

Package ‘Renvlp’

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Type Package

Title Computing Envelope Estimators

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Description Provides a general routine, `envMU()`, which allows estimation of the M envelope of $\text{span}(U)$ given root n consistent estimators of M and U . The routine `envMU()` does not presume a model. This package implements response envelopes (`env()`), partial response envelopes (`penv()`), envelopes in the predictor space (`xenv()`), heteroscedastic envelopes (`henv()`), simultaneous envelopes (`stenv()`), scaled response envelopes (`senv()`), scaled envelopes in the predictor space (`sxenv()`), groupwise envelopes (`genv()`), weighted envelopes (`weighted.env()`, `weighted.penv()` and `weighted.xenv()`), envelopes in logistic regression (`logit.env()`), and envelopes in Poisson regression (`pois.env()`). For each of these model-based routines the package provides inference tools including bootstrap, cross validation, estimation and prediction, hypothesis testing on coefficients are included except for weighted envelopes. Tools for selection of dimension include AIC, BIC and likelihood ratio testing. Background is available at Cook, R. D., Forzani, L. and Su, Z. (2016) <doi:10.1016/j.jmva.2016.05.006>. Optimization is based on a clockwise coordinate descent algorithm.

License GPL-2

NeedsCompilation no

Imports Rsolnp, stats

Suggests MASS, knitr

VignetteBuilder knitr

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Renvlp-package 3

Berkeley	5
boot.env	6
boot.genv	7
boot.henv	8
boot.logit.env	9
boot.penv	10
boot.pois.env	11
boot.senv	12
boot.stenv	13
boot.sxenv	14
boot.xenv	15
contr	16
cv.env	17
cv.genv	18
cv.henv	19
cv.logit.env	20
cv.penv	21
cv.pois.env	22
cv.senv	23
cv.stenv	24
cv.sxenv	25
cv.xenv	26
d.stenv	27
env	28
envMU	30
expan	31
fiberpaper	32
GE	32
genv	33
genvMU	35
ginv	36
henv	36
henvMU	38
horseshoecrab	39
logit.env	40
logit.envMU	42
penv	43
pois.env	45
pois.envMU	46
pred.env	47
pred.genv	48
pred.henv	49
pred.logit.env	50
pred.penv	51
pred.pois.env	52
pred.senv	53
pred.stenv	54
pred.sxenv	55

pred.xenv	56
pred2.env	57
sales	58
senv	59
senvMU	61
stenv	62
stenvMU	64
sxenv	65
sxenvMU	67
testcoef.env	68
testcoef.genv	69
testcoef.henv	70
testcoef.logit.env	71
testcoef.penv	73
testcoef.pois.env	74
testcoef.senv	75
testcoef.stenv	76
testcoef.sxenv	78
testcoef.xenv	79
u.env	80
u.genv	81
u.henv	82
u.logit.env	83
u.penv	84
u.pois.env	85
u.pred2.env	86
u.senv	87
u.stenv	88
u.sxenv	89
u.xenv	90
waterstrider	91
weighted.env	92
weighted.penv	93
weighted.pred.env	95
weighted.xenv	96
wheatprotein	98
xenv	99

Index**102**

Description

This package contains functions for estimating envelope models including response envelopes, partial response envelopes, envelopes in the predictor space, heteroscedastic envelopes, simultaneous envelopes, scaled response envelopes, scaled envelopes in the predictor space, groupwise envelopes, weighted envelopes, envelopes in logistic regression and envelopes in poisson regression.

Details

Package: Renvlp
Type: Package
Version: 2.5
Date: 2018-01-18
License: GPL-2
Imports: Rsolnp, stats
Suggests: Mass, knitr

Author(s)

Minji Lee and Zhihua Su.

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Cook, R. D., Zhang, X. (2015). Foundations for Envelope Models and Methods. *Journal of the American Statistical Association* 110, 599 - 611.

Berkeley

Berkeley Guidance Study Data

Description

Heights of children born in Berkeley

Usage

```
data("Berkeley")
```

Format

A data frame with 93 observations on the following 32 variables.

V1 Sex.

V2 Age 1.

V3 Age 1.25.

V4 Age 1.5.

V5 Age 1.75.

V6 Age 2.

V7 Age 3.

V8 Age 4.

V9 Age 5.

V10 Age 6.

V11 Age 7.

V12 Age 8.

V13 Age 8.5.

V14 Age 9.

V15 Age 9.5.

V16 Age 10.

V17 Age 10.5.

V18 Age 11.

V19 Age 11.5.

V20 Age 12.

V21 Age 12.5.

V22 Age 13.
 V23 Age 13.5.
 V24 Age 14.
 V25 Age 14.5.
 V26 Age 15.
 V27 Age 15.5.
 V28 Age 16.
 V29 Age 16.5.
 V30 Age 17.
 V31 Age 17.5.
 V32 Age 18.

Details

This data set contains measurements of heights of children born in 1928-29 in Berkeley, CA.

References

Tuddenham, R. D. and Snyder, M. M. (1954). Physical growth of California boys and girls from birth to eighteen years. *Publications in child developments*. University of California, Berkeley, 1(2), 183-364.

boot.env

Bootstrap for env

Description

Compute bootstrap standard error for the envelope estimator.

Usage

boot.env(X, Y, u, B)

Arguments

X	Predictors. An n by p matrix, p is the number of predictors. The predictors can be univariate or multivariate, discrete or continuous.
Y	Multivariate responses. An n by r matrix, r is the number of responses and n is number of observations. The responses must be continuous variables.
u	Dimension of the envelope. An integer between 0 and r .
B	Number of bootstrap samples. A positive integer.

Details

This function computes the bootstrap standard errors for the regression coefficients in the envelope model by bootstrapping the residuals.

Value

The output is an r by p matrix.

`bootse` The standard error for elements in beta computed by bootstrap.

Examples

```
data(wheatprotein)
X <- wheatprotein[, 8]
Y <- wheatprotein[, 1:6]

u <- u.env(X, Y)
u

B <- 100
bootse <- boot.env(X, Y, 1, B)
bootse
```

`boot.genv`

Bootstrap for genv

Description

Compute bootstrap standard error for the groupwise envelope.

Usage

```
boot.genv(X, Y, Z, u, B)
```

Arguments

<code>X</code>	Predictors. An n by p matrix, p is the number of predictors. The predictors can be univariate or multivariate, discrete or continuous.
<code>Y</code>	Multivariate responses. An n by r matrix, r is the number of responses and n is number of observations. The responses must be continuous variables.
<code>Z</code>	A group indicator vector of length n , where n denotes the number of observations.
<code>u</code>	Dimension of the groupwise envelope. An integer between 0 and r .
<code>B</code>	Number of bootstrap samples. A positive integer.

Details

This function computes the bootstrap standard errors for the regression coefficients in the groupwise envelope model by bootstrapping the residuals.

Value

The output is an p by r matrix.

bootse The standard error for elements in beta computed by bootstrap.

Examples

```
data(fiberpaper)
X <- fiberpaper[ , c(5, 7)]
Y <- fiberpaper[ , 1:3]
Z <- as.numeric(fiberpaper[ , 6] > mean(fiberpaper[ , 6]))

B <- 100
## Not run: res <- boot.genv(X, Y, Z, 2, B)
## Not run: res$bootse[[1]]
## Not run: res$bootse[[2]]
```

boot.henv

Bootstrap for henv

Description

Compute bootstrap standard error for the heteroscedastic envelope.

Usage

```
boot.henv(X, Y, u, B)
```

Arguments

X	A group indicator vector of length n , where n denotes the number of observations.
Y	Multivariate responses. An n by r matrix, r is the number of responses and n is number of observations. The responses must be continuous variables.
u	Dimension of the heteroscedastic envelope. An integer between 0 and r .
B	Number of bootstrap samples. A positive integer.

Details

This function computes the bootstrap standard errors for the regression coefficients in the heteroscedastic envelope model by bootstrapping the residuals.

Value

The output is an r by p matrix.

bootse The standard error for elements in beta computed by bootstrap.

Examples

```
data(waterstrider)
X <- waterstrider[, 1]
Y <- waterstrider[, 2:5]

B <- 100
## Not run: res <- boot.henv(X, Y, 2, B)
## Not run: res
```

boot.logit.env *Bootstrap for logit.env*

Description

Compute bootstrap standard error for the envelope estimator in logistic regression.

Usage

```
boot.logit.env(X, Y, u, B)
```

Arguments

X	Predictors. An n by p matrix, p is the number of predictors and n is number of observations. The predictors must be continuous variables.
Y	Response. An n by 1 matrix. The univariate response must be binary.
u	Dimension of the envelope. An integer between 0 and p .
B	Number of bootstrap samples. A positive integer.

Details

This function computes the bootstrap standard errors for the coefficients in the logistic regression envelope by the paired bootstrap.

Value

The output is a p by 1 matrix.

bootse The standard error for elements in beta computed by bootstrap.

Examples

```

data(horseshoecrab)
X1 <- as.numeric(horseshoecrab[, 1] == 2)
X2 <- as.numeric(horseshoecrab[, 1] == 3)
X3 <- as.numeric(horseshoecrab[, 1] == 4)
X4 <- as.numeric(horseshoecrab[, 2] == 2)
X5 <- as.numeric(horseshoecrab[, 2] == 3)
X6 <- horseshoecrab[, 3]
X7 <- horseshoecrab[, 5]
X <- cbind(X1, X2, X3, X4, X5, X6, X7)
Y <- as.numeric(iffelse(horseshoecrab[, 4] > 0, 1, 0))

B <- 100
## Not run: bootse <- boot.logit.env(X, Y, 1, B)
## Not run: bootse

```

boot.penv

Bootstrap for penv

Description

Compute bootstrap standard error for the partial envelope estimator.

Usage

```
boot.penv(X1, X2, Y, u, B)
```

Arguments

X1	Predictors of main interest. An n by p1 matrix, n is the number of observations, and p1 is the number of main predictors. The predictors can be univariate or multivariate, discrete or continuous.
X2	Covariates, or predictors not of main interest. An n by p2 matrix, p2 is the number of covariates.
Y	Multivariate responses. An n by r matrix, r is the number of responses and n is number of observations. The responses must be continuous variables.
u	Dimension of the partial envelope. An integer between 0 and r.
B	Number of bootstrap samples. A positive integer.

Details

This function computes the bootstrap standard errors for the regression coefficients beta1 in the partial envelope model by bootstrapping the residuals.

Value

The output is an r by p1 matrix.

bootse The standard error for elements in beta1 computed by bootstrap.

Examples

```
data(fiberpaper)
X1 <- fiberpaper[, 7]
X2 <- fiberpaper[, 5:6]
Y <- fiberpaper[, 1:4]

B <- 100
bootse <- boot.penv(X1, X2, Y, 1, B)
bootse
```

boot.pois.env

Bootstrap for pois.env

Description

Compute bootstrap standard error for the envelope estimator in poisson regression.

Usage

```
boot.pois.env(X, Y, u, B)
```

Arguments

X	Predictors. An n by p matrix, p is the number of predictors and n is number of observations. The predictors must be continuous variables.
Y	Response. An n by 1 matrix. The univariate response must be counts.
u	Dimension of the envelope. An integer between 0 and p.
B	Number of bootstrap samples. A positive integer.

Details

This function computes the bootstrap standard errors for the coefficients in the poisson regression envelope by the paired bootstrap.

Value

The output is a p by 1 matrix.

bootse	The standard error for elements in beta computed by bootstrap.
--------	--

Examples

```

data(horseshoecrab)
X1 <- as.numeric(horseshoecrab[, 1] == 2)
X2 <- as.numeric(horseshoecrab[, 1] == 3)
X3 <- as.numeric(horseshoecrab[, 1] == 4)
X4 <- as.numeric(horseshoecrab[, 2] == 2)
X5 <- as.numeric(horseshoecrab[, 2] == 3)
X6 <- horseshoecrab[, 3]
X7 <- horseshoecrab[, 5]
X <- cbind(X1, X2, X3, X4, X5, X6, X7)
Y <- horseshoecrab[, 4]

B <- 100
## Not run: bootse <- boot.pois.senv(X, Y, 1, B)
## Not run: bootse

```

boot.senv

Bootstrap for senv

Description

Compute bootstrap standard error for the scaled envelope estimator.

Usage

```
boot.senv(X, Y, u, B)
```

Arguments

X	Predictors. An n by p matrix, p is the number of predictors. The predictors can be univariate or multivariate, discrete or continuous.
Y	Multivariate responses. An n by r matrix, r is the number of responses and n is number of observations. The responses must be continuous variables.
u	Dimension of the scaled envelope. An integer between 0 and r .
B	Number of bootstrap samples. A positive integer.

Details

This function computes the bootstrap standard errors for the regression coefficients in the scaled envelope model by bootstrapping the residuals.

Value

The output is an r by p matrix.

bootse	The standard error for elements in beta computed by bootstrap.
--------	--

Examples

```

data(sales)
X <- sales[, 1:3]
Y <- sales[, 4:7]

u <- u.senv(X, Y)
u

## Not run: B <- 100
## Not run: bootse <- boot.stenv(X, Y, 2, B)
## Not run: bootse

```

boot.stenv

Bootstrap for stenv

Description

Compute bootstrap standard error for the simultaneous envelope estimator.

Usage

```
boot.stenv(X, Y, q, u, B)
```

Arguments

X	Predictors. An n by p matrix, p is the number of predictors. The predictors can be univariate or multivariate, discrete or continuous.
Y	Multivariate responses. An n by r matrix, r is the number of responses and n is number of observations. The responses must be continuous variables.
q	Dimension of the X-envelope. An integer between 0 and p.
u	Dimension of the Y-envelope. An integer between 0 and r.
B	Number of bootstrap samples. A positive integer.

Details

This function computes the bootstrap standard errors for the regression coefficients in the envelope model by bootstrapping the residuals.

Value

The output is an p by r matrix.

bootse	The standard error for elements in beta computed by bootstrap.
--------	--

Examples

```
data(fiberpaper)
X <- fiberpaper[, 5:7]
Y <- fiberpaper[, 1:4]
u <- u.stenv(X, Y)
u

B <- 100
bootse <- boot.stenv(X, Y, 2, 3, B)
bootse
```

boot.sxenv

Bootstrap for sxenv

Description

Compute bootstrap standard error for the scaled envelope in the predictor space estimator.

Usage

```
boot.sxenv(X, Y, u, R, B)
```

Arguments

X	Predictors. An n by p matrix, p is the number of predictors. The predictors can be univariate or multivariate, discrete or continuous.
Y	Multivariate responses. An n by r matrix, r is the number of responses and n is number of observations. The responses must be continuous variables.
u	Dimension of the scaled envelope in the predictor space. An integer between 0 and p .
R	The number of replications of the scales. A vector, the sum of all elements of R must be p .
B	Number of bootstrap samples. A positive integer.

Details

This function computes the bootstrap standard errors for the regression coefficients in the scaled envelope model in the predictor space by bootstrapping the residuals.

Value

The output is an p by r matrix.

bootse The standard error for elements in beta computed by bootstrap.

Examples

```

data(sales)
Y <- sales[, 1:3]
X <- sales[, 4:7]
R <- rep(1, 4)

u <- u.sxenv(X, Y, R)
u

B <- 100
## Not run: bootse <- boot.sxenv(X, Y, 2, R, B)
## Not run: bootse

```

boot.xenv

Bootstrap for xenv

Description

Compute bootstrap standard error for the envelope estimator.

Usage

```
boot.xenv(X, Y, u, B)
```

Arguments

X	Predictors. An n by p matrix, p is the number of predictors and n is number of observations. The predictors must be continuous variables.
Y	Responses. An n by r matrix, r is the number of responses. The response can be univariate or multivariate and must be continuous variable.
u	Dimension of the envelope. An integer between 0 and p.
B	Number of bootstrap samples. A positive integer.

Details

This function computes the bootstrap standard errors for the regression coefficients in the envelope model in predictor space by bootstrapping the residuals.

Value

The output is a p by r matrix.

bootse	The standard error for elements in beta computed by bootstrap.
--------	--

Examples

```
data(wheatprotein)
X <- wheatprotein[, 1:6]
Y <- wheatprotein[, 7]

B <- 100
## Not run: bootse <- boot.xenv(X, Y, 2, B)
## Not run: bootse
```

contr

Contraction matrix

Description

Generate contraction matrix.

Usage

```
contr(d)
```

Arguments

d Dimension of the contraction matrix. A positive integer.

Details

The contraction and expansion matrices are links between the "vec" operator and "vech" operator: for an d by d symmetric matrix A , $\text{vech}(A) = \text{contr}(d) * \text{vec}(A)$, and $\text{vec}(A) = \text{expan}(d) * \text{vech}(A)$. The "vec" operator stacks the matrix A into an d^2 dimensional vector columnwise. The "vech" operator stacks the lower triangle or the upper triangle of a symmetric matrix into an $d * (d + 1) / 2$ vector. For more details of "vec", "vech", contraction and expansion matrix, refer to Henderson and Searle (1979).

Value

The output is a matrix.

contrMatrix A contraction matrix that has dimension $d * (d + 1) / 2$ by d^2 .

References

Henderson, H. V., and Searle, S. R. (1979). Vec and Vech operators for matrices, with some uses in Jacobians and multivariate statistics. Canadian J. Statist. 7, 65 - 81.

Examples

```
contr(3)
```

cv.env *Cross validation for env*

Description

Compute the prediction error for the envelope estimator using m-fold cross validation.

Usage

```
cv.env(X, Y, u, m, nperm)
```

Arguments

X	Predictors. An n by p matrix, p is the number of predictors. The predictors can be univariate or multivariate, discrete or continuous.
Y	Multivariate responses. An n by r matrix, r is the number of responses and n is number of observations. The responses must be continuous variables.
u	Dimension of the envelope. An integer between 0 and r.
m	A positive integer that is used to indicate m-fold cross validation.
nperm	A positive integer indicating number of permutations of the observations, m-fold cross validation is run on each permutation.

Details

This function computes prediction errors using m-fold cross validation. For a fixed dimension u, the data is randomly partitioned into m parts, each part is in turn used for testing for the prediction performance while the rest m-1 parts are used for training. This process is repeated for nperm times, and average prediction error is reported. As Y is multivariate, the identity inner product is used for computing the prediction errors.

Value

The output is a real nonnegative number.

cvPE The prediction error estimated by m-fold cross validation.

Examples

```
data(wheatprotein)
X <- wheatprotein[, 8]
Y <- wheatprotein[, 1:6]
u <- u.env(X, Y)
u

m <- 5
nperm <- 50
cvPE <- cv.env(X, Y, 1, m, nperm)
cvPE
```

cv.genv

*Cross validation for genv***Description**

Compute the prediction error for the groupwise envelope estimator using m-fold cross validation.

