

# Package ‘bcv’

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**Title** Cross-Validation for the SVD (Bi-Cross-Validation)

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**Description** This package implements methods for choosing the rank of an SVD approximation via cross validation. It provides both Gabriel-style “block” holdouts and Wold-style “speckled” holdouts. Also included is an implementation of the SVDImpute algorithm. For more information about Bi-cross-validation, see Owen & Perry’s 2009 AOAS article (at <http://arxiv.org/abs/0908.2062>) and Perry’s 2009 PhD thesis (at <http://arxiv.org/abs/0909.3052>).

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## R topics documented:

bcv-package . . . . .	2
cv.svd . . . . .	2
impute.svd . . . . .	5
plot.cvsvd . . . . .	6
print.cvsvd . . . . .	7
summary.cvsvd . . . . .	8

<b>Index</b>	<b>10</b>
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bcv-package

*Cross-Validation for the SVD (Bi-Cross-Validation)*

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### Description

This package implements methods for choosing the rank of an SVD approximation via cross validation. It provides both Gabriel-style "block" holdouts and Wold-style "speckled" holdouts. Also included is an implementation of the SVDImpute algorithm.

### Details

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Basic usage is to call either [cv.svd.gabriel](#) or [cv.svd.wold](#).

### Author(s)

Patrick O. Perry <patperry@gmail.com>

### See Also

[impute.svd](#), [cv.svd.gabriel](#), [cv.svd.wold](#), [plot.cvsvd](#), [print.cvsvd](#) [summary.cvsvd](#)

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cv.svd

*Cross-Validation for choosing the rank of an SVD approximation.*

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### Description

Perform Wold- or Gabriel-style cross-validation for determining the appropriate rank SVD approximation of a matrix.

### Usage

```
cv.svd.gabriel(x, krow = 2, kcol = 2,  
              maxrank = floor(min(n - n/krow, p - p/kcol)))  
  
cv.svd.wold(x, k = 5, maxrank = 20, tol = 1e-4, maxiter = 20)
```

**Arguments**

x	the matrix to cross-validate.
k	the number of folds (for Wold-style CV).
krow	the number of row folds (for Gabriel-style CV).
kcol	the number of column folds (for Gabriel-style CV).
maxrank	the maximum rank to cross-validate up to.
tol	the convergence tolerance for <a href="#">impute.svd</a> .
maxiter	the maximum number of iterations for <a href="#">impute.svd</a> .

**Details**

These functions are for cross-validating the SVD of a matrix. They assume a model  $X = U D V' + E$  with the terms being signal and noise, and try to find the best rank to truncate the SVD of  $x$  at for minimizing prediction error. Here, prediction error is measured as sum of squares of residuals between the truncated SVD and the signal part.

For both types of cross-validation, in each replicate we leave out part of the matrix, fit an SVD approximation to the left-in part, and measure prediction error on the left-out part.

In Wold-style cross-validation, the holdout set is "speckled", a random set of elements in the matrix. The missing elements are predicted using [impute.svd](#).

In Gabriel-style cross-validation, the holdout set is "blocked". We permute the rows and columns of the matrix, and leave out the lower-right block. We use a modified Schur-complement to predict the held-out block. In Gabriel-style, there are  $krow * kcol$  total folds.

**Value**

call	the function call
msep	the mean square error of prediction (MSEP); this is a matrix whose columns contain the mean square errors in the predictions of the holdout sets for ranks 0, 1, ..., maxrank across the different replicates.
maxrank	the maximum rank for which prediction error is estimated; this is equal to $nrow(msep)+1$ .
krow	the number of row folds (for Gabriel-style only).
kcol	the number of column folds (for Gabriel-style only).
rowsets	the partition of rows into krow holdout sets (for Gabriel-style only).
colsets	the partition of the columns into kcol holdout sets (for Gabriel-style only).
k	the number of folds (for Wold-style only).
sets	the partition of indices into k holdout sets (for Wold-style only).

**Note**

Gabriel's version of cross-validation was for leaving out a single element of the matrix, which corresponds to n-by-p-fold. Owen and Perry generalized Gabriel's idea to larger holdouts, showing that 2-by-2-fold cross-validation often works better.

