Package 'glrt'

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R topics documented:

glrt-package	2
Aintmap	3
AlphaCross	4
Bisect	5
CensorType	5
Chisqstat3	6
cmv	7
	8
	8
gLRT	9
generation of the second s	12
g	13
gLRT3	15
gLRT4	17
Linkfunc	18

glrt-package

LinkfuncDir	1	9
ModifiedEMICM	2	20
ModifiedEMICMmac	2	22
PMGA	2	23
rescaleP	2	24
ScoreStat	2	24
ScoreTest	2	25
StartEnd	2	26
Teststat1	2	27
Teststat2	2	27
Teststat3	2	28
Teststat4	2	28
Var1	2	29
Var2		29
Var3	3	30
VarScoreStat	3	30
	1	32
	J	,4

Index

glrt-package

Generalized logrank tests for interval-censored failure time data

Description

Functions to conduct four nonparametric generalized logrank tests and a score test under a proportional hazards model

Details

Package:	glrt
Type:	Package
Version:	2.0
Date:	2014-12-24
License:	GPL-2
LazyLoad:	yes

The main function is gLRT, in which a method is selected. Depending on the method specified, one of the five functions (gLRT1, gLRT2, gLRT3, gLRT4, ScoreTest) is called to perform a generalized logrank test or a scor test. Before computing the test statistic in each test, function ModifiedEMICM is called to compute an NPMLE of the common survival function under the null hypothesis that all treatments have the same survival function except for in gLRT4, where ModifiedEMICM is used to estimate the survival function of each treatment group.

Author(s)

Qiang Zhao and Jianguo Sun

Aintmap

Maintainer: Qiang Zhao <qiang.zhao@txstate.edu>

References

Q. Zhao and J. Sun (2004), "Generalized Log-rank Test for Mixed-Censored Failure Time Data", Statistics in Medicine, 23: 1621-1629.

J. Sun, Q. Zhao, and X. Zhao (2005), "Generalized Log-rank Test for Interval-Censored Data", Scandinavian Journal of Statistics, 32: 45-57.

X. Zhao, Q. Zhao, J. Sun, Q. and J. S. Kim (2008), "Generalized Log-rank Tests for Partly Interval-Censored Failure Time Data", Biometrical Journal, 50 (3): 375-385.

X. Zhao, R. Duan, Q. Zhao, and J. Sun (2013), "A New Class of Generalized Log Rank Tests for Interval-censored Failure Time Data", Computational Statistics and Data Analysis. 60: 123-131.

Finkelstein, DM (1986), "A Proportional Hazards Model for Interval-censored Failure Time Data", Biometrics, 42: 845-854.

Q. Zhao (2012), "gLRT - A New R Package for Analyzing Interval-censored Survival Data", Interval-Censored Time-to-Event Data: Methods and Applications, CRC Press, 377-396.

See Also

gLRT, gLRT1, gLRT2, gLRT3, gLRT4, ScoreTest, ModifiedEMICM

Aintmap

Create A matrix and intmap

Description

This function is borrowed from package interval by Professor Michael Fay and used in function ModifiedEMICM to provide an NPMLE of a survival function. The A matrix is an n by m matrix of zeros and ones, where each row represents one of n failure times, and each column represents a possible interval for the nonparametric maximum likelihood estimate (NPMLE). The function Aintmap creates an A matrix and associated intmap from left and right intervals (L and R) which may not include the boundary of the interval (using Lin or Rin). The matrix intmap denotes the intervals of the potential jumps in the distribution of the NPMLE, and its attribute LRin denotes whether to include each of the interval or not.

Usage

Aintmap(L, R, Lin = NULL, Rin = NULL)

Arguments

L	numeric vector of left endpoints of censoring interval
R	numeric vector of right endpoints of censoring interval
Lin	logical vector, should L be included in the interval? (see details)
Rin	logical vector, should R be included in the interval? (see details)

Value

A list with two objects:

A	an n by m matrix of 0 and 1s
intmap	the associated intmap

Author(s)

Michael Fay

See Also

ModifiedEMICM

Examples

```
Aintmap(c(2,3,3,7),c(3,5,5,8),Lin=c(FALSE,TRUE,FALSE,FALSE),
Rin=c(TRUE,FALSE,TRUE,FALSE))
```

AlphaCross

Compute a matrix of at-risk indicators

Description

This function determines whether each observation in one group is at risk at different times or time intervals based on the observations of another group.

Note

It is used in Teststat4 and not to be called by the user.

Author(s)

Qiang Zhao and Jianguo Sun

See Also

Teststat4

Bisect

Description

Most of the optimization is Icens have a one dimensional root-finding component. Since the quantities involved are generally restricted to a subset of [0, 1] we use bisection to find the roots. This function is borrowed from package Icens.

Details

We search from pvec in the direction ndir to obtain the new value of pvec that maximizes the likelihood.

Note

It is used in ModifiedEMICMmac and not to be called by the user.

Author(s)

Alain Vandal and Robert Gentleman

References

Any book on optimization.

See Also

ModifiedEMICMmac

CensorType

Determine types of censoring based on censoring intervals

Description

This function determines types of censoring based on censoring intervals. It is called by function gLRT1, gLRT2, gLRT3, and gLRT4.

