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Title Twin Support Vector Machines

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Description Provides twin support vector machine classifiers and visualization tools for small to moderate classification problems. Includes one-vs-one multi-class classification and a standard support vector machine baseline for comparison.

License GPL-3

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`twinsvm-package` *twinsvm: Twin Support Vector Machines*

Description

Twin support vector machine classifiers with a standard C-SVC baseline.

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References

Jayadeva, Khemchandani, R., and Chandra, S. (2007). Twin support vector machines for pattern classification. *IEEE Transactions on Pattern Analysis and Machine Intelligence*, 29(5), 905-910.

Kumar, M. A. and Gopal, M. (2009). Least squares twin support vector machines for pattern classification. *Expert Systems with Applications*, 36(4), 7535-7543.

coef.tsvm *Extract Twin-SVM Coefficients*

Description

Extract Twin-SVM Coefficients

Usage

```
## S3 method for class 'tsvm'
coef(object, ...)
```

Arguments

object	A fitted tsvm object.
...	Unused.

Value

A list with the two plane coefficients.

Examples

```
dat <- gen_moons(30)
fit <- tsvm(dat$x, dat$y)
coef(fit)
```

compare_methods *Compare Twin-SVM and Standard SVM Boundaries*

Description

Fits least-squares twin SVM, original QP twin SVM, and the standard C-SVC SVM baseline on the same two-dimensional data, then plots the three decision boundaries side by side.

Usage

```
compare_methods(x, y, kernel = "rbf", gamma = 0.5, c1 = 1, c2 = 1, cost = 1)
```

Arguments

x	Numeric two-column matrix or data frame.
y	Two-class response.
kernel	Kernel name: "linear", "rbf", or "poly".
gamma	Kernel scale.
c1, c2	Positive twin-SVM regularization parameters.
cost	Positive C-SVC cost parameter.

Value

A faceted ggplot object.

See Also

Other visualization: kernel_lift(), lift_plot(), lift_plotly()

Examples

```
set.seed(30)
dat <- gen_moons(50, noise = 0.1)
compare_methods(dat$x, dat$y, gamma = 1, c1 = 0.2, c2 = 0.2, cost = 1)
```

---

confusion *Confusion Matrix and Accuracy*

Description

Predicts on x and returns a confusion matrix plus overall accuracy. This works for both binary and one-vs-one multiclass tsvm and svms fits.

Usage

```
confusion(object, x, y)
```

Arguments

object	A fitted tsvm, tsvm_multiclass, svms, or svms_multiclass object.
x	Numeric matrix or data frame of predictors.
y	True class labels.

Value

A list with table, a table(truth, predicted) confusion matrix, and accuracy, the overall classification accuracy.

See Also

Other multiclass: predict.svms_multiclass(), predict.tsvm_multiclass(), print.svms_multiclass(), print.tsvm_multiclass()

Examples

```
set.seed(50)
x <- rbind(
  matrix(rnorm(20, -2, 0.2), ncol = 2),
  matrix(rnorm(20, 0, 0.2), ncol = 2),
  matrix(rnorm(20, 2, 0.2), ncol = 2)
)
y <- factor(rep(c("a", "b", "c"), each = 10))
fit <- tsvm(x, y, kernel = "linear")
confusion(fit, x, y)
```

`cv_tsvm` *Cross-Validate Twin-SVM Hyperparameters*

Description

Runs k-fold cross-validation over `c1`, `c2`, and optionally `gamma`.

Usage

```
cv_tsvm(x, y, c1_grid, c2_grid, gamma_grid = NULL, k = 5, ...)
```

Arguments

`x`	Numeric matrix or data frame of predictors.
`y`	Two-class response.
`c1_grid`, `c2_grid`	Positive numeric vectors.
`gamma_grid`	Optional positive numeric vector. If `NULL`, `gamma` is left at the `tsvm()` default.
`k`	Number of folds.
`...`	Additional arguments passed to `tsvm()`.

Value

A `cv_tsvm` object with `best_params` and `results`.

Examples

```
set.seed(10)
dat <- gen_moons(40, noise = 0.1)
cv <- cv_tsvm(dat$x, dat$y, c1_grid = c(0.1, 1), c2_grid = c(0.1, 1), k = 3)
cv$best_params
```

gen_circles *Generate Concentric Circles Data*

Description

Generate Concentric Circles Data

Usage

```
gen_circles(n, noise = 0.05)
```

Arguments

n	Number of observations.
noise	Standard deviation of Gaussian noise.

