5: Generalized Linear Models – Logistic and Poisson Regression

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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. Poission 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 (){
    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))
}
```

```
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 + dvcat + 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 (){
    qqnorm(rpois(30, 5), ylab="", main="")
    qqnorm(rpois(30, 5), ylab="", main="")
}
```

```
fig5.5 <-
function (){
    if(!require(car))return("'car::spm' is not available; cannot do plot.")
    car::spm(~ . | habitat, data=moths, cex.labels=1.2,
        smooth=FALSE, reg.line=NA, diag="boxplot")
}
```

```
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))
}
```

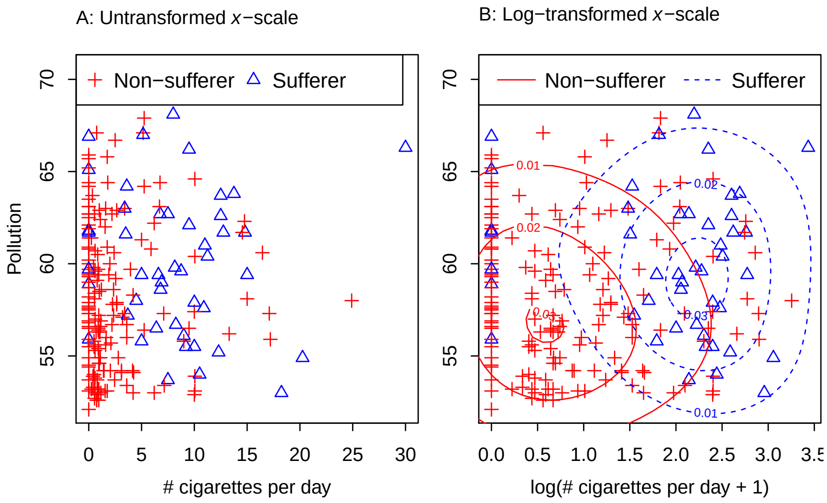
2 Show the Figures

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.

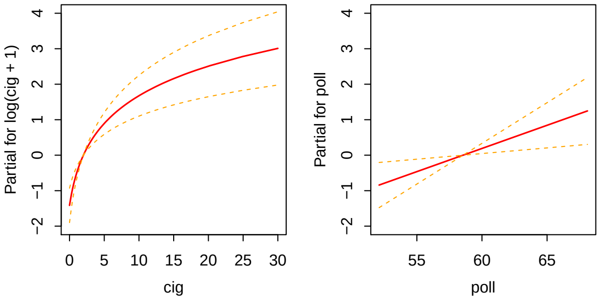
```
if(!exists("doFigs")) doFigs <- TRUE
```

