Poisson and Logistic Regression

Statistics 516, Homework 3

This homework assignment concerns the specification and interpretation of Poisson and logistic regression models. In comparison to the past two homework assignments, there is more emphasis here on *interpretation*, mainly by using rate ratios or odds ratios. So pay careful attention to your wording when interpreting a model using one of these ratios. An important part of statistical modeling is being able to understand and communicate what a model is saying about the statistical relationship between the expected response and the explanatory variable(s). You will need to have installed several packages for this assignment including **trtools**, **ggplot2**, **emmeans** (optional), **SMPracticals**, **dobson**, and **GLMsData**. Note that to be able to access data frames in the **GLMsData** package you will need to use the `data` function (see my code below).

Note: You may get an error saying `family not recongized` when using `glm` to estimate a Poisson regression model. The **dobson** package contains a data frame which is named `poisson` which will mask the `poisson` object that in R that is used in `family = poisson` in the `glm` function. To avoid this you can either use `family = stats::poisson` or explicitly name the link function such as `family = poisson(link = log)`.

Instructions

1. This assignment is due by 5:00 PM on Monday, April 4th. Email me your homework at trjohns@uidaho.edu. If possible, save/export your homework as a PDF file. Late assignments will be penalized by 10% if turned-in within 12 hours of the deadline, and 10% more for each additional 12 hour interval.
2. Your solutions must be **typed** and **very** neatly organized. I will not try to infer your solutions if they are not clearly presented. Mathematical expressions need not be typeset perfectly but they should be clear. You may substitute letters for symbols (e.g., b1 for β_1) and use other shortcuts for mathematical notation if no meaning is lost.
3. You must include with your solutions the relevant R output **and** R code that created them. Be sure that you provide sufficient code that I can replicate your results. Include both the code and the output within the text of your solutions (not in an appendix) using cut-and-paste. But edit your output so as to provide only that which is relevant to answering the questions. Use a monospace font (e.g., Courier or Monaco) for R code and output for clarity. Do not use a monospace font for text that is not R code or output.
4. Plots from R Studio can be exported in various formats or directly to the clipboard using the "export" menu in the top-left part of the plot panel.
5. It is permitted for you to discuss the homework with other students in the course. However your work including R code, output, and written answers must be your own.
6. You are very welcome to ask me questions. I will be happy to clarify what I am asking in any of the questions and will provide you some help with solving problems by showing you how to work through similar problems from class. I will also be open to helping with any R problems. If you email me with a R question, it will usually be helpful for you to include enough of your R script so that I can replicate your issue. But please avoid saving all your questions for just before the assignment is due. I can usually respond quickly to questions, but I will sometimes need time to respond.

