

Package ‘rCRM’

October 14, 2020

Type Package

Title Regularized Continual Reassessment Method

Version 0.1.1

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Description Fit a 2-parameter continual reassessment method (CRM) model (O’Quigley and Shen (1996), <doi: 10.2307/2532905>) regularized with L2 norm (Friedman et al. (2010), <doi: 10.18637/jss.v033.i01>) adjusted by the distance with the target dose limiting toxicity (DLT) rate.

License GPL (>= 2)

Encoding UTF-8

LazyData true

Imports Rcpp (>= 0.12.19)

LinkingTo Rcpp, RcppEigen

NeedsCompilation yes

Repository CRAN

Date/Publication 2020-10-14 16:34:47 UTC

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rCRM-package

Regularized CRM

Description

Fit a 2-parameter CRM model (O'Quigley and Shen 1996) regularized with L2 norm (Friedman et al. 2010) adjusted by the distance with the target DLT rate.

The package uses one-step coordinate descent algorithm and runs extremely fast.

Details

Package: rCRM
Type: Package
Version: 0.1
Date: 2018-11-06
License: GPL (>= 2)

Functions: [rCRM](#)

Author(s)

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References

O'Quigley, J., Shen, L.Z. (1996). *Continual reassessment method: a likelihood approach. Biometrics*, pp.673-684.
Friedman, J., Hastie, T. and Tibshirani, R. (2010). *Regularization paths for generalized linear models via coordinate descent, Journal of Statistical Software, Vol. 33(1), 1.*

Examples

```
set.seed(1213)

dose0=c(1:6)
prob0=c(0.007, 0.086, 0.294, 0.545, 0.731, 0.841)

m=3; Y=NULL; X=NULL
for (i in 1:length(dose0)) {
  Y=c(Y, rbinom(m, size=1, prob=prob0[i]))
  X=c(X, rep(i, m))
}
```

```
fiti=rCRM(X, Y, dose0, tp=0.3, mlambda=10)
# attributes(fiti)
```

print.rCRM *Print a rCRM Object*

Description

Print a summary of results

Usage

```
## S3 method for class 'rCRM'
print(x, digits = 3, ...)
```

Arguments

x	fitted rCRM object
digits	number of digits in printout
...	additional print arguments

Details

The performed model is printed, followed by the estimated probability of DLT from a fitted rCRM object.

Value

The data frame above is silently returned

Author(s)

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See Also

[rCRM](#)

Examples

```

set.seed(1213)

dose0=c(1:6)
prob0=c(0.007, 0.086, 0.294, 0.545, 0.731, 0.841)

m=3; Y=NULL; X=NULL
for (i in 1:length(dose0)) {
  Y=c(Y, rbinom(m, size=1, prob=prob0[i]))
  X=c(X, rep(i, m))
}

fiti=rCRM(X, Y, dose0, tp=0.3, mlambda=10)
# attributes(fiti)
fiti

```

rCRM

*Fit a 2-parameter CRM***Description**

Fit a 2-parameter CRM model (O'Quigley and Shen 1996) regularized with L2 norm (Friedman et al. 2010) adjusted by the distance with the target DLT rate.

Usage

```

rCRM(x, y, dose0, tp = 0.3, family = "2P", mlambda = 1, nlambda = 50, rlambda = NULL,
wldose = NULL, nfolds = length(y), foldid = NULL, keep.beta = FALSE,
thresh = 1e-07, maxit = 1e+04, threshP = 1e-06, threshB = 100)

```

Arguments

x	input vector of dose.
y	response variable. y is a binary vector with 0 (not DLT) and 1 (DLT).
dose0	dose regimen. x should be included in dose0.
tp	target toxicity probability. Default is 0.3.
family	type of CRM models. Now only supports 2-parameter CRM, 2P.
mlambda	maximum of tuning parameter lambda. The optimal lambda is selected by cross-validation.
nlambda	number of lambda values. Default is 50.
rlambda	fraction of mlambda to determine the smallest value for lambda. The default is rlambda = 0.0001 when the number of observations is larger than or equal to the number of variables; otherwise, rlambda = 0.01.
wldose	penalty weights used with L2 norm (adaptive L2). The wldose is a vector of non-negative values with the same length as dose0. Default is NULL indicating that weights are calculated based on MLE.

nfolds	number of folds. With nfolds = 1 and foldid = NULL, cross-validation is not performed. For cross-validation, smallest value allowable is nfolds = 3. Specifying foldid overrides nfolds. Default is nfolds=length(y) indicating leave-one-out cross-validation.
foldid	an optional vector of values between 1 and nfolds specifying which fold each observation is in. Default is foldid=NULL.
keep.beta	logical flag for returning estimates for all lambda values. For keep.beta = FALSE, only return the estimate with the minimum cross-validation value.
thresh	convergence threshold for coordinate descent. Default value is 1E-7.
maxit	maximum number of iterations for coordinate descent. Default is 1E+4.
threshP	boundary for calculating the probability of DLT. Default is 1E-6. The estimated probability is truncated between 1E-6 and 1-1E-6.
threshB	boundary for calculating the parameters. Default is 100. The estimates are truncated between -100 and 100.

Details

One-step coordinate descent algorithm is applied for each lambda. Cross-validation is used for tuning parameters.

Value

An object with S3 class "rCRM".

Beta	estimates in 2-parameter CRM model.
fit	a data.frame containing lambda and proportion of deviance. With cross-validation, additional results are reported, such as average cross-validation likelihood cvm and its standard error cvse, and index with '*' indicating the minimum cvm.
lambda.min	value of lambda that gives minimum cvm.
flag	convergence flag (for internal debugging). flag = 0 means converged.
prob	estimated probability of DLT at each dose0.
dose.close	the index of dose in dose0 with the prob closest to tp.
family	type of CRM models. 2P is 2-parameter CRM model.

Warning

It may terminate and return NULL.

Author(s)

Maintainer: Xiang Li <xli256@its.jnj.com>

References

- O'Quigley, J., Shen, L.Z. (1996). *Continual reassessment method: a likelihood approach. Biometrics*, 673-684.
- Friedman, J., Hastie, T. and Tibshirani, R. (2010). *Regularization paths for generalized linear models via coordinate descent, Journal of Statistical Software, Vol. 33(1), 1.*

Examples

```
set.seed(1213)

dose0=c(1:6)
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  X=c(X, rep(i, m))
}

fiti=rCRM(X, Y, dose0, tp=0.3, mlambda=10)
# attributes(fiti)
```

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