

5: Generalized Linear Models – Logistic and Poisson Regression

John H Maindonald

November 25, 2013

Ideas and issues illustrated by the graphs in this vignette

Generalized linear models (GLMs) are an extension of linear models. An important special case is models with a binary outcome. Poisson regression models are another special case. Graphs shown here illustrate important aspects of the use of these models.

1 Code for the Figures

```
fig5.1 <-  
function () {  
  opar <- par(mar=c(4,4,2.6,.1))  
  ylim <- range(bronchit$poll)+c(0,2.5)  
  par(fig=c(0,.525, 0,1))  
  plot(xlab="# cigarettes per day", ylab="Pollution", poll ~ cig,  
       col=c(2,4)[r+1], pch=(3:2)[r+1], data=bronchit, ylim=ylim)  
  legend(x="topleft", legend=c("Non-sufferer", "Sufferer"), ncol=2,  
        pch=c(3,2), col=c(2,4))  
  mtext(side=3, line=1.0,  
        expression("A: Untransformed " * italic(x) * "-scale"),  
        cex=0.95, adj=0)  
  par(fig=c(.475,1, 0,1), new=TRUE)  
  plot(poll ~ log(cig+1), col=c(2,4)[r+1], pch=(3:2)[r+1],  
       xlab="log(# cigarettes per day + 1)", ylab="",  
       data=bronchit, ylim=ylim)  
  xy1 <- with(subset(bronchit, r==0), cbind(x=log(cig+1), y=poll))  
  xy2 <- with(subset(bronchit, r==1), cbind(x=log(cig+1), y=poll))  
  est1 <- bkde2D(xy1, bandwidth=c(0.7, 3))  
  est2 <- bkde2D(xy2, bandwidth=c(0.7, 3))  
  lev <- pretty(c(est1$fhat, est2$fhat), 4)  
  contour(est1$x1, est1$x2, est1$fhat, levels=lev, add=TRUE, col=2)  
  contour(est2$x1, est2$x2, est2$fhat, levels=lev, add=TRUE, col=4,
```

```

        lty=2)
legend(x="topleft", legend=c("Non-sufferer","Sufferer"), ncol=2,
      lty=1:2, col=c(2,4), x.intersp=0.5)
mtext(side=3, line=1.0,
      expression("B: Log-transformed "*italic(x)*"-scale"),
      cex=0.95, adj=0)
par(fig=c(0,1,0,1))
par(opar)
}

```

```

fig5.2 <-
function (plotit=TRUE)
{
  par(mfrow=c(1,2))
  cig2.glm <- glm(r ~ log(cig+1) + poll, family=binomial,
                 data=bronchit)
  termplot(cig2.glm, se=TRUE, ylim=c(-2,4))
  par(mfrow=c(1,1))
}

```

```

fig5.3 <-
function ()
{
  nassnew <- subset(nassCDS,
                   !is.na(yearVeh) & yearVeh>=1986 & weight>0)
  nassnew.glm <- glm(dead ~ seatbelt + airbag + dvcac + yearVeh +
                    ageOFocc, weights=weight, family = quasibinomial,
                    data=nassnew)

  par(mfrow=c(1,2))
  termplot(nassnew.glm, terms=c("yearVeh","ageOFocc"),
           smooth=panel.smooth, se=TRUE)
  par(mfrow=c(1,1))
  par(fig=c(0,0.5,0,1), new=TRUE)
  mtext(side=3, line=1.0, "A", adj=0)
  par(fig=c(0.5,1,0,1), new=TRUE)
  mtext(side=3, line=1.0, "B", adj=0)
  par(fig=c(0,1,0,1))
}

```

```

fig5.4 <-
function (){
  opar <- par(mfrow=c(1,2), mar=c(3.6,3.6,1.6,0.6), mgp=c(2.25,.5,0))

```

```

qnorm(rpois(30, 5), ylab="", main="")
qnorm(rpois(30, 5), ylab="", main="")
par(opar)
}

```

```

fig5.5 <-
function (){
  if(!require(car))
    stop("Package 'car' must be installed")
  spm(~ . | habitat, data=moths, cex.labels=1.2,
      smooth=FALSE, reg.line=NA)
}

```

```

fig5.6 <-
function ()
{
  P.glm <- glm(P ~ habitat + log(meters), data=moths,
              family=quasipoisson)
  par(mfrow=c(2,2))
  plot(P.glm, which=1:4)
  par(mfrow=c(1,1))
}

```

2 Show the Figures

Unless `doFigs` is found in the workspace and is `FALSE`, then subject to checks that all necessary datasets and packages are available, the figures are now shown.

```

if(!exists("doFigs")) doFigs <- TRUE

