Package ‘CR’

February 19, 2015

Type Package

Title Power Calculation for Weighted Log-Rank Tests in Cure Rate Models

Version 1.0

Date 2012-06-18

Author Emil A. Cornea, Bahjat F. Qaqish, and Joseph G. Ibrahim

Maintainer Emil A. Cornea <ecornea@live.unc.edu>

Description This package contains R-functions to perform power calculation in a group sequential clinical trial with censored survival data and possibly unequal patient allocation between treatment and control groups. The functions can also be used to determine the study duration in a clinical trial with censored survival data as the sum of the accrual duration, which determines the sample size in a traditional sense, and the follow-up duration, which more or less controls the number of events to be observed. This package also contains R functions and methods to display the computed results.

License GPL-2

Depends methods

Repository CRAN

Date/Publication 2012-07-02 14:27:34

NeedsCompilation no

R topics documented:

CR-package .................................................. 2
curerate .......................................................... 4
CureRate-class ................................................ 7
show-methods ................................................ 9
showcr ......................................................... 9

Index 12
Description

This package contains R-functions to perform power calculation in a group sequential clinical trial with censored survival data and possibly unequal patient allocation between treatment and control groups. The functions can also be used to determine the study duration in a clinical trial with censored survival data as the sum of the accrual duration, which determines the sample size in a traditional sense, and the follow-up duration, which more or less controls the number of events to be observed. This package also contains R functions and methods to display the computed results.

Details

Package: CR
Type: Package
Version: 1.0
Date: 2012-06-18
License: GPL-2
Depends: methods

Author(s)

Emil A. Cornea, Bahjat F. Qaqish, and Joseph G. Ibrahim

Maintainer: Emil A. Cornea <ecornea@live.unc.edu>

References


See Also
curerate, CureRate-class, showcr, and show-methods
Examples

```r
## Input Data

# rho - specifies the value of rho in the G-rho test (Harrington and Fleming, 1982).
# rho = 0 gives the logrank test, and rho = 1 the Peto-Peto Wilcoxon test
# (and rho = -1 the test discussed by Gray and Tsatis, 1989).
rho = 0
numreps = 500

## cureobs - probability of cure on the observation arm of the study
cureobs = .359

## curerx - probability of cure on the treatment arm of the study
curerx = .459

## medobs - median survival among the non-cured on observation
medobs = .747

## medrx - median survival among the non-cured on treatment
medrx = .859

## acrate - rate at which patients accrue, combined over both
## observation and treatment arms of the study
acrate = 232

## probrx - probability of assignment to the treatment arm
probrx = .5

## actime - accrual duration
actime = c(3.3, 3.5, 3.8);

## futime - follow-up duration
futime = c(2.0, 2.5)

## info - vector of information times for the interim looks
## must be an increasing sequence in (0,1]
info = c(0.35, 0.56, 0.46, 1.0)

## crits - vector of critical values corresponding to the
## interim analysis time points specified in info
crits = c(3.6128, 2.6506, 2.1894, 2.0536)

mycr <- curerate(rho, numreps, cureobs, curerx, medobs, medrx, acrate, probrx, actime, futime, info, crits)

### (*)
show(mycr)  ### same as above
showcr(mycr) ### same as above
showcr(mycr, full.result=TRUE)
showcr(mycr, indac=2, indfu=1)
showcr(mycr, indac=2:3, indfu=2:1)
showcr(mycr, indac=c(1,3), indfu=2)

show(mycr)  ### same as (*) above
showcr(mycr) ### same as above
mycr  ### same as above
```

---

CR-package
curerate

### Peto & Peto modification of the Gehan-Wilcoxon test: rho=1

```r
rho=1
mycr<-curerate(rho, numreps, cureobs, curerx, medobs, medrx, acrate, probrx, actime, futime, info, crits)
mycr
```

---

**curerate**  
*Power Calculation for Weighted Log-Rank Tests in Cure Rate Models*

**Description**

This R-function performs power calculation in a group sequential clinical trial with censored survival data and possibly unequal patient allocation between treatment and control groups. The function can also be used to determine the study duration in a clinical trial with censored survival data as the sum of the accrual duration, which determines the sample size in a traditional sense, and the follow-up duration, which more or less controls the number of events to be observed.

