Package ‘ljr’

October 13, 2022

Version 1.4-0
Date 2016-4-30
Title Logistic Joinpoint Regression
Author Michal Czajkowski, Ryan Gill, Greg Rempala
Maintainer Ryan Gill <ryan.gill@louisville.edu>
Description Fits and tests logistic joinpoint models.
License GPL (>= 2)
NeedsCompilation yes
Repository CRAN
Date/Publication 2016-05-01 18:55:59

R topics documented:

  kcm ................................................................. 2
  ljr0 ................................................................. 2
  ljr01 ............................................................... 3
  ljr1 ................................................................. 5
  ljr11 ................................................................. 6
  ljrb ................................................................. 7
  ljrf ................................................................. 8
  ljrjk ................................................................. 9
  ljrk ................................................................. 10
  ljrkk ............................................................... 12

Index 14
**kcm**  
*Kentucky yearly cancer mortality from 1999-2005.*

**Description**

This table gives the yearly mortality counts due to neoplasms (ICD 10 codes C00-D48) and population sizes for Kentucky from 1999-2005. For more information, see http://wonder.cdc.gov/wonder/help/cmf.html.

**Usage**

data(kcm)

**Format**

A 7 by 3 data frame.

**Source**


---

**ljr0**  
*MLE with 0 joinpoints*

**Description**

Determines the maximum likelihood estimate of model coefficients in the logistic joinpoint regression model with no joinpoints.

**Usage**

ljr0(y,n,tm,X,ofst)

**Arguments**

- **y**  
  the vector of Binomial responses.
- **n**  
  the vector of sizes for the Binomial random variables.
- **tm**  
  the vector of observation times.
- **X**  
  a design matrix containing other covariates.
- **ofst**  
  a vector of known offsets for the logit of the response.
Details

The re-weighted log-likelihood is the log-likelihood divided by the largest component of \( n \).

Value

- **Coef**: A table of coefficient estimates.
- **wlik**: The maximum value of the re-weighted log-likelihood.

Author(s)

The authors are Michal Czajkowski, Ryan Gill, and Greg Rempala. The software is maintained by Ryan Gill <rsgill01@louisville.edu>.

References


See Also

- `ljr01`, `ljrb`, `ljrf`

Examples

```r
data(kcm)
attach(kcm)
ljr0(Count,Population,Year+.5)
```

---

**ljr01**

*Perform test of 0 vs 1 joinpoints.*

Description

This function tests the null hypothesis of 0 joinpoints versus the alternative of one joinpoint based on the likelihood ratio test statistic. The p-value is determined by a Monte Carlo method.

Usage

```r
ljr01(y,n,tm,X,ofst,R=1000,alpha=.05)
```
Arguments

- **y**: the vector of Binomial responses.
- **n**: the vector of sizes for the Binomial random variables.
- **tm**: the vector of ordered observation times.
- **X**: a design matrix containing other covariates.
- **ofst**: a vector of known offsets for the logit of the response.
- **R**: number of Monte Carlo simulations.
- **alpha**: significance level of the test.

Details

The re-weighted log-likelihood is the log-likelihood divided by the largest component of n.

Value

- **pval**: The estimate of the p-value via simulation.
- **Coeff**: A table of coefficient estimates.
- **Joinpoint**: The estimates of the joinpoint, if it is significant.
- **wlik**: The maximum value of the re-weighted log-likelihood.

Author(s)

The authors are Michal Czajkowski, Ryan Gill, and Greg Rempala. The software is maintained by Ryan Gill <rsgill01@louisville.edu>.

References


See Also

- **ljr0**, **ljr1**

Examples

```r
data(kcm)
attach(kcm)
set.seed(12345)
## Not run: ljr01(Count, Population, Year+.5, R=20)
```
Description

Determines the maximum likelihood estimates of model coefficients in the logistic joinpoint regression model with one joinpoint.

Usage

ljr1(y,n,tm,X,ofst,summ=TRUE)

Arguments

y       the vector of Binomial responses.
n       the vector of sizes for the Binomial random variables.
tm       the vector of ordered observation times.
X       a design matrix containing other covariates.
ofst       a vector of known offsets for the logit of the response.
summ       a boolean indicator of whether summary tables should be returned.

Details

The re-weighted log-likelihood is the log-likelihood divided by the largest component of n.

Value

Coef       A table of coefficient estimates.
Joinpoint       The estimate of the joinpoint.
wlik       The maximum value of the re-weighted log-likelihood.

Author(s)

The authors are Michal Czajkowski, Ryan Gill, and Greg Rempala. The software is maintained by Ryan Gill <rsgill01@louisville.edu>.

