Package ‘TestSurvRec’

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R topics documented:

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TestSurvRec-package  Statistical tests to compare survival curves of two groups with recurrent events.

Description

Recurrent events are common in many areas: psychology, engineering, medicine, physics, astronomy, biology, economics and so on. Such events are very common in the real world: viral diseases, carcinogenic tumors, machinery and equipment failures, births, murders, rains, industrial accidents, car accidents and so on. The availability of computerized tools for the analysis is indispensable. Survival analysis is a branch of the statistic that is used to model the time until the occurrence of events. The objectives of the survival analysis are: the modeling of the survival functions, the estimation of the risk functions of the occurrence of an event, the estimation of the probability of occurrence and the comparisons of survival curves of population groups. The development of tools for the statistical analysis of recurrent event is relatively recent and these are not fully known. The purpose of this package is to present statistical tests for the analysis of data with recurrent event. Martínez et al. (2009) published some statistical tests to compare survival curves on groups with recurrent events.

Details

The hypothesis is,

\( H_0 : S_1(t) = S_2(t) \)

\( H_1 : S_1(t) \neq S_2(t) \)

Where, \( S_1(t) \) and \( S_2(t) \) are the survival curves of the both group. The statistic of test is,

\[
Z = \frac{\sum_{t \leq z} w_z [\Delta N(s, z; r) - E{\Delta N(s, z; r)}]}{\sqrt{\sum_{t \leq z} w_z^2 Var{\Delta N(s, z; r)}}}
\]

The statistic \( Z \) has a normal asymptotic behavior. Its square has a chi-square approximate behavior with a degree of freedom. So,

\[ \Delta N(s, z; 1) = N(s, z + \Delta z; 1) - N(s, z; 1) \]

Now, if \( \Delta z \) is approaches to zero and \( \Delta N(s, z; 1) \) has a hypergeometric behavior and the expected value is,

\[ Y(s, z; 1)\Delta N(s, z)/Y(s, z) \]

and the variance is,

\[ Var[\Delta N(s, z; 1)] = \frac{Y(s, z) - Y(s, z; 1)}{Y(s, z) - 1} Y(s, z; 1) \Delta N(s, z)/Y(s, z) \left[ 1 - \frac{\Delta N(s, z)}{Y(s, z)} \right] \]

This author proposed various types of weights \((w_z)\),

\[
w_z = [S(z)]^\alpha [1 - S(z)]^\gamma \frac{[Y(s, z)]^\alpha}{[Y(s, z) + 1]^\beta}
\]
The appropriate selection of weights to the survival analysis depends on the behavior of its curves. With the selection of the values of the parameters \((\alpha, \beta, \gamma; \text{and } \eta)\) on our proposal, this statistical is able of adjustment to this behavior. With this proposal, we are able of make studies on survival analysis with recurrent events and of generate tests for analysis others, including the classical tests types: logrank, Gehan, Peto-Peto, Fleming-Harrington and so on. See, that if on the statistical all parameters are zero imply that \(w_z = 1\), it generate the test type logrank to the analysis with recurrent events. If \(\alpha = 1\) and the other parameters are zero \(w_z = Y(s, z)\), it generate the test type Gehan. If \(\gamma = 1\) and the other parameters are zero \(w_z = S(z)\), it generate the test of Peto-Peto. If \(\gamma = 1, \eta = 1\) and the rest of the parameters are zero, it generate the test of Fleming-Harrington. For that our statistical be able of generate the tests for the clasical survival analysis, all the study units have that experiment only one event or one censure. On the proposal, the statistical of comparison for recurrent events depends of the counting processes \(N\) and \(Y\), both are doubles indexed. With \(S\) index, we measure calendar time and with \(Z\) index, we measure the gap times. So, if the observation time tends to infinity and the event can only occur once on the unit, the test of comparison of the proposal becomes on the classical weighted test of comparison of groups on the survival analysis. We can conclude that, the tests proposed by Martínez et al. (2009) are useful on diverse fields of the research, such as: medicine, public health, insurance, social science, reliability and others.

