

Package: BlythStillCasellaCI (via r-universe)

May 11, 2026

Title Blyth-Still-Casella Exact Binomial Confidence Intervals

Version 1.1.0

Description Computes Blyth-Still-Casella exact binomial confidence intervals based on a refining procedure proposed by George Casella (1986) <[doi:10.2307/3314658](https://doi.org/10.2307/3314658)>.

License GPL-3

Encoding UTF-8

RoxygenNote 7.2.3

NeedsCompilation no

Author Ron Yu [aut, cre], Peiwen Wu [aut]

Maintainer Ron Yu <ronyu5135@gmail.com>

Repository <https://ronyu-gilead.r-universe.dev>

Date/Publication 2024-05-04 02:32:03 UTC

RemoteUrl <https://github.com/cran/BlythStillCasellaCI>

RemoteRef HEAD

RemoteSha cd65cdc7df9d774985e68fabd0b7372d29c45e35

Contents

blyth.still.casella	1
Index	3

blyth.still.casella *Blyth-Still-Casella Exact Binomial Confidence Intervals*

Description

blyth.still.casella() computes Blyth-Still-Casella exact binomial confidence intervals based on a refining procedure proposed by George Casella (1986).

Usage

```
blyth.still.casella(
  n,
  X = NULL,
  alpha = 0.05,
  digits = 2,
  CIs.init = NULL,
  additional.info = FALSE
)
```

Arguments

n	number of trials
X	number of successes (optional)
alpha	confidence level = 1 - alpha
digits	number of significant digits after the decimal point
CIs.init	initial confidence intervals from which the refinement procedure begins (default starts from Clopper-Pearson confidence intervals)
additional.info	additional information about the types of interval endpoints and their possible range is provided if TRUE (default = FALSE)

Value

If X is specified, the corresponding confidence interval will be returned, otherwise a list of n + 1 confidence intervals will be returned.

If additional.info = FALSE, only a list of confidence interval(s) will be returned. For any coincidental endpoint, midpoint of its range will be displayed.

If additional.info = TRUE, the following lists will be returned:

ConfidenceInterval	a list of confidence intervals
CoincidenceEndpoint	indices of coincidental lower endpoints (L.Index) and their corresponding upper endpoints (U.index)
Range	range for each endpoint

Examples

```
# to obtain 95% CIs for n = 30 and X = 0 to 30
blyth.still.casella(n = 30, alpha = 0.05, digits = 4)

# to obtain 90% CIs, endpoint types, indices of coincidental endpoints (if any),
# and range of each endpoint for n = 30 and X = 23
blyth.still.casella(n = 30, X = 23, alpha = 0.05, digits = 4, additional.info = TRUE)

# use initial confidence intervals defined by the user instead of Clopper-Pearson CIs
# CIs.input needs to be a (n + 1) x 2 matrix with sufficient coverage
CIs.input <- matrix(c(0,1), nrow = 11, ncol = 2, byrow = TRUE) # start with [0,1] intervals
blyth.still.casella(n = 10, alpha = 0.05, digits = 4, CIs.init = CIs.input, additional.info = TRUE)
```

Index

blyth.still.casella, 1