

# Package ‘pbivnorm’

July 2, 2014

**Title** Vectorized Bivariate Normal CDF

**Version** 0.5-1

**Date** 2012-10-31

**Author** Fortran code by Alan Genz. R code by Brenton Kenkel, based on Adelchi Azzalini's 'mnormt' package.

**Maintainer** Brenton Kenkel <brenton.kenkel@gmail.com>

**Description** Provides a vectorized R function for calculating probabilities from a standard bivariate normal CDF.

**License** GPL (>= 2)

**LazyLoad** yes

**Repository** CRAN

**Date/Publication** 2012-10-31 16:02:02

**NeedsCompilation** yes

## R topics documented:

pbivnorm . . . . .	2
<b>Index</b>	<b>4</b>

---

pbivnorm

*Standard bivariate normal CDF*

---

### Description

Calculate probabilities from the CDF of a standard bivariate normal distribution.

### Usage

```
pbivnorm(x, y, rho=0)
```

### Arguments

x	vector of upper integration limits for the CDF. May also be a two-column matrix, in which case y should not be used.
y	vector of upper integration limits, must be same length as x.
rho	correlation parameter. May be a vector of the same length as x, a scalar, or a vector of any other length that can be recycled to conform with x.

### Details

This function returns values identical to those of `biv.nt.prob` in the **mnormt** package, but is vectorized to reduce the number of Fortran calls required for computation of many probabilities.

### Value

Numeric vector of probabilities.

### Author(s)

Fortran code by Alan Genz (see references). R interface by Brenton Kenkel (<brenton.kenkel@gmail.com>), based on code from Adelchi Azzalini's **mnormt** package.

### References

- Genz, A. (1992). Numerical Computation of Multivariate Normal Probabilities. *J. Computational and Graphical Statist.*, **1**, 141–149.
- Genz, A. (1993). Comparison of methods for the computation of multivariate normal probabilities. *Computing Science and Statistics*, **25**, 400–405.
- Genz, A. Fortran code for MVTDSTPACK available at <http://www.math.wsu.edu/math/faculty/genz/software/fort77/mvtdstpack.f> (as of 2011-02-21).

**Examples**

```
x <- rnorm(10)
y <- rnorm(10)
rho <- runif(10)

pbivnorm(x, y, rho)

X <- cbind(x, y)
pbivnorm(X, rho = rho)

## rho can be a single value
rho <- runif(1)
pbivnorm(x, y, rho)
```

# Index

`pbivnorm`, [2](#)