Package ‘onlinePCA’

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Author David Degras [aut, cre], Herve Cardot [ctb]
Maintainer David Degras <ddegrasv@gmail.com>
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Online Principal Component Analysis

Description
Online PCA algorithms using perturbation methods (perturbationR pca), secular equations (secularR pca), incremental PCA (incR pca, incR pca.block, incR pca.rc), and stochastic optimization (bsoipca, cci pca, ghapca, sgapca, snlpca). impute handles missing data with the regression approach of Brand (2002). batchpca performs fast batch (offline) PCA using iterative methods. create.basis, coef2fd, fd2coef respectively create B-spline basis sets for functional data (FD), convert FD to basis coefficients, and convert basis coefficients back to FD. updateMean and updateCovariance update the sample mean and sample covariance.

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Author(s)
David Degras <ddegrasv@gmail.com>

References

### Description

This function performs the PCA of a data matrix or covariance matrix, returning the specified number of principal components (eigenvectors) and eigenvalues.

### Usage

```
batchpca(x, q, center, type = c("data","covariance"), byrow = FALSE)
```

### Arguments

- **x**: data or covariance matrix
- **q**: number of requested PCs
- **center**: optional centering vector for x
- **type**: type of the matrix x
- **byrow**: Are observation vectors stored in rows (TRUE) or in columns (FALSE)?

### Details

The PCA is efficiently computed using the functions `svds` or `eigs_sym` of package `RARPACK`, depending on the argument `type`. An Implicitly Restarted Arnoldi Method (IRAM) is used in the former case and an Implicitly Restarted Lanczos Method (IRLM) in the latter.

The arguments `center` and `byrow` are only in effect if `type` is "data". In this case a scaling factor $1/\sqrt{n}$ (not $1/\sqrt{n-1}$) is applied to $x$ before computing its singular values and vectors, where $n$ is the number of observation vectors stored in $x$.

### Value

A list with components

- **values**: the first $q$ squared singular values of $x$ if type="data"; the first $Q$ eigenvalues if type="covariance".
- **vectors**: the first $q$ PC of $x$.

### References

[http://www.caam.rice.edu/software/ARPACK/](http://www.caam.rice.edu/software/ARPACK/)
Examples

```r
## Not run:
## Simulate data
n <- 1e4
d <- 500
q <- 10
x <- matrix(runif(n*d), n, d)
x <- x %*% diag(sqrt(12*(1:d)))
# The eigenvalues of cov(x) are approximately 1, 2, ..., d
# and the corresponding eigenvectors are approximately
# the canonical basis of R^p
## PCA computation (from fastest to slowest)
system.time(pca1 <- batchpca(scale(x, scale=FALSE), q, byrow=TRUE))
system.time(pca2 <- batchpca(cov(x), q, type="covariance")
system.time(pca3 <- eigen(cov(x), TRUE))
system.time(pca4 <- svd(scale(x/sqrt(n-1), scale=FALSE), 0, q))
system.time(pca5 <- prcomp(x))
## End(Not run)
```

---

### bsoipca

**Block Stochastic Orthononal Iteration (BSOI)**

**Description**

The online PCA algorithm of Mitliagkas et al. (2013) is a block-wise stochastic variant of the classical power-method.

**Usage**

```r
bsoipca(x, q, U, B, center, byrow = FALSE)
```

**Arguments**

- `x` data matrix.
- `q` number of PC to compute.
- `U` matrix of initial PCs in columns (optional).
- `B` size of block updates (optional).
- `center` centering vector (optional).
- `byrow` are the data vectors in `x` stored in rows (TRUE) or columns (FALSE)?
ccipca

Details

The default value of $b$ is $\text{floor}(n/n_{\text{block}})$ with $n$ the number of data vectors in $x$, $d$ the number of variables, and $n_{\text{block}} = \text{ceiling} (\log(d))$ the number of blocks.

If $U$ is specified, $q$ defaults to $\text{ncol}(U)$; otherwise the initial PCs are computed from the first block of data and $q$ must be specified explicitly.

Although the algorithm does not give eigenvalues, they can easily be estimated by computing the variance of the data along the PCs.

Value

A matrix with the $q$ first eigenvectors/PCs in columns.

