

# Package ‘dcsvm’

January 10, 2025

**Type** Package

**Title** Density Convoluted Support Vector Machines

**Version** 0.0.1

**Date** 2025-01-08

**Description** Implements an efficient algorithm for solving sparse-penalized support vector machines with kernel density convolution. This package is designed for high-dimensional classification tasks, supporting lasso (L1) and elastic-net penalties for sparse feature selection and providing options for tuning kernel bandwidth and penalty weights. The ‘dcsvm’ is applicable to fields such as bioinformatics, image analysis, and text classification, where high-dimensional data commonly arise. Learn more about the methodology and algorithm at Wang, Zhou, Gu, and Zou (2023) <[doi:10.1109/TIT.2022.3222767](https://doi.org/10.1109/TIT.2022.3222767)>.

**Depends** Matrix

**Imports** grDevices, graphics, methods, stats

**License** GPL-2

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dcsvm-package	<i>Density-Convolved Support Vector Machines</i>
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## Description

This package provides tools to perform density-convolved support vector machine (DCSVM) modeling for high-dimensional data classification.

## Details

This package implements the density-convolved SVM for high-dimensional classification.

Package:	dcsvm
Type:	Package
Version:	0.0.1
Date:	2025-01-08
License:	GPL-2

The package `dcsvm` contains five main functions:

- `dcsvm`
- `cv.dcsvm`
- `coef.dcsvm`
- `plot.dcsvm`
- `plot.cv.dcsvm`

## Author(s)

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## References

Wang, B., Zhou, L., Gu, Y., and Zou, H. (2023) *Density-Convolved Support Vector Machines for High-Dimensional Classification*, *IEEE Transactions on Information Theory*, Vol. 69(4), 2523-2536,

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coef.cv.dcsvm	<i>Compute Coefficients from a "cv.dcsvm" Object</i>
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---

### Description

Computes the coefficients at specified lambda values for a cv.dcsvm object.

### Usage

```
## S3 method for class 'cv.dcsvm'
coef(object, s = c("lambda.1se", "lambda.min"), ...)
```

### Arguments

object	A fitted <a href="#">cv.dcsvm</a> object, obtained by conducting cross-validation on the sparse density-convoluted SVM model.
s	Value(s) of the L1 tuning parameter lambda for computing coefficients. Default is "lambda.1se", the largest lambda value achieving a cross-validation error within one standard error of the minimum. Alternatively, "lambda.min" corresponds to the lambda incurring the least cross-validation error. s can also be numeric, specifying the value(s) to use.
...	Other arguments that can be passed to <a href="#">dcsvm</a> .

### Details

Compute Coefficients from a "cv.dcsvm" Object

Computes coefficients at chosen values of lambda from the [cv.dcsvm](#) object.

This function computes the coefficients for lambda values suggested by cross-validation.

### Value

The returned object depends on the choice of s and any additional arguments passed to the [dcsvm](#) method.

### See Also

[cv.dcsvm](#) and [predict.cv.dcsvm](#) methods.

### Examples

```
data(colon)
colon$x <- colon$x[,1:100] # Use only the first 100 columns for this example
set.seed(1)
cv <- cv.dcsvm(colon$x, colon$y, lam2=1, nolds=5)
c1 <- coef(cv, s="lambda.1se")
```

coef.dcsvm

*Compute Coefficients for Sparse Density-Convolved SVM***Description**

Computes the coefficients or indices of nonzero coefficients at specified lambda values from a fitted dcsvm model.

**Usage**

```
## S3 method for class 'dcsvm'
coef(object, s = NULL, type = c("coefficients", "nonzero"), ...)
```

**Arguments**

object	A fitted <a href="#">dcsvm</a> object.
s	Value(s) of the L1 tuning parameter lambda for computing coefficients. Default is the entire lambda sequence obtained by <a href="#">dcsvm</a> .
type	"coefficients" or "nonzero"? "coefficients" computes the coefficients at given values for s; "nonzero" returns a list of the indices of the nonzero coefficients for each value of s. Default is "coefficients".
...	Not used. Other arguments to predict.

**Details**

Compute Coefficients for Sparse Density-Convolved SVM

Computes the coefficients or returns the indices of nonzero coefficients at chosen values of lambda from a fitted [dcsvm](#) object.

s is the vector of lambda values at which predictions are requested. If s is not in the lambda sequence used for fitting the model, the coef function uses linear interpolation. The new values are interpolated using a fraction of coefficients from both left and right lambda indices.