References


See Also

ljr01,ljrb,ljrf
Examples
data(kcm)
attach(kcm)
ljr1(Count,Population,Year+.5)

ljr11
Test coefficients conditioned on \(K=1\) joinpoint.

Description
This function performs the likelihood ratio tests to find p-values in testing the significance of each of
the coefficients as well as the intercept and ordered observation times. The p-values are determined
by a Monte Carlo method.

Usage
ljr11(y,n,tm,X,ofst,R=1000)

Arguments
\(y\) the vector of Binomial responses.
\(n\) the vector of sizes for the Binomial random variables.
\(tm\) the vector of ordered observation times.
\(X\) a design matrix containing other covariates.
ofst a vector of known offsets for the logit of the response.
\(R\) number of Monte Carlo simulations.

Details
The re-weighted log-likelihood is the log-likelihood divided by the largest component of \(n\).

Value
\(pvals\) The estimates of the p-values via simulation.

Author(s)
The authors are Michal Czajkowski, Ryan Gill, and Greg Rempala. The software is maintained by
Ryan Gill <rsgill01@louisville.edu>.

References
with applications to analyzing cohort mortality patterns. *Statistics in Medicine* 27, 1508-1526.
**ljrb**

**See Also**

`ljr1`

**Examples**

```r
data(kcm)
attach(kcm)
set.seed(12345)
## Not run: ljr11(Count,Population,Year+.5,R=20)
```

**ljrb**  
*Perform backward joinpoint selection algorithm with upper bound K.*

**Description**

This function performs the backward joinpoint selection algorithm with K maximum possible number of joinpoints based on the likelihood ratio test statistic. The p-value is determined by a Monte Carlo method.

**Usage**

```r
ljrb(K,y,n,tm,X,ofst,R=1000,alpha=.05)
```

**Arguments**

- `K`  
  the pre-specified maximum possible number of joinpoints
- `y`  
  the vector of Binomial responses.
- `n`  
  the vector of sizes for the Binomial random variables.
- `tm`  
  the vector of ordered observation times.
- `X`  
  a design matrix containing other covariates.
- `ofst`  
  a vector of known offsets for the logit of the response.
- `R`  
  number of Monte Carlo simulations.
- `alpha`  
  significance level of the test.

**Details**

The re-weighted log-likelihood is the log-likelihood divided by the largest component of n.

**Value**

- `pvals`  
  The estimates of the p-values via simulation.
- `Coeff`  
  A table of coefficient estimates.
- `Joinpoints`  
  The estimates of the joinpoint, if it is significant.
- `wlik`  
  The maximum value of the re-weighted log-likelihood.
Author(s)

The authors are Michal Czajkowski, Ryan Gill, and Greg Rempala. The software is maintained by Ryan Gill <rsgill01@louisville.edu>.

References


See Also

ljrk, ljrf

Examples

data(kcm)
attach(kcm)
set.seed(12345)
## Not run: ljrb(1, Count, Population, Year+.5, R=20)

ljrf

Perform forward joinpoint selection algorithm with unlimited upper bound.

Description

This function performs the full forward joinpoint selection algorithm based on the likelihood ratio test statistic. The p-value is determined by a Monte Carlo method.

Usage

ljrf(y, n, tm, X, ofst, R=1000, alpha=.05)

Arguments

y the vector of Binomial responses.

n the vector of sizes for the Binomial random variables.

tm the vector of ordered observation times.

X a design matrix containing other covariates.

ofst a vector of known offsets for the logit of the response.

R number of Monte Carlo simulations.

alpha significance level of the test.

Details

The re-weighted log-likelihood is the log-likelihood divided by the largest component of n.
**Value**

- **pvals**: The estimates of the p-values via simulation.
- **Coef**: A table of coefficient estimates.
- **Joinpoints**: The estimates of the joinpoint, if it is significant.
- **wlik**: The maximum value of the re-weighted log-likelihood.

**Author(s)**

The authors are Michal Czajkowski, Ryan Gill, and Greg Rempala. The software is maintained by Ryan Gill <rsgill01@louisville.edu>.

**References**


**See Also**

- `ljrk`, `ljrb`

**Examples**

```r
data(kcm)
attach(kcm)
set.seed(12345)
## Not run: ljrf(Count,Population,Year+.5,R=20)
```

---

**ljrjk**

*Perform test of j vs k joinpoints.*

**Description**

This function tests the null hypothesis of j joinpoint(s) versus the alternative of k joinpoint(s) based on the likelihood ratio test statistic. The p-value is determined by a Monte Carlo method.