References


Examples

```r
## Simulate Brownian Motion
n <- 100 # number of sample paths
d <- 50 # number of observation points
x <- matrix(rnorm(n*d, sd=1/sqrt(d)), n, d)
x <- t(apply(x, 1, cumsum)) # dim(x) = c(100, 50)

q <- 10 # number of PC to compute
B <- 20 # block size

## BSQI PCA
U <- bsoipca(x, q, B=B, byrow=TRUE) # PCs
lambda <- apply(x %*% U, 2, var) # eigenvalues
```

ccipca  
*Candid Covariance-Free Incremental PCA*

Description

Stochastic gradient ascent algorithm CCIPCA of Weng et al. (2003).

Usage

```
ccipca(lambda, U, x, n, q = length(lambda), l=2, center, tol = 1e-8, sort = TRUE)
```
Arguments

lambda  vector of eigenvalues.
U       matrix of eigenvectors (PC) stored in columns.
x       new data vector.
n       sample size before observing x.
q       number of eigenvectors to compute.
l       'amnesic' parameter.
center  optional centering vector for x.
tol     numerical tolerance.
sort    Should the new eigenpairs be sorted?

Details

The 'amnesic' parameter \( l \) determines the weight of past observations in the PCA update. If \( l=0 \), all observations have equal weight, which is appropriate for stationary processes. Otherwise, typical values of \( l \) range between 2 and 4. As \( l \) increases, more weight is placed on new observations and less on older ones. For meaningful results, the condition \( 0 \leq l < n \) should hold.

The CCIPCA algorithm iteratively updates the PCs while deflating \( x \). If at some point the Euclidean norm of \( x \) becomes less than \( tol \), the algorithm stops to prevent numerical overflow.

If sort is TRUE, the updated eigenpairs are sorted by decreasing eigenvalue. If FALSE, they are not sorted.

Value

A list with components

values    updated eigenvalues.
vectors   updated eigenvectors.

References


Examples

```r
## Simulation of Brownian motion
n <- 100  # number of paths
d <- 50  # number of observation points
q <- 10  # number of PCs to compute
x <- matrix(rnorm(n*d, sd=1/sqrt(d)), n, d)
x <- t(apply(x, 1, cumsum))

## Initial PCA
n0 <- 50
pca <- princomp(x[1:n0,])
xbar <- pca$center
```
coef2fd

Recover functional data from their B-spline coefficients

Description
This function computes functional data from their coefficients in a B-spline basis.

Usage
coef2fd(beta, basis, byrow = TRUE)

Arguments
beta  B-spline coefficients
basis object created by create.basis
byrow are the coefficients of each functional observation stored in rows (TRUE) or in columns (FALSE)?

Value
A matrix of functional data stored in the same format (row or columns) as the coefficients beta.

Note
In view of (online or offline) functional PCA, the coefficients beta are left- or right- multiplied by \(M^{1/2}\) (depending on their row/column format) before applying the B-spline matrix B, with M the Gram matrix associated to B.

See Also
create.basis, fd2coef
Examples

```r
n <- 100  # number of curves
d <- 500  # number of observation points
grid <- (1:d)/d  # observation points
p <- 50    # number of B-spline basis functions

# Simulate Brownian motion
x <- matrix(rnorm(n*d,sd=1/sqrt(d)),n,d)
x <- t(apply(x,1,cumsum))

# Create B-spline basis
mybasis <- create_basis(grid, p, 1e-4)

# Compute smooth basis coefficients
beta <- fd2coef(x, mybasis)

# Recover smooth functional data
x.smooth <- coef2fd(beta, mybasis)

# Standard PCA and Functional PCA
pca <- prcomp(x)
fpca <- prcomp(beta)
```

---

**create.basis**

Create a smooth B-spline basis

**Description**

This function creates a smooth B-spline basis and provides tools to find the coefficients of functional data in the basis and to recover functional data from basis coefficients.

**Usage**

`create.basis(x, p, sp = 1e-09, degree = 3, nderiv = 2)`

**Arguments**

- `x` vector of observation times
- `p` number of basis functions
- `sp` smoothing parameter
- `degree` degree of the B splines
- `nderiv` order of the derivative to penalize for smoothing

**Details**

The knots of the B-spline basis are taken as regular quantiles of `x`. The function output is intended for use with functions `coef2fd` and `fd2coef`.
Value

A list with fields

- **B**: matrix of B-splines evaluated at \( x \) (each column represents a basis function)
- **S**: matrix that maps functional data to their (smoothed) coefficients of their projection in the basis set. For the purpose of PCA, the coefficients are premultiplied by \( M^{\frac{1}{2}} \), where \( M \) is the Gram matrix associated with \( B \)
- **invsqrtM**: matrix \( M^{\frac{-1}{2}} \) used to recover functional data from their coefficients in the basis set