Value

A list with numeric matrix x and factor y.

Examples

```
dat <- gen_circles(20, noise = 0.05)
str(dat)
```

gen_moons *Generate Two-Moons Data*

Description

Generate Two-Moons Data

Usage

```
gen_moons(n, noise = 0.2)
```

Arguments

n	Number of observations.
noise	Standard deviation of Gaussian noise.

Value

A list with numeric matrix x and factor y.

Examples

```
dat <- gen_moons(20, noise = 0.1)
str(dat)
```

`kernel_lift` *Compatibility Alias for the RBF Kernel Lift Plot*

Description

`kernel_lift()` is kept for existing code. New code should call `lift_plot()`.

Usage

```
kernel_lift(x, y, gamma = 1, center = NULL)
```

Arguments

`x`	Numeric two-column matrix or data frame.
`y`	Two-class response.
`gamma`	Positive RBF scale.
`center`	Optional numeric length-two center for the RBF bump. If `NULL`, the centroid of the inner class is used.

Value

A `ggplot` object.

See Also

Other visualization: `compare_methods()`, `lift_plot()`, `lift_plotly()`

Examples

```
set.seed(22)
dat <- gen_circles(60, noise = 0.04)
kernel_lift(dat$x, dat$y, gamma = 1)
```

lift_plot *Static RBF Kernel Lift Plot*

Description

Maps two-dimensional data to a third RBF height and draws a static oblique projection. The height is `exp(-gamma * ||x - center||^2)`, so points near the center rise while points farther away stay low. A translucent plane is drawn halfway between the two class mean heights.

Usage

```
lift_plot(x, y, gamma = 1, center = NULL)
```

Arguments

`x`	Numeric two-column matrix or data frame.
`y`	Two-class response.
`gamma`	Positive RBF scale.
`center`	Optional numeric length-two center for the RBF bump. If `NULL`, the centroid of the inner class is used.

Value

A `ggplot` object.

See Also

Other visualization: `compare_methods()`, `kernel_lift()`, `lift_plotly()`

Examples

```
set.seed(20)
dat <- gen_circles(80, noise = 0.04)
lift_plot(dat$x, dat$y, gamma = 1)
```

lift_plotly *Interactive RBF Kernel Lift Plot*

Description

Draws the same RBF lift as `lift_plot()` as a rotatable `plotly` 3D chart. This function is optional; the package does not require `plotly` to build or check.

Usage

```
lift_plotly(x, y, gamma = 1, center = NULL)
```

Arguments

x	Numeric two-column matrix or data frame.
y	Two-class response.
gamma	Positive RBF scale.
center	Optional numeric length-two center for the RBF bump. If NULL, the centroid of the inner class is used.

Value

A plotly object.

See Also

Other visualization: compare_methods(), kernel_lift(), lift_plot()

Examples

```
set.seed(21)
dat <- gen_circles(80, noise = 0.04)
if (requireNamespace("plotly", quietly = TRUE)) {
  lift_plotly(dat$x, dat$y, gamma = 1)
}
```

---

morph_boundary *Animate a Decision Boundary Across a Hyperparameter Range*

Description

Refits a model over a sequence of hyperparameter values and returns a ganimate object showing the boundary change.

Usage

```
morph_boundary(
  x,
  y,
  param = c("gamma", "cost", "c1"),
  range,
  model = c("tsvm", "svms"),
  n = 30,
  ...
)
```

Arguments

x	Numeric two-column matrix or data frame.
y	Two-class response.
param	Hyperparameter to vary.
range	Numeric length-two range for the hyperparameter.
model	Model family: "tsvm" or "svms".
n	Number of frames.
...	Additional arguments passed to the model fit function.

Value

A gganim object.

Examples

```
if (interactive()) {
  dat <- gen_moons(40)
  morph_boundary(dat$x, dat$y, param = "gamma", range = c(0.5, 2), n = 4)
}
```

---

plot.cv_tsvm *Plot Twin-SVM Cross-Validation Results*

Description

Plot Twin-SVM Cross-Validation Results

Usage

```
## S3 method for class 'cv_tsvm'
plot(x, ...)
```

Arguments

x	A cv_tsvm object.
...	Unused.