Usage

CensorType(A, inf)

Arguments

A	a matrix containing the end points of censoring intervals in the first two columns
inf	value representing infinity

cens

a vector of censoring types with value 1 for left-censoring, 2 for interval-censoring, 3 for right-censoring, and 4 for exact observation

Author(s)

Qiang Zhao and Jianguo Sun

Examples

```
A = matrix(c(1, 3, 0, 4, 3, 100, 3, 3), ncol=2, byrow=TRUE)
CensorType(A, 100)
```

Chisqstat3	Compute the chi-square test statistic and degrees of freedom for test
	gLRT3

Description

This function computes the chi-square test statistic and degrees of freedom for test gLRT3. The degree of freedom depends on whether there are exact observations and proportions of exact observations in each treatment.

Usage

Chisqstat3(U, V, counts)

Arguments

U	k-vector of the test statistic in gLRT3, where k is number of treatments.
V	estimated k by k covariance matrix of U
counts	a k by 2 matrix containing number of exact and non-exact observations for each treatment

Value

chisq	chi-square test statistic
df	degrees of freedom used.

Note

This is not to be called by the user.

Author(s)

Qiang Zhao and Jianguo Sun

cmv

References

X. Zhao, Q. Zhao, J. Sun, Q. and J. S. Kim (2008), "Generalized Log-rank Tests for Partly Interval-Censored Failure Time Data", Biometrical Journal, 50 (3): 375-385.

Interval-censored data for times to cytomegalovirus (CMV) shedding in blood and urine

Description

The cmv data frame is based on an AIDS clinic trial on HIV-infected individuals. The data involve 204 patients who are classified into two groups based on whether patient's CD4 count is below 75 cells per μl or not. Among the 204 patients, 111 of them had a CD4 count below 75.

Usage

data(cmv)

Format

A data frame with 204 observations on the following 6 variables.

patient patient id

1b left end point of an censoring interval for time to CMV shedding in blood

rb right end point of an censoring interval for time to CMV shedding in blood

- lu left end point of an censoring interval for time to CMV shedding in urine
- ru right end point of an censoring interval for time to CMV shedding in urine

cd4ind group indicator if patient's baseline CD4 count is below 75 (1 for below 75 and 0 otherwise)

Details

The survival times are time to the presence of CMV in blood and ullrine, respectively. The censoring intervals are in the format of $(l_b, r_b]$ and $(l_u, r_u]$. For CMV in blood, there are 7 left-censored, 23 interval-censored, and 174 right-censored, but no exact observations. For CMV in urine, there are 49 left-censored, 67 interval-censored, and 88 right-censored, but no exact observations.

Source

J. Sun (2006), "The Statistical Analysis of Interval-censored Failure Time Data", Springer.

References

W. B. Goggins and D. M. Finkelstein (2000), "A proportional hazards model for multivariate interval-censored failure time data", Biometrics, 56: 940-943.

cosmesis

Description

The cosmesis data frame has 95 rows and 3 columns.

Usage

data(cosmesis)

Format

A data frame with the following 3 variables.

L left end point of the cosmetic deterioration interval

R right end point of the cosmetic deterioration interval

Trt treatment indicator. It is zero for those that received radiotherapy

Source

Borrowed from package Icens by Alain Vandal and Robert Gentleman.

References

A semiparametric model for regression analysis of interval-censored failure time data, D. M. Finkelstein and R. A. Wolfe, 1985, Biometrics.

diabetes

Interval-censored data for time from onset of diabetes to the onset of diabetic nephronpathy

Description

The diabetes data frame is based on a study conducted at the Steno Memorial Hospital in Denmark from 1933-1984. The data involve 731 patients (454 males and 277 females) and have 595 exact, 136 interval-censored, and no right-censored observations.

Usage

data(diabetes)

gLRT

Format

A data frame with 731 observations on the following 3 variables.

left left end point of an censoring interval

right right end point of an censoring interval

gender gender indicator (1 for male and 0 for female)

Details

The survival time is time from onset of diabetes to the onset of diabetic nephronpathy, a major complication of Type I diabetes.

Source

Kindly provided by Professor P. K. Andersen.

References

X. Zhao, Q. Zhao, J. Sun, Q. and J. S. Kim (2008), "Generalized Log-rank Tests for Partly Interval-Censored Failure Time Data", Biometrical Journal, 50 (3): 375-385.

gLRT

Do one of the four generalized logrank tests or a score test for intervalcensored data

Description

The gLRT function conducts four k(>=2)-sample tests for interval-censored survival data. Four of them are different nonparametric generalized logrank tests, and the other is a score test under a proportional hazards model. They are two-sided tests. The null hypothesis is that all k survival functions of the failure time are identical, and the alternative hypothesis hypothesis is that not all survival functions are the same. This function calls one of functions (gLRT1, gLRT2, gLRT3, gLRT4, ScoreTest) based on the method specified. However, each of these tests can be called individually to perform a test. Note that gLRT2 and gLRT4 do not allow exact observations. gLRT4 only allows k = 2 and is no longer called ScoreTest as in Zhao (2012).