See Also

`coef2fd`, `fd2coef`

Examples

```r
n <- 100 # number of curves
d <- 500 # number of observation points
grid <- (1:d)/d # observation points
p <- 50 # number of B-spline basis functions

# Simulate Brownian motion
x <- matrix(rnorm(n*d, sd=1/sqrt(d)), n, d)
x <- t(apply(x, 1, cumsum))

# Create B-spline basis
mybasis <- create.basis(grid, p, 1e-4)

# Compute smooth basis coefficients
beta <- fd2coef(x, mybasis)

# Recover smooth functional data
x.smooth <- coef2fd(beta, mybasis)

# Standard PCA and Functional PCA
pca <- prcomp(x)
fpca <- prcomp(beta)
```

**fd2coef**

Compute the coefficients of functional data in a B-spline basis

Description

This function computes the coefficients of functional data in a B-spline basis.

Usage

`fd2coef(x, basis, byrow = TRUE)`
Arguments

- **x**: matrix of functional data.
- **basis**: object created by `create.basis`.
- **byrow**: are the functional data stored in rows (TRUE) or in columns (FALSE)?

Value

A matrix of B-spline coefficients stored in the same format (row or columns) as functional data.

Note

In view of (online or offline) functional PCA, the coefficients are smoothed and premultiplied by $m^{1/2}$, with $m$ the Gram matrix associated to the B-spline matrix.

See Also

- `create.basis`, `coefRfd`

Examples

```r
n <- 100 # number of curves
d <- 500 # number of observation points
grid <- (1:d)/d # observation points
p <- 50 # number of B-spline basis functions

# Simulate Brownian motion
x <- matrix(rnorm(n*d, sd=1/sqrt(d)), n, d)
x <- t(apply(x, 1, cumsum))

# Create B-spline basis
mybasis <- create.basis(grid, p, 1e-4)

# Compute smooth basis coefficients
beta <- fd2coef(x, mybasis)

# Recover smooth functional data
xsmooth <- coefRfd(beta, mybasis)

# Standard PCA and Functional PCA
pca <- prcomp(x)
fpca <- prcomp(beta)
```

ghapca

*Generalized Hebbian Algorithm for PCA*

Description

Online PCA with the GHA of Sanger (1989).
ghapca

Usage
ghapca(lambda, U, x, gamma, q = length(lambda), center, sort = TRUE)

Arguments
lambda  optional vector of eigenvalues.
U        matrix of eigenvectors (PC) stored in columns.
x        new data vector.
gamma   vector of gain parameters.
q        number of eigenvectors to compute.
center  optional centering vector for x.
sort    Should the new eigenpairs be sorted?

Details
The vector gamma determines the weight placed on the new data in updating each eigenvector (the first coefficient of gamma corresponds to the first eigenvector, etc). It can be specified as a single positive number or as a vector of length ncol(U). Larger values of gamma place more weight on x and less on U. A common choice for (the components of) gamma is of the form c/n, with n the sample size and c a suitable positive constant.
If sort is TRUE and lambda is not missing, the updated eigenpairs are sorted by decreasing eigenvalue. Otherwise, they are not sorted.

Value
A list with components
values  updated eigenvalues or NULL.
vectors updated eigenvectors.

References

See Also
gapca, snlpc

Examples
## Initialization
n <- 1e4  # sample size
n0 <- 5e3 # initial sample size
d <- 10  # number of variables
q <- d # number of PC
x <- matrix(runif(n*d), n, d)
x <- x %*% diag(sqrt(12*(1:d)))
# The eigenvalues of \( X \) are close to 1, 2, \ldots, \( d \)
# and the corresponding eigenvectors are close to
# the canonical basis of \( \mathbb{R}^d \)

## GHA PCA

def princomp(x[1:n0,:])
xbar <- pca$center
pca <- list(values=pca$sdev[1:q]^2, vectors=pca$loadings[,1:q])
for (i in (n0+1):n) {
    xbar <- updateMean(xbar, x[i,], i-1)
    pca <- ghapca(pca$values, pca$vectors, x[i,], 2/i, q, xbar)
}

### impute

#### BLUP Imputation of Missing Values

**Description**

Missing values of a vector are imputed by best linear unbiased prediction (BLUP) assuming a multivariate normal distribution.