**Usage**

```
ljrjk(j,k,y,n,tm,X,ofst,R=1000,alpha=.05)
```

**Arguments**

- **j, k**: pre-specified number of joinpoints in the null and alternative hypotheses (the smaller is used for the null).
- **y**: the vector of Binomial responses.
- **n**: the vector of sizes for the Binomial random variables.
- **tm**: the vector of ordered observation times.
X a design matrix containing other covariates.
ofst a vector of known offsets for the logit of the response.
R number of Monte Carlo simulations.
alpha significance level of the test.

Details
The re-weighted log-likelihood is the log-likelihood divided by the largest component of n.

Value
pval The estimate of the p-value via simulation.
Coef A table of coefficient estimates.
Joinpoint The estimates of the joinpoint, if it is significant.
wlik The maximum value of the re-weighted log-likelihood.

Author(s)
The authors are Michal Czajkowski, Ryan Gill, and Greg Rempala. The software is maintained by Ryan Gill <rsgill01@louisville.edu>.

References

See Also
ljrk

Examples
data(kcm)
attach(kcm)
set.seed(12345)
## Not run: ljrjk(0,1,Count,Population,Year+.5,R=20)

ljrk MLE with k joinpoints

Description
Determines the maximum likelihood estimates of model coefficients in the logistic joinpoint regression model with k joinpoints.
Usage

\texttt{ljrk(k,y,n,tm,X,ofst)}

Arguments

- \texttt{k} \hspace{0.5cm} \text{the pre-specified number of joinpoints (with unknown locations).}
- \texttt{y} \hspace{0.5cm} \text{the vector of Binomial responses.}
- \texttt{n} \hspace{0.5cm} \text{the vector of sizes for the Binomial random variables.}
- \texttt{tm} \hspace{0.5cm} \text{the vector of ordered observation times.}
- \texttt{X} \hspace{0.5cm} \text{a design matrix containing other covariates.}
- \texttt{ofst} \hspace{0.5cm} \text{a vector of known offsets for the logit of the response.}

Details

The re-weighted log-likelihood is the log-likelihood divided by the largest component of \( n \).

Value

\begin{itemize}
  \item \texttt{Coef} \hspace{0.5cm} \text{A table of coefficient estimates.}
  \item \texttt{Joinpoints} \hspace{0.5cm} \text{The estimates of the joinpoints.}
  \item \texttt{wlik} \hspace{0.5cm} \text{The maximum value of the re-weighted log-likelihood.}
\end{itemize}

Author(s)

The authors are Michal Czajkowski, Ryan Gill, and Greg Rempala. The software is maintained by Ryan Gill <rsgill01@louisville.edu>.

References


See Also

\texttt{ljrb, ljrf}

Examples

\begin{verbatim}
data(kcm)
attach(kcm)
ljrk(1, Count, Population, Year+.5)
\end{verbatim}
Description

This function performs the likelihood ratio tests to find p-values in testing the significance of each of the coefficients as well as the intercept and ordered observation times. The p-values are determined by a Monte Carlo method.

Usage

\[ \text{ljrkk}(k, y, n, \text{tm}, X, \text{ofst}, R=1000) \]

Arguments

- \( k \) the pre-specified number of joinpoints (with unknown locations).
- \( y \) the vector of Binomial responses.
- \( n \) the vector of sizes for the Binomial random variables.
- \( \text{tm} \) the vector of ordered observation times.
- \( X \) a design matrix containing other covariates.
- \( \text{ofst} \) a vector of known offsets for the logit of the response.
- \( R \) number of Monte Carlo simulations.

Details

The re-weighted log-likelihood is the log-likelihood divided by the largest component of \( n \).

Value

- \( pvals \) The estimates of the p-values via simulation.

Author(s)

The authors are Michal Czajkowski, Ryan Gill, and Greg Rempala. The software is maintained by Ryan Gill <rsgill01@louisville.edu>.

References


See Also

\[ \text{ljrk} \]
Examples

data(kcm)
attach(kcm)
set.seed(12345)
## Not run: ljrkk(1,Count,Population,Year+.5,R=20)
Index

* datasets
  kcm, 2
* nonlinear
  ljr0, 2
  ljr01, 3
  ljr1, 5
  ljr11, 6
  ljrb, 7
  ljrf, 8
  ljrjk, 9
  ljrk, 10
  ljrkk, 12

kcm, 2

ljr0, 2, 4
ljr01, 3, 3, 5
ljr1, 4, 5, 7
ljr11, 6
ljrb, 3, 5, 7, 9, 11
ljrf, 3, 5, 8, 8, 11
ljrjk, 9
ljrk, 8–10, 10, 12
ljrkk, 12