# Package ‘TP.idm’

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TP.idm-package

Estimation of Transition Probabilities for the Illness-Death Model

Description


Details

The DESCRIPTION file:

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Index of help topics:

TP.idm-package Estimation of Transition Probabilities for the Illness-Death Model
TPidm Transition probabilities for the illness-death model
colonTP Chemotherapy for Stage B/C colon cancer
plot.TPIdm Plot method for a TPIdm object
print.TPIdm Print method for a TPIdm object
summary.TPIdm Summary method for a TPIdm object
test.mm Graphical tool to check the Markov assumption

This package incorporates the function TPidm which can be used to compute a nonparametric transition probability matrix for the illness-death model. For a complete list of functions use library(help=TP.idm).

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colonTP

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References


Examples

data(colonTP)

# create a TPidm object with s = 0, t = "last" (default),
# CI = TRUE (default) and method = "AJ":
aj0ci <- TPidm(colonTP, s = 0, method = "AJ")
summary(aj0ci) # summarizing the results
plot(aj0ci) # plotting all occupation probabilities

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ColonTP

Chemotherapy for Stage B/C Colon Cancer

Description

These are data from one of the first successful trials of adjuvant chemotherapy for colon cancer. Levamisole is a low-toxicity compound previously used to treat worm infestations in animals; 5-FU is a moderately toxic (as these things go) chemotherapy agent. This data frame reproduces the information in the colon object of the package survival, organized in a slightly different way (only one row is used for each individual).

Usage

data("colonTP")
Format

A data frame with 929 observations on the following 15 variables.

time
  Disease free survival time (time to recurrence, death, or censoring, whichever occurs first).
event
  Disease free survival indicator (1=dead or relapsed, 0=alive disease free).
Stime
  Time to death or censoring.
event
  Death indicator (1=dead, 0=alive).
rx
  Treatment - Observation, Lev(amisole), Lev(amisole)+FU.
sex
  1=male.
age
  Age in years.
obstruct
  Obstruction of colon by tumour.
perfor
  Perforation of colon.
adhere
  Adherence to nearby organs.
nodes
  Number of lymph nodes with detectable cancer.
differ
  Differentiation of tumour (1=well, 2=moderate, 3=poor).
extent
  Extent of local spread (1=submucosa, 2=muscle, 3=seros, 4=contiguous structures).
surg
  Time from surgery to registration (0=short, 1=long).
node4
  More than 4 positive lymph nodes.

Note

The study is originally described in Laurie et al. (1989). The main report is found in Moertel et al. (1990). This data set is closest to that of the final report in Moertel et al. (1991). A version of the data with less follow-up time was used in the paper by Lin (1994). This data set has been used for illustration purposes in a number of papers, including Meira-Machado et al. (2015) and de Uña-Álvarez and Meira-Machado (2015).

References


**Examples**

```r
data(colontp)
## maybe str(colontp); plot(colontp) ...
```
print.TPidm

### Description

Print method for an object of class ‘TPidm’.

### Usage

```r
# S3 method for class 'TPidm'
print(x, ...)
```

### Arguments

- `x` An object of class ‘TPidm’.
- `...` Further arguments to print.

### Value

A data.frame is returned with the following variables:

- `transition` The initial and final states “i j” for each particular transition.
- `probs` The transition probabilities $P_{ij}(s,t)$.

### Note

The print function displays the method used, the user-supplied times s and t, the possible transitions, the estimated transition probabilities and, optionally, confidence limits and variances.

If `cov` was specified, the print function provides the transition probabilities $P_{ij}(s,t)$ for each level of covariate.
Summary method for a TPidm object

Description

Summary method for an object of class ‘TPidm’.

Usage

```r
## S3 method for class 'TPidm'
summary(object, ...)  
```

Arguments

- `object` An object of class ‘TPidm’.
- `...` Further arguments to print.

Value

A data.frame is returned with the following variables:

- `transition` The initial and final states “i j” for each particular transition.
- `probs` The transition probabilities $P_{ij}(s,t)$.

Note

The summary function prints the method used, the user-supplied times s and t, the possible transitions, the estimated transition probabilities and, optionally, confidence limits and variances.

If `cov` is specified, the summary function provides the transition probabilities $P_{ij}(s,t)$ for each level of covariate.

Examples

```r
data(colonTP)  
# create a TPidm object with s = 365, t = 1095, cov = "rx",  
# CI = FALSE and method = "NM" (default):
nm365cov <- TPidm(colonTP, s = 365, t = 1095, cov = "rx", CI=FALSE)  
summary(nm365cov) # summarizing the results
```
Description

It constructs a PP-plot which compares the transition probabilities reported by the non-Markovian and Aalen-Johansen estimators. Under the Markov assumption the PP-plot should fit the straight line $y=x$. When the Markov assumption holds the Aalen-Johansen is preferred since it provides a smaller standard error. If the Markov assumption is violated, the Aalen-Johansen may be inconsistent and therefore the non-Markovian method is recommended.

Usage

test.nm(data, s, t = "last")

Arguments

data A data.frame including at least four columns named time1, event1, stime and event, which correspond to disease free survival time, disease free survival indicator, time to death or censoring, and death indicator, respectively.
s The current time for the transition probabilities to be computed.
t The future time for the transition probabilities to be computed. Default is “last” which means the largest time among the uncensored entry times for the intermediate state and the final absorbing state.