Toxicity of Sodium Bromide on Daphnia magna Reproduction

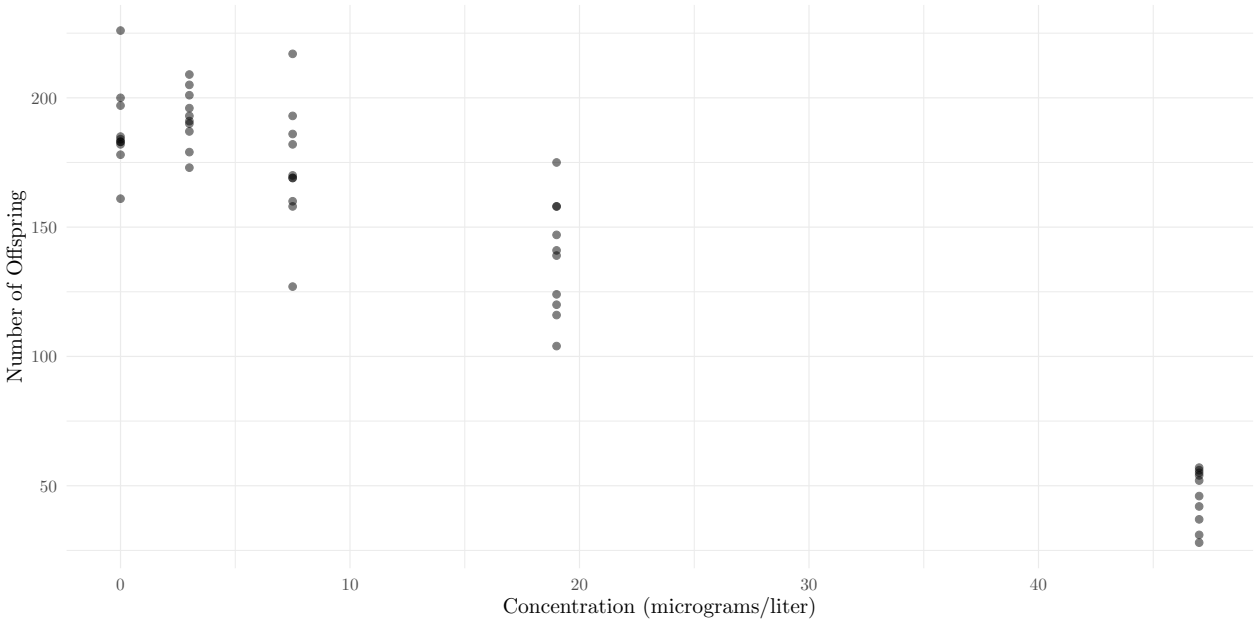
The data frame `nabr` in the **trtools** package is from a study of the toxicity of sodium bromide (NaBr) on the reproduction of Daphnia magna.[1] Sodium bromide is commonly used in oil and gas drilling and as an antiseptic. It can cause ecological problems if it finds its way into water systems. This study exposed Daphnia magna to different concentrations of sodium bromide over 23 days. The number of offspring per adult over that period was observed. As shown below the mean number of offspring decreased with the concentration of sodium bromide.

```
library(trtools)
library(dplyr)
nabr %>% group_by(concentration) %>% summarize(mean = mean(young))
```

```
# A tibble: 5 x 2
  concentration  mean
          <dbl> <dbl>
1             0   188.
2             3   192.
3             7.5 173.
4            19   138.
5            47    45.8
```

The figure below shows a plot of the data.

```
library(ggplot2)
p <- ggplot(nabr, aes(x = concentration, y = young)) +
  theme_minimal() + geom_point(alpha = 0.5) +
  labs(x = "Concentration (micrograms/liter)", y = "Number of Offspring")
plot(p)
```



Since the response variable is a count these data could maybe be modeled using Poisson regression.

1. Estimate two Poisson regression models with concentration as the explanatory variable and number of offspring as the response variable. For one model treat concentration as a quantitative explanatory

[1] Maul, A., El-Shaarawi, A. H., & Férard, J. F. (1991). Application of negative binomial regression models to the analysis of quantal bioassay data. *Environmetrics*, *2*, 253–261.

variable (i.e., as is), and for the other treat concentration as a categorical explanatory variable by converting it to a factor (either by converting it to a factor within the model formula using `factor(concentration)` or by creating a new variable with something like `nabr$concentrationf <- factor(nabr$concentration)`). Show the parameter estimates and their standard errors for each model using the `summary` function.

2. Create a plot showing the estimated expected number of offspring as a function of concentration for the model you estimated in the previous problem where concentration was treated as a *quantitative* explanatory variable.

3. Using the `contrast` function, estimate four rate ratios for comparing the expected number of offspring at concentrations of 3, 7.5, 19, and 47 micrograms/liter to the expected number of offspring at a concentration of zero micrograms/liter. Do this for *both* of the models you estimated earlier. Write a sentence to interpret each rate ratio in terms of what it shows about the effect of a given concentration relative to a zero concentration on the expected number of offspring.

4. For each of the two models you estimated earlier, create a residual plot of standardized or studentized residuals against the predicted values. Based on these residual plots, which model do you think better fits the data. Explain your reasoning.

