

# Package ‘CLAST’

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**Type** Package

**Title** Exact Confidence Limits after a Sequential Trial

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## Description

The user first provides design vectors  $n$ ,  $a$  and  $b$  as well as null ( $p_0$ ) and alternative ( $p_1$ ) benchmark values for the probability of success. The key function `mv.plots.SM()` calculates mean values of exact upper and lower limits based on four different rank ordering methods. These plots form the basis of selecting a rank ordering. The function `inference()` calculates exact limits from a provided realisation and ordering choice. For more information, see “Exact confidence limits after a group sequential single arm binary trial” by Lloyd, C.J. (2020), *Statistics in Medicine*, Volume 38, 2389-2399, <doi:10.1002/sim.8909>.

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## R topics documented:

CLAST-package . . . . .	2
CP.lower . . . . .	3
CP.stats.SM . . . . .	4
CP.upper . . . . .	5
cross . . . . .	5
errors.SM . . . . .	6
exact.lower.limits.SM . . . . .	7
exact.upper.limits.SM . . . . .	8
inference . . . . .	9
JT.rank.SM . . . . .	10
LR.lower . . . . .	11
LR.stats.SM . . . . .	12
LR.upper . . . . .	13

ML.rank.SM . . . . .	13
mv.plots.SM . . . . .	14
mv.SM . . . . .	15
plt.sample.space.SM . . . . .	16
prob.SM . . . . .	17
RANK . . . . .	18
sample.space . . . . .	19
sample.space.2 . . . . .	20
sample.space.SM . . . . .	21

<b>Index</b>	<b>22</b>
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CLAST-package	<i>Confidence Limits After Sequential Trial Exact Confidence Limits after a Sequential Trial</i>
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## Description

The user first provides design vectors  $n$ ,  $a$  and  $b$  as well as null ( $p_0$ ) and alternative ( $p_1$ ) benchmark values for the probability of success. The key function "mv.plots.SM()" calculates mean values of exact upper and lower limits based on four different rank ordering methods. These plots form the basis of selecting a rank ordering. The function "inference()" calculates exact limits from a provided realisation and ordering choice. For more information, see "Exact confidence limits after a group sequential single arm binary trial" by Lloyd, C.J. (2020), *Statistics in Medicine*, Volume 38, 2389-2399, <doi:10.1002/sim.8909>.

## Details

This package allows the user to compare different methods of calculating exact upper and lower limits for a probability after a group sequential trial.

## Author(s)

Chris J. Lloyd Maintainer: Chris J. Lloyd <c.lloyd@mbs.edu>

## References

Lloyd, C.J. (2020) Exact confidence limits after a group sequential single arm binary trial. *Statistics in Medicine*, Volume 38, 2389-2399. doi: [10.1002/sim.8909](https://doi.org/10.1002/sim.8909)

## Examples

```
# Example 1 in table 1 of Lloyd (2020)
n=c(5,6,5,9)
a=c(2,4,5,12)
b=c(5,9,11,13)
plt.sample.space.SM(n,a,b) # Produces figure 1 in reference
#
p0=.4
p1=.75
errors.SM(n,a,b,p0,p1) # Gives type 1 and type 2 errors
plt.sample.space.SM(n,a,b,p0,p1) # Add error rates into plot title
#
```

```

# Selection of type of limits is based on the diagnostic plots
# from the next command, which produces three panel graphic
# identical to Figure 2 in the main reference. The results here
# support method LR
  mv.plots.SM(n,a,b,p0=p0,p1=p1)
# Once we have an actual outcome we can calculate the limits.
  y=c(4,2,5) # Trial terminates on trial 2 since total successes is 11.
  inference(n,a,b,y,type="LR")
# Produces exact limits for specific outcome y.

