

Package ‘Homework1’

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Title Advanced Statistical Computing - Homework 1

Description This package contains functions for Homework 1 for Advanced Statistical Computing. It has functions for fast calculation of the beta coefficients in linear regression and for the fast calculation of the multivariate normal density.

Version 1.0

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Collate ‘dmvnorm.R’ ‘fastlm.R’

R topics documented:

dmvnorm	1
fastlm	2

Index	4
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dmvnorm	<i>Fast multivariate normal density</i>
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Description

Fast evaluation of the multivariate normal density

Usage

```
dmvnorm(x, mu, S, log = TRUE)
```

Arguments

x	The n by k matrix of points at which to evaluate the density. Each row of the matrix corresponds to one point (of dimension k).
mu	The length k vector of means of the multivariate normal.
S	The k by k covariance matrix of the multivariate normal.
log	If TRUE, returns the natural logarithm of the density. If FALSE, returns the density.

Details

This function checks that S is positive-definite. If not, the function will stop.

Value

A vector of length n containing the multivariate normal evaluated at the n points of x .

Author(s)

Leslie Myint

References

Roger Peng. http://rdpeng.github.io/Biostat778_HW1/

See Also

[mvnrm](#)

Examples

```
## Create the covariance matrix
n <- 10
n2 <- n^2
xg <- seq(0, 1, length = n)
yg <- xg
g <- data.matrix(expand.grid(xg, yg))
D <- as.matrix(dist(g))
phi <- 5

S <- exp(-phi * D)
mu <- rep(0, n2)
set.seed(1)
x <- matrix(rnorm(n2), byrow = TRUE, ncol = n2)

dmvnorm(x, mu, S, log = TRUE)
```

fastlm

Fast linear regression

Description

Efficiently calculate the beta coefficients and their variances in a standard linear model: $Y = X\beta + \epsilon$

Usage

```
fastlm(X, y, na.rm = FALSE)
```

Arguments

<code>X</code>	The design matrix of the linear model
<code>y</code>	The vector of observations
<code>na.rm</code>	Should missing values be removed? If TRUE, missing values are removed. If FALSE, missing values are not removed.

Details

This function is designed to be faster than `lm.fit`. It does not perform the entire suite of tasks that `lm` does.

Value

<code>coefficients</code>	A vector of the estimated beta coefficients
<code>vcov</code>	The variance-covariance matrix of the estimated beta coefficients

Author(s)

Leslie Myint

References

Roger Peng. http://rdpeng.github.io/Biostat778_HW1/

See Also

[lm](#), [lm.fit](#)

Examples

```
set.seed(2)
## Generate predictor matrix
n <- 1000
p <- 50
X <- cbind(1, matrix(rnorm(n * (p - 1)), n, p - 1))

## Coefficients
b <- rnorm(p)

## Response
y <- X

fit <- fastlm(X, y)
```

Index

`dmvnorm`, [1](#)

`fastlm`, [2](#)

`lm`, [3](#)

`lm.fit`, [3](#)

`mvrnorm`, [2](#)