

Joinpoint regression with R

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Contents

1	Introduction	1
2	Package installation	1
3	Data analysis	2
3.1	Data visualization	2
3.2	Simple trend analysis	3
4	Joinpoint analysis	5
4.1	Model for a given number of joinpoints	5
4.2	Model selection using LRT	6
4.3	Automatic method of model selection	7
5	References	9
6	Session information	9

1 Introduction

Objectives

- Understand the concept of Joinpoint regression
- Learn how to perform Joinpoint regression with R
- Perform data analyses where the scientific question is to determine changes in temporal trends (incidence or mortality rates)

2 Package installation

Package can be installed from CRAN

```
install.packages("ljr")
```

After that it is loaded as usual

```
library("ljr")
```

It contains the following functions:

```
ls(2)
## [1] "ljr0" "ljr01" "ljr1" "ljr11" "ljrb" "ljrf" "ljrjk" "ljrkk"
```

- *kcm*: Kentucky yearly cancer mortality from 1999-2005
- *ljr0*: MLE with 0 joinpoints
- *ljr01*: Perform test of 0 vs 1 joinpoints}
- *ljr1*: MLE with 1 joinpoint}
- *ljr11*: Test coefficients conditioned on K=1 joinpoint}

- *ljrb*: Perform backward joinpoint selection algorithm with upper bound K }
- *ljrf*: Perform forward joinpoint selection algorithm with unlimited upper bound
- *ljrk*: Perform test of j vs k joinpoints
- *ljrk*: MLE with k joinpoints}
- *ljrk*: Test coefficients conditioned on $K=k$ joinpoint}

3 Data analysis

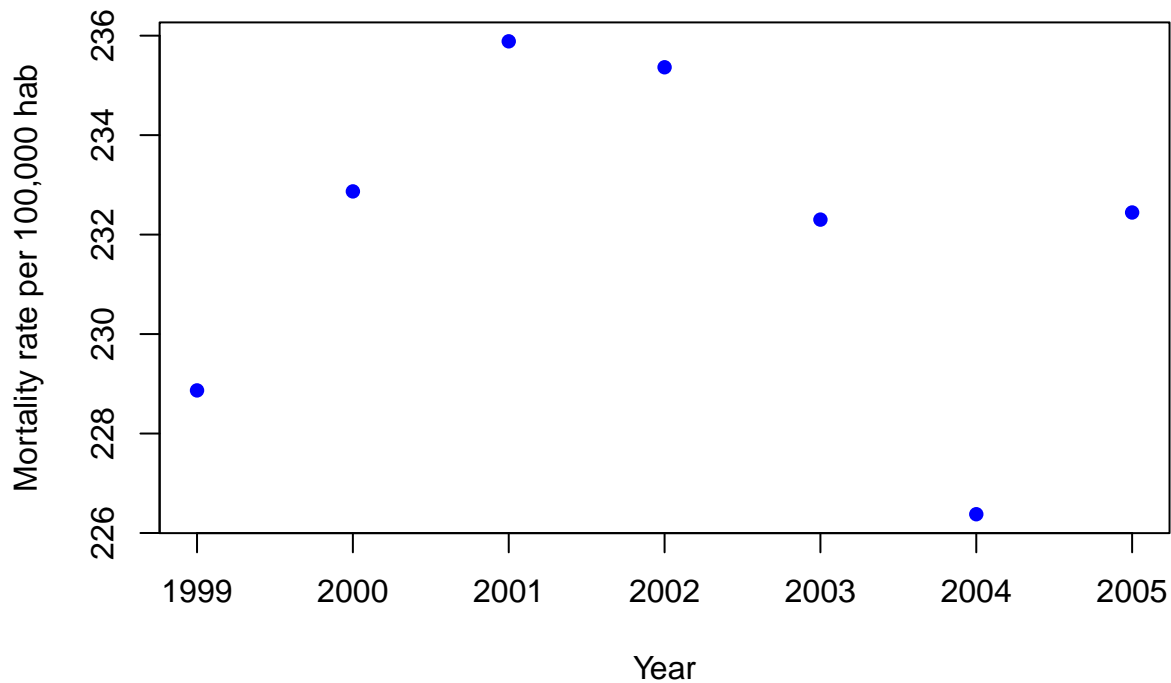
Let us use data available at the package

```
data(kcm)
head(kcm)
##   Year Count Population
## 1 1999  9196   4018053
## 2 2000  9412   4041769
## 3 2001  9595   4067643
## 4 2002  9624   4088977
## 5 2003  9558   4114489
## 6 2004  9373   4140427
```