```

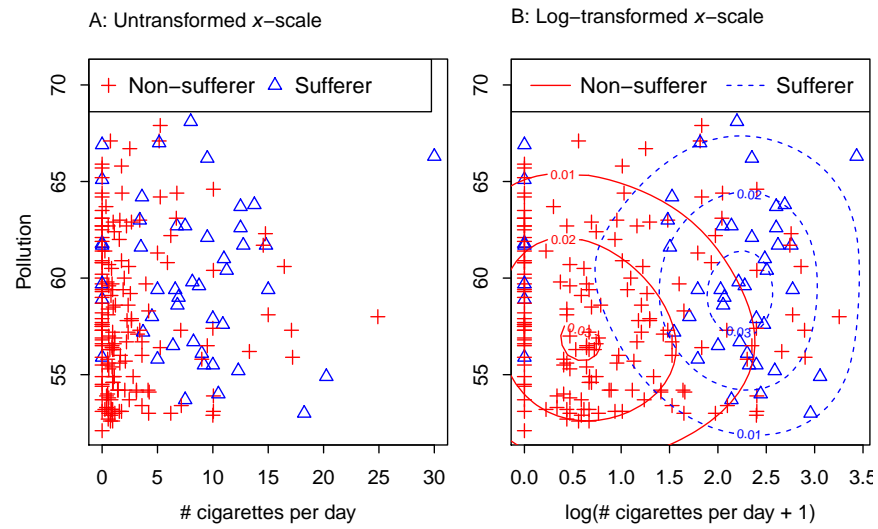
```

if(!exists("bronchit")){
  cat("Will try to load 'bronchit' from the SMIR package")
  if(!require(SMIR))stop("Package SMIR is not installed")
  library(SMIR)
  data(bronchit)
}
library(DAAG)
library(KernSmooth)

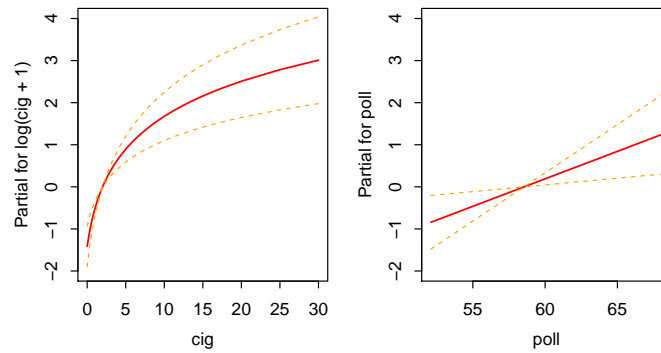
```

```
cig2.glm <- glm(r ~ log(cig+1) + poll, family=binomial,
               data=bronchit)
```

```
fig5.1()
```



```
fig5.2()
```



```
fig5.3()
```

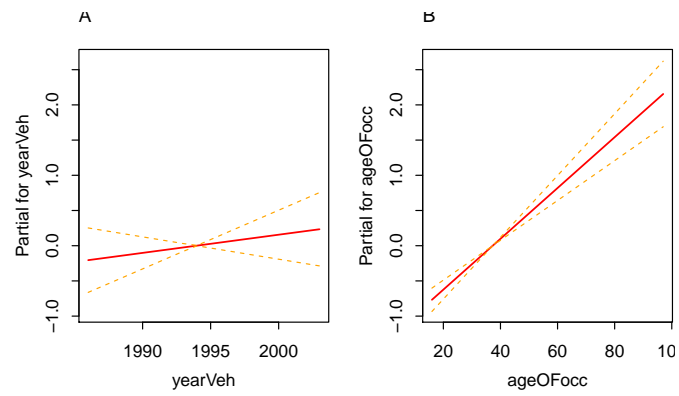


fig5.4()

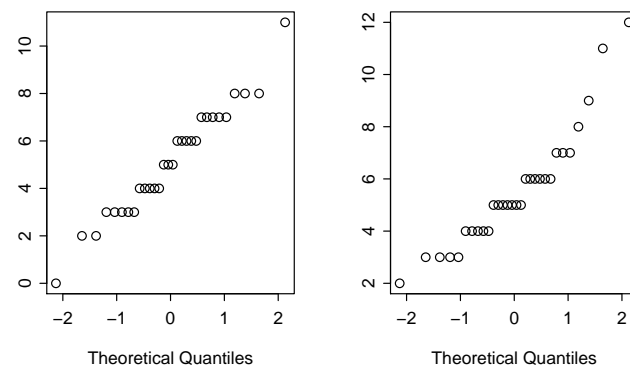
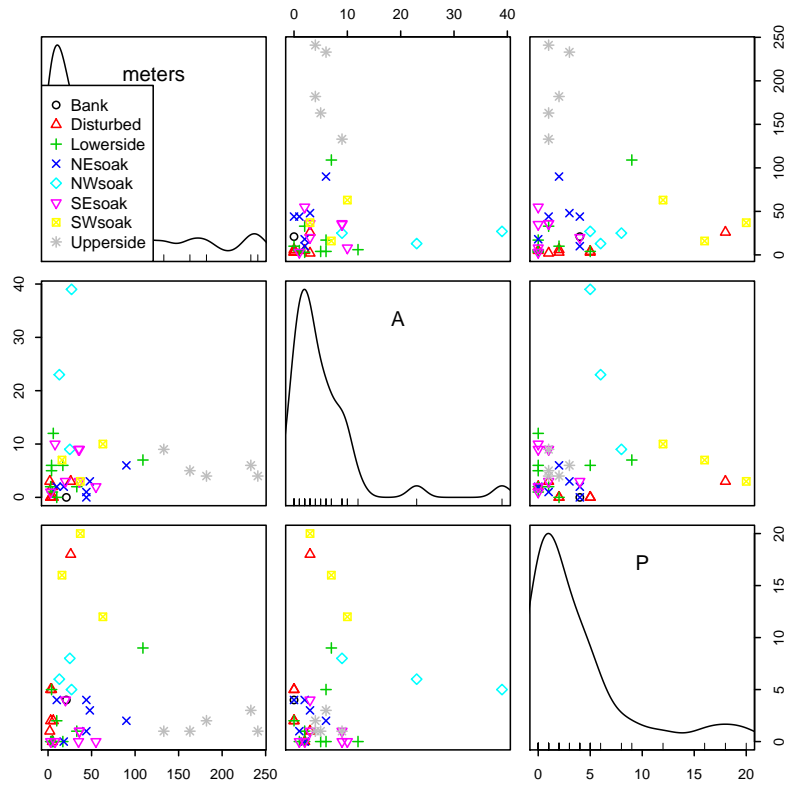


fig5.5()



```
fig5.6()
```

```
Warning: not plotting observations with leverage one:
40
```