```

---

CP.lower

*Calculates Clopper-Pearson lower limit*


---

### Description

Calculates the exact Clopper-Pearson lower limit for a binomial probability based on  $x$  successes from  $n$  trials

### Usage

```
CP.lower(x, n, a = 0.05)
```

### Arguments

$x$	number of successes (integer between 0 and $n$ inclusive)
$n$	number of binary trials
$a$	coverage error of limit

### Value

A numeric value between 0 and 1

### Author(s)

Chris J. Lloyd

### References

Clopper, C. and Pearson, E. S. (1934). The use of confidence or fiducial limits illustrated in the case of the binomial. *Biometrika*, 26 (4): 404-413. doi: [10.2307/2331986](https://doi.org/10.2307/2331986)

### Examples

```

# Find exact 99% lower limit for probability based on 20 successes from 55 trials.
CP.lower(20,55,a=0.01)
# Find exact (95%) lower limit for probability based on all failures.
CP.lower(0,5)

```

---

 CP.stats.SM

*Calculates all possible Clopper-Pearson limits.*


---

### Description

Calculates all possible Clopper-Pearson limits for  $p$  from an object that contains all possible data sets from a group sequential trial.

### Usage

```
CP.stats.SM(obj, alpha = 0.05, type = "upper")
```

### Arguments

obj	a list with elements S, M and design, containing all possible values of total successes S and stopping stage M based on the given design. Typically this is the output of function <code>sample.space</code> or <code>sample.space.2</code> and will also have elements Y and decision.
alpha	coverage error of exact limits
type	character, either "upper" or "lower"

### Value

a list with element "lims" as well as all elements of argument obj. The extra element contains the CP limit for each possible outcome.

### Author(s)

Chris J. LLoyd

### References

Clopper, C. and Pearson, E. S. (1934). The use of confidence or fiducial limits illustrated in the case of the binomial. *Biometrika*, 26 (4): 404-413. doi: [10.2307/2331986](https://doi.org/10.2307/2331986)

### Examples

```
n=c(5,6,5,9)
a=c(2,4,5,12)
b=c(5,9,11,13)
# There are 364 possible outcomes from this design which are
# listed in a natural systematic order by function sample.space.
all.samples=sample.space(n,a,b)
attributes(all.samples)
# Y contains the 364 possible sequential binary outcomes;
# M contains how many stages before the decision;
# S contains the total number of success that produces the decision;
# decision the final binary test result of H0 or H1.
CP.stats.SM(obj=all.samples)
```

---

 CP.upper

*Calculates Clopper-Pearson upper limit*


---

**Description**

Calculates the exact Clopper-Pearson upper limit for a binomial probability based on x successes from n trials

**Usage**

```
CP.upper(x, n, a = 0.05)
```

**Arguments**

x	number of successes (integer between 0 and n inclusive)
n	number of binary trials
a	coverage error of limit

**Value**

A numeric value between 0 and 1

**Author(s)**

Chris J. Lloyd

**References**

Clopper, C. and Pearson, E. S. (1934). The use of confidence or fiducial limits illustrated in the case of the binomial. *Biometrika*, 26 (4): 404-413. doi: [10.2307/2331986](https://doi.org/10.2307/2331986)

**Examples**

```
# Find exact 99% upper limit for probability based on 20 successes from 55 trials.
CP.upper(20,55,a=0.01)
# Find exact (95%) upper limit for probability from all successes.
CP.lower(5,5)
```

---

 cross

*Special combination of Matrix and Vector*


---

**Description**

This operation is useful in recursively generating all the possible path histories of a sequential design.

**Usage**

```
cross(A, v)
```

**Arguments**

A	An arbitrary matrix
v	An arbitrary vector

**Details**

For each component of v, the matrix A is duplicated with an extra right column equal to v[i]. This is added to the current output until the components of v are exhausted.

**Value**

A matrix with  $\dim(A)[2]+1$  columns and  $\dim(A)[1]*\text{length}(v)$  rows.

