

Mortalidad Por Causas

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26 junio, 2017

Extracción de los datos.

```
mort.caus <- read.table("mortcaushist.csv",sep=";",header=TRUE)
superv.larg<- read.table("supervivientes.csv",sep=";",header=TRUE)

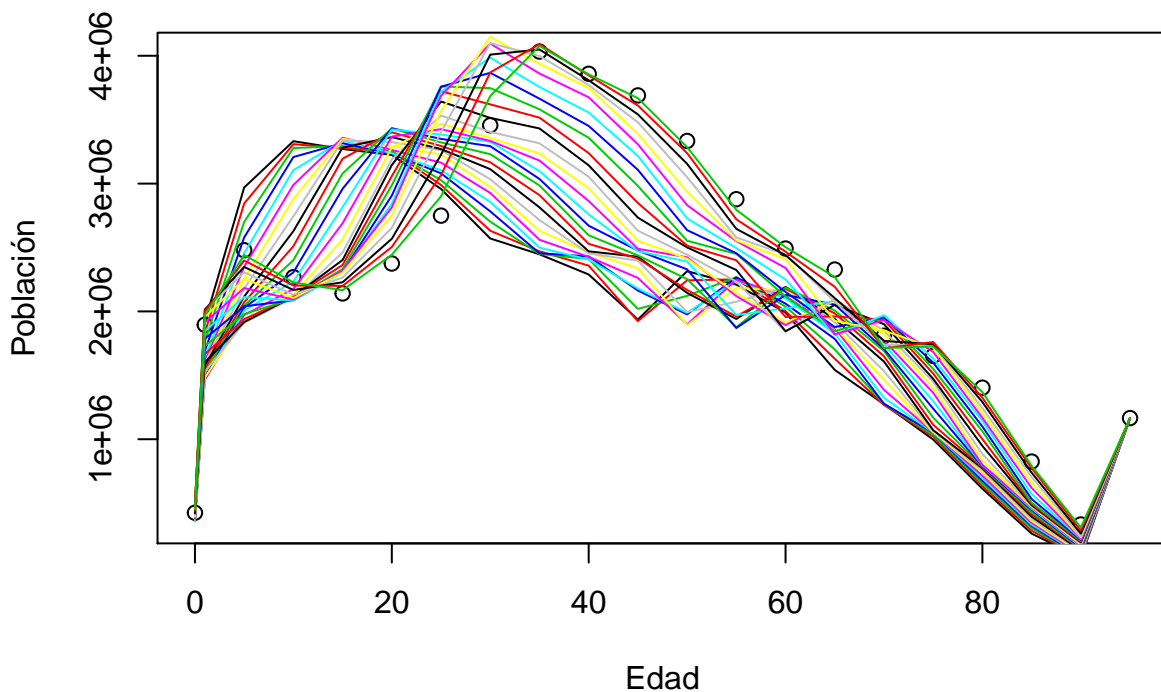
#Históricos de España con las edades por año
sup.spa <- read.table("suphistspa.csv",sep=";",header=TRUE)
defu.spa <- read.table("morthistspa.csv",sep=";",header=TRUE)
```

Extraemos los datos en matrices por separado, creando la lista de matrices D , que alberga en la primera matriz los fallecidos totales y en las siguientes los fallecidos para cada uno de los grupos causales en intervalos de 5 años de edad.

Evolución de la población

Dibujamos la evolución de la población española.

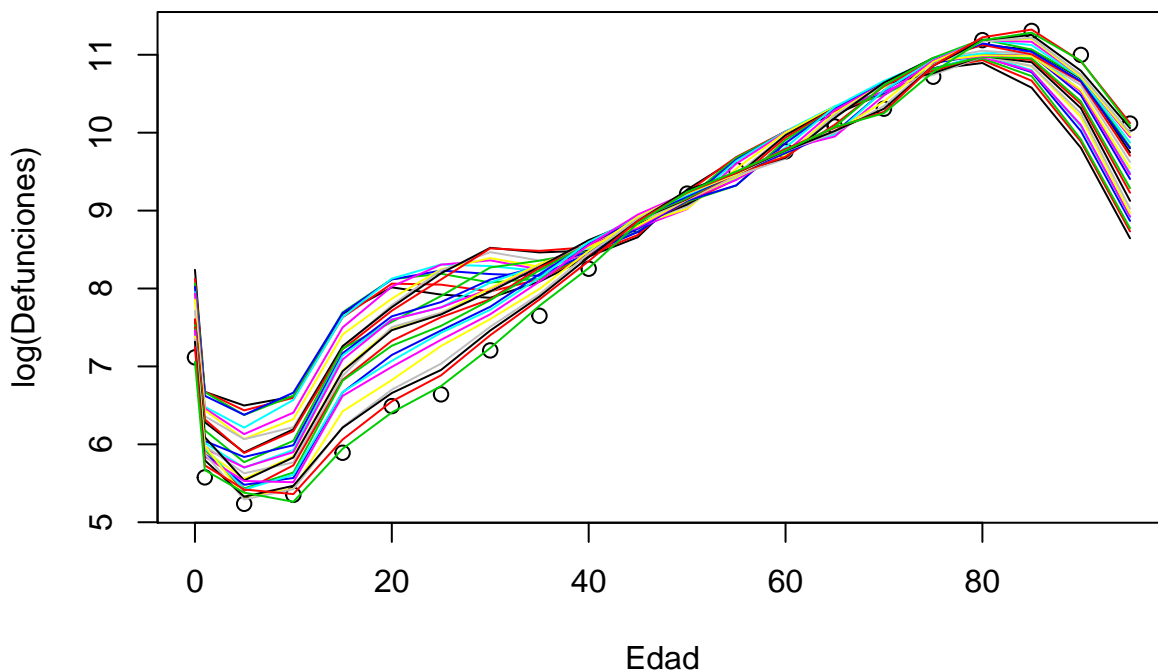
```
plot(x=c(0,1,seq(5,95,by=5)),y=sup[,nany],xlab = "Edad",ylab = "Población")
for(i in 1:(nany-1)){
  lines(c(0,1,seq(5,95,by=5)),sup[,i],col=i)
}
```



Evolución de la mortalidad

Dibujamos la evolución de la mortalidad total.

```
plot(x=c(0,1,seq(5,95,by=5)),y=log(D.total[,nany]),xlab = "Edad",ylab = "log(Defunciones)")
for(i in 1:(nany-1)){
  lines(c(0,1,seq(5,95,by=5)),log(D.total[,i]),col=i)
}
```



Probabilidades de cada causa

Creamos la lista T de probabilidades de cada causa suponiendo que ya ha fallecido.

$$T_i^j = P(\text{Fallecer de causa } j \text{ a la edad } i \mid \text{Ha fallecido})$$

```
T <- D #Sólo por generarla
for (k in 1:ncaus){
  for (i in 1:nint){
    for (j in 1:nany){
      T[[k]][i,j] <- D[[k]][i,j]/D.total[i,j]
    }
  }
}
```

Observamos que se ha realizado correctamente ya que la suma de todas las probabilidades de cada elemento da 1.

```
c <- Reduce("+",T)
```

```

#Creamos la matriz con los fallecimientos totales para cada año y para cada causa
def.caus.tot <- matrix(0,ncaus,nany)
for (j in 1:nany){
  for(i in 1:ncaus){
    def.caus.tot[i,j] <- sum(D[[i]][,j])
  }
}
colnames(def.caus.tot) <- colnames(D[[1]])

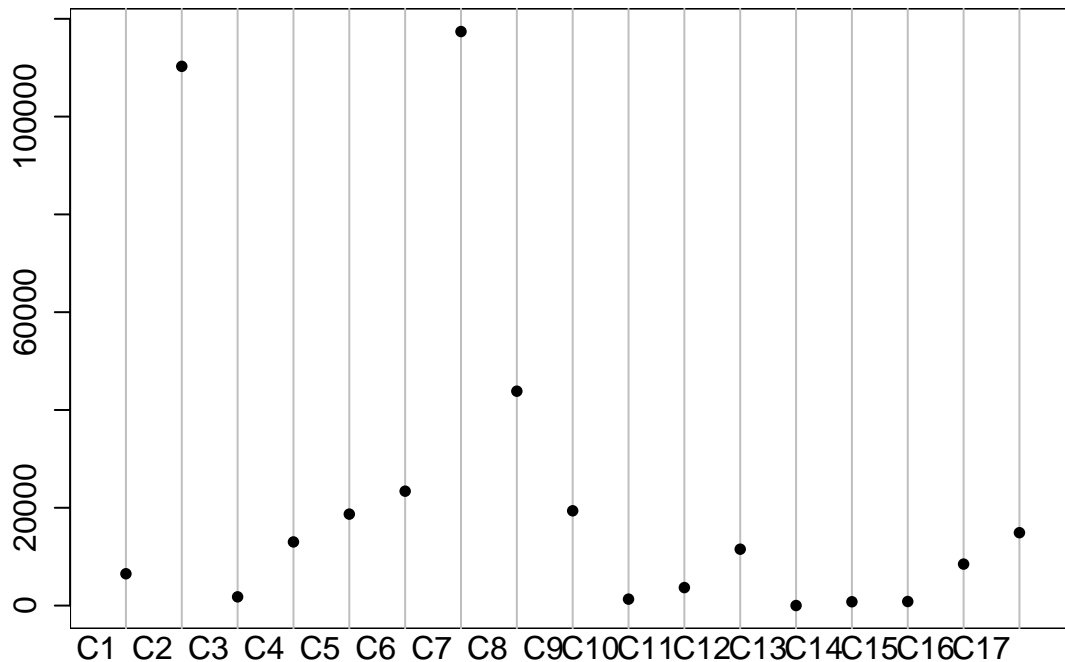
identical(sum(D.total),sum(def.caus.tot[,]))#Se ha realizado correctamente

## [1] TRUE

dotchart2(def.caus.tot[, "X2014"], labels=paste("C",c(1:17), sep=""),
  main="Defunciones por causa de fallecimiento (Cifras Absolutas) Año 2014",
  horizontal=FALSE)

```

Defunciones por causa de fallecimiento (Cifras Absolutas) Año 201

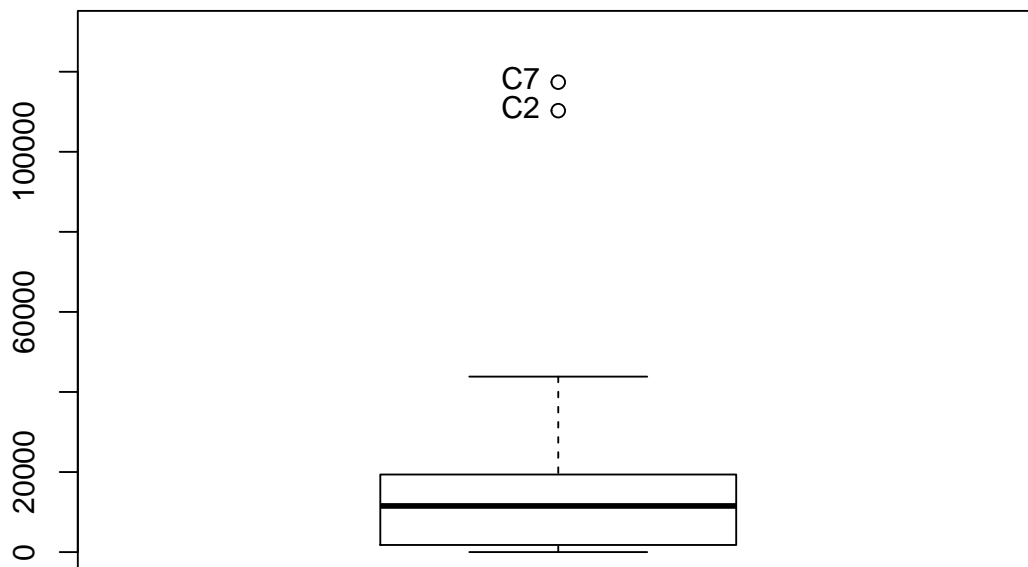


```

par(mar = c(3, 4, 4, 2))
Boxplot(def.caus.tot[, "X2014"], labels=paste("C",c(1:17), sep=""),
  main="Diagrama de caja y bigotes de las causas de fallecimiento (Cifras Absolutas) Año 2014",
  ylab="", ylim=c(0,130000), id.method="y")

```

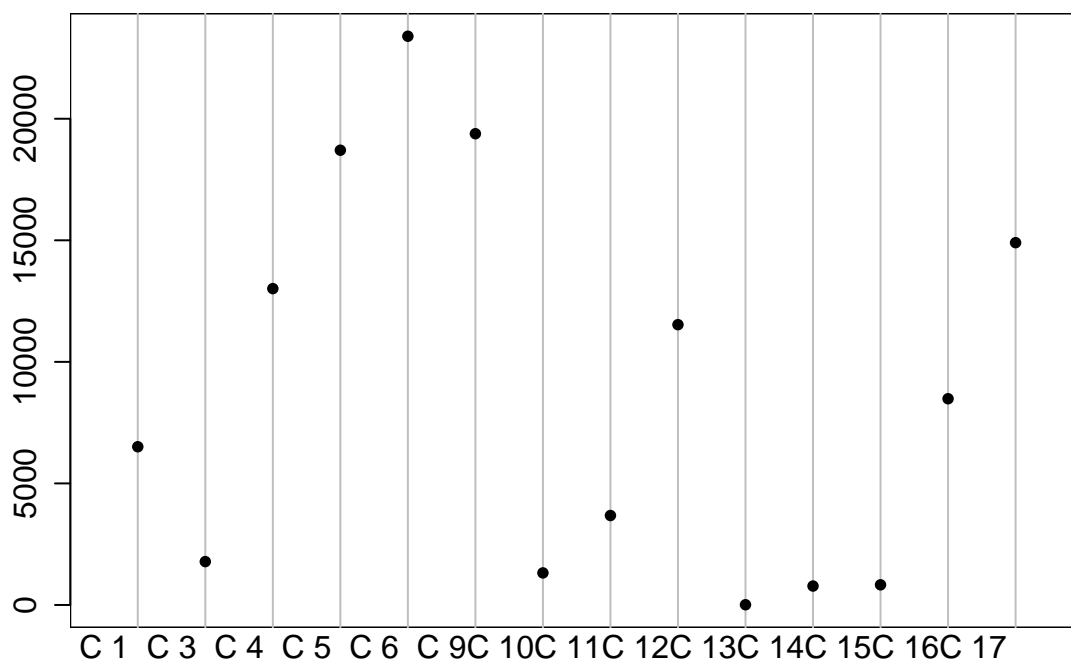
Diagrama de caja y bigotes de las causas de fallecimiento (Cifras Absolutas)



```
## [1] "C2" "C7"
```

```
dotchart2(def.caus.tot[-c(2,7,8),"X2014"],labels=c(paste("C",1),paste("C",3:6),paste("C",9:17),sep=""),
          main="Defunciones por causa de fallecimiento (Cifras Absolutas) Año 2014",
          horizontal=FALSE)
```

Defunciones por causa de fallecimiento (Cifras Absolutas) Año 201



```

Lista.causas <- matrix("a",ncaus,2)
colnames(Lista.causas) = c("Número","Nombre completo")
for(i in 1:ncaus){
  Lista.causas[i,1] <- paste("Grupo causal",i)
  Lista.causas[i,2] <- as.character(mort.caus[(22*(i-1)+1),1])
}

kable(Lista.causas, caption="Grupos causales",
      colnames = c("Número","Nombre completo"),
      align=c("c","l")
      )

```

Table 1: Grupos causales

Número	Nombre completo
Grupo causal 1	001-008 I.Enfermedades infecciosas y parasitarias (1)
Grupo causal 2	009-041 II.Tumores
Grupo causal 3	042-043 III.Enfermedades de la sangre y de los órganos hematopoyéticos, y ciertos trastornos que afectan
Grupo causal 4	044-045 IV.Enfermedades endocrinas, nutricionales y metabólicas
Grupo causal 5	046-049 V.Trastornos mentales y del comportamiento
Grupo causal 6	050-052 VI-VIII.Enfermedades del sistema nervioso y de los órganos de los sentidos
Grupo causal 7	053-061 IX.Enfermedades del sistema circulatorio
Grupo causal 8	062-067 X.Enfermedades del sistema respiratorio
Grupo causal 9	068-072 XI.Enfermedades del sistema digestivo
Grupo causal 10	073 XII.Enfermedades de la piel y del tejido subcutáneo
Grupo causal 11	074-076 XIII.Enfermedades del sistema osteomuscular y del tejido conjuntivo
Grupo causal 12	077-080 XIV.Enfermedades del sistema genitourinario
Grupo causal 13	081 XV.Embarazo, parto y puerperio
Grupo causal 14	082 XVI.Afecciones originadas en el periodo perinatal
Grupo causal 15	083-085 XVII.Malformaciones congénitas, deformidades y anomalías cromosómicas
Grupo causal 16	086-089 XVIII.Síntomas, signos y hallazgos anormales clínicos y de laboratorio, no clasificados en otra
Grupo causal 17	090-102 XX.Causas externas de mortalidad

```
xtable(Lista.causas)
```

```

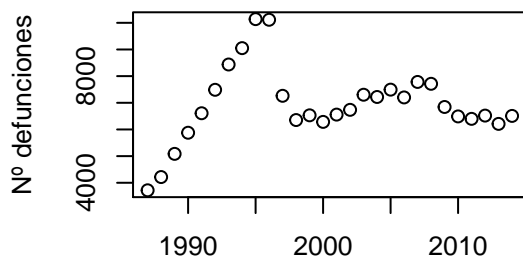
## % latex table generated in R 3.3.2 by xtable 1.8-2 package
## % Mon Jun 26 21:14:58 2017
## \begin{table}[ht]
## \centering
## \begin{tabular}{rll}
## \hline
## & Número & Nombre completo \\
## \hline
## 1 & Grupo causal 1 & 001-008 I.Enfermedades infecciosas y parasitarias (1) \\
## 2 & Grupo causal 2 & 009-041 II.Tumores \\
## 3 & Grupo causal 3 & 042-043 III.Enfermedades de la sangre y de los órganos hematopoyéticos, y \\
## 4 & Grupo causal 4 & 044-045 IV.Enfermedades endocrinas, nutricionales y metabólicas \\
## 5 & Grupo causal 5 & 046-049 V.Trastornos mentales y del comportamiento \\
## 6 & Grupo causal 6 & 050-052 VI-VIII.Enfermedades del sistema nervioso y de los órganos de los \\
## 7 & Grupo causal 7 & 053-061 IX.Enfermedades del sistema circulatorio

```

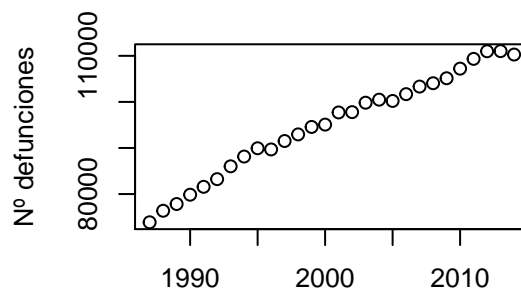
```
## 8 & Grupo causal 8 & 062-067 X.Enfermedades del sistema respiratorio \\
## 9 & Grupo causal 9 & 068-072 XI.Enfermedades del sistema digestivo \\
## 10 & Grupo causal 10 & 073 XII.Enfermedades de la piel y del tejido subcutáneo \\
## 11 & Grupo causal 11 & 074-076 XIII.Enfermedades del sistema osteomuscular y del tejido conjunt
## 12 & Grupo causal 12 & 077-080 XIV.Enfermedades del sistema genitourinario \\
## 13 & Grupo causal 13 & 081 XV.Embarazo, parto y puerperio \\
## 14 & Grupo causal 14 & 082 XVI.Afecciones originadas en el periodo perinatal \\
## 15 & Grupo causal 15 & 083-085 XVII.Malformaciones congénitas, deformidades y anomalías cromosó
## 16 & Grupo causal 16 & 086-089 XVIII.Síntomas, signos y hallazgos anormales clínicos y de labor
## 17 & Grupo causal 17 & 090-102 XX.Causas externas de mortalidad \\
## \hline
## \end{tabular}
## \end{table}
```

```
par(mfrow=c(2,2))
for(i in 1:ncaus){
  plot(c(1987:2014),def.caus.tot[i,],main=paste("Grupo causal",i),xlab="Años",ylab="Nº defunciones")
}
```