5. Consider the model you estimated earlier where concentration was treated as a quantitative variable. That model can be written as $\log E(Y_i) = \beta_0 + \beta_1 x_i$, where Y_i and x_i are the i-th observations of the number of offspring and concentration, respectively. We sometimes call this a log-linear model since the log of the expected response is a linear function. Now consider two other models: a *linear* Poisson regression model which can be written as $E(Y_i) = \beta_0 + \beta_1 x_i$, and a *quadratic* polynomial log-linear model which can be written as $\log E(Y_i) = \beta_0 + \beta_1 x_i + \beta_2 x_i^2$.[2] The linear model can be specified by using an "identity" rather than a log link function (i.e., use `link = identity` rather than `link = log` in the `glm` function). The polynomial log-linear model can be specified just like other Poisson regression models but using either the `I` inhibit function or the `poly` function to specify the polynomial (see the discussion of polynomial regression). Estimate each of these models using the `glm` function, reporting the parameter estimates and their standard errors using `summary`. Also plot the standardized or studentized residuals against the predicted values for each model. Based on these residual plots, how do the the four Poisson regression models that you have now estimated compare in terms of their fit to the data? Explain your reasoning. **Note**: This problem is *extra credit* for students in Stat 436, but is *required* for students in Stat 516.

Swedish Speed Limit Study

The data frame `nabr` in the **SMPracticals** package contains data from a observational study of the effects of speed limits on the number of traffic accidents.[3] This study was carried out in Sweden during the summers of 1961 and 1962 during comparable days (e.g., if an observation was made during the first Monday of July in 1961, an observation was also made during the first Monday of July in 1962). Periods of no speed limits were alternated with a posted speed limit of 90 km/h or 100 km/h. The number of traffic accidents with personal injuries that occurred and were reported each day during the study was recorded. The data are in "wide form" with each row showing observations from both 1961 and 1962.

```
library(SMPracticals)
head(limits)
```

```
  day lim1 lim2 y1 y2
```

[2]Typically when using Poisson regression a log link function is implied. But other link functions can be used, and it would still be appropriate to call such a model a Poisson regression model since it still assumes that the response variable has a Poisson distribution. Even though we are using a linear model, we are still assuming a Poisson distribution for the response variable, and the pattern of heteroscedasticity is still that of a Poisson distribution. But when we specify a logistic regression model the link function is a logit (i.e., log-odds) link function, and the assumed distribution of the observed count is assumed to be binomial. If we change the link function but still assume a binomial distribution (which we will consider in a future lecture) the model is no longer a logistic regression model. Instead we might call it a *binomial* (or *binary*) regression model.

[3]Svensson, A. (1981). On a goodness-of-fit test for multiplicative Poisson models. *Annals of Statistics*, *9*, 697–704.

```
1   1    0    0  9  9
2   2    0    0 11 20
3   3    0    0  9 15
4   4    0    0 20 14
5   5    0    0 31 30
6   6    0    0 26 23
```

Here `lim` and `lim2` are indicator variables for if a speed limit was posted on a given day in 1961 and 1962, respectively, and `y1` and `y2` are the number of traffic accidents on a given day in 1961 and 1962, respectively. For plotting and modeling it is useful to put the data into "long form" where each row is an observation from a given day in a given year.[4]

```
library(dplyr)
library(tidyr)
limitstudy <- limits %>%
  rename(limit_1961 = lim1, limit_1962 = lim2, y_1961 = y1, y_1962 = y2) %>%
  pivot_longer(cols = -day, names_to = c(".value", "year"), names_sep = "_") %>%
  mutate(limit = factor(limit, levels = c(0,1), labels = c("no","yes")))
head(limitstudy)
```