3.1 Data visualization

As in any other statistical data analysis, first, let us have a look at the data

```
kcm$rate <- (kcm$Count/kcm$Population)*100000
plot(kcm$Year, kcm$rate, xlab="Year",
     ylab="Mortality rate per 100,000 hab",
     type="n")
points(kcm$Year, kcm$rate, pch=16, col="blue")
```



3.2 Simple trend analysis

One may be interested in estimating a Poisson model to determine whether there is any change in global tren. Here the null hypothesis is that slope is 0.

```
modPoisson <- glm(Count~Year+offset(log(Population)),
                  family=poisson, data=kcm)
modPoisson
##
## Call:  glm(formula = Count ~ Year + offset(log(Population)), family = poisson,
##         data = kcm)
##
## Coefficients:
## (Intercept)      Year
## -4.1972066   -0.0009335
##
## Degrees of Freedom: 6 Total (i.e. Null);  5 Residual
## Null Deviance:      12.2
## Residual Deviance: 11.96    AIC: 92.94
```

Hence, the annual percentage change would be:

```
round((exp(modPoisson$coef[2])-1)*100, 2)
## Year
## -0.09
```

with confidence interval

```
round((exp(confint(modPoisson)[2,])-1)*100, 2)
## 2.5 % 97.5 %
## -0.47 0.29
```

In some occasions there is overdispersion and negative binomial (NB) distribution must be used instead. Dispersion can be estimated by using residual deviance (null deviance / df residual). When this coefficient is >1 Poisson distribution is not adequate and NB has to be used. Here you can see an approximate test. Other better tests can be found in the library `pscl`.

H_0 : There is no overdispersion

The p-value corresponding to this test can be obtained by

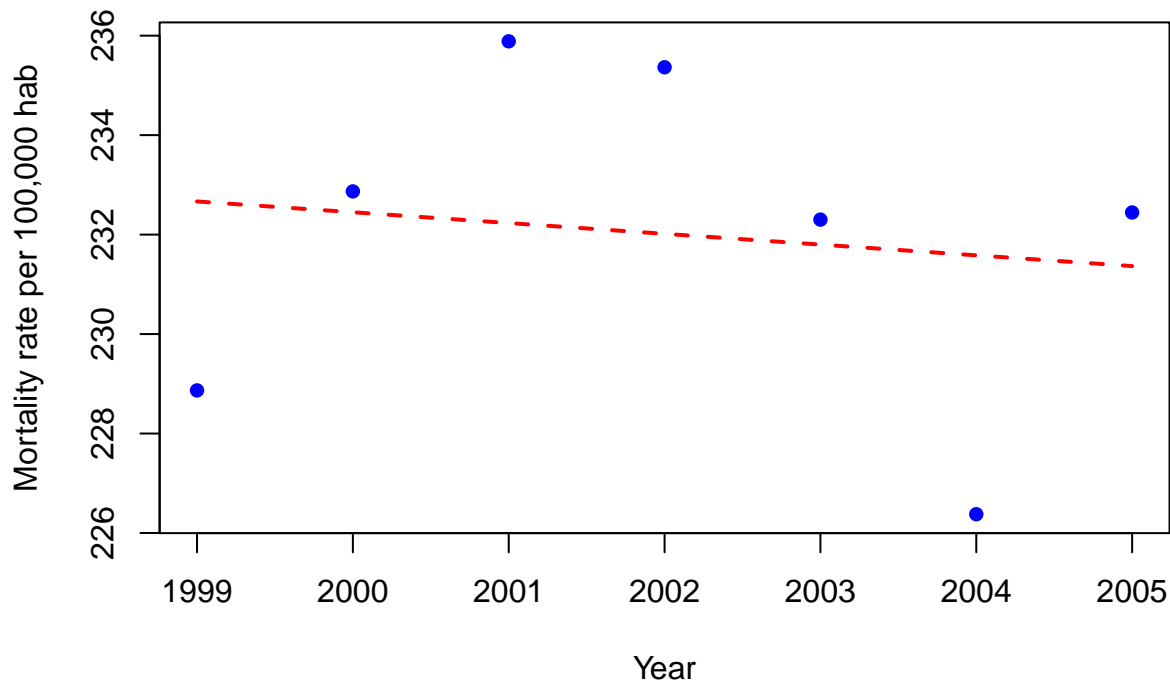
```
1 - pchisq(modPoisson$deviance, modPoisson$df.res)
## [1] 0.03527432
modPoisson
##
## Call: glm(formula = Count ~ Year + offset(log(Population)), family = poisson,
## data = kcm)
##
## Coefficients:
## (Intercept) Year
## -4.1972066 -0.0009335
##
## Degrees of Freedom: 6 Total (i.e. Null); 5 Residual
## Null Deviance: 12.2
## Residual Deviance: 11.96 AIC: 92.94
```