**Usage**

```r
curerate(rho = 0, numreps, cureobs, curerx, medobs, medrx, acrate, probrx, actime, futime, info, crits, alpha = 0.025)
```

**Arguments**

- `rho` numeric specifying the value of rho in the G-rho test (Harrington and Fleming, 1982), rho=0 (default) gives the log-rank test, rho=1 the Peto-Peto Wilcoxon test, and rho=-1 the test discuss by Gray and Tsiatis, 1989.
- `numreps` integer > 0 specifying the number of replications.
- `cureobs` numeric specifying the probability of cure on the observation arm of the study.
- `curerx` numeric specifying the probability of cure on the treatment arm of the study.
- `medobs` numeric > 0 specifying the median survival among the non-cured on observation.
- `medrx` numeric > 0 specifying the median survival among the non-cured on treatment.
- `acrate` numeric > 0 specifying the rate at which patients accrue, combined over both observation and treatment arms of the study.
- `probrx` numeric specifying the probability of assignment to the treatment arm, must be in [0,1].
- `actime` vector specifying the accrual durations.
- `futime` vector specifying the follow-up durations.
- `info` vector of information times for the interim looks; must be an increasing sequence in (0,1).
- `crits` vector of critical values corresponding to the interim analysis time points specified in info.
- `alpha` numeric specifying the one-sided level of significance; must be in (0,1); default value $0.025$; currently, it has no effect on the calculations, it is ignored in the current version of the software.
**Details**

The function `curerate` is used to calculate the power of weighted log-rank tests in cure rate models.

**Value**

An object of S4 class `CureRate` which has the following 22 components:

- `cureobs` numeric
- `medobs` numeric
- `curerx` numeric
- `medrx` numeric
- `actime` numeric vector
- `futime` numeric vector
- `info` numeric vector
- `crits` numeric vector
- `alpha` numeric
- `rho` numeric
- `acrate` numeric
- `probrx` numeric
- `numreps` integer
- `numobs` numeric matrix
- `timept` numeric 3D array
- `deaths` numeric 3D array
- `testname` character
- `power` numeric 3D array
- `numobs` numeric matrix
- `indac` vector of integers
- `indfu` vector of integers
- `printflag` integer

**Author(s)**

Emil A. Cornea, Bahjat F. Qaqish, and Joseph G. Ibrahim

Maintainer: Emil A. Cornea <ecornea@live.unc.edu>
References


See Also

CR-package, CureRate-class, showcr, and show-methods

Examples

```r
# Should be DIRECTLY executable !! ----
## Input Data

###
# rho - specifies the value of rho in the G-rho test (Harrington and Fleming, 1982).
# rho = 0 gives the logrank test, and rho = 1 the Peto-Peto Wilcoxon test
# (and rho = -1 the test discussed by Gray and Tsiatis, 1989).
rho = 0

numreps = 500

cureobs = 0.359

curerx = 0.459

medobs = 0.747

medrx = 0.859

acrate = 232

probrx = 0.5

actime = c(3.3, 3.5, 3.8);

futime = c(2.0, 2.5)

info = c(0.35, 0.61, 0.86, 1.0)

crits = c(3.6128, 2.6506, 2.1894, 2.0536)
```
### Log-rank test: rho=0 (default)

```r
crr <- curerate(rho, numreps, cureobs, curerx, medobs, medrx, acrate, probrx, actime, futime, info, crits)
crr
```

### (`*

```r
show(crr)  # same as above
showcr(crr, full.result = TRUE)
showcr(crr, indac = 2, indfu = 1)
showcr(crr, indac = 2:3, indfu = 2:1)
showcr(crr, indac = c(1, 3), indfu = 2)
```

### (`

```r
show(crr)  # same as (`* above
showcr(crr)  # same as above
```

```r
crr  # same as above
```

### Peto & Peto modification of the Gehan-Wilcoxon test: rho=1

```r
crr <- curerate(rho, numreps, cureobs, curerx, medobs, medrx, acrate, probrx, actime, futime, info, crits)
crr
```

---

**CureRate-class**

**Class** "CureRate"

---

**Description**

Class of objects like the output of function "curerate".

**Objects from the Class**

Objects can be created by calls of the form `new("CureRate", ...)`.  

**Slots**

- `cureobs`: Object of class "numeric"  
- `medobs`: Object of class "numeric"  
- `curerx`: Object of class "numeric"  
- `medrx`: Object of class "numeric"  
- `actime`: Object of class "vector"  
- `futime`: Object of class "vector"  
- `info`: Object of class "vector"  
- `crits`: Object of class "vector"  
- `alpha`: Object of class "numeric"
rho: Object of class "numeric"
acrate: Object of class "numeric"
probrx: Object of class "numeric"
umreps: Object of class "integer"
umobs: Object of class "matrix"
timept: Object of class "array"
deaths: Object of class "array"
testname: Object of class "character"
power: Object of class "array"
beta: Object of class "matrix"
indac: Vector of objects of class "integer"
indfu: Vector of objects of class "integer"
printflag: Object of class "integer"

Methods

show signature(object = "CureRate")

Author(s)

Emil A. Cornea, Bahjat F. Qaqish, and Joseph G. Ibrahim
Maintainer: Emil A. Cornea <ecornea@live.unc.edu>