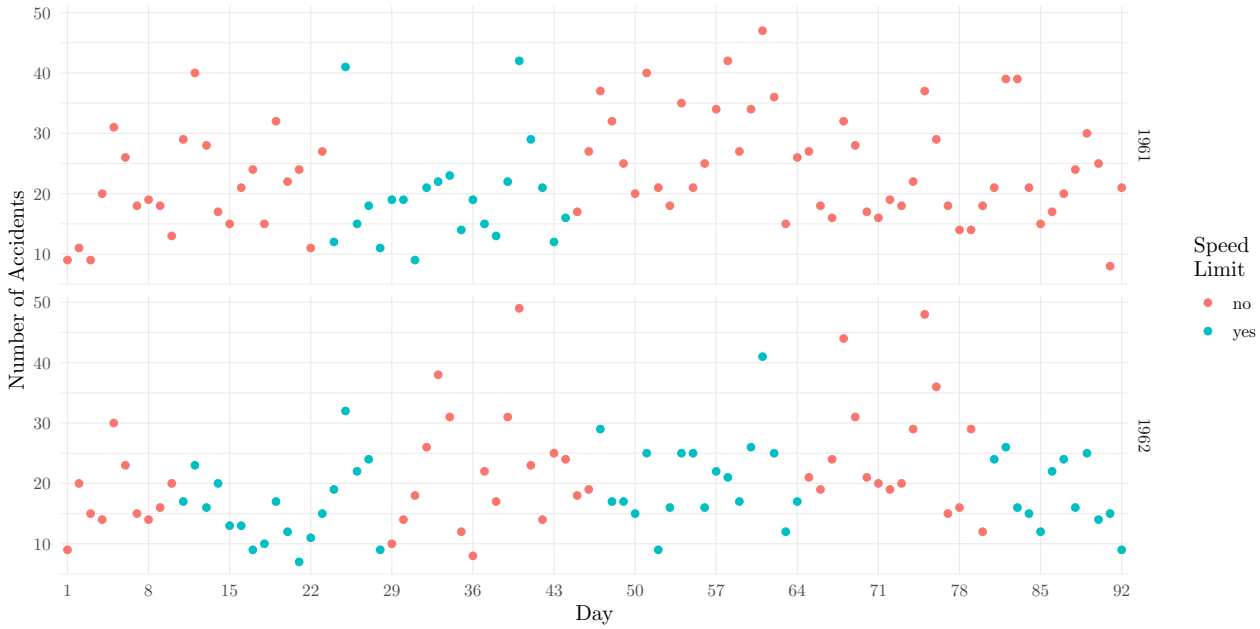
```
# A tibble: 6 x 4
  day   year  limit     y
  <fct> <chr> <fct> <int>
1 1     1961  no        9
2 1     1962  no        9
3 2     1961  no       11
4 2     1962  no       20
5 3     1961  no        9
6 3     1962  no       15
```

Compare the original data in `limits` to the new data frame `limitstudy` and you can see how the data have been "reshaped" by the code above. Also note that I formatted the `limit` into a factor with more clear level labels. Here is a plot of the data showing the number of accidents each day by year and whether or not a speed limit was posted.[5]

```
library(ggplot2)
p <- ggplot(limitstudy, aes(x = day, y = y, color = limit)) +
  theme_minimal() + geom_point() + facet_grid(year ~ .) +
  scale_x_discrete(breaks = seq(1, 92, by = 7)) +
  labs(x = "Day", y = "Number of Accidents", color = "Speed\nLimit")
plot(p)
```

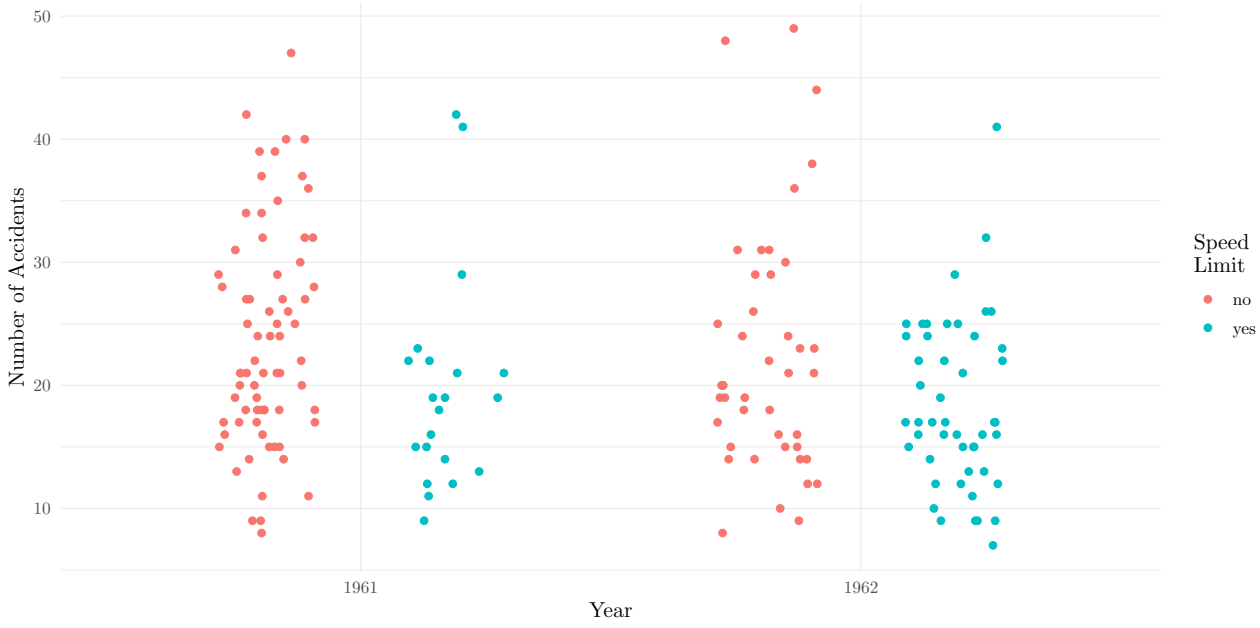
[4] Using `pivot_longer` effectively takes several columns that represent observations of the same variable and arranges them so that each observation is in a single row. This is relatively simple for a single variable, but gets a bit more complicated when there are two or more variables like there are here (i.e., the speed limit indicator and the number of accidents). I will admit the syntax is a bit cryptic. I actually copied this from an example that you can see if you use the command `vignette("pivot")`. The trick is to create variable names that can be parsed effectively by the `pivot_longer` function.