Wold's original version of cross-validation did not use the EM algorithm to estimate the SVD. He recommend using the NIPALS algorithm instead, which has since faded into obscurity.

Wold-style cross-validation takes a lot more computation than Gabriel-style. The `maxrank`, `tol`, and `maxiter` have been chosen to give up some accuracy in the name of expediency. They may need to be adjusted to get the best results.

**Author(s)**

Patrick O. Perry

**References**

Gabriel, K.R. (2002). Le biplot–outil d'exploration de données multidimensionnelles. *J. Roy. Stat. Soc. Series B* **40** 186–196.

Owen, A.B. and Perry, P.O. (2009). Bi-cross-validation of the SVD and the non-negative matrix factorization. *Annals of Applied Statistics* **3**(2) 564–594.

Wold, S. (1978). Cross-validatory estimation of the number of components in factor and principal components models. *Technometrics* **20**(4) 397–405.

**See Also**

[impute.svd](#), [plot.cvsvd](#), [print.cvsvd](#) [summary.cvsvd](#)

**Examples**

```
# generate a rank-2 matrix plus noise
n <- 50; p <- 20; k <- 2
u <- matrix( rnorm( n*k ), n, k )
v <- matrix( rnorm( p*k ), p, k )
e <- matrix( rnorm( n*p ), n, p )
x <- u %*% t(v) + e

# perform 5-fold Wold-style cross-validation
(cvw <- cv.svd.wold( x, 5, maxrank=10 ))

# perform (2,2)-fold Gabriel-style cross-validation
(cvg <- cv.svd.gabriel( x, 2, 2, maxrank=10 ))
```

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`impute.svd`*Missing value imputation via the SVDImpute algorithm*

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**Description**

Given a matrix with missing values, impute the missing entries using a low-rank SVD approximation estimated by the EM algorithm.

**Usage**

```
impute.svd(x, k = min(n, p), tol = max(n, p) * 1e-10, maxiter = 100)
```

**Arguments**

<code>x</code>	a matrix to impute the missing entries of.
<code>k</code>	the rank of the SVD approximation.
<code>tol</code>	the convergence tolerance for the EM algorithm.
<code>maxiter</code>	the maximum number of EM steps to take.

**Details**

Impute the missing values of `x` as follows: First, initialize all NA values to the column means, or 0 if all entries in the column are missing. Then, until convergence, compute the first `k` terms of the SVD of the completed matrix. Replace the previously missing values with their approximations from the SVD, and compute the RSS between the *non-missing* values and the SVD.

Declare convergence if  $\text{abs}(\text{rss0} - \text{rss1}) / (.Machine\$double.eps + \text{rss1}) < \text{tol}$ , where `rss0` and `rss1` are the RSS values computed from successive iterations. Stop early after `maxiter` iterations and issue a warning.

**Value**

<code>x</code>	the completed version of the matrix.
<code>rss</code>	the sum of squares between the SVD approximation and the non-missing values in <code>x</code> .
<code>iter</code>	the number of EM iterations before algorithm stopped.

**Author(s)**

Patrick O. Perry

**References**

Troyanskaya, O., Cantor, M., Sherlock, G., Brown, P., Hastie, T., Tibshirani, R., Botstein, D. and Altman, R.B. (2001). Missing value estimation methods for DNA microarrays. *Bioinformatics* **17**(6), 520–525.

**See Also**[cv.svd.wold](#)**Examples**

```
# Generate a matrix with missing entries
n <- 20
p <- 10
u <- rnorm( n )
v <- rnorm( p )
xfull <- u %*% rbind( v ) + rnorm( n*p )
miss <- sample( seq_len( n*p ), n )
x      <- xfull
x[miss] <- NA

# impute the missing entries with a rank-1 SVD approximation
xhat <- impute.svd( x, 1 )$x

# compute the prediction error for the missing entries
sum( ( xfull-xhat )^2 )
```

plot.cvsvd

*Plot the Result of an SVD Cross-Validation***Description**

Plot the result of [cv.svd.gabriel](#) or [cv.svd.wold](#), optionally with error bars.