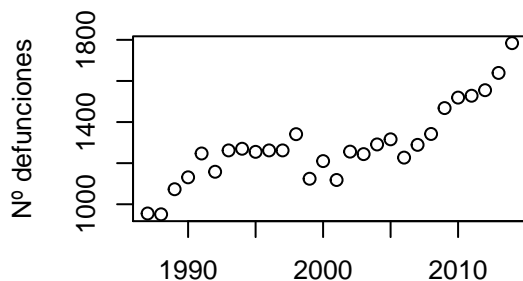
Grupo causal 1



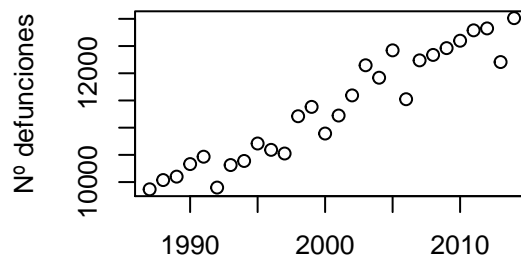
Grupo causal 2



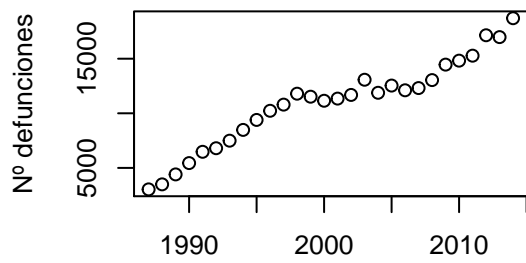
Grupo causal 3



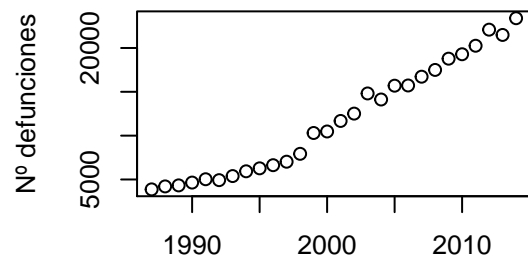
Grupo causal 4



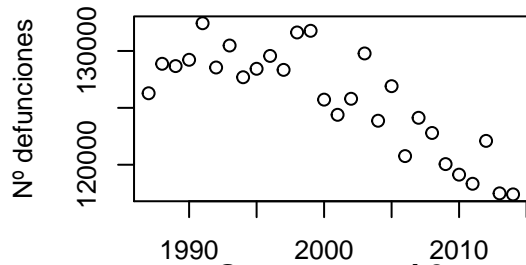
Grupo causal 5



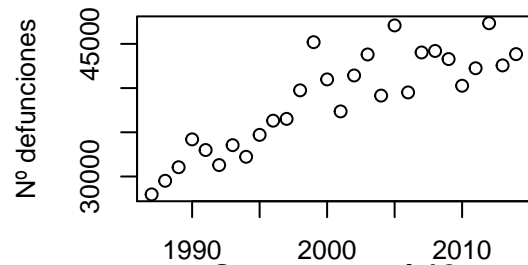
Grupo causal 6



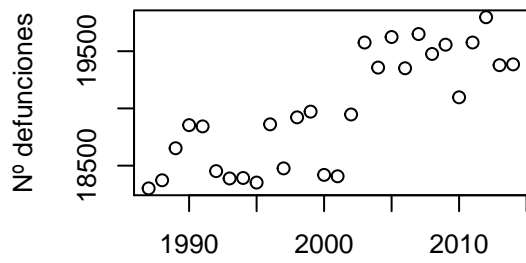
Grupo causal 7



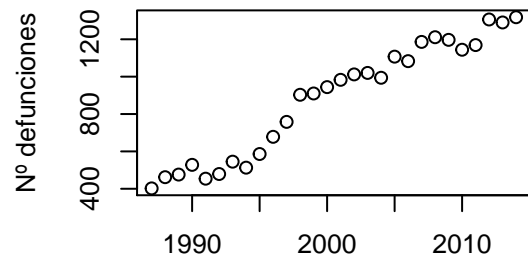
Grupo causal 8



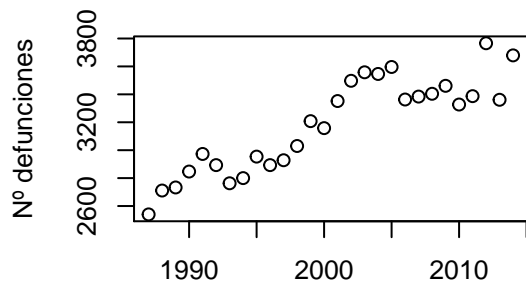
Grupo causal 9



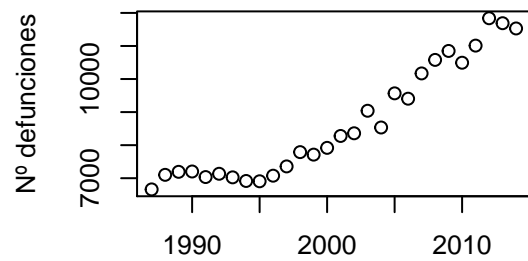
Grupo causal 10



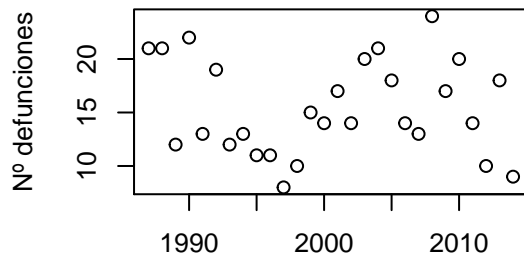
Grupo causal 11



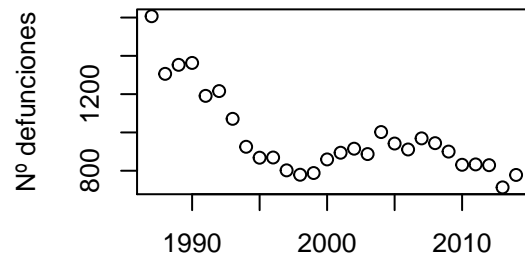
Grupo causal 12



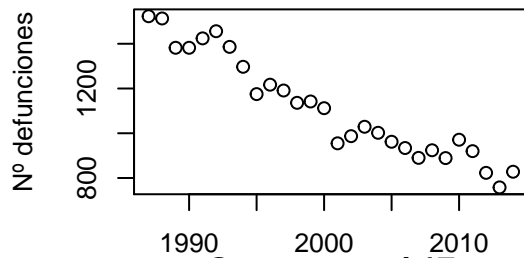
Grupo causal 13



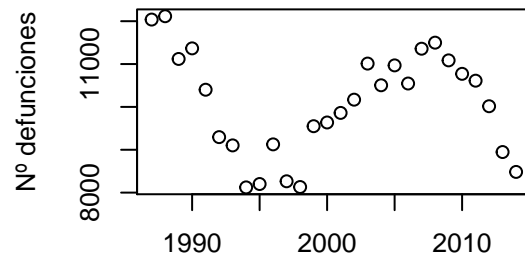
Grupo causal 14



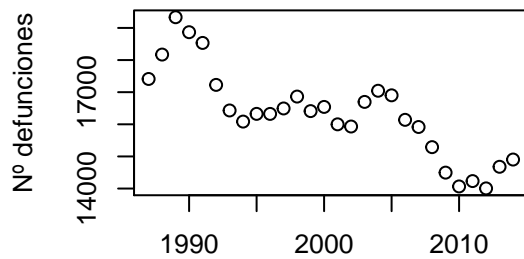
Grupo causal 15



Grupo causal 16



Grupo causal 17



Agrupación por correlaciones

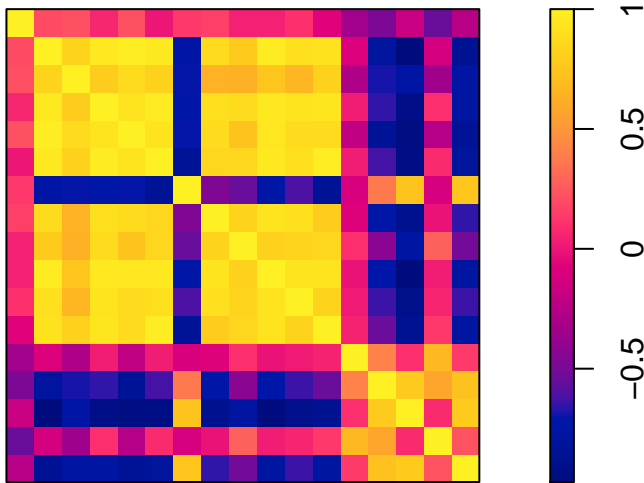
```
par(mfrow=c(1,1))
cor.def <- cor(t(def.caus.tot))
x <- as.character(c(1:17))
toString(x,width = 17)

## [1] "1, 2, 3, 4, 5...."

rownames(cor.def) <- as.character(c(1:17))
colnames(cor.def) <- as.character(c(1:17))

plot(im(cor.def[nrow(cor.def):1,]), main="Correlation Matrix Map")
```


Correlation Matrix Map



Como queremos agruparlos por correlaciones, comenzamos con la visualización de las distancias a partir de clústering jerárquico.

```
#Cogemos 4 tipos de disimilaridades
```

```
diss1 = 1 - cor.def
```

```
diss2 = (1 - cor.def)/2
```

```
diss3 = 1 - abs(cor.def)
```

```
diss4 = sqrt(1 - cor.def)
```

```
dist1 <- as.dist(diss1)
```

```
dist2 <- as.dist(diss2)
```

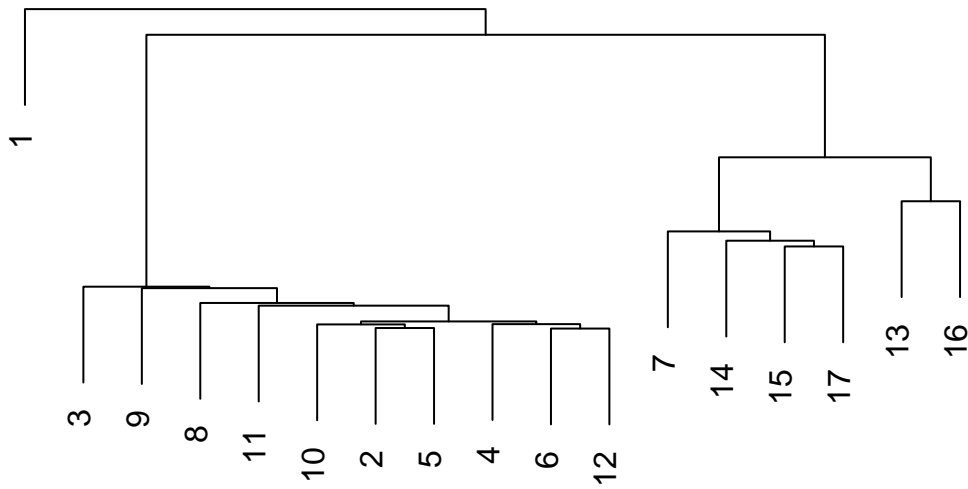
```
dist3 <- as.dist(diss3)
```

```
dist4 <- as.dist(diss4)
```

```
par(mfrow=c(1,1))
```

```
plot(hclust(dist1,method="single"),main="Dendograma con d = 1 - Corr",axes = FALSE,ylab =NULL,hang=0.
```

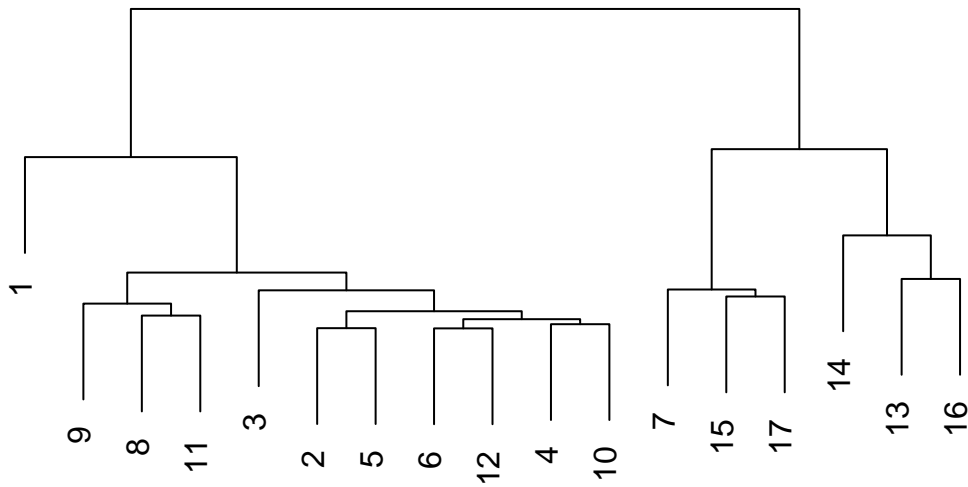
Dendrograma con $d = 1 - \text{Corr}$



Método Single

```
plot(hclust(dist1,method="complete"),main="Dendrograma con  $d = 1 - \text{Corr}$ ",axes = FALSE,ylab = NULL,hang=
```

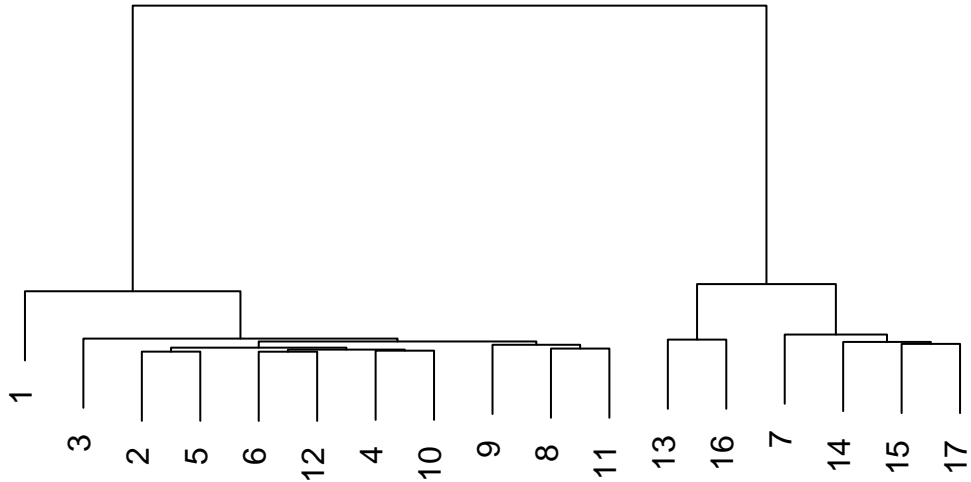
Dendrograma con $d = 1 - \text{Corr}$



Método Complete

```
plot(hclust(dist1,method="ward.D"),main="Dendograma con d = 1 - Corr",axes = FALSE,ylab =NULL,hang=0.
```

Dendograma con d = 1 - Corr



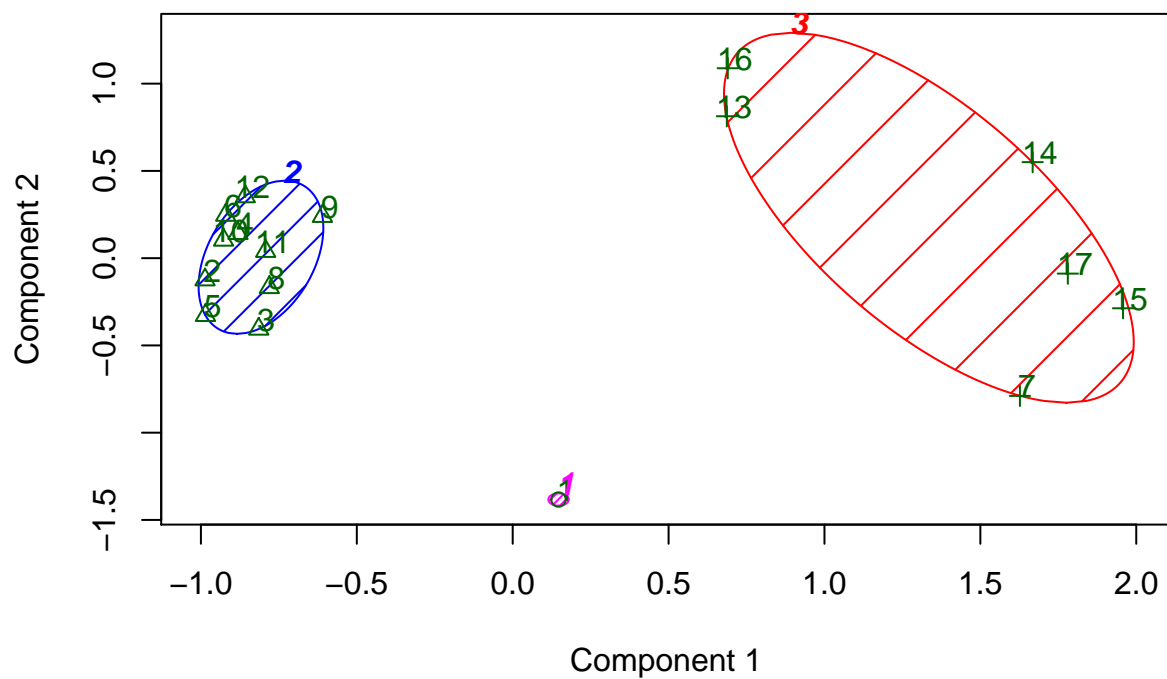
Método Ward

```
caus.km3<-kmeans(def.caus.tot,3)
caus.km4<-kmeans(def.caus.tot,4)
caus.km5<-kmeans(def.caus.tot,5)
```

```
pam.3 <- pam(dist1,k=3,diss=TRUE)
pam.4 <- pam(dist1,k=4,diss=TRUE)
pam.5 <- pam(dist1,k=5,diss=TRUE)
pam.6 <- pam(dist1,k=6,diss=TRUE)
```

```
clusplot(pam.3, color=TRUE, shade=TRUE, labels=2, lines=0,main="3 clústers")
```

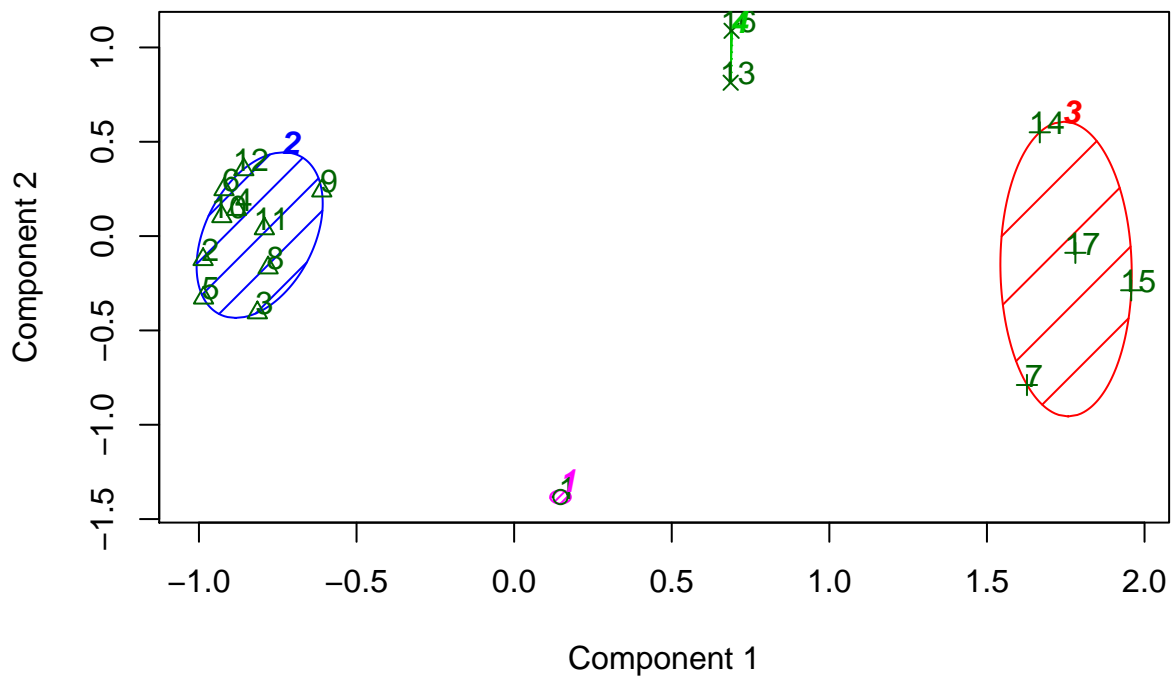
3 clústers



These two components explain 70.57 % of the point variability.

```
clusplot(pam.4, color=TRUE, shade=TRUE, labels=2, lines=0,main="4 clústers")
```

