_er")
mdat <- mmdata(samps[["scores"]], samps[["labels"]],
  modnames = samps[["modnames"]],
  dsids = samps[["dsids"]]
)

## Generate an smcurve object that contains ROC and Precision-Recall curves
smcurves <- evalmod(mdat)
smcurves

## Generate an smpoints object that contains basic evaluation measures
smpoints <- evalmod(mdat, mode = "basic")
smpoints

#####
### Multiple models & multiple test datasets
###

## Create sample datasets with 100 positives and 100 negatives
samps <- create_sim_samples(4, 100, 100, "all")
mdat <- mmdata(samps[["scores"]], samps[["labels"]],
  modnames = samps[["modnames"]],
  dsids = samps[["dsids"]]
)

## Generate an mmcurve object that contains ROC and Precision-Recall curves
mmcurves <- evalmod(mdat)
mmcurves

```



```

## Generate an mmpoints object that contains basic evaluation measures
mmpoints <- evalmod(mdat, mode = "basic")
mmpoints

#####
### N-fold cross validation datasets
###

## Load test data
data(M2N50F5)

## Specify necessary columns to create mdat
cvdat <- mmdata(
  nfold_df = M2N50F5, score_cols = c(1, 2),
  lab_col = 3, fold_col = 4,
  modnames = c("m1", "m2"), dsids = 1:5
)

## Generate an mmcurve object that contains ROC and Precision-Recall curves
cvcurves <- evalmod(cvdat)
cvcurves

## Generate an mmpoints object that contains basic evaluation measures
cvpoints <- evalmod(cvdat, mode = "basic")
cvpoints

## Specify mmdata arguments from evalmod
cvcurves2 <- evalmod(
  nfold_df = M2N50F5, score_cols = c(1, 2),
  lab_col = 3, fold_col = 4,
  modnames = c("m1", "m2"), dsids = 1:5
)
cvcurves2

#####
### AUC with the U statistic
###

## mode = "aucroc" returns 'aucroc' S3 object
data(P10N10)

# 'aucroc' S3 object
uauc1 <- evalmod(
  scores = P10N10$scores, labels = P10N10$labels,
  mode = "aucroc"
)

# print 'aucroc'
uauc1

# as.data.frame 'aucroc'

```

```

as.data.frame(uauc1)

## It is 2-3 times faster than mode = "rocprc"
# A sample of 100,000
samp1 <- create_sim_samples(1, 50000, 50000)

# a function to test mode = "rocprc"
func_evalmod_rocprc <- function(samp) {
  curves <- evalmod(scores = samp$scores, labels = samp$labels)
  aucs <- auc(curves)
}

# a function to test mode = "aucroc"
func_evalmod_aucroc <- function(samp) {
  uaucs <- evalmod(
    scores = samp$scores, labels = samp$labels,
    mode = "aucroc"
  )
  as.data.frame(uaucs)
}

# Process time
system.time(res1 <- func_evalmod_rocprc(samp1))
system.time(res2 <- func_evalmod_aucroc(samp1))

# AUCs
res1
res2

```

---

format\_nfold

*Create n-fold cross validation dataset from data frame*


---

## Description

The `format_nfold` function takes a data frame with scores, label, and n-fold columns and convert it to a list for `evalmod` and `mmdata`.

## Usage

```
format_nfold(nfold_df, score_cols, lab_col, fold_col)
```

## Arguments

<code>nfold_df</code>	A data frame that contains at least one score column, label and fold columns.
<code>score_cols</code>	A character/numeric vector that specifies score columns of <code>nfold_df</code> .
<code>lab_col</code>	A number/string that specifies the label column of <code>nfold_df</code> .
<code>fold_col</code>	A number/string that specifies the fold column of <code>nfold_df</code> .

**Value**

The `format_nfold` function returns a list that contains multiple scores and labels.

**See Also**

[evalmod](#) for calculation evaluation measures. [mmdata](#) for formatting input data. [join\\_scores](#) and [join\\_labels](#) for formatting scores and labels with multiple datasets.

**Examples**

```
#####  
### Convert dataframe with 2 models and 5-fold datasets  
###  
  
## Load test data  
data(M2N50F5)  
head(M2N50F5)  
  
## Convert with format_nfold  
nfold_list1 <- format_nfold(  
  nfold_df = M2N50F5, score_cols = c(1, 2),  
  lab_col = 3, fold_col = 4  
)  
  
## Show the list structure  
str(nfold_list1)  
str(nfold_list1$scores)  
str(nfold_list1$labels)  
  
#####  
### Specify a single score column  
###  
  
## Convert with format_nfold  
nfold_list2 <- format_nfold(  
  nfold_df = M2N50F5, score_cols = 1,  
  lab_col = 3, fold_col = 4  
)  
  
## Show the list structure  
str(nfold_list2)  
str(nfold_list2$scores)  
str(nfold_list2$labels)  
  
#####  
### Use column names  
###  
  
## Convert with format_nfold  
nfold_list3 <- format_nfold(  

```

```

nfold_df = M2N50F5,
score_cols = c("score1", "score2"),
lab_col = "label", fold_col = "fold"
)

## Show the list structure
str(nfold_list3)
str(nfold_list3$scores)
str(nfold_list3$labels)

```

---

fortify

---

*Convert a curves and points object to a data frame for ggplot2*


---

## Description

The `fortify` function converts an S3 object generated by `evalmod` to a data frame for **ggplot2**.

## Usage