**Usage**

```
## S3 method for class 'cvsvd'
plot(x, errorbars = TRUE, add = FALSE,
     xlab = "Rank", ylab = "Mean Sq. Prediction Error",
     col = "blue", col.errorbars = "gray50", ...)
```

**Arguments**

x	the result of a <a href="#">cv.svd.gabriel</a> or <code>link{cv.svd.wold}</code> computation.
errorbars	indicates whether or not to add error bars.
col	the color to use for showing prediction error.
col.errorbars	the color to use for the error bars.
add	indicates whether or not to add to the current plot.
xlab	the label for the x axis.
ylab	the label for the y axis.
...	additional arguments for plot.

**Details**

Plot the result of [cv.svd.gabriel](#) or [cv.svd.wold](#). This plots a the estimated prediction error as a function of rank, optionally with error bars.

If add is TRUE, the current plot is not cleared.

**Author(s)**

Patrick O. Perry

**See Also**

[cv.svd.gabriel](#), [cv.svd.wold](#), [print.cvsvd](#) [summary.cvsvd](#)

**Examples**

```
# generate a rank-2 matrix plus noise
n <- 50; p <- 20; k <- 2
u <- matrix( rnorm( n*k ), n, k )
v <- matrix( rnorm( p*k ), p, k )
e <- matrix( rnorm( n*p ), n, p )
x <- u %*% t(v) + e

# perform 5-fold Wold-style cross-validation
cvw <- cv.svd.wold( x, 5, maxrank=10 )

# perform (2,2)-fold Gabriel-style cross-validation
cvg <- cv.svd.gabriel( x, 2, 2, maxrank=10 )

# plot the results
par( mfrow=c(2,1) )
plot( cvw, main="Wold-style CV" )
plot( cvg, main="Gabriel-style CV" )
```

---

print.cvsvd

*Print the Result of an SVD Cross-Validation*


---

**Description**

Print the result of [cv.svd.gabriel](#) or [cv.svd.wold](#).

**Usage**

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

**Arguments**

x                    the result of a `cv.svd.gabriel` or `cv.svd.wold` computation.  
digits                the digits of precision to show in the output.  
...                    additional arguments to print.

**Details**

Print a table of the estimated prediction errors and the standard errors of the estimate. Put an asterisk (\*) next to the minimum and a plus (+) next to the "one standard error rule" choice.

**Author(s)**

Patrick O. Perry

**See Also**

[cv.svd.gabriel](#), [cv.svd.wold](#), [plot.cvsvd.summary.cvsvd](#)

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summary.cvsvd

*Summarize the Result of an SVD Cross-Validation*

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**Description**

Summarize the result of `cv.svd.gabriel` or `cv.svd.wold`.

**Usage**

```
## S3 method for class 'cvsvd'  
summary(object, ...)
```

**Arguments**

object                the result of a `cv.svd.gabriel` or `cv.svd.wold` computation.  
...                    additional arguments to `summary`.

**Details**

Print a table of the estimated prediction errors and the standard errors of the estimate. Put an asterisk (\*) next to the minimum and a plus (+) next to the "one standard error rule" choice.

**Value**

<code>nfolds</code>	the number of cross-validation folds
<code>maxrank</code>	the maximum rank for which prediction error is estimated.
<code>msep.mean</code>	the average mean square error of prediction (MSEP) accross all folds for ranks 0, 1, ..., <code>maxrank</code> .
<code>msep.se</code>	the standard errors of the <code>msep.mean</code> estimates.
<code>rank.best</code>	the rank with the minimum <code>msep.mean</code> value.
<code>rank.1se</code>	the smallest rank within one standard error of the minimum <code>msep.mean</code> value.

**Author(s)**

Patrick O. Perry

**See Also**

[cv.svd.gabriel](#), [cv.svd.wold](#), [plot.cvsvd](#) [print.cvsvd](#)

# Index

## \*Topic **package**

bcv-package, [2](#)

bcv (bcv-package), [2](#)

bcv-package, [2](#)

cv.svd, [2](#)

cv.svd.gabriel, [2](#), [6–9](#)

cv.svd.wold, [2](#), [6–9](#)

impute.svd, [2–4](#), [5](#)

plot.cvsvd, [2](#), [4](#), [6](#), [8](#), [9](#)

print.cvsvd, [2](#), [4](#), [7](#), [7](#), [9](#)

summary.cvsvd, [2](#), [4](#), [7](#), [8](#), [8](#)