Usage

```
cv.genv(X, Y, Z, u, m, nperm)
```

Arguments

X	Predictors. An n by p matrix, p is the number of predictors. The predictors can be univariate or multivariate, discrete or continuous.
Y	Multivariate responses. An n by r matrix, r is the number of responses and n is number of observations. The responses must be continuous variables.
Z	A group indicator vector of length n, where n denotes the number of observations.
u	Dimension of the groupwise envelope. An integer between 0 and r.
m	A positive integer that is used to indicate m-fold cross validation.
nperm	A positive integer indicating number of permutations of the observations, m-fold cross validation is run on each permutation.

Details

This function computes prediction errors using m-fold cross validation. For a fixed dimension u, the data is randomly partitioned into m parts, each part is in turn used for testing for the prediction performance while the rest m-1 parts are used for training. This process is repeated for nperm times, and average prediction error is reported. As Y is multivariate, the identity inner product is used for computing the prediction errors.

Value

The output is a real nonnegative number.

cvPE	The prediction error estimated by m-fold cross validation.
------	--

Examples

```
data(fiberpaper)
X <- fiberpaper[ , c(5, 7)]
Y <- fiberpaper[ , 1:3]
Z <- as.numeric(fiberpaper[ , 6] > mean(fiberpaper[ , 6]))

m <- 5
nperm <- 50
```

```
## Not run: cvPE <- cv.genv(X, Y, Z, 2, m, nperm)
## Not run: cvPE
```

cv.henv

Cross validation for henv

Description

Compute the prediction error for the heteroscedastic envelope estimator using m -fold cross validation.

Usage

```
cv.henv(X, Y, u, m, nperm)
```

Arguments

X	A group indicator vector of length n , where n denotes the number of observations.
Y	Multivariate responses. An n by r matrix, r is the number of responses and n is number of observations. The responses must be continuous variables.
u	Dimension of the heteroscedastic envelope. An integer between 0 and r .
m	A positive integer that is used to indicate m -fold cross validation.
$nperm$	A positive integer indicating number of permutations of the observations, m -fold cross validation is run on each permutation.

Details

This function computes prediction errors using m -fold cross validation. For a fixed dimension u , the data is randomly partitioned into m parts, each part is in turn used for testing for the prediction performance while the rest $m-1$ parts are used for training. This process is repeated for $nperm$ times, and average prediction error is reported. As Y is multivariate, the identity inner product is used for computing the prediction errors.

Value

The output is a real nonnegative number.

cvPE	The prediction error estimated by m -fold cross validation.
------	---

Examples

```

data(waterstrider)
X <- waterstrider[, 1]
Y <- waterstrider[, 2:5]

m <- 5
nperm <- 50

## Not run: cvPE <- cv.henv(X, Y, 2, m, nperm)
## Not run: cvPE

```

cv.logit.env

Cross validation for logit.env

Description

Compute the prediction error for the envelope estimator in logistic regression using m-fold cross validation.

Usage

```
cv.logit.env(X, Y, u, m, nperm)
```

Arguments

X	Predictors. An n by p matrix, p is the number of predictors and n is number of observations. The predictors must be continuous variables.
Y	Response. An n by 1 matrix. The univariate response must be binary.
u	Dimension of the envelope. An integer between 0 and p.
m	A positive integer that is used to indicate m-fold cross validation.
nperm	A positive integer indicating number of permutations of the observations, m-fold cross validation is run on each permutation.

Details

This function computes prediction errors using m-fold cross validation. For a fixed dimension u, the data is randomly partitioned into m parts, each part is in turn used for testing for the prediction performance while the rest m-1 parts are used for training. This process is repeated for nperm times, and average prediction error is reported.

Value

The output is a real nonnegative number.

cvPE	The prediction error estimated by m-fold cross validation.
------	--

Examples

```

data(horseshoecrab)
X1 <- as.numeric(horseshoecrab[, 1] == 2)
X2 <- as.numeric(horseshoecrab[, 1] == 3)
X3 <- as.numeric(horseshoecrab[, 1] == 4)
X4 <- as.numeric(horseshoecrab[, 2] == 2)
X5 <- as.numeric(horseshoecrab[, 2] == 3)
X6 <- horseshoecrab[, 3]
X7 <- horseshoecrab[, 5]
X <- cbind(X1, X2, X3, X4, X5, X6, X7)
Y <- as.numeric(iffelse(horseshoecrab[, 4] > 0, 1, 0))

m <- 5
nperm <- 50
## Not run: cvPE <- cv.logit.env(X, Y, 1, m, nperm)
## Not run: cvPE

```

cv.penv

Cross validation for penv

Description

Compute the prediction error for the partial envelope estimator using m-fold cross validation.

Usage

```
cv.penv(X1, X2, Y, u, m, nperm)
```

Arguments

X1	Predictors of main interest. An n by p1 matrix, n is the number of observations, and p1 is the number of main predictors. The predictors can be univariate or multivariate, discrete or continuous.
X2	Covariates, or predictors not of main interest. An n by p2 matrix, p2 is the number of covariates.
Y	Multivariate responses. An n by r matrix, r is the number of responses and n is number of observations. The responses must be continuous variables.
u	Dimension of the envelope. An integer between 0 and r.
m	A positive integer that is used to indicate m-fold cross validation.
nperm	A positive integer indicating number of permutations of the observations, m-fold cross validation is run on each permutation.

Details

This function computes prediction errors using m-fold cross validation. For a fixed dimension u , the data is randomly partitioned into m parts, each part is in turn used for testing for the prediction performance while the rest $m-1$ parts are used for training. This process is repeated for $nperm$ times, and average prediction error is reported. As Y is multivariate, the identity inner product is used for computing the prediction errors.

Value

The output is a real nonnegative number.

cvPE The prediction error estimated by m-fold cross validation.

Examples

```
data(fiberpaper)
X1 <- fiberpaper[, 7]
X2 <- fiberpaper[, 5:6]
Y <- fiberpaper[, 1:4]

m <- 5
nperm <- 50
cvPE <- cv.penv(X1, X2, Y, 1, m, nperm)
cvPE
```

cv.pois.env

Cross validation for pois.env

Description

Compute the prediction error for the envelope estimator in poisson regression using m-fold cross validation.

Usage

```
cv.pois.env(X, Y, u, m, nperm)
```

Arguments

X	Predictors. An n by p matrix, p is the number of predictors and n is number of observations. The predictors must be continuous variables.
Y	Response. An n by 1 matrix. The univariate response must be counts.
u	Dimension of the envelope. An integer between 0 and p .
m	A positive integer that is used to indicate m-fold cross validation.
$nperm$	A positive integer indicating number of permutations of the observations, m-fold cross validation is run on each permutation.

Details

This function computes prediction errors using m-fold cross validation. For a fixed dimension u , the data is randomly partitioned into m parts, each part is in turn used for testing for the prediction performance while the rest $m-1$ parts are used for training. This process is repeated for $nperm$ times, and average prediction error is reported.

Value

The output is a real nonnegative number.

cvPE The prediction error estimated by m-fold cross validation.

Examples

```
data(horseshoecrab)
X1 <- as.numeric(horseshoecrab[ , 1] == 2)
X2 <- as.numeric(horseshoecrab[ , 1] == 3)
X3 <- as.numeric(horseshoecrab[ , 1] == 4)
X4 <- as.numeric(horseshoecrab[ , 2] == 2)
X5 <- as.numeric(horseshoecrab[ , 2] == 3)
X6 <- horseshoecrab[ , 3]
X7 <- horseshoecrab[ , 5]
X <- cbind(X1, X2, X3, X4, X5, X6, X7)
Y <- horseshoecrab[ , 4]

m <- 5
nperm <- 50
## Not run: cvPE <- cv.pois.env(X, Y, 1, m, nperm)
## Not run: cvPE
```

cv.senv

Cross validation for senv

Description

Compute the prediction error for the scaled envelope estimator using m-fold cross validation.

Usage

```
cv.senv(X, Y, u, m, nperm)
```

Arguments

X Predictors. An n by p matrix, p is the number of predictors. The predictors can be univariate or multivariate, discrete or continuous.

Y Multivariate responses. An n by r matrix, r is the number of responses and n is number of observations. The responses must be continuous variables.

u	Dimension of the scaled envelope. An integer between 0 and r.
m	A positive integer that is used to indicate m-fold cross validation.
nperm	A positive integer indicating number of permutations of the observations, m-fold cross validation is run on each permutation.

Details

This function computes prediction errors using m-fold cross validation. For a fixed dimension u, the data is randomly partitioned into m parts, each part is in turn used for testing for the prediction performance while the rest m-1 parts are used for training. This process is repeated for nperm times, and average prediction error is reported. As Y is multivariate, the identity inner product is used for computing the prediction errors.

Value

The output is a real nonnegative number.

cvPE The prediction error estimated by m-fold cross validation.

Examples

```
data(sales)
X <- sales[, 1:3]
Y <- sales[, 4:7]

m <- 5
nperm <- 50
## Not run: cvPE <- cv.stenv(X, Y, 2, m, nperm)
## Not run: cvPE
```

cv.stenv

Cross validation for stenv

Description

Compute the prediction error for the simultaneous envelope estimator using m-fold cross validation.

Usage

```
cv.stenv(X, Y, q, u, m, nperm)
```

Arguments

X	Predictors. An n by p matrix, p is the number of predictors and n is number of observations. The predictors must be continuous variables.
Y	Responses. An n by r matrix, r is the number of responses. The response can be univariate or multivariate and must be continuous variable.
q	Dimension of the X-envelope. An integer between 0 and p.

u	Dimension of the Y-envelope. An integer between 0 and r.
m	A positive integer that is used to indicate m-fold cross validation.
nperm	A positive integer indicating number of permutations of the observations, m-fold cross validation is run on each permutation.

Details

This function computes prediction errors using m-fold cross validation. For a fixed dimension (q, u), the data is randomly partitioned into m parts, each part is in turn used for testing for the prediction performance while the rest m-1 parts are used for training. This process is repeated for nperm times, and average prediction error is reported. If Y is multivariate, the identity inner product is used for computing the prediction errors.

Value

The output is a real nonnegative number.

cvPE The prediction error estimated by m-fold cross validation.

Examples

```
data(fiberpaper)
X <- fiberpaper[, 5:7]
Y <- fiberpaper[, 1:4]

m <- 5
nperm <- 50
## Not run: cvPE <- cv.stenv(X, Y, 2, 3, m, nperm)
## Not run: cvPE
```

cv.sxenv

Cross validation for sxenv

Description

Compute the prediction error for the scaled envelope in the predictor space estimator using m-fold cross validation.

Usage

```
cv.sxenv(X, Y, u, R, m, nperm)
```

Arguments

X	Predictors. An n by p matrix, p is the number of predictors and n is number of observations. The predictors must be continuous variables.
Y	Responses. An n by r matrix, r is the number of responses. The response can be univariate or multivariate and must be continuous variable.
u	Dimension of the scaled envelope. An integer between 0 and r.
R	The number of replications of the scales. A vector, the sum of all elements of R must be p.
m	A positive integer that is used to indicate m-fold cross validation.
nperm	A positive integer indicating number of permutations of the observations, m-fold cross validation is run on each permutation.

Details

This function computes prediction errors using m-fold cross validation. For a fixed dimension u, the data is randomly partitioned into m parts, each part is in turn used for testing for the prediction performance while the rest m-1 parts are used for training. This process is repeated for nperm times, and average prediction error is reported. As Y is multivariate, the identity inner product is used for computing the prediction errors.

Value

The output is a real nonnegative number.

cvPE The prediction error estimated by m-fold cross validation.

Examples

```
data(sales)
Y <- sales[, 1:3]
X <- sales[, 4:7]
R <- rep(1, 4)

m <- 5
nperm <- 50
## Not run: cvPE <- cv.sxenv(X, Y, 2, R, m, nperm)
## Not run: cvPE
```

Description

Compute the prediction error for the envelope estimator using m-fold cross validation.

Usage

```
cv.xenv(X, Y, u, m, nperm)
```

Arguments

X	Predictors. An n by p matrix, p is the number of predictors and n is number of observations. The predictors must be continuous variables.
Y	Responses. An n by r matrix, r is the number of responses. The response can be univariate or multivariate and must be continuous variable.
u	Dimension of the envelope. An integer between 0 and p.
m	A positive integer that is used to indicate m-fold cross validation.
nperm	A positive integer indicating number of permutations of the observations, m-fold cross validation is run on each permutation.

Details

This function computes prediction errors using m-fold cross validation. For a fixed dimension u, the data is randomly partitioned into m parts, each part is in turn used for testing for the prediction performance while the rest m-1 parts are used for training. This process is repeated for nperm times, and average prediction error is reported. If Y is multivariate, the identity inner product is used for computing the prediction errors.

Value

The output is a real nonnegative number.

cvPE The prediction error estimated by m-fold cross validation.

Examples

```
data(wheatprotein)
X <- wheatprotein[, 1:6]
Y <- wheatprotein[, 7]

m <- 5
nperm <- 50
## Not run: cvPE <- cv.xenv(X, Y, 2, m, nperm)
## Not run: cvPE
```

d.stenv

Select the rank of beta

Description

This function outputs the rank selected by a chi-squared test developed by Bura and Cook (2003) with specified significance level for the beta.

Usage

```
d.stenv(X, Y, alpha = 0.01)
```

Arguments

X	Predictors. An n by p matrix, p is the number of predictors. The predictors can be univariate or multivariate, discrete or continuous.
Y	Multivariate responses. An n by r matrix, r is the number of responses and n is number of observations. The responses must be continuous variables.
alpha	Significance level for testing. The default is 0.01.

Details

This function estimate the rank of beta using a chi-squared test. The test statistic and degrees of freedom are described in Bura and Cook (2003).

Value

rank.beta	Rank of beta guided by the Bura-Cook estimator.
-----------	---

References

Bura, E. and Cook, R. D. (2003). Rank estimation in reduced-rank regression. *Journal of Multivariate Analysis*, 87, 159 - 176.

 env

Fit the envelope model

Description

Fit the envelope model in multivariate linear regression with dimension u.

Usage

```
env(X, Y, u, asy = TRUE, init = NULL)
```

Arguments

X	Predictors. An n by p matrix, p is the number of predictors. The predictors can be univariate or multivariate, discrete or continuous.
Y	Multivariate responses. An n by r matrix, r is the number of responses and n is number of observations. The responses must be continuous variables.
u	Dimension of the envelope. An integer between 0 and r.
asy	Flag for computing the asymptotic variance of the envelope estimator. The default is TRUE. When p and r are large, computing the asymptotic variance can take much time and memory. If only the envelope estimators are needed, the flag can be set to asy = FALSE.

`init` The user-specified value of Gamma for the envelope subspace. An r by u matrix. The default is the one generated by function `envMU`.

Details

This function fits the envelope model to the responses and predictors,

$$Y = \mu + \Gamma\eta X + \varepsilon, \Sigma = \Gamma\Omega\Gamma' + \Gamma_0\Omega_0\Gamma_0'$$

using the maximum likelihood estimation. When the dimension of the envelope is between 1 and $r-1$, the starting value and blockwise coordinate descent algorithm in Cook et al. (2016) is implemented. When the dimension is r , then the envelope model degenerates to the standard multivariate linear regression. When the dimension is 0, it means that X and Y are uncorrelated, and the fitting is different.

Value

The output is a list that contains the following components:

<code>beta</code>	The envelope estimator of the regression coefficients.
<code>Sigma</code>	The envelope estimator of the error covariance matrix.
<code>Gamma</code>	An orthonormal basis of the envelope subspace.
<code>Gamma0</code>	An orthonormal basis of the complement of the envelope subspace.
<code>eta</code>	The coordinates of <code>beta</code> with respect to <code>Gamma</code> .
<code>Omega</code>	The coordinates of <code>Sigma</code> with respect to <code>Gamma</code> .
<code>Omega0</code>	The coordinates of <code>Sigma</code> with respect to <code>Gamma0</code> .
<code>mu</code>	The estimated intercept.
<code>loglik</code>	The maximized log likelihood function.
<code>covMatrix</code>	The asymptotic covariance of <code>vec(beta)</code> . The covariance matrix returned are asymptotic. For the actual standard errors, multiply by $1/n$.
<code>asySE</code>	The asymptotic standard error for elements in <code>beta</code> under the envelope model. The standard errors returned are asymptotic, for actual standard errors, multiply by $1/\sqrt{n}$.
<code>ratio</code>	The asymptotic standard error ratio of the standard multivariate linear regression estimator over the envelope estimator, for each element in <code>beta</code> .
<code>n</code>	The number of observations in the data.

References

- Cook, R. D., Li, B. and Chiaromonte, F. (2010). Envelope Models for Parsimonious and Efficient Multivariate Linear Regression (with discussion). *Statist. Sinica* 20, 927- 1010.
- Cook, R. D., Forzani, L. and Su, Z. (2016) A Note on Fast Envelope Estimation. *Journal of Multivariate Analysis*. 150, 42-54.

Examples

```

data(wheatprotein)
X <- wheatprotein[, 8]
Y <- wheatprotein[, 1:6]
u <- u.env(X, Y)
u

m <- env(X, Y, 1)
m
m$beta

```

envMU

Estimate the envelope subspace

Description

Estimate the envelope subspace with specified dimension.

Usage

```
envMU(M, U, u)
```

Arguments

M	M matrix in the envelope objective function. An r by r semi-positive definite matrix.
U	U matrix in the envelope objective function. An r by r semi-positive definite matrix.
u	Dimension of the envelope. An integer between 0 and r .

Details

This function estimate the envelope subspace using an non-Grassmann optimization algorithm. The starting value and optimization algorithm is described in Cook et al. (2016).

Value

Gammahat	The orthonormal basis of the envelope subspace.
Gamma0hat	The orthonormal basis of the complement of the envelope subspace.
objfun	The minimized objective function.

References

Cook, R. D., Forzani, L. and Su, Z. (2016) A Note on Fast Envelope Estimation. *Journal of Multivariate Analysis*. 150, 42-54.

expan	<i>Expansion matrix</i>
-------	-------------------------

Description

Generate expansion matrix.

Usage

```
expan(d)
```

Arguments

d Dimension of the expansion matrix. A positive integer.

Details

The contraction and expansion matrices are links between the "vec" operator and "vech" operator: for an d by d symmetric matrix A , $\text{vech}(A) = \text{contr}(d) * \text{vec}(A)$, and $\text{vec}(A) = \text{expan}(d) * \text{vech}(A)$. The "vec" operator stacks the matrix A into an d^2 dimensional vector columnwise. The "vech" operator stacks the lower triangle or the upper triangle of a symmetric matrix into an $d * (d + 1) / 2$ vector. For more details of "vec", "vech", contraction and expansion matrix, refer to Henderson and Searle (1979).

