Package ‘rCRM’

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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.
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R topics documented:

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rCRM-package

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


Examples

```r
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))
}
```
print.rCRM

fiti=rCRM(X, Y, dose=0, 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)

do$0=c(1:6)
prob$0=c(0.007, 0.086, 0.294, 0.545, 0.731, 0.841)

m=3; Y=NULL; X=NULL
for (i in 1:length(dose$0)) {
  Y=c(Y, rbinom(m, size=1, prob=prob$0[i]))
  X=c(X, rep(i, m))
}

fiti=rCRM(X, Y, dose$0, 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, dose$0, 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).
- `dose$0` dose regimen. `x` should be included in `dose$0`.
- `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 `dose$0`. 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)

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References


Examples

```r
set.seed(123)

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)
```
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