Details

It constructs a PP-plot which compares the transition probabilities reported by the non-Markovian and Aalen-Johansen estimators. Under the Markov assumption the PP-plot should fit the straight line $y=x$. When the Markov assumption holds the Aalen-Johansen is preferred since it provides a smaller standard error. If the Markov assumption is violated, the Aalen-Johansen may be inconsistent and therefore the non-Markovian method is recommended. The PP-plot excludes $P_{11}(s,t)$ since both estimators agree in this case. Also, the user-supplied $s$ must be strictly positive, because the Markov assumption is not relevant for the estimation of occupation probabilities ($s=0$).

Examples

data(colonTP)
test.nm(colonTP, s = 0)
# nothig is displayed since the Markov condition is not relevant
# for the case s=0 (occupation probabilities)
test.nm(colonTP, s = 365, t = 1095)
Description

This function computes the transition probability matrix for the illness-death model, by using the Aalen-Johansen technique (suitable for Markov models) or alternatively a non-Markovian estimator. It creates a `TPidm` object.

Usage

```r
TPidm(data, s, t = "last", cov = NULL, CI = TRUE, level = 0.95,
      ci.transformation = "linear", method = "NM")
```

Arguments

data: A data.frame including at least four columns named `time1`, `event1`, `stime` and `event`, which correspond to disease free survival time, disease free survival indicator, time to death or censoring, and death indicator, respectively.
s: The current time for the transition probabilities to be computed; s=0 reports the occupation probabilities.
t: The future time for the transition probabilities to be computed. Default is “last” which means the largest time among the uncensored entry times for the intermediate state and the final absorbing state.
cov: A categorical variable for the optional by-group analysis; this variable must be a factor.
CI: If TRUE (default), confidence intervals are computed.
level: Level of confidence intervals. Default is 0.95 (corresponding to 95%).
ci.transformation: Transformation applied to compute confidence intervals. Possible choices are “linear”, “log”, “log-log” and “cloglog”. Default is “linear”.
method: The method used to compute the transition probabilities. Possible options are “AJ” (Aalen-Johansen) or “NM” (non-Markovian). Default is “NM”.

Details

If s = 0 this function TPidm reports the state occupation probabilities at time t. For s > 0, the transition probabilities are provided. The default method “NM” computes the estimator proposed by de Uña-Alvarez and Meira-Machado (2015), which is consistent regardless the Markov assumption. To fit a Markovian transition probability matrix, use the “AJ” method. Note that the Aalen-Johansen occupation probabilities are consistent even when the process is non-Markov (Datta and Satten, 2001), but this is not true for the Aalen-Johansen transition probabilities (Meira-Machado et al., 2006). If CI is TRUE (default), TPidm calculates the estimated variance and the confidence intervals by using the plug-in variance described in Balboa and de Uña-Alvarez (2018) (method = “NM”), or the standard formulas for Markovian processes (method = “AJ”, see Andersen et al., 1993).
**Value**

An object of class ‘TPidm’. It is a list containing the following objects:

- **s**
  
  The user-supplied current time for the transition probabilities.

- **t**
  
  The user-supplied future time for the transition probabilities.

- **method**
  
  The method used to compute the transition probabilities.

- **times**
  
  The uncensored entry times for the intermediate state and the final absorbing state which fall between s and t.

- **probs**
  
  A matrix with transition probability estimates $P_{ij}(s,t)$ for the user-supplied $(s, t)$ and each possible transition from state $i$ (rows) to state $j$ (columns). If CI is TRUE (default), it includes confidence limits and variances.

- **all.probs**
  
  An array with transition probability estimates $P_{ij}(s, t_k)$ for each possible transition, evaluated at all the event times $t_k$ falling between $s$ and $t$. If CI is TRUE (default), it includes confidence limits and variances.

- **p.trans**
  
  Possible transitions among the states. If $s = 0$, possible transitions are “1 1”, “1 2” and “1 3”; if $s > 0$ possible transitions are “1 1”, “1 2”, “1 3”, “2 2” and “2 3”.

- **CI**
  
  A logical value chosen by the user.

- **ci.transformation**
  
  Transformation chosen by the user to compute the confidence intervals.

**Note**

If time1=Stime and event1=event=1, the function TPidm assumes that a direct transition from the initial state to the final absorbing state has occurred. That is, zero sojourn times are not allowed for the intermediate state (replacing the zeros by a small positive amount is a way to introduce such cases).

If cov is specified, the main function provides estimations of transition probabilities for each level of the covariate.

**References**


Examples

data(colonTP)

# create a TPidm object with s = 0, t = "last" (default),
# CI = TRUE (default) and method = "AJ":
aj0ci <- TPidm(colonTP, s = 0, method = "AJ")
plot(aj0ci) # plotting all occupation probabilities

# or
# create a TPidm object with s = 365, t = "last" (default),
# CI = FALSE and method = "NM" (default):
nm365 <- TPidm(colonTP, s = 365, CI=FALSE)
summary(nm365) # summarizing the results

# or
# create a TPidm object with cov = "rx":
nm365cov <- TPidm(colonTP, s = 365, t = 1095, cov = "rx", CI=FALSE)
summary(nm365cov) # summarizing the results
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