Author(s)

Dr. Carlos Martínez, <cmmm7031@gmail.com>

References


See Also


Examples

data(TBCplapyr)
Plot.Event.Rec(TBCplapyr)
Dif.Surv.Rec(TBCplapyr,"all",1,1,0,0)
Dif.Surv.Rec(TBCplapyr,"Grec")
Print.Summary(TBCplapyr)
**DataColonDukesABvsC  Rehospitalization of patients with colorectal cancer**

**Description**
This data contains the rehospitalization times of patients diagnosed with stage AB and patients diagnosed with stage C.

**Usage**
```r
data(DataColonDukesABvsC)
```

**Format**
A data frame with 655 observations on the following 10 variables.
- **j**: Observation number
- **iden**: Identificator of each subject. Repeated for each recurrence
- **id**: Identificator of each subject. Repeated for each recurrence
- **tinicio**: Initial time of observation just before each recurrence
- **time**: Rehospitalization or censoring gap time
- **tcal**: Rehospitalization or censoring calendar time
- **event**: Censoring status. All events are 1 for each subject excepting last one that it is 0
- **chemoter**: Did patient receive chemotherapy? 1: No 2: Yes
- **dukes**: Dukes tumoral stage: 1:A-B 2:C
- **distance**: Distance from living place to hospital 1: less than 30 Km. 2: more than 30 Km.

**Details**
The patients included in the study have been operated between January 1996 and December 1998. For each patient, we have considered this date as the beginning of the observational period. All patients were followed until June 2002. Consequently, the length of the monitoring period can differ for each patient, depending on its surgery date. The first interoccurrence time has been considered as the time between the surgical intervention and the first hospitalization related to cancer. Four hundred and three patients with colon and rectum cancer have been included in the study. Information about their sex (male or female), age (< 60, 60-74 or ≥ 75), and tumoral stage using Dukes classification (A-B, C, or D) have been recorded. The following interoccurrence times have been considered as the difference between the last hospitalization and the current one. Only readmissions related to cancer have been considered.

**Source**
This data can be obtained upon request from González, JR et al.
References


Examples

data(DataColonDukesABvsD)
XLL=DataColonDukesABvsD
print(XL)

DataColonDukesABvsD  Rehospitalization of patients with colorectal cancer

Description

This data contains rehospitalization times of patients diagnosed with stage AB and patients diagnosed with stage D.

Usage

data(DataColonDukesABvsD)

Format

A data frame with 527 observations on the following 10 variables.

- **j**: Observation number
- **iden**: identifier of each subject. Repeated for each recurrence
- **id**: identifier of each subject. Repeated for each recurrence
- **tinicio**: Initial time of observation just before each recurrence
- **time**: rehospitalization or censoring gap time
- **tcal**: rehospitalization or censoring calendar time
- **event**: censoring status. All event are 1 for each subject excepting last one that it is 0
- **chemoter**: Did patient receive chemotherapy? 1: No 2: Yes
- **dukes**: Dukes tumoral stage: 1:A-B 3:D
- **distance**: distance from living place to hospital 1:less than 30 Km. 2: more than 30 Km.
Details

The patients included in the study have been operated between January 1996 and December 1998. For each patient, we have considered this date as the beginning of the observational period. All patients were followed until June 2002. Consequently, the length of the monitoring period can differ for each patient, depending on its surgery date. The first interoccurrence time has been considered as the time between the surgical intervention and the first hospitalization related to cancer. Four hundred and three patients with colon and rectum cancer have been included in the study. Information about their sex (male or female), age (≤ 60, 60-74 or ≥ 75), and tumoral stage using Dukes classification (A-B, C, or D) have been recorded. The following interoccurrence times have been considered as the difference between the last hospitalization and the current one. Only readmissions related to cancer have been considered.

Source

This data can be obtained upon request from González, JR et al.

References


Examples

data(DataColonDukesABvsD)
XL<-DataColonDukesABvsD
print(XL)

DataColonDukesCvsD  Rehospitalization of patients with colorectal cancer

Description

This data contains the rehospitalization times of patients diagnosed with stage C and patients diagnosed with stage D.