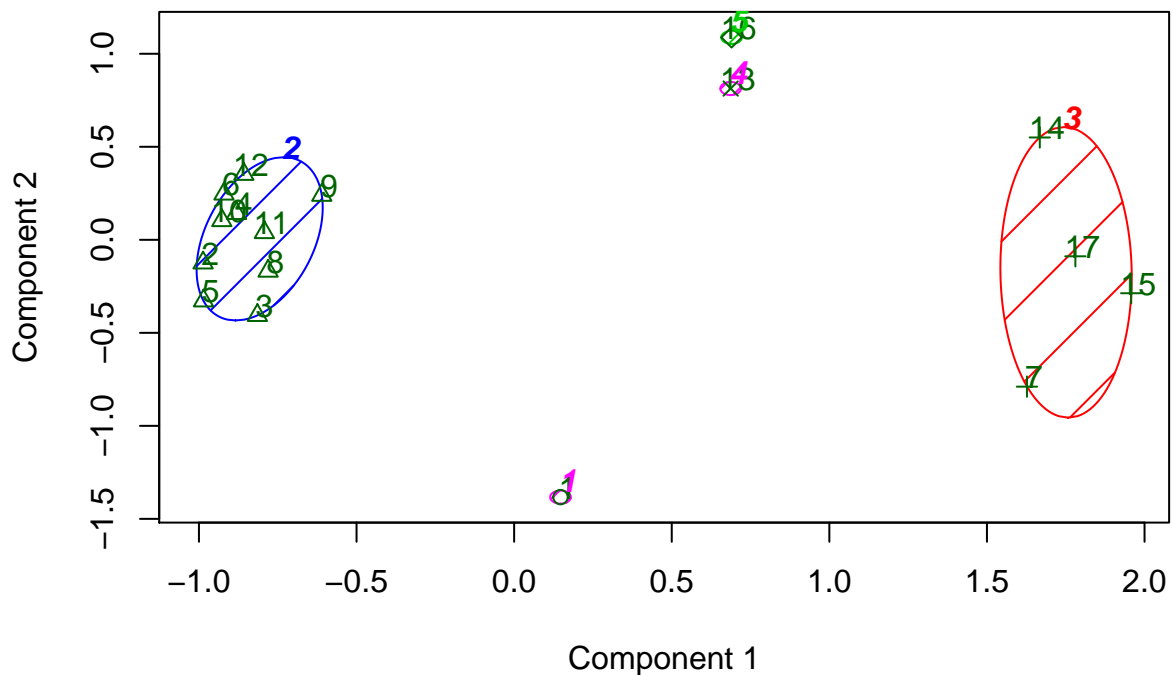
4 clústers



These two components explain 70.57 % of the point variability.

```
clusplot(pam.5, color=TRUE, shade=TRUE, labels=2, lines=0,main="5 clústers")
```

5 clústers



These two components explain 70.57 % of the point variability.

```
stats3 <- cluster.stats(dist1, pam.3$cluster)
stats4 <- cluster.stats(dist1, pam.4$cluster)
```

```
stats3$clus.avg.silwidths
```

```
##          1          2          3
## 0.0000000 0.8478620 0.4478921
```

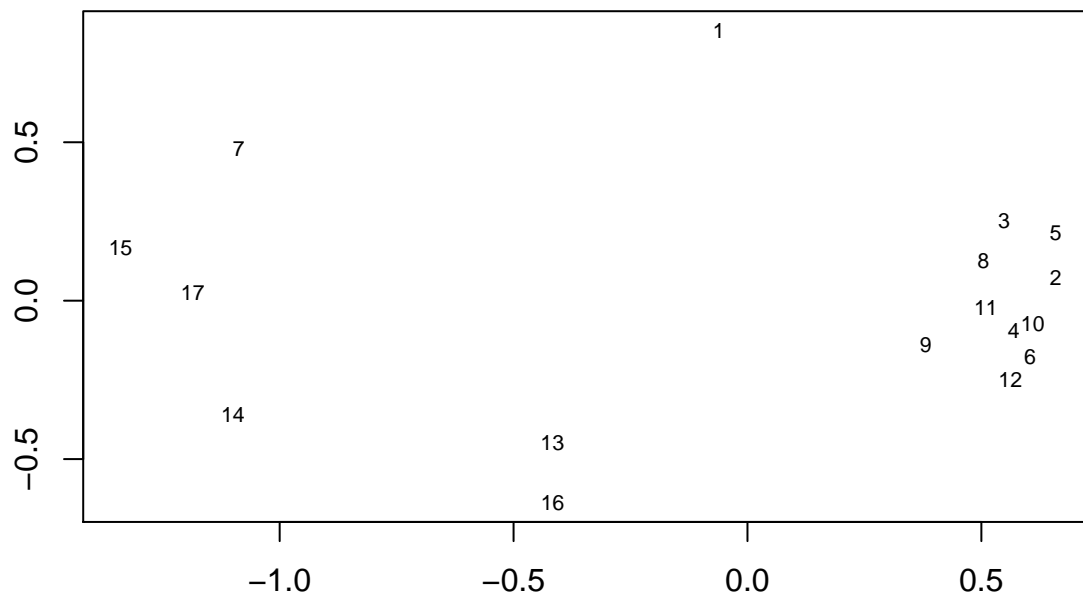
```
stats4$clus.avg.silwidths
```

```
##          1          2          3          4
## 0.0000000 0.8416253 0.5642511 0.6133732
```

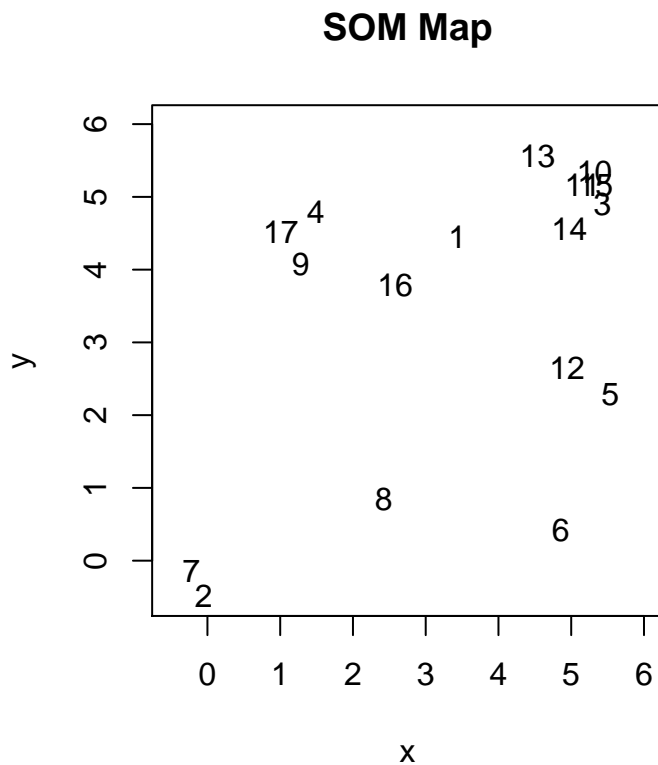
Para visualizar correctamente, realizaremos un escalado multidimensional y un SOM(Self Organized Map)

```
fit <- cmdscale(dist1,eig=TRUE, k=2) #Se puede realizar con cualquier otra disimilaridad
x <- fit$points[,1]
y <- fit$points[,2]
plot(x, y, xlab="", ylab="",
     main="Escalado Multidimensional", type="n")
text(x, y, labels = c(1:ncaus), cex=.7)
```

Escalado Multidimensional



```
mort.som<-som(def.caus.tot,6,6,rlen=1000)
xmx<-jitter(mort.som$visual$x,factor=3)
xmy<-jitter(mort.som$visual$y,factor=3)
par(mfrow=c(1,1),pty="s")
plot(xmx,xmy,type="n",pch=16,xlab="x",
      ylab="y",main="SOM Map",
      xlim=c(-0.5,6),ylim=c(-0.5,6))
text(xmx,xmy,c(1:17))
```



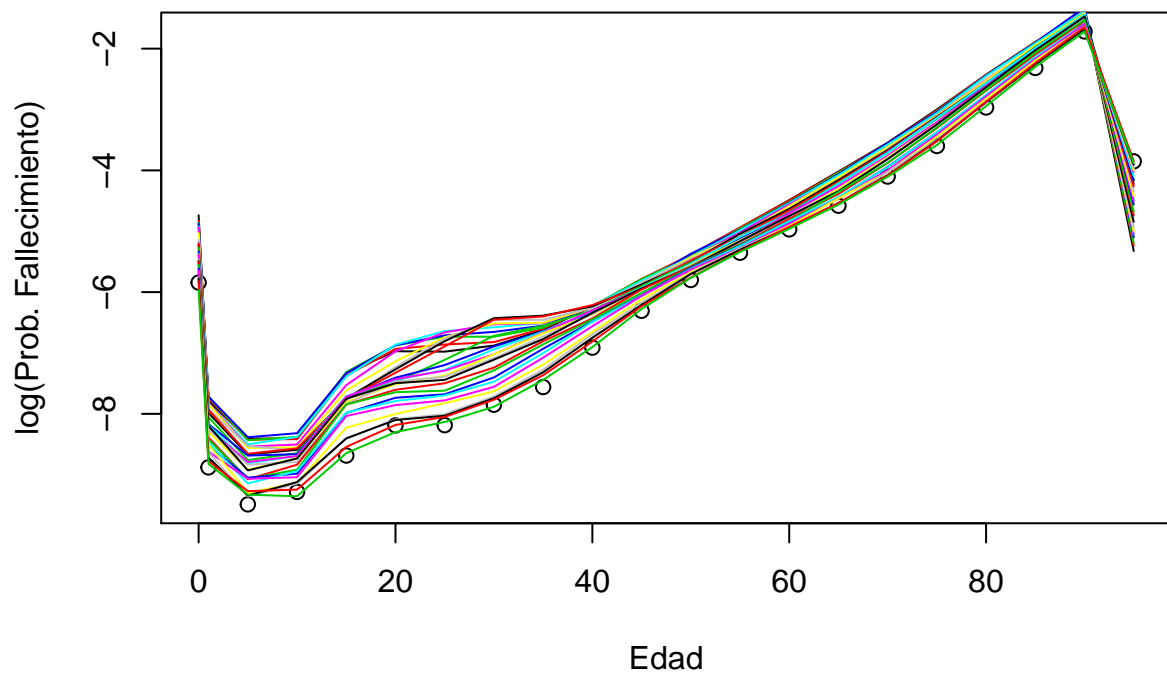
Cálculo de probabilidades

Ahora crearemos la lista de probabilidades de cada uno de los grupos causales de muerte(matriz Q).

$$Q_i^j = P(\text{Fallecer de causa } j \text{ a la edad } i \mid \text{No ha fallecido})$$

```
Q <- T #Sólo por generarla
for (k in 1:ncaus){
  for (i in 1:nint){
    for (j in 1:nany){
      Q[[k]][i,j] <- D[[k]][i,j]/sup[i,j]
    }
  }
}
Q.total <- Reduce("+",Q)

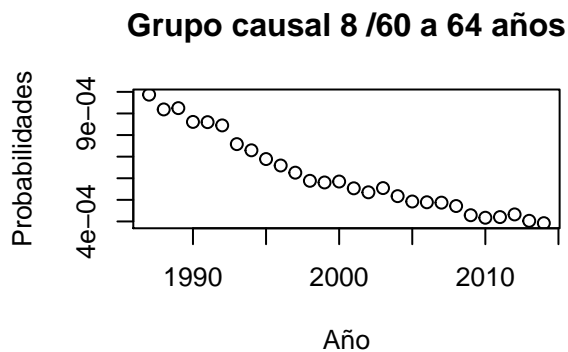
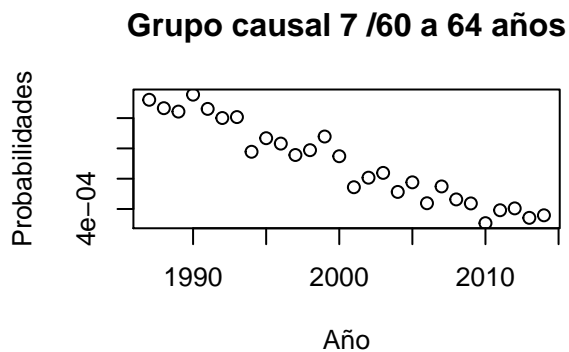
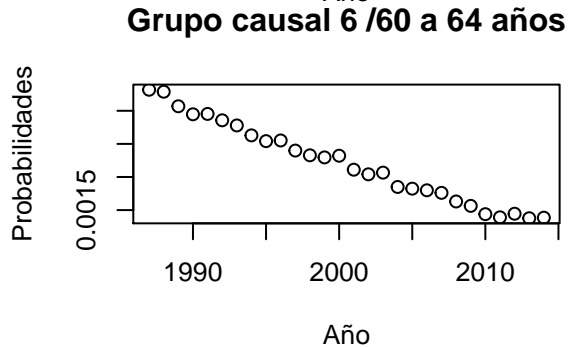
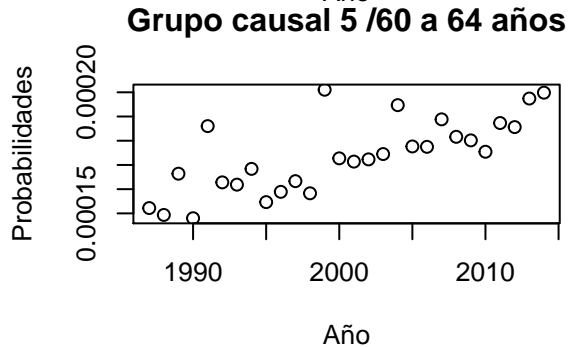
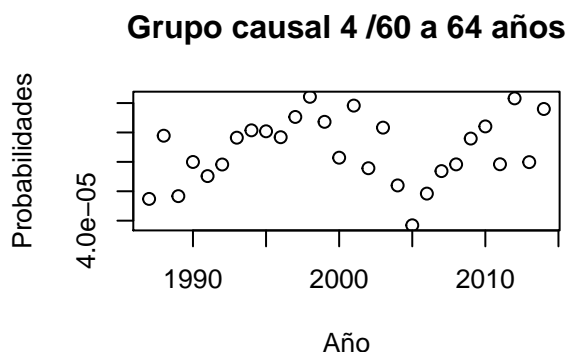
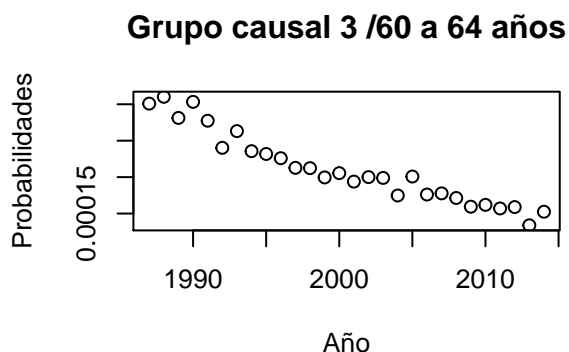
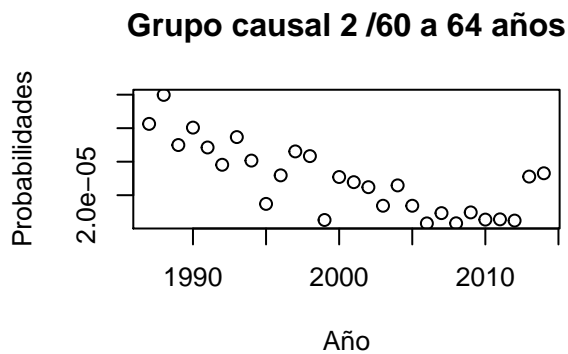
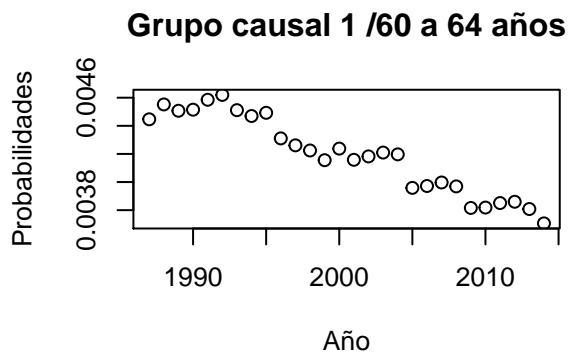
plot(x=c(0,1,seq(5,95,by=5)),y=log(Q.total[,nany]),xlab = "Edad",ylab = "log(Prob. Fallecimiento)")
for(i in 1:(nany-1)){
  lines(c(0,1,seq(5,95,by=5)),log(Q.total[,i]),col=i)
}
```

