Package ‘ljr’

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Title Logistic Joinpoint Regression
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Description Fits and tests logistic joinpoint models.
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**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**


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

Value

<table>
<thead>
<tr>
<th>Coef</th>
<th>A table of coefficient estimates.</th>
</tr>
</thead>
<tbody>
<tr>
<td>wlik</td>
<td>The maximum value of the re-weighted log-likelihood.</td>
</tr>
</tbody>
</table>

Author(s)

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

References


See Also

ljr01,ljrb,ljrf

Examples

data(kcm)
attach(kcm)
ljr01(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

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

data(kcm)
attach(kcm)
set.seed(12345)
## Not run: ljr01(Count, Population, Year+.5, R=20)
\textit{ljr1} \quad \textit{MLE with 1 joinpoint}

\textbf{Description}

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

\textbf{Usage}

\begin{verbatim}
\texttt{ljr1(y,n,tm,X,ofst,summ=TRUE)}
\end{verbatim}

\textbf{Arguments}

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

\textbf{Details}

The re-weighted log-likelihood is the log-likelihood divided by the largest component of \texttt{n}.

\textbf{Value}

- \texttt{Coeff} \quad A table of coefficient estimates.
- \texttt{Joinpoint} \quad The estimate of the joinpoint.
- \texttt{wlik} \quad The maximum value of the re-weighted log-likelihood.

\textbf{Author(s)}

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

\textbf{References}


\textbf{See Also}

\texttt{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

ljrb

See Also

ljr1

Examples

data(kcm)
attach(kcm)
set.seed(12345)
## Not run: ljr1(Count,Population,Year+.5,R=20)

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.
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.

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

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

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.
ljrjk

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

```r
ljrjk(j, k, y, n, tm, X, ofst, R=1000, alpha=0.05)
```

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.
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 <rstgill01@louisville.edu>.

References


See Also

- **ljrk**

Examples

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

---

**Description**

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

ljrk(k,y,n,tm,X,ofst)

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.
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.

Details

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

Value

Coef A table of coefficient estimates.
Joinpoints The estimates of the joinpoints.
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

ljrb,ljrf

Examples

data(kcm)
attach(kcm)
ljrk(1,Count,Population,Year+.5)
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

`ljrkk(k, y, n, tm, X, 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.
- `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 `<rsgill101@louisville.edu>`.

References


See Also

`ljrk`
Examples

data(kcm)
attach(kcm)
set.seed(12345)

## Not run: ljrkk(1,Count,Population,Year+.5,R=20)
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