R Code And Tasks Chapter 5 (MAS 6003)

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Chapter 5 Poisson regression

5.1 Introduction

pdf of poisson

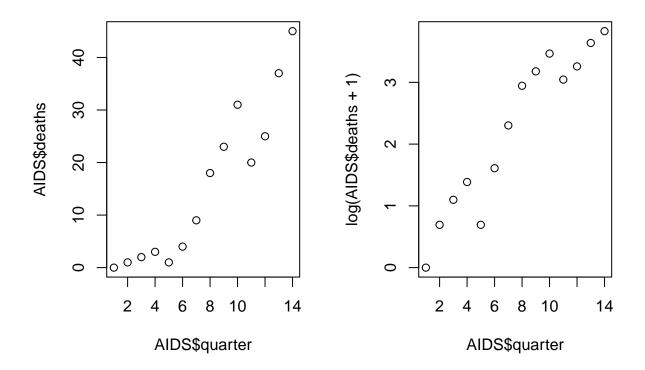
$$\frac{\lambda^k e^{-\lambda}}{k!}$$

5.2.1 Example: AIDS deaths over time (Task 15)

1 plot:

```
rm(list=ls())
load("data/MAS367-GLMs.RData", envir = e <- new.env())

AIDS <- e$AIDS
par(mfrow=c(1,2))
plot(AIDS$quarter, AIDS$deaths)
plot(AIDS$quarter, log(AIDS$deaths+1))</pre>
```



2 fit poisson with log link

```
glm.lin <- glm(deaths ~ quarter, data=AIDS, family=poisson(link='log'))
qchisq(0.95,glm.lin$df.residual)</pre>
```

[1] 21.02607

3 adding a quadratic term

```
glm.quad <- glm(deaths ~ quarter + I(quarter^2), data=AIDS, family=poisson(link='log'))
summary(glm.quad)</pre>
```

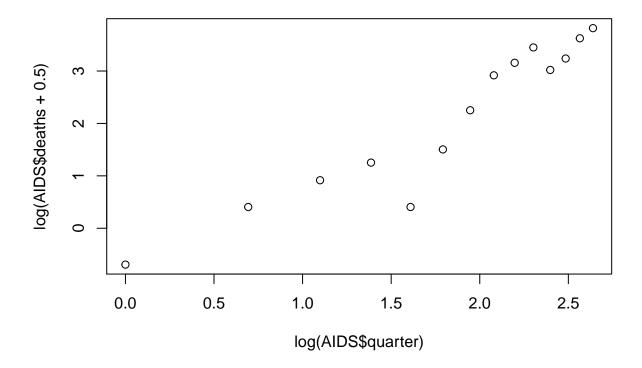
```
##
   glm(formula = deaths ~ quarter + I(quarter^2), family = poisson(link = "log"),
##
##
       data = AIDS)
##
## Deviance Residuals:
##
       Min
                  1Q
                       Median
                                    3Q
                                             Max
           -0.9385
##
  -1.7708
                       0.1304
                                0.8190
                                          1.4421
##
```

```
## Coefficients:
##
                Estimate Std. Error z value Pr(>|z|)
                           0.733108 -2.337 0.019432 *
## (Intercept) -1.713375
                0.746031
                           0.153391 4.864 1.15e-06 ***
## quarter
## I(quarter^2) -0.025836
                           0.007751 -3.333 0.000859 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## (Dispersion parameter for poisson family taken to be 1)
##
      Null deviance: 207.272 on 13 degrees of freedom
## Residual deviance: 16.371 on 11 degrees of freedom
## AIC: 75.298
##
## Number of Fisher Scoring iterations: 4
qchisq(0.95,glm.lin$df.residual)
## [1] 21.02607
4 a line predictor on log(x)
glm.logline <- glm(deaths ~ I(log(quarter)), data=AIDS, family=poisson(link='log'))</pre>
summary(glm.logline)
##
## Call:
## glm(formula = deaths ~ I(log(quarter)), family = poisson(link = "log"),
      data = AIDS)
##
## Deviance Residuals:
       Min
                  1Q
                        Median
                                      3Q
                                               Max
## -2.08992 -1.07141 -0.04657
                                 0.38956
##
## Coefficients:
                  Estimate Std. Error z value Pr(>|z|)
##
## (Intercept)
                   -1.9442
                               0.5116
                                       -3.80 0.000145 ***
## I(log(quarter))
                   2.1748
                               0.2150
                                       10.11 < 2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
      Null deviance: 207.272 on 13 degrees of freedom
## Residual deviance: 17.092 on 12 degrees of freedom
## AIC: 74.019
## Number of Fisher Scoring iterations: 4
```

```
qchisq(0.95,glm.logline$df.residual)
```

[1] 21.02607

plot(log(AIDS\$quarter), log(AIDS\$deaths+0.5))



5

Thus possible simple models are a line in logx or a quadratic in x, but there are reservations about both.

