MAST30027: Modern Applied Statistics

Week 4 Lab

1. The `cornnit` dataset in the `faraway` package contains data on the effect of nitrogen on the yield of corn. Fit a gamma regression to this data, using the `glm` command. You will need to pay attention to the choice of link function (inverse, identity or log), and consider transforming the predictor variable (your first step should be to plot the data).

   Note: For a linear model A nested within linear model B, under the null hypothesis that model A is correct we have

   $$\frac{(D^A - D^B)/s}{X^2/(n-p)} \sim F_{s,n-p}$$

   where we have n observations, A has $p - s$ paramters and B has p parameters.

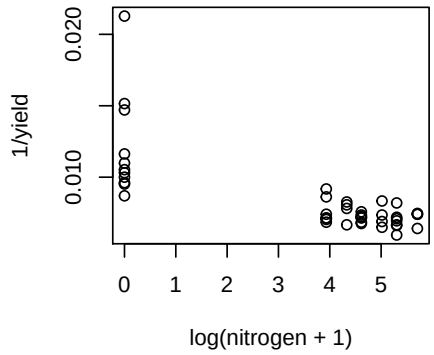
   In R X^2 (Pearson's chi-squared) is calculated using the fitted model B.

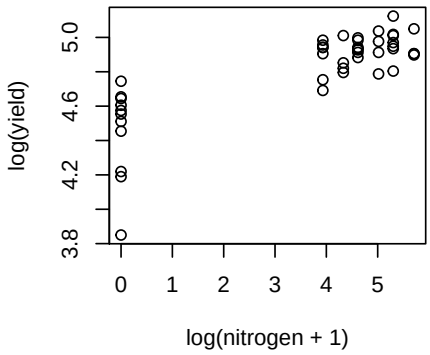
   For other GLM's this distributional result only holds approximately, but it can still be used for comparing models. In particular it can be used to compare gamma models.

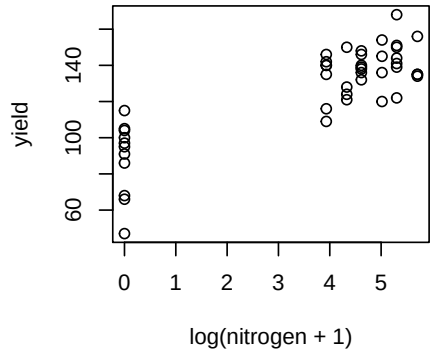
   Solution: As suggested we plot the data first, using different link functions. It was found that taking a log transform of the nitrogen variable improves the linearity in all cases (note that we add a small constant before taking the log because nitrogren has zero values).

   We suppose that the mean behaves like $g^{-1}(\eta)$, where in this case $\eta = \beta_0 + \beta_1 \log(1 + x)$ and x is the level of nitrogen. Thus a plot of $g(y)$ against $\log(1 + x)$ should look (vaguely) linear.

```
> library(faraway)
> data(cornnit)
> par(mfrow=c(2,2))
> plot(1/yield ~ log(nitrogen+1), data=cornnit)
> plot(log(yield) ~ log(nitrogen+1), data=cornnit)
> plot(yield ~ log(nitrogen+1), data=cornnit)
```





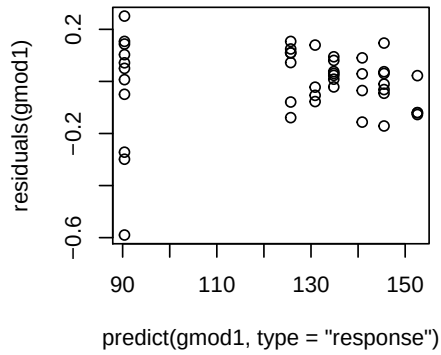


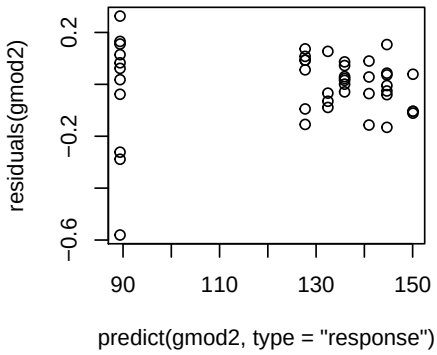
In all three plots there is an undesirable gap in the observed nitrogen values. We can reduce this a little by using the transform log(nitrogen + k) for larger k, but this impinges on the linearity.