Usage

data(DataColonDukesCvsD)

Format

A data frame with 537 observations on the following 10 variables.

This data.frame contains the following columns:

j Observation number
Iden identifier of each subject. Repeated for each recurrence
id  identifier of each subject. Repeated for each recurrence
Tinicio Initial time of observation just before each recurrence
time rehospitalization or censoring gap time
Tcal rehospitalization or censoring calendar time
event censoring status. All event are 1 for each subject excepting last one that it is 0
chemoter Did patient receive chemotherapy? 1: No 2: Yes
dukes Dukes tumoral stage: 2: C 3: D
distance distance from living place to hospital 1: less than 30 Km. 2: more than 30 Km.

Details

The patients included in the study have been operated between January 1996 and December 1998. For each patient, we have considered this date as the beginning of the observational period. All patients were followed until June 2002. Consequently, the length of the monitoring period can differ for each patient, depending on its surgery date. The first interoccurrence time has been considered as the time between the surgical intervention and the first hospitalization related to cancer. Four hundred and three patients with colon and rectum cancer have been included in the study. Information about their sex (male or female), age ( 60, 60-74 or 75), and tumoral stage using Dukes classification (A-B, C, or D) have been recorded. The following interoccurrence times have been considered as the difference between the last hospitalization and the current one. Only readmissions related to cancer have been considered.

Source

This data can be obtained upon request from González, JR et al.

References


Examples

data(DataColonDukesCvsD)
XL<-DataColonDukesCvsD
print(XL)
This function computes statistical difference between two survival curves.

Description

p-values of these tests are computed.

Usage

\texttt{Dif.Surv.Rec}(XX, \texttt{type, alfa, beta, gamma, eta})

Arguments

<table>
<thead>
<tr>
<th>XX</th>
<th>Object type recurrent events data</th>
</tr>
</thead>
<tbody>
<tr>
<td>\texttt{type}</td>
<td>&quot;LRrec&quot;,&quot;Grec&quot;,&quot;TWrec&quot;,&quot;PPrec&quot;,&quot;PMrec&quot;,&quot;FHrec&quot;,&quot;CMrec&quot;,&quot;Mrec&quot;,&quot;all&quot;</td>
</tr>
<tr>
<td>\texttt{alfa}</td>
<td>The appropriate choice, see ( w_z ). Defect value is equal zero</td>
</tr>
<tr>
<td>\texttt{beta}</td>
<td>The appropriate choice, see ( w_z ). Defect value is equal zero</td>
</tr>
<tr>
<td>\texttt{gamma}</td>
<td>The appropriate choice, see ( w_z ). Defect value is equal zero</td>
</tr>
<tr>
<td>\texttt{eta}</td>
<td>The appropriate choice, see ( w_z ). Defect value is equal zero</td>
</tr>
</tbody>
</table>

Details

This function contains tests to compare survival curves with recurrent events. The curves are estimated using \textbf{Peña-Strawderman-Hollander} estimator. \textbf{Peña et al. (2001)} defined the estimator of the survival function to recurrent events or \textbf{Kaplan-Meier} estimator \textbf{GPLE}. They used two counting processes \( N \) and \( Y \). The PSH estimator was defined as,

\[ \hat{S}(z) = \prod_{t \leq z} \left[ 1 - \frac{\Delta N(s, z)}{Y(s, z)} \right] \]

The authors considered two time scales: one related to calendar time (S) and other related to intercurrences time (T). So, the counting process \( N(s, z) \) represents the number of observed events in the calendar period \([0, s]\) with \( t \leq z \) and \( Y(s, z) \) represents the number of observed events in the period \([0, s]\) with \( t \geq z \). The produc-limit estimator was developed by \textbf{Peña, Strawderman} and \textbf{Hollander}, called \textbf{PSH}. This estimator is useful when the interoccurrence times are assumed to represents IID sample from some underlying distribution \( F \). \textbf{GPLE model} The \textbf{GPLE} estimator is defined as: A fundamental assumption of this approach is that individuals have been previously and properly classified in groups according to a stratification variable denote by \( r \). Thus, the estimator of the survival curve by each group is defined as,

\[ \hat{S}_r(z) = \prod_{t \leq z} \left[ 1 - \frac{\Delta N(s, z; r)}{Y(s, z; r)} \right] \quad r = 1, 2. \]