Value

The output is a matrix.

expanMatrix An expansion matrix that has dimension d^2 by $d * (d + 1) / 2$.

References

Henderson, H. V., and Searle, S. R. (1979). Vec and Vech operators for matrices, with some uses in Jacobians and multivariate statistics. *Canadian J. Statist.* 7, 65 - 81.

Examples

```
expan(3)
```

fiberpaper

Pulp and Paper Data

Description

Pulp and paper property

Usage

```
data("fiberpaper")
```

Format

A data frame with 62 observations on the following 8 variables.

V1 Breaking length.

V2 Elastic modulus.

V3 Stress at failure.

V4 Burst strength.

V5 Arithmetic fiber length.

V6 Long fiber fraction.

V7 Fine fiber fraction.

V8 Zero span tensile.

Details

This data set contains measurements of properties of pulp fibers and the paper made from them.

References

Johnson, R.A. and Wichern, D.W. (2007). Applied Multivariate Statistical Analysis, 6th edition.

GE

Gaussian elimination

Description

Gaussian elimination with partial pivoting.

Usage

```
GE(A)
```


Arguments

A An n by p matrix. n must be greater than or equal to p.

Details

This function performs Gaussian elimination to the input matrix and returns the locations of pivoting elements.

Value

The output is a vector of length n.

idx A vector of length n. The first p elements are the indices of the pivoting elements, ordered according to columns, and the rest n-p elements are the remaining indices from 1 to n.

genv *Fit the groupwise envelope model*

Description

Fit the groupwise envelope model in multivariate linear regression with dimension u.

Usage

genv(X, Y, Z, u, asy = TRUE, fit = TRUE, init = NULL)

Arguments

X Predictors. An n by p matrix, p is the number of predictors. The predictors can be univariate or multivariate, discrete or continuous.

Y Multivariate responses. An n by r matrix, r is the number of responses and n is number of observations. The responses must be continuous variables.

Z A group indicator vector of length n, where n denotes the number of observations.

u Dimension of the groupwise envelope. An integer between 0 and r.

asy Flag for computing the asymptotic variance of the envelope estimator. The default is TRUE. When p and r are large, computing the asymptotic variance can take much time and memory. If only the envelope estimators are needed, the flag can be set to asy = FALSE.

fit Flag for computing the fitted response. The default is TRUE.

init The user-specified value of Gamma for the groupwise envelope subspace. An r by u matrix. The default is the one generated by function genvMU.

Details

This function fits the groupwise envelope model to the responses and predictors,

$$Y_{(l)j} = \mu_{(l)} + \Gamma \eta_{(l)j} X_{(l)j} + \varepsilon_{(l)j}, \Sigma_{(l)} = \Gamma \Omega_{(l)} \Gamma' + \Gamma_0 \Omega_0 \Gamma_0'$$

for $l = 1, \dots, L$, using the maximum likelihood estimation. When the dimension of the groupwise envelope is between 1 and $r-1$, the starting value and blockwise coordinate descent algorithm in Cook et al. (2016) is implemented. When the dimension is r , then the envelope model degenerates to the standard multivariate linear regression. When the dimension is 0, it means that X and Y are uncorrelated, and the fitting is different. When L is 1, the groupwise envelope model degenerates to the envelope model in Cook et al. (2010).

Value

The output is a list that contains the following components:

beta	A list of r by p matrices for the estimator of regression coefficients. beta[[i]] indicates the estimator of regression coefficient for the i th group.
Sigma	A list of the estimator of error covariance matrix. Sigma[[i]] contains the estimated covariance matrix for the i th group.
Gamma	An orthonormal basis of the groupwise envelope subspace.
Gamma0	An orthonormal basis of the complement of the groupwise envelope subspace.
eta	The coordinates of beta with respect to Gamma.
Omega	The coordinates of Sigma with respect to Gamma.
Omega0	The coordinates of Sigma with respect to Gamma0.
mu	The estimator of group mean. A r by L matrix whose i th column contains the mean for the group.
loglik	The maximized log likelihood function.
covMatrix	A list of the asymptotic covariance of vec(beta). The covariance matrix returned are asymptotic. For the actual standard errors, multiply by $1 / n$. covMatrix[[i]] contains the asymptotic covariance matrix for the i th group.
asySE	A list of the asymptotic standard error for elements in beta under the groupwise envelope model. The standard errors returned are asymptotic, for actual standard errors, multiply by $1 / \sqrt{n}$. asySE[[i]] contains the asymptotic standard error for elements in beta[[i]].
ratio	A list of the asymptotic standard error ratio of the standard multivariate linear regression estimator over the groupwise envelope estimator, for each element in beta. ratio[[i]] contains the asymptotic standard error ratio for the i th group.
groupInd	A matrix containing the unique values of group indicators. The matrix has p rows.
n	The number of observations in the data.
ng	The number of observations in each group.
Yfit	Fitted responses.

References

- Park, Y., Su, Z. and Zhu, H. (2017) Groupwise envelope models for Imaging Genetic Analysis. *Biometrics*, to appear.
- Cook, R. D., Li, B. and Chiaromonte, F. (2010). Envelope Models for Parsimonious and Efficient Multivariate Linear Regression (with discussion). *Statist. Sinica* 20, 927- 1010.
- Cook, R. D., Forzani, L. and Su, Z. (2016) A Note on Fast Envelope Estimation. *Journal of Multivariate Analysis*. 150, 42-54.

Examples

```
data(fiberpaper)
X <- fiberpaper[ , c(5, 7)]
Y <- fiberpaper[ , 1:3]
Z <- as.numeric(fiberpaper[ , 6] > mean(fiberpaper[ , 6]))
u <- u.genv(X, Y, Z)
u
m <- genv(X, Y, Z, 2)
```

genvMU

Estimate the groupwise envelope subspace

Description

Estimate the groupwise envelope subspace with specified dimension.

Usage

```
genvMU(M, U, MU, u, n, ng, L)
```

Arguments

M	A matrix M for the non-Grassmann manifold optimization problem in Cook et al. (2016)
U	A matrix U for the non-Grassmann manifold optimization problem in Cook et al. (2016)
MU	Sum of matrix M and U.
u	A given dimension of the groupwise envelope space. It should be an interger between 0 and r .
n	The number of observations.
ng	A L by 1 vector of the number of observations in each group.
L	The number of groups.

Value

Gamma An r by u matrix for the orthonormal basis of the groupwise envelope subspace.
 Gamma0 An r by $(r - u)$ matrix for the orthonormal basis of the complement of the groupwise envelope subspace.

References

Cook, R. D., Forzani, L. and Su, Z. (2016) A Note on Fast Envelope Estimation. *Journal of Multivariate Analysis*. 150, 42-54.

ginv *Generalized Inverse of a Matrix*

Description

Calculates the Moore-Penrose generalized inverse of a matrix X.

Usage

```
ginv(X, tol = sqrt(.Machine$double.eps))
```

Arguments

X Matrix for which the Moore-Penrose inverse is required
 tol A relative tolerance to detect zero singular values

References

Venables, W.N. and Ripley, B.D. (1999) *Modern Applied statistics with S-PLUS*. Third Edition. Springer. p.100

henv *Fit the heteroscedastic envelope model*

Description

Fit the heteroscedastic envelope model with dimension u.

Usage

```
henv(X, Y, u, asy = TRUE, fit = TRUE, init = NULL)
```

Arguments

<code>X</code>	A group indicator vector of length n , where n denotes the number of observations.
<code>Y</code>	Multivariate responses. An n by r matrix, r is the number of responses and n is number of observations. The responses must be continuous variables.
<code>u</code>	Dimension of the heteroscedastic envelope. An integer between 0 and r .
<code>asy</code>	Flag for computing the asymptotic variance of the envelope estimator. The default is TRUE. When p and r are large, computing the asymptotic variance can take much time and memory. If only the envelope estimators are needed, the flag can be set to <code>asy = FALSE</code> .
<code>fit</code>	Flag for computing the fitted response. The default is TRUE.
<code>init</code>	The user-specified value of Gamma for the heteroscedastic envelope subspace. An r by u matrix. The default is the one generated by function <code>henvMU</code> .

Details

This function fits the heteroscedastic envelope model to the responses,

$$Y_{(i)j} = \mu + \Gamma\eta_{(i)} + \varepsilon_{(i)j}, \Sigma_{(i)} = \Gamma\Omega_{(i)}\Gamma' + \Gamma_0\Omega_0\Gamma_0'$$

for $i = 1, \dots, p$, using the maximum likelihood estimation. When the dimension of the heteroscedastic envelope is between 1 and $r-1$, the starting value and blockwise coordinate descent algorithm in Cook et al. (2016) is implemented. When the dimension is r , then the envelope model degenerates to the standard multivariate linear regression for comparing group means. When the dimension is 0, it means there is no any group effect, and the fitting is different.

Value

The output is a list that contains the following components:

<code>beta</code>	The heteroscedastic envelope estimator of the group main effect. An r by p matrix, the i th column of the matrix contains the main effect for the i th group.
<code>Sigma</code>	A list of the heteroscedastic envelope estimator of the error covariance matrix. <code>Sigma[[i]]</code> contains the estimated covariance matrix for the i th group.
<code>Gamma</code>	An orthonormal basis of the heteroscedastic envelope subspace.
<code>Gamma0</code>	An orthonormal basis of the complement of the heteroscedastic envelope subspace.
<code>eta</code>	A list of the coordinates of <code>beta</code> with respect to <code>Gamma</code> . <code>eta[[i]]</code> indicates the coordinates of the main effect of the i th group with respect to <code>Gamma</code> .
<code>Omega</code>	A list of the coordinates of <code>Sigma</code> with respect to <code>Gamma</code> . <code>Omega[[i]]</code> indicates the coordinates of the covariance matrix of the i th group with respect to <code>Gamma</code> .
<code>Omega0</code>	The coordinates of <code>Sigma</code> with respect to <code>Gamma0</code> .
<code>mu</code>	The heteroscedastic envelope estimator of the grand mean. A r by 1 matrix.
<code>mug</code>	A list of the heteroscedastic envelope estimator of the group mean. An r by p matrix, the i th column of the matrix contains the mean for the i th group.

loglik	The maximized log likelihood function.
covMatrix	The asymptotic covariance of $(\mu, \text{vec}(\beta))'$. An $r(p + 1)$ by $r(p + 1)$ matrix. The covariance matrix returned are asymptotic. For the actual standard errors, multiply by $1 / n$.
asySE	The asymptotic standard error for elements in β under the heteroscedastic envelope model. An r by p matrix. The standard errors returned are asymptotic, for actual standard errors, multiply by $1 / \text{sqrt}(n)$.
ratio	The asymptotic standard error ratio of the standard multivariate linear regression for comparing group means over the heteroscedastic envelope estimator, for each element in β . An r by p matrix.
groupInd	A matrix containing the unique values of group indicators. The matrix has p rows.
n	The number of observations in the data.
ng	The number of observations in each group.
Yfit	Fitted responses.

References

- Su, Z. and Cook, R. D. (2013) Estimation of Multivariate Means with Heteroscedastic Error Using Envelope Models. *Statistica Sinica*, 23, 213-230.
- Cook, R. D., Li, B. and Chiaromonte, F. (2010). Envelope Models for Parsimonious and Efficient Multivariate Linear Regression (with discussion). *Statist. Sinica* 20, 927- 1010.
- Cook, R. D., Forzani, L. and Su, Z. (2016) A Note on Fast Envelope Estimation. *Journal of Multivariate Analysis*. 150, 42-54.

Examples

```
data(waterstrider)
X <- waterstrider[ , 1]
Y <- waterstrider[ , 2:5]

## Not run: u <- u.henv(X, Y)
## Not run: u

## Not run: m <- henv(X, Y, 2)
```

henvMU

Estimate the heteroscedastic envelope subspace

Description

Estimate the heteroscedastic envelope subspace with specified dimension.

Usage

```
henvMU(M, U, MU, u, n, ng, L)
```

Arguments

M	A matrix M for the non-Grassmann manifold optimization problem in Cook et al. (2016)
U	A matrix U for the non-Grassmann manifold optimization problem in Cook et al. (2016)
MU	Sum of matrix M and U.
u	A given dimension of the heteroscedastic envelope space. It should be an integer between 0 and r .
n	The number of observations.
ng	A L by 1 vector of the number of observations in each group.
L	The number of groups.

Value

Gamma	An r by u matrix for the orthonormal basis of the heteroscedastic envelope subspace.
Gamma0	An r by $(r - u)$ matrix for the orthonormal basis of the complement of the heteroscedastic envelope subspace.

References

Cook, R. D., Forzani, L. and Su, Z. (2016) A Note on Fast Envelope Estimation. *Journal of Multivariate Analysis*. 150, 42-54.

horseshoecrab	<i>Horseshoe Crab Data</i>
---------------	----------------------------

Description

The number of satellite male crabs near a female crab upon characteristic of the female horseshoe crabs.

Usage

```
data("horseshoecrab")
```

Format

A data frame with 173 observations on the following 5 variables.

V1 Color.

V2 Condition of spine.

V3 Width of shell.

V4 Satellite.

V5 Weight.

Details

This data set contains the number of satellite male crabs and characteristics of the female horseshoe crabs.

References

Agresti, A. (2007). An Introduction to Categorical Data Analysis, 2nd edition.

logit.env

Fit the envelope model in logistic regression

Description

Fit the envelope model in logistic regression with dimension u .

Usage

```
logit.env(X, Y, u, asy = TRUE, init = NULL)
```

Arguments

X	Predictors. An n by p matrix, p is the number of predictors and n is number of observations. The predictors must be continuous variables.
Y	Response. An n by 1 matrix. The univariate response must be binary.
u	Dimension of the envelope. An integer between 0 and p .
asy	Flag for computing the asymptotic variance of the envelope estimator. The default is TRUE. When p and r are large, computing the asymptotic variance can take much time and memory. If only the envelope estimators are needed, the flag can be set to asy = FALSE.
init	The user-specified value of Gamma for the envelope subspace in logistic regression. An p by u matrix. The default is the one generated by function logit.envMU.

Details

This function fits the envelope model in logistic regression,

$$Y = \exp(\mu + \beta'X)/(1 + \exp(\mu + \beta'X)), \Sigma_X = \Gamma\Omega\Gamma' + \Gamma_0\Omega_0\Gamma_0'$$

using the maximum likelihood estimation. When the dimension of the envelope is between 1 and $p-1$, the starting value and blockwise coordinate descent algorithm in Cook et al. (2016) is implemented. This model works the best when X is multivariate normal.

Value

The output is a list that contains the following components:

beta	The envelope estimator of the canonical parameter.
SigmaX	The envelope estimator of the covariance matrix of X .
Gamma	An orthonormal basis of the envelope subspace.
Gamma0	An orthonormal basis of the complement of the envelope subspace.
eta	The estimated beta of the canonical parameter with respect to Gamma.
Omega	The coordinates of SigmaX with respect to Gamma.
Omega0	The coordinates of SigmaX with respect to Gamma0.
mu	The estimated intercept of the canonical parameter.
loglik	The maximized log likelihood function.
covMatrix	The asymptotic covariance of $\text{vec}(\text{beta})$. The covariance matrix returned are asymptotic. For the actual standard errors, multiply by $1/n$.
asySE	The asymptotic standard error for elements in beta under the envelope model. The standard errors returned are asymptotic, for actual standard errors, multiply by $1/\sqrt{n}$.
ratio	The asymptotic standard error ratio of the standard multivariate linear regression estimator over the envelope estimator, for each element in beta.
n	The number of observations in the data.

References

Cook, R. D., Zhang, X. (2015). Foundations for Envelope Models and Methods. Journal of the American Statistical Association 110, 599 - 611.

Cook, R. D., Forzani, L. and Su, Z. (2016) A Note on Fast Envelope Estimation. Journal of Multivariate Analysis. 150, 42-54.

Examples

```
data(horseshoecrab)
X1 <- as.numeric(horseshoecrab[, 1]) == 2)
X2 <- as.numeric(horseshoecrab[, 1]) == 3)
X3 <- as.numeric(horseshoecrab[, 1]) == 4)
X4 <- as.numeric(horseshoecrab[, 2]) == 2)
X5 <- as.numeric(horseshoecrab[, 2]) == 3)
```

```

X6 <- horseshoecrab[ , 3]
X7 <- horseshoecrab[ , 5]
X <- cbind(X1, X2, X3, X4, X5, X6, X7)
Y <- as.numeric(iffelse(horseshoecrab[ , 4] > 0, 1, 0))

u <- u.logit.env(X, Y)
u

m <- logit.env(X, Y, 1)
m$beta

```

logit.envMU

Estimate the envelope subspace in logistic regression

Description

Estimate the envelope subspace with specified dimension in logistic regression.

Usage

```
logit.envMU(X, Y, u)
```

Arguments

X	Predictors. An n by p matrix, p is the number of predictors. The predictors can be univariate or multivariate, discrete or continuous.
Y	Response. An n by 1 matrix. The univariate response must be binary.
u	Dimension of the envelope. An integer between 0 and p .

Details

This function estimate the envelope subspace in logistic regression using an non-Grassmann optimization algorithm. The starting value and optimization algorithm is described in Cook et al. (2016).

Value

Gammahat	The orthonormal basis of the envelope subspace.
Gamma0hat	The orthonormal basis of the complement of the envelope subspace.
muhat	The estimated intercept of the canonical parameter.
etahat	The estimated beta of the canonical parameter with respect to Gamma.
weighthat	The estimated weight defined as $C''(\theta) / E(C''(\theta))$ where $C(\theta)$ is the conditional log likelihood.
What	The estimated V defined as $V = \theta + (Y - \mu(\theta)) / W$.
avar	The asymptotic covariance of $\text{vec}(\beta)$.
objfun	The minimized objective function.

References

Cook, R. D., Forzani, L. and Su, Z. (2016) A Note on Fast Envelope Estimation. *Journal of Multivariate Analysis*. 150, 42-54.

penv

Fit the partial envelope model

Description

Fit the partial envelope model in multivariate linear regression with dimension u .

Usage

```
penv(X1, X2, Y, u, asy = TRUE, init = NULL)
```

Arguments

X1	Predictors of main interest. An n by p_1 matrix, n is the number of observations, and p_1 is the number of main predictors. The predictors can be univariate or multivariate, discrete or continuous.
X2	Covariates, or predictors not of main interest. An n by p_2 matrix, p_2 is the number of covariates.
Y	Multivariate responses. An n by r matrix, r is the number of responses and n is number of observations. The responses must be continuous variables.
u	Dimension of the partial envelope. An integer between 0 and r .
asy	Flag for computing the asymptotic variance of the partial envelope estimator. The default is TRUE. When p and r are large, computing the asymptotic variance can take much time and memory. If only the partial envelope estimators are needed, the flag can be set to <code>asy = FALSE</code> .
init	The user-specified value of Gamma for the partial envelope subspace. An r by u matrix. The default is the one generated by function <code>envMU</code> .