Usage

```
gLRT(A, k = 2, method = c("glrt1", "glrt2", "glrt3", "glrt4", "score"),
M = 50, rho = 0, gamma = 0, EMstep = TRUE, ICMstep = TRUE, tol = 1e-06,
maxiter = 1000, inf = Inf)
```

Arguments

A	an n by 3 data matrix with the censoring interval of the format (L, R] in columns 1 & 2 and treatmentment indicator ranging from 0 to $k - 1$ in column 3.
k	number of treatments. The default is 2.
method	a character string specifying the test to be performed: "glrt1", "glrt2", "glrt3", "glrt4", and "score".
М	number of multiple imputations used in estimating the covariance in function $gLRT1$. The default is 50.
rho	non-negative parameter in $[0, 1]$ of the link function used for calculating the test statistics in gLRT2, gLRT3, and gLRT4. It is the same as <i>b</i> in Zhao, Duan, Zhao, and Sun (2013). The default is 0.
gamma	non-negative parameter in $[0, 1]$ of the link function used for calculating the test statistics in gLRT2, gLRT3, and gLRT4. It is the same as c in Zhao, Duan, Zhao, and Sun (2013). The default is 0.
EMstep	a boolean variable indicating whether to take an EM step in the iteration when estimating the common distribution function. The default is TRUE.
ICMstep	a boolean variable indicating whether to take an ICM step in the iteration when estimating the common distribution function. The default is TRUE.
tol	the maximal L_1 distance between successive estimates before stopping iteration when estimating the common distribution function. The default is 1.0e-6.
maxiter	the maximal number of iterations to perform before stopping when estimating a distribution function. The default is 1000.
inf	value used in data for infinity. The default is Inf.

Details

For all tests, it is assumed that the censoring interval for each observation takes the form $(L_i, R_i]$. For exact observations, $L_i = R_i$; for left-censored observations, $L_i = 0$; and for right-censored observations, $R_i = inf$, infinity or a large number representing infinity.

Exact observations are not allowed in gLRT2. If no exactly observations exist, gLRT3 reduces to gLRT2 in terms of chi-square statistic and p-value.

When method="glrt1" is selected, gLRT1 is called to perform the test proposed by Zhao and Sun (2004). When method="glrt2" is selected, gLRT2 is called to perform the test proposed by Sun, Zhao, and Zhao (2005). When method="glrt3" is selected, gLRT3 is called to perform the test proposed by Zhao, Zhao, Sun, and Kim (2008). When method="score" is selected, ScoreTest is called to perform a score test under a proportional hazards model proposed by Finkelstein (1986). For the above methods, the NPMLE of the common distribution function under the null hypothesis is computed by function ModifiedEMICM. When method="glrt4" is selected, gLRT4 is called to perform the test proposed by Zhao, Duan, Zhao, and Sun (2013) where ModifiedEMICM is applied to each of the two groups.

The link function used in gLRT2, gLRT3, and gLRT4 is $\xi(x) = x log(x) x^{\rho} (1-x)^{\gamma}$.

gLRT

Value

The function returns an object containing the following components:

method	test procedure used
u	the test statistic
V	the estimated covariance of the test statistic u (NA for gLRT4)
chisq/fstat	the chi-square or f (for gLRT4) statistic
df	the degrees of freedom of the chis-square test or f-test
р	p-value of the test

Author(s)

Qiang Zhao and Jianguo Sun

References

Q. Zhao and J. Sun (2004), "Generalized Log-rank Test for Mixed-Censored Failure Time Data", Statistics in Medicine, 23: 1621-1629.

J. Sun, Q. Zhao, and X. Zhao (2005), "Generalized Log-rank Test for Interval-Censored Data", Scandinavian Journal of Statistics, 32: 45-57.

X. Zhao, Q. Zhao, J. Sun, Q. and J. S. Kim (2008), "Generalized Log-rank Tests for Partly Interval-Censored Failure Time Data", Biometrical Journal, 50 (3): 375-385.

X. Zhao, R. Duan, Q. Zhao, and J. Sun (2013), "A New Class of Generalized Log Rank Tests for Interval-censored Failure Time Data", Computational Statistics and Data Analysis. 60: 123-131.

Finkelstein, DM (1986), "A Proportional Hazards Model for Interval-censored Failure Time Data", Biometrics, 42: 845-854.

Q. Zhao (2012), "gLRT - A New R Package for Analyzing Interval-censored Survival Data", Interval-Censored Time-to-Event Data: Methods and Applications, CRC Press, 377-396.

See Also

gLRT1, gLRT2, gLRT3, gLRT4, ScoreTest

Examples

```
data(cosmesis)
gLRT(cosmesis, method="glrt1", M=20, inf=100)
gLRT(cosmesis, method="glrt2", rho=1, inf=100)
data(diabetes)
gLRT(diabetes, method="glrt3", gamma=1)
gLRT(diabetes, method="score")
data(cmv)
cmvBlood = cmv[,c(2,3,6)]
cmvUrine = cmv[, 4:6]
gLRT(cmvBlood, method="glrt4")
```

```
gLRT(cmvUrine, method="glrt4", rho=1, gamma=1)
# 3-sample test
data(cosmesis)
cosmesis[80:94, 3] = 2
gLRT(cosmesis, k=3, method="glrt3", rho=0, gamma=0, inf=100)
```

```
gLRT1
```

Conduct a generalized logrank test for interval-censored data

Description

Function gLRT1 conducts a k(>=2)-sample test for interval-censored survival data. The test is based on Zhao and Sun (2004). The null hypothesis is that all k survival functions of the failure time are the same, and the alternative hypothesis is that not all functions are the same.

