Package ‘ClinicalUtilityRecal’

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Title Recalibration Methods for Improved Clinical Utility of Risk Scores
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Description Recalibrate risk scores (predicting binary outcomes) to improve clinical utility of risk score using weighted logistic or constrained logistic recalibration methods. Additionally, produces plots to assess the potential for recalibration to improve the clinical utility of a risk model. Methods are described in detail in Mishra, A. (2019) `Methods for Risk Markers that Incorporate Clinical Utility’ <http://hdl.handle.net/1773/44068>.
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Description

Flexible function for plotting the calibration curve for a risk score and different recalibrations of a risk score. Histograms of risk score and recalibrated risk scores can be plotted using argument "hist=TRUE". Dotted guidelines for the risk threshold R are plotted and clinically relevant risk region [R_l, R_u] are plotted to help gauge calibration in clinically relevant.

Usage

calCurvPlot(y,p,p.std=NULL,p.recal=NULL,
stdPlot=FALSE, recalPlot=FALSE,
xlim=c(0,1),ylim=c(0,1),
label="Original Risk Score",
label2 = "Standard Recalibrated Risk Score",
label3 = "Weighted/Constrained Recalibrated Risk Score",
legendLab = c("Orig.", "Std.", "Wt."),
mainTitle="Calibration of Risk Score",
hist=TRUE,ylimHist = c(0,0.5),
r,r1 = -Inf, ru = Inf)

Arguments

y
Vector of binary outcomes, with 1 indicating event (case) and 0 indicating no event (controls)

p
Vector of risk score values

p.std
Vector of risk score values after standard logistic recalibration

p.recal
Vector of risk score values after weighted/contratined logistic recalibration

stdPlot
If TRUE plot calibration curve for standard logistic recalibrated risk score

recalPlot
If TRUE plot calibration curve for weighted/contratined recalibrated risk score

xlim
Limits for x-axis

ylim
Limits for y-axis

label
Label for x-axis corresponding to p vector

label2
Label for x-axis corresponding to p.std vector

label3
Label for x-axis corresponding to p.recal vector

legendLab
Label for legend

mainTitle
Main title for plot

hist
If true plot distribution of risk scores along with calibration curve

ylimHist
Limits for y-axis of histogram
**calCurvPlot**

- **r** Clinically relevant risk threshold used indicated with dotted line
- **r1** Lower bound of clinically relevant region indicated with dotted-dashed line
- **ru** Upper bound of clinically relevant region indicated with dotted-dashed line

**Value**

Prints calibration plot of risk model p, and optional histogram of risk score

**Author(s)**

Anu Mishra

**References**


**Examples**

```r
## Not run:
data("fakeData")

### get standard recalibrated risk score
stdRecal.res <- stdRecal(y = fakeData$y, p = fakeData$p)
p.std <- stdRecal.res$p

### Select tuning parameter lamba using 5-fold cross-validation repeated 25 times
grid <- RAWgrid(r = 0.3, rl = -Inf, ru = Inf, p = fakeData$p, y = fakeData$y, 
cvParm = "lambda", rl.raw = 0.25, ru.raw = 0.35)
repCV <- cvRepWtTuning(y = fakeData$y, p = fakeData$p, r = Inf, ru = Inf, r = 0.3, 
kFold = 5, cvRep = 25, cvParm = "lambda", tuneSeq = grid, stdErrRule = TRUE)

### Implement weighted logistic recalibration
wtRecal.res <- wtRecal(y = fakeData$y, p = fakeData$p, r = 0.3, rl = -Inf, ru = Inf, 
lambda = repCV$cv.lambda, delta=1)
p.recal <- wtRecal.res$p

### Calibration curve of only original risk score with histogram
calCurvPlot(y=fakeData$y, p=fakeData$p, p.std=NULL, p.recal=NULL, 
stdPlot=FALSE, recalPlot=FALSE, 
xlim=c(0,1), ylim=c(0,1), 
label="Original Risk Score", 
label2 = "Standard Recalibrated Risk Score", 
label3 = "Weighted/Constrained Recalibrated Risk Score", 
legendLab = c("Orig.", "Std.", "Wt."), 
mainTitle="Calibration of Risk Score", 
hist=TRUE, ylimHist = c(0,0.5), 
r=0.3, rl = -Inf, ru = Inf)

### Calibration curve of only original, standard and weighted recalibrated risk score
calCurvPlot(fakeData$y, p=fakeData$p, p.std=p.std, p.recal=p.recal, 
...)
```
\begin{verbatim}
studioCalRecal=TRUE, recalPlot=TRUE,
xlim=c(0,1), ylim=c(0,1),
label="Original Risk Score",
label2 = "Standard Recalibrated Risk Score",
label3 = "Weighted/Constrained Recalibrated Risk Score",
legendLab = c("Orig.", "Std.", "Wt."),
mainTitle="Calibration of Risk Score",
hist=TRUE, ylimHist = c(0,0.5),
r=0.3, r1 = -Inf, ru = Inf)
## End(Not run)
\end{verbatim}