**Value**

Either the coefficients at the requested values of lambda, or a list of the indices of the nonzero coefficients for each lambda.

**See Also**

[predict.dcsvm](#)

**Examples**

```
data(colon)
fit <- dcsvm(colon$x, colon$y, lam2=1)
c1 <- coef(fit, type="coefficients", s=c(0.1, 0.005))
c2 <- coef(fit, type="nonzero")
```

---

`colon`*Simplified Gene Expression Data from Alon et al. (1999)*

---

**Description**

This dataset contains 62 colon tissue samples with 2000 gene expression levels. Among these samples, 40 are tumor tissues (coded as 1) and 22 are normal tissues (coded as -1).

**Usage**

```
data(colon)
```

**Details**

Simplified Gene Expression Data from Alon et al. (1999)

Gene expression data (2000 genes for 62 samples) from a DNA microarray experiment of colon tissue samples (Alon et al., 1999).

**Value**

A list with the following elements:

- |                |                                                                                                                                                                                   |
|----------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>x</code> | A matrix of 62 rows and 2000 columns representing the gene expression levels of 62 colon tissue samples. Each row corresponds to a sample, and each column corresponds to a gene. |
| <code>y</code> | A numeric vector of length 62 representing the tissue type (1 for tumor; -1 for normal).                                                                                          |

**Source**

The data were introduced in Alon et al. (1999).

**References**

Alon, U., Barkai, N., Notterman, D.A., Gish, K., Ybarra, S., Mack, D., and Levine, A.J. (1999). "Broad patterns of gene expression revealed by clustering analysis of tumor and normal colon tissues probed by oligonucleotide arrays," *Proceedings of the National Academy of Sciences*, **96**(12), 6745–6750.

**Examples**

```
# Load the dcsvm library
library(dcsvm)

# Load the dataset
data(colon)

# Check the dimensions of the data
```

```
dim(colon$x)

# Count the number of samples in each class
sum(colon$y == -1)
sum(colon$y == 1)
```

---

cv.dcsvm

*Cross-Validation for Sparse Density-Convolved SVM*


---

## Description

Performs cross-validation for the sparse density-convolved SVM to estimate the optimal tuning parameter `lambda`.

## Usage

```
cv.dcsvm(x, y, lambda = NULL, hval = 1,
  pred.loss = c("misclass", "loss"), nfolds = 5, foldid, ...)
```

## Arguments

<code>x</code>	A matrix of predictors, i.e., the <code>x</code> matrix used in <a href="#">dcsvm</a> .
<code>y</code>	A vector of binary class labels, i.e., the <code>y</code> used in <a href="#">dcsvm</a> .
<code>lambda</code>	Default is <code>NULL</code> , and the sequence generated by <a href="#">dcsvm</a> is used. User can also provide a new <code>lambda</code> sequence for cross-validation.
<code>hval</code>	The bandwidth parameter for kernel smoothing. Default is 1.
<code>pred.loss</code>	"misclass" for classification error, "loss" for the density-convolved SVM loss.
<code>nfolds</code>	The number of folds. Default is 5. The allowable range is from 3 to the sample size. Larger <code>nfolds</code> increases computational time.
<code>foldid</code>	An optional vector with values between 1 and <code>nfolds</code> , representing the fold indices for each observation. If supplied, <code>nfolds</code> can be missing.
<code>...</code>	Other arguments that can be passed to <a href="#">dcsvm</a> .

## Details

Cross-Validation for Sparse Density-Convolved SVM

Conducts a `k`-fold cross-validation for [dcsvm](#) and returns the suggested values of the L1 parameter `lambda`.

This function runs [dcsvm](#) on the sparse density-convolved SVM by excluding each fold in turn, then computes the mean cross-validation error and standard deviation. It is adapted from the `cv` functions in the `gcdnet` and `glmnet` packages.