Usage

gLRT1(A, k = 2, M = 50, EMstep = TRUE, ICMstep = TRUE, tol = 1e-06, maxiter = 1000, inf = Inf)

Arguments

A	an n by 3 data matrix with the censoring interval of the format $(L, R]$ in columns 1 & 2 and treatmentment indicator ranging from 0 to $k - 1$ in column 3.
k	number of treatments. The default is 2.
М	number of multiple imputations used in estimating the covariance of the test statistic. The default is 50.
EMstep	a boolean variable indicating whether to take an EM step in the iteration when estimating the common distribution function. The default is TRUE.
ICMstep	a boolean variable indicating whether to take an ICM step in the iteration when estimating the common distribution function. The default is TRUE.
tol	the maximal L_1 distance between successive estimates before stopping iteration when estimating the common distribution function. The default is 1.0e-6.
maxiter	the maximal number of iterations to perform before stopping when estimating the common distribution function. The default is 1000.
inf	value used in data for infinity. The default is Inf.

Details

Under the null hypothesis, the NPMLE of the common distribution function is computed by function ModifiedEMICM.

Censoring interval for each observation take the form $(L_i, R_i]$. For exact observations, $L_i = R_i$.

The estimated covariance of the test statistic depends on random resampling. It is normal that two runs of the test gLRT1 yield different test results.

The chi-square test used in gLRT1 has k - 1 degrees of freedom.

12

gLRT2

Value

The function returns an object containing the following components:

method	test procedure used
u	the test statistic
V	the estimated covariance of the test statistic
chisq	the chisquare test statistic
df	the degrees of freedom of the test
р	p-value of the test

Author(s)

Qiang Zhao and Jianguo Sun

References

Q. Zhao and J. Sun (2004), "Generalized Log-rank Test for Mixed-Censored Failure Time Data", Statistics in Medicine, 23: 1621-1629.

Q. Zhao (2012), "gLRT - A New R Package for Analyzing Interval-censored Survival Data", Interval-Censored Time-to-Event Data: Methods and Applications, CRC Press, 377-396.

See Also

gLRT, gLRT2, gLRT3, gLRT4, ScoreTest

Examples

data(cosmesis)
gLRT1(cosmesis, inf=100)

data(diabetes)
gLRT1(diabetes, M=20)

gLRT2

Conduct a generalized logrank test for interval-censored data

Description

The gLRT2 function conducts a k(>=2)-sample test for interval-censored survival data. The test is based on Sun, Zhao, and Zhao (2005). The null hypothesis is that all k survival functions of the failure time are the same, and the alternative hypothesis is that not all functions are the same.

Usage

gLRT2(A, k = 2, rho = 0, gamma = 0, EMstep = TRUE, ICMstep = TRUE, tol = 1e-06, maxiter = 1000, inf = Inf)

Arguments

A	an n by 3 data matrix with the censoring interval of the format $(L, R]$ in columns 1 & 2 and treatmentment indicator ranging from 0 to $k - 1$ in column 3.
k	number of treatments. The default is 2.
rho	non-negative parameter of the link function used for calculating the test statis- tics. The default is 0.
gamma	non-negative parameter of the link function used for calculating the test statis- tics. The default is 0.
EMstep	a boolean variable indicating whether to take an EM step in the iteration when estimating the common distribution function. The default is TRUE.
ICMstep	a boolean variable indicating whether to take an ICM step in the iteration when estimating the common distribution function. The default is TRUE.
tol	the maximal L_1 distance between successive estimates before stopping iteration when estimating the common stribution function. The default is 1.0e-6.
maxiter	the maximal number of iterations to perform before stopping when estimating the common distribution function. The default is 1000.
inf	value used in data for infinity. The default is Inf.

Details

Under the null hypothesis, the NPMLE of the common distribution function is computed by function ModifiedEMICM.

Censoring interval for each observation take the form $(L_i, R_i]$. No exact observations are allowed, i.e., $L_i < R_i$.

The chi-square test used in gLRT2 has k-1 degrees of freedom.

The link function used in gLRT2 is $\xi(x) = x log(x) x^{\rho} (1-x)^{\gamma}$.

Value

The function returns an object containing the following components:

method	test procedure used
u	the test statistic
v	the estimated covariance of the test statistic
chisq	the chisquare test statistic
df	the degrees of freedom of the test
р	p-value of the test

Author(s)

Qiang Zhao and Jianguo Sun

gLRT3

References

J. Sun, Q. Zhao, and X. Zhao (2005), "Generalized Log-rank Test for Interval-Censored Data", Scandinavian Journal of Statistics, 32: 45-57.

