

Package: pbivnorm (via r-universe)

September 4, 2024

Title Vectorized Bivariate Normal CDF

Version 0.6.0

Date 2015-01-23

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.

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URL <https://github.com/brentonk/pbivnorm>

Repository <https://brentonk.r-universe.dev>

RemoteUrl <https://github.com/brentonk/pbivnorm>

RemoteRef HEAD

RemoteSha 1e611547811a36aaec97d1d8f3cdc6d1134d9762

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pbivnorm	<i>Standard bivariate normal CDF</i>
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Description

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

Usage

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

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.
rho	correlation parameter.
recycle	whether to automatically recycle the vectors x, y, and rho to conform to whichever is longest. If FALSE, all three must be the same length.

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, unless recycling is disallowed
rho <- runif(1)
pbivnorm(x, y, rho)
```

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