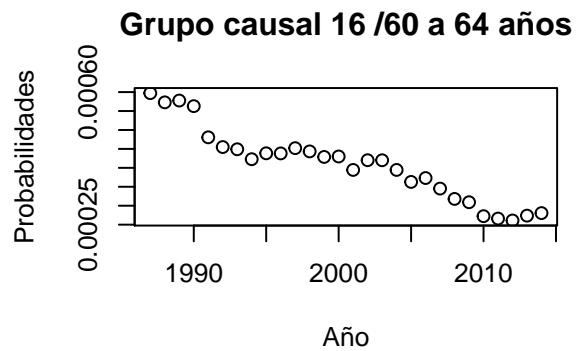
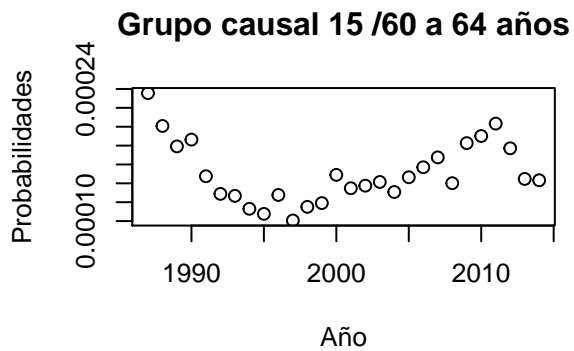
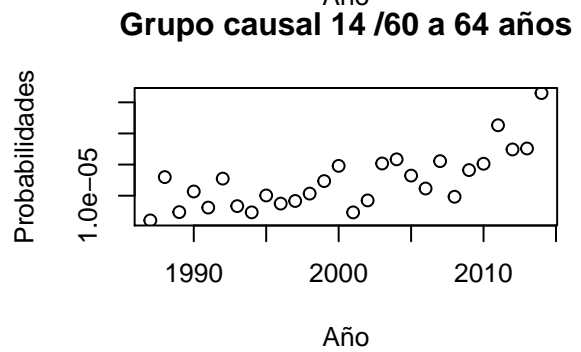
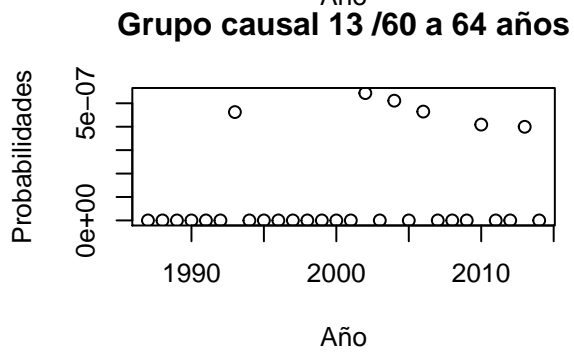
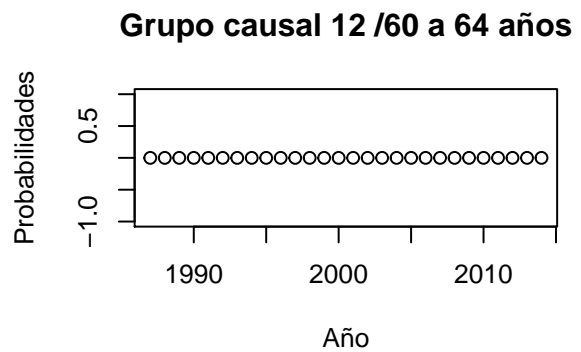
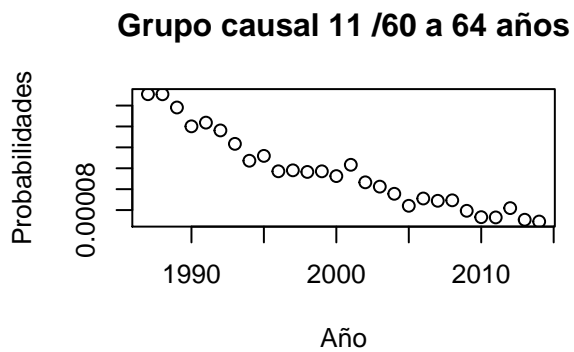
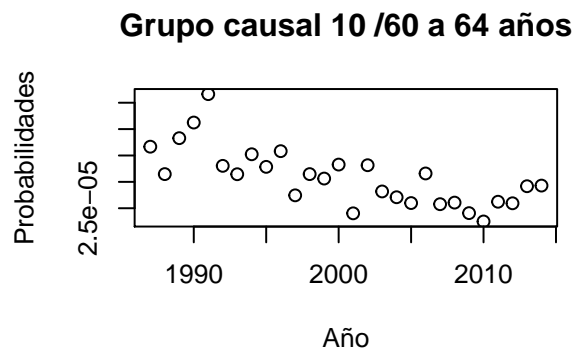
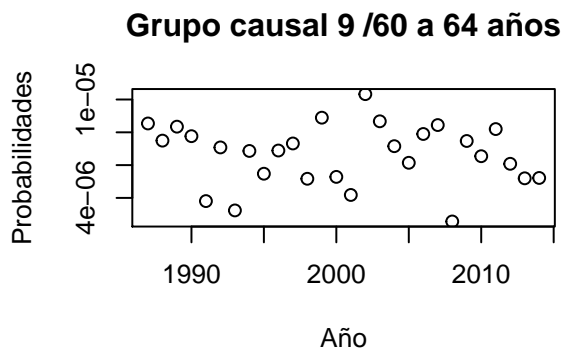



Evolución probabilidades de fallecimiento

Dibujemos las probabilidades de muerte según su evolución en los años para el grupo de edades de 60 a 65:

```
par(mfrow=c(2,2))
for(i in 2:ncaus){
  plot(x=c(1987:2014),y=as.vector(Q[[i]][14,]),main = paste("Grupo causal", i-1,"/60 a 64 años"),xlab=
}
```

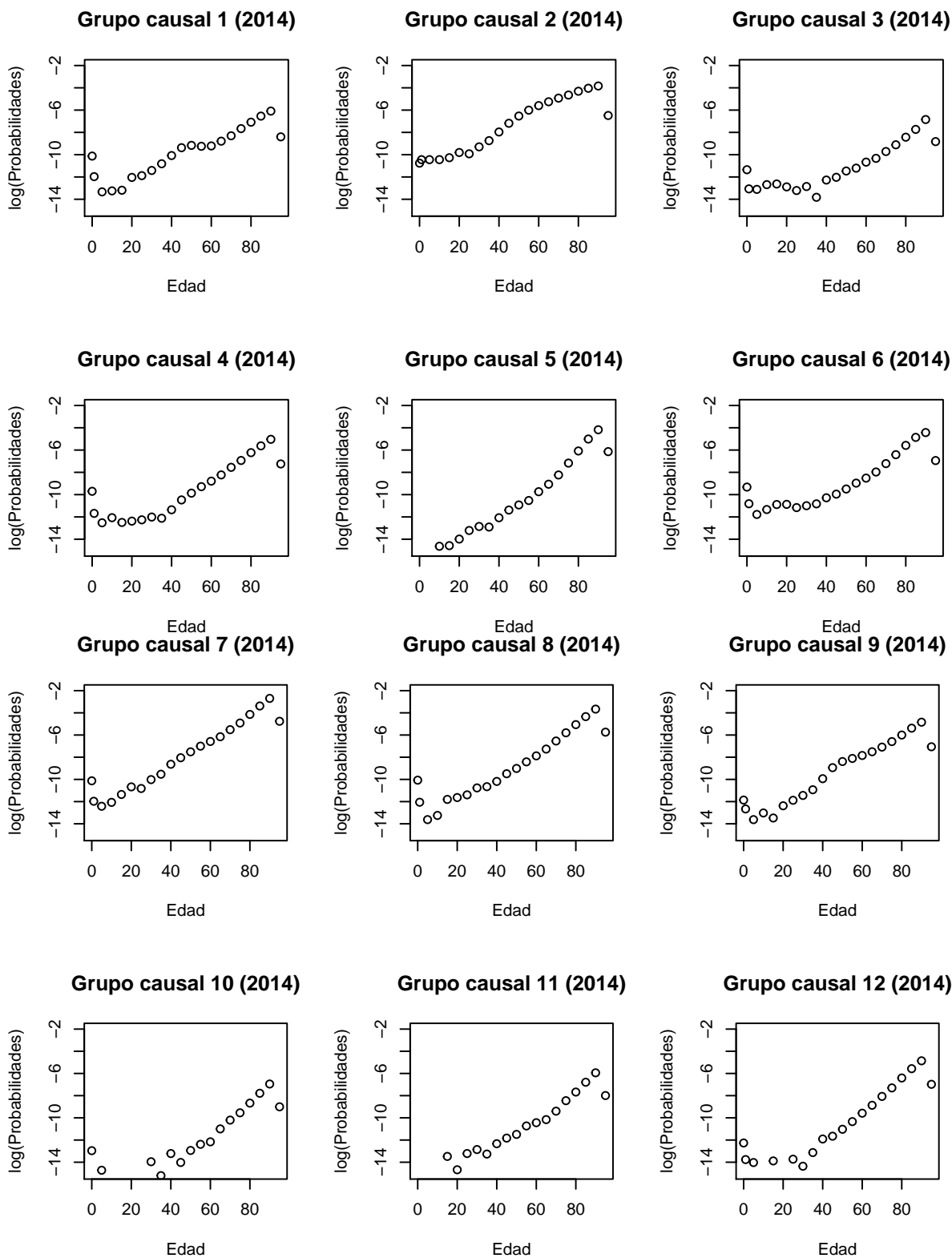


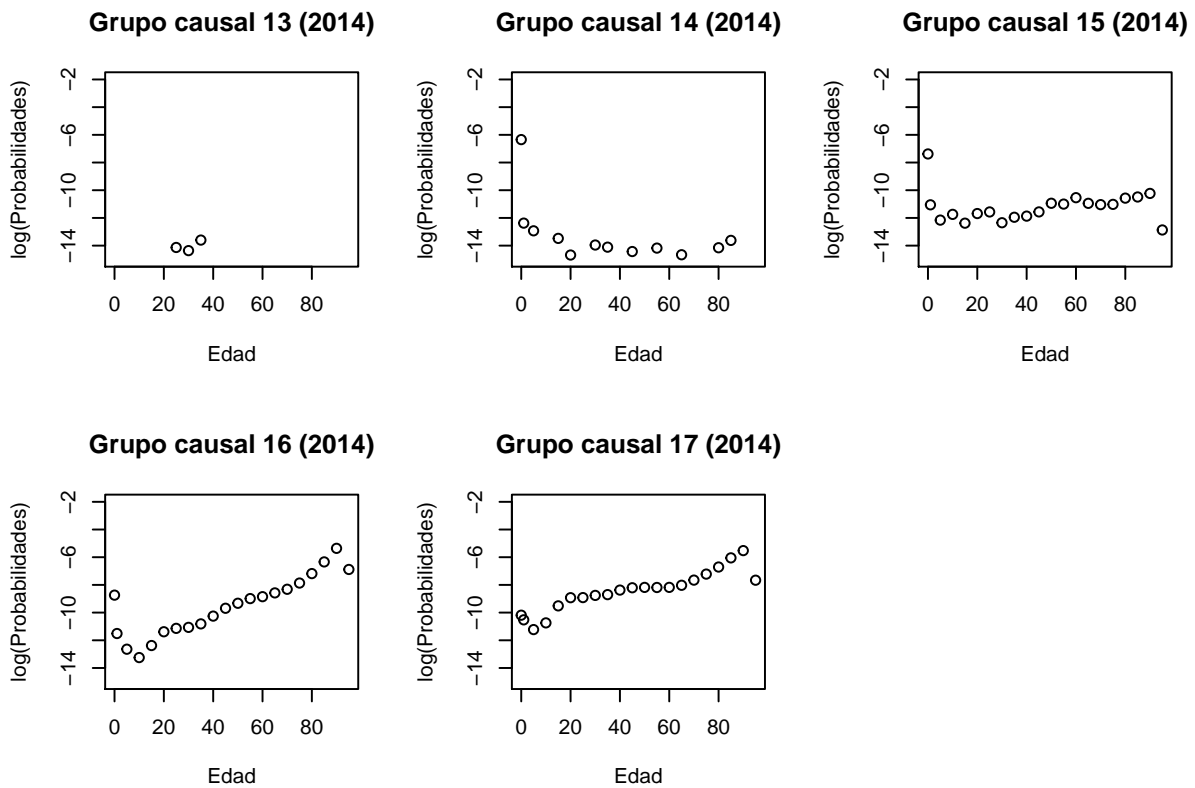


Evolución según la causa

Dibujemos ahora el logaritmo de las probabilidades de fallecimiento para cada una de las causas con los datos de 2014.

```
par(mfrow=c(2,3))
for(i in 1:ncaus) {
  plot(x=c(0,1,seq(5,95,by = 5)),y=log(Q[[i]][,nany]),ylim=c(-15,-2),main = paste("Grupo causal", i,"
  })
```





Unimos las causas más relacionadas

```
nclust <- 4
D.clust <- list()
D.clust[[1]] <- Reduce("+", D[1])
D.clust[[2]] <- Reduce("+", D[c(2,3,4,5,6,8,9,10,11,12)])
D.clust[[3]] <- Reduce("+", D[c(7,14,15,17)])
D.clust[[4]] <- Reduce("+", D[c(13,16)])

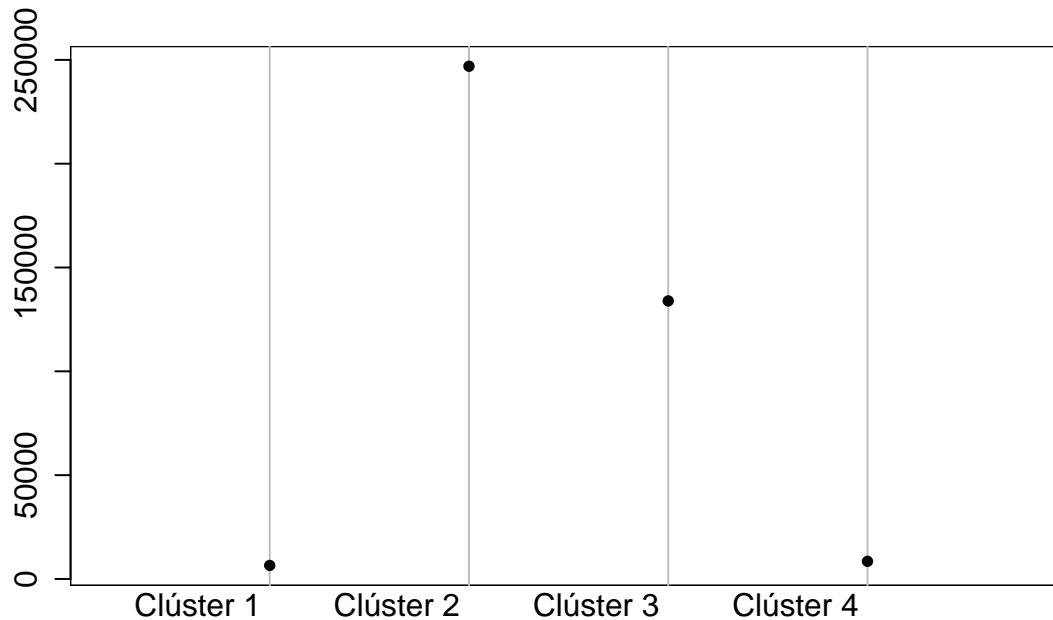
Q.clust <- D.clust
for (k in 1:nclust){
  for (i in 1:nint){
    for (j in 1:nany){
      Q.clust[[k]][i,j] <- D.clust[[k]][i,j]/sup[i,j]
    }
  }
}

par(mfrow=c(1,1))
D.total.clust <- cbind(sum(D.clust[[1]][, "X2014"]), sum(D.clust[[2]][, "X2014"]),
                      sum(D.clust[[3]][, "X2014"]), sum(D.clust[[4]][, "X2014"]))

labclust <- c(1:4)
for(i in 1:4){ labclust[i] <- paste("Clúster", i)}
dotchart2(D.total.clust, labels=labclust,
```

```
main="Distribución de defunciones de los clústers (Cifras absolutas) - 2014",
horizontal=FALSE)
```

Distribución de defunciones de los clústers (Cifras absolutas) – 201



```
Q.total.2 <- Reduce("+",Q.clust)
identical(Q.total,Q.total.2)#Aunque da falso, es por codificación

## [1] FALSE

identical(sum(Q.total),sum(Q.total.2))#Sí que suman lo mismo

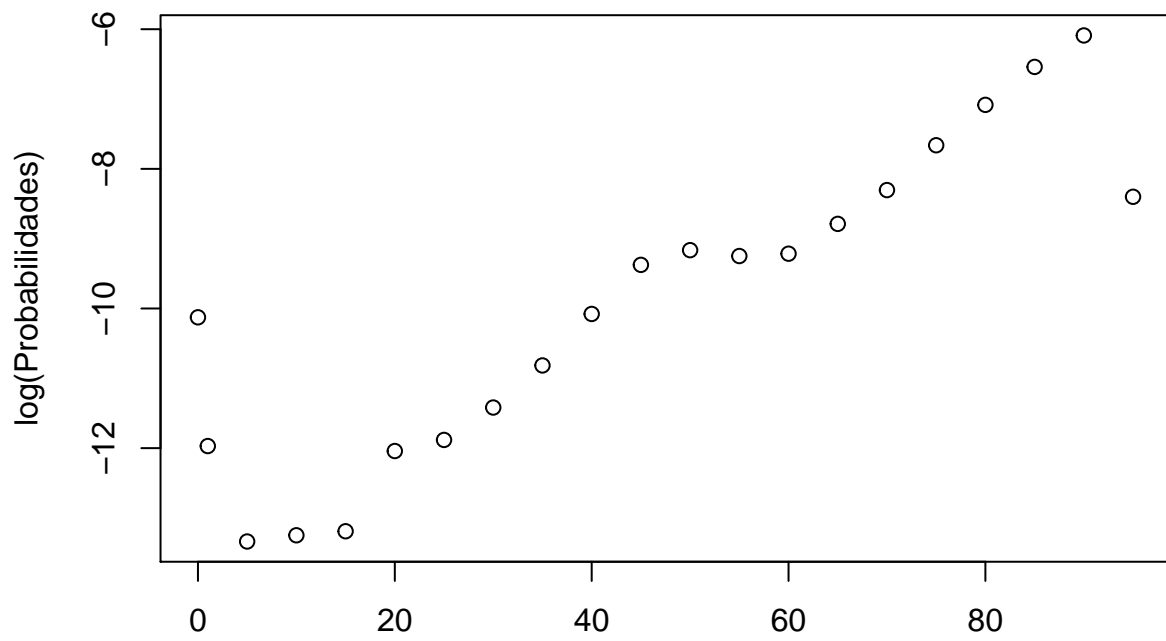
## [1] TRUE

#Fijarse que estos dos números son iguales pero el identical nos lo devuelve como falso
Q.total[nint,"X2013"]==Q.total.2[nint,"X2013"]

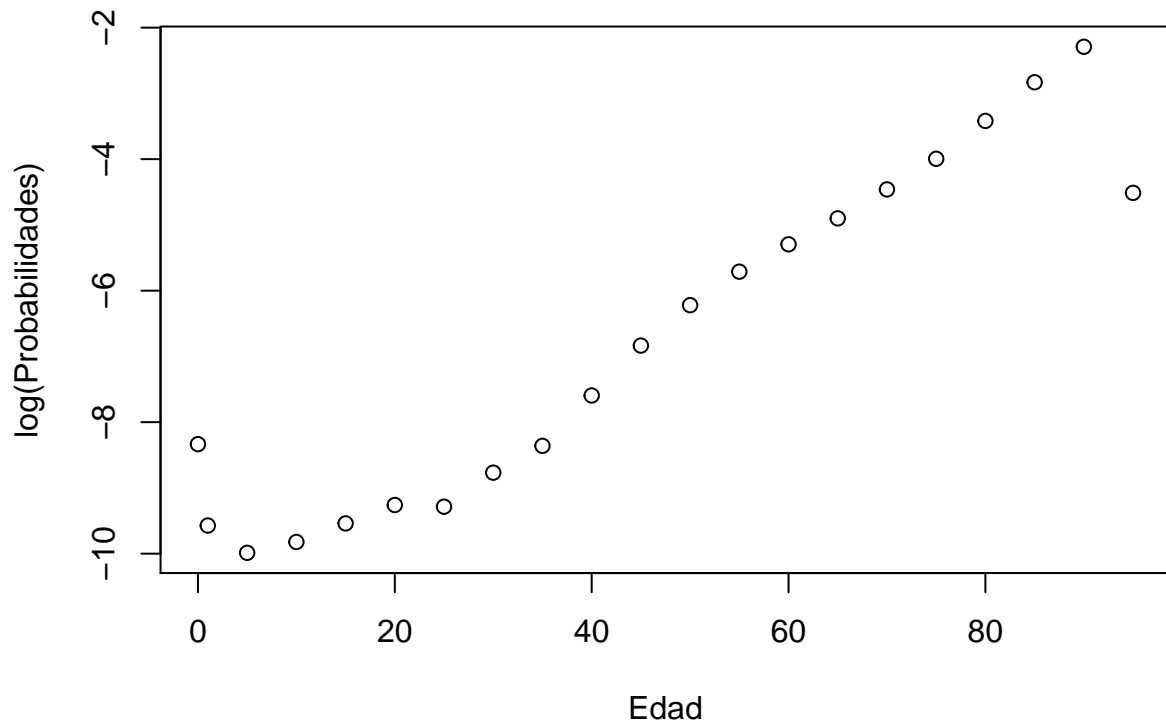
## [1] FALSE

par(mfrow=c(1,1))
for (i in 1:nclust){
  plot(x=c(0,1,seq(5,95,by =5)),
       y=log(Q.clust[[i]][,nany]),
       main=paste("Cluster",i),
       ylab="log(Probabilidades)",
       xlab="Edad")
}
```