5.3 Adjusting for exposure : offset (Task 16)

An explanation of offset which is brief and clear can be found here (but not in the lecture notes of MAS 6003).

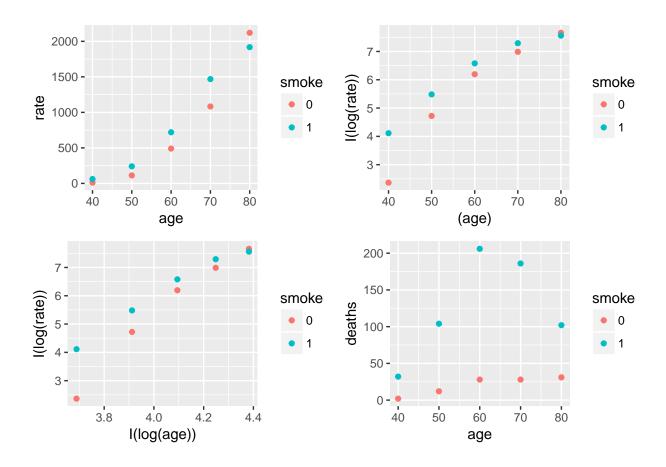
5.3.1 Example: Smoking and heart disease

1,2,3,4 death rates

library(ggplot2)

```
## Warning: package 'ggplot2' was built under R version 3.3.2
library(gridExtra)
## Warning: package 'gridExtra' was built under R version 3.3.2
smoking <- e$smoking</pre>
smoking$rate <- smoking$deaths/smoking$person.years * 1e5</pre>
lapply(smoking,class)
## $age
## [1] "integer"
##
## $smoke
## [1] "integer"
##
## $deaths
## [1] "integer"
## $person.years
## [1] "integer"
##
## $rate
## [1] "numeric"
smoking$smoke <- as.factor(smoking$smoke)</pre>
p1 <- ggplot(smoking, aes(age, rate, colour=smoke)) + geom_point()</pre>
p2 <- ggplot(smoking, aes((age), I(log(rate)), colour=smoke)) + geom_point()</pre>
p3 <- ggplot(smoking, aes(I(log(age)), I(log(rate)), colour=smoke)) + geom_point()
p4 <- ggplot(smoking, aes(age, deaths, colour=smoke)) + geom_point()
```

grid.arrange(p1,p2,p3,p4, ncol = 2)



5 The model

```
mod.offset <- glm(deaths~ offset(log(person.years)) + smoke * age + I(age^2), family = poisson, data=sm</pre>
summary(mod.offset)
##
## Call:
   glm(formula = deaths ~ offset(log(person.years)) + smoke * age +
       I(age^2), family = poisson, data = smoking)
##
##
## Deviance Residuals:
##
                               3
                                                   5
   -0.83049
              0.43820
                        0.13404
                                  -0.27329
                                             0.64107 -0.15265 -0.41058
##
                    9
##
          8
                              10
##
    0.23393 -0.01275
                       -0.05700
##
## Coefficients:
                 Estimate Std. Error z value Pr(>|z|)
##
## (Intercept) -1.970e+01 1.253e+00 -15.717 < 2e-16 ***
                2.364e+00 6.562e-01
                                        3.602 0.000316 ***
## smoke1
## age
                3.563e-01
                           3.632e-02
                                        9.810 < 2e-16 ***
               -1.977e-03 2.737e-04
                                      -7.223 5.08e-13 ***
## I(age^2)
```

smoke1:age -3.075e-02 9.704e-03 -3.169 0.001528 **

```
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1 ## ## (Dispersion parameter for poisson family taken to be 1) ## ## Null deviance: 935.0673 on 9 degrees of freedom ## Residual deviance: 1.6354 on 5 degrees of freedom ## AIC: 66.703 ## ## Number of Fisher Scoring iterations: 4 With smokers = 1 and 0 for nonsmokers: for non-smokers: -19.7 + 0.36x^2 - 0.02x^2 for smokers: -17.34 + 0.33x^2 - 0.02x^2
```

5.4 Non negative data with variance \propto means