---

**calWt**

*Calibration Weights*

**Description**
Calculates observation weights used for weighted calibration method using LOESS smoother. Observations with predicted risks outside clinically relevant interval \([R_l, R_u]\) are downweighted.

**Usage**

```r
calWt(rl, ru, p, y, r, lambda, delta, returnSmoothedEvent=FALSE)
```

**Arguments**

- `rl`: Lower bound of clinically relevant region
- `ru`: Upper bound of clinically relevant region
- `p`: Vector of risk score values
- `y`: Vector of binary outcomes, with 1 indicating event (cases) and 0 indicating no event (controls)
- `r`: Clinically relevant risk threshold
- `lambda`: Tuning parameter for weights inside relevant region
- `delta`: Weight assigned to observations outside relevant region
- `returnSmoothedEvent`: If TRUE returns smoothed observed event rate used for calculation of weights

**Details**
Computes observation weights for weighted recalibration method. Observations with risk scores near a pre-defined clinically relevant risk threshold \(r\) are given weights near 1, while observations far from the risk threshold are down-weighted.

For observations with risk scores within a pre-defined clinically relevant region \([R_l, R_u]\), the weighting function follows an exponential decay form with observations receiving smaller weights as they move farther from the clinically relevant risk threshold. Distance is measured by the squared
difference between the risk threshold and $o(p_i)$, where $o(p_i)$ is a smoothed observed event rate obtained via LOESS regression of $y$ on the risk scores $p_i$.

The amount of decay is set by the tuning parameter $\lambda$, with larger lambda indicating little down-weighting applied. For observations outside the clinically relevant risk interval, a weight of $\text{delta}$ is assigned. An indicator type weight can be choosen by select large $\lambda$ (e.g $\lambda = 10$). Clinically relevant region can be $[R_l, R_u] = [-\infty, \infty]$, and in these cases it is not necessary to specify $\text{delta}$. See Mishra et al (2020) for functional form of weights and more details.

Value

- **wt**: Vector of weights, between 0 and 1, to be used for weighted recalibration
- **o**: Vector of smoothed observed event rates

Author(s)

Anu Mishra

References


See Also

- wtRecal

Examples

```r
#load data
data(fakeData)

#exponential decay type weight
expWt <- calWt(rl=-Inf,ru=Inf,p=fakeData$p,y=fakeData$y,r=0.2,
               lambda=0.05,delta=0.2,returnSmoothedEvent = TRUE)
plot(expWt$o,expWt$wt,xlab="Smoothed Observed Event Rate",
     ylab="Calibration Weight",ylim=c(0,1))

#indicator type weight
indWt <- calWt(rl=0.1,ru=0.3,p=fakeData$p,y=fakeData$y,r=0.2,
               lambda=0.05,delta=0.2,returnSmoothedEvent = TRUE)
plot(indWt$o,indWt$wt,xlab="Smoothed Observed Event Rate",
     ylab="Calibration Weight",ylim=c(0,1))
```
constRecal  

**Constrained Logistic Recalibration**

**Description**

When recalibrating a risk model, where the intended purpose of the risk model is to prescribe an intervention to those deemed at high risk, it is desirable to have good calibration at the clinically relevant threshold used to define high risk (i.e. threshold used to identify who receives treatment). This can be achieved by maximizing the clinical utility of a risk model, which should in turn produce good calibration near the clinical relevant risk threshold. This function recalibrates risk scores (predicting binary outcome) by estimating the recalibration intercept and slope by maximizing the logistic likelihood over a restricted parameter space (Mishra et al. [2020]).

The restricted space only includes recalibration parameters $\alpha_0$ and $\alpha_1$ that produce a recalibrated risk model with high sNB. The restricted parameter space is defined all $\alpha$ parameters that result in a recalibrated risk score within one-standard-error of the maximum possible sNB. See Mishra et al (2020), for full details.