Value

A ggplot object.

Examples

```
set.seed(11)
dat <- gen_moons(40, noise = 0.1)
cv <- cv_tsvm(dat$x, dat$y, c1_grid = c(0.1, 1), c2_grid = c(0.1, 1), k = 3)
plot(cv)
```

plot.resample_accuracy *Plot the Accuracy Spread from Repeated Splits*

Description

Draws the per-split test accuracies as a boxplot, one box per model, so the dispersion is visible alongside the mean.

Usage

```
## S3 method for class 'resample_accuracy'
plot(x, ...)
```

Arguments

x	A resample_accuracy object.
...	Unused.

Value

A ggplot object.

Examples

```
set.seed(2)
dat <- gen_moons(120, noise = 0.15)
rs <- resample_accuracy(dat$x, dat$y, reps = 10, kernel = "rbf", gamma = 1)
plot(rs)
```

plot.svms *Plot a Standard SVM Decision Boundary*

Description

Plot a Standard SVM Decision Boundary

Usage

```
## S3 method for class 'svms'
plot(x, ...)
```

Arguments

x	A fitted svms object.
...	Unused.

Value

A ggplot object.

Examples

```
dat <- gen_moons(40)
fit <- svms(dat$x, dat$y, kernel = "linear")
plot(fit)
```

`plot.tsvm` *Plot a Twin-SVM Decision Boundary*

Description

Plot a Twin-SVM Decision Boundary

Usage

```
## S3 method for class 'tsvm'
plot(x, ...)
```

Arguments

x	A fitted tsvm object.
...	Unused.

Value

A ggplot object.

Examples

```
dat <- gen_moons(40)
fit <- tsvm(dat$x, dat$y)
plot(fit)
```

predict.svms *Predict from a Standard SVM*

Description

Predict from a Standard SVM

Usage

```
## S3 method for class 'svms'
predict(object, newdata, decision.values = FALSE, ...)
```

Arguments

object	A fitted svms object.
newdata	Numeric matrix or data frame.
decision.values	If TRUE, return raw decision values instead of class labels.
...	Unused.

Value

A factor of predicted classes, or a numeric vector when decision.values = TRUE.

Examples

```
set.seed(2)
dat <- gen_moons(30)
fit <- svms(dat$x, dat$y)
predict(fit, dat$x, decision.values = TRUE)
```

predict.svms_multiclass *Predict from a Multiclass Standard SVM*

Description

Predicts from a one-vs-one multiclass standard SVM. Each binary model votes for one class. Ties are resolved deterministically by choosing the class that appears first in the training factor level order.

Usage

```
## S3 method for class 'svms_multiclass'
predict(object, newdata, type = c("class", "votes"), ...)
```

Arguments

object	A fitted svms_multiclass object.
newdata	Numeric matrix or data frame.
type	Output type. "class" returns predicted class labels; "votes" returns the vote matrix.
...	Unused. decision.values is not supported for multiclass objects because OVO decision values do not have a single unambiguous scale.

Value

A factor of predicted classes, or an integer vote matrix when type = "votes".

See Also

Other multiclass: confusion(), predict.tsvm_multiclass(), print.svms_multiclass(), print.tsvm_multiclass()

Examples

```
set.seed(45)
x <- rbind(
  matrix(rnorm(8, -2, 0.2), ncol = 2),
  matrix(rnorm(8, 0, 0.2), ncol = 2),
  matrix(rnorm(8, 2, 0.2), ncol = 2)
)
y <- factor(rep(c("a", "b", "c"), each = 4))
fit <- svms(x, y, kernel = "linear", max_passes = 2, max_iter = 100)
predict(fit, x[1:3, , drop = FALSE])
```

---

predict.tsvm_multiclass

Predict from a Multiclass Twin SVM

Description

Predicts from a one-vs-one multiclass twin SVM. Each binary model votes for one class. Ties are resolved deterministically by choosing the class that appears first in the training factor level order.

Usage

```
## S3 method for class 'tsvm_multiclass'
predict(object, newdata, type = c("class", "votes"), ...)
```

Arguments

object	A fitted tsvm_multiclass object.
newdata	Numeric matrix or data frame.
type	Output type. "class" returns predicted class labels; "votes" returns the vote matrix.
...	Unused. decision.values is not supported for multiclass objects because OVO decision values do not have a single unambiguous scale.