**Author(s)**

Chris J. Lloyd

**Examples**

```
A=cbind(c(1,2),c(3,4))
v=c(5,6)
cross(A,v)
#      [,1] [,2] [,3]
#[1,]  1   3   5
#[2,]  2   4   5
#[3,]  1   3   6
#[4,]  2   4   6
```

---

errors.SM

*Exact error rates of specified sequential design*

---

**Description**

For a given sequential design defined by vectors a, b and n, calculate the probability of a type 1 error (assuming  $p=p_0$ ) and type 2 error (assuming  $p=p_1$ )

**Usage**

```
errors.SM(n, a, b, p0, p1)
```

**Arguments**

n	Design vector of planned sample sizes
a	Design vector of lower futility boundaries
b	Design vector of upper superiority boundaries
p0	Lower benchmark for success probability
p1	Upper benchmark for success probability

**Value**

list with attributes type1 and type 2

**Author(s)**

Chris J. Lloyd

**Examples**

```
# Example 1 in table 1 of Lloyd (2020)
n=c(5,6,5,9)
a=c(2,4,5,12)
b=c(5,9,11,13)
p0=.4
p1=.75
errors.SM(n,a,b,p0,p1)
# $type1
# [1] 0.09590162
# $type2
# [1] 0.1060701
```

---

exact.lower.limits.SM *Calculates all exact lower limits.*

---

**Description**

Calculates Buehler lower limit for all possible data sets based on a provided ranking function.

**Usage**

```
exact.lower.limits.SM(obj, lims = NULL, alpha = 0.05, set = FALSE)
```

**Arguments**

obj	list with components \$count, \$\$, \$N, typically the output of LR.stats.SM, CP.stats.SM, JT.rank.SM or ML.rank.SM. In this case, it will also have element \$lims.
lims	a vector of same length as obj\$count, most often an approximate lower limits. If this is missing, then it should be an element of obj\$lims.
alpha	exact coverage error
set	If true, exact limits of 1 are replaced by the largest limit less than 1. This will never be chosen by the user and is there for certain numerical investigations.

**Value**

A numeric vector of same length as obj\$lims, giving the exact lower limit for each possible outcome as listed in components obj\$M and obj\$S.

**Author(s)**

Chris J. Lloyd

**References**

Lloyd, C.J. (2020) Exact confidence limits after a group sequential single arm binary trial. *Statistics in Medicine*, Volume 38, 2389-2399.

**Examples**

```
# Example 1 in table 1 of Lloyd (2020)
n=c(5,6,5,9)
a=c(2,4,5,12)
b=c(5,9,11,13)
# There are 364 possible outcomes from this design which are
# listed in a natural systematic order by function sample.space.
all.samples=sample.space.SM(n,a,b)
attributes(all.samples)
# Y contains the 364 possible sequential binary outcomes;
# M contains how many stages before the decision;
# S contains the total number of success that produces the decision;
# decision the final binary test result of H0 or H1.
all.CP=CP.stats.SM(all.samples,type="lower")
all.CP$lims # These limits are based on fixed sample size so are not exact.
all.exact=exact.lower.limits.SM(all.CP)
plot(all.CP$lims,all.exact)
```

---

exact.upper.limits.SM *Calculates all exact upper limits.*

---

**Description**

Calculates Buehler upper limit for all possible data sets based on ranking function provided in obj\$lims.

**Usage**

```
exact.upper.limits.SM(obj, lims = NULL, alpha = 0.05, set = FALSE)
```

**Arguments**

obj	list with components \$count, \$\$, \$N, typically the output of LR.stats.SM, CP.stats.SM, JT.rank.SM or ML.rank.SM. In this case, it will also have element \$lims.
lims	a vector of same length as obj\$count, most often an approximate lower limits. If this is missing, then it should be an element of obj\$lims.
alpha	exact coverage error
set	If true, exact limits of 0 are replaced by the smallest limit greater than 1. This will never be chosen by the user and is there for certain numerical investigations.