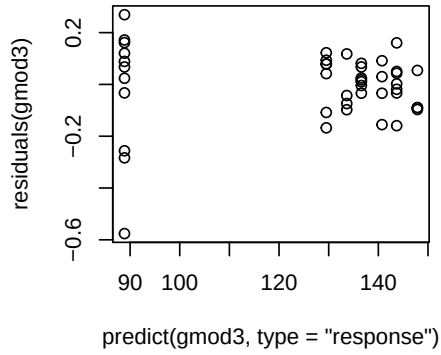
In the first and second plots there is noticably more variance in $g(y)$ when nitrogen is zero. For a gamma model the variance should be proportional to the mean squared. Thus when the yield is larger we expect the data to be more variable, which is not what we see here. However, when we transform the responses we transform their variances as well as their means, and both the inverse and log links have larger slopes at small values, so this will be magnifying the variance when the yield is small. Unfortunately we can't really disentangle these two effects using these plots (but see the residual plots below).

Of the three I think the plot of yield against log(nitrogen + 1) looks most linear, but the other two are not unreasonable. Accordingly we will try all three link functions are compare the residuals.

```
> par(mfrow=c(2,2))
> gmod1 <- glm(yield ~ log(nitrogen+1), data=cornnit, family=Gamma(link="inverse"))
> plot(predict(gmod1,type="response"), residuals(gmod1))
> gmod2 <- glm(yield ~ log(nitrogen+1), data=cornnit, family=Gamma(link="log"))
> plot(predict(gmod2,type="response"), residuals(gmod2))
> gmod3 <- glm(yield ~ log(nitrogen+1), data=cornnit, family=Gamma(link="identity"))
> plot(predict(gmod3,type="response"), residuals(gmod3))
```







There is not much difference between these plots. In all three cases there is slightly more variation when the fitted values are small, but for a gamma model we would expect the variance to grow as the fitted values got larger. Thus all three models are problematic, however if we look at the AIC for each model we see that it is smallest for the model with the identity link (just), so we will take this model from here on.

```
> gmod1$aic

[1] 383.7435

> gmod2$aic

[1] 382.4205

> gmod3$aic

[1] 381.7124
```

(a) Extract the Pearson residuals from the fitted model using the `residuals` function, then use them to estimate the dispersion parameter. Check that your answer agrees with the summary output from your model.

Solution: From the summary we see the dispersion parameter is estimated to be 0.01810, which we can reproduce using Pearson's chi-squared statistic. Note that the model has 42 d.f.

```
> summary(gmod3)

Call:
glm(formula = yield ~ log(nitrogen + 1), family = Gamma(link = "identity"),
    data = cornnit)
```

```
Deviance Residuals:
     Min        1Q    Median        3Q       Max
-0.57604  -0.07789   0.02067   0.07948   0.26927

Coefficients:
                 Estimate Std. Error t value Pr(>|t|)
(Intercept)         88.875      3.571   24.89  < 2e-16 ***
log(nitrogen + 1)   10.337      1.009   10.24 5.46e-13 ***
---
Signif. codes:  0 âĂŸ***âĂŹ 0.001 âĂŸ**âĂŹ 0.01 âĂŸ*âĂŹ 0.05 âĂŸ.âĂŹ 0.1 âĂŸ âĂŹ 1

(Dispersion parameter for Gamma family taken to be 0.01810187)

    Null deviance: 2.40614  on 43  degrees of freedom
Residual deviance: 0.87603  on 42  degrees of freedom
AIC: 381.71

Number of Fisher Scoring iterations: 4
```

```
> (phihat <- sum(residuals(gmod3, "pearson")^2)/42)
```

```
[1] 0.01810169
```

(b) Suppose your fitted model is `gmod`, then the command `anova(gmod, test="F")` will compare your model against the null model, using an F test. Using the deviances and dispersion estimates reported by `summary(gmod)`, check that the F statistic reported by the `anova` function is correct.