When rejecting the null hypothesis, negative binomial model can be fitted as

```
library(MASS)
modNB <- glm.nb(Count~Year+ offset(log(Population)),
               data=kcm)
modNB
##
## Call: glm.nb(formula = Count ~ Year + offset(log(Population)), data = kcm,
## init.theta = 13398.06067, link = log)
##
## Coefficients:
## (Intercept) Year
## -4.2218596 -0.0009212
##
## Degrees of Freedom: 6 Total (i.e. Null); 5 Residual
## Null Deviance: 7.141
## Residual Deviance: 7.01 AIC: 93.73
```

However, as illustrated in the next plot, linear trend is not valid

```
counts.pred <- predict(modPoisson, type="response")
rate.pred <- (counts.pred/kcm$Population)*100000
plot(kcm$Year, kcm$rate, xlab="Year",
     ylab="Mortality rate per 100,000 hab",
     type="n")
points(kcm$Year, kcm$rate, pch=16, col="blue")
lines(kcm$Year, rate.pred, lwd=2, lty=2, col="red")
```



4 Joinpoint analysis

4.1 Model for a given number of joinpoints

In general, one may be interested in estimating the best model for a given number of joinpoints (obtained by visually inspecting the overall trend). For example, for 1 joinpoint the model is estimated with the function `ljrk`

```
ljrk(1, kcm$Count, kcm$Population, kcm$Year+.5)
## Model:
## y~Binom(n,p) where p=invlogit(eta)
## eta=b0+g0*t+g1*max(t-tau1,0)
##
##      Variables      Coef
## b0      Intercept -40.81272431
## g0          t      0.01737196
## g1 max(t-tau1,0) -0.02418284
##
## Joinpoints:
##
## 1 tau1= 2001.273
## $Coef
##      Intercept          t max(t-tau1,0)
## -40.81272431    0.01737196   -0.02418284
##
```

```
## $Joinpoints
##   tau1=
## 2001.273
##
## $wlik
## [1] -0.112523
```

Notice that we have used the Year variable +0.5 for interpreting purposes. The model for 2 joinpoints is estimated by

```
ljrk(2, kcm$Count, kcm$Population, kcm$Year+.5)
## Model:
## y~Binom(n,p) where p=invlogit(eta)
## eta=b0+g0*t+g1*max(t-tau1,0)+g2*max(t-tau2,0)
##
##      Variables      Coef
## b0      Intercept -36.31521597
## g0           t      0.01512302
## g1 max(t-tau1,0) -0.03460547
## g2 max(t-tau2,0)  0.04383173
##
## Joinpoints:
##
## 1 tau1= 2004.500
## 2 tau2= 2002.039
## $Coef
##      Intercept          t max(t-tau1,0) max(t-tau2,0)
## -36.31521597    0.01512302   -0.03460547    0.04383173
##
## $Joinpoints
##   tau1=   tau2=
## 2004.500 2002.039
##
## $wlik
## [1] -0.1125223
```

4.2 Model selection using LRT

When two different models may fit the data, we can select the best one by using a likelihood ratio test (LRT) where the p-value is computed by using Montecarlo method. The function for that purpose is `ljrjk` and can be fitted in the case of comparing 1 and 2 joinpoints by executing

```
ljrjk(1, 2, kcm$Count, kcm$Population, kcm$Year+.5,
      R=1000,alpha=.05)
## Testing H0: 1 joinpoint(s) vs. H1: 2 joinpoints
## p-value= 0.05
## Null hypothesis is rejected
##
## Model:
## y~Binom(n,p) where p=invlogit(eta)
## eta=b0+g0*t+g1*max(t-tau1,0)+g2*max(t-tau2,0)
##
##      Variables      Coef
## b0      Intercept -36.31521597
## g0           t      0.01512302
```

```
## g1 max(t-tau1,0) -0.03460547
## g2 max(t-tau2,0) 0.04383173
##
## Joinpoints:
##
## 1 tau1= 2004.500
## 2 tau2= 2002.039
## $Coef
##      Intercept          t max(t-tau1,0) max(t-tau2,0)
## -36.31521597    0.01512302   -0.03460547    0.04383173
##
## $Joinpoint
##      tau1=      tau2=
## 2004.500 2002.039
##
## $wlik
## [1] -0.1125223
##
## $pval
## [1] 0.05
```