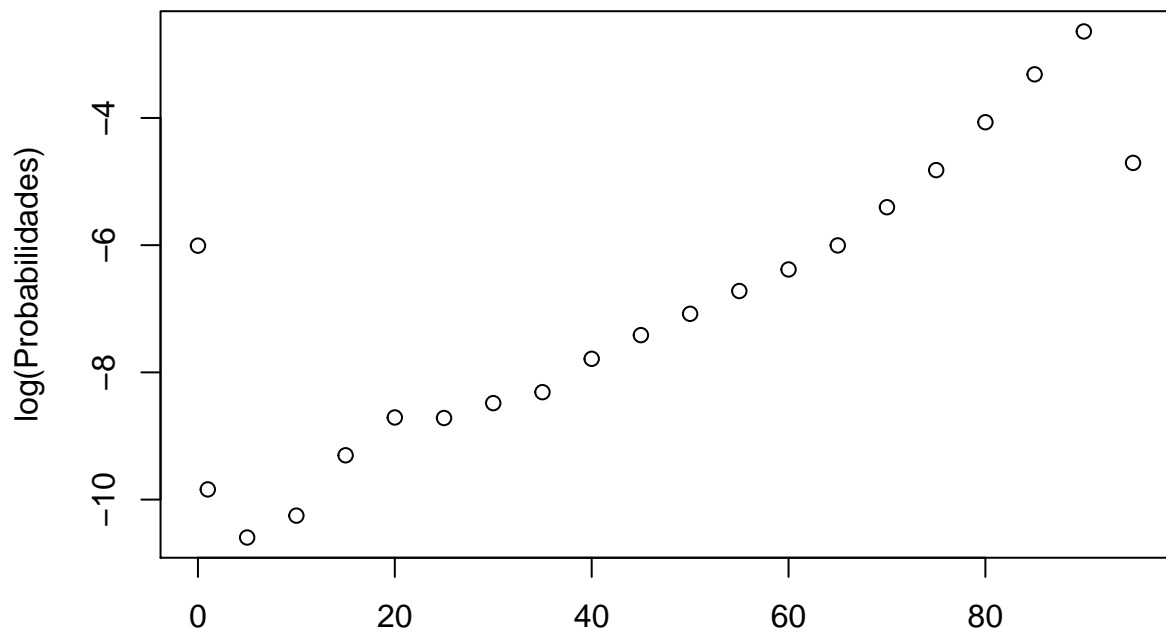
Cluster 1



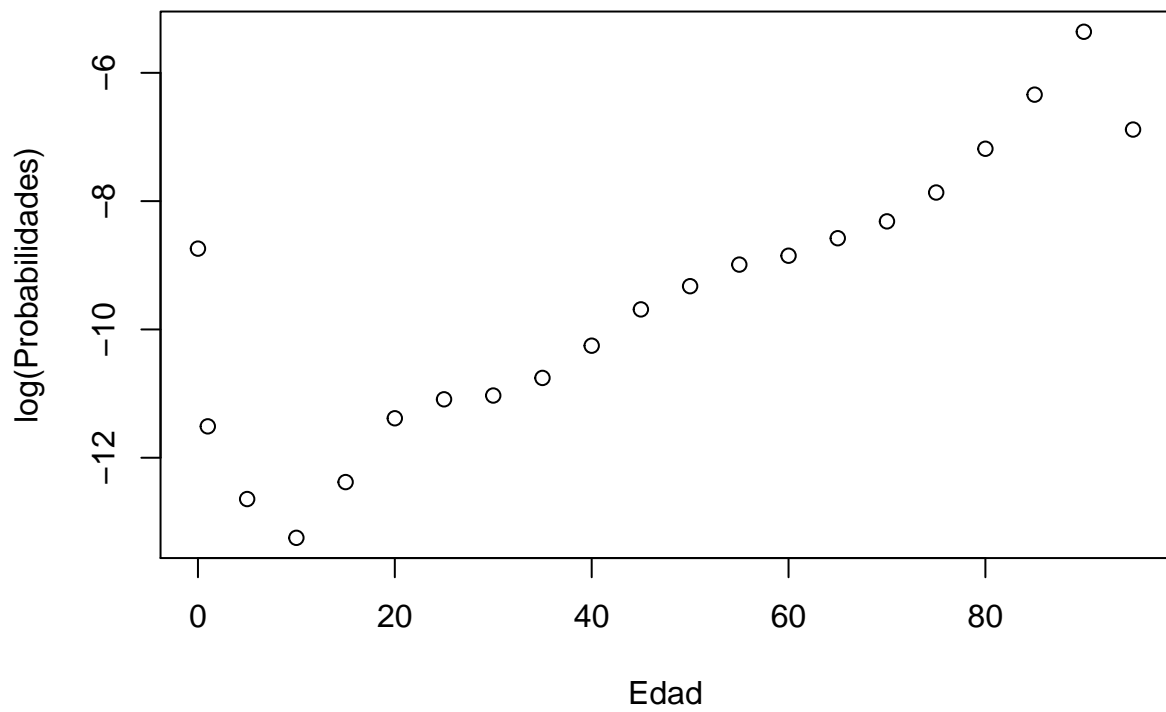
Cluster 2



Cluster 3



Cluster 4

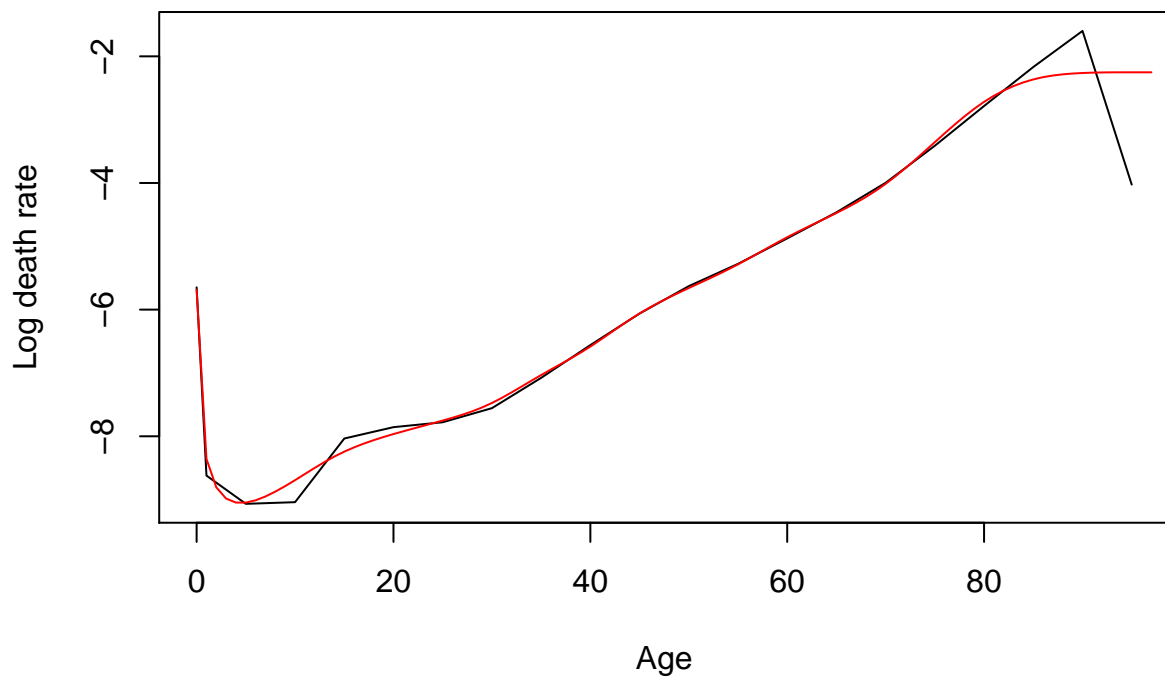


Lee-Carter - Introducción de datos

```
#ages=c(0.5,1.5,seq(7.5,97.5,5))
demog.total<-demogdata(Q.total, sup,ages=c(0,1,seq(5,95,5)),
                      years=c(1987:2014),
                      type="mortality", name="Total", label="España")

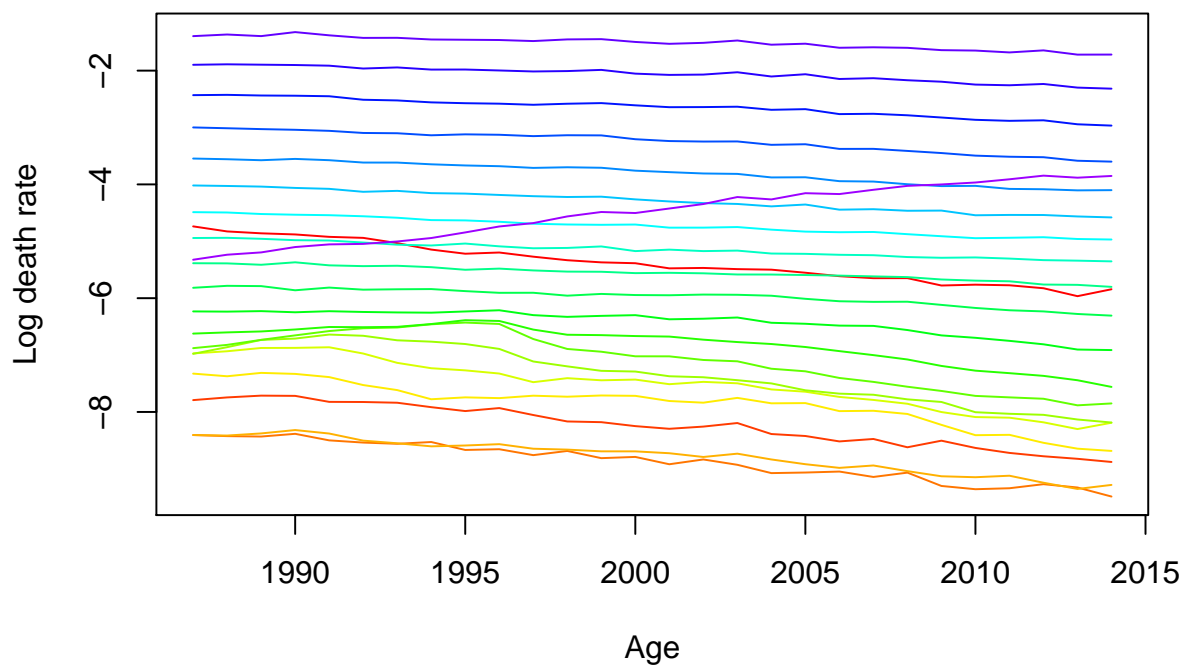
demog.total.suave <- smooth.demogdata(demog.total)
plot(demog.total,year=2008)
lines(demog.total.suave,year=2008,col="red")
```

España: total death rates (2008)



```
plot.demogdata(demog.total,plot.type="time") #each age is shown as a separate time series in a time plot
```

España: total death rates (1987–2014)



```
tablamort <- lifetable(demog.total,type="period",years=2008,max.age=90)
```

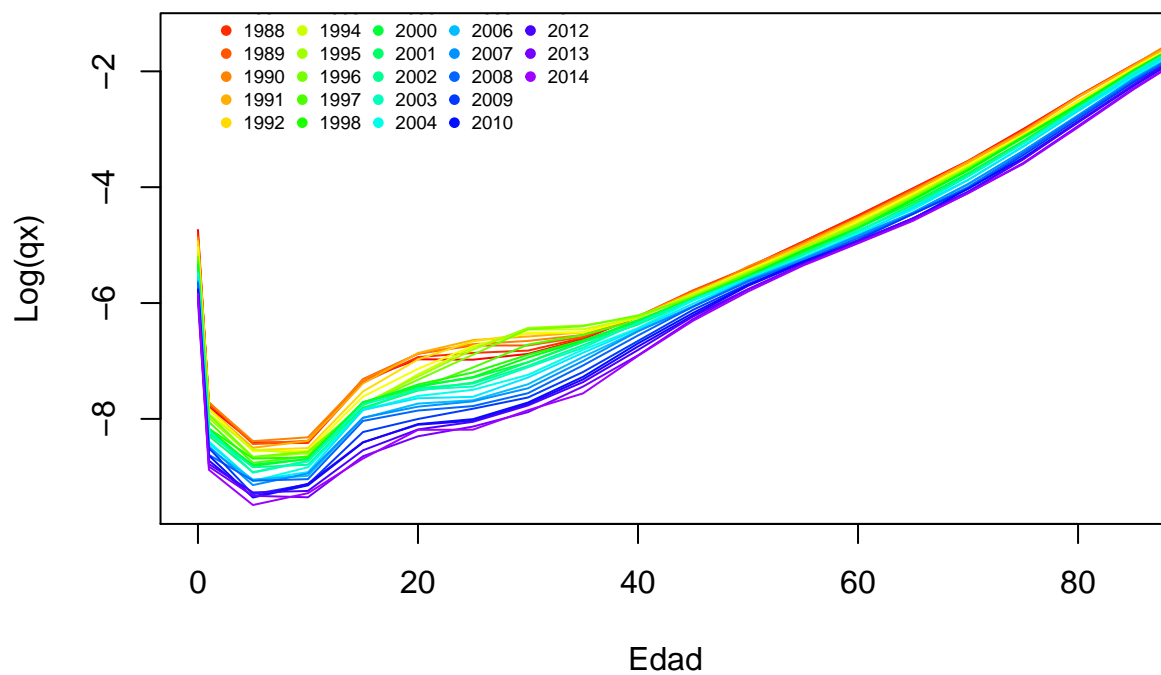
```
plot.demogdata(demog.total,plot.type="function",xlim=c(0,85), main = "España: tantos de mortalidad (1
```

```
fr.mort_age = extract.ages(demog.total,0:85,F)
```

```
fr.mort_age_yr = extract.years(fr.mort_age,1987:2014)
```

```
legend(1,-0.5,legend=unique(fr.mort_age_yr$year),
      col=rainbow(length(fr.mort_age_yr$year)*1.25), ncol=5, pch=19, cex=0.6, bty="n")
```

España: tantos de mortalidad (1987–2014)



```
#lines(mean(demog.total.suave),lwd=2,col=2)
```

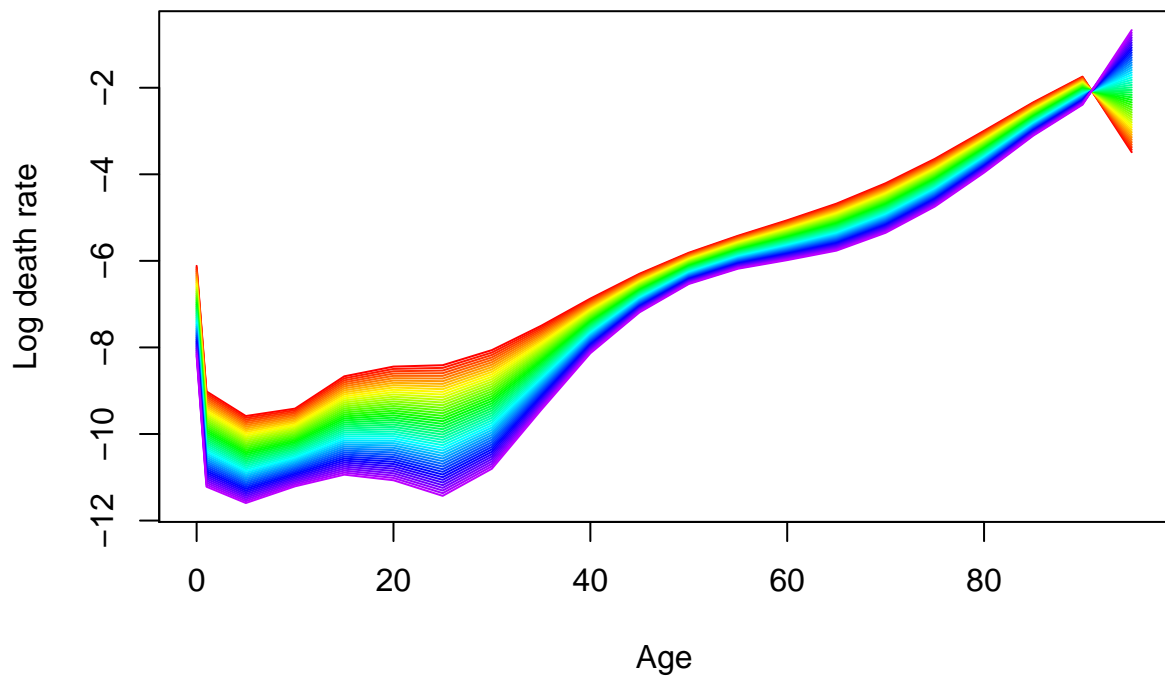
```
#lines(median(demog.total.suave),lwd=2,col=2)
```

Lee-Carter - Parámetros

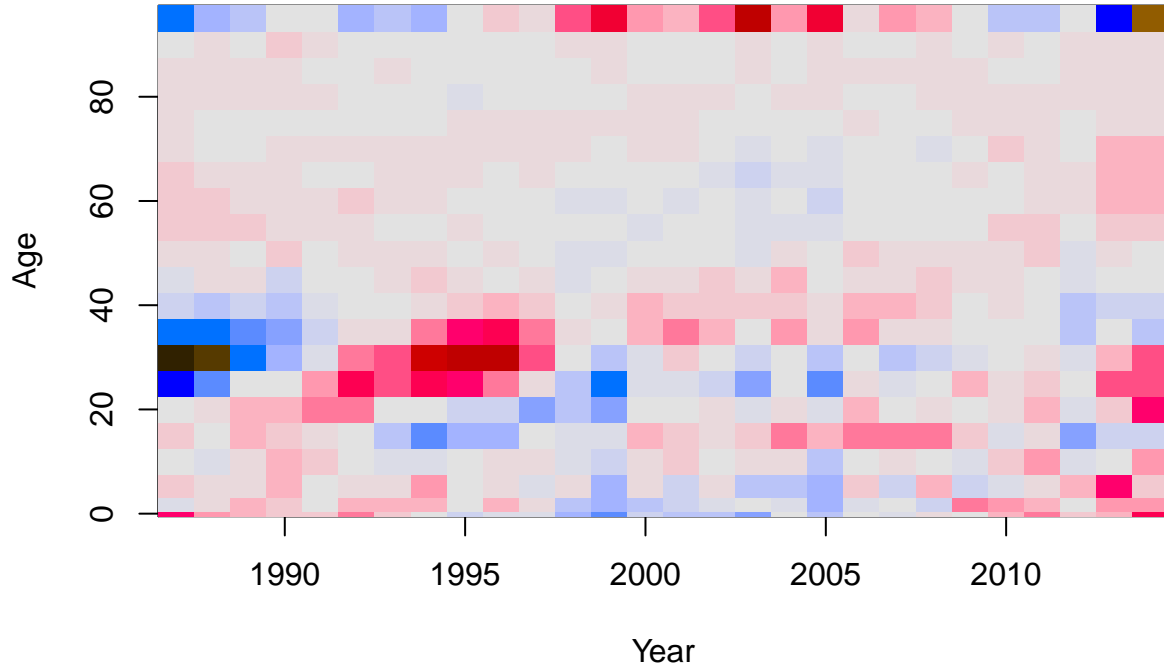
```
lc.model<- lca(demog.total,interpolate = TRUE)
fc.total <- forecast.lca(lc.model,50,jumpchoice="fit",se = "innovdrift")

plot(fc.total)
```