Solution:

```
> anova(gmod3, test="F")
```

```
Analysis of Deviance Table

Model: Gamma, link: identity

Response: yield

Terms added sequentially (first to last)


                 Df Deviance Resid. Df Resid. Dev      F    Pr(>F)
NULL                                43    2.40614
log(nitrogen + 1)  1   1.5301        42    0.87603 84.528 1.297e-11 ***
---
Signif. codes:  0 âĂŸ***âĂŹ 0.001 âĂŸ**âĂŹ 0.01 âĂŸ*âĂŹ 0.05 âĂŸ.âĂŹ 0.1 âĂŸ âĂŹ 1
```

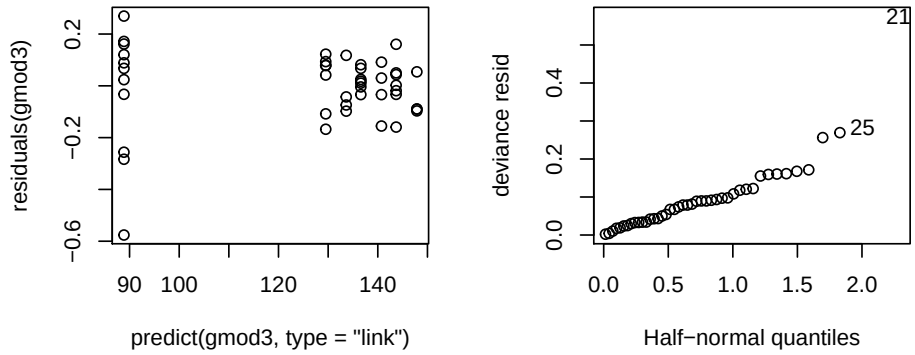
```
> model_dev <- .87603
> null_dev <- 2.40614
> (F_statistic <- (null_dev - model_dev)/phihat)
```

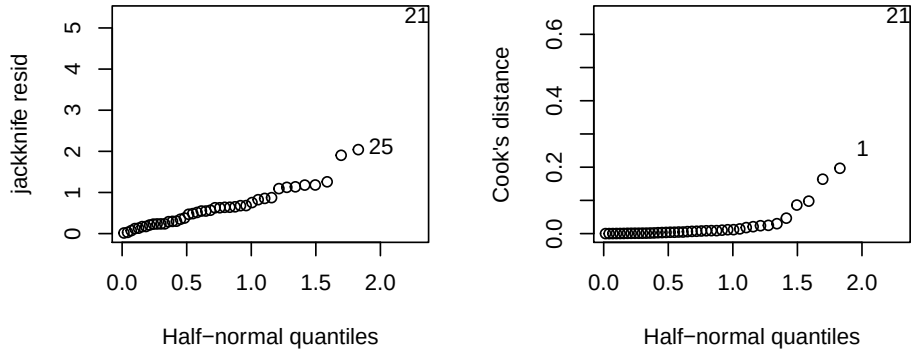
```
[1] 84.52857
```

(c) Now do some diagnostic plots. Can you identify a potential outlier? [Solve this problem in week 5 after learning diagnostics for GLMs.]

