Recent diabetes incidence ratesin Denmark

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Contents

Chapter 1

Introduction

First we introduce the relevant packages

```
> options( width=120 )
> library( Epi )
> library( splines )
```

1.1 Incidence rates

We model the incidence rates from a tabulation of the diabetes register made in conjunction with the annual update of the register. The analytical units are the Lexis triangles, classified by age, period and cohort ($\blacktriangledown$ and $\blacktriangle$):

```
> load( "C:/Bendix/Steno/DM-register/NDR/2009/data/inc.Rdata" )
> head( inc )
```

```
  sex         A        P        C D upper        Y      dm.Y   well.Y
1   K 0.6666667 1995.333 1994.667 2     1 17100.67 0.1300479 17100.54
2   K 0.3333333 1995.667 1995.333 0     0 17025.50 0.0000000 17025.50
3   K 0.6666667 1996.333 1995.667 4     1 17069.17 1.8617385 17067.30
4   K 0.3333333 1996.667 1996.333 4     0 16469.50 1.4455852 16468.05
5   K 0.6666667 1997.333 1996.667 2     1 16501.83 1.9835729 16499.85
6   K 0.3333333 1997.667 1997.333 0     0 16434.00 0.0000000 16434.00
```

```
> dim( inc )
```

```
[1] 6000    9
```

```
> with( inc, addmargins( xtabs( D ~ floor(P) + sex ) ) )
```

```
        sex
floor(P)      K      M    Sum
    1995   7145   7748  14893
    1996   7392   8022  15414
    1997   7533   7927  15460
    1998   8044   8814  16858
    1999   8555   9307  17862
    2000   8883   9631  18514
    2001   9477  10211  19688
    2002  10912  11197  22109
    2003  11506  12477  23983
    2004  11615  12553  24168
    2005  10636  11663  22299
    2006  10930  12092  23022
    2007  11763  12703  24466
    2008  12641  13995  26636
    2009  12297  14242  26539
    Sum  149329 162582 311911
```

Thus the dataset has the variable `D` for the number of DM-cases and the variable `well.Y` for the amount of follow-up among the non-diabetic part of the population, the latter is the correct denominator for analysis of the rates. The covariates of interest are of course `A`, `P` and `C` with values for age, period and cohort at the midpoints of the Lexis-triangles.