**Usage**

```r
impute(lambda, U, x, center, tol = 1e-07)
```

**Arguments**

- `lambda`: vector of eigenvalues of length \( q \).
- `U`: matrix of eigenvectors (principal components) of dimension \( p \times q \).
- `x`: vector of observations of length \( p \) with missing entries.
- `center`: centering vector for \( x \). Default is zero.
- `tol`: tolerance in the calculation of the pseudoinverse.

**Details**

The vector \( x \) is assumed to arise from a multivariate normal distribution with mean vector \( \text{center} \) and covariance matrix \( U \text{diag}(\lambda) U^T \).

**Value**

The imputed vector \( x \).

**References**

Examples

```r
set.seed(10)
lambda <- c(1,2,5)
U <- qr.Q(qr(matrix(rnorm(30),10,3)))
x <- U %*% diag(sqrt(lambda)) %*% rnorm(3) + rnorm(10, sd = .05)
x.na <- x
x.na[c(1,3,7)] <- NA
x.imputed <- impute(lambda,U,x.na)
cbind(x,x.imputed)
```

Description

Online PCA using the incremental SVD method of Brand (2002) and Arora et al. (2012).

Usage

`incRpca(lambda, U, x, n, f = 1/n, q = length(lambda), center, tol = 1e-7)`

Arguments

- `lambda`: vector of eigenvalues.
- `U`: matrix of eigenvectors (principal components) stored in columns.
- `x`: new data vector.
- `n`: sample size before observing x.
- `f`: forgetting factor: a number in (0,1).
- `q`: number of eigenvectors to compute.
- `center`: optional centering vector for x.
- `tol`: numerical tolerance.

Details

If the Euclidean distance between x and U is more than tol, the number of eigenpairs increases to length(lambda)+1 before eventual truncation at order q. Otherwise, the eigenvectors remain unchanged and only the eigenvalues are updated.

The forgetting factor f can be interpreted as the inverse of the number of observation vectors effectively used in the PCA: the "memory" of the PCA algorithm goes back 1/f observations in the past. For larger values of f, the PCA update gives more relative weight to the new data x and less to the current PCA (lambda,U). For nonstationary processes, f should be closer to 1.

Only one of the arguments n and f needs being specified. If it is n, then f is set to 1/n by default (usual PCA of sample covariance matrix where all data points have equal weight). If f is specified, its value overrides any eventual specification of n.
Value

A list with components

- values updated eigenvalues in decreasing order.
- vectors updated eigenvectors.

References


Examples

```r
## Simulate Brownian motion
n <- 100 # number of sample paths
d <- 50 # number of observation points
q <- 10 # number of PCs to compute
n0 <- 50 # number of sample paths used for initialization
x <- matrix(rnorm(n*d, sd=1/sqrt(d)), n, d)
x <- t(apply(x, 1, cumsum))
dim(x) # (100,50)

## Incremental PCA (IPCA, centered)
pca <- prcomp(x[1:n0,]) # initialization
xbar <- pca$center
pca <- list(values=pca$dev[1:q]^2, vectors=pca$rotation[,1:q])
for (i in (n0+1):n)
{
  xbar <- updateMean(xbar, x[i,], i-1)
  pca <- incRpca(pca$values, pca$vectors, x[i,], i-1, q = q, center = xbar)
}

## Incremental PCA (IPCA, uncentered)
pca <- prcomp(x[1:n0,], center=FALSE) # initialization
pca <- list(values = pca$sdev[1:q]^2, vectors = pca$rotation[,1:q])
for (i in (n0+1):n)
  pca <- incRpca(pca$values, pca$vectors, x[i,], i-1, q = q)
```

Description

Sequential Karhunen-Loeve (SKL) algorithm of Levy and Lindenbaum (2000). The PCA can be updated with respect to a data matrix (not just a data vector).
Usage

```r
incR pca.block(x, B, lambda, U, n0 = 0, f, q = length(lambda), center, byrow = FALSE)
```

Arguments

- `x`: data matrix
- `B`: block size
- `lambda`: initial eigenvalues (optional)
- `U`: initial eigenvectors/PCs (optional)
- `n0`: initial sample size (optional)
- `f`: vector of forgetting factors
- `q`: number of requested PCs
- `center`: centering vector for `x` (optional)
- `byrow`: Are the data vectors in `x` stored in rows (TRUE) or columns (FALSE)?