Solution: We have already observed more variation than we would like when the responses are small. It also looks like point 21 could be an outlier.

```
> par(mfrow=c(2,2))
> plot(predict(gmod3, type="link"), residuals(gmod3))
> halfnorm(residuals(gmod3), ylab="deviance resid")
> halfnorm(rstudent(gmod3), ylab="jackknife resid")
> halfnorm(cooks.distance(gmod3), ylab="Cook's distance")
```





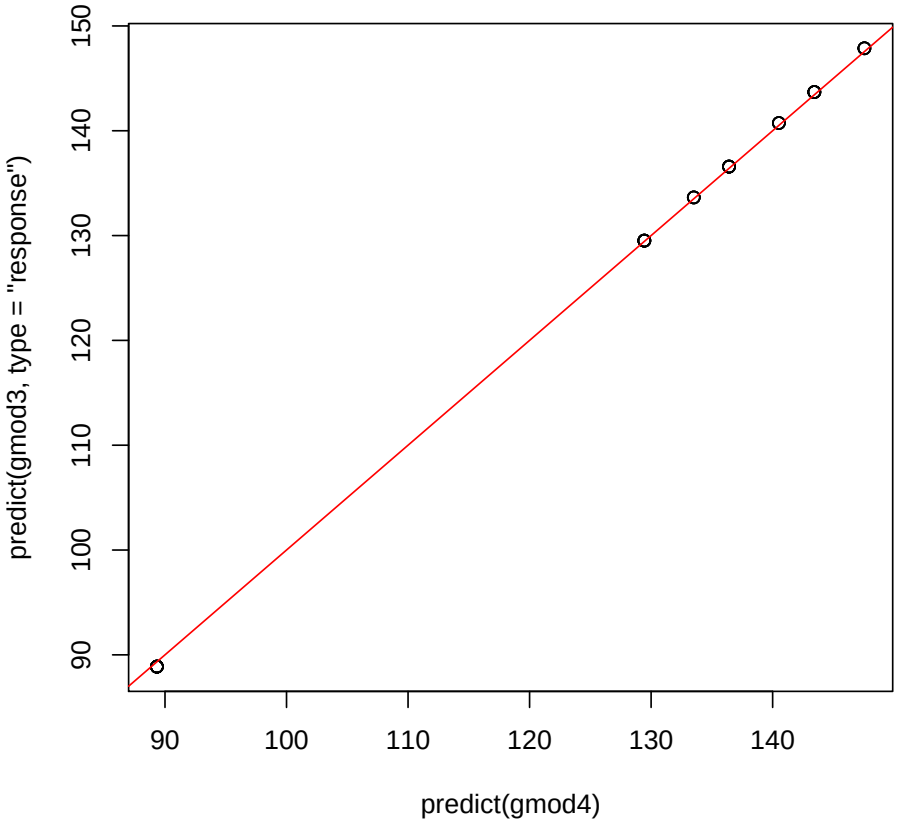
(d) Fit a linear model to the `cornnit` data.

Which do you prefer, the linear model or the gamma model, and why?

Solution: A gamma variable with a large mean looks a lot like a normal, so we expect a linear model fit to look a lot like our gamma model fit, and it does. We can see this by plotting the fitted values for the two models against each other, and seeing that the points lie very close to the diagonal.

```
> gmod4 <- lm(yield ~ log(nitrogen+1), data=cornnit)
> summary(gmod4)

Call:
lm(formula = yield ~ log(nitrogen + 1), data = cornnit)

Residuals:
    Min      1Q  Median      3Q     Max
-42.335 -10.261   2.126  10.558  25.665

Coefficients:
                 Estimate Std. Error t value Pr(>|t|)
(Intercept)        89.335      4.227   21.13  < 2e-16 ***
log(nitrogen + 1)  10.201      1.017   10.03 1.03e-12 ***
---
Signif. codes:  0 âĂŸ***âĂŹ 0.001 âĂŸ**âĂŹ 0.01 âĂŸ*âĂŹ 0.05 âĂŸ.âĂŹ 0.1 âĂŸ âĂŹ 1

Residual standard error: 14.34 on 42 degrees of freedom
Multiple R-squared:  0.7055,        Adjusted R-squared:  0.6985
F-statistic: 100.6 on 1 and 42 DF,  p-value: 1.025e-12
```

```
> par(mfrow=c(1,1))
> plot(predict(gmod4), predict(gmod3, type="response"))
> abline(0, 1, col="red")
```



However, for a linear model we expect the variance to stay fixed, rather than grow with the mean, and this is more in keeping with this data, so we should go with the linear model.

