

# Package ‘FastBandChol’

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**Type** Package

**Title** Fast Estimation of a Covariance Matrix by Banding the Cholesky Factor

**Version** 0.1.1

**Author** Aaron Molstad <molst029@umn.edu>

**Maintainer** Aaron Molstad <molst029@umn.edu>

**Description** Fast and numerically stable estimation of a covariance matrix by banding the Cholesky factor using a modified Gram-Schmidt algorithm implemented in RcppArmadillo. See <<http://stat.umn.edu/~molst029>> for details on the algorithm.

**License** GPL-2

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FastBandChol-package    *Fast estimation of covariance matrix by banded Cholesky factor*

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## Description

Fast and numerically stable estimation of covariance matrix by banding the Cholesky factor using a modified Gram-Schmidt algorithm implemented in RcppArmadillo. See <<https://stat.umn.edu/~molst029>> for details on the algorithm.

## Details

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## Author(s)

Aaron Molstad

## References

Rothman, A.J., Levina, E., and Zhu, J. (2010). A new approach to Cholesky-based covariance regularization in high dimensions. *Biometrika*, 97(3):539-550.

## Examples

```
## set sample size and dimension
n = 20
p = 100

## create covariance with AR1 structure
Sigma = matrix(0, nrow=p, ncol=p)
for(l in 1:p){
  for(m in 1:p){
    Sigma[l,m] = .5^(abs(l-m))
  }
}

## simulation Normal data
eo1 = eigen(Sigma)
Sigma.sqrt = eo1$vec%%diag(eo1$val^.5)%*%t(eo1$vec)
X = t(Sigma.sqrt%%matrix(rnorm(n*p), nrow=p, ncol=n))
```

```
## compute estimates
est.sample = banded.sample(X, bandwidth=4)$est
est.chol = banded.chol(X, bandwidth=4)$est
```

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banded.chol	<i>Computes estimate of covariance matrix by banding the Cholesky factor</i>
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### Description

Computes estimate of covariance matrix by banding the Cholesky factor using a modified Gram Schmidt algorithm implemented in RcppArmadillo.

### Usage

```
banded.chol(X, bandwidth, centered = FALSE)
```

### Arguments

<code>X</code>	A data matrix with $n$ rows and $p$ columns. Rows are assumed to be independent realizations from a $p$ -variate distribution with covariance $\Sigma$ .
<code>bandwidth</code>	A positive integer. Must be less than $n - 1$ and $p - 1$ .
<code>centered</code>	Logical. Is data matrix centered? Default is <code>centered = FALSE</code>

### Value

A list with	
<code>est</code>	The estimated covariance matrix.

### Examples

```
## set sample size and dimension
n=20
p=100

## create covariance with AR1 structure
Sigma = matrix(0, nrow=p, ncol=p)
for(l in 1:p){
  for(m in 1:p){
    Sigma[l,m] = .5^(abs(l-m))
  }
}

## simulation Normal data
e01 = eigen(Sigma)
Sigma.sqrt = e01$vec%*%diag(e01$val^.5)%*%t(e01$vec)
```

```
X = t(Sigma.sqrt%%matrix(rnorm(n*p), nrow=p, ncol=n))

## compute estimate
out1 = banded.chol(X, bandwidth=4)
```

---

banded.chol.cv

*Selects bandwidth for Cholesky factorization by cross validation*


---

## Description

Selects bandwidth for Cholesky factorization by k-fold cross validation

## Usage

```
banded.chol.cv(X, bandwidth, folds = 3, est.eval = TRUE, Frob = TRUE)
```

## Arguments

X	A data matrix with $n$ rows and $p$ columns. Rows are assumed to be independent realizations from a $p$ -variate distribution with covariance $\Sigma$ .
bandwidth	A vector of candidate bandwidths. Candidate bandwidths can only positive integers such that the maximum is less than the sample size outside of the $k$ th fold.
folds	The number of folds used for cross validation. Default is <code>folds = 3</code> .
est.eval	Logical: <code>est.eval = TRUE</code> returns a list with both the selected bandwidth and the estimated covariance matrix. <code>est.eval=FALSE</code> returns a list with only the selected bandwidth. The default is <code>est.eval = TRUE</code> .
Frob	Logical: <code>Frob = TRUE</code> uses squared Frobenius norm loss for cross-validation. <code>Frob = FALSE</code> uses operator norm loss. Default is <code>Frob = TRUE</code> .