```

## S3 method for class 'sscurves'
fortify(model, data, raw_curves = NULL, reduce_points = FALSE, ...)

## S3 method for class 'mscurves'
fortify(model, data, raw_curves = NULL, reduce_points = FALSE, ...)

## S3 method for class 'smcurves'
fortify(model, data, raw_curves = NULL, reduce_points = FALSE, ...)

## S3 method for class 'mmcurves'
fortify(model, data, raw_curves = NULL, reduce_points = FALSE, ...)

## S3 method for class 'sspoints'
fortify(model, data, raw_curves = NULL, reduce_points = FALSE, ...)

## S3 method for class 'mspoints'
fortify(model, data, raw_curves = NULL, reduce_points = FALSE, ...)

## S3 method for class 'smpoints'
fortify(model, data, raw_curves = NULL, reduce_points = FALSE, ...)

## S3 method for class 'mmpoints'
fortify(model, data, raw_curves = NULL, reduce_points = FALSE, ...)

```

## Arguments

`model` An S3 object generated by `evalmod`. The `fortify` function takes one of the following S3 objects.

## 1. ROC and Precision-Recall curves (mode = "rocprc")

S3 object	# of models	# of test datasets
sscurves	single	single
mcurves	multiple	single
smcurves	single	multiple
mmcurves	multiple	multiple

## 2. Basic evaluation measures (mode = "basic")

S3 object	# of models	# of test datasets
sspoin	single	single
mspoin	multiple	single
smspoin	single	multiple
mmspoin	multiple	multiple

See the **Value** section of [evalmod](#) for more details.

data	Not used by this method.
raw_curves	A Boolean value to specify whether raw curves are shown instead of the average curve. It is effective only when raw_curves is set to TRUE of the <a href="#">evalmod</a> function.
reduce_points	A Boolean value to decide whether the points should be reduced. The points are reduced according to x_bins of the <a href="#">evalmod</a> function. The default values is FALSE.
...	Not used by this method.

**Value**

The fortify function returns a data frame for [ggplot2](#).

**See Also**

[evalmod](#) for generating S3 objects with performance evaluation measures. [autoplot](#) for plotting with [ggplot2](#).

**Examples**

```
## Not run:

## Load library
library(ggplot2)

#####
### Single model & single test dataset
###

## Load a dataset with 10 positives and 10 negatives
data(P10N10)
```

```

## Generate an sscurve object that contains ROC and Precision-Recall curves
sscurves <- evalmod(scores = P10N10$scores, labels = P10N10$labels)

## Let ggplot internally call fortify
p_rocprc <- ggplot(sscurves, aes(x = x, y = y))
p_rocprc <- p_rocprc + geom_line()
p_rocprc <- p_rocprc + facet_wrap(~curvetype)
p_rocprc

## Explicitly fortify sscurves
ssdf <- fortify(sscurves)

## Plot a ROC curve
p_roc <- ggplot(subset(ssdf, curvetype == "ROC"), aes(x = x, y = y))
p_roc <- p_roc + geom_line()
p_roc

## Plot a Precision-Recall curve
p_prc <- ggplot(subset(ssdf, curvetype == "PRC"), aes(x = x, y = y))
p_prc <- p_prc + geom_line()
p_prc

## Generate an sspoints object that contains basic evaluation measures
sspoints <- evalmod(
  mode = "basic", scores = P10N10$scores,
  labels = P10N10$labels
)
## Fortify sspoints
ssdf <- fortify(sspoints)

## Plot normalized ranks vs. precision
p_prec <- ggplot(subset(ssdf, curvetype == "precision"), aes(x = x, y = y))
p_prec <- p_prec + geom_point()
p_prec

#####
### Multiple models & single test dataset
###

## Create sample datasets with 10 positives and 10 negatives
samps <- create_sim_samples(1, 10, 10, "all")
mdat <- mmdata(samps[["scores"]], samps[["labels"]],
  modnames = samps[["modnames"]]
)

## Generate an mscurve object that contains ROC and Precision-Recall curves
mscurves <- evalmod(mdat)

## Let ggplot internally call fortify
p_rocprc <- ggplot(mscurves, aes(x = x, y = y, color = modname))
p_rocprc <- p_rocprc + geom_line()
p_rocprc <- p_rocprc + facet_wrap(~curvetype)

```

```

p_rocprc

## Explicitly fortify mscurves
msdf <- fortify(mscurves)

## Plot ROC curve
df_roc <- subset(msdf, curvetype == "ROC")
p_roc <- ggplot(df_roc, aes(x = x, y = y, color = modname))
p_roc <- p_roc + geom_line()
p_roc

## Fortified data frame can be used for plotting a Precision-Recall curve
df_prc <- subset(msdf, curvetype == "PRC")
p_prc <- ggplot(df_prc, aes(x = x, y = y, color = modname))
p_prc <- p_prc + geom_line()
p_prc

## Generate an mspoints object that contains basic evaluation measures
mspoints <- evalmod(mdat, mode = "basic")

## Fortify mspoints
msdf <- fortify(mspoints)

## Plot normalized ranks vs. precision
df_prec <- subset(msdf, curvetype == "precision")
p_prec <- ggplot(df_prec, aes(x = x, y = y, color = modname))
p_prec <- p_prec + geom_point()
p_prec

#####
### Single model & multiple test datasets
###

## Create sample datasets with 10 positives and 10 negatives
samps <- create_sim_samples(5, 10, 10, "good_er")
mdat <- mmdata(samps[["scores"]], samps[["labels"]],
  modnames = samps[["modnames"]],
  dsids = samps[["dsids"]]
)