**Usage**

```r
constRecal(y,p,r,int=NULL,alphaLB=c(-10,0),
           alphaUB=c(10,10),ftol=1e-8,xtol=1e-4,maxeval=1e6)
```

**Arguments**

- **y**  
  Vector of binary outcomes, with 1 indicating event (case) and 0 indicating no event (controls)
- **p**  
  Vector of risk score values
- **r**  
  Clinically relevant risk threshold
- **int**  
  Two-dimensional vector of initial recalibration parameter ($\alpha$) values. If not specified the recalibration parameters estimated under standard logistic recalibration will be used
- **alphaLB**  
  Lower bound of box-constrained search space
- **alphaUB**  
  Upper bound of box-constrained search space
- **ftol**  
  Controls tolerance of optimization procedure with respect to changes in sNB
- **xtol**  
  Controls tolerance of optimization procedure with respect to changes in alpha
- **maxeval**  
  Maximum number of iterations performed during optimization procedure

**Details**

To solve this optimization problem the DIRECT optimization method is implemented via the NLOPTR package. See Jones et al (1993) and Ypma et al (2014) for full description of optimization method and implementation details. Note this is not a convex optimization problem, so a global optimizer is used.
Value

alpha  
Recalibration parameters obtained from Constrained Logistic Recalibration

y  
Vector of binary outcomes, with 1 indicating event (case) and 0 indicating no event (controls)

p.const  
Vector of constrained logistic recalibrated risk scores

snbLB  
Lower bound used to define constraint region. The solution is constrained to the region where recalibration parameters result in risk model with $sNB$ greater or equal to this bound. This is one-standard error lower than the maximum $sNB$

optimRes  
Full output from the NLOPTR optimization routine

Author(s)

Anu Mishra

References


Examples

```r
## Not run:
### Load data ##
data(fakeData)

## Implementing standard logistic recalibration
stdRecal.res <- stdRecal(y = fakeData$y,p = fakeData$p)
stdRecal.res$alpha #standard recalibration parameters
p.std <- stdRecal.res$p.std

## Look at potential sNB under recalibration plot
snbRecalPlot(p = fakeData$p,p.std = p.std,y = fakeData$y,r = 0.3)

## Implementing constrained logistic recalibration
constRecal.res <- constRecal(y = fakeData$y,p = fakeData$p,r = 0.3)
constRecal.res$alpha #constrained logistic recalibration parameters
p.recal <- constRecal.res$p.const

## comparing standardized net benefit of the two
nb(y = fakeData$y,p = fakeData$p,r = 0.3)$snb #original
nb(y = stdRecal.res$y,p = stdRecal.res$p.std,r = 0.3)$snb #std recal
nb(y = constRecal.res$y,p = constRecal.res$p.const,r = 0.3)$snb #weighted

## Generate calibration plots
```
### Calibration curve of only original, standard and weighted recalibrated risk score

```r
calCurvPlot(y=fakeData$y,p=fakeData$p,p.std=p.std,p.recal=p.recal,
            stdPlot=TRUE, recalPlot=TRUE,
            xlim=c(0,1),ylim=c(0,1),
            label="Original Risk Score",
            label2 = "Standard Recalibrated Risk Score",
            label3 = "Weighted/Constrained Recalibrated Risk Score",
            legendLab = c("Orig.", "Std.", "Wt."),
            mainTitle="Calibration of Risk Score",
            hist=TRUE,ylimHist = c(0,0.5),
            r=0.3,rl = -Inf, ru = Inf)
```

## End(Not run)

---

**cvRepWtTuning**

*Repeated Cross Validation for Weight Tuning Parameter Selection*

---

**Description**

Calibration weights require specification of tuning parameter *delta* or *lambda*. Since a single round of cross-validation can be noisy, cross-validation can be repeated multiple times with independent random partitions and the results be averaged. This function implements a repeated K-fold cross-validation where tuning parameter *lambda* or *delta* is selected by maximizing standardized net benefit (sNB) (i.e. repeated cvWtTuning procedure).

A "one-standard error" rule can be used for selecting tuning parameters. Under the "one-standard error" rule the calibration weight tuning parameter (*lambda* or *delta*) is selected such that corresponding cross-validated sNB is within one-standard deviation of the maximum cross-validated sNB. This provides protection against overfitting the data and selecting a tuning parameter that is too extreme. If the "one-standard error" rule is not implemented, then the tuning parameter with the largest average cross-validated sNB (across folds and repetition) will be selected.