Value

# Dif.Surv.Rec(TBCplapyr,"all",0,0,0,0). Values returned
### Dif.Surv.Rec

<table>
<thead>
<tr>
<th>Nomb.Est</th>
<th>Chi.square</th>
<th>p.value</th>
</tr>
</thead>
<tbody>
<tr>
<td>LRrec</td>
<td>0.3052411</td>
<td>0.5806152</td>
</tr>
<tr>
<td>Grec</td>
<td>1.4448446</td>
<td>0.2293570</td>
</tr>
<tr>
<td>TWrec</td>
<td>0.9551746</td>
<td>0.3284056</td>
</tr>
<tr>
<td>PPrec</td>
<td>1.1322772</td>
<td>0.2872901</td>
</tr>
<tr>
<td>PMrec</td>
<td>1.1430319</td>
<td>0.2850126</td>
</tr>
<tr>
<td>PPrrec</td>
<td>1.1834042</td>
<td>0.2766641</td>
</tr>
<tr>
<td>HFrec</td>
<td>0.3052411</td>
<td>0.5806152</td>
</tr>
<tr>
<td>CMrec</td>
<td>0.3052411</td>
<td>0.5806152</td>
</tr>
<tr>
<td>Mrec</td>
<td>1.5298763</td>
<td>0.2161310</td>
</tr>
</tbody>
</table>

### Author(s)

Dr. Carlos Martínez, <cmmm7031@gmail.com>

### References


### See Also


### Examples

```r
data(TBCplapyr)
#Return the p-values of the all tests
Dif.Surv.Rec(TBCplapyr,"all",0,0,0,0)
#Return the p-value of the LRrec test
Dif.Surv.Rec(TBCplapyr)
#Return the p-value of the Grec test
Dif.Surv.Rec(TBCplapyr,"Grec")
#Return the p-values of the CMrec tests
#The CMrec test with this parameters generates LRrec test
Dif.Surv.Rec(TBCplapyr,"all",0,0,0,0)
#The CMrec test with this parameters generates Grec test
Dif.Surv.Rec(TBCplapyr,"all",0,0,1,0)
#The CMrec test with this parameters generates TWrec test
Dif.Surv.Rec(TBCplapyr,"all",0,0,0.5,0)
#The CMrec test with this parameters generates PPrec test
Dif.Surv.Rec(TBCplapyr,"all",1,0,0,0)
#The CMrec test with this parameters generates HFrec test
Dif.Surv.Rec(TBCplapyr,"all",1,1,0,0)
```
Plot.Data.Events

Plot data with recurrent events

Description

This function plot data with recurrent events

Usage

Plot.Data.Events(\texttt{yy, paciente, inicio, dias, censored, especiales, coevent="red", colcensor="blue"})

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>\texttt{yy}</td>
<td>Data type recurrent events. Examples: TBCplapyr</td>
</tr>
<tr>
<td>\texttt{paciente}</td>
<td>Vector of number of units on the data base</td>
</tr>
<tr>
<td>\texttt{inicio}</td>
<td>Vector, its assumed that the units are observed from one time equal to zero.</td>
</tr>
<tr>
<td>\texttt{dias}</td>
<td>Vector of the periods of observations of the study units</td>
</tr>
<tr>
<td>\texttt{censored}</td>
<td>Vector of times of censorship for each unit</td>
</tr>
<tr>
<td>\texttt{especiales}</td>
<td>Three-column matrix containing the identification of the units, times of occurrence of the event and type of event.</td>
</tr>
<tr>
<td>\texttt{coevent}</td>
<td>Color event identifier.</td>
</tr>
<tr>
<td>\texttt{colcensor}</td>
<td>Color censored data identifier.</td>
</tr>
</tbody>
</table>

Details

The plot shows the recurrence of the events on the time.

