Package: NNTbiomarker (via r-universe)

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Type Package

Title Calculate Design Parameters for Biomarker Validation Studies

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Description Helps a clinical trial team discuss the clinical goals of a well-defined biomarker with a diagnostic, staging, prognostic, or predictive purpose. From this discussion will come a statistical plan for a (non-randomized) validation trial. Both prospective and retrospective trials are supported. In a specific focused discussion, investigators should determine the range of ``discomfort'' for the NNT, number needed to treat. The meaning of the discomfort range, [NNTlower, NNTupper], is that within this range most physicians would feel discomfort either in treating or withholding treatment. A pair of NNT values bracketing that range, NNTpos and NNTneg, become the targets of the study's design. If the trial can demonstrate that a positive biomarker test yields an NNT less than NNTlower, and that a negative biomarker test yields an NNT less than NNTlower, then the biomarker may be useful for patients. A highlight of the package is visualization of a ``contra-Bayes'' theorem, which produces criteria for retrospective case-controls studies.

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Imports shiny, xtable, stringr, magrittr, mvbutils

Collate aaa.R ifVerboseCat.R sesp-pv-NNT.R achievable.se.sp.R binom.confint.R NNTintervals.R run.R ROCplots.R argmin.R zzz.R

Suggests testthat (>= 0.8.1), knitr (>= 1.6), rmarkdown, ggplot2, plyr

VignetteBuilder knitr

Repository https://professorbeautiful.r-universe.dev

RemoteUrl https://github.com/professorbeautiful/nntbiomarkerhome

RemoteRef HEAD

RemoteSha dc7702f3e626a189fcf400dcdc8fb546704571b3

Contents

`NNTbiomarker-package` *Plan a biomarker validation study by focusing on desired clinical actionability.*

Description

Clarifying what performance would suffice if the test is to improve medical care makes it possible to design meaningful validation studies.

Details

Package:	NNTbiomarker
Type:	Package
Version:	0.1
Date:	2015-03-21
License:	What license is it under?

This package bases the design of a biomarker study on the idea of "number needed to treat" (NNT). It postulates a "range of discomfort" for NNT, within which the clinical decision is uncomfortable for a treating physician. provides a `shiny` window for eliciting the boundaries of the range of number needed to

Author(s)

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References

See author for unpublished manuscript.

Examples

```
NNT.to.pv(NNTpos=5, NNTneg=28)
NNT.from.sesp(se=0.7, sp=0.9, prev=0.1)
pv.to.sesp(pv = cbind(ppv=seq(.5, .9, .1), npv=0.9), prev = 0.2)
```

`argmin` *argmin Argmin function for a vector.*

Description

Return the index minimizing distance from v to target.

Usage

```
argmin(v, target = 0)
```

Arguments

`v`	The vector to compare to target.
`target`	The value sought in the vector; default=0.

Value

The index in v of the value which is closest to target.

`binom.confint` *binom.confint*

Description

Exact confidence intervals for a binomial proportion parameter.

Usage

```
binom.confint(k, n, alpha = 0.05, side = c("two", "upper", "lower"))
```

Arguments

`k`	#"heads"
`n`	sample size
`alpha`	Confidence level
`side`	Sidedness of the hypothesis: c("two", "upper", "lower")

`NNT.to.pv` *NNT.to.pv*

Description

Convert between (NNTpos, NNTneg) and (PPV, NPV).

Usage

```
NNT.to.pv(NNTpos, NNTneg, NNT, prev, calculate.se.sp = F)
```

Arguments

`NNTpos`	NNT for a patient with positive test result
`NNTneg`	NNT for a patient with negative test result
`NNT`	A matrix or vector of (NNTpos, NNTneg) values.
`prev`	Prevalence of the "BestToTreat" group before testing.
`calculate.se.sp`	(default=FALSE) If TRUE, also calculate the sensitivity and specificity using the contra-Bayes theorem.

Value

For matrix input, cbind(ppv=ppv, npv=npv). For vector input, c(ppv=ppv, npv=npv).