**Value**

A numeric vector of same length as obj\$lims, giving the exact lower limit for each possible outcome as listed in components obj\$M and obj\$S.

**Author(s)**

Chris J. Lloyd

**References**

Lloyd, C.J. (2020) Exact confidence limits after a group sequential single arm binary trial. *Statistics in Medicine*, Volume 38, 2389-2399.



**Examples**

```
# Example 1 in table 1 of Lloyd (2020)
n=c(5,6,5,9)
a=c(2,4,5,12)
b=c(5,9,11,13)
# There are 364 possible outcomes from this design which are
# listed in a natural systematic order by function sample.space.
all.samples=sample.space.SM(n,a,b)
attributes(all.samples)
# Y contains the 364 possible sequential binary outcomes;
# M contains how many stages before the decision;
# S contains the total number of success that produces the decision;
# decision the final binary test result of H0 or H1.
all.CP=CP.stats.SM(all.samples,type="upper")
all.CP$lims # These limits are based on fixed sample size so are not exact.
all.exact=exact.upper.limits.SM(all.CP)
plot(all.CP$lims,all.exact)
```

inference

*Exact limits from outcome***Description**

Calculates exact upper and lower confidence limits from the outcome of a multi-stage group sequential trial.

**Usage**

```
inference(n, a, b, y, alpha, type)
```

**Arguments**

n	Design vector of planned sample sizes
a	Design vector of lower futility boundaries
b	Design vector of upper superiority boundaries
y	Actual outcome of experiment
alpha	exact coverage error
type	character, either "LR", "CP", "JT" or "ML"

**Value**

list with components	
lower	exact lower limit, type dependent
upper	exact lower limit, type dependent
est	ML estimate
type	selected ordering function "LR", "CP", "JT" or "ML"

**Author(s)**

Chris J. Lloyd

## References

Lloyd, C.J. (2020) Exact confidence limits after a group sequential single arm binary trial. *Statistics in Medicine*, Volume 38, 2389-2399.

## Examples

```
# Example from table 1 of Lloyd (2020)
n=c(5,6,5,9)
a=c(2,4,5,12)
b=c(5,9,11,13)
y=c(4,2,5) # This is the actual outcome. The trial stopped for
# superiority at stage m=3 with s=11 successes.
inference(n,a,b,y,type="CP")
# Results happen to be identical for type="LR" but different
# for the alternative ordering functions "JT" and "ML"
```

---

JT.rank.SM

*Calculates Jennison & Turnbull ranking of sample space*

---

## Description

Calculates the Jennison & Turnbull (1983) ranking of each possible outcome of the sample space generated from a sequential design.

## Usage

```
JT.rank.SM(obj)
```

## Arguments

**obj** a list with elements S, M and design, containing all possible values of total successes S and stopping stage M based on the given design. Typically this is the output of function `sample.space` or `sample.space.2` and will also have elements Y and decision.

## Value

a list with element "lims" as well as all elements of argument obj. The extra element contains the JT rank of each possible the outcome.

## Author(s)

Chris J. Lloyd

## References

Jennison C, Turnbull BW. Confidence intervals for a binomial parameter following a multistage test with application to MIL-STD 105D and medical trials. *Technometrics*. 1983(25), 49-58. doi: [10.1080/00401706.1983.10487819](https://doi.org/10.1080/00401706.1983.10487819)

**Examples**

```

n=c(5,6,5,9)
a=c(2,4,5,12)
b=c(5,9,11,13)
# There are 364 possible outcomes from this design which are
# listed in a natural systematic order by function sample.space.
all.samples=sample.space(n,a,b)
attributes(all.samples)
# Y contains the 364 possible sequential binary outcomes;
# M contains how many stages before the decision;
# S contains the total number of success that produces the decision;
# decision the final binary test result of H0 or H1.
JT.rank.SM(obj=all.samples)
# Component "lims" contains the rank of each sequential binary
# outcome. The same rank is assigned to outcomes with the same
# values of (S,M).