**Usage**

```r
cvRepWtTuning(y,p,r,r1,ru,kFold=5,cvRep=25,cvParm,tuneSeq,stdErrRule=TRUE,int.seed=11111)
```

**Arguments**

- `y` Vector of binary outcomes, with 1 indicating event (cases) and 0 indicating no event (controls)
- `p` Vector of risk score values
- `r` Clinically relevant risk threshold
- `r1` Lower bound of clinically relevant region
- `ru` Upper bound of clinically relevant region
- `kFold` Number of folds for cross-validation
cvRepWtTuning

**cvRep**
Number of cross-validation repititions

**cvParm**
Parameter to be selected via cross-validation. Can be either delta the weight assigned to observations outside the clinically relevant region \([R_l,R_u]\), or the lambda tuning parameter controlling exponential decay within the clinically relevant region \([R_l,R_u]\)

**tuneSeq**
Sequence of values of tuning parameters to perform cross-validation over

**stdErrRule**
Use "one-standard" error rule selecting tuning parameter

**int.seed**
Initial seed set for random splitting of data into K folds

**Details**
To estimate the standard deviation of the cross-validated sNV, the dependence between the different partitions of cross-validation needs to be accounted for. Gelman (1992) give a variance estimator of convergence diagnostic statistic used when Markov Chain Monte Carlo with multiple chains are performed. The variance estimator accounts for both the variability of the statistic "within" a single chain, and the variance of the statistic across, or "between", chains. Analogously, we can use this framework to estimate the "within" repetition variance (i.e. variation in sNB from a single round of K-fold cross-validation) and the "between" repetition variance. We denote the "within" repetition variance as W and the "between" repetition variance as B . We augment this formula slightly from that given in Gelman (1992) to account for the fact that as the number of cross-validation repetitions increases, the between-repetition variability should decrease. See Mishra et al (2020) for full expressions of B and W.

**Value**

<table>
<thead>
<tr>
<th>Variable</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>cv.sNB</td>
<td>Standardized net benefit (sNB) of tuning parameter selected via cross-validated tuning parameter</td>
</tr>
<tr>
<td>cv.RAW</td>
<td>Corresponding RAW value given cross-validated selected tuning parameter</td>
</tr>
<tr>
<td>cv.lambda</td>
<td>lambda value selected via cross-validation if cvParm = lambda, otherwise user specified lambda value</td>
</tr>
<tr>
<td>cv.delta</td>
<td>delta value selected via cross-validation if cvParm = delta, otherwise user specified lambda value</td>
</tr>
<tr>
<td>avgCV.res</td>
<td>Averaged (across-replications) cross-validated sNB for sequence of tuning parameters</td>
</tr>
<tr>
<td>W</td>
<td>Estimate of &quot;with-in&quot; repetition variance. Will only return if stdErrRule==TRUE</td>
</tr>
<tr>
<td>B</td>
<td>Estimate of &quot;between&quot; repetition variance. Will only return if stdErrRule==TRUE</td>
</tr>
<tr>
<td>fullList</td>
<td>List of cross-validation results for all fold and repetitions</td>
</tr>
</tbody>
</table>

**Author(s)**

Anu Mishra

**References**


See Also

calWt, RAWgrid, nb, cvWtTuning

Examples

```r
### Load data ##
## Not run:
data(fakeData)

### Get grid of tuning parameters ###
grid <- RAWgrid(r = 0.3,rl = -Inf,ru = Inf,p = fakeData$p,y = fakeData$y,
cvParm = "lambda",rl.raw = 0.25,ru.raw = 0.35)

### Implement repeated k-fold cross validation
repCV <- cvRepWtTuning(y = fakeData$p,y = fakeData$p,r = 0.3,
 kFold = 5,cvRep = 25,cvParm = "lambda",tuneSeq = grid,stdErrRule = TRUE)

## cross-validation results
repCV$avgCV.res

## cross-validation selected lambda, RAW, and sNB
cv.lambda <- repCV$cv.lambda
cv.RAW <- repCV$cv.RAW
cv.RAW <- repCV$cv.sNB

## End(Not run)
```

cvWtTuning

Cross-validation for Selecting Weight Tuning Parameter

Description

Calibration weights require specification of tuning parameter \( \delta \) or \( \lambda \). This function uses K-fold cross-validation to select tuning parameter used for calibration weights, with standardized net benefit (sNB) as objective function. Either one of \( \delta \) or \( \lambda \) must be specified. The sequence of tuning parameters can be obtained from the RAWgrid function.