## Generate an smcurve object that contains ROC and Precision-Recall curves
smcurves <- evalmod(mdat, raw_curves = TRUE)

## Let ggplot internally call fortify
p_rocprc <- ggplot(smcurves, aes(x = x, y = y, group = dsid))
p_rocprc <- p_rocprc + geom_smooth(stat = "identity")
p_rocprc <- p_rocprc + facet_wrap(~curvetype)
p_rocprc

## Explicitly fortify smcurves
smdf <- fortify(smcurves, raw_curves = FALSE)

```

```

## Plot average ROC curve
df_roc <- subset(smdf, curvetype == "ROC")
p_roc <- ggplot(df_roc, aes(x = x, y = y, ymin = ymin, ymax = ymax))
p_roc <- p_roc + geom_smooth(stat = "identity")
p_roc

## Plot average Precision-Recall curve
df_prc <- subset(smdf, curvetype == "PRC")
p_prc <- ggplot(df_prc, aes(x = x, y = y, ymin = ymin, ymax = ymax))
p_prc <- p_prc + geom_smooth(stat = "identity")
p_prc

## Generate an smpoints object that contains basic evaluation measures
smpoints <- evalmod(mdat, mode = "basic")

## Fortify smpoints
smdf <- fortify(smpoints)

## Plot normalized ranks vs. precision
df_prec <- subset(smdf, curvetype == "precision")
p_prec <- ggplot(df_prec, aes(x = x, y = y, ymin = ymin, ymax = ymax))
p_prec <- p_prec + geom_ribbon(aes(min = ymin, ymax = ymax),
  stat = "identity", alpha = 0.25,
  fill = "grey25"
)
p_prec <- p_prec + geom_point(aes(x = x, y = y))
p_prec

#####
### Multiple models & multiple test datasets
###

## Create sample datasets with 10 positives and 10 negatives
samps <- create_sim_samples(5, 10, 10, "all")
mdat <- mmdata(samps[["scores"]], samps[["labels"]],
  modnames = samps[["modnames"]],
  dsids = samps[["dsids"]]
)

## Generate an mscurve object that contains ROC and Precision-Recall curves
mmcurves <- evalmod(mdat, raw_curves = TRUE)

## Let ggplot internally call fortify
p_rocprc <- ggplot(mmcurves, aes(x = x, y = y, group = dsid))
p_rocprc <- p_rocprc + geom_smooth(aes(color = modname), stat = "identity")
p_rocprc <- p_rocprc + facet_wrap(~curvetype)
p_rocprc

## Explicitly fortify mmcurves
mmdf <- fortify(mmcurves, raw_curves = FALSE)

## Plot average ROC curve

```



```

df_roc <- subset(mmdf, curvetype == "ROC")
p_roc <- ggplot(df_roc, aes(x = x, y = y, ymin = ymin, ymax = ymax))
p_roc <- p_roc + geom_smooth(aes(color = modname), stat = "identity")
p_roc

## Plot average Precision-Recall curve
df_prc <- subset(mmdf, curvetype == "PRC")
p_prc <- ggplot(df_prc, aes(x = x, y = y, ymin = ymin, ymax = ymax))
p_prc <- p_prc + geom_smooth(aes(color = modname), stat = "identity")
p_prc

## Generate an mmpoints object that contains basic evaluation measures
mmpoints <- evalmod(mdat, mode = "basic")

## Fortify mmpoints
mmdf <- fortify(mmpoints)

## Plot normalized ranks vs. precision
df_prec <- subset(mmdf, curvetype == "precision")
p_prec <- ggplot(df_prec, aes(x = x, y = y, ymin = ymin, ymax = ymax))
p_prec <- p_prec + geom_ribbon(aes(min = ymin, ymax = ymax, group = modname),
  stat = "identity", alpha = 0.25,
  fill = "grey25"
)
p_prec <- p_prec + geom_point(aes(x = x, y = y, color = modname))
p_prec

## End(Not run)

```

---

 IB1000

---

*Imbalanced data with 1000 positives and 10000 negatives.*


---

## Description

A list contains labels and scores of five different performance levels. All scores were randomly generated.

## Usage

```
data(IB1000)
```

## Format

A list with 8 items.

**np** number of positives: 1000

**nn** number of negatives: 10000

**labels** labels of observed data

**random\_scores** scores of a random performance level

**poor\_er\_scores** scores of a poor early retrieval level

**good\_er\_scores** scores of a good early retrieval level

**excel\_scores** scores of an excellent level

**perf\_scores** scores of the perfect level

---

IB500

*Imbalanced data with 500 positives and 5000 negatives.*

---

### Description

A list contains labels and scores of five different performance levels. All scores were randomly generated.

### Usage

```
data(IB500)
```

### Format

A list with 8 items.

**np** number of positives: 500

**nn** number of negatives: 5000

**labels** labels of observed data

**random\_scores** scores of a random performance level

**poor\_er\_scores** scores of a poor early retrieval level

**good\_er\_scores** scores of a good early retrieval level

**excel\_scores** scores of an excellent level

**perf\_scores** scores of the perfect level

---

join_labels	<i>Join observed labels of multiple test datasets into a list</i>
-------------	---

---

**Description**

join\_labels takes observed labels and converts them to a list.

**Usage**

```
join_labels(..., byrow = FALSE, chklen = TRUE)
```

**Arguments**

...	Multiple datasets. They can be vectors, arrays, matrices, data frames, and lists.
byrow	A Boolean value to specify whether row vectors are used for matrix, data frame, and array.
chklen	A Boolean value to specify whether all list items must be the same lengths.

**Value**

The join\_labels function returns a list that contains all combined label data.

**See Also**

[evalmod](#) for calculation evaluation measures. [mmdata](#) for formatting input data. [join\\_scores](#) for formatting scores with multiple datasets.

**Examples**