2. The `dvisits` data in the `faraway` package comes from the Australian Health Survey of 1977–78 and consist of 5190 observations on single adults, where young and old have been oversampled.

   (a) Build a Poisson regression model with `doctorco` as the response and `sex, age, agesq, income, levyplus, freepoor, freerepa, illness, actdays, hscore, chcond1` and `chcond2` as possible predictor variables. Considering the deviance of this model, does this model fit the data?

   Solution: Using stepwise model selection based on the AIC, we end up with the model `doctorco sex + age + income + levyplus + freepoor + illness + actdays + hscore`. The deviance of 4385.5 is clearly not significant given that we have 5181 degrees of freedom, though note that the responses are not that large, so the deviance may not be close to a chi-squared distribution.

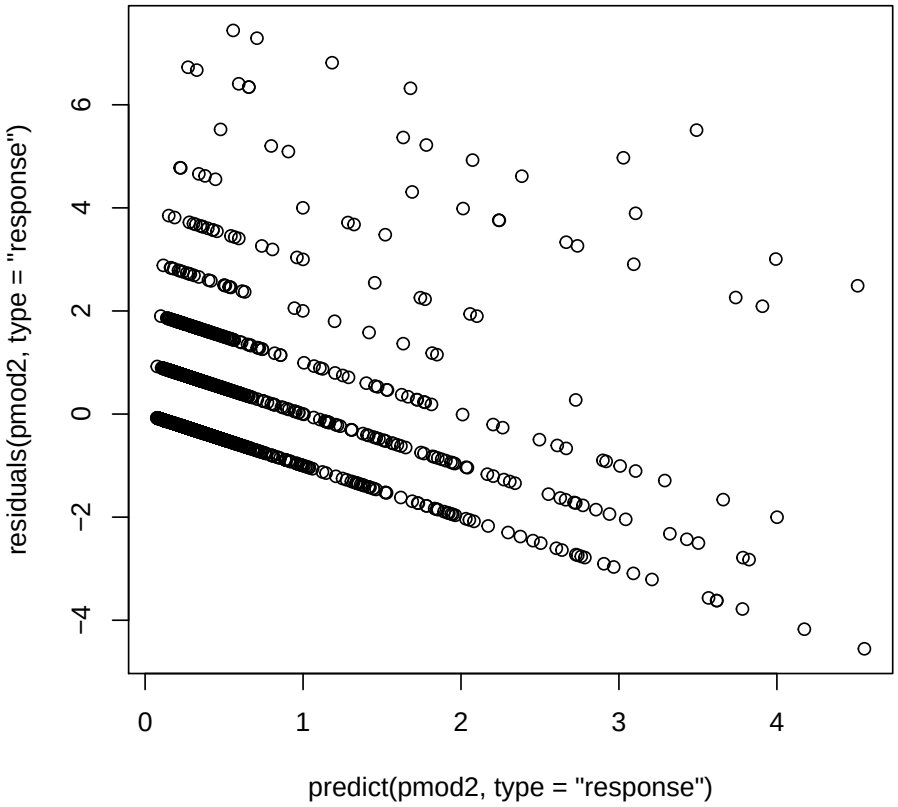
```
> data(dvisits)
> pmod <- glm(doctorco ~ sex + age + agesq + income + levyplus + freepoor
+             + freerepa + illness + actdays + hscore + chcond1,
+             family=poisson, data=dvisits)
> pmod2 <- step(pmod, scope=~., trace=0)
> summary(pmod2)

Call:
glm(formula = doctorco ~ sex + age + income + levyplus + freepoor +
```

```
    illness + actdays + hscore, family = poisson, data = dvisits)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-3.0180  -0.6811  -0.5772  -0.4916   5.6590

Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept) -2.072446   0.100191 -20.685  < 2e-16 ***
sex          0.167591   0.055604   3.014 0.002578 **
age          0.437894   0.137070   3.195 0.001400 **
income      -0.203978   0.084206  -2.422 0.015420 *
levyplus     0.087156   0.053501   1.629 0.103304
freepoor    -0.465788   0.176364  -2.641 0.008265 **
illness      0.196366   0.017603  11.155  < 2e-16 ***
actdays      0.127994   0.004905  26.097  < 2e-16 ***
hscore       0.032854   0.009961   3.298 0.000973 ***
---
Signif. codes:  0 âĂŸ***âĂŹ 0.001 âĂŸ**âĂŹ 0.01 âĂŸ*âĂŹ 0.05 âĂŸ.âĂŹ 0.1 âĂŸ âĂŹ 1

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 5634.8  on 5189  degrees of freedom
Residual deviance: 4385.5  on 5181  degrees of freedom
AIC: 6735

Number of Fisher Scoring iterations: 6
```

