MATH 588

HW8

Md Ismail Hossain

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Question 1

```
library(Sleuth3)
lymph = ex1914
names(lymph) = casefold(names(lymph))

lymphA = array(t(cbind(lymph$survive,lymph$died)),
dim=c(2,2,17),
dimnames = list(
outcome=c("survived","died"),
group=c("radiation","no"),
months=lymph$months[seq(1,by=2,length=17)]))
lymphA = aperm(lymphA,c(2,1,3))
```

```
woolf <- function(x) {
x <- x + 1 / 2
k <- dim(x)[3]
or <- apply(x, 3, function(x) (x[1,1]*x[2,2])/(x[1,2]*x[2,1]))
w <- apply(x, 3, function(x) 1 / sum(1 / x))
1 - pchisq(sum(w * (log(or) - weighted.mean(log(or), w)) ^ 2), k - 1)
}
woolf(lymphA)
```

```
## [1] 0.9465877
```

```
mantelhaen.test(lymphA)
```

```
##
##  Mantel-Haenszel chi-squared test with continuity correction
##
## data:  lymphA
## Mantel-Haenszel X-squared = 2.3938, df = 1, p-value = 0.1218
## alternative hypothesis: true common odds ratio is not equal to 1
## 95 percent confidence interval:
##  0.1762224 1.1012146
## sample estimates:
## common odds ratio
##         0.4405209
```

Question 2

```
trout = ex2116
names(trout)=casefold(names(trout))
trout$noTumor = trout$total - trout$tumor
trout$invDose = 1/trout$dose
trlr = glm(cbind(tumor,noTumor)~invDose, trout, family="binomial")
```

```
qtr=glm(cbind(tumor,noTumor)~invDose, trout, family="quasibinomial")
```

```
1 - pchisq(summary(qtr)$dispersion * trlr$df.residual, trlr$df.residual)
```

```
## [1] 0.0007922717
```

```
summary(qtr)
```

```
## 
## Call:
## glm(formula = cbind(tumor, noTumor) ~ invDose, family = "quasibinomial",
##     data = trout)
## 
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -2.4440  -1.0363   0.3803   1.0666   2.6503
## 
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.636552   0.135625    12.07 4.61e-10 ***
## invDose     -0.046664   0.004069  -11.47 1.04e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## (Dispersion parameter for quasibinomial family taken to be 2.390595)
## 
##     Null deviance: 667.195  on 19  degrees of freedom
## Residual deviance:  41.809  on 18  degrees of freedom
## AIC: NA
## 
## Number of Fisher Scoring iterations: 4
```

Question 3

```
mate = case2201
names(mate)=casefold(names(mate))
m1 = glm(matings ~ age, mate, family="poisson")
qm1 = glm(matings ~ age, mate, family="quasipoisson")
1 - pchisq(summary(qm1)$dispersion * m1$df.residual, m1$df.residual)
```

```
## [1] 0.2308694
```

```
plot(m1)
```

Residuals vs Fitted

Predicted values
glm(matings ~ age)

Normal Q–Q

Std. Pearson resid.

Theoretical Quantiles
glm(matings ~ age)

Scale–Location

√|Std. Pearson resid.|

Predicted values
glm(matings ~ age)

Residuals vs Leverage

glm(matings ~ age)