```
#####
### Add three numeric vectors
###
l1 <- c(1, 0, 1, 1)
l2 <- c(1, 1, 0, 0)
l3 <- c(0, 1, 0, 1)
labels1 <- join_labels(l1, l2, l3)

## Show the list structure
str(labels1)

#####
### Add a matrix and a numeric vector
###
a1 <- matrix(rep(c(1, 0), 4), 4, 2)
labels2 <- join_labels(a1, l3)

## Show the list structure
str(labels2)
```

```
#####
### Use byrow
###
a2 <- matrix(rep(c(1, 0), 4), 2, 4, byrow = TRUE)
labels3 <- join_labels(a2, 13, byrow = TRUE)

## Show the list structure
str(labels3)

#####
### Use chklen
###
l4 <- c(-1, 0, -1)
l5 <- c(0, -1)
labels4 <- join_labels(l4, l5, chklen = FALSE)

## Show the list structure
str(labels4)
```

---

join\_scores

*Join scores of multiple models into a list*


---

### Description

The `join_scores` function takes predicted scores from multiple models and converts them to a list.

### Usage

```
join_scores(..., byrow = FALSE, chklen = TRUE)
```

### Arguments

<code>...</code>	Multiple datasets. They can be vectors, arrays, matrices, data frames, and lists.
<code>byrow</code>	A Boolean value to specify whether row vectors are used for matrix, data frame, and array.
<code>chklen</code>	A Boolean value to specify whether all list items must be the same lengths.

### Value

The `join_scores` function returns a list that contains all combined score data.

### See Also

[evalmod](#) for calculation evaluation measures. [mmdata](#) for formatting input data. [join\\_labels](#) for formatting labels with multiple datasets.

**Examples**

```
#####
### Add three numeric vectors
###
s1 <- c(1, 2, 3, 4)
s2 <- c(5, 6, 7, 8)
s3 <- c(2, 4, 6, 8)
scores1 <- join_scores(s1, s2, s3)

## Show the list structure
str(scores1)

#####
### Add a matrix and a numeric vector
###
a1 <- matrix(seq(8), 4, 2)
scores2 <- join_scores(a1, s3)

## Show the list structure
str(scores2)

#####
### Use byrow
###
a2 <- matrix(seq(8), 2, 4, byrow = TRUE)
scores3 <- join_scores(a2, s3, byrow = TRUE)

## Show the list structure
str(scores3)

#####
### Use chklen
###
s4 <- c(1, 2, 3)
s5 <- c(5, 6, 7, 8)
scores4 <- join_scores(s4, s5, chklen = FALSE)

## Show the list structure
str(scores4)
```

---

M2N50F5

*5-fold cross validation sample.*


---

**Description**

A data frame contains labels and scores for 5-fold test sets.

**Usage**

```
data(M2N50F5)
```

**Format**

A data frame with 4 columns.

**score1** 50 random scores

**score2** 50 random scores

**label** 50 labels as 'pos' or 'neg'

**fold** 50 fold IDs as 1:5

---

mmdata

*Reformat input data for performance evaluation calculation*


---

**Description**

The `mmdata` function takes predicted scores and labels and returns an `mdat` object. The `evalmod` function takes an `mdat` object as input data to calculate evaluation measures.

**Usage**

```
mmdata(
  scores,
  labels,
  modnames = NULL,
  dsids = NULL,
  posclass = NULL,
  na_worst = TRUE,
  ties_method = "equiv",
  expd_first = NULL,
  mode = "rocprc",
  nfold_df = NULL,
  score_cols = NULL,
  lab_col = NULL,
  fold_col = NULL,
  ...
)
```

**Arguments**

scores	A numeric dataset of predicted scores. It can be a vector, a matrix, an array, a data frame, or a list. The <code>join_scores</code> function can be useful to make scores with multiple datasets.
labels	A numeric, character, logical, or factor dataset of observed labels. It can be a vector, a matrix, an array, a data frame, or a list. The <code>join_labels</code> function can be useful to make labels with multiple datasets.

modnames	A character vector for the names of the models. The <code>evalmod</code> function automatically generates default names as "m1", "m2", "m3", and so on when it is NULL.
dsids	A numeric vector for test dataset IDs. The <code>evalmod</code> function automatically generates the default ID as 1 when it is NULL.
posclass	A scalar value to specify the label of positives in labels. It must be the same data type as labels. For example, <code>posclass = -1</code> changes the positive label from 1 to -1 when labels contains 1 and -1. The positive label will be automatically detected when <code>posclass</code> is NULL.
na_worst	A Boolean value for controlling the treatment of NAs in scores. <b>TRUE</b> All NAs are treated as the worst scores <b>FALSE</b> All NAs are treated as the best scores
ties_method	A string for controlling ties in scores. <b>"equiv"</b> Ties are equivalently ranked <b>"first"</b> Ties are ranked in an increasing order as appeared <b>"random"</b> Ties are ranked in random order
expd_first	A string to indicate which of the two variables - model names or test dataset IDs should be expanded first when they are automatically generated. <b>"modnames"</b> Model names are expanded first. For example, The <code>mmdata</code> function generates <code>modnames</code> as <code>c("m1", "m2")</code> and <code>dsids</code> as <code>c(1, 1)</code> when two vectors are passed as input, and <code>modnames</code> and <code>dsids</code> are unspecified. <b>"dsids"</b> Test dataset IDs are expanded first. For example, The <code>mmdata</code> function generates <code>modnames</code> as <code>c("m1", "m1")</code> and <code>dsids</code> as <code>c(1, 2)</code> when two vectors are passed as input, and <code>modnames</code> and <code>dsids</code> are unspecified.
mode	A string that specifies the types of evaluation measures that the <code>evalmod</code> function calculates. <b>"rocprc"</b> ROC and Precision-Recall curves <b>"prcroc"</b> Same as above <b>"basic"</b> Normalized ranks vs. accuracy, error rate, specificity, sensitivity, precision, Matthews correlation coefficient, and F-score. <b>"aucroc"</b> Fast AUC(ROC) calculation with the U statistic
ifold_df	A data frame that contains at least one score column, label and fold columns.
score_cols	A character/numeric vector that specifies score columns of <code>ifold_df</code> .
lab_col	A number/string that specifies the label column of <code>ifold_df</code> .
fold_col	A number/string that specifies the fold column of <code>ifold_df</code> .
...	Not used by this method.

### Value

The `mmdata` function returns an `mdat` object that contains formatted labels and score ranks. The object can be used as input data for the `evalmod` function.

**See Also**

[evalmod](#) for calculation evaluation measures. [join\\_scores](#) and [join\\_labels](#) for formatting scores and labels with multiple datasets. [format\\_nfold](#) for creating n-fold cross validation dataset from data frame.

**Examples**

