Package ‘ljr’

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Title Logistic Joinpoint Regression

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Description Fits and tests logistic joinpoint models.

License GPL (>= 2)

NeedsCompilation yes

Repository CRAN

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Contents

`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

Centers for Disease Control and Prevention, National Center for Health Statistics. Compressed Mortality File 1999-2005. CDC WONDER On-line Database, compiled from Compressed Mortality File 1999-2005 Series 20 No. 2K, 2008. Accessed at http://wonder.cdc.gov/cmf-icd10.html on May 5, 2008.

`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

Czajkowski, M., Gill, R. and Rempala, G. (2008). Model selection in logistic joinpoint regression with applications to analyzing cohort mortality patterns. *Statistics in Medicine* 27, 1508-1526.

See Also

`ljr01`,`ljrb`,`ljrf`

Examples

```
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

```
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.
`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

Czajkowski, M., Gill, R. and Rempala, G. (2008). Model selection in logistic joinpoint regression with applications to analyzing cohort mortality patterns. *Statistics in Medicine* 27, 1508-1526.

See Also

`ljr0`,`ljr1`

Examples

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

`ljr1` *MLE with 1 joinpoint*

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

Czajkowski, M., Gill, R. and Rempala, G. (2008). Model selection in logistic joinpoint regression with applications to analyzing cohort mortality patterns. *Statistics in Medicine* 27, 1508-1526.

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

Czajkowski, M., Gill, R. and Rempala, G. (2008). Model selection in logistic joinpoint regression with applications to analyzing cohort mortality patterns. *Statistics in Medicine* 27, 1508-1526.

See Also

`ljr1`

Examples

```
 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

```
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.

Author(s)

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

References

Czajkowski, M., Gill, R. and Rempala, G. (2008). Model selection in logistic joinpoint regression with applications to analyzing cohort mortality patterns. *Statistics in Medicine* 27, 1508-1526.

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

Czajkowski, M., Gill, R. and Rempala, G. (2008). Model selection in logistic joinpoint regression with applications to analyzing cohort mortality patterns. *Statistics in Medicine* 27, 1508-1526.

See Also

`ljrk`, `ljrb`

Examples

```
 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 hpyotheses (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

Czajkowski, M., Gill, R. and Rempala, G. (2008). Model selection in logistic joinpoint regression with applications to analyzing cohort mortality patterns. *Statistics in Medicine* 27, 1508-1526.

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

```
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

Czajkowski, M., Gill, R. and Rempala, G. (2008). Model selection in logistic joinpoint regression with applications to analyzing cohort mortality patterns. *Statistics in Medicine* 27, 1508-1526.

See Also

`ljrb`,`ljrf`

Examples

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

`ljrkk` *Test coefficients conditioned on K=k 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

```
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 `<rsgill01@louisville.edu>`.

References

Czajkowski, M., Gill, R. and Rempala, G. (2008). Model selection in logistic joinpoint regression with applications to analyzing cohort mortality patterns. *Statistics in Medicine* 27, 1508-1526.

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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