Package 'sglr'

April 19, 2022

Type Package

Title Sequential Generalized Likelihood Ratio Decision Boundaries
Proposed by Shih, Lai, Heyse and Chen (2010,
<doi:10.1002/Sim.4036>)

Version 0.8

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Description We provide functions for computing the decision boundaries for pre-licensure vaccine trials using the Generalized Likelihood Ratio tests proposed by Shih, Lai, Heyse and Chen (2010, <doi:10.1002/sim.4036>).

Depends R (>= 2.7)

Imports rlang, ggplot2, shiny

License GPL (>= 2)

NeedsCompilation no

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R topics documented:

1

| sglr-package | *A package for computing the boundaries for sequential generalized likelihood ratio test for pre-licensure vaccine studies* |

Description

This package is an implementation of the methodology of Shih, Lai, Heyse, and Chen (to appear in Statistics in Medicine) for computing Generalized Likelihood Ratio test boundaries for pre-licensure vaccine studies

Details

Package:	sglr
Type:	Package
Version:	0.05
Date:	2010-04-20
License:	GPL (version 2 or later)
LazyLoad:	yes

The package provides several functions. The function `glrSearch` computes boundaries for testing a given p_0 versus p_1 (specified as a two-dimensional vector) given a significance level α and a type II error β. The function `computeBoundary` computes the boundary in terms of a more understandable and usable quantity, such as the number of adverse events in a pre-licensure vaccine study for example. It takes as input a set of given boundaries for the GLR statistic. The third function is `plotBoundary` which also takes the same arguments as $computeBoundary$ and produces a plot. The last two functions can make use of statistics computed previously for the problem, which can be specified as an argument; otherwise, the statistics are computed from scratch.

Author(s)

Balasubramanian Narasimhan with input from Tze Lai and Mei-Chiung Shih. Maintainer: Balasubramanian Narasimhan <naras@stat.stanford.edu>

References

"Sequential Generalized Likelihood Ratio Tests for Vaccine Safety Evaluation" doi: 10.1002/sim.4036.

Examples

```
library(sglr)
result <- glrSearch(p=c(.5, .75), alpha=0.05, beta=0.10)
## print(result)  ## large amounts of output possible!
result[1:3]
```

| computeBoundary | *A function to compute the boundary of the decision region in terms of the number of adverse events (AEs) of interest, such as vaccine AEs.* |

Description

This function computes the boundary of the decision region in a manner that can be employed in the field, as a table, for example. See section 4.2 of the reference below.

Usage

```
computeBoundary(b1, b0, p, glrTables = NULL, tol=1e-7)
```

Arguments

b1	The acceptance boundary value (corresponds to the boundary b_1 in the appendix of reference)
b0	The rejection boundary value (corresponds to the boundary b_0 in the appendix of reference)
p	The vector of probabilities, (p_0, p_1) with $p_0 < p_1$.
glrTables	A previously computed set of likelihood functions, to speed up computation for the *same hypothesis testing problem*. Otherwise, it is computed ab initio, resulting in a longer running time.
tol	A numerical tolerance, defaults to 1e-7

Details

This essentially computes the probabilities of hitting the boundaries using a recursion.

Value

upper	The upper boundary that indicates rejection of the null hypothesis
lower	The upper boundary that indicates acceptance of the null hypothesis
estimate	The estimated α and β values corresponding to the two boundaries

Author(s)

Balasubramanian Narasimhan

References

"Sequential Generalized Likelihood Ratio Tests for Vaccine Safety Evaluation" doi: 10.1002/sim.4036.

See Also

See Also glrSearch

Examples

```
computeBoundary(b1=2.8, b0=3.3, p=c(.5, .75))
```

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glrSearch	*This function searches through a space of design boundaries (scalar values a and b) to find values that achieve close to specified type I and type II errors for the sequential generalized likelihood ratio test of p0 versus p1 (specified respectively as vector of length 2) in pre-licensure vaccine trials*

Description

The search through the space of b_1 (corresponds to b_1 in paper) and b_0 (corresponds to b_0 in paper) is greedy initially. Then refinements to the boundary are made by adjusting the boundaries by the step-size. It is entirely possible that the step-size is so small that a maximum number of iterations can be reached. Depending on how close p_0 and p_1 are the memory usage can grow significantly. The process is computationally intensive being dominated by a recursion deep in the search.

