# Package ‘NPHMC’

February 15, 2013

**Type**  Package  
**Title**  Sample Size Calculation for the Proportional Hazards Cure Model  
**Version**  2.0  
**Date**  2013-01-13  
**Author**  Chao Cai, Songfeng Wang, Wenbin Lu, Jiajia Zhang  
**Maintainer**  Chao Cai <caic@email.sc.edu>  
**Description**  An R-package for calculating sample size based on Proportional Hazard Mixture Cure (PHMC) Model  
**Depends**  survival, smcure  
**License**  GPL-2  
**LazyLoad**  yes  
**Repository**  CRAN  
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1
An R-package for Estimating Sample Size of Proportional Hazards Mixture Cure Model

Description


Details

Package: NPHMC
Type: Package
Version: 1.0
Date: 2013-01-13
License: GPL-2
LazyLoad: yes

Author(s)

Chao Cai, Songfeng Wang, Wenbin Lu, Jiajia Zhang
Maintainer: Chao Cai <caic@email.sc.edu>

References


Examples

# parametric
NPHMC(power=0.90, alpha=0.05, accrualtime=3, followuptime=4, p=0.5, accrualdist="uniform", hazardratio=2/2.5, oddsratio=2.25, pi0=0.1, survdist="exp", k=1, lambda0=0.5)

# nonparametric
data(e1684szdata)
NPHMC(power=0.80, alpha=0.05, accrualtime=4, followuptime=3, p=0.5, accrualdist="uniform", data=e1684szdata)
**Description**

Sample Size Calculation Example Data

**Usage**

```r
data(e1684szdata)
```

**Format**

A data frame with 285 observations on the following 3 variables.

- **Time**: observed relapse-free time
- **Status**: censoring indicator, 1=event of interest happens, and 0=censoring
- **X**: arm indicator, 0=control and 1=treatment

**Examples**

```r
data(e1684szdata)
```

---

**f1**

*function one*

**Description**

The first integrate function

**Usage**

```r
f1(t, survdist, k, lambda0)
```

**Arguments**

- **t**: time variable
- **survdist**: survival distribution of uncured patients, it can be "exp" or "weib"
- **k**: the shape parameter of weibull distribution. By default, it is set to be 1 for exponential distribution
- **lambda0**: the scale parameter of exponential distribution or weibull distribution
**f2**

*function two*

**Description**

The second integrate function

**Usage**

\[ f2(t, \text{accrualt ime}, \text{followuptime}, \text{accrualdist}, \text{survdist}, k, \lambda_0) \]

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>(t)</td>
<td>time variable</td>
</tr>
<tr>
<td>\text{accrualt ime}</td>
<td>accrual time. The default is 3</td>
</tr>
<tr>
<td>\text{followuptime}</td>
<td>follow up time. The default is 4</td>
</tr>
<tr>
<td>\text{accrualdist}</td>
<td>accrual rate distribution. It can be &quot;uniform&quot;, &quot;increasing&quot; or &quot;decreasing&quot;.</td>
</tr>
<tr>
<td>\text{survdist}</td>
<td>survival distribution of uncured patients, it can be &quot;exp&quot; or &quot;weib&quot;</td>
</tr>
<tr>
<td>(k)</td>
<td>the shape parameter of weibull distribution. By default, it is set to be 1 for exponential distribution</td>
</tr>
<tr>
<td>\lambda_0</td>
<td>the scale parameter of exponential distribution or weibull distribution</td>
</tr>
</tbody>
</table>

**f3**

*function three*

**Description**

The third integrate function

**Usage**

\[ f3(t, \beta_0, \gamma_0, \pi_0, \text{survdist}, k, \lambda_0) \]

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
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</thead>
<tbody>
<tr>
<td>(t)</td>
<td>time variable</td>
</tr>
<tr>
<td>\beta_0</td>
<td>log hazard ratio of uncured patients</td>
</tr>
<tr>
<td>\gamma_0</td>
<td>log odds ratio of cure rates between the two groups</td>
</tr>
<tr>
<td>\pi_0</td>
<td>cure rate for control group. The default is 0.1</td>
</tr>
<tr>
<td>\text{survdist}</td>
<td>survival distribution of uncured patients, it can be &quot;exp&quot; or &quot;weib&quot;</td>
</tr>
<tr>
<td>(k)</td>
<td>the shape parameter of weibull distribution. By default, it is set to be 1 for exponential distribution</td>
</tr>
<tr>
<td>\lambda_0</td>
<td>the scale parameter of exponential distribution or weibull distribution</td>
</tr>
</tbody>
</table>
**f4**

*function four*

**Description**

the fourth integrate function

**Usage**

\[ f4(t, \text{accrualtime}, \text{followuptime}, \text{accrualdist}, \text{beta0}, \text{gamma0}, \text{pi0}, \text{survdist}, k, \text{lambda0}) \]