(b) Plot the response residuals against the fitted values. Why are there lines of observations on the plot?

Solution: The lines appear because the response reisuals are given by $y_i - g(\eta_i)$ and y_i only takes on finitely many values. Each line corresponds to a different possible value.

```
> plot(predict(pmod2, type="response"), residuals(pmod2, type="response"))
> table(dvisits$doctorco)

   0    1    2    3    4    5    6    7    8    9
4141  782  174   30   24    9   12   12    5    1
```



(c) Use backward elimination with a critical p-value of 5% to reduce the model as much as possible.

Solution: Using backward elimination and chi-squared tests we end up with the model `doctorco  sex + age + income + freepoor + illness + actdays + hscore`, which is slightly smaller than the model achieved using the AIC and forward-backward elimination (just missing levyplus).

Note that the `step` function uses the AIC, so we have to use `drop1` instead. Here I just give the final step, which shows that we don't need to drop any more variables.

```
> pmod3 <- glm(doctorco ~ sex + age +income + freepoor + illness + actdays
+              + hscore, family=poisson, data=dvisits)
> drop1(pmod3, scope=~., test="Chisq")
Single term deletions

Model:
doctorco ~ sex + age + income + freepoor + illness + actdays +
    hscore
         Df Deviance    AIC    LRT  Pr(>Chi)
<none>        4388.1 6735.7
sex       1   4398.2 6743.8  10.14  0.001453 **
age       1   4398.2 6743.7  10.06  0.001518 **
income    1   4392.5 6738.1   4.43  0.035274 *
freepoor  1   4397.4 6742.9   9.27  0.002335 **
illness   1   4508.9 6854.5 120.82 < 2.2e-16 ***
actdays   1   4956.5 7302.1 568.41 < 2.2e-16 ***
hscore    1   4398.4 6744.0  10.31  0.001322 **
---
Signif. codes:  0 âĂŸ***âĂŹ 0.001 âĂŸ**âĂŹ 0.01 âĂŸ*âĂŹ 0.05 âĂŸ.âĂŹ 0.1 âĂŸ âĂŹ 1
```

(d) What sort of person would be predicted to visit the doctor the most under your selected model?

Solution Using a log link we have $\mu = e^{\eta}$, so we wish to maximise $\eta = \mathbf{x}^T\beta$. Looking at the coefficients this means female; as old as possible; no income; not entitled to free health care; very ill in the past two weeks; many days of reduced activity in the last two weeks; and a high hscore.

```
> pmod3$coefficients
```

```
(Intercept)         sex         age      income    freepoor     illness
-2.05196250  0.17552865  0.43353243 -0.17105283 -0.49632492  0.19600786
    actdays      hscore
 0.12779329  0.03243268
```

(e) For the last person in the dataset, compute the predicted probability distribution for their visits to the doctor, i.e., give the probability they visit 0,1,2, etc. times.