Usage

```
glrSearch(p, alpha, beta, stepSize = 0.5, tol = 1e-7,
          startB1 = log(1/beta), startB0 = log(1/alpha),
          maxIter = 25, gridIt = FALSE, nGrid = 5, verbose = FALSE)
```

Arguments

p	The vector of p_0 and p_1, with $p_0 < p_1$
alpha	A value for type I error α between 0 and 1 typically 0.05 which is the default value
beta	A value for type II error (β) between 0 and 1 typically below .2, default 0.10
stepSize	A value to use for moving the boundaries during the search, 0.5 default seems to work.
tol	A value that is used for deciding when to terminate the search. A euclidean metric is used. Default 1e-7.
startB1	A starting value for the futility boundary, default is log of reciprocal type I error
startB0	A starting value for the rejection boundary, default is log of reciprocal type II error
maxIter	A maximum number of iterations to be used for the search. This allows for a bailout if the step size is too small.
gridIt	A logical value indicating if a grid of values should be evaluated once the boundaries are bracketed in the search.
nGrid	The number of grid points to use, default 5
verbose	A logical flag indicating if you want verbose output during search. Useful for situations where the code gets confused.

Details

One should not use this code without a basic understanding of the Shih, Lai, Heyse and Chen paper cited below, particularly the section on the pre-licensure vaccine trials.

As the search can be computationally intensive, the program needs to use some variables internally by reference, particularly large tables that stay constant.

In our experiments, starting off with the default step size has usually worked, but in other cases the step size and the maximum number of iterations may need to be adjusted.

Value

`b1`	The explored values of the futility boundary b_1 (corresponds to the boundary b_1 in the appendix of reference)
`b0`	The explored values of the rejection boundary b_0 (corresponds to the boundary b_0 in the appendix of reference)
`estimate`	The estimated α and β values corresponding to the explored boundaries (a 2-column matrix); first column is α, second is β
`glrTables`	The constant values of the log likelihoods under p_0, p_1 and the estimate probability of terminating at that step. The first two, are, in turn, lists of length n where n is the maximum number of adverse events that might be needed for the test. The last element is a matrix of 2 columns, specifying the probability of terminating at each value of n
`alphaTable`	a matrix (nGrid x nGrid) of α values corresponding to the combinations of boundaries b and a (which are the row and column names of the matrix). This is computed only if `gridIt=TRUE`
`betaTable`	a matrix (nGrid x nGrid) of β values corresponding to the combinations of boundaries b and a (which are the row and column names of the matrix). This is computed only if `gridIt=TRUE`
`b1Vals`	the vector of b_1 (or equivalently b_1) values used in the grid, computed only if `gridIt=TRUE`
`b0Vals`	the vector of b_0 (or equivalently b_0) values used in the grid, computed only if `gridIt=TRUE`
`iterations`	The number of iterations actually used

Author(s)

Balasubramanian Narasimhan

References

"Sequential Generalized Likelihood Ratio Tests for Vaccine Safety Evaluation" doi: 10.1002/sim.4036.

Examples

```
library(sglr)
result <- glrSearch(p=c(.5, .75), alpha=0.05, beta=0.10)
```

```
result <- glrSearch(p=c(.5, .75), alpha=0.05, beta=0.10, verbose=TRUE)

result <- glrSearch(p=c(.5, .75), alpha=0.05, beta=0.10, gridIt=TRUE)
print(result$alphaTable)
print(result$betaTable)

## takes a while
result <- glrSearch(p=c(.5, 2/3), alpha=0.05, beta=0.10)
print(names(result))

##result <- glrSearch(p=c(.5, 2/3), alpha=0.05, beta=0.10, gridIt=TRUE)
##print(result$alphaTable)
##print(result$betaTable)
```

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plotBoundary *A function to plot the boundary of the decision region*

Description

This function attempts to plot the boundary of the decision region, but currently falls flat. Will be rewritten.

Usage

```
plotBoundary(b1, b0, p, glrTables = NULL, tol = 1e-7,
             legend =FALSE, textXOffset = 2, textYSkip = 2)
```

Arguments

b1	The acceptance boundary value (corresponds to the boundary b_1 in the appendix of reference)
b0	The rejection boundary value (corresponds to the boundary b_0 in the appendix of reference)
p	The vector of probabilities, (p_0, p_1) with $p_0 < p_1$.
glrTables	A previously computed set of likelihood functions, to speed up computation for the *same hypothesis testing problem*. This can speed up computations.
tol	The tolerance, default of 1e-7
legend	A flag indicating if a legend is desired or not, default false
textXOffset	Horizontal offset for legend text
textYSkip	Vertical skip for legend text

Details

This essentially computes the recursion and the probabilities of hitting the boundaries and returns a ggplot2 object

Value

A ggplot2 object

Author(s)

Balasubramanian Narasimhan

See Also

See Also `glrSearch`

Examples

```
plotBoundary(b1=2.8, b0=3.3, p=c(.5, .75))
```

Index