

# Package ‘Homework1’

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**Title** Advanced Computing Homework 1

**Description** Improves R’s base linear regression function and adds support for multivariate normal density evaluation.

**Version** 1.0-0

**Depends** R (>= 3.0.1)

**License** GPL-3

**LazyData** true

**Author** James Pringle

**Maintainer** James Pringle <james\_pringle@jhu.edu>

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**URL** [https://github.com/jkpr/Biostat778\\_HW1](https://github.com/jkpr/Biostat778_HW1)

**Collate** ‘dmvnorm.R’ ‘fastlm.R’

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dmvnorm	<i>Evaluate the density of a multivariate normal distribution</i>
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## Description

Evaluate the density of a multivariate normal distribution

## Usage

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

**Arguments**

<code>x</code>	an $n \times k$ matrix to represent $n$ vectors of length $k$
<code>mu</code>	the mean of the distribution: a numeric vector of length $k$
<code>S</code>	the variance-covariance matrix with dimensions $k \times k$
<code>log</code>	a boolean that indicates if the log of the density should be returned

**Value**

numeric vector with length  $n$ , corresponding to the density of the  $n$  vectors in  $x$  evaluated under a multivariate normal distribution defined by mean  $\mu$  and variance-covariance  $S$

**Examples**

```
x <- matrix(rnorm(10*9), ncol=9)
mu <- rep(0,9)
xg <- seq(0, 1, length = 3)
yg <- xg
g <- data.matrix(expand.grid(xg, yg))
D <- as.matrix(dist(g))
S <- exp(D * -1)
dmvnorm(x, mu, S)
```

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fastlm

*Fast linear regression*


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**Description**

Fast linear regression

**Usage**

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

**Arguments**

<code>X</code>	an $n \times p$ design matrix
<code>y</code>	a numeric vector of length $n$
<code>na.rm</code>	a boolean to indicate if NA values should be removed

**Value**

`fastlm()` returns a list with the following components:

<code>coefficients</code>	A numeric vector of length $p$ containing the regression coefficients estimated by maximum likelihood.
<code>vcov</code>	the $p \times p$ covariance matrix of the estimated regression coefficients.

**Examples**

```
X <- matrix(rnorm(10),ncol=2)
y <- rnorm(5)
fastlm(X, y)
```

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