`NNTintervalsRetrospective` *NNTintervalsRetrospective*

Description

Bayes predictive intervals for sensitivity, specificity, NNTpos and NNTneg in a case-control retrospective study.

Usage

```
NNTintervalsRetrospective(Ncases = 10, Ncontrols = 30, NposCases = 6,
  NposControls = 2, prev = 0.15, alpha = 0.025, prior = c(1/2, 1/2))
```

Arguments

Ncases	Number of cases in the study
Ncontrols	Number of controls in the study
NposCases	Number of cases with positive test
NposControls	Number of controls with positive test
prev	Prevalence of the BestToTreat (versus BestToWait)
alpha	Significance level for interval.
prior	Beta parameters for prior. Default is the Jeffreys prior = c(1/2,1/2). Jaynes prior = c(0,0) won't work when #fp=1.

Value

A list with 3 components containing intervals (predictive or otherwise), with names intervalsForSN, intervalsForSP, intervalsForNNT. The intervals derive from assuming independent Jeffreys priors for SN and SP, sampling from joint independent posteriors for SN and SP incorporating the anticipated results, and applying NNT.from.sesp (Bayes theorem) to each sampled pair to obtain a sample of NNTpos and NNTneg.

ROCplots *ROCplots*

Description

A variety of ROC-related plots for a binary target and a single continuous predictor.

Usage

```
ROCplots(data, whichPlots = c("density", "raw", "ROC", "pv", "nnt",
  "nntRange"), NNTlower = 3, NNTupper = 10, N = 1000, prev = 0.2,
  diffInSD = 2, ...)
```

Arguments

data	Data frame with columns "class" (binary target variable) and "X" (predictor).
whichPlots	Which plots to do. Options are c("density", "raw", "ROC", "pv", "nnt")
NNTlower	Subjective input. If NNT < NNTlower, the decision is clearly to Treat.
NNTupper	Subjective input. If NNT > NNTupper, the decision is clearly to Wait.
N	For simulated data: sample size
prev	For simulated data: Prevalence
diffInSD	For simulated data: Difference: E(X | group=1) - E(X | group=0),measured in units of S.D (common to the 2 groups).
...	Extra arguments for a plot. Do not supply unless length(whichPlots)==1.

Details

The plots display the values achievable by changing the cutoff, in comparison with the desired values as determined by NNTlower and NNTupper. The "whichPlots" options are as follows:

- "density"Marginal density of X, with rug.
- "raw"X versus class.
- "ROC"Standard ROC curve.
- "pv"Plot of ppv versus npv, with indication of the acceptable range for cutoff.
- "nnt"Plot of NNTpos versus NNTneg, with indication of the acceptable region
- "nntRange"Plot of NNTpos and NNTneg versus cutoff, with indication of the acceptable range.

  By default, all the plots are made.

`run` *run*

Description

Run a shiny app for this package.

Usage

```
run(shinyDir)
```

Arguments

`shinyDir`	Current options are "shinyElicit" and "shinyCombinePlots". If not provided, a menu of the options is provided.

Details

The selected shiny app is run. See the vignette Using_the_NNTbiomarker_package for details, and the vignette The_Biomarker_Crisis for an overview.

runCombinePlots *runCombinePlots*

Description

Run a shiny app connecting a visual scale for NNT quantities and a "contra-Bayes" plot for mapping from predictive values to sensitivity/specificity (Bayes theorem in reverse).

Usage

```
runCombinePlots()
```

See Also

run

runElicit *runElicit*

Description

Run a shiny app outlining the process of specifying a design for a biomarker validation study.

Usage

```
runElicit()
```

See Also

run

setVerboseCatOption *setVerboseCatOption*

Description

Allows user to toggle on and off printing messages on a per-function basis. Should be usable in other packages, but not by importing.

Usage

```
setVerboseCatOption(fname, value)
```

Arguments

fname	Name of the function to control.
value	Boolean value: should this function print out messages?

Value

The new value of the namespace option for fname ifVerboseCat

%&% *%&% string concatenation*

Description

From mvbutils

Usage

```
a %&% b
```

Arguments

a	a string
b	another string

Value

paste0(a, b)

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