[5] The "\n" in the label for color is an escape character which adds a new line so that the label "Speed Limit" spans two lines of text instead of one.



It might be important to account for the effect of day since the risk of accidents may vary over time, and the figure above shows that the speed limits were not randomly or uniformly distributed over days. But for this problem you will ignore any effect of day and just focus on how the expected number of accidents varies by year and by whether or not a speed limit was posted.[6] The table below shows the data without accounting for day.

```
set.seed(111)
p <- ggplot(limitstudy, aes(x = year, y = y, color = limit)) +
  theme_minimal() + geom_point(position = position_jitterdodge()) +
  labs(x = "Year", y = "Number of Accidents", color = "Speed\nLimit")
plot(p)
```



[6] We may return to these data and see how we might account for the effect of day using a fixed or random effects model.

The sample statistics show that the number of accidents was, on average, lower when speed limits were posted.

```
limitstudy %>% group_by(year, limit) %>% summarize(mean = mean(y))
```

```
# A tibble: 4 x 3
# Groups:   year [2]
  year  limit  mean
  <chr> <fct> <dbl>
1 1961  no     23.7
2 1961  yes    19.7
3 1962  no     22.2
4 1962  yes    18.4
```

In this problem you will consider using regression models for inferences concerning the relationship between the posting of a speed limit and the expected number of accidents. The main focus here is on how posting a speed limit is related to the expected number of accidents, but controlling for year by including it as an explanatory variable is important since the accident rate may have varied by year and year is partially confounded with speed limit since speed limits were posted more often in 1962 than in 1961. Be sure you use the data frame `limitstudy` created above for your model.

1. Estimate a Poisson regression model with the number of accidents as the response variable and the speed limit (yes or no) and year (1961 or 1962) as explanatory variables. Do not include an interaction in your model. Year here should be treated as a categorical variable (i.e., a factor) but it is not necessary to convert it to a factor since it is stored in the data frame as a character variable and not a number, so R will automatically interpret it as a factor when it is used as an explanatory variable.[7]

2. Using either `contrast` or functions from the **emmeans** package, produce estimates and confidence intervals for the expected number of accidents with and without a posted speed limit in 1961, and again in 1962.

3. Using either `contrast` or functions from the **emmeans** package, estimate the rate ratio for the expected number of accidents when a speed limit was posted versus when it was not. Note that while you can estimate a separate rate ratio for 1961 and another for 1962, they should be equal since the model does not include an interaction. Report the rate ratio and its confidence interval, and write a sentence that interprets the value of the rate ratio in terms of the the expected number of accidents when a speed limit was posted versus when it was not.