Usage

cvWtTuning(p,y,r,rl,ru,kFold=5,cvParm,tuneSeq,cv.seed=1111)
cvWtTuning

Arguments

- **y**: Vector of binary outcomes, with 1 indicating event (cases) and 0 indicating no event (controls)
- **p**: Vector of risk score values
- **r**: Clinically relevant risk threshold
- **rl**: Lower bound of clinically relevant region
- **ru**: Upper bound of clinically relevant region
- **kFold**: Number of folds for cross-validation
- **cvParm**: Parameter to be selected via cross-validation. Can be either \( \delta \) the weight assigned to observations outside the clinically relevant region \([R_L,R_u]\), or the \( \lambda \) tuning parameter controlling exponential decay within the clinically relevant region \([R_L,R_u]\)
- **tuneSeq**: Sequence of values of tuning parameters to perform cross-validation over
- **cv.seed**: Initial seed set for random splitting of data into K folds

Value

- **cv.res**: Matrix containing sequence of tuning parameters and corresponding cross-validation
- **cv.param**: Value of tuning parameter selected via cross validation
- **cv.full**: Matrix of cross-validation results for all folds

Note

Note this function does not split data into training and validation set, but performs the K-fold cross-validation procedure on all data included. We advise that a separate, validation subset should be split from the data used in this function.

Author(s)

Anu Mishra

References


See Also

*calWt, RAWgrid, nb, cvRepWtTuning*
fakeData  
*Dataset for Recalibration Purposes*

**Description**

Simulated dataset that can be used for recalibration purposes.

**Usage**

```r
data("fakeData")
```

**Format**

A data frame with 1000 observations on the following 2 variables.

- `p` a numeric vector or risk scores bounded between 0 and 1
- `y` a numeric vector of indicator of events (cases) and non-events (control)

**Details**

See Mishra et al (2020) for description of simulation settings to generate data (simulation example 3).

**References**


**Examples**

```r
data(fakeData)
```

---

**nb**  
*Net Benefit*

**Description**

Estimates the net benefit and standardized net benefit of a risk score given a risk threshold R. Additionally estimates the standardized net benefit of a "treat-all" (everyone receives intervention) treatment rule.

**Usage**

```r
nb(y, p, r)
```
Arguments

$y$ Vector of binary outcomes, with 1 indicating event (case) and 0 indicating no event (controls)

$p$ Vector of risk score values

$r$ Clinically relevant risk threshold

Value

$nb$ Net benefit of risk score $p$

$snb$ Standardized net benefit of risk score $p$. Net benefit of $p$ dived by the prevalence

$snb.all$ Standardized net benefit of a decision rule where everyone recieves treatment

Author(s)

Anu Mishra

References


Description

Tuning parameters for calibration weights may not be intuitive. Instead, relative average weight (RAW) can be used to find sensible tuning parameters. The RAW is the average weight of observations within the RAW region, $[R_l,RAW, R_u,RAW]$, divided by the average weight of observations outside RAW region.

This function elicits a grid of tuning parameter lambda or delta given a sequence of relative average weights (RAW) values, to be used for cross-validation. One tuning parameter delta or lambda must be specified.

Two clinically relevant lower and upper bound values must be specified. The first, $[R_l, R_u]$, define the clinically relevant region used for the weighting function. The second, $[R_l,RAW, R_u,RAW]$, define the complementarly regions used for defining relative average weights.

Usage

RAWgrid(r, r1, ru, p, y, rawSeq=seq(0.1,0.9,0.1), cvParm, delta = NULL, lambda = NULL, r1.raw, ru.raw)
Arguments

- **r**: Clinically relevant risk threshold
- **rl**: Lower bound of clinically relevant region
- **ru**: Upper bound of clinically relevant region
- **p**: Vector of risk score values
- **y**: Vector of binary outcomes, with 1 indicating event (cases) and 0 indicating no event (controls)
- **rawSeq**: Sequence of relative average weights
- **cvParm**: Tuning parameter that will be selected via cross-validation. Can either be 'lambda' or 'delta'
- **delta**: Calibration weight for observations outside clinically relevant region [rl, ru]. Needs to be specified if cvParm="lambda", otherwise should be left blank, and function will generate a sequence of delta for cross-validation.
- **lambda**: Tuning parameter for controlling exponential decay of calibration weights. Needs to be specified if cvParm="delta", otherwise should be left blank, and function will generate a sequence of lambda for cross-validation.
- **rl.raw**: Lower bound for defining the relative average weight region of interest
- **ru.raw**: Upper bound for defining the relative average weight region of interest