Value

This function returned the pictorial representation of the set of recurrence events data

Note

We recommend users to use routines similar to the example.

Author(s)

Dr. Carlos Martinez, <cmmm7031@gmail.com>
References


See Also

Plot.Surv.Rec, Print.Summary

Examples

data(TBcpelayr)
X<-data.frame(TBcpelayr)
p<-ncol(X)
N<-nrow(X)
censor<-matrix(X$event)
especiales<-matrix(data=0,nrow(X),3)
especiales[,1]<-matrix(X$id)
especiales[,2]<-matrix(X$Tcal)
especiales[,3]<-matrix(X$event)
niveles<-levels(factor(especiales[,1]))
for(i in 1:N){
  for(j in 1:nrow(matrix(niveles))){
    if (as.character(especiales[i,1])==niveles[j] especiales[i,1]<-j})
StudyPeriod<-matrix(data=0,nrow(matrix(niveles)),1)
start<-matrix(data=0,nrow(matrix(niveles)),1)
k<-0
for(j in 1:N){if (X$event[j]==0){k<-k+1;StudyPeriod[k,1]<-X$Tcal[j]}}
units<-matrix(1:nrow(matrix(niveles)),nrow(matrix(niveles)),1)
Plot.Data.Events(X,units,start,StudyPeriod,censor, especiales,"black","blue")
Plot.Data.Events(X,units,start,StudyPeriod,censor, especiales,"red","black")

Plot.Event.Rec   This function plots the occurrence of one recurrent event on two scales time, a gap time and a calendars time.

Description

Recurrent events are plotted. A plot is returned. The counting processes are a powerful tools in survival analysis. These process consider two scale time, a calendar time and a gap time. This idea originally provides from Gill (1981) and the concept was extended by Peña et al. (2001).
Usage

Plot.Event.Rec(yy, xy, xf)

Arguments

yy Object type recurrent events data. Example: TBCplapyr
xy Identification of the unit to plotted. xy = 1 is defect value.
xf Argument to plot the occurrence events of the unit xf. xf = 1 is defect value.

Value

Plot is returned. Peña et al. (2001) designed a special graphic, that allows to count the occurrence of events per unit time. Doubly indexed processes illustration for an case. The graphic shows a case followed during 24.01 months. This patient presents four recurrences at months 7, 10, 16 and 24 from the beginning of study. This fact implies that interoccurrence times are 7, 3, 6, 8 and the censored time correspond to 0.01 months. Let us assume that we are interested in computing the single processes, N(t) and Y (t) for a selected interoccurrence time t = 5. In this case N(t = 5) = 1 and Y (t = 5) = 3. For the calendar time scale, s = 20, we have N(s = 20) = 3 and Y (s = 20) = 1. Now, let us assume that we would like to know double-indexed processes for both selected interoccurrence and calendar times. Using both time scales we observe that \( N_{14}(s = 20, t = 5) = 1 \), \( Y_{14}(s = 20, t = 5) = 2 \) and \( \Delta N_{14}(s = 20, t = 6) = 1 \).

Author(s)

Dr. Carlos Martínez <cmmm7031@gmail.com>

References


See Also

Dif.Surv.Rec

Examples

data(TBCplapyr)
# See, the unit number 14
Plot.Event.Rec(TBCplapyr,14,14)
# See, the unit number 5
Plot.Event.Rec(TBCplapyr,5,5)
Plot.Surv.Rec

**Description**

The survival curves are plotted. Both curves are estimates using survrec package. This package is available in language R. This important clearly, that the PHS estimator is of valid use, when it assumed that the inter-occurrence times are IID. Its obvious that this assumption is restrictive in biomedical applications and its use is more valid on the field of engineering.

**Usage**

```
Plot.Surv.Rec (XX)
```

**Arguments**

- `XX` Data type recurrent events. Example: TBCplapyr

**Value**

The survival curves for both groups are plotted.