See Also

curerate, show-methods, showcr

Examples

showClass("CureRate")

## Input Data

# rho - specifies the value of rho in the G-rho test (Harrington and Fleming, 1982).
# rho = 0 gives the logrank test, and rho = 1 the Peto-Peto Wilcoxon test
#(and rho = -1 the test discussed by Gray and Tsiatis, 1989).
rho = 0

numreps = 500
##cureobs - probability of cure on the observation arm of the study
cureobs = .359
##curerx - probability of cure on the treatment arm of the study
curerx = .459
##medobs - median survival among the non-cured on observation
medobs = .747
##medrx - median survival among the non-cured on treatment
medrx = .859
## Show-methods

---

### Description

Method for function `show`

### Methods

#### signature(object = "CureRate")

---

### showcr

Function for displaying objects of class `CureRate`

#### Description

R function for customized display of an object of class `CureRate`. It allows the user to display the full info for any pair set of pairs (`object@actime[]`, `object@futime[]`). The default is the display of the summary power table. For more info, see the section Arguments below.
showcr(cr, full.results = FALSE, indac = 0, indfu = 0)

Arguments

- **cr**: object of class CureRate
- **full.results**: logical, if TRUE, the full results are displayed, and the values of indac and indfu are disregarded; if FALSE (default), the summary power table is displayed only, unless both indac and indfu are specified as (sub)vectors of indices of cr@actime and cr@futime when the corresponding detailed info is displayed for each pair (cr@actime[indac[i]].cr@futime[indac[j]]).
- **indac**: vector of integers, subvector of indices of cr@actime vector; use only when full.results = FALSE and indfu is specified too; default value 0.
- **indfu**: vector of integers, subvector of indices of cr@futime vector; use only when full.results = FALSE and indac is specified too; default value 0.

Details

The object cr of class CureRate must be specified. If full.results, indac, and indfu are not specified, they assume the default values TRUE, 0, and 0, respectively, then the summary power table for the specified object cr is displayed only. If full.results is not specified, but both indac and indfu are specified, then full.results assumes the default value TRUE and all the info for each pair of (cr@actime[indac[]].cr@futime[indfu[]]) are displayed together with the summary power table. If full.results is specified as TRUE, then the values of indac, and indfu, specified or not, all info for all pairs (cr@actime[],cr@futime[]) are displayed together with the summary power table.

Author(s)

Emil A. Cornea, Bahjat F. Qaqish, and Joseph G. Ibrahim

Maintainer: Emil A. Cornea <ecornea@live.unc.edu>

See Also

CR-package, curerate, CureRate-class, and show-methods

Examples

```r
## Should be DIRECTLY executable !! ----
## Input Data

# rho - specifies the value of rho in the G-rho test (Harrington and Fleming, 1982).
# rho = 0 gives the logrank test, and rho = 1 the Peto-Peto Wilcoxon test
#(and rho = -1 the test discussed by Gray and Tsiatis, 1989).
 rho = 0
numreps = 500

cureobs - probability of cure on the observation arm of the study
cureobs = .359
```
showcr

### curerx - probability of cure on the treatment arm of the study

curerx = .459

### medobs - median survival among the non-cured on observation

medobs = .747

### medrx - median survival among the non-cured on treatment

medrx = .859

### acrate - rate at which patients accrue, combined over both observation and treatment arms of the study

acrate = 232

### probdx - probability of assignment to the treatment arm

probdx = .5

### actime - accrual duration

actime = c(3.3, 3.5, 3.8);

### futime - followup duration

futime = c(2.0, 2.5)

### info - vector of information times for the interim looks

# must be an increasing sequence in (0,1)

info = c(.35, .61, .86, 1.0)

### crits - vector of critical values corresponding to the interim analysis time points specified in info

crits = c(3.6128, 2.6506, 2.1894, 2.0536)


#############################################################

### Log-rank test: rho=0 (default)

curerate(rho ,numreps,cureobs,curerx,medobs,medrx,acrate, probdx,actime,futime,info,crits)

mycr### (*)

show(mycr)  ### same as above

showcr(mycr)  ### same as above

unclass(mycr)

showcr(mycr,full.results=TRUE)

showcr(mycr,indac=3,indfu=1)
Index

*Topic **classes**
  CureRate-class, 7

*Topic **functions**
  curerate, 4
  showcr, 9

*Topic **methods**
  show-methods, 9

*Topic **object display**
  showcr, 9

*Topic **package**
  CR-package, 2

CR (CR-package), 2
CR-curerate (curerate), 4
CR-CureRate-method (CureRate-class), 7
CR-package, 2
CR-showcr (showcr), 9
curerate, 2, 4, 8, 10
CureRate-class, 7

show, CureRate-method (show-methods), 9
show-methods, 9
showcr, 2, 6, 8, 9