1.1.1 Models for incidence rates

Based on this we can now derive the location of the knots for this model:

```
> source( "c:/stat/r/bxc/library.sources/useful/r/Ns.r" )
> nk.a <- 25
> nk.p <- 10
> nk.c <- 8
> qn <- function(n) seq( 1/(3*n), 1-1/(3*n),,n)
> ( ki.a <- with( inc, quantile( rep(A,D), qn(nk.a) ) ) )

1.333333% 5.388889% 9.444444%     13.5% 17.55556% 21.61111% 25.66667% 29.72222% 33.77778% 37.83333%
 15.33333  32.66667  39.66667  44.33333  47.33333  50.33333  52.33333  54.33333  56.33333  58.33333
      50% 54.05556% 58.11111% 62.16667% 66.22222% 70.27778% 74.33333% 78.38889% 82.44444%     86.5%
 62.66667  64.33333  65.66667  67.33333  69.33333  70.66667  72.66667  74.33333  76.33333  78.66667
98.66667%
 89.66667

> ( ki.p <- with( inc, quantile( rep(P,D), qn(nk.p) ) ) )

3.333333%  13.7037% 24.07407% 34.44444% 44.81481% 55.18519% 65.55556% 75.92593%  86.2963% 96.66667%
 1995.667  1997.667  1999.667  2001.333  2002.667  2004.333  2005.667  2007.333  2008.333  2009.667

> ( ki.c <- with( inc, quantile( rep(C,D), qn(nk.c) ) ) )

4.166667%  17.2619% 30.35714% 43.45238% 56.54762% 69.64286%  82.7381% 95.83333%
 1916.333  1926.333  1932.667  1938.333  1943.667  1948.667  1956.667  1973.667

> m.inc.ap <- glm( D ~ Ns(A,knots=ki.a) + Ns(P,knots=ki.p),
+                      offset = log(well.Y/1000), family=poisson,
+                      data = subset(inc,sex=="M") )
> f.inc.ap  <- update( m.inc.ap, data = subset(inc,sex=="K") )
> np <- 100
> a.pt <- seq(0,90,,np)
> p.rf <- 2004
> p.pt <- seq(1995,2010,,np)
> CP   <- Ns(    p.pt    ,knots=ki.p)
> CPr  <- Ns(rep(p.rf,np),knots=ki.p)
> m10.rr <- ci.exp( m.inc.ap, subset="P", ctr.mat=CP-CPr )
> f10.rr <- ci.exp( f.inc.ap, subset="P", ctr.mat=CP-CPr )
> nk.p <- 5
> ( ki.p <- with( inc, quantile( rep(P,D), qn(nk.p) ) ) )

6.666667% 28.33333%       50% 71.66667% 93.33333%
 1996.333  2000.333  2003.667  2006.667  2009.333

> m.inc.ap <- glm( D ~ Ns(A,knots=ki.a) + Ns(P,knots=ki.p),
+                      offset = log(well.Y/1000), family=poisson,
+                      data = subset(inc,sex=="M") )
> f.inc.ap  <- update( m.inc.ap, data = subset(inc,sex=="K") )
> CA   <- Ns(    a.pt    ,knots=ki.a)
> CP   <- Ns(    p.pt    ,knots=ki.p)
> CPr  <- Ns(rep(p.rf,np),knots=ki.p)
> m5.rr <- ci.exp( m.inc.ap, subset="P", ctr.mat=CP-CPr )
> f5.rr <- ci.exp( f.inc.ap, subset="P", ctr.mat=CP-CPr )
```

We can now plot the RR by calendar time:

```
> par( mar=c(3,3,1,1), mgp=c(3,1,0)/1.6 )
> matplot( p.pt, cbind( m5.rr, f5.rr ), type="n",
+          log="y", las=1, ylim=c(0.5,1.5),
+          xlab="Date of follow-up",
+          ylab="DM incidence rate ratio")
> abline( v=1990:2020, h=seq(0.5,2,0.1), col=gray(0.8) )
> abline( h=1 )
> matlines( p.pt, cbind( m10.rr, m5.rr,
+                        f10.rr, f5.rr ), lty=rep(c(3,1),c(3,3)), lwd=c(3,1,1),
+                  col=rep(c("blue","red"),each=6) )
> points( p.rf, 1, pch=16, cex=1.1, col="white")
> points( p.rf, 1, pch=1 , cex=1.1, col="black", lwd=3 )
```

The next point is to extract the age-specific incidence rates at 1.1.2004:

```
> m5.inc <- ci.exp( m.inc.ap, ctr.mat=cbind(1,CA,CPr) )
> f5.inc <- ci.exp( f.inc.ap, ctr.mat=cbind(1,CA,CPr) )
> par( mar=c(3,3,1,1), mgp=c(3,1,0)/1.6 )
```

