# Package 'rCRM'

November 30, 2018

**Type** Package

**Title** Regularized Continual Reassessment Method

**Version** 0.1

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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** 2018-11-30 16:40:03 UTC

## R topics documented:

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rCRM-package | *Regularized CRM*

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### 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](rCRM)

## Examples

```
set.seed(1213)

dose0=c(1:6)
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m=3; Y=NULL; X=NULL
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  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*

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## 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-paraemter 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` cloest 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

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```

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