**Value**

A `cv.dcsvm` object is returned, which includes the cross-validation fit:

<code>lambda</code>	The lambda sequence used in <code>dcsvm</code> .
<code>cvm</code>	A vector of length <code>length(lambda)</code> for the mean cross-validated error.
<code>cvsd</code>	A vector of length <code>length(lambda)</code> for estimates of standard error of <code>cvm</code> .
<code>cvupper</code>	The upper curve: <code>cvm + cvsd</code> .
<code>cvlower</code>	The lower curve: <code>cvm - cvsd</code> .
<code>nzero</code>	Number of non-zero coefficients at each lambda.
<code>name</code>	"Mis-classification error", for plotting purposes.
<code>dcsvm.fit</code>	A fitted <code>dcsvm</code> object using the full data.
<code>lambda.min</code>	The lambda incurring the minimum cross-validation error <code>cvm</code> .
<code>lambda.1se</code>	The largest value of lambda such that error is within one standard error of the minimum.
<code>cv.min</code>	The minimum cross-validation error.
<code>cv.1se</code>	The cross-validation error associated with <code>lambda.1se</code> .

**See Also**

`dcsvm`, `plot.cv.dcsvm`, `predict.cv.dcsvm`, and `coef.cv.dcsvm` methods.

**Examples**

```
data(colon)
colon$x <- colon$x[,1:100] # Use only the first 100 columns for this example
n <- nrow(colon$x)
set.seed(1)
id <- sample(n, trunc(n / 3))
cvfit <- cv.dcsvm(colon$x[-id, ], colon$y[-id], lam2=1, nolds=5)
plot(cvfit)
predict(cvfit, newx=colon$x[id, ], s="lambda.min")
```

**Description**

Fits the density-convolved support vector machine (DCSVM) through kernel density convolutions.

**Usage**

```

dcsvm(
  x,
  y,
  nlambda = 100,
  lambda.factor = ifelse(nobs < nvars, 0.01, 1e-04),
  lambda = NULL,
  lam2 = 0,
  kern = c("gaussian", "uniform", "epanechnikov"),
  hval = 1,
  pf = rep(1, nvars),
  pf2 = rep(1, nvars),
  exclude,
  dfmax = nvars + 1,
  pmax = min(dfmax * 1.2, nvars),
  standardize = TRUE,
  eps = 1e-08,
  maxit = 1e+06,
  istrong = TRUE
)

```

**Arguments**

<code>x</code>	A numeric matrix with $N$ rows and $p$ columns representing predictors. Each row corresponds to an observation, and each column corresponds to a variable.
<code>y</code>	A numeric vector of length $N$ representing binary responses. Elements must be either -1 or 1.
<code>nlambda</code>	Number of lambda values in the sequence. Default is 100.
<code>lambda.factor</code>	Ratio of the smallest to the largest lambda in the sequence: <code>lambda.factor = min(lambda) / max(lambda)</code> . The default value is 0.0001 if $N \geq p$ or 0.01 if $N < p$ . Takes no effect if a lambda sequence is specified.
<code>lambda</code>	An optional user-specified sequence of lambda values. If <code>lambda = NULL</code> (default), the sequence is computed based on <code>nlambda</code> and <code>lambda.factor</code> . The program automatically sorts user-defined lambda sequences in decreasing order.
<code>lam2</code>	Users may tune $\lambda_2$ , which controls the L2 regularization strength. Default is 0 (lasso).
<code>kern</code>	Type of kernel method for smoothing. Options are "gaussian", "uniform", and "epanechnikov". Default is "epanechnikov".
<code>hval</code>	The bandwidth parameter for kernel smoothing. Default is 1.
<code>pf</code>	A numeric vector of length $p$ representing the L1 penalty weights for each coefficient. A common choice is $(\beta + 1/n)^{-1}$ , where $n$ is the sample size and $\beta$ is obtained from L1 DCSVM or enet DCSVM. Default is 1 for all predictors.
<code>pf2</code>	A numeric vector of length $p$ representing the L2 penalty weights for each coefficient. A value of 0 indicates no L2 shrinkage. Default is 1 for all predictors.
<code>exclude</code>	Indices of predictors to exclude from the model. Equivalent to assigning an infinite penalty factor. Default is none.



dfmax	Maximum number of nonzero coefficients allowed in the model. Default is $p+1$ . Useful for large $p$ when a partial path is acceptable.
pmax	Maximum number of variables allowed to ever be nonzero during the computation. Default is $\min(\text{dfmax} * 1.2, p)$ .
standardize	Logical indicating whether predictors should be standardized to unit variance. Default is TRUE. Note that predictors are always centered.
eps	Convergence threshold. The algorithm stops when $4 \max_j (\beta_j^{\text{new}} - \beta_j^{\text{old}})^2$ is less than eps. Default is $1e-8$ .
maxit	Maximum number of iterations allowed. Default is $1e6$ . Consider increasing maxit if the algorithm does not converge.
istrong	Logical indicating whether to use the strong rule for faster computation. Default is TRUE.

