Local_poison_regression

Gregoire Gasparini, Aurora Hofman, Sarah Musiol, Beatriu Tort

22 de marzo de 2020

Bandwidth choice for the local Poisson regression

The functions from ATENEA are modified to fit a local Poisson regression.

```
#The first function is not modified
h.cv.sm.poison <- function(x,y,rg.h=NULL,1.h=10,method=loglik.CV){
   cv.h <- numeric(1.h)</pre>
   if (is.null(rg.h)){
      hh <- c(h.select(x,y,method="cv"),</pre>
            h.select(x,y,method="aicc"))
      rg.h \leftarrow range(hh)*c(1/1.1, 1.5)
   }
   i <- 0
   gr.h <- exp( seq(log(rg.h[1]), log(rg.h[2]), l=1.h))
   for (h in gr.h){
      i <- i+1
      cv.h[i] <- method(x,y,h)</pre>
   return(list(h = gr.h,
               cv.h = cv.h,
               h.cv = gr.h[which.min(cv.h)]))
}
# method loglik.CV: leave-one-out log-likelihood
#Modifications: sm.poisson and the return function is the loglikelihood
#of the density of the poison distribution.
loglik.CV <- function(x,y,h){</pre>
 n <- length(x)
 pred <- sapply(1:n,</pre>
      function(i,x,y,h){
         sm.poisson(x=x[-i],y=y[-i],h=h,eval.points=x[i],display="none")$estimate
  #faculty <- sapply(1:n, function(i, y){prod(1:y[i])},</pre>
  # if one wants the scalingfactor uncomment the line above
  return(-sum(y*log(pred)-pred)) #-log(faculty) only a scale
```

Local Poisson regression for Country Development Data

Consider the country development dataset containing information on development indicators measured in 179 countries

```
countries<-read.csv2(file="HDI.2017.subset.csv",row.names = 1)
le.fm.r <- round(countries$le.fm)</pre>
```

Fit a local Poisson regression modeling le.fm.0 as a function of Life.expec. Use sm.poisson from R package. library(sm)

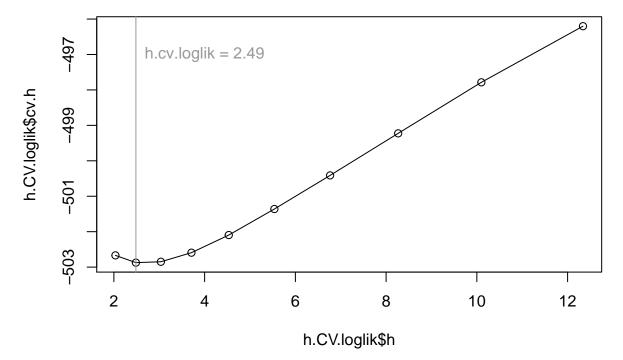
```
## Warning in fun(libname, pkgname): couldn't connect to display ":0"
## Package 'sm', version 2.2-5.6: type help(sm) for summary information
x<- countries$Life.expec
y<- le.fm.r
h.cv.sm.poison(countries$Life.expec, le.fm.r)$h.cv</pre>
```

[1] 2.485047

Plot of the loglikelihood as a function of Bandwidth.

```
h.CV.loglik <- h.cv.sm.poison(countries$Life.expec,le.fm.r, l.h = 10)
plot(h.CV.loglik$h,h.CV.loglik$cv.h)
lines(h.CV.loglik$h,h.CV.loglik$cv.h)
abline(v=h.CV.loglik$h.cv, col = "gray60")
text(4, -497, paste("h.cv.loglik = ",round(h.CV.loglik$h.c,2),sep=""), col = "gray60")
title("Bandwidth cross - validation plot")</pre>
```

Bandwidth cross - validation plot



In this plot it can be seen that the optimal bandwidth is around 2.5, which is where the -loglikelihood is at

its minimum.

Now we make a local poison regression where le.fm.r is plotted against life.expectensy.

```
aux <- sm.poisson(countries$Life.expec,le.fm.r,h=h.CV.loglik$h.cv)
title(main=paste("h.cv.loglik = ",round(h.CV.loglik$h.cv,2),sep=""))</pre>
```

h.cv.loglik = 2.49