```
#####
### Single model & single test dataset
###

## Load a dataset with 10 positives and 10 negatives
data(P10N10)

## Generate mdat object
ssmdat1 <- mmdata(P10N10$scores, P10N10$labels)
ssmdat1
ssmdat2 <- mmdata(1:8, sample(c(0, 1), 8, replace = TRUE))
ssmdat2

#####
### Multiple models & single test dataset
###

## Create sample datasets with 100 positives and 100 negatives
samps <- create_sim_samples(1, 100, 100, "all")

## Multiple models & single test dataset
msmdat1 <- mmdata(samps[["scores"]], samps[["labels"]],
  modnames = samps[["modnames"]]
)
msmdat1

## Use join_scores and join_labels
s1 <- c(1, 2, 3, 4)
s2 <- c(5, 6, 7, 8)
scores <- join_scores(s1, s2)

l1 <- c(1, 0, 1, 1)
l2 <- c(1, 0, 1, 1)
labels <- join_labels(l1, l2)

msmdat2 <- mmdata(scores, labels, modnames = c("ms1", "ms2"))
msmdat2

#####
### Single model & multiple test datasets
###

## Create sample datasets with 100 positives and 100 negatives
```



```

samps <- create_sim_samples(10, 100, 100, "good_er")

## Single model & multiple test datasets
smmdat <- mmdat(samps[["scores"]], samps[["labels"]],
  modnames = samps[["modnames"]],
  dsids = samps[["dsids"]]
)
smmdat

#####
### Multiple models & multiple test datasets
###

## Create sample datasets with 100 positives and 100 negatives
samps <- create_sim_samples(10, 100, 100, "all")

## Multiple models & multiple test datasets
mmdat <- mmdat(samps[["scores"]], samps[["labels"]],
  modnames = samps[["modnames"]],
  dsids = samps[["dsids"]]
)
mmdat

#####
### N-fold cross validation datasets
###

## Load test data
data(M2N50F5)
head(M2N50F5)

## Specify necessary columns to create mdat
cvdat1 <- mmdat(
  nfold_df = M2N50F5, score_cols = c(1, 2),
  lab_col = 3, fold_col = 4,
  modnames = c("m1", "m2"), dsids = 1:5
)
cvdat1

## Use column names
cvdat2 <- mmdat(
  nfold_df = M2N50F5, score_cols = c("score1", "score2"),
  lab_col = "label", fold_col = "fold",
  modnames = c("m1", "m2"), dsids = 1:5
)
cvdat2

```

**Description**

A list contains labels and scores for 10 positives and 10 negatives.

**Usage**

```
data(P10N10)
```

**Format**

A list with 4 items.

**np** number of positives: 10

**nn** number of negatives: 10

**labels** 20 labels of observed data

**scores** 20 scores with some ties

---

 part

---

*Calculate partial AUCs*


---

**Description**

The part function takes an S3 object generated by [evalmod](#) and calculate partial AUCs and Standardized partial AUCs of ROC and Precision-Recall curves. Standardized pAUCs are standardized to the range between 0 and 1.

**Usage**

```
part(curves, xlim = NULL, ylim = NULL, curvetype = NULL)
```

```
## S3 method for class 'sscurves'
```

```
part(curves, xlim = c(0, 1), ylim = c(0, 1), curvetype = c("ROC", "PRC"))
```

```
## S3 method for class 'mscurves'
```

```
part(curves, xlim = c(0, 1), ylim = c(0, 1), curvetype = c("ROC", "PRC"))
```

```
## S3 method for class 'smcurves'
```

```
part(curves, xlim = c(0, 1), ylim = c(0, 1), curvetype = c("ROC", "PRC"))
```