Details

This function fits the partial envelope model to the responses Y and predictors X_1 and X_2 ,

$$Y = \mu + \Gamma\eta X_1 + \beta_2 X_2 + \varepsilon, \Sigma = \Gamma\Omega\Gamma' + \Gamma_0\Omega_0\Gamma_0'$$

using the maximum likelihood estimation. When the dimension of the envelope is between 1 and $r - 1$, we implemented the algorithm in Su and Cook (2011), but the partial envelope subspace is estimated using the blockwise coordinate descent algorithm in Cook et al. (2016). When the dimension is r , then the partial envelope model degenerates to the standard multivariate linear regression with Y as the responses and both X_1 and X_2 as predictors. When the dimension is 0, X_1 and Y are uncorrelated, and the fitting is the standard multivariate linear regression with Y as the responses and X_2 as the predictors.

Value

The output is a list that contains the following components:

beta1	The partial envelope estimator of beta1, which is the regression coefficients for X1.
beta2	The partial envelope estimator of beta2, which is the regression coefficients for X2.
Sigma	The partial envelope estimator of the error covariance matrix.
Gamma	An orthonormal basis of the partial envelope subspace.
Gamma0	An orthonormal basis of the complement of the partial envelope subspace.
eta	The coordinates of beta1 with respect to Gamma.
Omega	The coordinates of Sigma with respect to Gamma.
Omega0	The coordinates of Sigma with respect to Gamma0.
mu	The estimated intercept in the partial envelope model.
loglik	The maximized log likelihood function.
covMatrix	The asymptotic covariance of $\text{vec}(\beta)$, while $\beta = (\beta_1, \beta_2)$. The covariance matrix returned are asymptotic. For the actual standard errors, multiply by $1 / n$.
asySE1	The asymptotic standard error for elements in beta1 under the partial envelope model. The standard errors returned are asymptotic, for actual standard errors, multiply by $1 / \sqrt{n}$.
asySE2	The asymptotic standard error for elements in beta2 under the partial envelope model. The standard errors returned are asymptotic, for actual standard errors, multiply by $1 / \sqrt{n}$.
ratio	The asymptotic standard error ratio of the standard multivariate linear regression estimator over the partial envelope estimator, for each element in beta1.
n	The number of observations in the data.

References

- Su, Z. and Cook, R.D. (2011). Partial envelopes for efficient estimation in multivariate linear regression. *Biometrika* 98, 133 - 146.
- Cook, R. D., Forzani, L. and Su, Z. (2016) A Note on Fast Envelope Estimation. *Journal of Multivariate Analysis*. 150, 42-54.

Examples

```
data(fiberpaper)
X1 <- fiberpaper[, 7]
X2 <- fiberpaper[, 5:6]
Y <- fiberpaper[, 1:4]
u <- u.penv(X1, X2, Y)
u

m <- penv(X1, X2, Y, 1)
m
m$beta1
```

pois.env

*Fit the envelope model in poisson regression***Description**

Fit the envelope model in poisson regression with dimension u .

Usage

```
pois.env(X, Y, u, asy = TRUE, init = NULL)
```

Arguments

X	Predictors. An n by p matrix, p is the number of predictors and n is number of observations. The predictors must be continuous variables.
Y	Response. An n by 1 matrix. The univariate response must be counts.
u	Dimension of the envelope. An integer between 0 and p .
<code>asy</code>	Flag for computing the asymptotic variance of the envelope estimator. The default is TRUE. When p and r are large, computing the asymptotic variance can take much time and memory. If only the envelope estimators are needed, the flag can be set to <code>asy = FALSE</code> .
<code>init</code>	The user-specified value of Gamma for the envelope subspace in poisson regression. An p by u matrix. The default is the one generated by function <code>pois.envMU</code> .

Details

This function fits the envelope model in poisson regression,

$$Y = \exp(\mu + \beta' X), \Sigma_X = \Gamma\Omega\Gamma' + \Gamma_0\Omega_0\Gamma_0'$$

using the maximum likelihood estimation. When the dimension of the envelope is between 1 and $p-1$, the starting value and blockwise coordinate descent algorithm in Cook et al. (2016) is implemented. This model works the best when X is multivariate normal.

Value

The output is a list that contains the following components:

<code>beta</code>	The envelope estimator of the canonical parameter.
<code>SigmaX</code>	The envelope estimator of the covariance matrix of X .
<code>Gamma</code>	An orthonormal basis of the envelope subspace.
<code>Gamma0</code>	An orthonormal basis of the complement of the envelope subspace.
<code>eta</code>	The estimated beta of the canonical parameter with respect to Gamma.
<code>Omega</code>	The coordinates of <code>SigmaX</code> with respect to Gamma.

<code>Omega0</code>	The coordinates of Σ_X with respect to Γ_0 .
<code>mu</code>	The estimated intercept of the canonical parameter.
<code>loglik</code>	The maximized log likelihood function.
<code>covMatrix</code>	The asymptotic covariance of $\text{vec}(\beta)$. The covariance matrix returned are asymptotic. For the actual standard errors, multiply by $1 / n$.
<code>asySE</code>	The asymptotic standard error for elements in β under the envelope model. The standard errors returned are asymptotic, for actual standard errors, multiply by $1 / \sqrt{n}$.
<code>ratio</code>	The asymptotic standard error ratio of the standard multivariate linear regression estimator over the envelope estimator, for each element in β .
<code>n</code>	The number of observations in the data.

References

Cook, R. D., Zhang, X. (2015). Foundations for Envelope Models and Methods. *Journal of the American Statistical Association* 110, 599 - 611.

Cook, R. D., Forzani, L. and Su, Z. (2016) A Note on Fast Envelope Estimation. *Journal of Multivariate Analysis*. 150, 42-54.

Examples

```
data(horseshoecrab)
X1 <- as.numeric(horseshoecrab[ , 1] == 2)
X2 <- as.numeric(horseshoecrab[ , 1] == 3)
X3 <- as.numeric(horseshoecrab[ , 1] == 4)
X4 <- as.numeric(horseshoecrab[ , 2] == 2)
X5 <- as.numeric(horseshoecrab[ , 2] == 3)
X6 <- horseshoecrab[ , 3]
X7 <- horseshoecrab[ , 5]
X <- cbind(X1, X2, X3, X4, X5, X6, X7)
Y <- horseshoecrab[ , 4]

u <- u.pois.env(X, Y)
u

m <- pois.env(X, Y, 1)
m$beta
```

pois.envMU

Estimate the envelope subspace in poisson regression

Description

Estimate the envelope subspace with specified dimension in poisson regression.

Usage

```
pois.envMU(X, Y, u)
```

Arguments

X Predictors. An n by p matrix, p is the number of predictors. The predictors can be univariate or multivariate, discrete or continuous.

Y Response. An n by 1 matrix. The univariate response must be counts.

u Dimension of the envelope. An integer between 0 and p .

Details

This function estimate the envelope subspace in poisson regression using an non-Grassmann optimization algorithm. The starting value and optimization algorithm is described in Cook et al. (2016).

Value

Gammahat The orthonormal basis of the envelope subspace.

Gamma0hat The orthonormal basis of the complement of the envelope subspace.

muhat The estimated intercept of the canonical parameter.

etahat The estimated beta of the canonical parameter with respect to Γ .

weighthat The estimated weight defined as $C''(\theta) / E(C''(\theta))$ where $C(\theta)$ is the conditional log likelihood.

Vhat The estimated V defined as $V = \theta + (Y - \mu(\theta)) / W$.

avar The asymptotic covariance of $\text{vec}(\beta)$.

objfun The minimized objective function.

References

Cook, R. D., Forzani, L. and Su, Z. (2016) A Note on Fast Envelope Estimation. *Journal of Multivariate Analysis*. 150, 42-54.

pred.env *Estimation or prediction for env*

Description

Perform estimation or prediction under the envelope model.

Usage

```
pred.env(m, Xnew)
```

Arguments

m	A list containing estimators and other statistics inherited from env.
Xnew	The value of X with which to estimate or predict Y. A p dimensional vector.

Details

This function evaluates the envelope model at new value Xnew. It can perform estimation: find the fitted value when $X = X_{\text{new}}$, or prediction: predict Y when $X = X_{\text{new}}$. The covariance matrix and the standard errors are also provided.

Value

The output is a list that contains following components.

value	The fitted value or the predicted value evaluated at Xnew.
covMatrix.estm	The covariance matrix of the fitted value at Xnew.
SE.estm	The standard error of the fitted value at Xnew.
covMatrix.pred	The covariance matrix of the predicted value at Xnew.
SE.pred	The standard error of the predicted value at Xnew.

Examples

```
data(wheatprotein)
X <- wheatprotein[, 8]
Y <- wheatprotein[, 1:6]
u <- u.env(X, Y)
u

m <- env(X, Y, 1)
m

X <- as.matrix(X)
pred.res <- pred.env(m, X[2, ])
pred.res
```

pred.genv

Estimation or prediction for genv

Description

Perform estimation or prediction under the groupwise envelope model.

Usage

```
pred.genv(m, Xnew, Znew)
```


Arguments

m	A list containing estimators and other statistics inherited from env.
Xnew	The value of X with which to estimate or predict Y. A p dimensional vector.
Znew	A group indicator of X.

Details

This function evaluates the envelope model at new value Xnew. It can perform estimation: find the fitted value when $X = X_{\text{new}}$ with a group indicator $Z = Z_{\text{new}}$, or prediction: predict Y when $X = X_{\text{new}}$ with a group indicator $Z = Z_{\text{new}}$. The covariance matrix and the standard errors are also provided.

Value

The output is a list that contains following components.

value	The fitted value or the predicted value evaluated at Znew.
covMatrix.estm	The covariance matrix of the fitted value at Znew.
SE.estm	The standard error of the fitted value at Znew.
covMatrix.pred	The covariance matrix of the predicted value at Znew.
SE.pred	The standard error of the predicted value at Znew.

Examples

```
data(fiberpaper)
X <- fiberpaper[ , c(5, 7)]
Y <- fiberpaper[ , 1:3]
Z <- as.numeric(fiberpaper[ , 6] > mean(fiberpaper[ , 6]))
u <- u.genv(X, Y, Z)
u

m <- genv(X, Y, Z, 2)
m

X <- as.matrix(X)
pred.res <- pred.genv(m, X[2, ], Z[2])
pred.res
```

pred.henv

Estimation or prediction for henv

Description

Perform estimation or prediction under the heteroscedastic envelope model.

Usage

```
pred.henv(m, Xnew)
```

Arguments

m A list containing estimators and other statistics inherited from `henv`.
Xnew The value of `X` with which to estimate or predict `Y`. An `r` by 1 vector.

Details

This function evaluates the heteroscedastic envelope model at new value `Xnew`. It can perform estimation: find the fitted value when $X = X_{\text{new}}$, or prediction: predict `Y` when $X = X_{\text{new}}$. The covariance matrix and the standard errors are also provided.

Value

The output is a list that contains following components.

value The fitted value or the predicted value evaluated at `Xnew`.
covMatrix.estm The covariance matrix of the fitted value at `Xnew`.
SE.estm The standard error of the fitted value at `Xnew`.
covMatrix.pred The covariance matrix of the predicted value at `Xnew`.
SE.pred The standard error of the predicted value at `Xnew`.

Examples

```
data(waterstrider)
X <- waterstrider[, 1]
Y <- waterstrider[, 2:5]

## Not run: u <- u.henv(X, Y)
## Not run: u

## Not run: m <- henv(X, Y, 2)

## Not run: pred.res <- pred.henv(m, X[2])
```

pred.logit.env

Estimation or prediction for logit.env

Description

Perform estimation or prediction under the envelope model in logistic regression.

Usage

```
pred.logit.env(m, Xnew)
```

Arguments

m	A list containing estimators and other statistics inherited from xenv.
Xnew	The value of X with which to estimate or predict Y. A p dimensional vector.

Details

This function evaluates the envelope model at new value Xnew. It can perform estimation: find the fitted value when $X = X_{\text{new}}$. The covariance matrix of estimation and the standard errors of estimation are also provided.

Value

The output is a list that contains following components.

value	The fitted value or predicted value evaluated at Xnew.
covMatrix.estm	The covariance matrix of the fitted value at Xnew.
SE.estm	The standard error of the fitted value at Xnew.

Examples

```
data(horseshoecrab)
X1 <- as.numeric(horseshoecrab[ , 1] == 2)
X2 <- as.numeric(horseshoecrab[ , 1] == 3)
X3 <- as.numeric(horseshoecrab[ , 1] == 4)
X4 <- as.numeric(horseshoecrab[ , 2] == 2)
X5 <- as.numeric(horseshoecrab[ , 2] == 3)
X6 <- horseshoecrab[ , 3]
X7 <- horseshoecrab[ , 5]
X <- cbind(X1, X2, X3, X4, X5, X6, X7)
Y <- as.numeric(ifelse(horseshoecrab[ , 4] > 0, 1, 0))

m <- logit.env(X, Y, 1)

pred.res <- pred.logit.env(m, X[1, ])
pred.res
```

pred.penv *Estimation or prediction for penv*

Description

Perform estimation or prediction under the partial envelope model.

Usage

```
pred.penv(m, X1new, X2new)
```

Arguments

m	A list containing estimators and other statistics inherited from penv.
X1new	The value of X1 with which to estimate or predict Y. A p1 dimensional vector.
X2new	The value of X2 with which to estimate or predict Y. A p2 dimensional vector.

Details

This function evaluates the partial envelope model at new value Xnew. It can perform estimation: find the fitted value when $X = X_{new}$, or prediction: predict Y when $X = X_{new}$. The covariance matrix and the standard errors are also provided.

Value

The output is a list that contains following components.

value	The fitted value or the predicted value evaluated at X1new and X2new.
covMatrix.estm	The covariance matrix of the fitted value at X1new and X2new.
SE.estm	The standard error of the fitted value at X1new and X2new.
covMatrix.pred	The covariance matrix of the predicted value at X1new and X2new.
SE.pred	The standard error of the predicted value at X1new and X2new.

Examples

```
data(fiberpaper)
X1 <- fiberpaper[, 7]
X2 <- fiberpaper[, 5:6]
Y <- fiberpaper[, 1:4]
m <- penv(X1, X2, Y, 1)

pred.res <- pred.penv(m, X1[1], X2[1, ])
pred.res
```

pred.pois.env

Estimation or prediction for pois.env

Description

Perform estimation or prediction under the envelope model in poisson regression.

Usage

```
pred.pois.env(m, Xnew)
```

Arguments

m	A list containing estimators and other statistics inherited from xenv.
Xnew	The value of X with which to estimate or predict Y. A p dimensional vector.

Details

This function evaluates the envelope in poisson regression at new value X_{new} . It can perform estimation: find the fitted value when $X = X_{new}$, or prediction: predict Y when $X = X_{new}$. The covariance matrix of estimation and the standard errors of estimation are also provided.

Value

The output is a list that contains following components.

value The fitted value or the predicted value evaluated at X_{new} .
 covMatrix.estm The covariance matrix of the fitted value at X_{new} .
 SE.estm The standard error of the fitted value at X_{new} .

Examples

```
data(horseshoecrab)
X1 <- as.numeric(horseshoecrab[ , 1] == 2)
X2 <- as.numeric(horseshoecrab[ , 1] == 3)
X3 <- as.numeric(horseshoecrab[ , 1] == 4)
X4 <- as.numeric(horseshoecrab[ , 2] == 2)
X5 <- as.numeric(horseshoecrab[ , 2] == 3)
X6 <- horseshoecrab[ , 3]
X7 <- horseshoecrab[ , 5]
X <- cbind(X1, X2, X3, X4, X5, X6, X7)
Y <- horseshoecrab[ , 4]

m <- pois.env(X, Y, 1)

pred.res <- pred.pois.env(m, X[1, ])
pred.res
```

pred.senv

Estimation or prediction for senv

Description

Perform estimation or prediction under the scaled envelope model.

Usage

```
pred.senv(m, Xnew)
```

Arguments

m A list containing estimators and other statistics inherited from scale.env.
 Xnew The value of X with which to estimate or predict Y . A p dimensional vector.

Details

This function evaluates the scaled envelope model at new value X_{new} . It can perform estimation: find the fitted value when $X = X_{\text{new}}$, or prediction: predict Y when $X = X_{\text{new}}$. The covariance matrix and the standard errors are also provided.

Value

The output is a list that contains following components.

value	The fitted value or the predicted value evaluated at X_{new} .
covMatrix.estm	The covariance matrix of the fitted value at X_{new} .
SE.estm	The standard error of the fitted value at X_{new} .
covMatrix.pred	The covariance matrix of the predicted value at X_{new} .
SE.pred	The standard error of the predicted value at X_{new} .

Examples

```
data(sales)
X <- sales[, 1:3]
Y <- sales[, 4:7]

m <- senv(X, Y, 2)

pred.res <- pred.senv(m, X[2, ])
pred.res
```

pred.stenv

Estimation or prediction for stenv

Description

Perform estimation or prediction under the simultaneous envelope model.

Usage

```
pred.stenv(m, Xnew)
```

Arguments

m	A list containing estimators and other statistics inherited from stenv.
Xnew	The value of X with which to estimate or predict Y . A p dimensional vector.

Details

This function evaluates the simultaneous envelope model at new value X_{new} . It can perform estimation: find the fitted value when $X = X_{\text{new}}$, or prediction: predict Y when $X = X_{\text{new}}$. The covariance matrix and the standard errors are also provided.

Value

The output is a list that contains following components.

value	The fitted value or the predicted value evaluated at Xnew.
covMatrix.estm	The covariance matrix of the fitted value at Xnew.
SE.estm	The standard error of the fitted value at Xnew.
covMatrix.pred	The covariance matrix of the predicted value at Xnew.
SE.pred	The standard error of the predicted value at Xnew.

Examples

```
data(fiberpaper)
X <- fiberpaper[ , 5:7]
Y <- fiberpaper[ , 1:4]

m <- stenv(X, Y, 2, 3)
m

pred.res <- pred.stenv(m, X[1, ])
pred.res
```

pred.sxenv

Estimation or prediction for sxenv

Description

Perform estimation or prediction under the scaled envelope model in the predictor space.