```
pkgs <- c("DAAG","KernSmooth","car")
z <- sapply(pkgs, require, character.only=TRUE, warn.conflicts=FALSE)
if(any(!z)){
  notAvail <- paste(names(z)[!z], collapse=", ")
  print(paste("The following packages should be installed:", notAvail))
}
if(!exists("bronchit")){
  getData <- try(data("bronchit", package="SMIR"))
}
if(getData != "bronchit") print("Dataset 'bronchit' is not available")
```

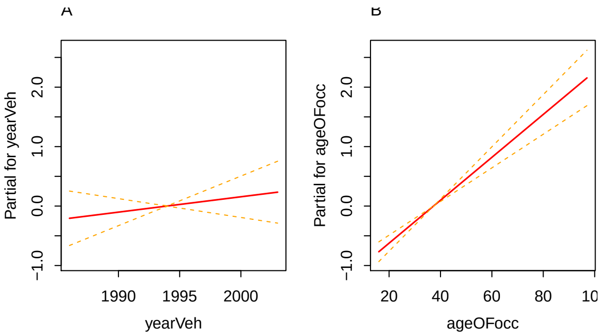
```
if(doFigs)if(exists("bronchit"))fig5.1() else return("Data set 'bronchit' is not available")
```



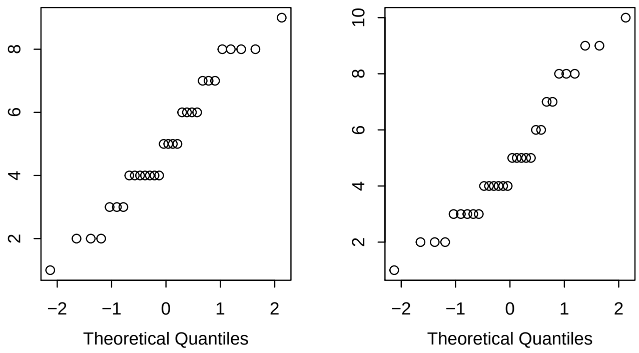
```
if(doFigs)if(exists("bronchit"))fig5.2() else return("Data set 'bronchit' is not available")
```



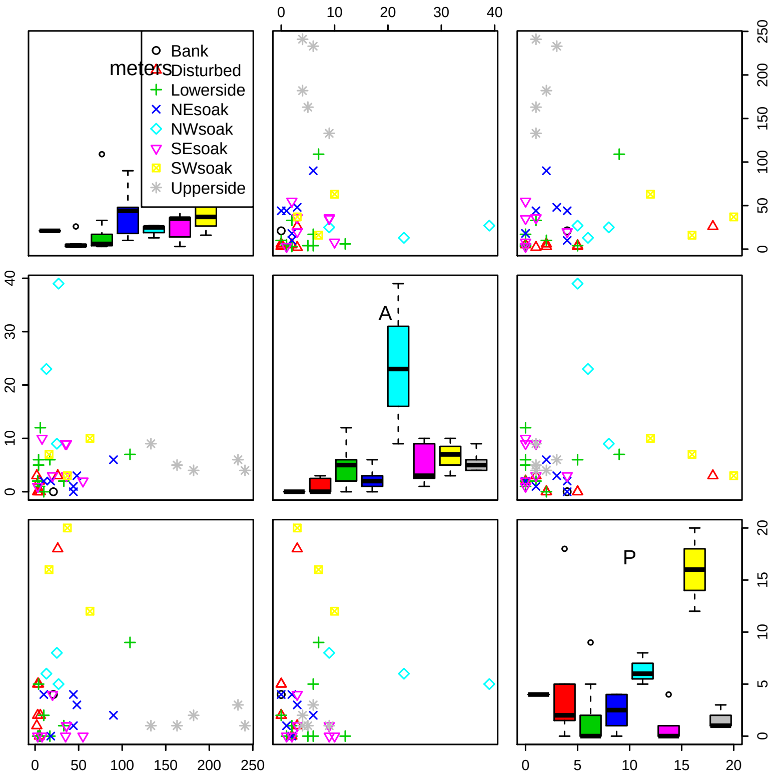
```
if(doFigs)fig5.3()
```



```
if(doFigs)fig5.4()
```

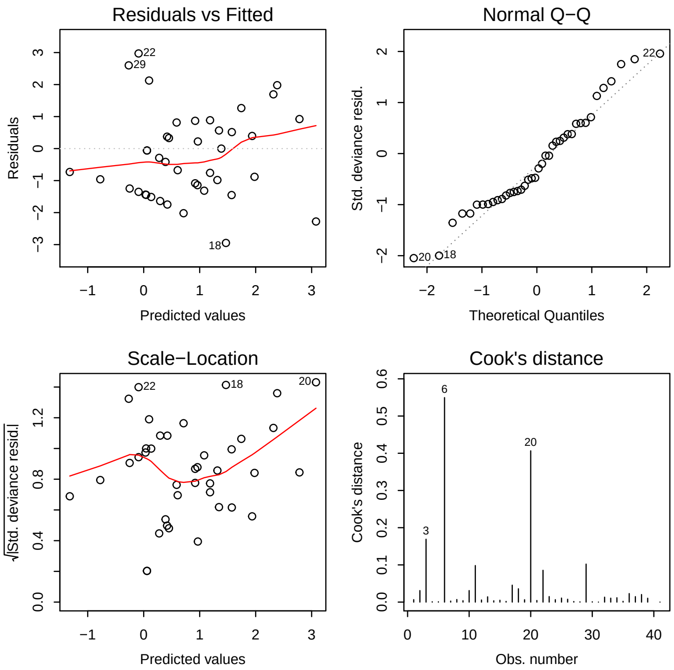


```
if(require(DAAG)) fig5.5() else return("Dataset 'moths' is from 'DAAG', not available")
```



```
if(doFigs)if(require(DAAG)) fig5.6() else return("Dataset 'moths' is from 'DAAG', not availa

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


Residuals vs Fitted
Residuals
Predicted values
−3
−2
−1
0
1
2
3
−1
0
1
2
3
22
29
18
Normal Q−Q
Std. deviance resid.
Theoretical Quantiles
−2
−1
0
1
2
22
20
18
Scale−Location
√|Std. deviance resid.|
Predicted values
0.0
0.4
0.8
1.2
22
18
20
Cook's distance
Cook's distance
Obs. number
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0
10
20
30
40
3
6
20