```
## S3 method for class 'mmcurves'
```

```
part(curves, xlim = c(0, 1), ylim = c(0, 1), curvetype = c("ROC", "PRC"))
```

**Arguments**

**curves** An S3 object generated by [evalmod](#). The part function accepts the following S3 objects.

S3 object	# of models	# of test datasets
sscurves	single	single
mcurves	multiple	single
smcurves	single	multiple
mmcurves	multiple	multiple

See the **Value** section of [evalmod](#) for more details.

xlim	A numeric vector of length two to specify x range between two points in [0, 1]
ylim	A numeric vector of length two to specify y range between two points in [0, 1]
curvetype	A character vector with the following curve types.

curvetype	description
ROC	ROC curve
PRC	Precision-Recall curve

Multiple curvetype can be combined, such as `c("ROC", "PRC")`.

### Value

The `part` function returns the same S3 object specified as input with calculated pAUCs and standardized pAUCs.

### See Also

[evalmod](#) for generating S3 objects with performance evaluation measures. [pauc](#) for retrieving a dataset of pAUCs.

### Examples

```
## Not run:

## Load library
library(ggplot2)

#####
### Single model & single test dataset
###

## Load a dataset with 10 positives and 10 negatives
data(P10N10)

## Generate an sscurve object that contains ROC and Precision-Recall curves
sscurves <- evalmod(scores = P10N10$scores, labels = P10N10$labels)

## Calculate partial AUCs
sscurves.part <- part(sscurves, xlim = c(0.25, 0.75))

## Show AUCs
sscurves.part
```

```

## Plot partial curve
plot(sscurves.part)

## Plot partial curve with ggplot
autoplot(sscurves.part)

#####
### Multiple models & single test dataset
###

## Create sample datasets with 100 positives and 100 negatives
samps <- create_sim_samples(1, 100, 100, "all")
mdat <- mmdata(samps[["scores"]], samps[["labels"]],
  modnames = samps[["modnames"]]
)

## Generate an mscurve object that contains ROC and Precision-Recall curves
mscurves <- evalmod(mdat)

## Calculate partial AUCs
mscurves.part <- part(mscurves, xlim = c(0, 0.75), ylim = c(0.25, 0.75))

## Show AUCs
mscurves.part

## Plot partial curves
plot(mscurves.part)

## Plot partial curves with ggplot
autoplot(mscurves.part)

#####
### Single model & multiple test datasets
###

## Create sample datasets with 100 positives and 100 negatives
samps <- create_sim_samples(4, 100, 100, "good_er")
mdat <- mmdata(samps[["scores"]], samps[["labels"]],
  modnames = samps[["modnames"]],
  dsids = samps[["dsids"]]
)

## Generate an smcurve object that contains ROC and Precision-Recall curves
smcurves <- evalmod(mdat)

## Calculate partial AUCs
smcurves.part <- part(smcurves, xlim = c(0.25, 0.75))

## Show AUCs
smcurves.part

```

```

## Plot partial curve
plot(smcurves.part)

## Plot partial curve with ggplot
autoplot(smcurves.part)

#####
### Multiple models & multiple test datasets
###

## Create sample datasets with 100 positives and 100 negatives
samps <- create_sim_samples(4, 100, 100, "all")
mdat <- mmdata(samps[["scores"]], samps[["labels"]],
  modnames = samps[["modnames"]],
  dsids = samps[["dsids"]]
)

## Generate an mscurve object that contains ROC and Precision-Recall curves
mmcurves <- evalmod(mdat, raw_curves = TRUE)

## Calculate partial AUCs
mmcurves.part <- part(mmcurves, xlim = c(0, 0.25))

## Show AUCs
mmcurves.part

## Plot partial curves
plot(mmcurves.part)

## Plot partial curves with ggplot
autoplot(mmcurves.part)

## End(Not run)

```

---

pauc

*Retrieve a data frame of pAUC scores*


---

## Description

The `auc` function takes an S3 object generated by `part` and `evalmod` and retrieves a data frame with the partial AUC scores of ROC and Precision-Recall curves.

## Usage

```

pauc(curves)

## S3 method for class 'aucs'
pauc(curves)

```

**Arguments**

curves An S3 object generated by [part](#) and [evalmod](#). The `pauc` function accepts the following S3 objects.

S3 object	# of models	# of test datasets
sscurves	single	single
mcurves	multiple	single
smcurves	single	multiple
mmcurves	multiple	multiple

See the **Value** section of [evalmod](#) for more details.

**Value**

The `auc` function returns a data frame with pAUC scores.

**See Also**

[evalmod](#) for generating S3 objects with performance evaluation measures. [part](#) for calculation of pAUCs. [auc](#) for retrieving a dataset of AUCs.

**Examples**

```
#####
### Single model & single test dataset
###

## Load a dataset with 10 positives and 10 negatives
data(P10N10)

## Generate an sscurve object that contains ROC and Precision-Recall curves
sscurves <- evalmod(scores = P10N10$scores, labels = P10N10$labels)

## Calculate partial AUCs
sscurves.part <- part(sscurves, xlim = c(0.25, 0.75))

## Shows pAUCs
pauc(sscurves.part)

#####
### Multiple models & single test dataset
###

## Create sample datasets with 100 positives and 100 negatives
samps <- create_sim_samples(1, 100, 100, "all")
mdat <- mmdata(samps[["scores"]], samps[["labels"]],
              modnames = samps[["modnames"]])
)

## Generate an mscurve object that contains ROC and Precision-Recall curves
mcurves <- evalmod(mdat)
```

```

## Calculate partial AUCs
mscurves.part <- part(mscurves, xlim = c(0, 0.75), ylim = c(0.25, 0.75))

## Shows pAUCs
pauc(mscurves.part)

#####
### Single model & multiple test datasets
###

## Create sample datasets with 100 positives and 100 negatives
samps <- create_sim_samples(4, 100, 100, "good_er")
mdat <- mmdata(samps[["scores"]], samps[["labels"]],
  modnames = samps[["modnames"]],
  dsids = samps[["dsids"]]
)