**Author(s)**

Dr. **Carlos Martinez** <cmmm7031@gmail.com>

**References**


**See Also**

Plot.Event.Rec, Dif.Surv.Rec

**Examples**

```
data(TBCplapyr)
Plot.Surv.Rec(TBCplapyr)
```
Print.Summary

Function to print summary of statistics tests to comparison of the survival curves of the groups with recurrent events

Description

Returns matrices that contain the estimations of the survival curves for both groups. The estimations of survival curves of both groups are made using PSH estimator. The p.values of the tests are returned.

Usage

Print.Summary(XX)

Arguments

XX Object type recurrent events data

Details

See Dif.Surv.Rec(XX,...)

Value

Put object type recurrent events data. Group= 0

<table>
<thead>
<tr>
<th>time</th>
<th>n.event</th>
<th>n.risk</th>
<th>surv</th>
<th>std.error</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>2</td>
<td>127</td>
<td>0.984</td>
<td>0.0110</td>
</tr>
<tr>
<td>2</td>
<td>9</td>
<td>124</td>
<td>0.913</td>
<td>0.0243</td>
</tr>
<tr>
<td>3</td>
<td>14</td>
<td>113</td>
<td>0.800</td>
<td>0.0340</td>
</tr>
<tr>
<td>4</td>
<td>9</td>
<td>98</td>
<td>0.726</td>
<td>0.0380</td>
</tr>
<tr>
<td>...</td>
<td>...</td>
<td>...</td>
<td>.....</td>
<td>.....</td>
</tr>
<tr>
<td>29</td>
<td>1</td>
<td>18</td>
<td>0.244</td>
<td>0.0422</td>
</tr>
<tr>
<td>31</td>
<td>1</td>
<td>13</td>
<td>0.225</td>
<td>0.0427</td>
</tr>
<tr>
<td>35</td>
<td>1</td>
<td>9</td>
<td>0.200</td>
<td>0.0439</td>
</tr>
</tbody>
</table>

Group= 1

<table>
<thead>
<tr>
<th>time</th>
<th>n.event</th>
<th>n.risk</th>
<th>surv</th>
<th>std.error</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>3</td>
<td>84</td>
<td>0.964</td>
<td>0.0199</td>
</tr>
<tr>
<td>2</td>
<td>6</td>
<td>81</td>
<td>0.893</td>
<td>0.0327</td>
</tr>
<tr>
<td>3</td>
<td>12</td>
<td>73</td>
<td>0.746</td>
<td>0.0447</td>
</tr>
<tr>
<td>4</td>
<td>10</td>
<td>61</td>
<td>0.624</td>
<td>0.0494</td>
</tr>
<tr>
<td>...</td>
<td>...</td>
<td>...</td>
<td>.....</td>
<td>.....</td>
</tr>
<tr>
<td>...</td>
<td>...</td>
<td>...</td>
<td>.....</td>
<td>.....</td>
</tr>
</tbody>
</table>
15 1 17 0.283 0.0514
42 1 6 0.236 0.0582
44 1 5 0.189 0.0599

Group Median

<table>
<thead>
<tr>
<th>Group</th>
<th>Median</th>
</tr>
</thead>
<tbody>
<tr>
<td>Pooled Group</td>
<td>8</td>
</tr>
<tr>
<td>1er Group</td>
<td>9</td>
</tr>
<tr>
<td>2do Group</td>
<td>6</td>
</tr>
</tbody>
</table>

Nomb.Est   Chi.square   p.value
-------------   ---------------   --------
LRrec   0.3052411   0.5806152
Grec     1.4448446   0.2293570
TWrec    0.9551746   0.3284056
PPrec    1.1322772   0.2872901
PMrec    1.1430319   0.2850126
PPrec    1.1834042   0.2766641
HFrec    0.3052411   0.5806152
CMrec    0.3052411   0.5806152
Mrec     1.5298763   0.2161310

Author(s)

Dr. Carlos Martinez <cmmn703@mmail.com>

References


See Also

Dif.Surv.Rec, Plot.Surv.Rec

Examples

data(TBcplapyr)
Print.Summary(TBcplapyr)
**TBCplapyr**

**Data of tumor recurrence in patients with bladder cancer. Patients were treated with placebo and pyridoxine**

---

**Description**

This database corresponds to the time of recurrence of tumors in 78 patients with bladder cancer. Patients were randomly assigned to treatments: placebo (47 patients) and piridoxine (31 patients). Data type data.frame with 222 observations on 8 variables.