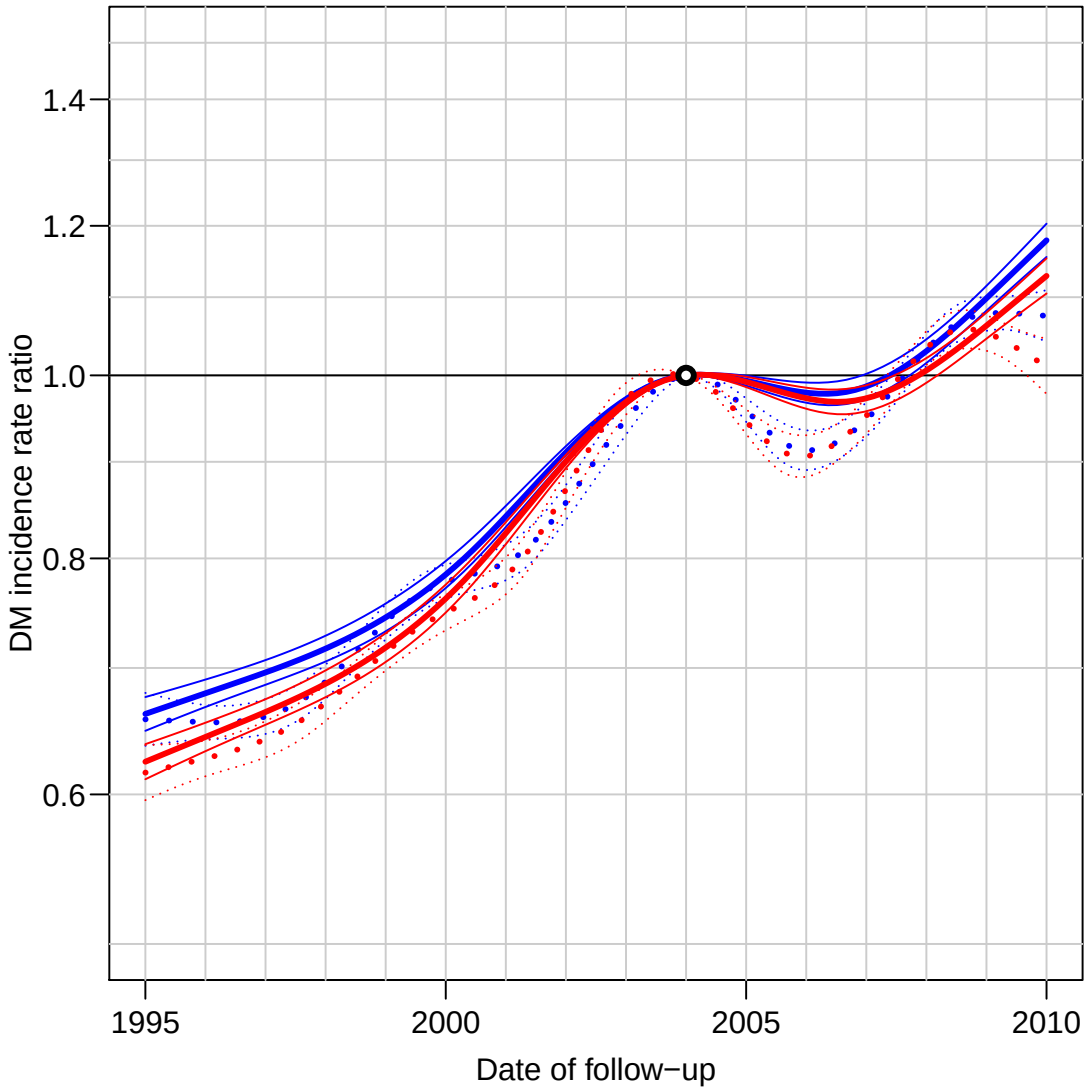

Figure 1.1: *Rate-ratio relative to 1.1.2004, separately for men (blue) and women (red), dotted lines are with 10-knot splines, full lines with 5-knot splines. Clearly the 5-knot spline is the more appropriate, indicatin that there is an increase in incidence rates after around 2007.*

```
> matplot( a.pt, cbind( m5.inc, f5.inc ), type="l",
+          log="y", las=1, ylim=c(0.1,20),
+          xlab="Date of follow-up",
+          ylab="DM incidence rate per 1000 PY")
> abline( v=seq(0,90,5), h=c(1:9/10,1:25), col=gray(0.8) )
> abline( h=1 )
> matlines( a.pt, cbind( m5.inc, f5.inc ), lty=1, lwd=c(3,1,1),
+                 col=rep(c("blue","red"),each=3) )
> box()
```