Solution:

```
> dim(dvisits)
```

```
[1] 5190   19
```

```
> lambda <- exp(predict(pmod3, dvisits[5190,]))
> dpois(0:9, lambda)
```

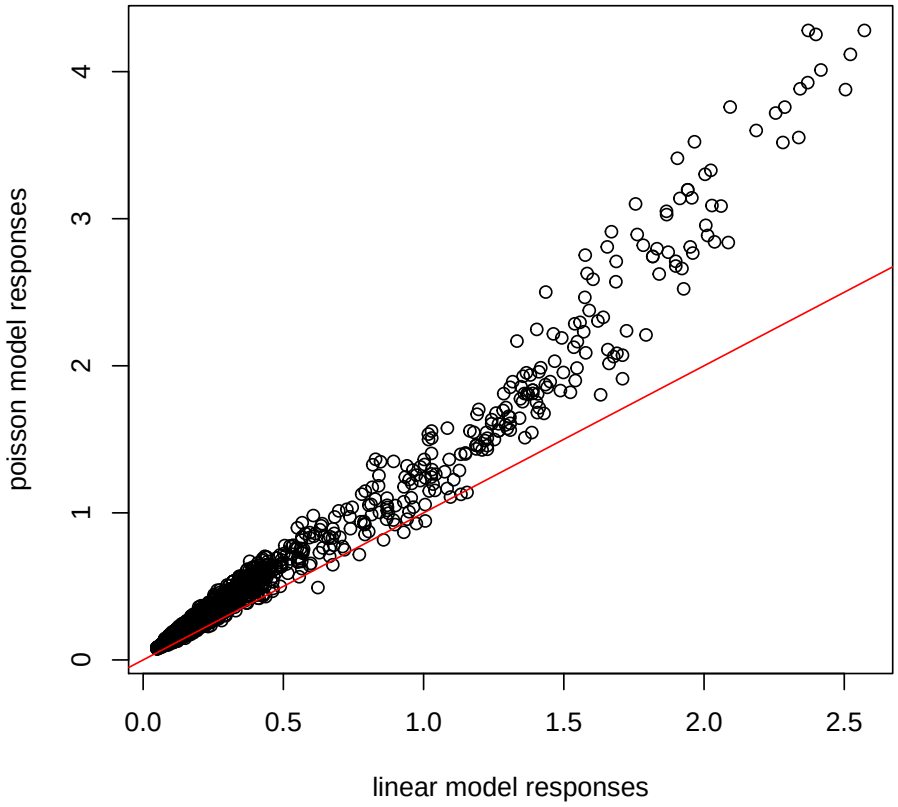
```
 [1] 8.451821e-01 1.421623e-01 1.195608e-02 6.703505e-04 2.818878e-05
 [6] 9.482888e-07 2.658420e-08 6.387927e-10 1.343087e-11 2.510129e-13
```

(f) Fit a comparable (Gaussian) linear model and graphically compare the fits. Describe how the Gaussian and Poisson models differ.

Solution: We get a better fit by taking the log of the response (offset by 0.1, as the response can take zero values). The resulting linear model produces fitted values a lot like those of the poisson model.

Note that the mean of a log-normal random variable is given by $\exp(\mu + \sigma^2/2)$. Thus if Y is log-normal, and we estimate the mean μ and variance σ^2 of $\log(Y)$, then our estimate for $\mathbb{E}Y$ is $\exp(\hat{\mu} + \hat{\sigma}^2/2)$.

```
> mod <- lm(log(doctorco + .1) ~ sex + age + agesq + income + levyplus
+           + freepoor + freerepa + illness + actdays + hscore + chcond1,
+           data=dvisits)
> mod2 <- step(mod, scope=~., trace=0)
> mod2si2 <- deviance(mod2)/mod2$df.residual
> plot(exp(predict(mod2) + mod2si2/2) - .1, predict(pmod3, type="response"),
+      xlab="linear model responses", ylab="poisson model responses")
> abline(0, 1, col="red")
```



Although the linear model does surprisingly well, its fitted values are all a little smaller than the corresponding fitted values for the poisson model. The most important difference between how these two models are fitted is their variance structure. The poisson model assumes that $\operatorname{Var} Y \propto \mathbb{E}Y$ and the linear model assumes that $\operatorname{Var} \log Y$ and hence $\operatorname{Var} Y$ is constant. Thus the linear model will be giving too much weight to large responses.