Package ‘cbinom’

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Type Package

Title Continuous Analog of a Binomial Distribution

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Description Implementation of the d/p/q/r family of functions for a continuous analog to the standard discrete binomial with continuous size parameter and continuous support with x in [0, size + 1], following Ilienko (2013) <arXiv:1303.5990>.

License GPL (>= 2)

Imports Rcpp (>= 0.12.0)

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Continuous Analog of a Binomial Distribution

Description

Implementation of the d/p/q/r family of functions for a continuous analog to the standard discrete binomial with continuous size parameter and continuous support with x in [0, size + 1].

Details

Included in the package are functions dcbinom(x, size, prob, log = FALSE), pcbinom(q, size, prob, lower.tail = TRUE, log.p = FALSE), qcbinom(p, size, prob, lower.tail = TRUE, log.p = FALSE), and rcbinom(n, size, prob).
Usage closely parallels that of the binom family of functions in the stats R package.

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References


See Also

pcbinom

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cbinom

The Continuous Binomial Distribution

Description

Density, distribution function, quantile function and random generation for a continuous analog to the binomial distribution with parameters size and prob. The usage and help pages are modeled on the d-p-q-r families of functions for the commonly-used distributions (e.g., dbinom) in the stats package.

Heuristically speaking, this distribution spreads the standard probability mass (dbinom) at integer x to the interval [x, x + 1] in a continuous manner. As a result, the distribution looks like a smoothed version of the standard, discrete binomial but shifted slightly to the right. The support of the continuous binomial is [0, size + 1], and the mean is approximately size * prob + 1/2.
Usage

dcbionm(x, size, prob, log = FALSE)
dcbionm(q, size, prob, lower.tail = TRUE, log.p = FALSE)
dcbionm(p, size, prob, lower.tail = TRUE, log.p = FALSE)
dcbionm(n, size, prob)

Arguments

x, q vector of quantiles.
p vector of probabilities.
n number of observations. If length(n) > 1, the length is taken to be the number required.
size the size parameter.
prob the prob parameter.
log, log.p logical; if TRUE, probabilities p are given as log(p)
lower.tail logical; if TRUE (default), probabilities are P[X <= x], otherwise, P[X > x]

Details

The cbinom package is an implementation of Ilienko’s (2013) continuous binomial distribution.
The continuous binomial distribution with size = N and prob = p has cumulative distribution function

\[ F(x) = \frac{B(x, N + 1 - x, p)}{B(x, N + 1 - x)} \]

for x in [0, N + 1], where

\[ B(x, N + 1 - x, p) = \int_{p}^{1} t^{x-1} (1 - t)^{y-1} dt \]

is the incomplete beta function and

\[ B(x, N + 1 - x) = \int_{0}^{1} t^{x-1} (1 - t)^{y-1} dt \]

is the beta function (or \( \text{beta}(x, N - x + 1) \) in R). The CDF can be expressed in R as \( F(x) = 1 - \text{pbeta}(\text{prob}, x, \text{size} - x + 1) \) and the mean calculated as \( \text{integrate}(\text{function}(x) \, \text{pbeta}(\text{prob}, x, \text{size} - x + 1), \text{lower} = 0, \text{upper} = \text{size} + 1) \).

If an element of x is not in [0, N + 1], the result of dcbionm is zero. The PDF dcbionm(x, size, prob) is computed via numerical differentiation of the CDF = 1 - pbeta(prob, x, size - x + 1).

Value

dcbionm is the density, pcbinom is the distribution function, qcbinom is the quantile function, and rcbinom generates random deviates.
The length of the result is determined by n for rbinom, and is the maximum of the lengths of the numerical arguments for the other functions.
The numerical arguments other than n are recycled to the length of the result.
References


Examples

```r
require(graphics)
# Compare continuous binomial to a standard binomial
size <- 20
prob <- 0.2
x <- 0:20
xx <- seq(0, 21, length = 200)
plot(x, pbinom(x, size, prob), xlab = "x", ylab = "P(X <= x)"
lines(xx, pcbinom(xx, size, prob))
legend('bottomright', legend = c("standard binomial", "continuous binomial"),
       pch = c(1, NA), lty = c(NA, 1))
mtext(side = 3, line = 1.5, text = "pcbinom resembles pbinom but continuous and shifted")

# Use "log = TRUE" for more accuracy in the tails and an extended range:

n <- 1000
k <- seq(0, n, by = 20)
print(cbind(exp(dcbinom(k, n, .481, log = TRUE)), dcbinom(k, n, .481)))
```
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