**Usage**

data(TBCplapyr)

**Format**

This data.frame contains the following columns:
- j : Observation number
- id : ID of each unit. Repeated for each recurrence
- Tinicio: Inicial time
- time : recurrence o censoring time. For each unit the last time is censored.
- event : censoring status. '1' = occurrence of the event in the unit and '0' right censored time.
- strata : Number of strata
- trt : Factor w/ 2 levels "Placebo","Pyridoxine"
- group : a factor with levels. Group identifier.

**Details**

Experiment Byar (1980). The database Byar experiment is used and the time (months) of recurrence of tumors in 116 sick patients with superficial bladder cancer is measured. These patients were randomly allocated to the following treatments: placebo (47 patients), pyridoxine (31 patients) and thiotepa (38 patients).

**Source**


**References**

**Examples**

```r
data(TBCplathy)
XL<-data.frame(TBCplathy)
print(XL)
Print.Summary(TBCplathy)
```

| TBCplathy | Data of tumor recurrence in patients with bladder cancer. Patients were treated as placebo and thiotepa |

**Description**

This database corresponds to the time of recurrence of tumors of 85 patients with bladder cancer. Patients were randomly assigned to treatments: placebo (47 patients) and thiotepa (38 patients). Data type data.frame with 217 observations on 8 variables.

**Usage**

```r
data(TBCplathi)
```

**Format**

This data frame contains the following columns:

- **j**: Observation number
- **id**: ID of each unit. Repeated for each recurrence
- **Tinicio**: Inicial time
- **time**: recurrence o censoring time
- **event**: censoring status.
- **strata**: Number of strata
- **trt**: Factor w/ 2 levels "Placebo","Thiotepa"
- **group**: a factor with levels. Group identificator.

**Details**

Experiment Byar (1980). The database Byar experiment is used and the time (months) of recurrence of tumors in 116 sick patients with superficial bladder cancer is measured. These patients were randomly allocated to the following treatments: placebo (47 patients), pyridoxine (31 patients) and thiotepa (38 patients).

**Source**

**References**


**Examples**

```r
data(TBCplathip)
XL<-data.frame(TBCplathip)
print(XL)
Print.Summary(TBCplathip)
```

**TBCpyrthi**  
*Data of tumor recurrence in patients with bladder cancers. Patients were treated with pyridoxine and thiotepa.*

**Description**

This database corresponds to the time of recurrence of tumors of 69 patients with bladder cancer. Patients were randomly assigned to treatments: pyridoxine (38 patients) and thiotepa (31 patients). Data type data.frame with 171 observations on 8 variables.

**Usage**

```r
data(TBCpyrthi)
```

**Format**

This data frame contains the following columns:

- j: Observation number
- id: ID of each unit. Repeated for each recurrence
- Tinicio: Initial time
- time: recurrence or censoring time
- event: censoring status.
- strata: Number of strata
- trt: Factor w/ 2 levels "Pyridoxine", "Thiotepa"
- group: a factor with levels. Group identifier.

**Details**

Experiment Byar (1980). The database Byar experiment is used and the time (months) of recurrence of tumors in 116 sick patients with superficial bladder cancer is measured. These patients were randomly allocated to the following treatments: placebo (47 patients), pyridoxine (31 patients) and thiotepa (38 patients).
Source


References


Examples

data(TBCpyrthi)
XLC<-data.frame(TBCpyrthi)
print(XL)
Print.Summary(TBCpyrthi)
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