Q. Zhao (2012), "gLRT - A New R Package for Analyzing Interval-censored Survival Data", Interval-Censored Time-to-Event Data: Methods and Applications, CRC Press, 377-396.

See Also

gLRT, gLRT1, gLRT3, gLRT4, ScoreTest

Examples

```
data(cosmesis)
gLRT2(cosmesis, rho=0, gamma=1, inf=100)
```

```
gLRT3
```

Conduct a generalized logrank test for interval-censored data

Description

Function gLRT3 conducts a k(>=2)-sample test for interval-censored survival data. The test is based on Zhao, Zhao, Sun, and Kim (2008). The null hypothesis is that all *k*hel survival functions of the failure time are the same, and the alternative hypothesis is that not all functions are the same.

Usage

gLRT3(A, k = 2, rho = 0, gamma = 0, EMstep = TRUE, ICMstep = TRUE, tol = 1e-06, maxiter = 1000, inf = Inf)

Arguments

A	an n by 3 data matrix with the censoring interval of the format $(L, R]$ in columns 1 & 2 and treatmentment indicator ranging from 0 to $k - 1$ in column 3.
k	number of treatments. The default is 2.
rho	non-negative parameter of the link function used for calculating the test statis- tics. The default is 0.
gamma	non-negative parameter of the link function used for calculating the test statis- tics. The default is 0.
EMstep	a boolean variable indicating whether to take an EM step in the iteration when estimating the common distribution function. The default is TRUE.
ICMstep	a boolean variable indicating whether to take an ICM step in the iteration when estimating the common distribution function. The default is TRUE.
tol	the maximal L_1 distance between successive estimates before stopping iteration when estimating the common distribution function. The default is 1.0e-6.
maxiter	the maximal number of iterations to perform before stopping when estimating the common distribution function. The default is 1000.
inf	value used in data for infinity. The default is Inf.

Details

Under the null hypothesis, the NPMLE of the common distribution function is computed by function ModifiedEMICM.

Censoring interval for each observation take the form $(L_i, R_i]$. For exact observations, $L_i = R_i$.

The chi-square test in gLRT3 has either k or k - 1 degrees of freedom depending on the existence and proportion of exact observations in each treatment. See Zhao, Zhao, Sun, and Kim (2008) for more details.

The link function used in gLRT3 is $\xi(x) = x log(x) x^{\rho} (1-x)^{\gamma}$.

Value

The function returns an object containing the following components:

method	test procedure used
u	the test statistic
v	the estimated covariance of the test statistic
chisq	the chisquare test statistic
df	the degrees of freedom of the test
р	p-value of the test

Author(s)

Qiang Zhao and Jianguo Sun

References

X. Zhao, Q. Zhao, J. Sun, Q. and J. S. Kim (2008), "Generalized Log-rank Tests for Partly Interval-Censored Failure Time Data", Biometrical Journal, 50 (3): 375-385.

Q. Zhao (2012), "gLRT - A New R Package for Analyzing Interval-censored Survival Data", Interval-Censored Time-to-Event Data: Methods and Applications, CRC Press, 377-396.

See Also

gLRT, gLRT1, gLRT2, gLRT4, ScoreTest

Examples

```
data(cosmesis)
gLRT3(cosmesis, rho=1, inf=100)
```

data(diabetes) gLRT3(diabetes, gamma=0)

16

gLRT4

Description

Function gLRT4 conducts a k(=2)-sample test for interval-censored survival data. The test is based on Zhao, Duan, Zhao, and Sun (2013). The null hypothesis is that the two survival functions of the failure time are the same, and the alternative hypothesis is that the two functions are not the same.

Usage

gLRT4(A, k = 2, rho = 0, gamma = 0, EMstep = TRUE, ICMstep = TRUE, tol = 1e-06, maxiter = 1000, inf = Inf)

Arguments

A	an <i>n</i> by 3 data matrix with the censoring interval of the format $(L, R]$ in columns 1 & 2 and treatment indicator ranging from 0 to $k-1$ in column 3. No exact observations (i.e., $L = R$) are allowed.
k	number of treatments. Only $k = 2$ is allowed.
rho	non-negative parameter in $[0, 1]$ of the link function used for calculating the test statistics. It is the same as b in Zhao, Duan, Zhao, and Sun (2013). The default is 0.
gamma	non-negative parameter in $[0, 1]$ of the link function used for calculating the test statistics. It is the same as c in Zhao, Duan, Zhao, and Sun (2013). The default is 0.
EMstep	a boolean variable indicating whether to take an EM step in the iteration when estimating the common distribution function. The default is TRUE.
ICMstep	a boolean variable indicating whether to take an ICM step in the iteration when estimating the common distribution function. The default is TRUE.
tol	the maximal L_1 distance between successive estimates before stopping iteration when estimating the common distribution function. The default is 1.0e-6.
maxiter	the maximal number of iterations to perform before stopping when estimating the common distribution function. The default is 1000.
inf	value used in data for infinity. The default is Inf.

Details

The NPMLE of the distribution function for each treatment group is computed by function ModifiedEMICM.