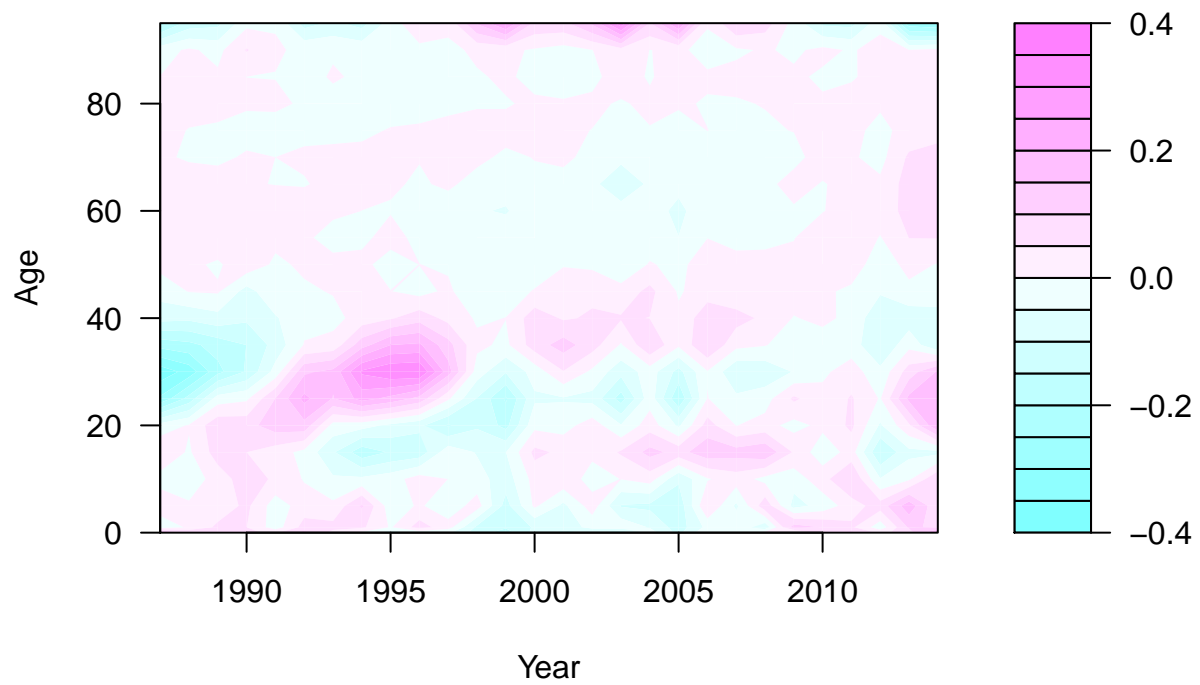
España: total death rates (2015–2064)



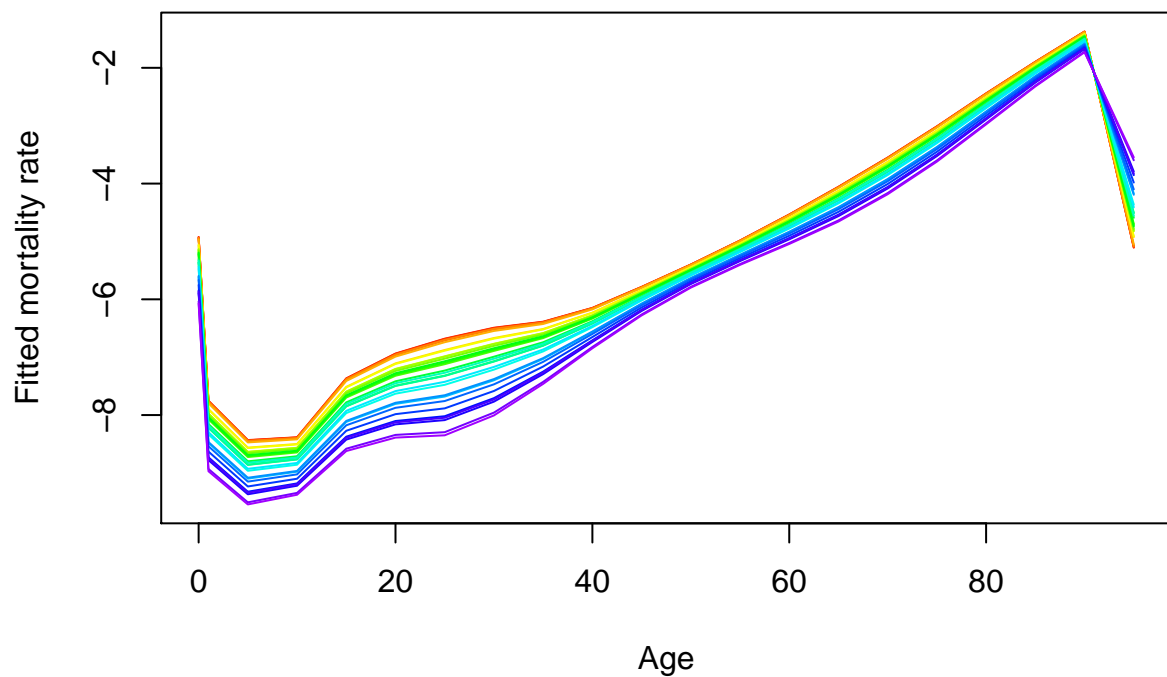
```
plot(residuals(lc.model))
```



```
plot(residuals(lc.model), type = "filled.contour") #Alternativo
```



```
plot(fitted(lc.model))
```



Lee-Carter - Simulaciones

```
lc.model.total<- lca(demog.total.suave,interpolate = TRUE)
fc.total <- forecast.lca(lc.model.total,50,jumpchoice="fit",se = "innovdrift")
```

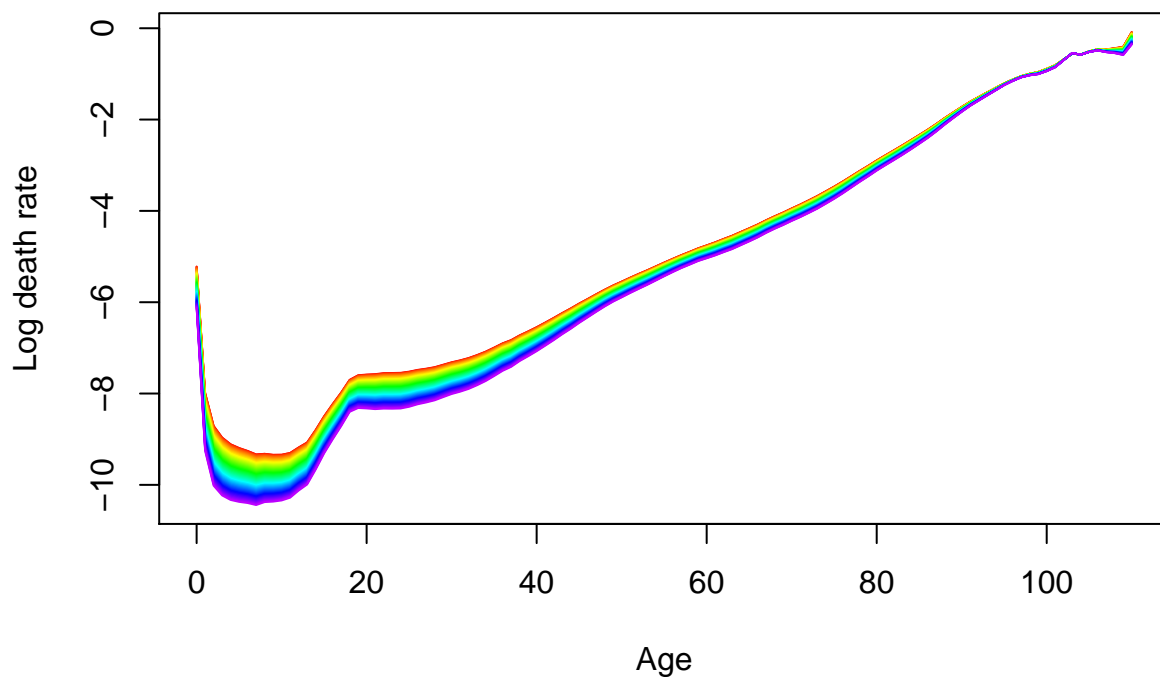
Francia

```
str(fr.mort)

## List of 7
## $ type : chr "mortality"
## $ label : chr "FRATNP"
## $ lambda: num 0
## $ year : int [1:191] 1816 1817 1818 1819 1820 1821 1822 1823 1824 1825 ...
## $ age : num [1:111] 0 1 2 3 4 5 6 7 8 9 ...
## $ rate :List of 3
## ..$ total : num [1:111, 1:191] 0.2053 0.0467 0.0341 0.023 0.016 ...
## .. ..- attr(*, "dimnames")=List of 2
## .. .. ..$ : chr [1:111] "0" "1" "2" "3" ...
## .. .. ..$ : chr [1:191] "1816" "1817" "1818" "1819" ...
## ..$ female: num [1:111, 1:191] 0.187 0.0467 0.0339 0.0229 0.016 ...
## .. ..- attr(*, "dimnames")=List of 2
## .. .. ..$ : chr [1:111] "0" "1" "2" "3" ...
## .. .. ..$ : chr [1:191] "1816" "1817" "1818" "1819" ...
## ..$ male : num [1:111, 1:191] 0.2229 0.0467 0.0343 0.0232 0.0161 ...
## .. ..- attr(*, "dimnames")=List of 2
## .. .. ..$ : chr [1:111] "0" "1" "2" "3" ...
## .. .. ..$ : chr [1:191] "1816" "1817" "1818" "1819" ...
## $ pop :List of 3
## ..$ total : num [1:111, 1:191] 834355 782273 714855 686823 674203 ...
## .. ..- attr(*, "dimnames")=List of 2
## .. .. ..$ : chr [1:111] "0" "1" "2" "3" ...
## .. .. ..$ : chr [1:191] "1816" "1817" "1818" "1819" ...
## ..$ female: num [1:111, 1:191] 408224 382452 351454 337733 331576 ...
## .. ..- attr(*, "dimnames")=List of 2
## .. .. ..$ : chr [1:111] "0" "1" "2" "3" ...
## .. .. ..$ : chr [1:191] "1816" "1817" "1818" "1819" ...
## ..$ male : num [1:111, 1:191] 426130 399821 363401 349090 342627 ...
## .. ..- attr(*, "dimnames")=List of 2
## .. .. ..$ : chr [1:111] "0" "1" "2" "3" ...
## .. .. ..$ : chr [1:191] "1816" "1817" "1818" "1819" ...
## - attr(*, "class")= chr "demogdata"

france.fit <- fdm(fr.mort,year=2000:2006, order = 2)
france.fcast <- forecast(france.fit, 50)
plot(france.fcast)
```

FRATNP: total death rates (2007–2056)



```
models(france.fcast)
```

```
##
## -- Coefficient 1 --
## Series: xx[, i]
## ARIMA(1,1,1) with drift
##
## Coefficients:
##      ar1      ma1      drift
##      0.6383 -0.8145 -0.1265
## s.e.  0.1481  0.1120  0.0411
##
## sigma^2 estimated as 1.206: log likelihood=-285.97
## AIC=579.95  AICc=580.16  BIC=592.93
##
## -- Coefficient 2 --
## Series: xx[, i]
## ARIMA(2,1,1)
##
## Coefficients:
##      ar1      ar2      ma1
##      0.3818  0.2926 -0.9679
## s.e.  0.0758  0.0745  0.0280
##
## sigma^2 estimated as 0.9067: log likelihood=-259.4
## AIC=526.79  AICc=527.01  BIC=539.78
```


Española total

```
par(mfrow=c(1,1))
defu.spa <- rev(defu.spa)
rownames(defu.spa) <- defu.spa[,43]
defu.spa <- defu.spa[,c(-1,-43)]

sup.spa <- rev(sup.spa)
rownames(sup.spa) <- sup.spa[,43]
sup.spa <- sup.spa[,c(-1,-43)]
colnames(sup.spa) <- colnames(defu.spa)

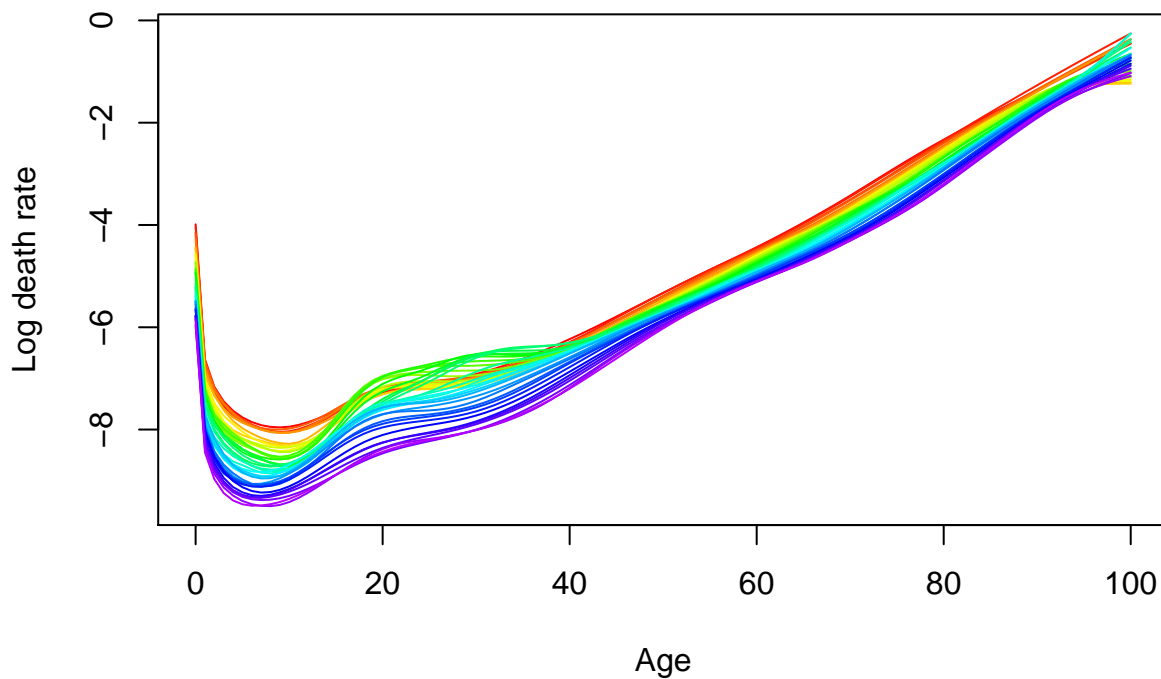
q.tot.hist <- defu.spa/sup.spa

demog.spain<-demogdata(q.tot.hist, sup.spa,ages=c(0:100),
                      years=c(1975:2015),
                      type="mortality", name="Total", label="Spain 1975-2015")

demog.spain.smooth <- smooth.demogdata(demog.spain)

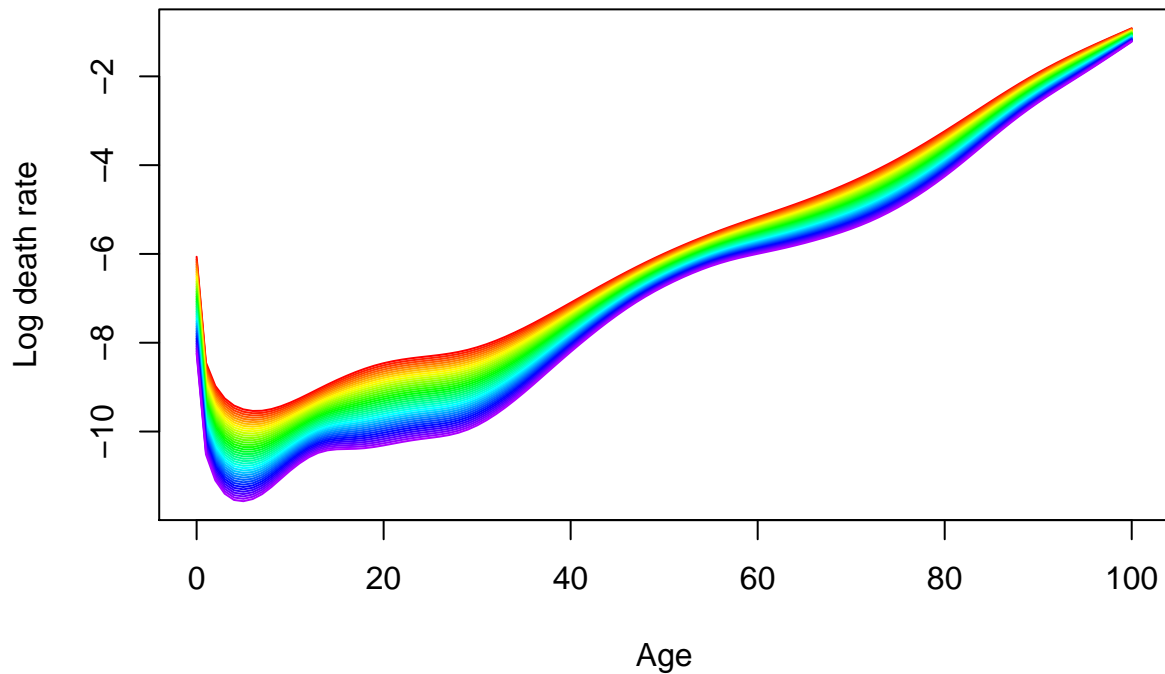
spa.fit <- fdm(demog.spain.smooth, order = 2)
plot(demog.spain.smooth)
```

Spain 1975–2015: total death rates (1975–2015)



```
spa.fcast <- forecast(spa.fit, 40)
plot(spa.fcast)
```

Spain 1975–2015: total death rates (2016–2055)



Tasas de variación

```
#Tasas de orden 1
tasas.1 <- Q

for(k in 1:ncaus){
  for (i in 1:nint){
    for (j in 2:nany){

      tasas.1[[k]][i,j] <- (Q[[k]][i,j]-Q[[k]][i,j-1])/Q[[k]][i,j-1]

    }
  }
}
for(k in 1:ncaus){
  tasas.1[[k]] <- tasas.1[[k]][,-1]
}

#Tasas de orden 2
tasas.2 <- Q
```

```

for(k in 1:ncaus){
  for (i in 1:nint){
    for (j in 3:nany){

      tasas.2[[k]][i,j] <- (Q[[k]][i,j]-Q[[k]][i,j-2])/Q[[k]][i,j-2]

    }
  }
}
for(k in 1:ncaus){
  tasas.2[[k]] <- tasas.1[[k]][,c(-1,-2)]
}

```

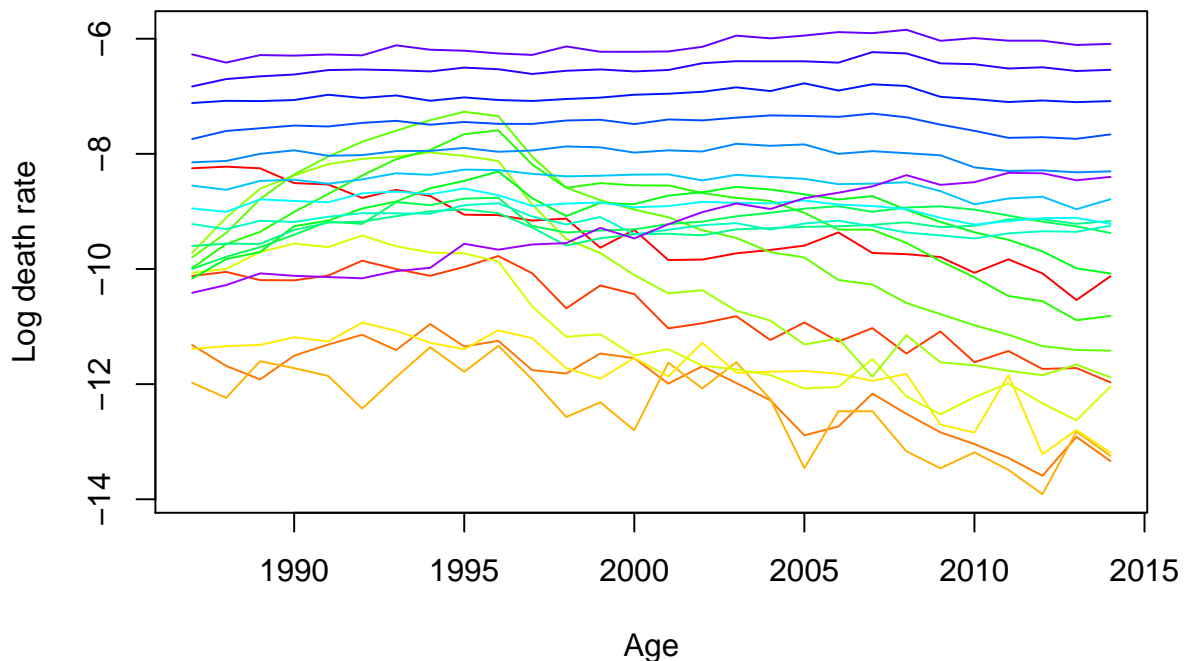
Modelización de las causas(clústers)

```

#Clúster1
demog.clust1<-demogdata(Q.clust[[1]], sup,ages=c(0,1,seq(5,95,5)),
  years=c(1987:2014),
  type="mortality", name="Cluster 1", label="España")
demog.clust1.suave <- smooth.demogdata(demog.clust1)
plot.demogdata(demog.clust1,plot.type="time") #each age is shown as a separate time series in a time

