Package: spcr (via r-universe)

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Type Package

Title Sparse Principal Component Regression

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Description The sparse principal component regression is computed. The regularization parameters are optimized by cross-validation.

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Contents

cv.spcr *Cross-validation for spcr*

Description

This function performs cross-validation for spcr. cv.spcr enables us to determine two regularization parameters λ_β and λ_γ objectively.

Usage

```
cv.spcr(x, y, k, w=0.1, xi=0.01, nfolds=5, adaptive=FALSE,
 center=TRUE, scale=FALSE, lambda.B.length=10, lambda.gamma.length=10,
 lambda.B=NULL, lambda.gamma=NULL)
```

Arguments

x	A data matrix.
y	A response vector.
k	The number of principal components.
w	Weight parameter with $0 \leq w \leq 1$. The default is 0.1.
xi	The elastic net mixing parameter with $0 \leq \alpha \leq 1$. The default is 0.01.
nfolds	The number of folds. The default is 5.
adaptive	If "TRUE", the adaptive SPCR is used.
center	If "TRUE", the data matrix is centered.
scale	If "TRUE", the data matrix is scaled.
lambda.B.length	The number of candidates for the parameter λ_β. The default is 10.
lambda.gamma.length	The number of candidates for the parameter λ_γ. The default is 10.
lambda.B	Optional user-supplied candidates for the parameter λ_β. The default is NULL.
lambda.gamma	Optional user-supplied candidates for the parameter λ_γ. The default is NULL.

Value

lambda.gamma.seq	The values of lambda.gamma in the fit.
lambda.B.seq	The values of lambda.B in the fit.
CV.mat	Matrix of the mean values of cross-validation. The row shows a sequence of lambda.gamma. The column shows a sequence of lambda.B.
lambda.gamma.cv	The value of lambda.gamma selected by cross-validation.
lambda.B.cv	The value of lambda.B selected by cross-validation.
cvm	The minimum of the mean cross-validated error.

Author(s)

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References

Kawano, S., Fujisawa, H., Takada, T. and Shiroishi, T. (2015). *Sparse principal component regression with adaptive loading. Compuational Statistics & Data Analysis, 89, 192–203.*

See Also

`spcr`

Examples

```
#data
n <- 50
np <- 5
set.seed(1)
nu0 <- c(-1, 1)
x <- matrix( rnorm(np*n), n, np )
e <- rnorm(n)
y <- nu0[1]*x[ ,1] + nu0[2]*x[ ,2] + e

#fit
cv.spcr.fit <- cv.spcr(x=x, y=y, k=2)
cv.spcr.fit

#fit (adaptive SPCR)
cv.adaspcr.fit <- cv.spcr(x=x, y=y, k=2, adaptive=TRUE)
cv.adaspcr.fit
```

`cv.spcrglm` *Cross-validation for spcr-glm*

Description

This function performs cross-validation for SPCR-glm. `cv.spcrglm` enables us to determine two regularization parameters λ_β and λ_γ objectively.

Usage

```
cv.spcrglm(x, y, k, family=c("binomial","poisson","multinomial"),
 w=0.1, xi=0.01, nfolds=5, adaptive=FALSE, q=1, center=TRUE,
 scale=FALSE, lambda.B.length=10, lambda.gamma.length=10,
 lambda.B=NULL, lambda.gamma=NULL)
```

Arguments

x	A data matrix.
y	A response vector.
k	The number of principal components.
family	Response type.
w	Weight parameter with $w \geq 0$. The default is 0.1.
xi	The elastic net mixing parameter with $0 \leq \alpha \leq 1$. The default is 0.01.
nfolds	The number of folds. The default is 5.
adaptive	If "TRUE", the adaptive SPCR-glm (aSPCR-glm) is used.
q	The tuning parameter that controls weights in aSPCR-glm. The default is 1.
center	If "TRUE", the data matrix is centered.
scale	If "TRUE", the data matrix is scaled.
lambda.B.length	The number of candidates for the parameter λ_β. The default is 10.
lambda.gamma.length	The number of candidates for the parameter λ_γ. The default is 10.
lambda.B	Optional user-supplied candidates for the parameter λ_β. The default is NULL.
lambda.gamma	Optional user-supplied candidates for the parameter λ_γ. The default is NULL.

Value

lambda.gamma.seq	The values of lambda.gamma in the fit.
lambda.B.seq	The values of lambda.B in the fit.
CV.mat	Matrix of the mean values of cross-validation. The row shows a sequence of lambda.gamma. The column shows a sequence of lambda.B.
lambda.gamma.cv	The value of lambda.gamma selected by cross-validation.
lambda.B.cv	The value of lambda.B selected by cross-validation.
cvm	The minimum of the mean cross-validated error.