Here we can conclude that

Once the model is selected, we can compute the anual percentage of change of each segment by

```
mod <- ljrK(2, kcm$Count, kcm$Population, kcm$Year+.5)
## Model:
## y~Binom(n,p) where p=invlogit(eta)
## eta=b0+g0*t+g1*max(t-tau1,0)+g2*max(t-tau2,0)
##
##      Variables      Coef
## b0      Intercept -36.31521597
## g0          t      0.01512302
## g1 max(t-tau1,0) -0.03460547
## g2 max(t-tau2,0) 0.04383173
##
## Joinpoints:
##
## 1 tau1= 2004.500
## 2 tau2= 2002.039
cbind(year=c(1999, mod$Joinpoints),
      APC=round((exp(mod$Coef[-1])-1)*100,2))
##      year  APC
##      1999.000 1.52
## tau1= 2004.500 -3.40
## tau2= 2002.039 4.48
```

4.3 Automatic method of model selection

In some occasion the user is interested in selecting the best model by using an automatic method by using backward or forward approaches. Si queremos escoger el modelo de forma automática, utilizamos un método de selección 'backward' o 'forward'. This can be performed by using the function `ljrb` or `ljrf`. Note that in 'backward' method the argument `K` is required. This indicates the maximum number of joinpoints to be tested. The 'forward' method starts from the null model (e.g. linear trend or no joinpoints) and tests whether the inclusion of a new joinpoint is statistically significant or not.

```

ljrb(K=3, kcm$Count, kcm$Population, kcm$Year+.5)
## Backward algorithm for determining the number of joinpoints:
## Step 1 : Test H0: 0 joinpoint(s) vs H1: 3 joinpoint(s)
## p-value= 0.023
## Step 2 : Test H0: 0 joinpoint(s) vs H1: 2 joinpoint(s)
## p-value= 0.011
## Step 3 : Test H0: 1 joinpoint(s) vs H1: 2 joinpoint(s)
## p-value= 0.042
##
## Estimated number of joinpoints= 1
##
## Model:
## y~Binom(n,p) where p=invlogit(eta)
## eta=ofst+b0+g0*t+g1*max(t-tau1,0)
##
##      Variables      Coef
## b0      Intercept -40.81272431
## g0              t    0.01737196
## g1 max(t-tau1,0) -0.02418284
##
## Joinpoints:
##
## 1 tau1= 2001.273
## $Coef
##      Intercept      t max(t-tau1,0)
## -40.81272431    0.01737196 -0.02418284
##
## $Joinpoints
##      tau1=
## 2001.273
##
## $wlik
## [1] -0.112523
##
## $pvals
## [1] 0.023 0.011 0.042

```

```

ljrf(kcm$Count, kcm$Population, kcm$Year+.5)
## Forward algorithm for determining the number of joinpoints:
## Step 1 : Test H0: 0 joinpoint(s) vs H1: 1 joinpoint(s)
## p-value= 0.05
##
## Estimated number of joinpoints= 0
##
## Model:
## y~Binom(n,p) where p=invlogit(eta)
## eta=b0+g0*t
##
##      Variables      Coef
## b0 Intercept -4.190069631
## g0          t -0.000935695
## $Coef
##      Intercept      t
## -4.190069631 -0.000935695

```



```
##  
## $wlik  
## [1] -0.1125237  
##  
## $pvals  
## [1] 0.05 0.00 0.00 0.00 0.00
```

We observe that

5 References

- The [pscl](#) package

6 Session information

```
## R version 3.3.2 (2016-10-31)  
## Platform: x86_64-w64-mingw32/x64 (64-bit)  
## Running under: Windows 10 x64 (build 14393)  
##  
## locale:  
## [1] LC_COLLATE=Spanish_Spain.1252 LC_CTYPE=Spanish_Spain.1252  
## [3] LC_MONETARY=Spanish_Spain.1252 LC_NUMERIC=C  
## [5] LC_TIME=Spanish_Spain.1252  
##  
## attached base packages:  
## [1] stats      graphics  grDevices  utils      datasets  methods   base  
##  
## other attached packages:  
## [1] MASS_7.3-45      ljr_1.4-0      knitr_1.15.1    BiocStyle_2.2.1  
##  
## loaded via a namespace (and not attached):  
## [1] backports_1.0.5 magrittr_1.5    rprojroot_1.2   tools_3.3.2  
## [5] htmltools_0.3.5 yaml_2.1.14     Rcpp_0.12.9     stringi_1.1.2  
## [9] rmarkdown_1.3    stringr_1.1.0  digest_0.6.11   evaluate_0.10
```