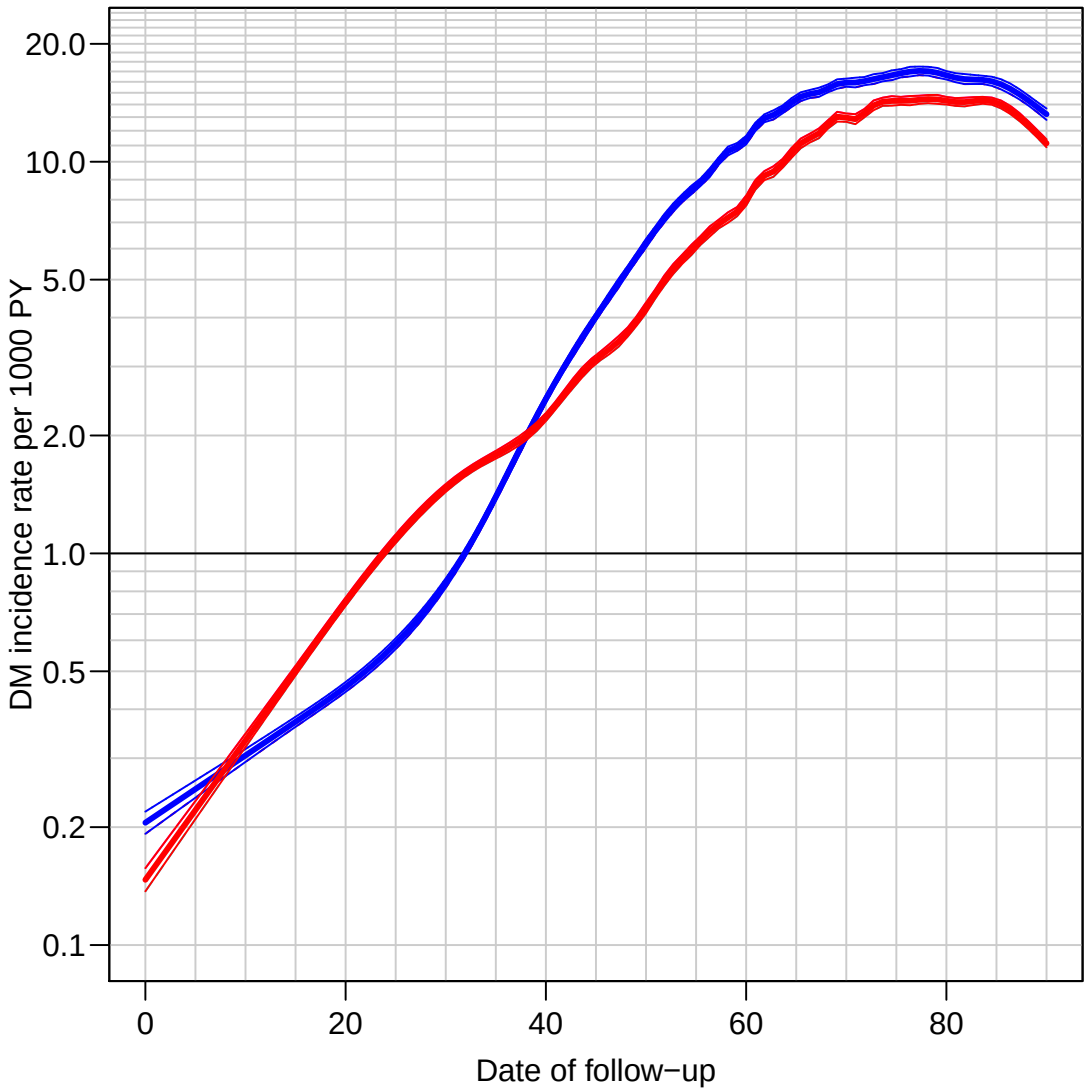

Figure 1.2: *Incidence rates of DM at 1.1.2004, separately for men (blue) and women (red).*