

# 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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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>
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**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.
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**Author(s)**

The authors are Michal Czajkowski, Ryan Gill, and Greg Rempala. The software is maintained by Ryan Gill <rgill01@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: ljrjk(Count,Population,Year+.5,R=20)
```

---

ljrjk	<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**

```
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

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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