```

LR.lower

*Calculates likelihood ratio based lower limit***Description**

Calculates approximate lower limit for a probability from  $x$  successes out of  $n$  binary trials based on the signed root likelihood ratio.

**Usage**

```
LR.lower(x, n, a = 0.05, epsilon = 1e-18)
```

**Arguments**

<code>x</code>	number of successes (integer between 0 and $n$ inclusive)
<code>n</code>	number of binary trials
<code>a</code>	coverage error of limit
<code>epsilon</code>	Tolerance supplied to <code>uniroot</code> .

**Value**

A numeric values between 0 and 1

**Author(s)**

Chris J. Lloyd

**Examples**

```

# Find approximate 99% lower limit for probability based on 20 successes from 55 trials.
LR.lower(20,55,a=0.01)
# Find exact (95%) lower limit for probability based on all failures.
LR.lower(0,5)

```

---

LR.stats.SM

*Calculates all possible LR limits.*


---

### Description

Calculates all possible LR based limits for  $p$  from an object that contains all possible data sets from a group sequential trial.

### Usage

```
LR.stats.SM(obj, alpha = 0.05, type = "upper")
```

### Arguments

obj	a list with elements S, M and design, containing all possible values of total successes S and stopping stage M based on the given design. Typically this is the output of function <code>sample.space</code> or <code>sample.space.2</code> and will also have elements Y and decision.
alpha	nominal coverage error of approximate LR based limits
type	character, either "upper" or "lower"

### Value

a list with element "lims" as well as all elements of argument obj. The extra element contains the LR exact limit for each possible outcome.

### Author(s)

Chris J. Lloyd

### Examples

```
n=c(5,6,5,9)
a=c(2,4,5,12)
b=c(5,9,11,13)
# There are 364 possible outcomes from this design which are
# listed in a natural systematic order by function sample.space.
all.samples=sample.space(n,a,b)
attributes(all.samples)
# Y contains the 364 possible sequential binary outcomes;
# M contains how many stages before the decision;
# S contains the total number of success that produces the decision;
# decision the final binary test result of H0 or H1.
LR.stats.SM(obj=all.samples)
```

---

LR.upper                      *Calculates likelihood ratio based upper limit*

---

**Description**

Calculates approximate upper limit for a probability from x successes out of n binary trials based on the signed root likelihood ratio.

**Usage**

```
LR.upper(x, n, a = 0.05, epsilon = 1e-18)
```

**Arguments**

x	number of successes (integer between 0 and n inclusive)
n	number of binary trials
a	coverage error of limit
epsilon	Tolerance supplied to uniroot.

**Value**

A numeric values between 0 and 1

**Author(s)**

Chris J. Lloyd

**Examples**

```
# Find approximate 99% upper limit for probability based on 20 successes from 55 trials.
LR.upper(20,55,a=0.01)
# Find exact (95%) upper limit for probability from all successes.
LR.upper(5,5)
```

---

ML.rank.SM                      *Maximum likelihood estimator of p.*

---

**Description**

Calculates the ML estimator for each possible outcome of the sample space generated from a sequential design.

**Usage**

```
ML.rank.SM(obj)
```

**Arguments**

obj a list with elements S, M and design, containing all possible values of total successes S and stopping stage M based on the given design. Typically this is the output of function sample.space or sample.space.2 and will also have elements Y and decision.

**Value**

a list with element "lims" as well as all elements of argument obj. The extra element contains the ML estimator of p for each possible outcome.