Value

A factor of predicted classes, or an integer vote matrix when type = "votes".

See Also

Other multiclass: confusion(), predict.svms_multiclass(), print.svms_multiclass(), print.tsvm_multiclass()

Examples

```
set.seed(40)
x <- rbind(
  matrix(rnorm(20, -2, 0.2), ncol = 2),
  matrix(rnorm(20, 0, 0.2), ncol = 2),
  matrix(rnorm(20, 2, 0.2), ncol = 2)
)
y <- factor(rep(c("a", "b", "c"), each = 10))
fit <- tsvm(x, y, kernel = "linear")
predict(fit, x[1:3, , drop = FALSE])
```

---

print.svms_multiclass *Print a Multiclass Standard SVM*

Description

Print a Multiclass Standard SVM

Usage

```
## S3 method for class 'svms_multiclass'
print(x, ...)
```

Arguments

x	A fitted svms_multiclass object.
...	Unused.

Value

The input object, invisibly.

See Also

Other multiclass: `confusion()`, `predict.svms_multiclass()`, `predict.tsvm_multiclass()`, `print.tsvm_multiclass()`

Examples

```
set.seed(46)
x <- rbind(
  matrix(rnorm(8, -2, 0.2), ncol = 2),
  matrix(rnorm(8, 0, 0.2), ncol = 2),
  matrix(rnorm(8, 2, 0.2), ncol = 2)
)
y <- factor(rep(c("a", "b", "c"), each = 4))
print(svms(x, y, kernel = "linear", max_passes = 2, max_iter = 100))
```

---

print.tsvm_multiclass *Print a Multiclass Twin SVM*

Description

Print a Multiclass Twin SVM

Usage

```
## S3 method for class 'tsvm_multiclass'
print(x, ...)
```

Arguments

x	A fitted `tsvm_multiclass` object.
...	Unused.

Value

The input object, invisibly.

See Also

Other multiclass: `confusion()`, `predict.svms_multiclass()`, `predict.tsvm_multiclass()`, `print.svms_multiclass()`

Examples

```
set.seed(41)
x <- rbind(
  matrix(rnorm(20, -2, 0.2), ncol = 2),
  matrix(rnorm(20, 0, 0.2), ncol = 2),
  matrix(rnorm(20, 2, 0.2), ncol = 2)
)
y <- factor(rep(c("a", "b", "c"), each = 10))
print(tsvm(x, y, kernel = "linear"))
```

`resample_accuracy` *Accuracy and Its Spread over Repeated Random Splits*

Description

Evaluates a classifier by repeated random holdout: the data are split into training and test sets `reps` times, the model is refitted on each training set, and test accuracy is recorded. Reporting the mean **together with its between-split standard deviation and standard error** turns a single accuracy number into an estimate with a stated uncertainty, so that differences between methods can be read against the noise rather than taken at face value.

Usage

```
resample_accuracy(
  x,
  y,
  model = c("both", "tsvm", "svms"),
  reps = 50L,
  prop = 0.7,
  seed = NULL,
  ...
)
```

Arguments

`x`	Numeric matrix or data frame of predictors.
`y`	Response factor with at least two classes.
`model`	Which classifier(s) to evaluate: `"both"` (the default, `tsvm()` and `svms()` on the same splits), `"tsvm"`, or `"svms"`.
`reps`	Number of random splits (at least 2; the spread is estimated across them).
`prop`	Proportion of observations used for training in each split, between 0 and 1.
`seed`	Optional integer seed. Set it for reproducible splits; because the splits are fixed before any model is fitted, the comparison is stable even though the SMO solver in `svms()` itself draws random numbers.
`...`	Further arguments passed to the fitter(s), e.g. `kernel`, `gamma`, `cost` (standard SVM), or `c1`, `c2`, `method` (twin SVM). Each argument is forwarded only to the fitter(s) that accept it, so a single call such as `kernel = "rbf", gamma = 1` works for `model = "both"`.

Details

The splits are drawn once, up front, and shared by every model, so when `model = "both"` the twin SVM and the standard SVM are compared on identical training and test sets (a paired comparison). Splits are stratified by class, so each class keeps roughly its overall proportion in both parts.

