

Package: ljr (via r-universe)

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Title Logistic Joinpoint Regression

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Description Fits and tests logistic joinpoint models.

License GPL (>= 2)

NeedsCompilation yes

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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/cm.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/cm.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 | <i>MLE with 1 joinpoint</i> |
|------|-----------------------------|

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 <rgsill01@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 | <i>Perform backward joinpoint selection algorithm with upper bound K.</i> |
|------|---|

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: ljr(1,Count,Population,Year+.5,R=20)
```

| | |
|------|--|
| ljrf | <i>Perform forward joinpoint selection algorithm with unlimited upper bound.</i> |
|------|--|

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: ljjrf(Count,Population,Year+.5,R=20)
```

| | |
|-------|---|
| ljjrk | <i>Perform test of j vs k joinpoints.</i> |
|-------|---|

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

```
ljjrk(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

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: ljrk(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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