### Value

An object of class dcsvm containing the following components:

b0	Intercept values for each lambda.
beta	Sparse matrix of coefficients for each lambda. Use <code>as.matrix()</code> to convert.
df	Number of nonzero coefficients for each lambda.
dim	Dimensions of the coefficient matrix.
lambda	Sequence of lambda values used.
npasses	Total number of iterations across all lambda values.
jerr	Warnings and errors. 0 if no errors.
call	The matched call.

### See Also

`print.dcsvm`, `predict.dcsvm`, `coef.dcsvm`, `plot.dcsvm`, and `cv.dcsvm`.

### Examples

```
# Load the data
data(colon)
# Fit the elastic-net penalized DCSVM with lambda2 to be 1
fit <- dcsvm(colon$x, colon$y, lam2 = 1)
print(fit)
# Coefficients at some lambda value
c1 <- coef(fit, s = 0.005)
# Make predictions
predict(fit, newx = colon$x[1:10, ], s = c(0.01, 0.005))
```

---

`plot.cv.dcsvm`*Plot the Cross-Validation Curve of Sparse Density-Convolved SVM*

---

**Description**

Depicts the cross-validation curves for the sparse density-convoluted SVM.

**Usage**

```
## S3 method for class 'cv.dcsvm'  
plot(x, sign.lambda, ...)
```

**Arguments**

<code>x</code>	A fitted <code>cv.dcsvm</code> object.
<code>sign.lambda</code>	Specifies whether to plot against $\log(\lambda)$ (default) or its negative if <code>sign.lambda = -1</code> .
<code>...</code>	Other graphical parameters to plot.

**Details**

Plot the Cross-Validation Curve of Sparse Density-Convolved SVM

Plots the cross-validation curve against a function of lambda values, including upper and lower standard deviation curves.

This function visualizes the cross-validation curves for a `cv.dcsvm` object, which plots the relationship between lambda values and cross-validation error.

**Value**

No return value, only called for plots.

**See Also**

[cv.dcsvm](#).

**Examples**

```
data(colon)  
colon$x <- colon$x[,1:100] # Use only the first 100 columns for this example  
set.seed(1)  
cv <- cv.dcsvm(colon$x, colon$y, lam2=1, nolds=5)  
plot(cv)
```

---

plot.dcsvm *Plot Coefficients for Sparse Density-Convolutd SVM*

---

### Description

Plots the solution paths as a coefficient profile plot for a fitted dcsvm model.

### Usage

```
## S3 method for class 'dcsvm'
plot(x, xvar = c("norm", "lambda"), color = FALSE, label = FALSE, ...)
```

### Arguments

x	A fitted <code>dcsvm</code> model.
xvar	Specifies the X-axis. If <code>xvar == "norm"</code> , plots against the L1-norm of the coefficients; if <code>xvar == "lambda"</code> , plots against the log-lambda sequence.
color	If TRUE, plots the curves with rainbow colors; otherwise, with gray colors (default).
label	If TRUE, labels the curves with variable sequence numbers. Default is FALSE.
...	Other graphical parameters to plot.

### Details

Plot Coefficients for Sparse Density-Convolutd SVM

Plots the solution paths for a fitted `dcsvm` object.

This function generates a coefficient profile plot showing the solution paths of the sparse density-convolutd SVM.

### Value

No return value, only called for plots.

### See Also

`print.dcsvm`, `predict.dcsvm`, `coef.dcsvm`, `plot.dcsvm`, and `cv.dcsvm`.

### Examples

```
data(colon)
fit <- dcsvm(colon$x, colon$y)
oldpar <- par(mfrow = c(1,3)) #changes par() and stores original par()
# Plots against the L1-norm of the coefficients
plot(fit)
# Plots against the log-lambda sequence
plot(fit, xvar="lambda", label=TRUE)
# Plots with colors
```

```
plot(fit, color=TRUE)
# Reset to user's option
par(oldpar)
```

---

predict.cv.dcsvm      *Make Predictions from a "cv.dcsvm" Object*

---

### Description

Predicts class labels for new data based on the cross-validated lambda values from a `cv.dcsvm` object.