Value

- **rrWt.seq**: Matrix containing the input RAW sequence, and corresponding weight tuning parameter lambda and weight value delta (with one fixed depending on cvParm selection). If 'NA' is returned there may be too few events within the weight clinically relevant RAW region, meaning that RAW value is not possible.

Warning

Event rate outside RAW interval, widen RAW intervalIf no or too cases are inside RAW interval [R_l,R_u], cross-validation procedure may not be stable, so this warning indicates RAW interval should widen to include more cases.

Author(s)

Anu Mishra

References


See Also

calWt, cvWtTuning, cvRepWtTuning
Examples

```R
### Load data ###
data(fakeData)

### Get Grid of Tuning Parameters ###
grid <- RAWgrid(r = 0.3, rl = -Inf, ru = Inf, p = fakeData$p, y = fakeData$y,
cvParm = "lambda", delta=1, rl.raw = 0.25, ru.raw = 0.35)
```

---

### snbRecalPlot ---

**Plot of Potential sNB Under Recalibration**

**Description**

Function for producing a graphical device to help assess the potential for recalibration to improve the clinical utility of a risk model.

This function plots the sNB for a given risk score (p) and cost benefit ratio (R/1-R) against the threshold used to prescribe intervention. The peak of the curve estimates the maximum possible sNB that can be obtained via recalibration. The estimated sNB of the original risk score and the recalibrated risk score under standard logistic recalibration are also plotted on the curves. The dotted line "stdErrThresh" controls. The plot includes a dotted horizontal line one standard error (or any number of standard errors, controlled by stdErrThresh) below the maximum, to help gauge much room for improvement in sNB there is for original or standard recalibrated risk score from maximum possible sNB.

**Usage**

```R
snbRecalPlot(p, p.std, y, r, stdErrThresh=1, ylim=NULL,
titlePlot = "Potential sNB Under Recalibration", risk.model.std=TRUE)
```

**Arguments**

- `p` Vector of risk score values
- `p.std` Vector of risk score values after standard logistic recalibration
- `y` Vector of binary outcomes, with 1 indicating event (case) and 0 indicating no event (controls)
- `r` Clinically relevant risk threshold
- `stdErrThresh` Indicates how many standard errors line drawn below the maximum of the sNB curve should be
- `ylim` Y axis limits
- `titlePlot` Title for plot
- `risk.model.std` Plot standard error bars for sNB of plotted risk models

**Value**

Prints plot of potential sNB of risk score p under recalibration
Author(s)

Anu Mishra

References


Examples

data("fakeData")

### get standard recalibrated risk score
stdRecal.res <- stdRecal(y = fakeData$y,p = fakeData$p)
p.std <- stdRecal.res$p.std

## make plot
snbRecalPlot(p = fakeData$p,p.std = p.std,y = fakeData$y,r = 0.3)

## both original and std logistic recalibrated risk score are below 1 std err from maximum
## indicating that alternative recalibration methods could improve

---

**stdRecal**  
*Standard Logistic Recalibration*

Description

Produces recalibration intercept, slope and corresponding recalibrated risk scores using standard logistic recalibration. Recalibration slope and intercept using logistic recalibration method, develop by Cox (1958), then used to calculated the recalibrated risk score

Usage

`stdRecal(y,p)`

Arguments

- **y**  
  Vector of binary outcomes, with 1 indicating event (case) and 0 indicating no event (controls)

- **p**  
  Vector of risk score values

Value

- **stdRisk**  
  Vector of recalibrated risks under standard logistic recalibration

- **alpha**  
  Two-element vector containing logistic recalibration intercept and slope
wtRecal

Author(s)
Anu Mishra

References

Examples
#load data
data(fakeData)
res <- stdRecal(p=fakeData$p, y=fakeData$y)
p.std <- res$stdRecal
coef.dt <- res$alpha

wtRecal | Weighted Logistic Recalibration
---------|--------------------------------------------------

Description
When recalibrating a risk model, where the intended purpose of the risk model is to prescribe an intervention to those deemed at high risk, it is desirable to have good calibration at the clinically relevant threshold used to define high risk (i.e. threshold used to identify who receives treatment). This function recalibrates risk scores (predicting binary outcome) using the weighted logistic recalibration method (Mishra et al. [2020]).

