36-402/608 Homework #12 due 10:30AM 4/22

1. Lymphoma and radiation (34 points)

   Read problem 19.14 on page 574. Using ex1914.csv, load the data into R using this code:

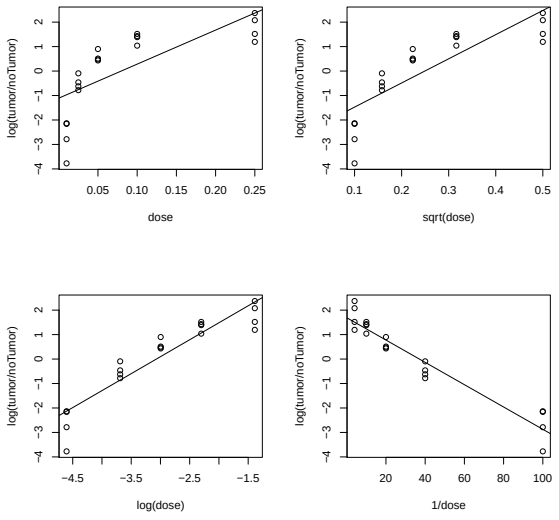
```
lymph = read.csv("ex1914.csv")
lymphA = array(t(cbind(lymph$survive,lymph$died)),
               dim=c(2,2,17),
               dimnames = list(
                 outcome=c("survived","died"),
                 group=c("radiation","no"),
                 months=lymph$months[seq(1,by=2,length=17)]))
lymphA = aperm(lymphA,c(2,1,3))
```

   Perform the Woolf test (see HO20), and turn in the p-value and its interpretation.

   Perform the Mantel-Haenszel test (two-sided). Turn in the M-H p-value, the estimate of the common odds ratio and its CI, and a careful statement of how these are interpreted.

2. Trout tumors (33 points)

   Read problem 21.16 and load the data from ex2116.csv. Add the variable "noTumors" to the data frame.



   The EDA plots shown here demonstrate that the inverse of the dose is a good transformation to achieve linearity with the log odds of getting a tumor. Add an "invDose" variable to the data frame.

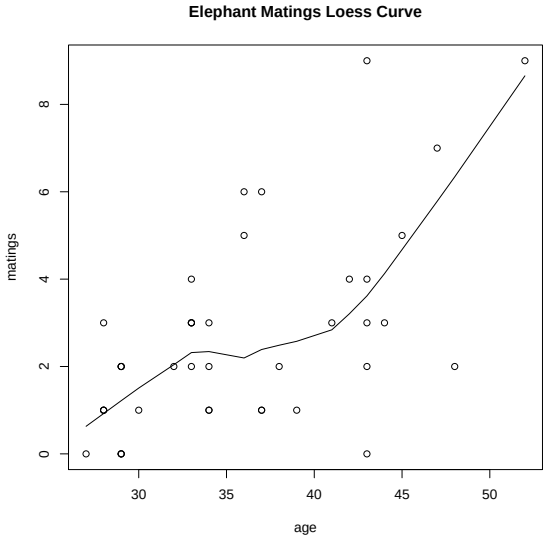
Perform binomial logistic regression to model the log odds of a tumor vs. the inverse dose. Save the glm() object for later use.

Perform quasibinomial logistic regression for the same model. Using the code on page 6 of HO21, obtain a p-value for the test with the null hypothesis of no over-dispersion. Turn in the p-value.

Based on the over-dispersion p-value, we must use the quasibinomial results to correct for over-dispersion (extra-binomial variation). Turn in the summary() for this model and an interpretation of $\exp(b_x)$ where x is the inverse dose. (You do not need to try to "undo" the meaning of the transformation.) Also roughly state in what way the quasibinomial results change our conclusions about the effects of dose on tumor production.

3. Mating Elephants (33 points) Turn in R code and a brief summary of your conclusions for the mating elephant problem on page 645 using data from case2201.csv.

   An EDA plot is shown here.



   Include a residual plot, as well as a check for extra-Poisson variation using family=quasipoisson with your results.