

# Package ‘Homework1’

November 12, 2013

**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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**Date** 2013-11-13

**License** GPL-3

**Collate** ‘dmvnorm.R’ ‘fastlm.R’

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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/](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)
```

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fastlm

*Fast linear regression*


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**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/](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)
```

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