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

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

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.

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Author(s)

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

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References

Ewell, M. and Ibrahim, J.G. (1997). The Large Sample Distribution of the Weighted Log Rank Statistic Under General Local Alternatives. Lifetime Data Analysis,3, 5-12.

Kim, K. (1992). Study Duration for Group Sequential Clinical Trials with Censored Survival Data Adjusting for Stratification.Statistics in Medicine, Vol. 11, 1477-1788.

Harrington, D. P. and Fleming, T. R. (1982). A class of rank test procedures for censored survival data. Biometrika 69, 553-566.

Gray, R.J. and Tsiatis, A.A. (1989). A linear rank test for use when the main interest is in differences in cure rates. Biometrics 45, 899-904.

See Also

curerate, CureRate-class, showcr, and show-methods

Examples

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

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
```

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

```
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 assigment 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

Ewell, M. and Ibrahim, J.G. (1997). The Large Sample Distribution of the Weighted Log Rank Statistic Under General Local Alternatives. Lifetime Data Analysis,3,5-12

Kim, K. (1992). Study Duration for Group Sequential Clinical Trials with Censored Survival Data Adjusting for Stratification. Statistics in Medicine, Vol. 11, 1477-1788

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Gray, R.J. and Tsiatis, A.A. (1989). A linear rank test for use when the main interest is in differences in cure rates. Biometrics 45, 899-904.

See Also

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

Examples

```
##---- 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
##curerx - probability of cure on the treatment arm of the study
curerx = .459
##medobs - median survival among the non-cured on observation
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##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  - 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)
mycr<-curerate(rho,numreps,cureobs,curerx,medobs,medrx,acrate,
         probrx,actime,futime,info,crits)
mycr        ### (*)

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

### Peto & Peto modification of the Gehan-Wilcoxon test: rho=1
rho=1
mycr<-curerate(rho,numreps,cureobs,curerx,medobs,medrx,acrate,
         probrx,actime,futime,info,crits)
mycr
```

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"`

numreps: Object of class `"integer"`

numobs: 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)

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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
```

```
##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  - followup duration
futime = c(2.0,  2.5)
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###############################################################

### Log-rank test: rho=0 (default)
mycr<-curerate(rho ,numreps,cureobs,curerx,medobs,medrx,acrate,
          probrx,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)
```

---

  show-methods   *Methods for Function* show

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.

Usage

```
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)

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See Also

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

Examples

```
##---- 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).
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numreps = 500
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```
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################################################################

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

show(mycr)   ### same as above
showcr(mycr)   ### same as above
unclass(mycr)
showcr(mycr,full.results=TRUE)
showcr(mycr,indac=3,indfu=1)
```

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