**Arguments**

- \( t \): time variable
- \( \text{accrualtime} \): accrual time. The default is 3
- \( \text{followuptime} \): follow up time. The default is 4
- \( \text{accrualdist} \): accrual rate distribution. It can be "uniform", "increasing" or "decreasing"
- \( \text{beta0} \): log hazard ratio of uncured patients
- \( \text{gamma0} \): log odds ratio of cure rates between the two groups
- \( \text{pi0} \): cure rate for control group. The default is 0.1
- \( \text{survdist} \): survival distribution of uncured patients, it can be "exp" or "weib"
- \( k \): the shape parameter of weibull distribution. By default, it is set to be 1 for exponential distribution
- \( \text{lambda0} \): the scale parameter of exponential distribution or weibull distribution

**H0**

*Cumulative Hazard Function*

**Description**

Cumulative Hazard Function for Exponential and Weibull Distributions

**Usage**

\[ H0(t, \text{survdist}, k, \text{lambda0}) \]

**Arguments**

- \( t \)
- \( \text{survdist} \): survival distribution of uncured patients, it can be exponential or weibull
- \( k \): the shape parameter of weibull distribution. By default, it is set to be 1 for exponential distribution
- \( \text{lambda0} \): the scale parameter of exponential distribution or weibull distribution
m $M$ function

Description

M integrate function

Usage

m(t, beta0, gamma0, pi0, survdist, k, lambda0)

Arguments

t time variable
beta0 log hazard ratio of uncured patients
gamma0 log hazard ratio of uncured patients
pi0 cure rate for control group. The default is 0.1
survdist survival distribution of uncured patients, it can be exponential or weibull
k the shape parameter of weibull distribution. By default, it is set to be 1 for exponential distribution
lambda0 the scale parameter of exponential distribution or weibull distribution

NPHMC

An R-package for Estimating Sample Size of Proportional Hazard Cure Models

Description


Usage

NPHMC(power = 0.8, alpha = 0.05, accrualtime = 3, followuptime = 4, p = 0.5, accrualdist = c("uniform", "normal"), accrualtime = c(3, 6), followuptime = c(4, 8), p = c(0.5, 0.7))

Arguments

t  power specifies the required power. The default power is 0.8
alpha specifies the level significance of the statistical test. The default is 0.05.
accrualtime accrual time. The default is 3
followuptime follow up time. The default is 4
p specifies the proportion of subjects in each arm. The default p is 0.5
accrualdist specifies the accrual rate distribution. It can be "uniform", "increasing" or "decreasing".

hazardratio specifies the hazard ratio of uncured patients between two arms, which is equivalent to $e^{\beta_0} = \lambda_1(t)/\lambda_0(t)$. The value must be greater than 0.

oddsratio specifies the odds ratio of cure rates between control and treatment arms, which is calculated by $e^{\gamma_0} = \pi_1/(1-\pi_1)/\pi_0/(1-\pi_0)$. The value should be greater than 0 if cure rates exist. It can be 0 if there's no cure rate.

p10 specifies the cure rate for control arm which is between 0 and 1. The default is 0.1.

survdist specifies the survival distribution of uncured patients, it can be "exp" or "weib".

k if survdist = "weib", the shape parameter k needs to be specified. By default, k = 1, which refers to the exponential distribution.

lambda0 specifies the scale parameter of exponential distribution or Weibull distribution for survival times of uncured patients in the control arm. The default lambda0 = 1. The density function of Weibull distribution with shape parameter k and scale parameter lambda0 is given by

$$f(t) = \lambda_0k(\lambda_0t)^{k-1}\exp(-\lambda_0t^k)$$

for $t > 0$

data if observed/historical data is available, the sample size can be calculated based on the nonparametric estimators from the proportional hazards mixture model by 'smcure' package in R. The data must contain three columns with order of "Time","Status" and "X" where "Time" refers to time to event of interest, "Status" refers to censoring indicator, 1=event of interest happens, and 0=censoring and "X" refers to arm indicator, 0=control and 1=treatment.

Details
None

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**S0 Function**

Description
Baseline Survival Function for Mixture Cure Model

Usage
S0(t, pi0, survdist, k, lambda0)
Arguments

- **t**: time variable
- **pi0**: cure rate for control group. The default is 0.1
- **survdist**: survival distribution of uncured patients, it can be "exp" or "weib"
- **k**: the shape parameter of weibull distribution. By default, it is set to be 1 for exponential distribution
- **lambda0**: the scale parameter of exponential distribution or weibull distribution

Description

Survival Distribution of Censoring times

Usage

```r
Sc(t, accrualtime, followuptime, accrualdist)
```

Arguments

- **t**: time variable
- **accrualtime**: accrual time. The default is 3
- **followuptime**: follow up time. The default is 4
- **accrualdist**: accrual rate distribution. It can be "uniform", "increasing" or "decreasing"
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