Details

This incremental PCA algorithm utilizes QR factorization and RSVD. It generalizes the algorithm `incR pca` from vector to matrix/block updates. However, `incR pca` should be preferred for vector updates as it is faster.

If `lambda` and `U` are specified, they are taken as the initial PCA. Otherwise, the PCA is initialized by the SVD of the first block of data in `x` (B data vectors). The number `n0` is the sample size before observing `x` (default value = 0). The number `B` is the size of blocks to be used in the PCA updates. Ideally, `B` should be a divisor of the number of data vectors in `x` (otherwise the last smaller block is discarded). If `U` is provided, then `B` and `q` default to the number of columns (=PC) of `U`.

The argument `f` determines the relative weight of current PCA and new data in each block update. Its length should be equal to the number of blocks in `x`, say `nbblock`. If `n0` and `B` are provided, then `f` defaults to `B/((n0+(B:(nbblock-1))*B))`, i.e., the case where all data points have equal weights.

The values in `f` should be in (0,1), with higher values giving more weight to new data and less to the current PCA.

Value

A list with components

- `values`: first `q` eigenvalues.
- `vectors`: first `q` eigenvectors/PCs.

References


See Also

`incR pca, incR pca.rc`
### Examples

```r
## Simulate Brownian Motion
n <- 100  # number of sample paths
d <- 50  # number of observation points
x <- matrix(rnorm(n*d, sd=1/sqrt(d)), n, d)
x <- t(apply(x, 1, cumsum))  # dim(x) = c(100, 50)
q <- 10  # number of PC to compute
B <- 20  # block size
n0 <- B  # initial sample size (if relevant)

## PCA without initial values
res1 <- incRpca.block(x, B, q=q)  # data vectors in columns
res2 <- incRpca.block(x, B, q=q, byrow=TRUE)  # data vectors in rows
all.equal(res1, res2)  # TRUE

## PCA with initial values
svd0 <- svd(x[1:n0,], 0, n0)  # use first block for initialization
lambda <- svd0$$d[1:n0]*2/n0  # initial eigenvalues
U <- svd0$u  # initial PC
res3 <- incRpca.block(x[-(1:n0),], B, lambda, n0, q=q, byrow=TRUE)
# run PCA with this initialization on rest of the data
all.equal(res1, res3)  # compare with previous PCA: TRUE

## Compare with function incRpca
res4 <- list(values=lambda, vectors=U)
for (i in (n0+1):n)
res4 <- incRpca(res4$values, res4$ vectors, x[i,], i-1, q=q)
B <- 1  # vector update
res5 <- incRpca.block(x[-(1:n0),], B, lambda, n0, q=q, byrow=TRUE)
ind <- which(sign(res5$ vectors[1,]) != sign(res4$ vectors[1,]))
res5$ vectors[, ind] <- -res5$ vectors[, ind]  # align PCs (flip orientation as needed)
all.equal(res4, res5)  # TRUE
```

---

**incRpca.rc**  
*Incremental PCA With Reduced Complexity*

### Description

The incremental PCA is computed without rotating the updated projection space (Brand, 2002; Arora et al., 2012). Specifically, PCs are specified through a matrix of orthogonal vectors $\mathbf{u}_t$ that spans the PC space and a rotation matrix $\mathbf{u}_s$ such that the PC matrix is $\mathbf{u}_t\mathbf{u}_s$. Given a new data vector, the PCA is updated by adding one column to $\mathbf{u}_t$ and recalculating the low-dimensional rotation matrix $\mathbf{u}_s$. This reduces complexity and helps preserving orthogonality. Eigenvalues are updated as the usual incremental PCA algorithm.

### Usage

```r
incRpca.rc(lambda, U, Us, x, n, f = 1/n, center, tol = 1e-07)
```
Arguments

- \texttt{lambda}: vector of eigenvalues.
- \texttt{Ut}: matrix of orthogonal vectors stored in columns.
- \texttt{Us}: rotation matrix.
- \texttt{x}: new data vector.
- \texttt{n}: sample size before observing \texttt{x}.
- \texttt{f}: forgetting factor: a number in \((0,1)\).
- \texttt{center}: optional centering vector for \texttt{x}.
- \texttt{tol}: numerical tolerance for eigenvalues.