## Generate an smcurve object that contains ROC and Precision-Recall curves
smcurves <- evalmod(mdat, raw_curves = TRUE)

## Calculate partial AUCs
smcurves.part <- part(smcurves, xlim = c(0.25, 0.75))

## Shows pAUCs
pauc(smcurves.part)

#####
### Multiple models & multiple test datasets
###

## Create sample datasets with 100 positives and 100 negatives
samps <- create_sim_samples(4, 100, 100, "all")
mdat <- mmdata(samps[["scores"]], samps[["labels"]],
  modnames = samps[["modnames"]],
  dsids = samps[["dsids"]]
)

## Generate an mscurve object that contains ROC and Precision-Recall curves
mmcurves <- evalmod(mdat, raw_curves = TRUE)

## Calculate partial AUCs
mmcurves.part <- part(mmcurves, xlim = c(0, 0.25))

## Shows pAUCs
pauc(mmcurves.part)

```

## Description

The `plot` function creates a plot of performance evaluation measures.

## Usage

```
## S3 method for class 'sscurves'
plot(x, y = NULL, ...)

## S3 method for class 'mscurves'
plot(x, y = NULL, ...)

## S3 method for class 'smcurves'
plot(x, y = NULL, ...)

## S3 method for class 'mmcurves'
plot(x, y = NULL, ...)

## S3 method for class 'sspoinst'
plot(x, y = NULL, ...)

## S3 method for class 'mspoinst'
plot(x, y = NULL, ...)

## S3 method for class 'smpoinst'
plot(x, y = NULL, ...)

## S3 method for class 'mmpoinst'
plot(x, y = NULL, ...)
```

## Arguments

`x` An S3 object generated by `evalmod`. The `plot` function accepts the following S3 objects.

1. ROC and Precision-Recall curves (mode = "rocprc")

S3 object	# of models	# of test datasets
sscurves	single	single
mscurves	multiple	single
smcurves	single	multiple
mmcurves	multiple	multiple

2. Basic evaluation measures (mode = "basic")

S3 object	# of models	# of test datasets
sspoinst	single	single
mspoinst	multiple	single
smpoinst	single	multiple
mmpoinst	multiple	multiple



See the **Value** section of [evalmod](#) for more details.

y Equivalent with `curvetype`.  
 ... All the following arguments can be specified.

**curvetype** 1. ROC and Precision-Recall curves (mode = "rocprc")

<b>curvetype</b>	<b>description</b>
ROC	ROC curve
PRC	Precision-Recall curve

Multiple `curvetype` can be combined, such as `c("ROC", "PRC")`.

2. Basic evaluation measures (mode = "basic")

<b>curvetype</b>	<b>description</b>
error	Normalized ranks vs. error rate
accuracy	Normalized ranks vs. accuracy
specificity	Normalized ranks vs. specificity
sensitivity	Normalized ranks vs. sensitivity
precision	Normalized ranks vs. precision
mcc	Normalized ranks vs. Matthews correlation coefficient
fscore	Normalized ranks vs. F-score

Multiple `curvetype` can be combined, such as `c("precision", "sensitivity")`.

**type** A character to specify the line type as follows.

"l" lines  
 "p" points  
 "b" both lines and points

**show\_cb** A Boolean value to specify whether point-wise confidence bounds are drawn. It is effective only when `calc_avg` of the [evalmod](#) function is set to TRUE.

**raw\_curves** A Boolean value to specify whether raw curves are shown instead of the average curve. It is effective only when `raw_curves` of the [evalmod](#) function is set to TRUE.

**show\_legend** A Boolean value to specify whether the legend is shown.

## Value

The `plot` function shows a plot and returns NULL.

## See Also

[evalmod](#) for generating an S3 object. [autoplot](#) for plotting the equivalent curves with [ggplot2](#).

## Examples

```
## Not run:
#####
### Single model & single test dataset
```

```

###

## Load a dataset with 10 positives and 10 negatives
data(P10N10)

## Generate an sscurve object that contains ROC and Precision-Recall curves
sscurves <- evalmod(scores = P10N10$scores, labels = P10N10$labels)

## Plot both ROC and Precision-Recall curves
plot(sscurves)

## Plot a ROC curve
plot(sscurves, curvetype = "ROC")

## Plot a Precision-Recall curve
plot(sscurves, curvetype = "PRC")

## Generate an sspoints object that contains basic evaluation measures
sspoints <- evalmod(
  mode = "basic", scores = P10N10$scores,
  labels = P10N10$labels
)

## Plot normalized ranks vs. basic evaluation measures
plot(sspoints)

## Plot normalized ranks vs. precision
plot(sspoints, curvetype = "precision")

#####
### Multiple models & single test dataset
###

## Create sample datasets with 100 positives and 100 negatives
samps <- create_sim_samples(1, 100, 100, "all")
mdat <- mmdata(samps[["scores"]], samps[["labels"]],
  modnames = samps[["modnames"]]
)

## Generate an mscurve object that contains ROC and Precision-Recall curves
mscurves <- evalmod(mdat)

## Plot both ROC and Precision-Recall curves
plot(mscurves)

## Hide the legend
plot(mscurves, show_legend = FALSE)

## Generate an mspoints object that contains basic evaluation measures
mspoints <- evalmod(mdat, mode = "basic")

## Plot normalized ranks vs. basic evaluation measures

```

```

plot(mspoints)