Usage

```
pred.sxenv(m, Xnew)
```

Arguments

m	A list containing estimators and other statistics inherited from stenv.
Xnew	The value of X with which to estimate or predict Y. A p dimensional vector.

Details

This function evaluates the scaled envelope model in the predictor space at new value Xnew. It can perform estimation: find the fitted value when $X = X_{\text{new}}$, or prediction: predict Y when $X = X_{\text{new}}$. The covariance matrix and the standard errors are also provided.

Value

The output is a list that contains following components.

value	The fitted value or the predicted value evaluated at Xnew.
covMatrix.estm	The covariance matrix of the fitted value at Xnew.
SE.estm	The standard error of the fitted value at Xnew.
covMatrix.pred	The covariance matrix of the predicted value at Xnew.
SE.pred	The standard error of the predicted value at Xnew.

Examples

```
data(sales)
Y <- sales[, 1:3]
X <- sales[, 4:7]
R <- rep(1, 4)

m <- sxenv(X, Y, 2, R)

pred.res <- pred.sxenv(m, X[1, ])
pred.res
```

pred.xenv

Estimation or prediction for xenv

Description

Perform estimation or prediction under the envelope model in predictor space.

Usage

```
pred.xenv(m, Xnew)
```

Arguments

m	A list containing estimators and other statistics inherited from xenv.
Xnew	The value of X with which to estimate or predict Y. A p dimensional vector.

Details

This function evaluates the envelope model at new value Xnew. It can perform estimation: find the fitted value when $X = X_{\text{new}}$, or prediction: predict Y when $X = X_{\text{new}}$. The covariance matrix and the standard errors are also provided.

Value

The output is a list that contains following components.

value	The fitted value or the predicted value evaluated at Xnew.
covMatrix.estm	The covariance matrix of the fitted value at Xnew.
SE.estm	The standard error of the fitted value at Xnew.
covMatrix.pred	The covariance matrix of the predicted value at Xnew.
SE.pred	The standard error of the predicted value at Xnew.

Examples

```
data(wheatprotein)
X <- wheatprotein[, 1:6]
Y <- wheatprotein[, 7]

m <- xenv(X, Y, 2)
m

pred.res <- pred.xenv(m, X[1, ])
pred.res
```

pred2.env

Estimation or prediction for env

Description

Perform estimation or prediction under the envelope model through partial envelope model.

Usage

```
pred2.env(X, Y, u, Xnew)
```

Arguments

X	Predictors. An n by p matrix, p is the number of predictors. The predictors can be univariate or multivariate, discrete or continuous.
Y	Multivariate responses. An n by r matrix, r is the number of responses and n is number of observations. The responses must be continuous variables.
u	The dimension of the constructed partial envelope model.
Xnew	The value of X with which to estimate or predict Y. A p dimensional vector.

Details

This function evaluates the envelope model at new value X_{new} . It can perform estimation: find the fitted value when $X = X_{new}$, or prediction: predict Y when $X = X_{new}$. The covariance matrix and the standard errors are also provided. Compared to `predict.env`, this function performs prediction through partial envelope model, which can be more accurate if the partial envelope is of smaller dimension and contains less variant material information. The constructed partial envelope model is obtained by the following: Let A_0 by a p by $p-1$ matrix, such that $A = (X_{new}, A_0)$ has full rank. Let $\phi_1 = \beta * X_{new}$, $\phi_2 = \beta * A_0$, $\phi = (\phi_1, \phi_2)$ and $X = \text{inverse of } A * X = (Z_1, Z_2)'$. Then the model $Y = \alpha + \beta * X + \epsilon$ can be reparameterized as $Y = \alpha + \phi_1 * Z_1 + \phi_2 * Z_2 + \epsilon$. We then fit a partial envelope model with Z_1 as the predictor of interest, and predict at $(Z_1, Z_2)' = \text{inverse of } A * X_{new}$.

Value

The output is a list that contains following components.

<code>value</code>	The fitted value or the predicted value evaluated at X_{new} .
<code>covMatrix.estm</code>	The covariance matrix of the fitted value at X_{new} .
<code>SE.estm</code>	The standard error of the fitted value at X_{new} .
<code>covMatrix.pred</code>	The covariance matrix of the predicted value at X_{new} .
<code>SE.pred</code>	The standard error of the predicted value at X_{new} .

Examples

```
data(fiberpaper)
X <- fiberpaper[, 5:7]
Y <- fiberpaper[, 1:4]

u <- u.pred2.env(X, Y, X[10, ])
pred.res <- pred2.env(X, Y, u$u.bic, X[10, ])
pred.res$SE.estm
pred.res$SE.pred
```

sales

Sales staff Data

Description

On the performance of a firm's sales staff

Usage

```
data("sales")
```

Format

A data frame with 50 observations on the following 7 variables.

V1 Index of sales growth.

V2 Index of sales profitability.

V3 Index of new account sales.

V4 Score on creativity.

V5 Score on mechanical reasoning test.

V6 Score on abstract reasoning test.

V7 Score on Mathematics test.

Details

This data set contains 3 measures of performance and 4 tests scores.

References

Johnson, R.A., Wichern, D.W. (2007). Applied Multivariate Statistical Analysis, 6th edition.

senv

Fit the scaled envelope model

Description

Fit the scaled envelope model in multivariate linear regression with dimension u .

Usage

```
senv(X, Y, u, asy = TRUE, init = NULL)
```

Arguments

X	Predictors. An n by p matrix, p is the number of predictors. The predictors can be univariate or multivariate, discrete or continuous.
Y	Multivariate responses. An n by r matrix, r is the number of responses and n is number of observations. The responses must be continuous variables.
u	Dimension of the scaled envelope. An integer between 0 and r .
<code>asy</code>	Flag for computing the asymptotic variance of the envelope estimator. The default is TRUE. When p and r are large, computing the asymptotic variance can take much time and memory. If only the scaled envelope estimators are needed, the flag can be set to <code>asy = FALSE</code> .
<code>init</code>	The user-specified value of Gamma for the scaled envelope subspace. An r by u matrix. The default is the one generated by function <code>senvMU</code> .

Details

This function fits the scaled envelope model to the responses and predictors,

$$Y = \mu + \Lambda\Gamma\eta X + \varepsilon, \Sigma = \Lambda\Gamma\Omega\Gamma'\Lambda + \Lambda\Gamma_0\Omega_0\Gamma_0'\Lambda$$

using the maximum likelihood estimation. When the dimension of the scaled envelope is between 1 and $r-1$, the starting value and blockwise coordinate descent algorithm in Cook et al. (2016) is implemented. When the dimension is r , then the scaled envelope model degenerates to the standard multivariate linear regression. When the dimension is 0, it means that X and Y are uncorrelated, and the fitting is different.

Value

The output is a list that contains the following components:

beta	The scaled envelope estimator of the regression coefficients.
Sigma	The scaled envelope estimator of the error covariance matrix.
Lambda	The matrix of estimated scale.
Gamma	An orthonormal basis of the scaled envelope subspace.
Gamma0	An orthonormal basis of the complement of the scaled envelope subspace.
eta	The coordinates of beta with respect to Gamma.
Omega	The coordinates of Sigma with respect to Gamma.
Omega0	The coordinates of Sigma with respect to Gamma0.
mu	The estimated intercept.
loglik	The maximized log likelihood function.
covMatrix	The asymptotic covariance of $\text{vec}(\text{beta})$. The covariance matrix returned are asymptotic. For the actual standard errors, multiply by $1/n$.
asySE	The asymptotic standard error for elements in beta under the envelope model. The standard errors returned are asymptotic, for actual standard errors, multiply by $1/\sqrt{n}$.
ratio	The asymptotic standard error ratio of the standard multivariate linear regression estimator over the envelope estimator, for each element in beta.
n	The number of observations in the data.

References

- Cook, R. D., Su, Z. (2013). Scaled Envelopes: scale Invariant and Efficient Estimation in Multivariate Linear Regression. *Biometrika* 100, 939 - 954.
- Cook, R. D., Forzani, L. and Su, Z. (2016) A Note on Fast Envelope Estimation. *Journal of Multivariate Analysis*. 150, 42-54.

Examples

```

data(sales)
X <- sales[, 1:3]
Y <- sales[, 4:7]

u <- u.senv(X, Y)
u

m <- senv(X, Y, 2)
m$beta

```

senvMU

*Estimate the scaled envelope subspace***Description**

Estimate the scaled envelope subspace with specified dimension.

Usage

```
senvMU(X, Y, u)
```

Arguments

X	Predictors. An n by p matrix, p is the number of predictors. The predictors can be univariate or multivariate, discrete or continuous.
Y	Multivariate responses. An n by r matrix, r is the number of responses and n is number of observations. The responses must be continuous variables.
u	Dimension of the envelope. An integer between 0 and r.

Details

This function estimate the scaled envelope subspace using an non-Grassmann optimization algorithm and nonlinear optimization using augmented Lagrange method.

Value

Gammahat	The orthonormal basis of the scaled envelope subspace.
Gamma0hat	The orthonormal basis of the complement of the scaled envelope subspace.
Lambdahat	The matrix of estimated scales.
objfun	The minimized objective function.

References

Cook, R. D., Forzani, L. and Su, Z. (2016) A Note on Fast Envelope Estimation. *Journal of Multivariate Analysis*. 150, 42-54.

Ye, Y., Interior algorithms for linear, quadratic, and linearly constrained non linear programming, PhD Thesis, Departments of EES stanford University, Stanford CA.

stenv

Fit the simultaneous envelope model

Description

Fit the simultaneous envelope model in multivariate linear regression with dimension (q, u) .

Usage

```
stenv(X, Y, q, u, asy = TRUE, Pinit = NULL, Ginit = NULL)
```

Arguments

X	Predictors. An n by p matrix, p is the number of predictors. The predictors can be univariate or multivariate, discrete or continuous.
Y	Multivariate responses. An n by r matrix, r is the number of responses and n is number of observations. The responses must be continuous variables.
q	Dimension of the X-envelope. An integer between 0 and p .
u	Dimension of the Y-envelope. An integer between 0 and r .
asy	Flag for computing the asymptotic variance of the envelope estimator. The default is TRUE. When p and r are large, computing the asymptotic variance can take much time and memory. If only the envelope estimators are needed, the flag can be set to <code>asy = FALSE</code> .
Pinit	The user-specified value of Phi for the X-envelope subspace. An p by q matrix. The default is the one generated by function <code>stenvMU</code> .
Ginit	The user-specified value of Gamma for the Y-envelope subspace. An r by u matrix. The default is the one generated by function <code>stenvMU</code> .

Details

This function fits the envelope model to the responses and predictors simultaneously,

$$Y = \mu + \Gamma\eta'\Phi'X + \varepsilon, \Sigma_{Y|X} = \Gamma\Omega\Gamma' + \Gamma_0\Omega_0\Gamma_0', \Sigma_X = \Phi\Delta\Phi' + \Phi_0\Delta_0\Phi_0'$$

using the maximum likelihood estimation. When the dimension of the Y-envelope is between 1 and $r-1$ and the dimension of the X-envelope is between 1 and $p-1$, the starting value and blockwise coordinate descent algorithm in Cook et al. (2016) is implemented. When the dimension is (p, r) , then the envelope model degenerates to the standard multivariate linear regression. When the dimension of the Y-envelope is r , then the envelope model degenerates to the standard envelope model. When the dimension of X-envelope is p , then the envelope model degenerates to the envelope model in the predictor space. When the dimension is 0, it means that X and Y are uncorrelated, and the fitting is different.

Value

The output is a list that contains the following components:

beta	The envelope estimator of the regression coefficients.
SigmaYcX	The envelope estimator of the error covariance matrix.
SigmaX	The envelope estimator of the covariance matrix of X.
Gamma	An orthonormal basis of the Y-envelope subspace.
Gamma0	An orthonormal basis of the complement of the Y-envelope subspace.
eta	The coordinates of beta with respect to Gamma and Phi.
Omega	The coordinates of SigmaYcX with respect to Gamma.
Omega0	The coordinates of SigmaYcX with respect to Gamma0.
mu	The estimated intercept.
Phi	An orthonormal basis of the X-envelope subspace.
Phi0	An orthonormal basis of the complement of the X-envelope subspace.
Delta	The coordinates of SigmaX with respect to Phi.
Delta0	The coordinates of SigmaX with respect to Phi0.
loglik	The maximized log likelihood function.
covMatrix	The asymptotic covariance of vec(beta). The covariance matrix returned are asymptotic. For the actual standard errors, multiply by 1 / n.
asySE	The asymptotic standard error for elements in beta under the envelope model. The standard errors returned are asymptotic, for actual standard errors, multiply by 1 / sqrt(n).
ratio	The asymptotic standard error ratio of the standard multivariate linear regression estimator over the envelope estimator, for each element in beta.
n	The number of observations in the data.

References

- Cook, R. D., Zhang, X. (2015). Simultaneous Envelopes for Multivariate Linear Regression. *Technometrics* 57, 11 - 25.
- Cook, R. D., Forzani, L. and Su, Z. (2016) A Note on Fast Envelope Estimation. *Journal of Multivariate Analysis*. 150, 42-54.

Examples

```
data(fiberpaper)
X <- fiberpaper[, 5:7]
Y <- fiberpaper[, 1:4]
u <- u.stenv(X, Y)
u

m <- stenv(X, Y, 2, 3)
m
m$beta
```

 stenvMU

Estimate the simultaneous envelope subspace

Description

Estimate the simultaneous envelope subspace with specified dimension.

Usage

```
stenvMU(X, Y, q, u)
```

Arguments

X	Predictors. An n by p matrix, p is the number of predictors. The predictors can be univariate or multivariate, discrete or continuous.
Y	Multivariate responses. An n by r matrix, r is the number of responses and n is number of observations. The responses must be continuous variables.
q	Dimension of the X-envelope. An integer between 0 and p.
u	Dimension of the Y-envelope. An integer between 0 and r.

Details

This function estimate the simultaneous envelope subspace using an non-Grassmann optimization algorithm.

Value

Gammahat	The orthonormal basis of the Y-envelope subspace.
Gamma0hat	The orthonormal basis of the complement of the Y-envelope subspace.
Phihat	The orthonormal basis of the X-envelope subspace.
Phi0hat	The orthonormal basis of the complement of the X-envelope subspace.
objfun	The minimized objective function.

References

Cook, R. D., Forzani, L. and Su, Z. (2016) A Note on Fast Envelope Estimation. Journal of Multivariate Analysis. 150, 42-54.

 sxenv

Fit the scaled envelope model in the predictor space

Description

Fit the scaled envelope model in the predictor space in multivariate linear regression with dimension u .

Usage

```
sxenv(X, Y, u, R, asy = TRUE, init = NULL)
```

Arguments

X	Predictors. An n by p matrix, p is the number of predictors. The predictors can be univariate or multivariate, discrete or continuous.
Y	Multivariate responses. An n by r matrix, r is the number of responses and n is number of observations. The responses must be continuous variables.
u	Dimension of the scaled envelope in the predictor space. An integer between 0 and p .
R	The number of replications of the scales. A vector, the sum of all elements of R must be p .
<code>asy</code>	Flag for computing the asymptotic variance of the envelope estimator. The default is TRUE. When p and r are large, computing the asymptotic variance can take much time and memory. If only the envelope estimators are needed, the flag can be set to <code>asy = FALSE</code> .
<code>init</code>	The user-specified value of Gamma for the scaled envelope subspace in the predictor space. An p by u matrix. The default is the one generated by function <code>sxenvMU</code> .

Details

This function fits the scaled envelope model in the predictor space to the responses and predictors,

$$Y = \mu_Y + \eta' \Gamma' \Lambda^{-1} (X - \mu_X) + \varepsilon, \Sigma_X = \Lambda \Gamma \Omega \Gamma' \Lambda + \Lambda \Gamma_0 \Omega_0 \Gamma_0' \Lambda$$

using the maximum likelihood estimation. When the dimension of the scaled envelope in the predictor space is between 1 and $p-1$, the starting value and blockwise coordinate descent algorithm in Cook et al. (2016) is implemented. When the dimension is p , then the scaled envelope model in the predictor space degenerates to the standard multivariate linear regression. When the dimension is 0, it means that X and Y are uncorrelated, and the fitting is different.

Value

The output is a list that contains the following components:

beta	The scaled envelope estimator of the regression coefficients.
Sigma	The scaled envelope estimator of the error covariance matrix.
Lambda	The matrix of estimated scale.
Gamma	An orthonormal basis of the scaled envelope subspace.
Gamma0	An orthonormal basis of the complement of the scaled envelope subspace.
eta	The coordinates of beta with respect to Gamma.
Omega	The coordinates of Sigma with respect to Gamma.
Omega0	The coordinates of Sigma with respect to Gamma0.
muY	The mean of Y.
muX	The mean of X.
loglik	The maximized log likelihood function.
covMatrix	The asymptotic covariance of vec(beta). The covariance matrix returned are asymptotic. For the actual standard errors, multiply by 1 / n.
asySE	The asymptotic standard error for elements in beta under the envelope model. The standard errors returned are asymptotic, for actual standard errors, multiply by 1 / sqrt(n).
ratio	The asymptotic standard error ratio of the standard multivariate linear regression estimator over the envelope estimator, for each element in beta.
n	The number of observations in the data.

References

- Cook, R. D., Su, Z. (2016). Scaled Predictor Envelopes and Partial Least Squares Regression. *Technometrics* 58, 155 - 165.
- Cook, R. D., Forzani, L. and Su, Z. (2016) A Note on Fast Envelope Estimation. *Journal of Multivariate Analysis*. 150, 42-54.

Examples

```
data(sales)
Y <- sales[, 1:3]
X <- sales[, 4:7]
R <- rep(1, 4)

u <- u.sxenv(X, Y, R)
u

m <- sxenv(X, Y, 2, R)
m$beta
```

 sxenvMU

Estimate the scaled envelope subspace in the predictor space

Description

Estimate the scaled envelope subspace in the predictor space with specified dimension.

Usage

```
sxenvMU(X, Y, u, R)
```

Arguments

X	Predictors. An n by p matrix, p is the number of predictors. The predictors can be univariate or multivariate, discrete or continuous.
Y	Multivariate responses. An n by r matrix, r is the number of responses and n is number of observations. The responses must be continuous variables.
u	Dimension of the scaled envelope in the predictor space. An integer between 0 and p .
R	The number of replications of the scales. A vector, the sum of all elements of R must be p .

Details

This function estimate the scaled envelope subspace in the predictor space using an non-Grassmann optimization algorithm and nonlinear optimization using augmented Lagrange method.

Value

Gammahat	The orthonormal basis of the scaled envelope subspace in the predictor space.
Gamma0hat	The orthonormal basis of the complement of the scaled envelope subspace in the predictor space.
Lambdahat	The matrix of estimated scales.
objfun	The minimized objective function.