```

España: cluster 1 death rates (1987–2014)



```

#Clúster2
demog.clust2<-demogdata(Q.clust[[2]], sup,ages=c(0,1,seq(5,95,5)),
  years=c(1987:2014),

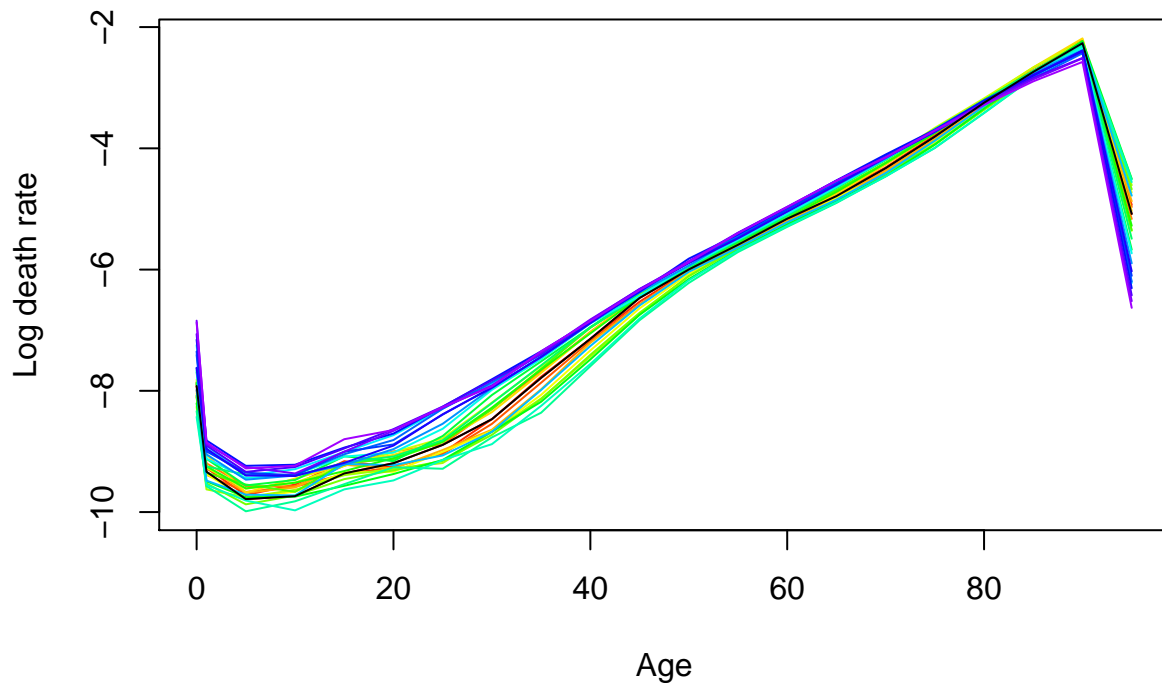
```

```

type="mortality", name="Cluster 2", label="España")
demog.clust2.suave <- smooth.demogdata(demog.clust2)
plot.demogdata(demog.clust2,plot.type="density") #each age is shown as a separate time series in a time series

```

España: cluster 2 death rates (1987–2014)

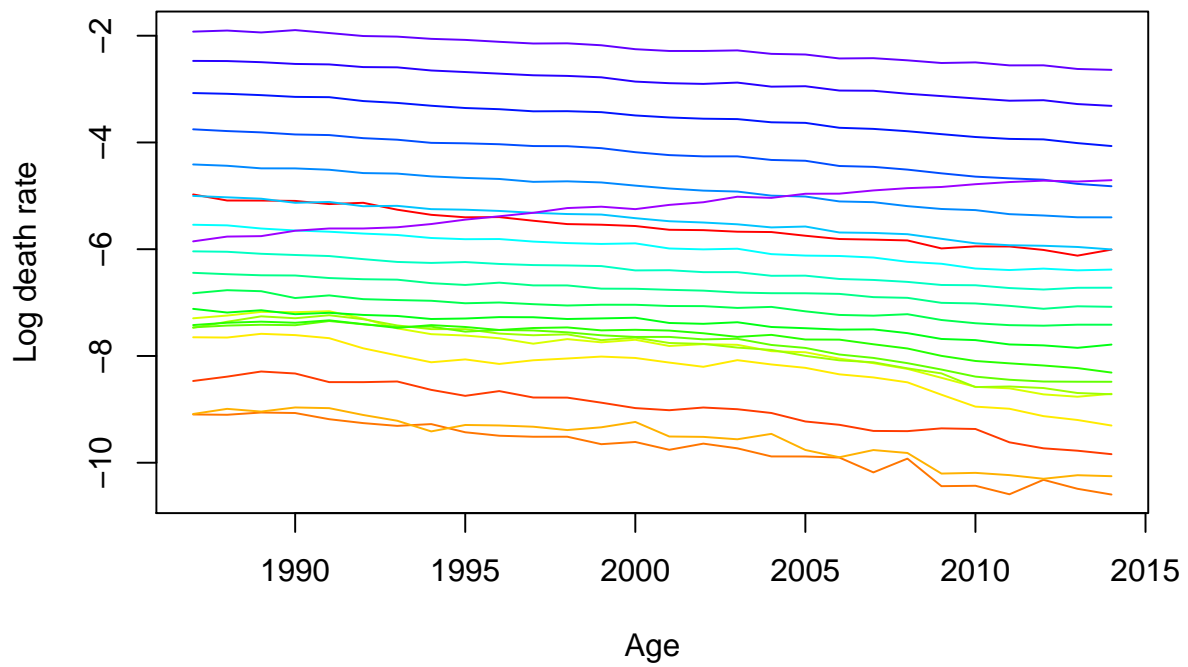


```

#Clúster3
demog.clust3<-demogdata(Q.clust[[3]], sup,ages=c(0,1,seq(5,95,5)),
years=c(1987:2014),
type="mortality", name="Cluster 3", label="España")
demog.clust3.suave <- smooth.demogdata(demog.clust3)
plot.demogdata(demog.clust3,plot.type="time") #each age is shown as a separate time series in a time series

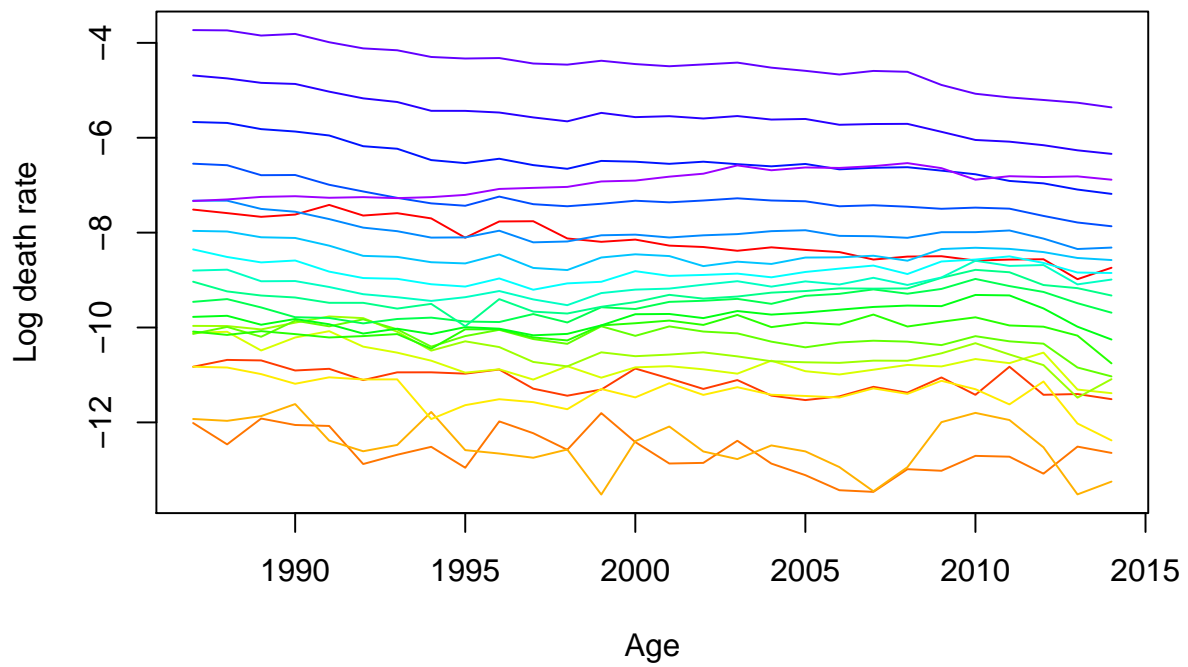
```

España: cluster 3 death rates (1987–2014)

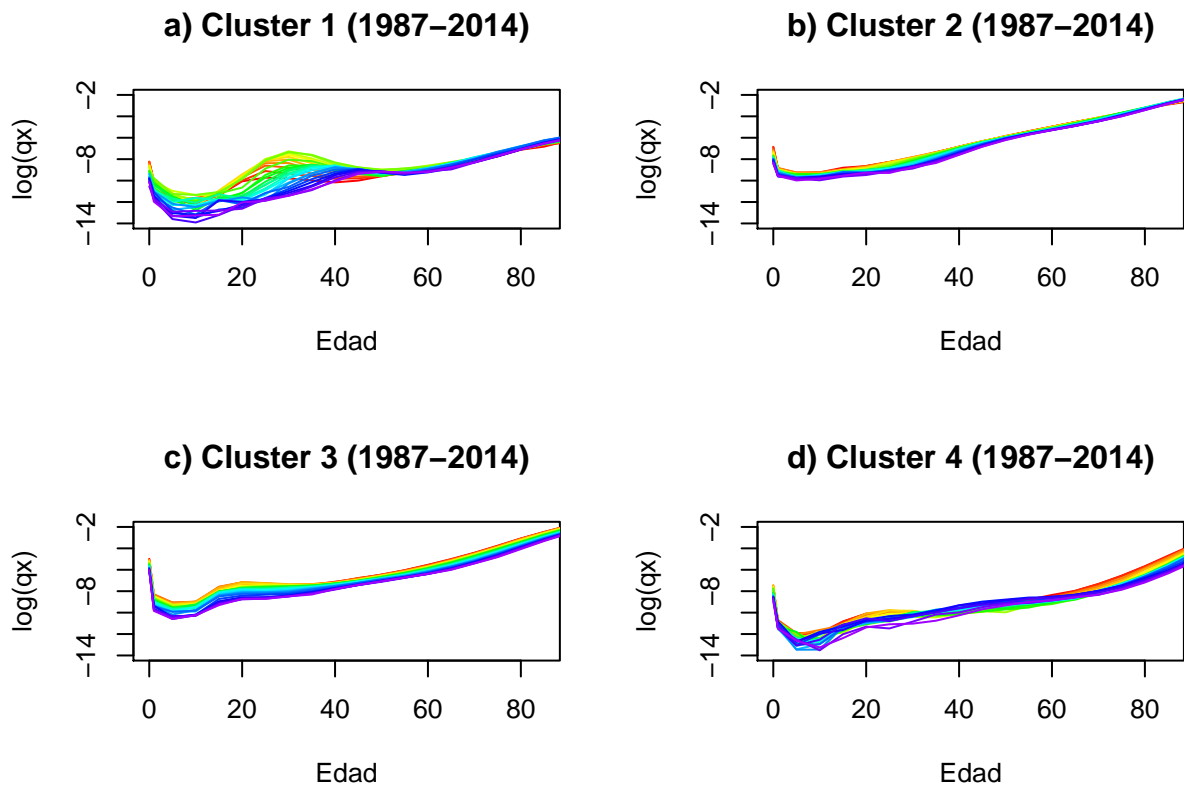


```
#Clúster4
demog.clust4<-demogdata(Q.clust[[4]], sup,ages=c(0,1,seq(5,95,5)),
                        years=c(1987:2014),
                        type="mortality", name="Cluster 4", label="España")
demog.clust4.suave <- smooth.demogdata(demog.clust4)
plot.demogdata(demog.clust4,plot.type="time") #each age is shown as a separate time series in a time
```

España: cluster 4 death rates (1987–2014)



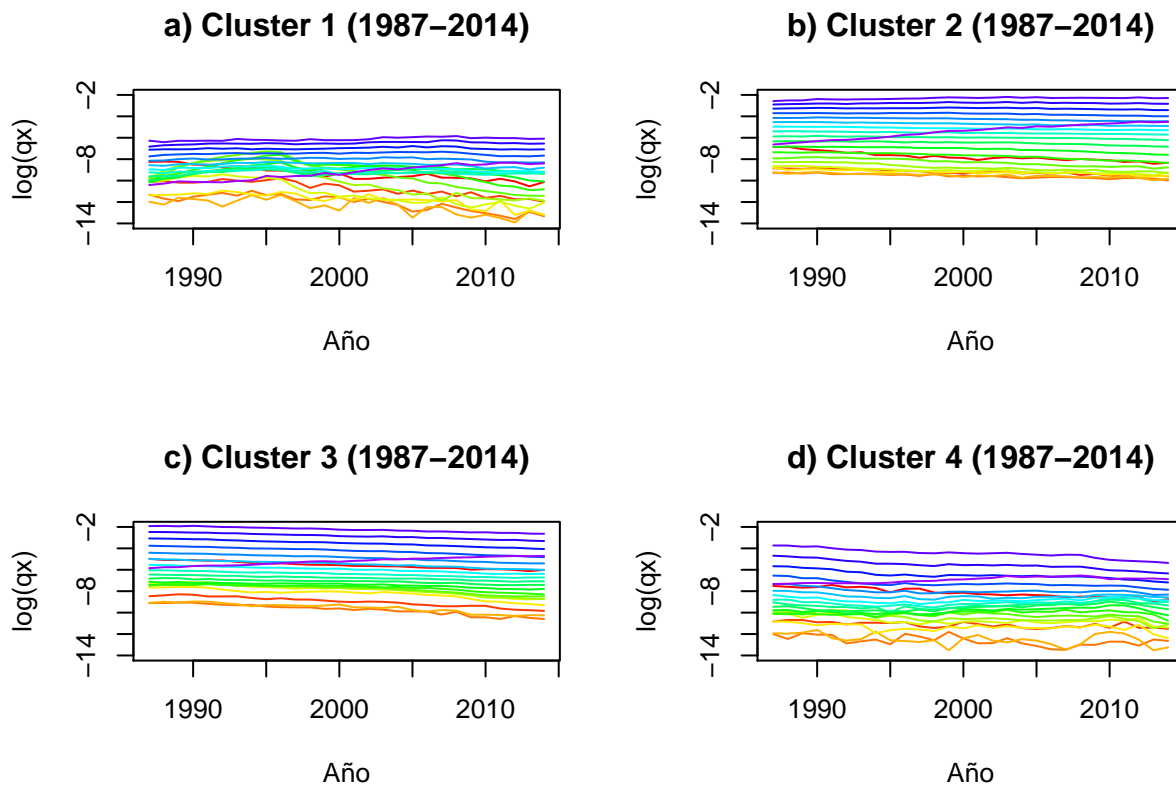
```
par(mfrow=c(2,2))
plot.demogdata(demog.clust1,plot.type="function",ylim=c(-14,-2),main = "a) Cluster 1 (1987-2014)"
, xlab="Edad",ylab="log(qx)",xlim=c(0,85))
plot.demogdata(demog.clust2,plot.type="function",ylim=c(-14,-2),main = "b) Cluster 2 (1987-2014)"
, xlab="Edad",ylab="log(qx)",xlim=c(0,85))
plot.demogdata(demog.clust3,plot.type="function",ylim=c(-14,-2),main = "c) Cluster 3 (1987-2014)"
, xlab="Edad",ylab="log(qx)",xlim=c(0,85))
plot.demogdata(demog.clust4,plot.type="function",ylim=c(-14,-2),main = "d) Cluster 4 (1987-2014)"
, xlab="Edad",ylab="log(qx)",xlim=c(0,85))
```



```

par(mfrow=c(2,2))
plot.demogdata(demog.clust1,plot.type="time",ylim=c(-14,-2),main = "a) Cluster 1 (1987-2014)"
, xlab="Año",ylab="log(qx)")
plot.demogdata(demog.clust2,plot.type="time",ylim=c(-14,-2),main = "b) Cluster 2 (1987-2014)"
, xlab="Año",ylab="log(qx)")
plot.demogdata(demog.clust3,plot.type="time",ylim=c(-14,-2),main = "c) Cluster 3 (1987-2014)"
, xlab="Año",ylab="log(qx)")
plot.demogdata(demog.clust4,plot.type="time",ylim=c(-14,-2),main = "d) Cluster 4 (1987-2014)"
, xlab="Año",ylab="log(qx)")

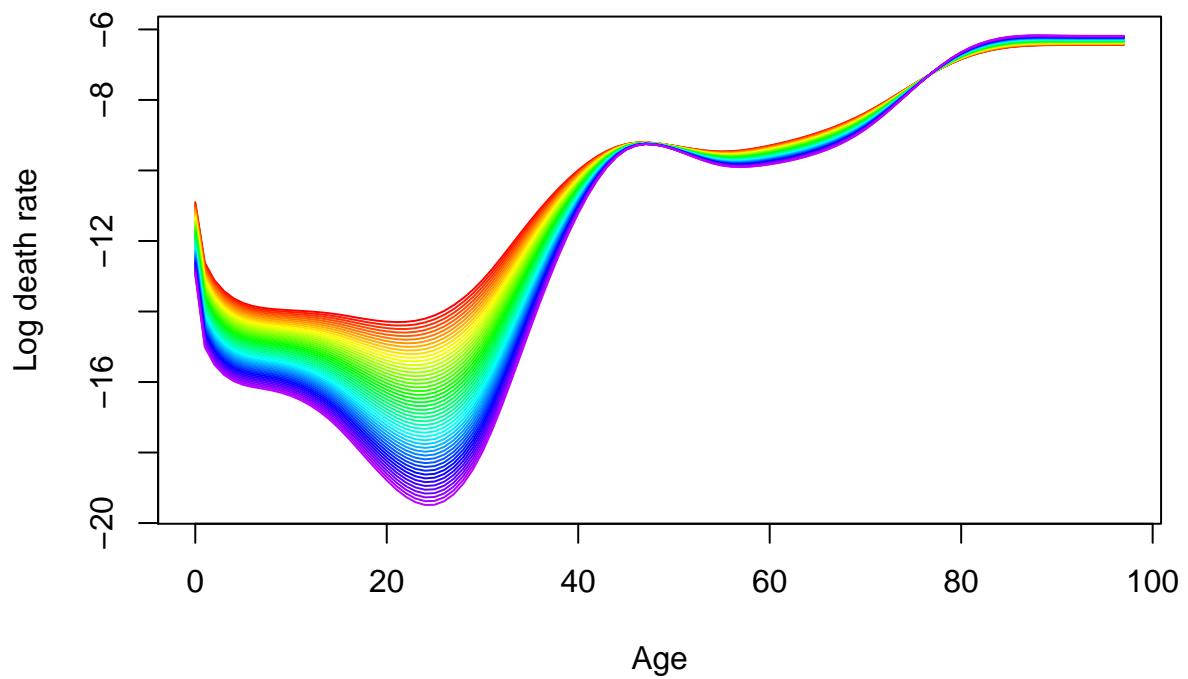
```



```
par(mfrow=c(1,1))
lc.model.clust1<- lca(demog.clust1.suave,interpolate = TRUE)

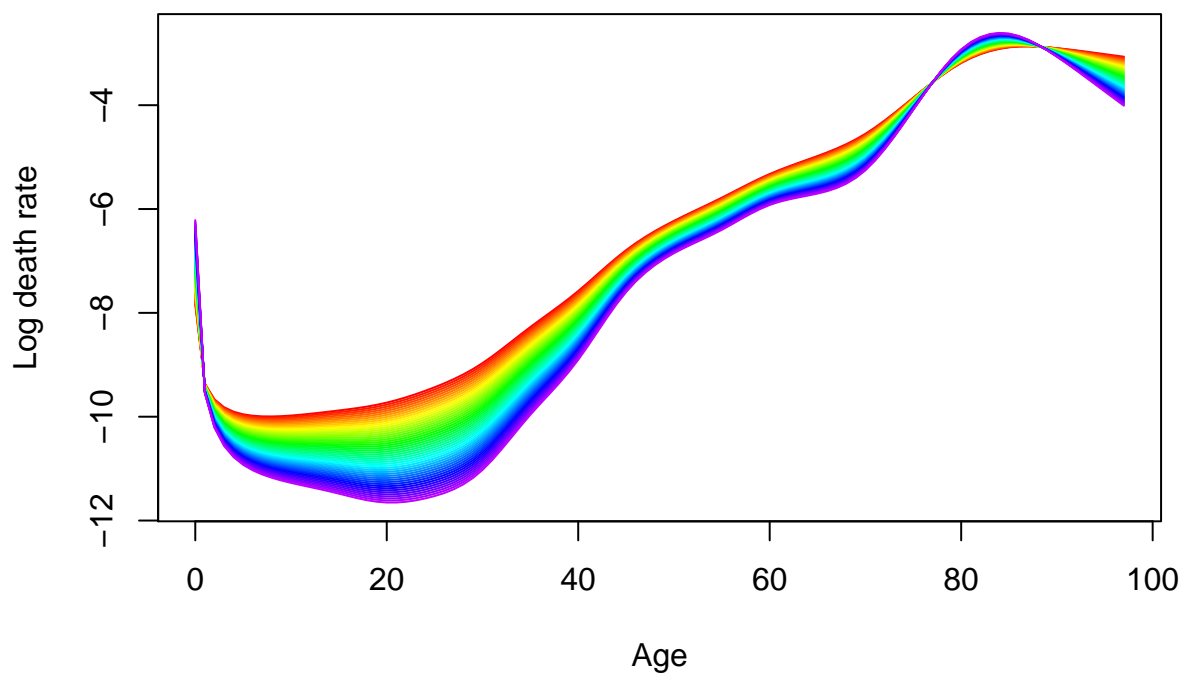
## Warning in newroot(FUN, guess, ...): No root exists. Returning closest
## Warning in newroot(FUN, guess, ...): No root exists. Returning closest
## Warning in newroot(FUN, guess, ...): No root exists. Returning closest
## Warning in newroot(FUN, guess, ...): No root exists. Returning closest
fc.clust1 <- forecast.lca(lc.model.clust1,50,jumpchoice="fit",se = "innovdrift")
plot(fc.clust1)
```