Details

For large datasets, this algorithm is considerably faster than its counterpart \texttt{incR pca}, reducing the time complexity of each update from \(O(qd^2)\) to \(O(qd + q^3)\) flops with \(d\) the length of \(x\). A consequence of not rotating the PC basis at each update is that the dimension of the PCA decomposition increases whenever a new observation vector is not entirely contained in the PC space. To keep the number of PCs and eigenvalues from getting too large, it is necessary to multiply the matrices \(U_t\) and \(U_s\) at regular time intervals so as to recover the individual PCs and retain only the largest ones.

Value

A list with components

- \texttt{values}: updated eigenvalues in decreasing order.
- \texttt{Ut}: updated projection space.
- \texttt{Us}: updated rotation matrix.

References


See Also

\texttt{incR pca}, \texttt{incR pca.block}

Examples

```r
## Not run:
# Data generation
n <- 400  # number of units
d <- 10000  # number of variables
n0 <- 200  # initial sample
q <- 20  # required number of PCs
x <- matrix(rnorm(n*d,sd=1/sqrt(d)),n,d)  # data matrix
```

perturbationR pca

Recursive PCA using a rank 1 perturbation method

Description

This function recursively updates the PCA with respect to a single new data vector, using the (fast) perturbation method of Hegde et al. (2006).
### Usage

```r
dperturbationRpca(lambda, U, x, n, f = 1/n, center, sort = TRUE)
```

### Arguments

- `lambda`: vector of eigenvalues.
- `U`: matrix of eigenvectors (PC) stored in columns.
- `x`: new data vector.
- `n`: sample size before observing `x`.
- `f`: forgetting factor: a number between 0 and 1.
- `center`: optional centering vector for `x`.
- `sort`: Should the eigenpairs be sorted?

### Details

The forgetting factor `f` can be interpreted as the inverse of the number of observation vectors effectively used in the PCA: the "memory" of the PCA algorithm goes back `1/f` observations in the past. For larger values of `f`, the PCA update gives more relative weight to the new data `x` and less to the current PCA (`lambda`, `U`). For nonstationary processes, `f` should be closer to 1. Only one of the arguments `n` and `f` needs being specified. If it is `n`, then `f` is set to `1/n` by default (usual PCA of sample covariance matrix where all data points have equal weight). If `f` is specified, its value overrides any eventual specification of `n`. If `sort` is TRUE, the updated eigenpairs are sorted by decreasing eigenvalue. Otherwise, they are not sorted.

### Value

A list with components

- `values`: updated eigenvalues.
- `vectors`: updated eigenvectors.

### Note

This perturbation method is based on large sample approximations. It tends to be highly inaccurate for small/medium sized samples and should not be used in this case.

### References


### See Also

`secularRpca`
Examples

n <- 1e3
n0 <- 5e2
d <- 10
x <- matrix(runif(n*d), n, d)
x <- x %*% diag(sqrt(12*(1:d)))
# The eigenvalues of cov(x) are approximately equal to 1, 2, ..., d
# and the corresponding eigenvectors are approximately equal to
# the canonical basis of R^d

## Perturbation-based recursive PCA
# Initialization: use factor 1/n0 (princomp) rather
# than factor 1/(n0-1) (prcomp) in calculations
pca <- princomp(x[1:n0,], center=FALSE)
xbar <- pca$center
pca <- list(values=pca$sdev^2, vectors=pca$loadings)
for (i in (n0+1):n) {
xbar <- updateMean(xbar, x[i,], i-1)
pca <- perturbationR pca(pca$values, pca$vectors, x[i,],
i-1, center=xbar) }

secularrpca

Recursive PCA Using Secular Equations

Description

The PCA is recursively updated after observation of a new vector (rank one modification of the
covariance matrix). Eigenvalues are computed as roots of a secular equation. Eigenvectors (principal
components) are deduced by explicit calculation (Bunch et al., 1978) or approximated with the

Usage

secularrpca(lambda, U, x, n, f = 1/n, center, tol = 1e-10, reortho = FALSE)

Arguments

lambda vector of eigenvalues.
U matrix of eigenvectors (PCs) stored in columns.
x new data vector.
n sample size before observing x.
f forgetting factor: a number in (0,1).
center centering vector for x (optional).
tol tolerance for the computation of eigenvalues.
reortho if FALSE, eigenvectors are explicitly computed using the method of Bunch et al.
(1978). If TRUE, they are approximated with the method of Gu and Eisenstat
(1994).
Details

The method of secular equations provides accurate eigenvalues in all but pathological cases. On the other hand, the perturbation method implemented by \texttt{perturbationR pca} typically runs much faster but is only accurate for a large sample size \( n \).