**Author(s)**

Chris J. Lloyd

**Examples**

```
n=c(5,6,5,9)
a=c(2,4,5,12)
b=c(5,9,11,13)
# There are 364 possible outcomes from this design which are
# listed in a natural systematic order by function sample.space.
all.samples=sample.space(n,a,b)
attributes(all.samples)
# Y contains the 364 possible sequential binary outcomes;
# M contains how many stages before the decision;
# S contains the total number of success that produces the decision;
# decision the final binary test result of H0 or H1.
ML.rank.SM(obj=all.samples)$lims
# Component "lims" contains the value of the ML estimate i.e.
# total successes S divided by total trials N. The same ML
# estimator occurs for outcomes with the same values of (S,M).
```

---

mv.plots.SM

*Diagnostic mean values plots.*


---

**Description**

Plots mean value of upper limit, lower limit and interval width for four different ranking methods. This function is basically a wrapper for mv.plot.

**Usage**

```
mv.plots.SM(n, a, b, type = "interval",
B = 100, offset = TRUE, plt = c(1, 1, 1), p0 = NULL, p1 = NULL, focus = FALSE)
```

**Arguments**

n Design vector of planned sample sizes  
a Design vector of lower futility boundaries  
b Design vector of upper superiority boundaries  
type Either "upper", "lower" or "interval" (default)

B	Integer controlling fineness of plot (default=100)
offset	if TRUE then ML mean value is subtracted
plt	Logical vector indicating output plots of upper, lower and interval (default=c(1,1,1))
p0	Lower (null) benchmark for success probability
p1	Upper (alternative) benchmark for success probability
focus	Logical. If true, plots are restricted to p between p0 and p1. (default=FALSE)

**Value**

NULL

**Author(s)**

Chris J. Lloyd

**References**

Lloyd, C.J. (2021) Exact confidence limits after a group sequential single arm binary trial. *Statistics in Medicine*, Volume 38, 2389-2399. doi: [10.1002/sim.8909](https://doi.org/10.1002/sim.8909)

**Examples**

```
# Figure 2 in Lloyd (2020)
n=c(5,6,5,9)
a=c(2,4,5,12)
b=c(5,9,11,13)
p0=.4
p1=.75
mv.plots.SM(n,a,b,p0=p0,p1=p1)
# Produces three panel graphic identical to Figure 2 in reference
mv.plots.SM(n,a,b,p0=p0,p1=p1,focus=TRUE)
# Produces alternative graphic focussed on relevant values of p.
# In both cases LR (in blue) appears best. CP can perform poorly
# for values of p outside the range of interest.
```

mv.SM

*Mean value of upper limits.***Description**

Calculates mean value of a provided vector of upper limits as a function of p

**Usage**

```
mv.SM(obj, lims = NULL, p = NULL, B = 99, offset = TRUE, wgt = TRUE)
```

**Arguments**

obj	list with components \$S, \$N, \$count and optionally \$lims, typically the output of sample.space.SM
lims	if not a component of obj
p	vector of values of p at which to calculate mean value
B	number of evenly spaced values of p if not provided
offset	if TRUE then ML mean value is subtracted
wgt	if TRUE than assign zero probability weight to extreme limits of 1 or 0.

**Value**

list with elements \$x (containing grid of B values of probability) and \$y (containing corresponding mean values)

**Author(s)**

Chris J. Lloyd

**Examples**

```
n=c(5,6,5,9)
a=c(2,4,5,12)
b=c(5,9,11,13)
# Enumerate all possible elements of the sufficiency reduced samples
# space i.e. all values of S and M. Also listed are the counts and
# subcounts of these outcomes, the test decision and the vector
# n, a, and b in $design

data.SM=sample.space.SM(n,a,b) # There are 26 elements.

# Calculate all approximate LR upper limits for these 26 outcomes.
all.LR.high=LR.stats.SM(data.SM,type="upper")$lims
# Calculate all approximate LR upper limits for these 26 outcomes.
all.LR.low=LR.stats.SM(data.SM,type="lower")$lims

# Calculate the mean values of these lims as a function of p
mv.high=mv.SM(data.SM,all.LR.high,p=(1:99)/100,offset=FALSE)
mv.low=mv.SM(data.SM,all.LR.low,p=(1:99)/100,offset=FALSE)
plot(c(0,1),c(0,1),ylab="mean value",xlab="p",type="n")
lines(mv.high)
lines(mv.low)
abline(0,1,lty=3)
title(main="Mean value of upper and lower limits by p")
```