Value

An object of class `resample_accuracy`, a list with

`summary` a data frame with one row per model giving `mean`, `sd`, `se` and `n` of the test accuracy;

`accuracy` a long data frame of the per-split accuracies (`model`, `rep`, `accuracy`);

`reps`, `prop`, `models`, `call` the settings used.

The plot() method draws the accuracy distributions as boxplots.

Examples

```
set.seed(1)
dat <- gen_moons(120, noise = 0.15)
rs <- resample_accuracy(dat$x, dat$y, model = "both",
                        reps = 10, kernel = "rbf", gamma = 1, seed = 1)
rs                 # mean, sd and se per model
plot(rs)           # accuracy spread as boxplots
```

---

svms *Fit a Standard C-SVC Support Vector Machine*

Description

Fits a C-SVC support vector machine with a Platt SMO solver. With two classes this uses the validated binary path. With three or more classes, the function fits one binary SVM for each class pair and predicts by majority vote. Multiclass ties are resolved by choosing the class that appears first in the factor level order.

Usage

```
svms(
  x,
  y,
  kernel = c("linear", "rbf", "poly"),
  cost = 1,
  gamma = NULL,
  degree = 3,
  coef0 = 1,
  tol = 0.001,
  max_passes = 10L,
  max_iter = 10000L
)
```

Arguments

x	Numeric matrix or data frame of predictors.
y	Response with at least two classes. In the binary path, level 1 is the negative class and level 2 is the positive class.
kernel	Kernel name: "linear", "rbf", or "poly".
cost	Positive C-SVC cost parameter.
gamma	Kernel scale. Defaults to 1 / ncol(x).
degree	Polynomial degree.
coef0	Polynomial offset.
tol	SMO tolerance.
max_passes	Maximum consecutive passes without alpha changes.
max_iter	Maximum SMO iterations.

Value

A fitted svms object for two classes, or a svms_multiclass object for three or more classes.

Examples

```
set.seed(1)
dat <- gen_moons(40, noise = 0.1)
fit <- svms(dat$x, dat$y, kernel = "linear", cost = 1)
predict(fit, dat$x[1:3, ])
```

---

tsvm *Fit a Twin Support Vector Machine*

Description

Fits a twin support vector machine. With two classes this uses the validated binary twin-SVM path: level 1 of y is class B, level 2 is class A, plane 1 is close to class A, and plane 2 is close to class B. With three or more classes, the function fits one binary twin SVM for each class pair and predicts by majority vote. Multiclass ties are resolved by choosing the class that appears first in the factor level order.

Usage

```
tsvm(
  x,
  y,
  method = c("ls", "twin"),
  kernel = c("linear", "rbf", "poly"),
  c1 = 1,
  c2 = 1,
```

```
  gamma = NULL,
  degree = 3,
  coef0 = 1,
  eps = 1e-06
)
```

Arguments

x	Numeric matrix or data frame of predictors.
y	Response with at least two classes.
method	Twin-SVM method. "ls" fits least-squares twin SVM; "twin" fits the original box-constrained dual formulation.
kernel	Kernel name.
c1, c2	Positive regularization parameters.
gamma	Kernel scale. Defaults to 1 / ncol(x).
degree	Polynomial degree.
coef0	Polynomial offset.
eps	Ridge term added to every linear solve.

Value

A fitted tsvm object for two classes, or a tsvm_multiclass object for three or more classes.

References

Jayadeva, Khemchandani, R., and Chandra, S. (2007). Twin support vector machines for pattern classification. *IEEE Transactions on Pattern Analysis and Machine Intelligence*, 29(5), 905-910.

Kumar, M. A. and Gopal, M. (2009). Least squares twin support vector machines for pattern classification. *Expert Systems with Applications*, 36(4), 7535-7543.

Examples

```
set.seed(3)
dat <- gen_moons(50, noise = 0.05)
fit <- tsvm(dat$x, dat$y)
predict(fit, dat$x[1:4, ])
```

---

twomoons *Example Two-Moons Data*

Description

A small two-class two-moons data set for examples and tests.

Usage

```
data(twomoons)
```

Format

A data frame with 120 rows and 3 variables:

x1 First coordinate.

x2 Second coordinate.

y Two-class factor with levels `B` and `A`.

Examples

```
data(twomoons)
str(twomoons)
```

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