References

- Cook, R. D., Forzani, L. and Su, Z. (2016) A Note on Fast Envelope Estimation. *Journal of Multivariate Analysis*. 150, 42-54.
- Ye, Y., Interior algorithms for linear, quadratic, and linearly constrained non linear programming, PhD Thesis, Departments of EES stanford University, Stanford CA.

testcoef.env

Hypothesis test of the coefficients of the envelope model

Description

This function tests the null hypothesis $L * \beta * R = A$ versus the alternative hypothesis $L * \beta * R \neq A$, where β is estimated under the envelope model.

Usage

```
testcoef.env(m, L, R, A)
```

Arguments

m	A list containing estimators and other statistics inherited from env.
L	The matrix multiplied to beta on the left. It is a d_1 by r matrix, while d_1 is less than or equal to r .
R	The matrix multiplied to beta on the right. It is a p by d_2 matrix, while d_2 is less than or equal to p .
A	The matrix on the right hand side of the equation. It is a d_1 by d_2 matrix. Note that inputs L, R and A must be matrices, if not, use <code>as.matrix</code> to convert them.

Details

This function tests for hypothesis $H_0: L \beta R = A$, versus $H_a: L \beta R \neq A$. The β is estimated by the envelope model. If $L = I_r$, $R = I_p$ and $A = 0$, then the test is equivalent to the standard F test on if $\beta = 0$. The test statistic used is $\text{vec}(L \beta R - A) \hat{\Sigma}^{-1} \text{vec}(L \beta R - A)^T$, where β is the envelope estimator and $\hat{\Sigma}$ is the estimated asymptotic covariance of $\text{vec}(L \beta R - A)$. The reference distribution is chi-squared distribution with degrees of freedom $d_1 * d_2$.

Value

The output is a list that contains following components.

chisqStatistic	The test statistic.
dof	The degrees of freedom of the reference chi-squared distribution.
pValue	p-value of the test.
covMatrix	The covariance matrix of $\text{vec}(L \beta R)$.

Examples

```

data(wheatprotein)
X <- wheatprotein[, 8]
Y <- wheatprotein[, 1:6]
m <- env(X, Y, 1)
m

L <- diag(6)
R <- as.matrix(1)
A <- matrix(0, 6, 1)

test.res <- testcoef.env(m, L, R, A)
test.res

```

testcoef.genv

Hypothesis test of the coefficients of the groupwise envelope model

Description

This function tests the null hypothesis $L * \beta * R = A$ versus the alternative hypothesis $L * \beta * R \neq A$, where β is estimated under the groupwise envelope model.

Usage

```
testcoef.genv(m, L, R, A)
```

Arguments

m	A list containing estimators and other statistics inherited from genv.
L	The matrix multiplied to beta on the left. It is a d_1 by r matrix, while d_1 is less than or equal to r .
R	The matrix multiplied to beta on the right. It is a p by d_2 matrix, while d_2 is less than or equal to p .
A	The matrix on the right hand side of the equation. It is a d_1 by d_2 matrix. Note that inputs L, R and A must be matrices, if not, use <code>as.matrix</code> to convert them.

Details

This function tests for hypothesis $H_0: L \beta R = A$, versus $H_a: L \beta R \neq A$. The β is estimated by the groupwise envelope model. If $L = I_r$, $R = I_p$ and $A = 0$, then the test is equivalent to the standard F test on if $\beta = 0$. The test statistic used is $\text{vec}(L \beta R - A) \hat{\Sigma}^{-1} \text{vec}(L \beta R - A)^T$, where β is the envelope estimator and $\hat{\Sigma}$ is the estimated asymptotic covariance of $\text{vec}(L \beta R - A)$. The reference distribution is chi-squared distribution with degrees of freedom $d_1 * d_2$.

Value

The output is a list that contains following components.

`chisqStatistic` The test statistic.
`dof` The degrees of freedom of the reference chi-squared distribution.
`pValue` p-value of the test.
`covMatrix` The covariance matrix of $\text{vec}(L\beta R)$.

Examples

```
data(fiberpaper)
X <- fiberpaper[ , c(5, 7)]
Y <- fiberpaper[ , 1:3]
Z <- as.numeric(fiberpaper[ , 6] > mean(fiberpaper[ , 6]))
u <- u.genv(X, Y, Z)
u

m <- genv(X, Y, Z, 2)
m

L <- diag(3)
R <- diag(2)
A <- matrix(0, 3, 2)

test.res <- testcoef.genv(m, L, R, A)
test.res
```

testcoef.henv	<i>Hypothesis test of the coefficients of the heteroscedastic envelope model</i>
---------------	--

Description

This function tests the null hypothesis $L * \beta * R = A$ versus the alternative hypothesis $L * \beta * R \neq A$, where β is estimated under the heteroscedastic envelope model.

Usage

```
testcoef.henv(m, L, R, A)
```

Arguments

`m` A list containing estimators and other statistics inherited from `genv`.
`L` The matrix multiplied to β on the left. It is a d_1 by r matrix, while d_1 is less than or equal to r .
`R` The matrix multiplied to β on the right. It is a p by d_2 matrix, while d_2 is less than or equal to p .

A The matrix on the right hand side of the equation. It is a $d1$ by $d2$ matrix.
Note that inputs L, R and A must be matrices, if not, use `as.matrix` to convert them.

Details

This function tests for hypothesis $H_0: L\beta R = A$, versus $H_a: L\beta R \neq A$. The beta is estimated by the heteroscedastic envelope model. If $L = I_r$, $R = I_p$ and $A = 0$, then the test is equivalent to the standard F test on if $\beta = 0$. The test statistic used is $\text{vec}(L\beta R - A) \hat{\Sigma}^{-1} \text{vec}(L\beta R - A)^T$, where beta is the envelope estimator and $\hat{\Sigma}$ is the estimated asymptotic covariance of $\text{vec}(L\beta R - A)$. The reference distribution is chi-squared distribution with degrees of freedom $d1 * d2$.

Value

The output is a list that contains following components.

`chisqStatistic` The test statistic.
`dof` The degrees of freedom of the reference chi-squared distribution.
`pValue` p-value of the test.
`covMatrix` The covariance matrix of $\text{vec}(L\beta R)$.

Examples

```
data(waterstrider)
X <- waterstrider[, 1]
Y <- waterstrider[, 2:5]

## Not run: m <- henv(X, Y, 2)
## Not run: m

L <- diag(4)
R <- matrix(c(1, -1, 0), 3, 1)
A <- matrix(0, 4, 1)

## Not run: test.res <- testcoef.henv(m, L, R, A)
## Not run: test.res
```

testcoef.logit.env *Hypothesis test of the coefficients of the envelope model*

Description

This function tests the null hypothesis $L * \beta = A$ versus the alternative hypothesis $L * \beta \neq A$, where beta is estimated under the envelope model in logistic regression.

Usage

```
testcoef.logit.env(m, L, A)
```

Arguments

<code>m</code>	A list containing estimators and other statistics inherited from <code>logit.env</code> .
<code>L</code>	The matrix multiplied to beta on the left. It is a $d1$ by p matrix, while $d1$ is less than or equal to p .
<code>A</code>	The matrix on the right hand side of the equation. It is a $d1$ by 1 matrix. Note that inputs <code>L</code> and <code>A</code> must be matrices, if not, use <code>as.matrix</code> to convert them.

Details

This function tests for hypothesis $H_0: L\beta = A$, versus $H_a: L\beta \neq A$. The beta is estimated by the envelope model in predictor space. If $L = I_p$ and $A = 0$, then the test is equivalent to the standard F test on if $\beta = 0$. The test statistic used is $\text{vec}(L\hat{\beta} - A) \hat{\Sigma}^{-1} \text{vec}(L\hat{\beta} - A)^T$, where $\hat{\beta}$ is the envelope estimator and $\hat{\Sigma}$ is the estimated asymptotic covariance of $\text{vec}(L\hat{\beta} - A)$. The reference distribution is chi-squared distribution with degrees of freedom $d1$.

Value

The output is a list that contains following components.

<code>chisqStatistic</code>	The test statistic.
<code>dof</code>	The degrees of freedom of the reference chi-squared distribution.
<code>pValue</code>	p-value of the test.
<code>covMatrix</code>	The covariance matrix of $\text{vec}(L\hat{\beta})$.

Examples

```
data(horseshoecrab)
X1 <- as.numeric(horseshoecrab[, 1] == 2)
X2 <- as.numeric(horseshoecrab[, 1] == 3)
X3 <- as.numeric(horseshoecrab[, 1] == 4)
X4 <- as.numeric(horseshoecrab[, 2] == 2)
X5 <- as.numeric(horseshoecrab[, 2] == 3)
X6 <- horseshoecrab[, 3]
X7 <- horseshoecrab[, 5]
X <- cbind(X1, X2, X3, X4, X5, X6, X7)
Y <- as.numeric(ifelse(horseshoecrab[, 4] > 0, 1, 0))

m <- logit.env(X, Y, 1)

L <- diag(7)
A <- matrix(0, 7, 1)

test.res <- testcoef.logit.env(m, L, A)
test.res
```


testcoef.penv

*Hypothesis test of the coefficients of the partial envelope model***Description**

This function tests the null hypothesis $L * \beta_1 * R = A$ versus the alternative hypothesis $L * \beta_1 * R \neq A$, where β_1 is estimated under the partial envelope model.

Usage

```
testcoef.penv(m, L, R, A)
```

Arguments

<code>m</code>	A list containing estimators and other statistics inherited from <code>penv</code> .
<code>L</code>	The matrix multiplied to β_1 on the left. It is a d_1 by r matrix, while d_1 is less than or equal to r .
<code>R</code>	The matrix multiplied to β_1 on the right. It is a p_1 by d_2 matrix, while d_2 is less than or equal to p_1 .
<code>A</code>	The matrix on the right hand side of the equation. It is a d_1 by d_2 matrix. Note that inputs <code>L</code> , <code>R</code> and <code>A</code> must be matrices, if not, use <code>as.matrix</code> to convert them.

Details

This function tests for hypothesis $H_0: L \beta_1 R = A$, versus $H_a: L \beta_1 R \neq A$. The β_1 is estimated by the partial envelope model. If $L = I_r$, $R = I_{p_1}$ and $A = 0$, then the test is equivalent to the standard F test on if $\beta_1 = 0$. The test statistics used is $\text{vec}(L \beta_1 R - A) \hat{\Sigma}^{-1} \text{vec}(L \beta_1 R - A)^T$, where β_1 is the envelope estimator and $\hat{\Sigma}$ is the estimated asymptotic covariance of $\text{vec}(L \beta_1 R - A)$. The reference distribution is chi-squared distribution with degrees of freedom $d_1 * d_2$.

Value

The output is a list that contains following components.

<code>chisqStatistic</code>	The test statistic.
<code>dof</code>	The degrees of freedom of the reference chi-squared distribution.
<code>pValue</code>	p-value of the test.
<code>covMatrix</code>	The covariance matrix of $\text{vec}(L \beta_1 R)$.

Examples

```

data(fiberpaper)
X1 <- fiberpaper[, 7]
X2 <- fiberpaper[, 5:6]
Y <- fiberpaper[, 1:4]
m <- penv(X1, X2, Y, 1)
m

L <- diag(4)
R <- as.matrix(1)
A <- matrix(0, 4, 1)

test.res <- testcoef.penv(m, L, R, A)
test.res

```

testcoef.pois.env	<i>Hypothesis test of the coefficients of the envelope model</i>
-------------------	--

Description

This function tests the null hypothesis $L * \beta = A$ versus the alternative hypothesis $L * \beta \neq A$, where β is estimated under the envelope model in poisson regression.

Usage

```
testcoef.pois.env(m, L, A)
```

Arguments

m	A list containing estimators and other statistics inherited from pois.env.
L	The matrix multiplied to β on the left. It is a $d1$ by p matrix, while $d1$ is less than or equal to p .
A	The matrix on the right hand side of the equation. It is a $d1$ by 1 matrix. Note that inputs L and A must be matrices, if not, use <code>as.matrix</code> to convert them.

Details

This function tests for hypothesis $H_0: L \beta = A$, versus $H_a: L \beta \neq A$. The β is estimated by the envelope model in predictor space. If $L = I_p$ and $A = 0$, then the test is equivalent to the standard F test on if $\beta = 0$. The test statistic used is $\text{vec}(L \beta - A) \hat{\Sigma}^{-1} \text{vec}(L \beta - A)^T$, where β is the envelope estimator and $\hat{\Sigma}$ is the estimated asymptotic covariance of $\text{vec}(L \beta - A)$. The reference distribution is chi-squared distribution with degrees of freedom $d1$.

Value

The output is a list that contains following components.

`chisqStatistic` The test statistic.
`dof` The degrees of freedom of the reference chi-squared distribution.
`pValue` p-value of the test.
`covMatrix` The covariance matrix of $\text{vec}(L \beta)$.

Examples

```
data(horseshoecrab)
X1 <- as.numeric(horseshoecrab[, 1] == 2)
X2 <- as.numeric(horseshoecrab[, 1] == 3)
X3 <- as.numeric(horseshoecrab[, 1] == 4)
X4 <- as.numeric(horseshoecrab[, 2] == 2)
X5 <- as.numeric(horseshoecrab[, 2] == 3)
X6 <- horseshoecrab[, 3]
X7 <- horseshoecrab[, 5]
X <- cbind(X1, X2, X3, X4, X5, X6, X7)
Y <- horseshoecrab[, 4]

m <- pois.env(X, Y, 1)

L <- diag(7)
A <- matrix(0, 7, 1)

test.res <- testcoef.pois.env(m, L, A)
test.res
```

testcoef.senv

Hypothesis test of the coefficients of the scaled envelope model

Description

This function tests the null hypothesis $L * \beta * R = A$ versus the alternative hypothesis $L * \beta * R \neq A$, where β is estimated under the scaled envelope model.

Usage

```
testcoef.senv(m, L, R, A)
```

Arguments

`m` A list containing estimators and other statistics inherited from `scale.env`.
`L` The matrix multiplied to β on the left. It is a d_1 by r matrix, while d_1 is less than or equal to r .

R	The matrix multiplied to beta on the right. It is a p by d2 matrix, while d2 is less than or equal to p.
A	The matrix on the right hand side of the equation. It is a d1 by d2 matrix. Note that inputs L, R and A must be matrices, if not, use <code>as.matrix</code> to convert them.

Details

This function tests for hypothesis $H_0: L\beta R = A$, versus $H_a: L\beta R \neq A$. The beta is estimated by the scaled envelope model. If $L = I_r$, $R = I_p$ and $A = 0$, then the test is equivalent to the standard F test on if $\beta = 0$. The test statistic used is $\text{vec}(L\beta R - A) \hat{\Sigma}^{-1} \text{vec}(L\beta R - A)^T$, where beta is the envelope estimator and $\hat{\Sigma}$ is the estimated asymptotic covariance of $\text{vec}(L\beta R - A)$. The reference distribution is chi-squared distribution with degrees of freedom $d_1 * d_2$.

Value

The output is a list that contains following components.

<code>chisqStatistic</code>	The test statistic.
<code>dof</code>	The degrees of freedom of the reference chi-squared distribution.
<code>pValue</code>	p-value of the test.
<code>covMatrix</code>	The covariance matrix of $\text{vec}(L\beta R)$.

Examples

```
data(sales)
X <- sales[, 1:3]
Y <- sales[, 4:7]

m <- senv(X, Y, 2)

L <- diag(4)
R <- as.matrix(c(1, 0, 0))
A <- matrix(0, 4, 1)

test.res <- testcoef.senv(m, L, R, A)
test.res
```

testcoef.stenv

Hypothesis test of the coefficients of the simultaneous envelope model

Description

This function tests the null hypothesis $L * \beta * R = A$ versus the alternative hypothesis $L * \beta * R \neq A$, where beta is estimated under the simultaneous envelope model.

Usage

```
testcoef.stenv(m, L, R, A)
```

Arguments

m	A list containing estimators and other statistics inherited from stenv.
L	The matrix multiplied to beta on the left. It is a d_1 by p matrix, while d_1 is less than or equal to p .
R	The matrix multiplied to beta on the right. It is an r by d_2 matrix, while d_2 is less than or equal to r .
A	The matrix on the right hand side of the equation. It is a d_1 by d_2 matrix. Note that inputs L, R and A must be matrices, if not, use <code>as.matrix</code> to convert them.

Details

This function tests for hypothesis $H_0: L\beta R = A$, versus $H_a: L\beta R \neq A$. The beta is estimated by the simultaneous envelope model. If $L = I_p$, $R = I_r$ and $A = 0$, then the test is equivalent to the standard F test on if $\beta = 0$. The test statistic used is $\text{vec}(L\beta R - A) \hat{\Sigma}^{-1} \text{vec}(L\beta R - A)^T$, where beta is the envelope estimator and $\hat{\Sigma}$ is the estimated asymptotic covariance of $\text{vec}(L\beta R - A)$. The reference distribution is chi-squared distribution with degrees of freedom $d_1 * d_2$.

Value

The output is a list that contains following components.

chisqStatistic	The test statistic.
dof	The degrees of freedom of the reference chi-squared distribution.
pValue	p-value of the test.
covMatrix	The covariance matrix of $\text{vec}(L\beta R)$.

Examples

```
data(fiberpaper)
X <- fiberpaper[ , 5:7]
Y <- fiberpaper[ , 1:4]
m <- stenv(X, Y, 2, 3)

L <- diag(3)
R <- as.matrix(c(1, 0, 0, 0), nrow = 4)
A <- matrix(0, 3, 1)

test.res <- testcoef.stenv(m, L, R, A)
test.res
```

testcoef.sxenv	<i>Hypothesis test of the coefficients of the scaled envelope model in the predictor space</i>
----------------	--

Description

This function tests the null hypothesis $L * \beta * R = A$ versus the alternative hypothesis $L * \beta * R \neq A$, where β is estimated under the scaled envelope model in the predictor space.

Usage

```
testcoef.sxenv(m, L, R, A)
```

Arguments

m	A list containing estimators and other statistics inherited from scale.sxenv.
L	The matrix multiplied to β on the left. It is a d_1 by p matrix, while d_1 is less than or equal to p .
R	The matrix multiplied to β on the right. It is an r by d_2 matrix, while d_2 is less than or equal to r .
A	The matrix on the right hand side of the equation. It is a d_1 by d_2 matrix. Note that inputs L, R and A must be matrices, if not, use <code>as.matrix</code> to convert them.