---

plt.sample.space.SM    *Sample space for given sequential design.*

---

**Description**

Plots decision function in S-M space with boundary vectors "a" and "b". If p0 and p1 are provided then the type 1 and type 2 error are displayed in the main graphic title



**Usage**

```
plt.sample.space.SM(n, a, b, p0 = NULL, p1 = NULL)
```

**Arguments**

n	Design vector of sample sizes
a	Design vector of lower boundaries
b	Design vector of upper boundaries
p0	Lower benchmark for success probability
p1	Upper benchmark for success probability

**Value**

NULL

**Author(s)**

Chris J. Lloyd

**References**

Lloyd, C.J. (2020) Exact confidence limits after a group sequential single arm binary trial. *Statistics in Medicine*, Volume 38, 2389-2399. doi: [10.1002/sim.8909](https://doi.org/10.1002/sim.8909)

**Examples**

```
# Figure 1 of Lloyd (2020)
n=c(5,6,5,9)
a=c(2,4,5,12)
b=c(5,9,11,13)
plt.sample.space.SM(n,a,b)
# produces plots in Figure 1 or reference.
```

---

prob.SM

*Probability of sufficient statistics (S,M).*

---

**Description**

Calculates probability distribution of sufficient statistics (S,M) from sample space object.

**Usage**

```
prob.SM(data, p, m = NULL, s = NULL)
```

**Arguments**

data	list with components \$Y, \$S, \$M, \$design, \$count. This will typically be the output of sample.space or sample.space.2.
p	value of binary probability
m	number of stages at end of sequential trial
s	number of successes at end of sequential trial

**Value**

list with component \$prob, \$count, \$subcount and matrix \$data giving the \$subcount different binary sequential outcomes that lead to \$prob.

**Author(s)**

Chris J. Lloyd

**References**

Lloyd, C.J. (2020) Exact confidence limits after a group sequential single arm binary trial. *Statistics in Medicine*, Volume 38, 2389-2399. doi: [10.1002/sim.8909](https://doi.org/10.1002/sim.8909)

**Examples**

```
n=c(5,6,5,9)
a=c(2,4,5,12)
b=c(5,9,11,13)
# There are 364 possible outcomes from this design which are
# listed in a natural systematic order by function sample.space.
all.samples=sample.space(n,a,b)
attributes(all.samples)
# Y contains the 364 possible sequential binary outcomes;
# M contains how many stages before the decision;
# S contains the total number of success that produces the decision;
# decision the final binary test result of H0 or H1.
prob.SM(all.samples,p=.5,m=3,s=11)
```

---

RANK

*Produces ranks of entries of vector*

---

**Description**

An alternative to the function rank (which replaces ties by average rank). This function instead gives each tied value the same rank. The output will have the same length as x but contain integer values from 1 to length(unique(x)).

**Usage**

RANK(x)

**Arguments**

x                    a numeric vector

**Value**

Vector of integer ranks of the same length as x.

**Author(s)**

Chris J. Lloyd

**Examples**

```
x=c(5,4,4,7,6)
rank(x)
# 3.0 1.5 1.5 5.0 4.0
RANK(x)
# 2 1 1 4 3
```

---

sample.space

*Sample space enumeration (K>2)*


---

**Description**

Creates all possible samples from a multi-stage group sequential trial with  $K>2$ . If  $K=2$ , use the function `sample.space.2` instead.