The default eigendecomposition method is that of Bunch et al. (1978). This algorithm consists in three stages: initial deflation, nonlinear solution of secular equations, and calculation of eigenvectors. The calculation of eigenvectors (PCs) is accurate for the first few eigenvectors but loss of accuracy and orthogonality may occur for the next ones. In contrast the method of Gu and Eisenstat (1994) is robust against small errors in the computation of eigenvalues. It provides eigenvectors that may be less accurate than the default method but for which strict orthogonality is guaranteed.

The forgetting factor \( f \) can be interpreted as the inverse of the number of observation vectors effectively used in the PCA: the "memory" of the PCA algorithm goes back \( 1/f \) observations in the past. For larger values of \( f \), the PCA update gives more relative weight to the new data \( x \) and less to the current PCA \((\lambda_l, \mathbf{u})\). For nonstationary processes, \( f \) should be closer to 1. Only one of the arguments \( n \) and \( f \) needs being specified. If it is \( n \), then \( f \) is set to \( 1/n \) by default (usual PCA of sample covariance matrix where all data points have equal weight). If \( f \) is specified, its value overrides any eventual specification of \( n \).

Value

A list with components

- \texttt{values} updated eigenvalues in decreasing order.
- \texttt{vectors} updated eigenvectors (PCs).

References


See Also

\texttt{perturbationR pca}

Examples

```r
# Initial data set
n <- 100
d <- 50
x <- matrix(runif(n*d),n,d)
xbar <- colMeans(x)
pca0 <- eigen(cov(x))

# New observation
newx <- runif(d)

# Recursive PCA with secular equations
xbar <- updateMean(xbar, newx, n)
```
sgapca

Stochastic Gradient Ascent PCA

Description

Online PCA with the SGA algorithm of Oja (1992).

Usage

sgapca(lambda, U, x, gamma, q = length(lambda), center,
        type = c("exact", "nn"), sort = TRUE)

Arguments

lambda optional vector of eigenvalues.
U matrix of eigenvectors (PC) stored in columns.
x new data vector.
gamma vector of gain parameters.
q number of eigenvectors to compute.
center optional centering vector for x.
type algorithm implementation: "exact" or "nn" (neural network).
sort Should the new eigenpairs be sorted?

Details

The gain vector gamma determines the weight placed on the new data in updating each principal component. The first coefficient of gamma corresponds to the first principal component, etc.. It can be specified as a single positive number (which is recycled by the function) or as a vector of length ncol(U). For larger values of gamma, more weight is placed on x and less on U. A common choice for (the components of) gamma is of the form c/n, with n the sample size and c a suitable positive constant.

The Stochastic Gradient Ascent PCA can be implemented exactly or through a neural network. The latter is less accurate but faster.

If sort is TRUE and lambda is not missing, the updated eigenpairs are sorted by decreasing eigenvalue. Otherwise, they are not sorted.

Value

A list with components

values updated eigenvalues or NULL.
 vectors updated principal components.
snlpca

References

See Also
ghapca, snlpca

Examples

```
## Initialization
n <- 1e4  # sample size
do <- 10  # number of variables
d <- do  # number of PC to compute
x <- matrix(rnorm(n*d), n, d)
x <- x %*% diag(sqrt(12*(1:d)))
# The eigenvalues of x are close to 1, 2, ..., d
# and the corresponding eigenvectors are close to
# the canonical basis of R^d

## SGA PCA
xbar <- colMeans(x[1:n0,])
pca <- batchpca(x[1:n0,], q, center=xbar, byrow=TRUE)
for (i in (n0+1):n) {
  xbar <- updateMean(xbar, x[i,], i-1)
  pca <- sgapca(pca$values, pca$vectors, x[i,], 2/i, q, xbar)
}
pca
```

snlpca

Subspace Network Learning PCA

Description
Online PCA with the SNL algorithm of Oja (1992).

Usage

```
snlpca(lambda, U, x, gamma, q = length(lambda), center,
       type = c("exact", "nn"), sort = TRUE)
```

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>lambda</td>
<td>optional vector of eigenvalues.</td>
</tr>
<tr>
<td>U</td>
<td>matrix of eigenvectors (PC) stored in columns.</td>
</tr>
<tr>
<td>x</td>
<td>new data vector.</td>
</tr>
<tr>
<td>gamma</td>
<td>vector of learning rates.</td>
</tr>
</tbody>
</table>
q          number of eigenvectors to compute.
center     optional centering vector for x.
type       algorithm implementation: "exact" or "nn" (neural network).
sort       Should the new eigenpairs be sorted?