Details

This function tests for hypothesis $H_0: L \beta R = A$, versus $H_a: L \beta R \neq A$. The β is estimated by the scaled envelope model in the predictor space. If $L = I_p$, $R = I_r$ and $A = 0$, then the test is equivalent to the standard F test on if $\beta = 0$. The test statistic used is $\text{vec}(L \beta R - A) \hat{\Sigma}^{-1} \text{vec}(L \beta R - A)^T$, where β is the envelope estimator and $\hat{\Sigma}$ is the estimated asymptotic covariance of $\text{vec}(L \beta R - A)$. The reference distribution is chi-squared distribution with degrees of freedom $d_1 * d_2$.

Value

The output is a list that contains following components.

chisqStatistic	The test statistic.
dof	The degrees of freedom of the reference chi-squared distribution.
pValue	p-value of the test.
covMatrix	The covariance matrix of $\text{vec}(L \beta R)$.

Examples

```

data(sales)
Y <- sales[, 1:3]
X <- sales[, 4:7]
R <- rep(1, 4)

u <- u.sxenv(X, Y, R)
u

m <- sxenv(X, Y, 2, R)

L <- diag(4)
R <- as.matrix(c(1, 0, 0))
A <- matrix(0, 4, 1)

test.res <- testcoef.sxenv(m, L, R, A)
test.res

```

testcoef.xenv

Hypothesis test of the coefficients of the envelope model

Description

This function tests the null hypothesis $L * \beta * R = A$ versus the alternative hypothesis $L * \beta * R \neq A$, where β is estimated under the envelope model in predictor space.

Usage

```
testcoef.xenv(m, L, R, A)
```

Arguments

<code>m</code>	A list containing estimators and other statistics inherited from <code>xenv</code> .
<code>L</code>	The matrix multiplied to β on the left. It is a d_1 by p matrix, while d_1 is less than or equal to p .
<code>R</code>	The matrix multiplied to β on the right. It is an r by d_2 matrix, while d_2 is less than or equal to r .
<code>A</code>	The matrix on the right hand side of the equation. It is a d_1 by d_2 matrix. Note that inputs <code>L</code> , <code>R</code> and <code>A</code> must be matrices, if not, use <code>as.matrix</code> to convert them.

Details

This function tests for hypothesis $H_0: L \beta R = A$, versus $H_a: L \beta R \neq A$. The β is estimated by the envelope model in predictor space. If $L = I_p$, $R = I_r$ and $A = 0$, then the test is equivalent to the standard F test on if $\beta = 0$. The test statistic used is $\text{vec}(L \beta R - A) \hat{\Sigma}^{-1} \text{vec}(L \beta R - A)^T$, where β is the envelope estimator and $\hat{\Sigma}$ is the estimated asymptotic covariance of $\text{vec}(L \beta R - A)$. The reference distribution is chi-squared distribution with degrees of freedom $d_1 * d_2$.

Value

The output is a list that contains following components.

`chisqStatistic` The test statistic.
`dof` The degrees of freedom of the reference chi-squared distribution.
`pValue` p-value of the test.
`covMatrix` The covariance matrix of $\text{vec}(L \beta R)$.

Examples

```
data(wheatprotein)
X <- wheatprotein[, 1:6]
Y <- wheatprotein[, 7]
m <- xenv(X, Y, 2)
m

L <- diag(6)
R <- as.matrix(1)
A <- matrix(0, 6, 1)

test.res <- testcoef.xenv(m, L, R, A)
test.res
```

u.env

Select the dimension of env

Description

This function outputs dimensions selected by Akaike information criterion (AIC), Bayesian information criterion (BIC) and likelihood ratio testing with specified significance level for the envelope model.

Usage

```
u.env(X, Y, alpha = 0.01)
```

Arguments

`X` Predictors. An n by p matrix, p is the number of predictors. The predictors can be univariate or multivariate, discrete or continuous.

`Y` Multivariate responses. An n by r matrix, r is the number of responses and n is number of observations. The responses must be continuous variables.

`alpha` Significance level for testing. The default is 0.01.

Value

u.aic	Dimension of the envelope subspace selected by AIC.
u.bic	Dimension of the envelope subspace selected by BIC.
u.lrt	Dimension of the envelope subspace selected by the likelihood ratio testing procedure.
loglik.seq	Log likelihood for dimension from 0 to r.
aic.seq	AIC value for dimension from 0 to r.
bic.seq	BIC value for dimension from 0 to r.

Examples

```
data(wheatprotein)
X <- wheatprotein[, 8]
Y <- wheatprotein[, 1:6]
u <- u.env(X, Y)
u
```

u.genv

Select the dimension of genv

Description

This function outputs dimensions selected by Akaike information criterion (AIC), Bayesian information criterion (BIC) and likelihood ratio testing with specified significance level for the group-wise envelope model.

Usage

```
u.genv(X, Y, Z, alpha = 0.01)
```

Arguments

X	Predictors. An n by p matrix, p is the number of predictors. The predictors can be univariate or multivariate, discrete or continuous.
Y	Multivariate responses. An n by r matrix, r is the number of responses and n is number of observations. The responses must be continuous variables.
Z	A group indicator vector of length n , where n denotes the number of observations.
alpha	Significance level for testing. The default is 0.01.

Value

u.aic	Dimension of the groupwise envelope subspace selected by AIC.
u.bic	Dimension of the groupwise envelope subspace selected by BIC.
u.lrt	Dimension of the groupwise envelope subspace selected by the likelihood ratio testing procedure.
loglik.seq	Log likelihood for dimension from 0 to r.
aic.seq	AIC value for dimension from 0 to r.
bic.seq	BIC value for dimension from 0 to r.

Examples

```
data(fiberpaper)
X <- fiberpaper[ , c(5, 7)]
Y <- fiberpaper[ , 1:3]
Z <- as.numeric(fiberpaper[ , 6] > mean(fiberpaper[ , 6]))

u <- u.genv(X, Y, Z)
u
```

u.henv

Select the dimension of henv

Description

This function outputs dimensions selected by Akaike information criterion (AIC), Bayesian information criterion (BIC) and likelihood ratio testing with specified significance level for the heteroscedastic envelope model.

Usage

```
u.henv(X, Y, alpha = 0.01)
```

Arguments

X	A group indicator vector of length n , where n denotes the number of observations.
Y	Multivariate responses. An n by r matrix, r is the number of responses and n is number of observations. The responses must be continuous variables.
alpha	Significance level for testing. The default is 0.01.

Value

u.aic	Dimension of the heteroscedastic envelope subspace selected by AIC.
u.bic	Dimension of the heteroscedastic envelope subspace selected by BIC.
u.lrt	Dimension of the heteroscedastic envelope subspace selected by the likelihood ratio testing procedure.
loglik.seq	Log likelihood for dimension from 0 to r.
aic.seq	AIC value for dimension from 0 to r.
bic.seq	BIC value for dimension from 0 to r.

Examples

```
data(waterstrider)
X <- waterstrider[, 1]
Y <- waterstrider[, 2:5]

## Not run: u <- u.henv(X, Y)
## Not run: u
```

u.logit.env

Select the dimension of logit.env

Description

This function outputs dimensions selected by Akaike information criterion (AIC), Bayesian information criterion (BIC) and likelihood ratio testing with specified significance level for the envelope model in logistic regression.

Usage

```
u.logit.env(X, Y, alpha = 0.01)
```

Arguments

X	Predictors. An n by p matrix, p is the number of predictors and n is number of observations. The predictors must be continuous variables.
Y	Response. An n by 1 matrix. The univariate response must be binary.
alpha	Significance level for testing. The default is 0.01.

Value

u.aic	Dimension of the envelope subspace selected by AIC.
u.bic	Dimension of the envelope subspace selected by BIC.
u.lrt	Dimension of the envelope subspace selected by the likelihood ratio testing procedure.
loglik.seq	Log likelihood for dimension from 0 to p.
aic.seq	AIC value for dimension from 0 to p.
bic.seq	BIC value for dimension from 0 to p.

Examples

```

data(horseshoecrab)
X1 <- as.numeric(horseshoecrab[, 1] == 2)
X2 <- as.numeric(horseshoecrab[, 1] == 3)
X3 <- as.numeric(horseshoecrab[, 1] == 4)
X4 <- as.numeric(horseshoecrab[, 2] == 2)
X5 <- as.numeric(horseshoecrab[, 2] == 3)
X6 <- horseshoecrab[, 3]
X7 <- horseshoecrab[, 5]
X <- cbind(X1, X2, X3, X4, X5, X6, X7)
Y <- as.numeric(iffelse(horseshoecrab[, 4] > 0, 1, 0))

u <- u.logit.env(X, Y)
u

```

u.penv

Select the dimension of penv

Description

This function outputs dimensions selected by Akaike information criterion (AIC), Bayesian information criterion (BIC) and likelihood ratio testing with specified significance level for the partial envelope model.

Usage

```
u.penv(X1, X2, Y, alpha = 0.01)
```

Arguments

X1	Predictors of main interest. An n by p1 matrix, n is the number of observations, and p1 is the number of main predictors. The predictors can be univariate or multivariate, discrete or continuous.
X2	Covariates, or predictors not of main interest. An n by p2 matrix, p2 is the number of covariates.
Y	Multivariate responses. An n by r matrix, r is the number of responses and n is number of observations. The responses must be continuous variables.
alpha	Significance level for testing. The default is 0.01.

Value

u.aic	Dimension of the partial envelope subspace selected by AIC.
u.bic	Dimension of the partial envelope subspace selected by BIC.
u.lrt	Dimension of the partial envelope subspace selected by the likelihood ratio testing procedure.
loglik.seq	Log likelihood for dimension from 0 to r.
aic.seq	AIC value for dimension from 0 to r.
bic.seq	BIC value for dimension from 0 to r.

Examples

```

data(fiberpaper)
X1 <- fiberpaper[, 7]
X2 <- fiberpaper[, 5:6]
Y <- fiberpaper[, 1:4]

u <- u.penv(X1, X2, Y)
u

```

u.pois.env

Select the dimension of pois.env

Description

This function outputs dimensions selected by Akaike information criterion (AIC), Bayesian information criterion (BIC) and likelihood ratio testing with specified significance level for the envelope model in poisson regression.

Usage

```
u.pois.env(X, Y, alpha = 0.01)
```

Arguments

X	Predictors. An n by p matrix, p is the number of predictors and n is number of observations. The predictors must be continuous variables.
Y	Response. An n by 1 matrix. The univariate response must be counts.
alpha	Significance level for testing. The default is 0.01.

Value

u.aic	Dimension of the envelope subspace selected by AIC.
u.bic	Dimension of the envelope subspace selected by BIC.
u.lrt	Dimension of the envelope subspace selected by the likelihood ratio testing procedure.
loglik.seq	Log likelihood for dimension from 0 to p.
aic.seq	AIC value for dimension from 0 to p.
bic.seq	BIC value for dimension from 0 to p.

Examples

```

data(horseshoecrab)
X1 <- as.numeric(horseshoecrab[, 1] == 2)
X2 <- as.numeric(horseshoecrab[, 1] == 3)
X3 <- as.numeric(horseshoecrab[, 1] == 4)
X4 <- as.numeric(horseshoecrab[, 2] == 2)
X5 <- as.numeric(horseshoecrab[, 2] == 3)
X6 <- horseshoecrab[, 3]
X7 <- horseshoecrab[, 5]
X <- cbind(X1, X2, X3, X4, X5, X6, X7)
Y <- horseshoecrab[, 4]

u <- u.pois.env(X, Y)
u

```

u.pred2.env	<i>Select the dimension of the constructed partial envelope for prediction based on envelope model</i>
-------------	--

Description

This function outputs dimensions selected by Akaike information criterion (AIC), Bayesian information criterion (BIC) and likelihood ratio testing with specified significance level for the constructed partial envelope model.

Usage

```
u.pred2.env(X, Y, Xnew, alpha = 0.01)
```

Arguments

X	Predictors. An n by p matrix, p is the number of predictors. The predictors can be univariate or multivariate, discrete or continuous.
Y	Multivariate responses. An n by r matrix, r is the number of responses and n is number of observations. The responses must be continuous variables.
Xnew	The value of X with which to estimate or predict Y. A p dimensional vector.
alpha	Significance level for testing. The default is 0.01.

Value

u.aic	Dimension of the constructed partial envelope subspace selected by AIC.
u.bic	Dimension of the constructed partial envelope subspace selected by BIC.
u.lrt	Dimension of the constructed partial envelope subspace selected by the likelihood ratio testing procedure.
loglik.seq	Log likelihood for dimension from 0 to r.
aic.seq	AIC value for dimension from 0 to r.
bic.seq	BIC value for dimension from 0 to r.

Examples

```

data(fiberpaper)
X <- fiberpaper[, 5:7]
Y <- fiberpaper[, 1:4]

u <- u.pred2.env(X, Y, X[10, ])
u

```

u.senv

Select the dimension of senv

Description

This function outputs dimensions selected by Akaike information criterion (AIC), Bayesian information criterion (BIC).

Usage

```
u.senv(X, Y)
```

Arguments

X	Predictors. An n by p matrix, p is the number of predictors. The predictors can be univariate or multivariate, discrete or continuous.
Y	Multivariate responses. An n by r matrix, r is the number of responses and n is number of observations. The responses must be continuous variables.

Value

u.aic	Dimension of the scaled envelope subspace selected by AIC.
u.bic	Dimension of the scaled envelope subspace selected by BIC.
aic.seq	AIC value for dimension from 0 to r.
bic.seq	BIC value for dimension from 0 to r.

Examples

```

data(sales)
X <- sales[, 1:3]
Y <- sales[, 4:7]

u <- u.senv(X, Y)
u

```

`u.stenv`*Select the dimension of stenv*

Description

This function outputs dimensions selected by Akaike information criterion (AIC), Bayesian information criterion (BIC) and likelihood ratio testing with specified significance level for the simultaneous envelope model.

Usage

```
u.stenv(X, Y, alpha = 0.01)
```

Arguments

<code>X</code>	Predictors. An n by p matrix, p is the number of predictors. The predictors can be univariate or multivariate, discrete or continuous.
<code>Y</code>	Multivariate responses. An n by r matrix, r is the number of responses and n is number of observations. The responses must be continuous variables.
<code>alpha</code>	Significance level for testing. The default is 0.01.

Value

<code>d</code>	Rank of beta selected by the Bura-Cook estimator.
<code>u.aic</code>	Dimension of the simultaneous envelope subspace selected by AIC.
<code>u.bic</code>	Dimension of the simultaneous envelope subspace selected by BIC.
<code>u.lrt</code>	Dimension of the simultaneous envelope subspace selected by the likelihood ratio testing procedure.
<code>loglik.mat</code>	Log likelihood for dimension from (1, 1) to (r, p).
<code>aic.mat</code>	AIC value for dimension from (1, 1) to (r, p).
<code>bic.mat</code>	BIC value for dimension from (1, 1) to (r, p).

Examples

```
data(fiberpaper)
X <- fiberpaper[, 5:7]
Y <- fiberpaper[, 1:4]

u <- u.stenv(X, Y)
u
```

`u.sxenv`*Select the dimension of sxenv*

Description

This function outputs dimensions selected by Akaike information criterion (AIC), Bayesian information criterion (BIC) for the scaled envelope model in the predictor space.

Usage

```
u.sxenv(X, Y, R)
```

Arguments

X	Predictors. An n by p matrix, p is the number of predictors. The predictors can be univariate or multivariate, discrete or continuous.
Y	Multivariate responses. An n by r matrix, r is the number of responses and n is number of observations. The responses must be continuous variables.
R	The number of replications of the scales. A vector, the sum of all elements of R must be p.

Value

u.aic	Dimension of the scaled envelope subspace in the predictor space selected by AIC.
u.bic	Dimension of the scaled envelope subspace in the predictor space selected by BIC.
aic.seq	AIC value for dimension from 0 to p.
bic.seq	BIC value for dimension from 0 to p.

Examples

```
data(sales)
Y <- sales[, 1:3]
X <- sales[, 4:7]
R <- rep(1, 4)

u <- u.sxenv(X, Y, R)
u
```

`u.xenv`*Select the dimension of xenv*

Description

This function outputs dimensions selected by Akaike information criterion (AIC), Bayesian information criterion (BIC) and likelihood ratio testing with specified significance level for the envelope model.

Usage

```
u.xenv(X, Y, alpha = 0.01)
```

Arguments

<code>X</code>	Predictors. An n by p matrix, p is the number of predictors and n is number of observations. The predictors must be continuous variables.
<code>Y</code>	Responses. An n by r matrix, r is the number of responses. The response can be univariate or multivariate and must be continuous variable.
<code>alpha</code>	Significance level for testing. The default is 0.01.

Value

<code>u.aic</code>	Dimension of the envelope subspace selected by AIC.
<code>u.bic</code>	Dimension of the envelope subspace selected by BIC.
<code>u.lrt</code>	Dimension of the envelope subspace selected by the likelihood ratio testing procedure.
<code>loglik.seq</code>	Log likelihood for dimension from 0 to p .
<code>aic.seq</code>	AIC value for dimension from 0 to p .
<code>bic.seq</code>	BIC value for dimension from 0 to p .

Examples

```
data(wheatprotein)
X <- wheatprotein[, 1:6]
Y <- wheatprotein[, 7]

u <- u.xenv(X, Y)
u
```

waterstrider	<i>Water strider data</i>
--------------	---------------------------

Description

Measures of characteristics of the water striders

Usage

```
data("waterstrider")
```

Format

A data frame with 90 observations on the following 9 variables.

- V1 Index of water strider species.
- V2 Logarithm of length of the first antennal segment.
- V3 Logarithm of length of the second antennal segment.
- V4 Logarithm of length of the third antennal segment.
- V5 Logarithm of length of the fourth antennal segment.
- V6 Logarithm of length of fomora of middle leg.
- V7 Logarithm of length of tibiae of middle leg.
- V8 Logarithm of length of fomora of hind leg.
- V9 Logarithm of length of tibiae of hind leg.

Details

This data set contains 8 measures of water striders and an indicator of the species of water striders.

References

Klingenberg, C. R. and Spence, J. R. (1993). Heterochrony and Allometry Lessons from the Water Strider Genus *Limnopus*. *Evolution* 47, 1834-1853

weighted.env	<i>Weighted envelope estimator</i>
--------------	------------------------------------

Description

Compute the weighted envelope estimator with weights computed from BIC.