The f-test in gLRT4 is based on an F distribution with degrees of freedom 1 and 1.

The link function used in gLRT4 is $\xi(x) = x log(x) x^{\rho} (1-x)^{\gamma} = x log(x) x^{b} (1-x)^{c}$.

Value

The function returns an object containing the following components:

method	test procedure used
u	the test statistic
v	NA is returned
fstat	the f-test statistic
df	the numerator and denominator degrees of freedom of the f-test, i.e., (1, 1)
р	p-value of the f-test

Author(s)

Qiang Zhao and Jianguo Sun

References

X. Zhao, R. Duan, Q. Zhao, and J. Sun (2013), "A New Class of Generalized Log Rank Tests for Interval-censored Failure Time Data", Computational Statistics and Data Analysis. 60: 123-131.

See Also

gLRT, gLRT1, gLRT2, gLRT3, ScoreTest

Examples

```
data(cmv)
cmvBlood = cmv[,c(2,3,6)]
cmvUrine = cmv[, 4:6]
gLRT4(cmvBlood)
gLRT4(cmvUrine, rho=1, gamma=1)
```

Linkfunc

A link function used in tests gLRT2, gLRT3, and gLRT4

Description

A link function over (0, 1) used in gLRT2, gLRT3, and gLRT4, which is a function of the original link function $\xi(x) = x \log(x) x^{\rho} (1-x)^{\gamma}$.

Usage

Linkfunc(x, rho = 0, gamma = 0)

LinkfuncDir

Arguments

х	a value between 0 and 1
rho	a non-negative parameter in $[0, 1]$
gamma	a non-negative parameter in $[0, 1]$

Details

This function $\eta(x) = 1 - \xi(1 - x)$.

Value

Function value is returned.

Note

This is not to be called by the user.

Author(s)

Qiang Zhao and Jianguo Sun

References

X. Zhao, Q. Zhao, J. Sun, Q. and J. S. Kim (2008), "Generalized Log-rank Tests for Partly Interval-Censored Failure Time Data", Biometrical Journal, 50 (3): 375-385.

See Also

LinkfuncDir

Examples

Linkfunc(0.2, rho=0, gamma=1)

LinkfuncDir Direvative of the link function

Description

Direvative of the link function $\eta(x), \eta'(x)$, used in gLRT2, gLRT3, and gLRT4,.

Usage

LinkfuncDir(x, rho = 0, gamma = 0)

Arguments

х	a value between 0 and 1
rho	a non-negative parameter in $[0, 1]$
gamma	a non-negative parameter in $\left[0,1\right]$

Value

The first derivative of the function.

Note

This is not to be called by the user.

Author(s)

Qiang Zhao and Jianguo Sun

References

X. Zhao, Q. Zhao, J. Sun, Q. and J. S. Kim (2008), "Generalized Log-rank Tests for Partly Interval-Censored Failure Time Data", Biometrical Journal, 50 (3): 375-385.

See Also

Linkfunc

Examples

LinkfuncDir(0.2, rho=0, gamma=1)

ModifiedEMICM Estimate the distribution function using the hybrid EM-ICM approach

Description

A modified version of function EMICM in package Icens by incorporating function Aintmap in package interval. By defult, the function provides an NPMLE for the distribution function of the survival time.

Usage

```
ModifiedEMICM(A, EMstep = TRUE, ICMstep = TRUE, keepiter = FALSE,
tol = 1e-06, maxiter = 1000)
```

ModifiedEMICM

Arguments

A	an n by 2 matrix with containing the end points of censoring intervals of the format (Li, Ri].
EMstep	a boolean variable indicating whether to take an EM step in the iteration when estimating the common distribution function. The default is TRUE.
ICMstep	a boolean variable indicating whether to take an ICM step in the iteration when estimating the common distribution function. The default is TRUE.
keepiter	TRUE/FALSE determining whether to keep the iteration states.
tol	the maximal L1 distance between successive estimates before stopping iteration when estimating the common distribution function. The default is 1.0e-6.
maxiter	the maximal number of iterations to perform before stopping when estimating the common distribution function. The default is 1000.

Details

After incorporating function Aintmap, function ModifiedEMICM often produces intmap with smaller size than function EMICM, especially when exact observations ($L_i = R_i$) exist. In addition, object ppairs is returned for later use in computing the test statistics in functions gLRT1, gLRT2, gLRT3, gLRT4, and ScoreTest. Also, a bug was identified in using EMICM when ICMstep=F is specified. The problem is fixed by calling ModifiedEMICMmac, a modified version of function EMICMmac from package Icens.

Either EM, ICM, or both steps can be taken in the estimation. When ICMstep = FALSE, the function computes a self-consistent estimate, the same results as obtained from function icfit in package interval.

Value

An object containing the following components:

pf	Estimated probabilities
sigma	NPMLE/self-consistant estimate of the distribution function
weights	the diagonal of the likelihood functions's second derivative
lastchange	a vector of differences between the last two iterations
numiter	number of iterations performed
iter	only present if keepiter is true; state of sigma during the iteration
intmap	the real representation associated with the probabilities reported in pf
startend	the indices for L_i and R_i identifying the end points in intmap where a subject is at risk.