España: cluster 1 death rates (2015–2064)



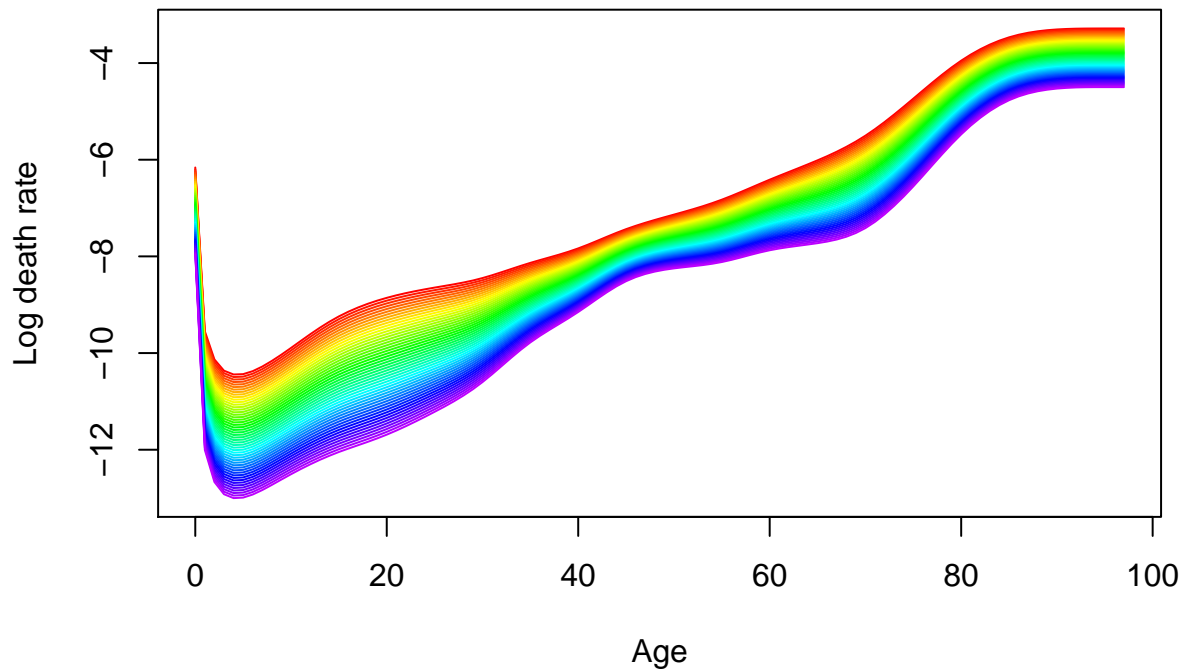
```
lc.model.clust2<- lca(demog.clust2.suave,interpolate = TRUE)  
fc.clust2 <- forecast.lca(lc.model.clust2,50,jumpchoice="fit",se = "innovdrift")  
plot(fc.clust2)
```

España: cluster 2 death rates (2015–2064)



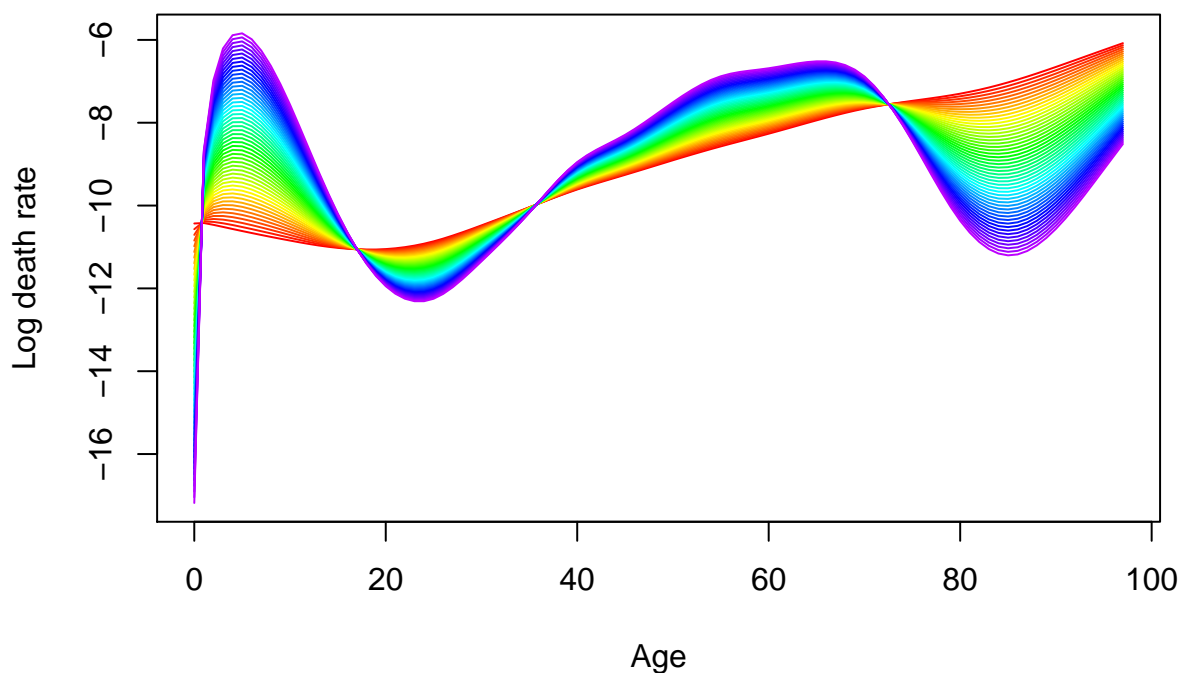
```
lc.model.clust3<- lca(demog.clust3.suave,interpolate = TRUE)  
fc.clust3 <- forecast.lca(lc.model.clust3,50,jumpchoice="fit",se = "innovdrift")  
plot(fc.clust3)
```

España: cluster 3 death rates (2015–2064)



```
lc.model.clust4<- lca(demog.clust4.suave,interpolate = TRUE)  
fc.clust4 <- forecast.lca(lc.model.clust4,50,jumpchoice="fit",se = "innovdrift")  
plot(fc.clust4)
```

España: cluster 4 death rates (2015–2064)



```
fc.total.agr <- fc.clust1$rate$`Cluster 1` +fc.clust2$rate$`Cluster 2`+fc.clust3$rate$`Cluster 3`+fc.
fc.clust2$e0
```

```
## Time Series:
```

```
## Start = 2015
```

```
## End = 2064
```

```
## Frequency = 1
```

```
## [1] 91.60776 91.80231 91.99867 92.19690 92.39705 92.59918 92.80335
```

```
## [8] 93.00963 93.21807 93.42873 93.64167 93.85695 94.07464 94.29480
```

```
## [15] 94.51748 94.74275 94.97067 95.20131 95.43472 95.67097 95.91013
```

```
## [22] 96.15226 96.39742 96.64567 96.89709 97.15174 97.40968 97.67098
```

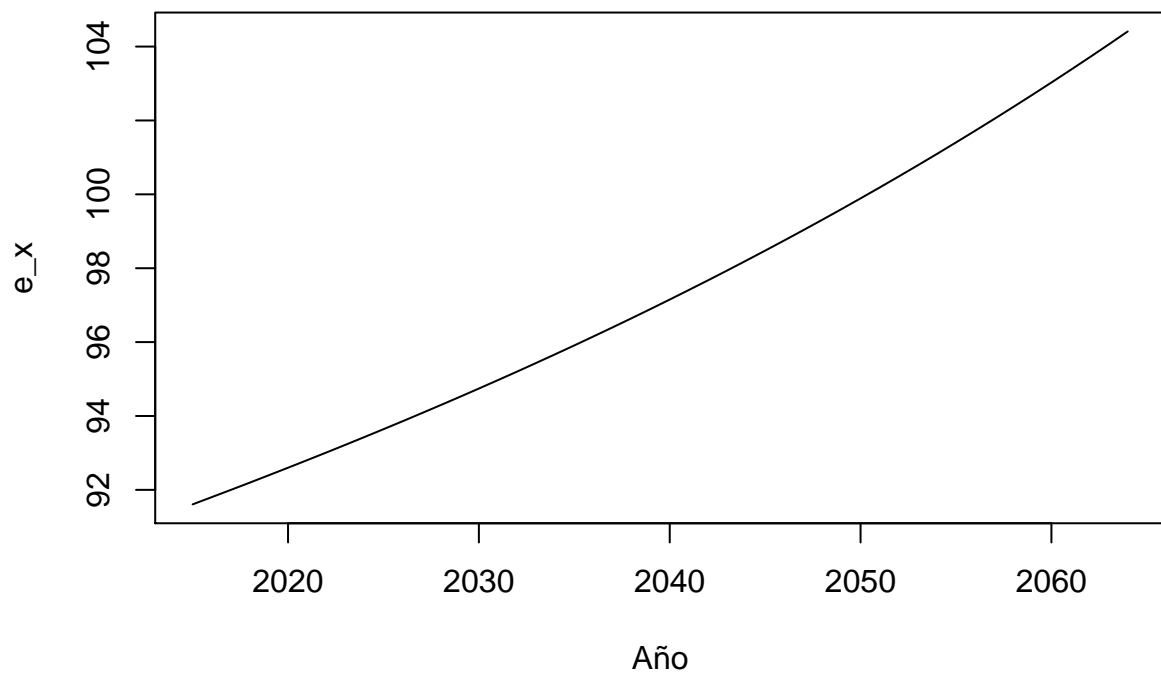
```
## [29] 97.93570 98.20393 98.47571 98.75112 99.03024 99.31311 99.59983
```

```
## [36] 99.89045 100.18505 100.48369 100.78645 101.09340 101.40461 101.72015
```

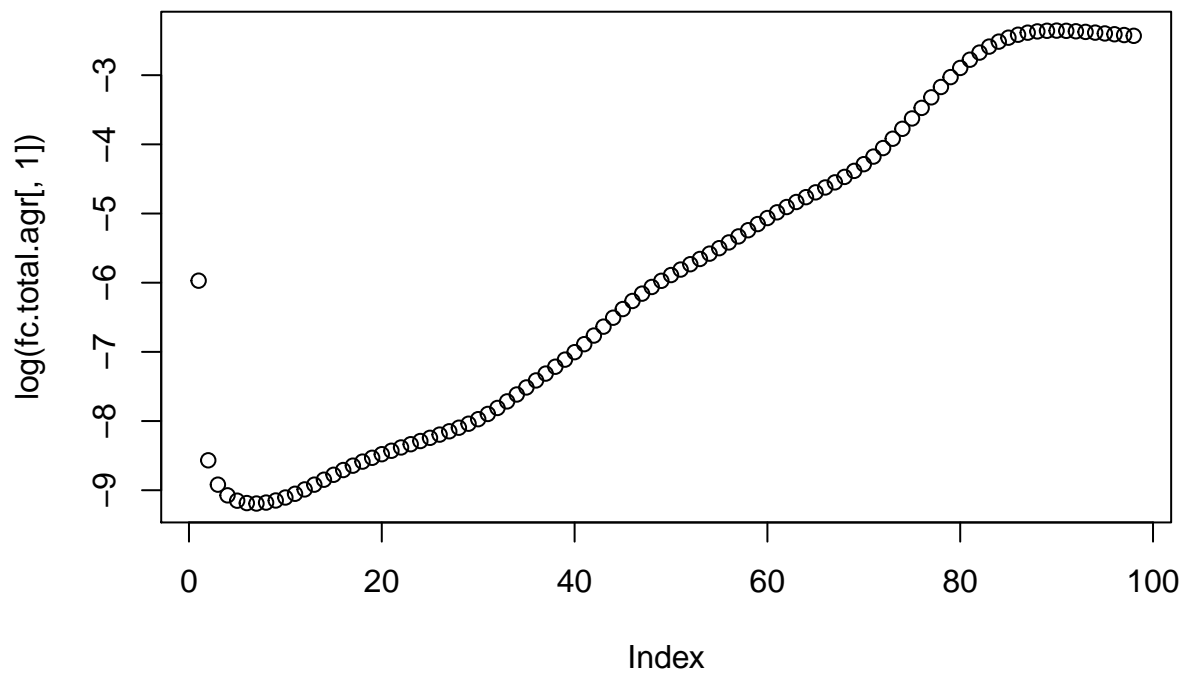
```
## [43] 102.04009 102.36451 102.69348 103.02708 103.36537 103.70844 104.05635
```

```
## [50] 104.40918
```

```
plot(fc.clust2$e0,xlab="Año",ylab="e_x")
```



```
plot(log(fc.total.agr[,1]))
```



```
#ax y bx
par.edad <- cbind(lc.model.total$ax,lc.model.total$bx,
  lc.model.clust1$ax,lc.model.clust1$bx,
  lc.model.clust2$ax,lc.model.clust2$bx,
  lc.model.clust3$ax,lc.model.clust3$bx,
  lc.model.clust4$ax,lc.model.clust4$bx)
colnames(par.edad)=c("ax_total","bx_total","ax_clust1","bx_clust1")
```

```

, "ax_clust2", "bx_clust2", "ax_clust3", "bx_clust3", "ax_clust4", "bx_clust4")

write.csv(par.edad, "Parámetros_edad.csv")

#kt

par.tiempo <- cbind(lc.model.total$kt,
  lc.model.clust1$kt,
  lc.model.clust2$kt,
  lc.model.clust3$kt,
  lc.model.clust4$kt)
colnames(par.tiempo)=c("kt_total", "kt_clust1", "kt_clust2", "kt_clust3", "kt_clust4")
rownames(par.tiempo) <- c(1987:2014)
write.csv(par.tiempo, "Parámetros_tiempo.csv")

xtable(par.tiempo)

## % latex table generated in R 3.3.2 by xtable 1.8-2 package
## % Mon Jun 26 21:15:36 2017
## \begin{table}[ht]
## \centering
## \begin{tabular}{rrrrrr}
## \hline
## & kt\_total & kt\_clust1 & kt\_clust2 & kt\_clust3 & kt\_clust4 \\
## \hline
## 1987 & 41.09 & -29.38 & 14.95 & 45.13 & 1.68 \\
## 1988 & 41.88 & -47.34 & 18.50 & 44.77 & 1.63 \\
## 1989 & 40.71 & 4.98 & 19.95 & 42.56 & 1.31 \\
## 1990 & 41.65 & 24.36 & 26.38 & 40.63 & 1.36 \\
## 1991 & 39.49 & 36.79 & 23.50 & 38.99 & 1.00 \\
## 1992 & 33.30 & 45.65 & 18.93 & 32.36 & 0.60 \\
## 1993 & 34.40 & 53.63 & 22.76 & 31.39 & 0.52 \\
## 1994 & 29.52 & 56.43 & 22.01 & 25.01 & 0.05 \\
## 1995 & 28.55 & 61.58 & 23.19 & 22.00 & 0.01 \\
## 1996 & 26.14 & 60.41 & 20.55 & 18.71 & 0.13 \\
## 1997 & 22.20 & 32.24 & 20.08 & 14.26 & -0.29 \\
## 1998 & 2.49 & 17.59 & 1.42 & 13.67 & -0.40 \\
## 1999 & 2.95 & 14.62 & 6.24 & 10.43 & 0.04 \\
## 2000 & -3.23 & 8.75 & -0.71 & 3.15 & -0.07 \\
## 2001 & -8.66 & 9.71 & -5.19 & -2.32 & -0.13 \\
## 2002 & -8.56 & 11.64 & -3.52 & -3.96 & -0.08 \\
## 2003 & -5.77 & 22.67 & 1.78 & -3.77 & 0.04 \\
## 2004 & -15.22 & 18.33 & -10.02 & -11.78 & -0.18 \\
## 2005 & -13.27 & 19.07 & -3.88 & -13.27 & -0.20 \\
## 2006 & -24.76 & 10.10 & -17.88 & -23.16 & -0.44 \\
## 2007 & -23.69 & 18.46 & -15.65 & -23.98 & -0.24 \\
## 2008 & -28.38 & 12.29 & -19.33 & -29.85 & -0.30 \\
## 2009 & -34.01 & -29.66 & -22.17 & -36.70 & -0.65 \\
## 2010 & -39.30 & -166.57 & -30.09 & -40.26 & -0.58 \\
## 2011 & -42.23 & -117.78 & -30.04 & -45.12 & -0.77

```

```

##    2012 & -38.54 & -115.51 & -21.18 & -44.27 & -1.01 \\
##    2013 & -47.97 & -113.51 & -34.72 & -50.64 & -1.51 \\
##    2014 & -48.58 & -111.27 & -33.11 & -52.61 & -1.89 \\
##    \hline
## \end{tabular}
## \end{table}

```