Usage

```
weighted.env(X, Y, bstrpNum = 0, min.u = 1, max.u = ncol(Y), boot.resi = "full")
```

Arguments

<code>X</code>	Predictors. An n by p matrix, p is the number of predictors. The predictors can be univariate or multivariate, discrete or continuous.
<code>Y</code>	Multivariate responses. An n by r matrix, r is the number of responses and n is number of observations. The responses must be continuous variables.
<code>bstrpNum</code>	Number of bootstrap samples. A positive integer.
<code>min.u</code>	Lower bound of the range of u to compute bootstrap error. A positive integer between 1 and p . This argument is relevant only when <code>bstrpNum</code> >0.
<code>max.u</code>	Upper bound of the range of u to compute bootstrap error. A positive integer between 1 and p . This argument is relevant only when <code>bstrpNum</code> >0.
<code>boot.resi</code>	A string that can be "full" or "weighted" indicating the model from which the residuals are calculated. If the input is "full", then the residuals are obtained using the standard estimators; and if the input is "weighted", then the residuals are obtained using the weighted envelope estimators. This argument is for computing residuals in residual bootstrap, and it is relevant only when <code>bstrpNum</code> >0. Note that inputs <code>X</code> and <code>Y</code> must be matrices, if not, use <code>as.matrix</code> to convert them.

Details

This function computes the weighted envelope estimator in a standard multivariate linear regression. And the weighted envelope estimator takes the form

$$\hat{\beta}_w = \sum_{j=1}^r w_j \hat{\beta}_j,$$

where $\hat{\beta}_j$ is the envelope estimator of β with $u = j$ and w_j 's are the weights computed from BIC values

$$w_j = \frac{\exp(-b_j)}{\sum_{k=1}^r \exp(-b_k)},$$

where b_j is the BIC criterion evaluated at the envelope estimator $\hat{\beta}_j$. For details, see Eck and Cook (2017).

The variation of the weighted envelope estimator is estimated by residual bootstrap. The user can specify the range for bootstrap $u = (\text{min.u}, \text{max.u})$, if the weights outside of the range are small.

Value

The output is a list that contains the following components:

beta	The weighted envelope estimator of the regression coefficients.
mu	The weighted estimated intercept.
Sigma	The weighted envelope estimator of the error covariance matrix.
w	Weights computed based on BIC.
loglik	The log likelihood function computed with weighted envelope estimator.
n	The number of observations in the data.
bootse	The standard error for elements in beta computed by residual bootstrap. This output is available only when bstrpNum>0.
ratios	The bootstrap standard error ratio of the standard multivariate linear regression estimator over the weighted envelope estimator for each element in beta. This output is available only when bstrpNum>0.
bic_select	A table that lists how many times BIC selected each candidate dimension. If BIC never selects a dimension, this dimension does not appear on the table. This output is available only when bstrpNum>0.

References

Eck, D. J. and Cook, R. D. (2017). Weighted Envelope Estimation to Handle Variability in Model Selection. *Biometrika*. To appear.

Examples

```
data(wheatprotein)
X <- wheatprotein[, 8]
Y <- wheatprotein[, 1:6]
m <- weighted.env(X, Y)
m$w
m$beta

## Not run: m2 <- weighted.env(X, Y, bstrpNum = 100, min.u = 1, max.u = 6, boot.resi = "full")
## Not run: m2$bic_select
## Not run: m2$bootse
```

 weighted.penv

Weighted partial envelope estimator

Description

Compute the weighted partial envelope estimator with weights computed from BIC.

Usage

```
weighted.penv(X1, X2, Y, bstrpNum = 0, min.u = 1, max.u = ncol(Y), boot.resi = "full")
```

Arguments

X1	Predictors of main interest. An n by p1 matrix, n is the number of observations, and p1 is the number of main predictors. The predictors can be univariate or multivariate, discrete or continuous.
X2	Covariates, or predictors not of main interest. An n by p2 matrix, p2 is the number of covariates.
Y	Multivariate responses. An n by r matrix, r is the number of responses and n is number of observations. The responses must be continuous variables.
bstrpNum	Number of bootstrap samples. A positive integer.
min.u	Lower bound of the range of u to compute bootstrap error. A positive integer between 1 and p. This argument is relevant only when bstrpNum>0.
max.u	Upper bound of the range of u to compute bootstrap error. A positive integer between 1 and p. This argument is relevant only when bstrpNum>0.
boot.resi	A string that can be "full" or "weighted" indicating the model from which the residuals are calculated. If the input is "full", then the residuals are obtained using the standard estimators; and if the input is "weighted", then the residuals are obtained using the weighted envelope estimators. This argument is for computing residuals in residual bootstrap, and it is relevant only when bstrpNum>0. Note that inputs X and Y must be matrices, if not, use as.matrix to convert them.

Details

This function computes the weighted partial envelope estimator in a standard multivariate linear regression. And the weighted partial envelope estimator takes the form

$$\hat{\beta}_w = \sum_{j=1}^r w_j \hat{\beta}_j,$$

where $\hat{\beta}_j$ is the partial envelope estimator of β with $u = j$ and w_j 's are the weights computed from BIC values

$$w_j = \frac{\exp(-b_j)}{\sum_{k=1}^r \exp(-b_k)},$$

where b_j is the BIC criterion evaluated at the partial envelope estimator $\hat{\beta}_j$. For details, see Eck and Cook (2017).

The variation of the weighted partial envelope estimator is estimated by residual bootstrap. The user can specify the range for bootstrap $u = (\text{min.u}, \text{max.u})$, if the weights outside of the range are small.

Value

The output is a list that contains the following components:

beta	The weighted partial envelope estimator of the regression coefficients.
mu	The weighted estimated intercept.

Sigma	The weighted partial envelope estimator of the error covariance matrix.
w	Weights computed based on BIC.
loglik	The log likelihood function computed with weighted partial envelope estimator.
n	The number of observations in the data.
bootse	The standard error for elements in beta1 computed by residual bootstrap. This output is available only when bstrpNum>0.
ratios	The bootstrap standard error ratio of the standard multivariate linear regression estimator over the weighted partial envelope estimator for each element in beta1. This output is available only when bstrpNum>0.
bic_select	A table that lists how many times BIC selected each candidate dimension. If BIC never selects a dimension, this dimension does not appear on the table. This output is available only when bstrpNum>0.

References

Eck, D. J. and Cook, R. D. (2017). Weighted Envelope Estimation to Handle Variability in Model Selection. *Biometrika*. To appear.

Examples

```
data(fiberpaper)
X1 <- fiberpaper[, 7]
X2 <- fiberpaper[, 5:6]
Y <- fiberpaper[, 1:4]
m <- weighted.penv(X1, X2, Y)
m$w
m$beta1

m2 <- penv(X1, X2, Y, 2)
m2$beta1

## Not run: m3 <- weighted.penv(X1, X2, Y, bstrpNum = 100, boot.resi = "full")
## Not run: m3$w
## Not run: m3$bic_select
## Not run: m3$bootse

## Not run: boot.penv(X1, X2, Y, 2, 100)
```

weighted.pred.env

Estimation or prediction using weighted partial envelope

Description

Perform estimation or prediction through weighted partial envelope model.

Usage

```
weighted.pred.env(X, Y, Xnew)
```

Arguments

X	Predictors. An n by p matrix, p is the number of predictors. The predictors can be univariate or multivariate, discrete or continuous.
Y	Multivariate responses. An n by r matrix, r is the number of responses and n is number of observations. The responses must be continuous variables.
Xnew	The value of X with which to estimate or predict Y. A p dimensional vector.

Details

This function evaluates the envelope model at new value Xnew. It can perform estimation: find the fitted value when $X = X_{\text{new}}$, or prediction: predict Y when $X = X_{\text{new}}$. But it does not provide the estimation or prediction error. This function performs prediction using the same procedure as in `pred2.env`, except that the partial envelope estimator with dimension u is replaced by a weighted partial envelope estimator. The weights are decided based on BIC values.

Value

value	The fitted value or the predicted value evaluated at Xnew.
-------	--

Examples

```
data(fiberpaper)
X <- fiberpaper[, 5:7]
Y <- fiberpaper[, 1:4]

pred.res <- weighted.pred.env(X, Y, X[10, ])
```

 weighted.xenv

Weighted predictor envelope estimator

Description

Compute the weighted predictor envelope estimator with weights computed from BIC.

Usage

```
weighted.xenv(X, Y, bstrpNum = 0, min.u = 1, max.u = ncol(X), boot.resi = "full")
```


Arguments

X	Predictors. An n by p matrix, p is the number of predictors and n is number of observations. The predictors must be continuous variables.
Y	Responses. An n by r matrix, r is the number of responses. The response can be univariate or multivariate and must be continuous variable.
bstrpNum	Number of bootstrap samples. A positive integer.
min.u	Lower bound of the range of u to compute bootstrap error. A positive integer between 1 and p. This argument is relevant only when bstrpNum>0.
max.u	Upper bound of the range of u to compute bootstrap error. A positive integer between 1 and p. This argument is relevant only when bstrpNum>0.
boot.resi	A string that can be "full" or "weighted" indicating the model from which the residuals are calculated. If the input is "full", then the residuals are obtained using the standard estimators; and if the input is "weighted", then the residuals are obtained using the weighted predictor envelope estimators. This argument is for computing residuals in residual bootstrap, and it is relevant only when bstrpNum>0. Note that inputs X and Y must be matrices, if not, use <code>as.matrix</code> to convert them.

Details

This function computes the weighted predictor envelope estimator in a standard multivariate linear regression. And the weighted predictor envelope estimator takes the form

$$\hat{\beta}_w = \sum_{j=1}^p w_j \hat{\beta}_j,$$

where $\hat{\beta}_j$ is the predictor envelope estimator of β with $u = j$ and w_j 's are the weights computed from BIC values

$$w_j = \frac{\exp(-b_j)}{\sum_{k=1}^p \exp(-b_k)},$$

where b_j is the BIC criterion evaluated at the predictor envelope estimator $\hat{\beta}_j$. For details, see Eck and Cook (2017).

The variation of the weighted predictor envelope estimator is estimated by residual bootstrap. The user can specify the range for bootstrap $u = (\text{min.u}, \text{max.u})$, if the weights outside of the range are small.

Value

The output is a list that contains the following components:

beta	The weighted predictor envelope estimator of the regression coefficients.
mu	The weighted estimated intercept.
SigmaX	The weighted predictor envelope estimator of the covariance matrix of X.
SigmaYcX	The weighted predictor envelope estimator of the error covariance matrix.

w	Weights computed based on BIC.
loglik	The log likelihood function computed with weighted predictor envelope estimator.
n	The number of observations in the data.
bootse	The standard error for elements in beta computed by residual bootstrap. This output is available only when bstrpNum>0.
ratios	The bootstrap standard error ratio of the standard multivariate linear regression estimator over the weighted predictor envelope estimator for each element in beta. This output is available only when bstrpNum>0.
bic_select	A table that lists how many times BIC selected each candidate dimension. If BIC never selects a dimension, this dimension does not appear on the table. This output is available only when bstrpNum>0.

References

Eck, D. J. and Cook, R. D. (2017). Weighted Envelope Estimation to Handle Variability in Model Selection. *Biometrika*. To appear.

Examples

```
data(wheatprotein)
X <- wheatprotein[, 1:6]
Y <- wheatprotein[, 7]
m <- weighted.xenv(X, Y)
m$w
m$beta

## Not run: m2 <- weighted.xenv(X, Y, bstrpNum = 100, min.u = 2, max.u = 4, boot.resi = "full")
## Not run: m2$w
## Not run: m2$bootse
```

wheatprotein

Wheat Protein Data

Description

The protein content of ground wheat samples.

Usage

```
data(wheatprotein)
```

Format

A data frame with 50 observations on the following 8 variables.

- V1 Measurements of the reflectance of NIR radiation by the wheat samples at 1680nm. The measurements were made on the $\log(1/\text{reflectance})$ scale.
- V2 Measurements of the reflectance of NIR radiation by the wheat samples at 1806nm.
- V3 Measurements of the reflectance of NIR radiation by the wheat samples at 1932nm.
- V4 Measurements of the reflectance of NIR radiation by the wheat samples at 2058nm.
- V5 Measurements of the reflectance of NIR radiation by the wheat samples at 2184nm.
- V6 Measurements of the reflectance of NIR radiation by the wheat samples at 2310nm.
- V7 The protein content of each sample (in percent).
- V8 Binary indicator, 0 for high protein content and 1 for low protein content. The cut off point is if the protein content is smaller than 9.75.

Details

The data are the result of an experiment to calibrate a near infrared reflectance (NIR) instrument for measuring the protein content of ground wheat samples. The protein content of each sample (in percent) was measured by the standard Kjeldahl method. In Fearn (1983), the problem is to find a linear combination of the measurements that predicts protein content. The estimated coefficients can then be entered into the instrument allowing the protein content of future samples to be read directly. The first 24 cases were used for calibration and the last 26 samples were used for prediction.

References

Fearn, T. (1983). A misuse of ridge regression in the calibration of a near infrared reflectance instrument.

xenv

Fit the envelope model in the predictor space

Description

Fit the envelope model in the predictor space with dimension u under linear regression.

Usage

```
xenv(X, Y, u, asy = TRUE, init = NULL)
```

Arguments

X	Predictors. An n by p matrix, p is the number of predictors and n is number of observations. The predictors must be continuous variables.
Y	Responses. An n by r matrix, r is the number of responses. The response can be univariate or multivariate and must be continuous variable.
u	Dimension of the envelope. An integer between 0 and p.
asy	Flag for computing the asymptotic variance of the envelope estimator. The default is TRUE. When p and r are large, computing the asymptotic variance can take much time and memory. If only the envelope estimators are needed, the flag can be set to asy = FALSE.
init	The user-specified value of Gamma for the envelope subspace in the predictor space. An p by u matrix. The default is the one generated by function envMU.

Details

This function fits the envelope model in the predictor space,

$$Y = \mu + \eta' \Omega^{-1} \Gamma' X + \varepsilon, \Sigma_X = \Gamma \Omega \Gamma' + \Gamma_0 \Omega_0 \Gamma_0'$$

using the maximum likelihood estimation. When the dimension of the envelope is between 1 and p-1, the starting value and blockwise coordinate descent algorithm in Cook et al. (2016) is implemented. When the dimension is p, then the envelope model degenerates to the standard multivariate linear regression. When the dimension is 0, it means that X and Y are uncorrelated, and the fitting is different.

Value

The output is a list that contains the following components:

beta	The envelope estimator of the regression coefficients.
SigmaX	The envelope estimator of the covariance matrix of X.
Gamma	An orthonormal basis of the envelope subspace.
Gamma0	An orthonormal basis of the complement of the envelope subspace.
eta	The estimated eta. According to the envelope parameterization, beta = Gamma * Omega^-1 * eta.
Omega	The coordinates of SigmaX with respect to Gamma.
Omega0	The coordinates of SigmaX with respect to Gamma0.
mu	The estimated intercept.
SigmaYcX	The estimated conditional covariance matrix of Y given X.
loglik	The maximized log likelihood function.
covMatrix	The asymptotic covariance of vec(beta). The covariance matrix returned are asymptotic. For the actual standard errors, multiply by 1 / n.
asySE	The asymptotic standard error for elements in beta under the envelope model. The standard errors returned are asymptotic, for actual standard errors, multiply by 1 / sqrt(n).

ratio	The asymptotic standard error ratio of the standard multivariate linear regression estimator over the envelope estimator, for each element in beta.
n	The number of observations in the data.

References

Cook, R. D., Helland, I. S. and Su, Z. (2013). Envelopes and Partial Least Squares Regression. *Journal of the Royal Statistical Society: Series B* 75, 851 - 877.

Cook, R. D., Forzani, L. and Su, Z. (2016) A Note on Fast Envelope Estimation. *Journal of Multivariate Analysis*. 150, 42-54.

See Also

[simpls.fit](#) for partial least squares (PLS).

Examples

```
## Fit the envelope in the predictor space
data(wheatprotein)
X <- wheatprotein[, 1:6]
Y <- wheatprotein[, 7]
u <- u.xenv(X, Y)
u

m <- xenv(X, Y, 4)
m
m$beta

## Not run: m1 <- pls::simpls.fit(X, Y, 4)
## Not run: m1$coefficients
```

Index

*Topic **datasets**

- Berkeley, [5](#)
- fiberpaper, [32](#)
- horseshoecrab, [39](#)
- sales, [58](#)
- waterstrider, [91](#)
- wheatprotein, [98](#)

- Berkeley, [5](#)
- boot.env, [6](#)
- boot.genv, [7](#)
- boot.henv, [8](#)
- boot.logit.env, [9](#)
- boot.penv, [10](#)
- boot.pois.env, [11](#)
- boot.senv, [12](#)
- boot.stenv, [13](#)
- boot.sxenv, [14](#)
- boot.xenv, [15](#)

- contr, [16](#)
- cv.env, [17](#)
- cv.genv, [18](#)
- cv.henv, [19](#)
- cv.logit.env, [20](#)
- cv.penv, [21](#)
- cv.pois.env, [22](#)
- cv.senv, [23](#)
- cv.stenv, [24](#)
- cv.sxenv, [25](#)
- cv.xenv, [26](#)

- d.stenv, [27](#)

- env, [28](#)
- envMU, [30](#)
- expan, [31](#)

- fiberpaper, [32](#)

- GE, [32](#)

- genv, [33](#)
- genvMU, [35](#)
- ginv, [36](#)
- henv, [36](#)
- henvMU, [38](#)
- horseshoecrab, [39](#)

- logit.env, [40](#)
- logit.envMU, [42](#)

- penv, [43](#)
- pois.env, [45](#)
- pois.envMU, [46](#)
- pred.env, [47](#)
- pred.genv, [48](#)
- pred.henv, [49](#)
- pred.logit.env, [50](#)
- pred.penv, [51](#)
- pred.pois.env, [52](#)
- pred.senv, [53](#)
- pred.stenv, [54](#)
- pred.sxenv, [55](#)
- pred.xenv, [56](#)
- pred2.env, [57](#)

- Renvlp-package, [3](#)
- Revnlp-package (Renvlp-package), [3](#)

- sales, [58](#)
- senv, [59](#)
- senvMU, [61](#)
- simpls.fit, [101](#)
- stenv, [62](#)
- stenvMU, [64](#)
- sxenv, [65](#)
- sxenvMU, [67](#)

- testcoef.env, [68](#)
- testcoef.genv, [69](#)
- testcoef.henv, [70](#)

testcoef.logit.env, 71
testcoef.penv, 73
testcoef.pois.env, 74
testcoef.senv, 75
testcoef.stenv, 76
testcoef.sxenv, 78
testcoef.xenv, 79

u.env, 80
u.genv, 81
u.henv, 82
u.logit.env, 83
u.penv, 84
u.pois.env, 85
u.pred2.env, 86
u.senv, 87
u.stenv, 88
u.sxenv, 89
u.xenv, 90

waterstrider, 91
weighted.env, 92
weighted.penv, 93
weighted.pred.env, 95
weighted.xenv, 96
wheatprotein, 98

xenv, 99