Author(s)

Qiang Zhao and Jianguo Sun

References

Function EMICM by Alain Vandal and Robert Gentleman .

J. A. Wellner and Y. Zhan (1997), "A hybrid algorithm for computation of the nonparametric maximum likelihood estimator from censored data", JASA.

See Also

Aintmap, ModifiedEMICMmac

Examples

```
data(diabetes)
ModifiedEMICM(diabetes[,1:2])
```

data(cosmesis)
ModifiedEMICM(cosmesis[,1:2])

ModifiedEMICMmac An interval function in package "Icens"

Description

A modified version of EMICMmac in package Icens to avoid the error when calling function EMICM when specifying ICMstep = FALSE. The error is caused by changing the type of an undeclared vector weights.

Note

It is used in ModifiedEMICM and not to be called by the user.

Author(s)

Qiang Zhao and Jianguo Sun

See Also

ModifiedEMICM

22

PMGA

Description

For isotonization problems some increase in speed and decrease in complexity can be achieved through the use of the pool monotone groups algorithm of Y.L. Zhang and M.A. Newton (1997). It isotonizes a weighted and ordered set of values. This function is borrowed from package Icens.

Usage

PMGA(est, ww=rep(1, length(est)))

Arguments

est	The vector of values, in the appropriate order.
WW	The weight vector.

Details

To be supplied at some later date.

Value

An Object containing the following components:

est	The isotonized estimates.
WW	The weight associated with the isotonized estimates.
poolnum	The number of values pooled in the current estimate.
passes	The number of passes which were required to isotonize the list.

Note

It is used in ModifiedEMICMmac and not to be called by the user.

Author(s)

Alain Vandal and Robert Gentleman

References

Y. L. Zhang and M. A. Newton (1997), http://www.stat.wisc.edu/~newton/newton.html.

See Also

ModifiedEMICMmac

rescaleP

Description

An internal function borrowed from Icens.

Note

It is not to be called by the user.

Author(s)

Alain Vandal and Robert Gentleman

See Also

Bisect

ScoreStat

Compute the test statistic of the score test

Description

The function computes the test statistic of the score test proposed by Finkelstein (1986).

Note

It is not to be called by the user.

Author(s)

Qiang Zhao and Jianguo Sun

References

Finkelstein, DM (1986), "A Proportional Hazards Model for Interval-censored Failure Time Data", Biometrics, 42: 845-854.

See Also

ScoreTest

ScoreTest

Description

The ScoreTest function conducts a k(>=2)-sample test for interval-censored survival data. The test is based on Finkelstein (1986). The null hypothesis is that all k survival functions of the failure time are the same, and the alternative hypothesis is that not all functions are the same. It is not referred as gLRT4 as in Zhao (2012).

Usage

```
ScoreTest(A, k = 2, EMstep = TRUE, ICMstep = TRUE, tol = 1e-06,
maxiter = 1000, inf = Inf)
```

Arguments

A	an n by 3 data matrix with the censoring interval of the format $(L, R]$ in columns 1 & 2 and treatmentment indicator ranging from 0 to $k - 1$ in column 3.
k	number of treatments. The default is 2.
EMstep	a boolean variable indicating whether to take an EM step in the iteration when estimating the common distribution function. The default is TRUE.
ICMstep	a boolean variable indicating whether to take an ICM step in the iteration when estimating the common distribution function. The default is TRUE.
tol	the maximal L_1 distance between successive estimates before stopping iteration when estimating the common distribution function. The default is 1.0e-6.
maxiter	the maximal number of iterations to perform before stopping when estimating the common distribution function. The default is 1000.
inf	value used in data for infinity. The default is Inf.

Details

Under the null hypothesis that k survival functions are the same, the NPMLE of the common survival function is computed by function ModifiedEMICM.

The chi-square test in ScoreTest has k-1 degrees of freedom.

Value

The function returns an object containing the following components:

method	test procedure used
u	the test statistic
V	the estimated covariance of the test statistic
chisq	the chisquare test statistic
df	the degrees of freedom of the test
р	p-value of the test

Author(s)

Qiang Zhao and Jianguo Sun

References

Finkelstein, DM (1986), "A Proportional Hazards Model for Interval-censored Failure Time Data", Biometrics, 42: 845-854.

Q. Zhao (2012), "gLRT - A New R Package for Analyzing Interval-censored Survival Data", Interval-Censored Time-to-Event Data: Methods and Applications, CRC Press, 377-396.

See Also

ModifiedEMICM, gLRT, gLRT1, gLRT2, gLRT3, gLRT4

Examples

```
data(cosmesis)
ScoreTest(cosmesis, inf=100)
```

data(diabetes)
ScoreTest(diabetes)

StartEnd

Compute the indices for the end points of censoring intervals

Description

The function computes the indices for the end points of censoring intervals over the intmaps when estimating a survival function when called in function ModifiedEMICM. It is also used in Teststat4 of gLRT4.

Note

It is not to be called by the user.

Author(s)

Qiang Zhao and Jianguo Sun

See Also

ModifiedEMICM, Teststat4

Teststat1

Description

The function computes the test statistics of the test proposed by Zhao and Sun (2004).

