

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. 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 (){  
  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 x"),
      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 + dvcats + 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 (){
  par(mar=c(3.6,3.6,1.6,0.6), mgp=c(2.25,.5,0), mfrow=c(2,2))
  msg <- "As 'car::spm' is not available, cannot do plot."
  if(!require(car))return(msg)
  if(packageVersion('car') < '3.0.0'){ diag <- "boxplot"
  car::spm(~ . | habitat, data=moths, cex.labels=1.2,
           col=rep(1,8), var.labels=c("", "A", "P"), smooth=FALSE,
           reg.line=NA, diagonal=diag)
  } else {
    diag <- list(method="boxplot")
    car::spm(~ . | habitat, data=moths, cex.labels=1.2,
             col=rep(1,8), var.labels=c("", "A", "P"), smooth=FALSE,
             regLine=FALSE, diagonal=diag)
  }
}

```

```

fig5.6 <-
function ()
{
  par(mar=c(3.6,3.6,1.6,0.6), mgp=c(2.25,.5,0), mfrow=c(2,2))
  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

```

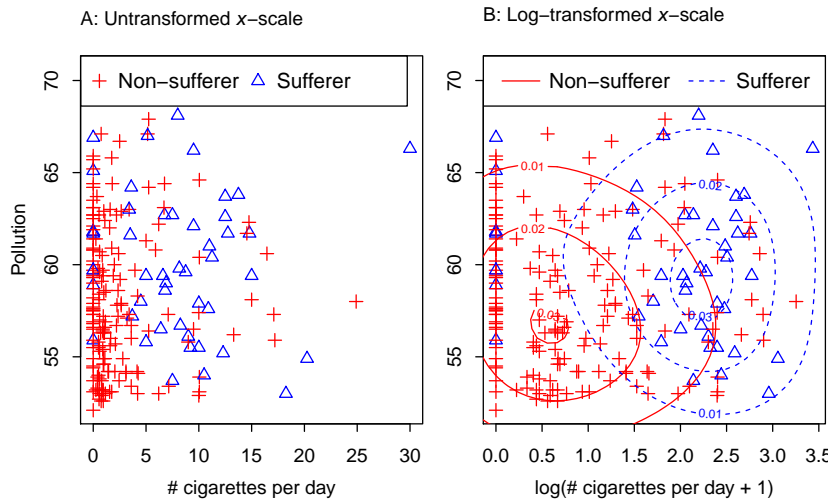
pkgs <- c("DAAG", "KernSmooth", "car")
z <- sapply(pkgs, require, character.only=TRUE, warn.conflicts=FALSE)
if(any(!z)){
  notAvail <- paste(names(z)[!z], collapse=", ")
  print(paste("The following packages should be installed:", notAvail))
}
if(!exists("bronchit")){
  if(require("SMIR")) data("bronchit",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

```

```

if(exists("bronchit"))fig5.1() else
  return("Cannot locate data set 'bronchit', get from 'SMIR'")

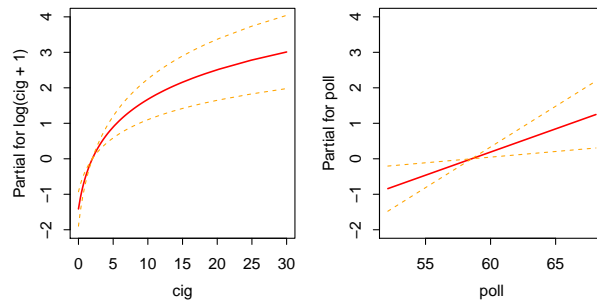
```



```

if(exists("bronchit"))fig5.2() else
  return("Cannot locate data set 'bronchit', get from 'SMIR'")

```



```

fig5.3()

```

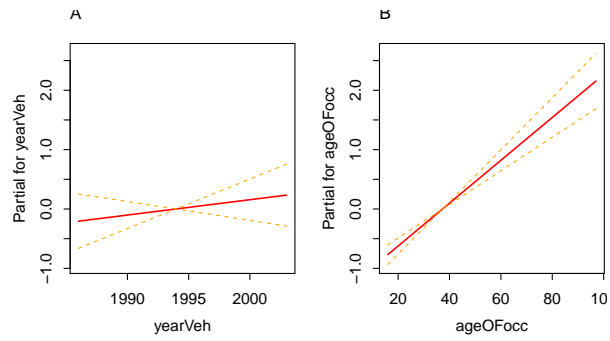
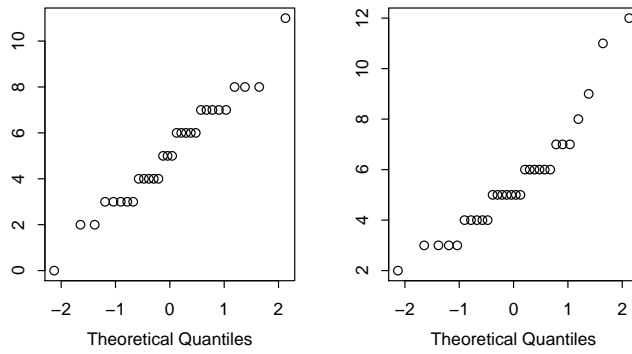
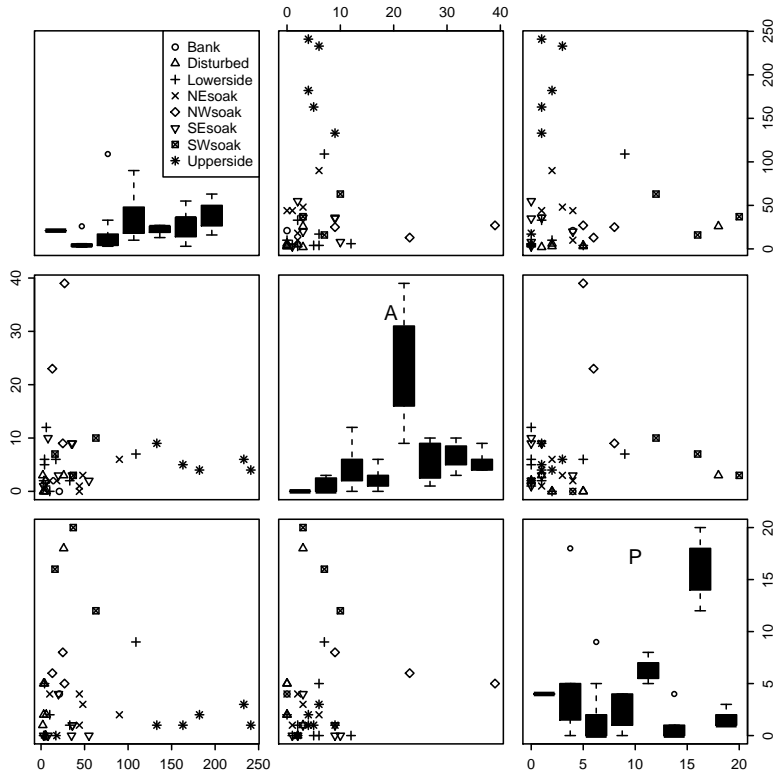


fig5.4()



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



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

Warning: not plotting observations with leverage:
40