### Usage

```
## S3 method for class 'cv.dcsvm'
predict(object, newx, s = c("lambda.1se", "lambda.min"), ...)
```

### Arguments

<code>object</code>	A fitted <code>cv.dcsvm</code> object.
<code>newx</code>	A matrix of new values for <code>x</code> at which predictions are to be made. Must be a matrix. See documentation for <code>predict.dcsvm</code> .
<code>s</code>	Value(s) of the L1 tuning parameter <code>lambda</code> for making predictions. Default is <code>s = "lambda.1se"</code> saved in the <code>cv.dcsvm</code> object. An alternative choice is <code>s = "lambda.min"</code> . <code>s</code> can also be numeric, representing the specific value(s) to use.
<code>...</code>	Not used. Other arguments to <code>predict</code> .

### Details

Make Predictions from a "cv.dcsvm" Object

This function predicts the class labels of new observations using the sparse density-convoluted SVM at the lambda values suggested by `cv.dcsvm`.

This function uses the cross-validation results to make predictions. It is adapted from the `predict.cv` function in the `glmnet` and `gcdnet` packages.

### Value

Predicted class labels or fitted values, depending on the choice of `s` and any arguments passed to the `dcsvm` method.

### See Also

`cv.dcsvm`, and `coef.cv.dcsvm` methods.

**Examples**

```
data(colon)
colon$x <- colon$x[ , 1:100] # Use only the first 100 columns for this example
set.seed(1)
cv <- cv.dcsvm(colon$x, colon$y, lam2=1, nfolds=5)
predict(cv$dcsvm.fit, newx=colon$x[2:5, ],
        s=cv$lambda.1se, type="class")
```

---

predict.dcsvm

*Make Predictions for Sparse Density-Convolved SVM*


---

**Description**

Predicts binary class labels or fitted values for a `dcsvm` model using new data.

**Usage**

```
## S3 method for class 'dcsvm'
predict(object, newx, s = NULL, type = c("class", "link"), ...)
```

**Arguments**

<code>object</code>	A fitted <code>dcsvm</code> object.
<code>newx</code>	A matrix of new values for <code>x</code> at which predictions are to be made. Note that <code>newx</code> must be a matrix; vectors or other formats are not accepted.
<code>s</code>	Value(s) of the L1 tuning parameter <code>lambda</code> for computing coefficients. Default is the entire <code>lambda</code> sequence obtained by <code>dcsvm</code> .
<code>type</code>	"class" or "link"? "class" produces the predicted binary class labels, while "link" returns the fitted values. Default is "class".
<code>...</code>	Not used. Other arguments to <code>predict</code> .

**Details****Make Predictions for Sparse Density-Convolved SVM**

This function predicts the binary class labels or the fitted values of a `dcsvm` object.

`s` represents the new `lambda` values for making predictions. If `s` is not part of the original `lambda` sequence generated by `dcsvm`, `predict.dcsvm` uses linear interpolation to compute predictions by combining adjacent `lambda` values in the original sequence. This functionality is adapted from the `predict` methods in the `glmnet` and `gcdnet` packages.

**Value**

Returns either the predicted class labels or the fitted values, depending on the choice of `type`.

**See Also**[coef.dcsvm](#)**Examples**

```
data(colon)
fit <- dcsvm(colon$x, colon$y, lam2=1)
print(predict(fit, type="class", newx=colon$x[2:5, ]))
```

---

`print.dcsvm`*Print a DCSVM Object*

---

**Description**

Prints a summary of the `dcsvm` object, showing the solution paths.

**Usage**

```
## S3 method for class 'dcsvm'
print(x, digits = max(3, getOption("digits") - 3), ...)
```

**Arguments**

<code>x</code>	A fitted <code>dcsvm</code> object.
<code>digits</code>	Specifies the significant digits to use in the output. Default is <code>max(3, getOption("digits") - 3)</code> .
<code>...</code>	Additional arguments to <code>print</code> .

**Details**

Print a DCSVM Object

Print a summary of the `dcsvm` solution paths.

This function prints a two-column matrix with columns `Df` and `Lambda`. The `Df` column shows the number of nonzero coefficients, and the `Lambda` column displays the corresponding lambda value. It is adapted from the `print` function in the `gcdnet` and `glmnet` packages.

**Value**

A two-column matrix with one column showing the number of nonzero coefficients and the other column showing the lambda values.

**See Also**

`print.dcsvm`, `predict.dcsvm`, `coef.dcsvm`, `plot.dcsvm`, and `cv.dcsvm`.

**Examples**

```
data(colon)
fit <- dcsvm(colon$x, colon$y)
print(fit)
```

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