**Usage**

```
sample.space(n, a, b)
```

**Arguments**

n	Design vector of planned sample sizes
a	Design vector of lower futility boundaries
b	Design vector of upper superiority boundaries

**Value**

list with components \$Y, \$M, \$S, \$decision and \$design

**Author(s)**

Chris J. Lloyd

**References**

Lloyd, C.J. (2020) Exact confidence limits after a group sequential single arm binary trial. *Statistics in Medicine*, Volume 38, 2389-2399. doi: [10.1002/sim.8909](https://doi.org/10.1002/sim.8909)

**Examples**

```
n=c(5,6,5,9)
a=c(2,4,5,12)
b=c(5,9,11,13)
# There are 364 possible outcomes from this design which are
# listed in a natural systematic order by function sample.space.
all.samples=sample.space(n,a,b)
attributes(all.samples)
# Y contains the 364 possible sequential binary outcomes;
# M contains how many stages before the decision;
# S contains the total number of success that produces the decision;
# decision the final binary test result of H0 or H1.
```

---

 sample.space.2

*Sample space enumeration (K=2)*


---

### Description

Creates all possible samples from a multi-stage group sequential trial with  $K=2$ . If  $K>2$ , use the function `sample.space` instead.

### Usage

```
sample.space.2(n, a, b)
```

### Arguments

n	Design vector of planned sample sizes
a	Design vector of lower futility boundaries
b	Design vector of upper superiority boundaries

### Value

list with components \$Y, \$M, \$S, \$decision and \$design

### Author(s)

Chris J. Lloyd

### References

Lloyd, C.J. (2020) Exact confidence limits after a group sequential single arm binary trial. *Statistics in Medicine*, Volume 38, 2389-2399. doi: [10.1002/sim.8909](https://doi.org/10.1002/sim.8909)

### Examples

```
n=c(5,6)
a=c(2,6)
b=c(5,7)
# There are 18 possible outcomes from this design which are
# listed in a natural systematic order by function sample.space.
all.samples=sample.space.2(n,a,b)
attributes(all.samples)
# Y contains the 18 possible sequential binary outcomes;
# M contains how many stages before the decision;
# S contains the total number of success that produces the decision;
# decision the final binary test result of H0 or H1.
```

---

sample.space.SM	<i>Sample space enumeration</i>
-----------------	---------------------------------

---

**Description**

Creates all possible samples from a multi-stage group sequential trial for  $K \geq 2$  by calling `sample.space` or `sample.space.2`.

**Usage**

```
sample.space.SM(n, a, b)
```

**Arguments**

n	Design vector of planned sample sizes
a	Design vector of lower futility boundaries
b	Design vector of upper superiority boundaries

**Value**

list with components

M	number of trials for each possible trial outcome
S	number of responses for each possible trial outcome
N	number of patients for each possible trial outcome
count	combinatoric multiplier for probability distribution
subcountM	combinatoric components for probability distribution
decision	test decision for each possible trial outcome
design	list giving design vectors

**Author(s)**

Chris J. Lloyd

**References**

Lloyd, C.J. (2020) Exact confidence limits after a group sequential single arm binary trial. *Statistics in Medicine*, Volume 38, 2389-2399. doi: [10.1002/sim.8909](https://doi.org/10.1002/sim.8909)

**Examples**

```
# Example 1 in table 1 of Lloyd (2020)
n=c(5,6,5,9)
a=c(2,4,5,12)
b=c(5,9,11,13)
sample.space.SM(n,a,b)
# Object describing all 26 possible outcomes for (s,m).
```

# Index

## \*Topic **package**

CLAST-package, 2

CLAST (CLAST-package), 2

CLAST-package, 2

CP.lower, 3

CP.stats.SM, 4

CP.upper, 5

cross, 5

errors (errors.SM), 6

errors.SM, 6

exact.lower.limits.SM, 7

exact.upper.limits.SM, 8

inference, 9

JT.rank.SM, 10

LR.lower, 11

LR.stats.SM, 12

LR.upper, 13

ML.rank.SM, 13

mv.plots.SM, 14

mv.SM, 15

plt.sample.space.SM, 16

prob.SM, 17

RANK, 18

sample.space, 19

sample.space.2, 20

sample.space.SM, 21