Under this method, a recalibration intercept and slope are estimated via weighted logistic regression. Weights are constructed such that observations further from the clinically relevant risk threshold are down-weighted, meaning observations closer to the clinically relevant risk threshold have higher contribution to the risk threshold. The resulting estimated weighted recalibration slope and intercept are used to scale and shift the existing risk score, producing better calibrated risk scores near the risk threshold and potentially increasing the net benefit of the risk score.

Usage
wtRecal(y,p,r,r1,ru,lambda,delta)

Arguments
| y | Vector of binary outcomes, with 1 indicating event (case) and 0 indicating no event (controls) |
| p | Vector of risk score values |
| r | Clinically relevant risk threshold |
wtRecal

rl Lower bound of clinically relevant region
ru Upper bound of clinically relevant region
lambda Tuning parameter for weights inside relevant region
delta Weight assigned to observations outside relevant region

Value

y Vector of binary outcomes, with 1 indicating event (case) and 0 indicating no event (controls)
p.wt Vector of weighted recalibrated risk scores
alpha.wt Weighted recalibration slope and intercept
wt Calibration weights
wt.conv Indicator of convergence of the weighted logistic regression model. 1 indicates model convergence, 0 indicates model did not converge

Author(s)
Anu Mishra

References

See Also
calWt

Examples

## Not run:
### Load data ##
data(fakeData)

## Implement standard logistic recalibration
stdRecal.res <- stdRecal(y = fakeData$y, p = fakeData$p)
stdRecal.res$alpha #standard recalibration parameters
p.std <- stdRecal.res$p.std

## Look at potential sNB under recalibration plot
snbRecalPlot(p = fakeData$p, p.std = p.std, y = fakeData$y, r = 0.3)
## both original and std logistic recalibrated risk score are below 1 std err from maximum
## indicating that alternative recalibration methods could improve

### Get grid of tuning parameters ###
## In this example keeping delta fixed, and selecting lambda
grid <- RAWgrid(r = 0.3, rl = -Inf, ru = Inf, p = fakeData$p, y = fakeData$y,
                 cvParm = "lambda", rl.raw = 0.25, ru.raw = 0.35)
### Select tuning parameter lambda using 5-fold cross-validation repeated 25 times
### with one standard error rule implemented

```r
repCV <- cvRepWtTuning(y = fakeData$y, p = fakeData$p, rl = -Inf, ru = Inf, r = 0.3,
                        kFold = 5, cvRep = 25, cvParm = "lambda", tuneSeq = grid, stdErrRule = TRUE)
```

## Implement weighted logistic recalibration

```r
wtRecal.res <- wtRecal(y = fakeData$y, p = fakeData$p, r = 0.3, rl = -Inf, ru = Inf,
                        lambda = repCV$cv.lambda, delta=1)
```

# note that delta here is set to 1 as a place holder, but not used since the clinically
# relevant region is [-Inf, Inf]

```r
wtRecal.res$alpha.wt  # weighted recalibration parameters
```

## comparing standardized net benefit of the two

```r
nb(y = fakeData$y, p = fakeData$p, r = 0.3)$snb  # original
nb(y = stdRecal.res$y, p = stdRecal.res$p.std, r = 0.3)$snb  # std recal
nb(y = wtRecal.res$y, p = wtRecal.res$p.wt, r = 0.3)$snb  # weighted
```

### Calibration curve of only original, standard and weighted recalibrated risk score

```r
calCurvPlot(y = fakeData$y, p = fakeData$p, p.std=p.std, p.recal=p.recal,
            stdPlot=TRUE, recalPlot=TRUE,
            xlim=c(0,1), ylim=c(0,1),
            label="Original Risk Score",
            label2 = "Standard Recalibrated Risk Score",
            label3 = "Weighted/Constrained Recalibrated Risk Score",
            legendLab = c("Orig.", "Std.", "Wt."),
            mainTitle="Calibration of Risk Score",
            hist=TRUE, ylimHist = c(0,0.5),
            r=0.3, rl = -Inf, ru = Inf)
```

## End(Not run)
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