## Hide the legend
plot(mspoints, show_legend = FALSE)

#####
### Single model & multiple test datasets
###

## Create sample datasets with 100 positives and 100 negatives
samps <- create_sim_samples(10, 100, 100, "good_er")
mdat <- mmdata(samps[["scores"]], samps[["labels"]],
  modnames = samps[["modnames"]],
  dsids = samps[["dsids"]]
)

## Generate an smcurve object that contains ROC and Precision-Recall curves
smcurves <- evalmod(mdat, raw_curves = TRUE)

## Plot average ROC and Precision-Recall curves
plot(smcurves, raw_curves = FALSE)

## Hide confidence bounds
plot(smcurves, raw_curves = FALSE, show_cb = FALSE)

## Plot raw ROC and Precision-Recall curves
plot(smcurves, raw_curves = TRUE, show_cb = FALSE)

## Generate an smpoints object that contains basic evaluation measures
smpoints <- evalmod(mdat, mode = "basic")

## Plot normalized ranks vs. average basic evaluation measures
plot(smpoints)

#####
### Multiple models & multiple test datasets
###

## Create sample datasets with 100 positives and 100 negatives
samps <- create_sim_samples(10, 100, 100, "all")
mdat <- mmdata(samps[["scores"]], samps[["labels"]],
  modnames = samps[["modnames"]],
  dsids = samps[["dsids"]]
)

## Generate an mscurve object that contains ROC and Precision-Recall curves
mmcurves <- evalmod(mdat, raw_curves = TRUE)

## Plot average ROC and Precision-Recall curves
plot(mmcurves, raw_curves = FALSE)

```

```

## Show confidence bounds
plot(mmcurves, raw_curves = FALSE, show_cb = TRUE)

## Plot raw ROC and Precision-Recall curves
plot(mmcurves, raw_curves = TRUE)

## Generate an mmpoints object that contains basic evaluation measures
mmpoints <- evalmod(mdat, mode = "basic")

## Plot normalized ranks vs. average basic evaluation measures
plot(mmpoints)

#####
### N-fold cross validation datasets
###

## Load test data
data(M2N50F5)

## Specify necessary columns to create mdat
cvdat <- mmdata(
  nfold_df = M2N50F5, score_cols = c(1, 2),
  lab_col = 3, fold_col = 4,
  modnames = c("m1", "m2"), dsids = 1:5
)

## Generate an mmcurve object that contains ROC and Precision-Recall curves
cvcurves <- evalmod(cvdat)

## Average ROC and Precision-Recall curves
plot(cvcurves)

## Show confidence bounds
plot(cvcurves, show_cb = TRUE)

## Generate an mmpoints object that contains basic evaluation measures
cvpoints <- evalmod(cvdat, mode = "basic")

## Normalized ranks vs. average basic evaluation measures
plot(cvpoints)

## End(Not run)

```

---

```
precrec
```

```
precrec: A package for computing accurate ROC and Precision-Recall
curves
```

---

## Description

The precrec package contains several functions and S3 generics to provide a robust platform for performance evaluation of binary classifiers.

## Functions

The precrec package provides the following six functions.

Function	Description
<code>evalmod</code>	Main function to calculate evaluation measures
<code>mmdata</code>	Reformat input data for performance evaluation calculation
<code>join_scores</code>	Join scores of multiple models into a list
<code>join_labels</code>	Join observed labels of multiple test datasets into a list
<code>create_sim_samples</code>	Create random samples for simulations
<code>format_nfold</code>	Create n-fold cross validation dataset from data frame

## S3 generics

The precrec package provides nine different S3 generics for the S3 objects generated by the `evalmod` function.

S3 generic	Library	Description
<code>print</code>	base	Print the calculation results and the summary of the test data
<code>as.data.frame</code>	base	Convert a precrec object to a data frame
<code>plot</code>	graphics	Plot performance evaluation measures
<code>autoplot</code>	ggplot2	Plot performance evaluation measures with ggplot2
<code>fortify</code>	ggplot2	Prepare a data frame for ggplot2
<code>auc</code>	precrec	Make a data frame with AUC scores
<code>part</code>	precrec	Calculate partial curves and partial AUC scores
<code>pauc</code>	precrec	Make a data frame with pAUC scores
<code>auc_ci</code>	precrec	Calculate confidence intervals of AUC scores

## Performance measure calculations

The `evalmod` function calculates ROC and Precision-Recall curves and returns an S3 object. The generated S3 object can be used with several different S3 generics, such as `print` and `plot`. The `evalmod` function can also calculate basic evaluation measures - error rate, accuracy, specificity, sensitivity, precision, Matthews correlation coefficient, and F-Score.

## Data preparation

The `mmdata` function creates an input dataset for the `evalmod` function. The generated dataset contains formatted scores and labels.

`join_scores` and `join_labels` are helper functions to combine multiple scores and labels.

The `create_sim_samples` function creates test datasets with five different performance levels.

## Data visualization

`plot` takes an S3 object generated by `evalmod` as input and plot corresponding curves.

`autoplot` uses ggplot to plot curves.

**Result retrieval**

`as.data.frame` takes an S3 object generated by `evalmod` as input and returns a data frame with calculated curve points.

`auc` and `pauc` returns a data frame with AUC scores and partial AUC scores, respectively. `auc_ci` returns confidence intervals of AUCs for both ROC and precision-recall curves.

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**See Also**

Useful links:

- <https://github.com/evalclass/precrec>
- Report bugs at <https://github.com/evalclass/precrec/issues>

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