## Value

a list with	
bandwidth.min	The bandwidth minimizing cross-validation error.
est	The estimated covariance matrix computed with <code>bandwidth=bandwidth.min</code> .

## Examples

```
## set sample size and dimension
n=20
p=100

## create covariance with AR1 structure
Sigma = matrix(0, nrow=p, ncol=p)
for(l in 1:p){
  for(m in 1:p){
```

```

        Sigma[l,m] = .5^(abs(l-m))
      }
    }

## simulation Normal data
eo1 = eigen(Sigma)
Sigma.sqrt = eo1$vec%*%diag(eo1$val^.5)%*%t(eo1$vec)
X = t(Sigma.sqrt%*%matrix(rnorm(n*p), nrow=p, ncol=n))

## perform cross validation
k = 4:7
out1.cv = banded.chol.cv(X, bandwidth=k, folds = 5)

```

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banded.sample

*Computes banded sample covariance matrix*


---

### Description

Estimates a covariance matrix by banding the sample covariance matrix

### Usage

```
banded.sample(X, bandwidth, centered = FALSE)
```

### Arguments

<code>X</code>	A data matrix with $n$ rows and $p$ columns. Rows are assumed to be independent realizations from a $p$ -variate distribution with covariance $\Sigma$ .
<code>bandwidth</code>	A positive integer. Must be less than $p - 1$ .
<code>centered</code>	Logical. Is data matrix centered? Default is <code>centered = FALSE</code>

### Value

A list with	
<code>est</code>	The estimated covariance matrix.

### Examples

```

## set sample size and dimension
n=20
p=100

## create covariance with AR1 structure
Sigma = matrix(0, nrow=p, ncol=p)
for(l in 1:p){
  for(m in 1:p){
    Sigma[l,m] = .5^(abs(l-m))
  }
}

```

```

    }
  }

  ## simulation Normal data
  eo1 = eigen(Sigma)
  Sigma.sqrt = eo1$vec%*%diag(eo1$val^.5)%*%t(eo1$vec)
  X = t(Sigma.sqrt%*%matrix(rnorm(n*p), nrow=p, ncol=n))

  ## compute estimate
  out2 = banded.sample(X, bandwidth=4)

```

---

banded.sample.cv

*Selects bandwidth for sample covariance matrix by cross validation*


---

### Description

Selects bandwidth for sample covariance matrix by k-fold cross validation

### Usage

```
banded.sample.cv(X, bandwidth, folds = 3, est.eval = TRUE, Frob = TRUE)
```

### Arguments

<code>X</code>	A data matrix with $n$ rows and $p$ columns. Rows are assumed to be independent realizations from a $p$ -variate distribution with covariance $\Sigma$ .
<code>bandwidth</code>	A vector of candidate bandwidths. Candidate bandwidths can only positive integers such that the maximum is less than $p - 1$ .
<code>folds</code>	The number of folds used for cross validation. Default is <code>folds = 3</code> .
<code>est.eval</code>	Logical: <code>est.eval = TRUE</code> returns a list with both the selected bandwidth and the estimated covariance matrix. <code>est.eval=FALSE</code> returns a list with only the selected bandwidth. The default is <code>est.eval = TRUE</code> .
<code>Frob</code>	Logical: <code>Frob = TRUE</code> uses squared Frobenius norm loss for cross-validation. <code>Frob = FALSE</code> uses operator norm loss. Default is <code>Frob = TRUE</code> .

### Value

A list with

<code>bandwidth.min</code>	the bandwidth minimizing cv error
<code>est</code>	the sample covariance matrix at <code>bandwidth.min</code>

**Examples**

```
## set sample size and dimension
n=20
p=100

## create covariance with AR1 structure
Sigma = matrix(0, nrow=p, ncol=p)
for(l in 1:p){
  for(m in 1:p){
    Sigma[l,m] = .5^(abs(l-m))
  }
}

## simulation Normal data
eo1 = eigen(Sigma)
Sigma.sqrt = eo1$vec%*%diag(eo1$val^.5)%*%t(eo1$vec)
X = t(Sigma.sqrt%*%matrix(rnorm(n*p), nrow=p, ncol=n))

## perform cross validation
k = 4:7
out2.cv = banded.sample.cv(X, bandwidth=k, folds=5)
```

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