Note

It is not to be called by the user.

Author(s)

Qiang Zhao and Jianguo Sun

References

Q. Zhao and J. Sun (2004), "Generalized Log-rank Test for Mixed-Censored Failure Time Data", Statistics in Medicine, 23: 1621-1629.

See Also

gLRT1

Teststat2 Compute the test statistic in test gLRT2

Description

The function computes the test statistics of the test proposed by Sun, Zhao, and Zhao (2005).

Note

It is not to be called by the user.

Author(s)

Qiang Zhao and Jianguo Sun

References

J. Sun, Q. Zhao, and X. Zhao (2005), "Generalized Log-rank Test for Interval-Censored Data", Scandinavian Journal of Statistics, 32: 45-57.

See Also

gLRT2

Teststat3

Description

The function computes the test statistics of the test proposed by Zhao, Zhao, Sun, and Kim (2008).

Note

It is not to be called by the user.

Author(s)

Qiang Zhao and Jianguo Sun

References

X. Zhao, Q. Zhao, J. Sun, Q. and J. S. Kim (2008), "Generalized Log-rank Tests for Partly Interval-Censored Failure Time Data", Biometrical Journal, 50 (3): 375-385.

See Also

gLRT3

Teststat4 Compute the test statistic in test gLRT4

Description

The function computes the test statistics of the test proposed by Zhao, Duan, Zhao, and Sun (2013).

Note

It is not to be called by the user.

Author(s)

Qiang Zhao and Jianguo Sun

References

X. Zhao, R. Duan, Q. Zhao, and J. Sun (2013), "A New Class of Generalized Log Rank Tests for Interval-censored Failure Time Data", Computational Statistics and Data Analysis. 60: 123-131.

See Also

gLRT4

Var1

Description

The function computes the estimate of the covariance of test statistics of the test proposed by Zhao and Sun (2004).

Note

It is not to be called by the user.

Author(s)

Qiang Zhao and Jianguo Sun

References

Q. Zhao and J. Sun (2004), "Generalized Log-rank Test for Mixed-Censored Failure Time Data", Statistics in Medicine, 23: 1621-1629.

See Also

gLRT1

Var2

Compute the estimate of the covariance of the test statistic in test gLRT2

Description

The function computes the estimate of the covariance of the test statistics of the test proposed by Sun, Zhao, and Zhao (2005).

Note

It is not to be called by the user.

Author(s)

Qiang Zhao and Jianguo Sun

References

J. Sun, Q. Zhao, and X. Zhao (2005), "Generalized Log-rank Test for Interval-Censored Data", Scandinavian Journal of Statistics, 32: 45-57.

See Also

gLRT2

Compute the estimate of the covariance of the test statistic in test gLRT3

Description

Var3

The function computes the estimate of the covariance of the test statistics of the test proposed by Zhao, Zhao, Sun, and Kim (2008).

Note

It is not to be called by the user.

Author(s)

Qiang Zhao and Jianguo Sun

References

X. Zhao, Q. Zhao, J. Sun, Q. and J. S. Kim (2008), "Generalized Log-rank Tests for Partly Interval-Censored Failure Time Data", Biometrical Journal, 50 (3): 375-385.

See Also

gLRT3

VarScoreStat Compute the estimate of the covariance of the test statistic in the score test

Description

The function computes the estimate of the covariance of the test statistic of the score test proposed by Finkelstein (1986).

Note

It is not to be called by the user.

Author(s)

Qiang Zhao and Jianguo Sun

30

VarScoreStat

References

Finkelstein, DM (1986), "A Proportional Hazards Model for Interval-censored Failure Time Data", Biometrics, 42: 845-854.

See Also

ScoreTest

Index

Aintmap, 3, 20, 22 AlphaCross, 4 Bisect, 5, 24 CensorType, 5 Chisqstat3,6 cmv, 7 cosmesis, 8diabetes, 8 gLRT, 2, 3, 9, 13, 15, 16, 18, 26 glrt (glrt-package), 2 glrt-package, 2 gLRT1, 2, 3, 5, 9–11, 12, 15, 16, 18, 21, 26, 27, 29 gLRT2, 2, 3, 5, 9–11, 13, 13, 16, 18, 19, 21, 26, 27, 30 gLRT3, 2, 3, 5, 6, 9–11, 13, 15, 15, 18, 19, 21, 26, 28, 30 gLRT4, 2, 3, 5, 9–11, 13, 15, 16, 17, 18, 19, 21, 26, 28 Linkfunc, 18, 20 LinkfuncDir, 19, 19 ModifiedEMICM, 2-4, 10, 12, 14, 16, 17, 20, 22, 25, 26 ModifiedEMICMmac, 5, 21, 22, 22, 23 PMGA, 23 rescaleP, 24 ScoreStat, 24 ScoreTest, 2, 3, 9-11, 13, 15, 16, 18, 21, 24, 25, 31 StartEnd, 26 Teststat1, 27

Teststat2, 27 Teststat3, 28 Teststat4, *4*, 26, 28 Var1, 29 Var2, 29 Var3, 30 VarScoreStat, 30