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References

Kawano, S., Fujisawa, H., Takada, T. and Shiroishi, T. (2018). *Sparse principal component regression for generalized linear models. Compuational Statistics & Data Analysis, 124, 180–196.*

See Also

spcrglm

Examples

```
# binomial
n <- 100
np <- 3
nu0 <- c(-1, 1)
set.seed(4)
x <- matrix( rnorm(np*n), n, np )
y <- rbinom(n,1,1-1/(1+exp(  (nu0[1]*x[ ,1] + nu0[2]*x[ ,2]  ))))
cv.spcrglm.fit <- cv.spcrglm(x=x, y=y, k=1, family="binomial")
cv.spcrglm.fit

# Poisson
set.seed(5)
y <- rpois(n, 1)
cv.spcrglm.fit <- cv.spcrglm(x=x, y=y, k=1, family="poisson")
cv.spcrglm.fit

# multinomial
set.seed(4)
y <- sample(1:4, n, replace=TRUE)
cv.spcrglm.fit <- cv.spcrglm(x=x, y=y, k=1, family="multinomial")
cv.spcrglm.fit
```

---

spcr *Fit a sparse principal component regression (SPCR)*

Description

This function computes a principal component regression model via sparse regularization.

Usage

```
spcr(x, y, k, lambda.B, lambda.gamma, w=0.1, xi=0.01,
 adaptive=FALSE, center=TRUE, scale=FALSE)
```

Arguments

x	A data matrix.
y	A response vector.
k	The number of principal components.
lambda.B	The regularization parameter for the parameter B.
lambda.gamma	The regularization parameter for the coefficient vector γ.
w	Weight parameter with $0 \leq w \leq 1$. The default is 0.1.
xi	The elastic net mixing parameter with $0 \leq \alpha \leq 1$. The default is 0.01.
adaptive	If "TRUE", the adaptive SPCR is used.
center	If "TRUE", the data matrix is centered.
scale	If "TRUE", the data matrix is scaled.

Value

loadings.B	the loading matrix B
gamma	the coefficient
gamma0	intercept
loadings.A	the loading matrix A

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References

Kawano, S., Fujisawa, H., Takada, T. and Shiroishi, T. (2015). *Sparse principal component regression with adaptive loading. Compuational Statistics & Data Analysis, 89, 192–203.*

See Also

cv.spcr

Examples

```
#data
n <- 100
np <- 5
set.seed(4)
nu0 <- c(-1, 1)
x <- matrix( rnorm(np*n), n, np )
e <- rnorm(n)
y <- nu0[1]*x[ ,1] + nu0[2]*x[ ,2] + e

#fit
spcr.fit <- spcr(x=x, y=y, k=2, lambda.B=6, lambda.gamma=2)
spcr.fit

#fit (adaptive SPCR)
adaspcr.fit <- spcr(x=x, y=y, k=2, lambda.B=6, lambda.gamma=2, adaptive=TRUE)
adaspcr.fit
```

---

spcrglm — *Fit a sparse principal component regression for generalized linear models (SPCR-glm)*

Description

This function computes a principal component regression for generalized linear models via sparse regularization.

Usage

```
spcrglm(x, y, k, family=c("binomial","poisson","multinomial"), lambda.B,
 lambda.gamma, w=0.1, xi=0.01, adaptive=FALSE, q=1, center=TRUE, scale=FALSE)
```

Arguments

x	A data matrix.
y	A response data.
k	The number of principal components.
family	Response type.
lambda.B	The regularization parameter for the parameter B.
lambda.gamma	The regularization parameter for the coefficient vector γ.
w	Weight parameter with $w \geq 0$. The default is 0.1.
xi	The elastic net mixing parameter with $0 \leq \alpha \leq 1$. The default is 0.01.
adaptive	If "TRUE", the adaptive SPCR-glm (aSPCR-glm) is used.
q	The tuning parameter that controls weights in aSPCR-glm. The default is 1.
center	If "TRUE", the data matrix is centered.
scale	If "TRUE", the data matrix is scaled.

Value

loadings.B	the loading matrix B
gamma	the coefficient
gamma0	intercept
loadings.A	the loading matrix A

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References

Kawano, S., Fujisawa, H., Takada, T. and Shiroishi, T. (2018). *Sparse principal component regression for generalized linear models. Compuational Statistics & Data Analysis, 124, 180–196.*

See Also

cv.spcrglm

Examples

```
# binomial
n <- 100
np <- 5
nu0 <- c(-1, 1)
set.seed(4)
x <- matrix( rnorm(np*n), n, np )
y <- rbinom(n,1,1-1/(1+exp(  (nu0[1]*x[ ,1] + nu0[2]*x[ ,2]  ))))
spcrglm.fit <- spcrglm(x=x, y=y, k=2, family="binomial", lambda.B=2, lambda.gamma=1)
spcrglm.fit

# Poisson
set.seed(4)
y <- rpois(n, exp(  (nu0[1]*x[ ,1] + nu0[2]*x[ ,2] ) ))
spcrglm.fit <- spcrglm(x=x, y=y, k=2, family="poisson", lambda.B=2, lambda.gamma=1)
spcrglm.fit

# multinomial
set.seed(4)
y <- sample(1:4, n, replace=TRUE)
spcrglm.fit <- spcrglm(x=x, y=y, k=2, family="multinomial", lambda.B=2, lambda.gamma=2)
spcrglm.fit
```

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