Details

The vector gamma determines the weight placed on the new data in updating each PC. For larger values of gamma, more weight is placed on x and less on u. A common choice is of the form c/n, with n the sample size and c a suitable positive constant. Argument gamma can be specified as a single positive number (common to all PCs) or as a vector of length q.

If sort is TRUE and lambda is not missing, the updated eigenpairs are sorted by decreasing eigenvalue. Otherwise, they are not sorted.

Value

A list with components

values     updated eigenvalues or NULL.
vectors    updated (rotated) eigenvectors.

Note

The Subspace Network Learning PCA can be implemented exactly or through a neural network. The latter is less accurate but much faster. Unlike the GHA and SGA algorithms, the SNL algorithm does not consistently estimate principal components. It provides only the linear space spanned by the PCs.

References


See Also

ghapca, sgapca

Examples

```r
# Initialization
n <- 1e4    # sample size
n0 <- 5e3  # initial sample size
d <- 10    # number of variables
q <- d     # number of PC to compute
x <- matrix(rnorm(n*d), n, d)
x <- x * diag(sqrt(12*(1:1:d)))
# The eigenvalues of x are close to 1, 2, ..., d
# and the corresponding eigenvectors are close to
# the canonical basis of R^d
```
updateCovariance

## Description

This function recursively updates a covariance matrix without entirely recomputing it when new observations arrive.

## Usage

```r
updateCovariance(C, x, n, xbar, f, byrow = TRUE)
```

## Arguments

- `C` : covariance matrix.
- `x` : vector/matrix of new data.
- `n` : sample size before observing `x`.
- `xbar` : mean vector before observing `x`.
- `f` : forgetting factor: a number between 0 and 1.
- `byrow` : Are the observation vectors in `x` stored in rows?

## Details

The forgetting factor `f` determines the balance between past and present observations in the PCA update: the closer it is to 1 (resp. to 0), the more weight is placed on current (resp. past) observations. At least one of the arguments `n` and `f` must be specified. If `f` is specified, its value overrides the argument `n`. The default `f=1/n` corresponds to a stationary observation process.

The argument `byrow` should be set to `TRUE` (default value) if the data vectors in `x` are stored in rows and to `FALSE` if they are stored in columns. The function automatically handles the case where `x` is a single vector.

## Value

The updated covariance matrix.

## See Also

- `updateMean`
Examples

```r
n <- 1e4
n0 <- 5e3
d <- 10
x <- matrix(rnorm(n*d), n, d)

## Direct computation of the covariance
C <- cov(x)

## Recursive computation of the covariance
xbar0 <- colMeans(x[,1:n0,])
C0 <- cov(x[,1:n0,])
Crec <- updateCovariance(C0, x[(n0+1):n,], n0, xbar0)

## Check equality
all.equal(C, Crec)
```

---

**updateMean**

*Update the Sample Mean Vector*

**Description**

Recursive update of the sample mean vector.

**Usage**

```r
updateMean(xbar, x, n, f, byrow = TRUE)
```

**Arguments**

- `xbar` current mean vector.
- `x` vector or matrix of new data.
- `n` sample size before observing `x`.
- `f` forgetting factor: a number in (0,1).
- `byrow` Are the observation vectors in `x` stored in rows (TRUE) or in columns (FALSE)?

**Details**

The forgetting factor `f` determines the balance between past and present observations in the PCA update: the closer it is to 1 (resp. to 0), the more weight is placed on current (resp. past) observations. At least one of the arguments `n` and `f` must be specified. If `f` is specified, its value overrides the argument `n`. For a given argument `n`, the default value of `f` is $\frac{k}{n+k}$, with $k$ the number of new vector observations. This corresponds to a stationary observation process.

**Value**

The updated mean vector.
updateMean

See Also

updateCovariance

Examples

n <- 1e4
n0 <- 5e3
d <- 10
x <- matrix(rnorm(n*d), n, d)

## Direct computation
xbar1 <- colMeans(x)

## Recursive computation
xbar2 <- colMeans(x[1:n0,])
xbar2 <- updateMean(xbar2, x[(n0+1):n,], n0)

## Check equality
all.equal(xbar1, xbar2)
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