Modeling Death Rates from Cervical Cancer

The data frame `cervical` in the **GLMsData** package is an observational study of the death rates due to cervical cancer by age group in four countries/regions in Europe.[8] The data are shown below. Note that using `data(cervical)` is necessary here to make the data frame accessible.[9]

```
library(GLMsData)
data(cervical)
cervical
```

```
    Country    Age Deaths Wyears
1  EngWales 25to34    192 153999
2  EngWales 35to44    860  14268
```

[7] You can see that `year` is a character variable when you look at the data frame. At the top is it labeled as type `<chr>` which identifies it as a character variable. You can also see this if you use `str(limitstudy)`

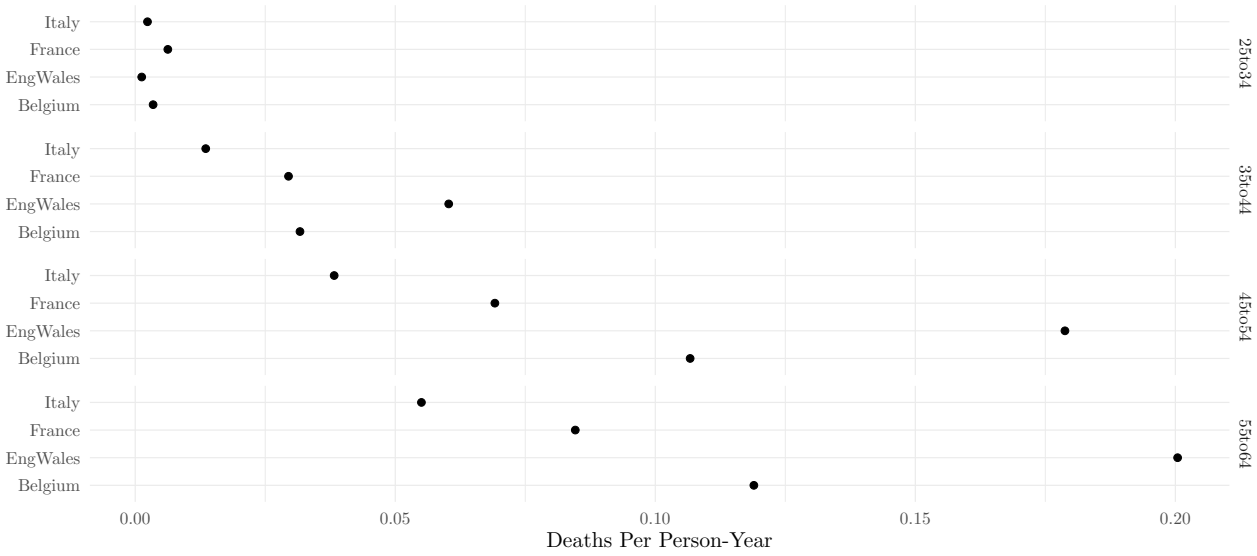
[8] Whittermore, A. S. & Gong, G. (1991). Poisson regression with misclassified counts: Applications to cervical cancer mortality rates. *Applied Statistics*, *40(1)*, 81–93.

[9] The `data` function was originally intended to allow users to not have to load large data frames into memory until needed. But that is no longer necessary because packages can now use what is called lazy loading meaning that a data frame will only be loaded into memory if and when it is used. Package developers are encouraged to set their packages to use lazy loading so use of `data` is not necessary, but not everyone does this.

```
3  EngWales 45to54   2762  15450
4  EngWales 55to64   3035  15142
5   Belgium 25to34      8   2328
6   Belgium 35to44     81   2557
7   Belgium 45to54    242   2268
8   Belgium 55to64    268   2253
9    France 25to34     96  15324
10   France 35to44    477  16186
11   France 45to54    998  14432
12   France 55to64   1117  13201
13    Italy 25to34     45  19115
14    Italy 35to44    255  18811
15    Italy 45to54    621  16234
16    Italy 55to64    839  15246
```

The observed death rate can be computed by dividing the number of deaths (`Deaths`) by the number of woman-years (`Wyears`). The latter, which is usually called "person-years" in gender-neutral applications, is a unit of measurement that takes into account both the number of people and the amount of time they are being observed.[10] For example, if we had ten people each observed for five years then that would be 50 person-years. Or if we had one person observed for five years and another observed for two that would be a total of seven person-years. The rate can then be defined in terms of number of deaths due to cervical cancer per person-year, or per person per year. The plot below shows the observed rate of deaths to cervical cancer by country and age group.

```
library(ggplot2)
p <- ggplot(cervical, aes(x = Deaths / Wyears, y = Country)) +
   theme_minimal() + geom_point() + facet_grid(Age ~ .) +
   labs(y = NULL, x = "Deaths Per Person-Year")
plot(p)
```

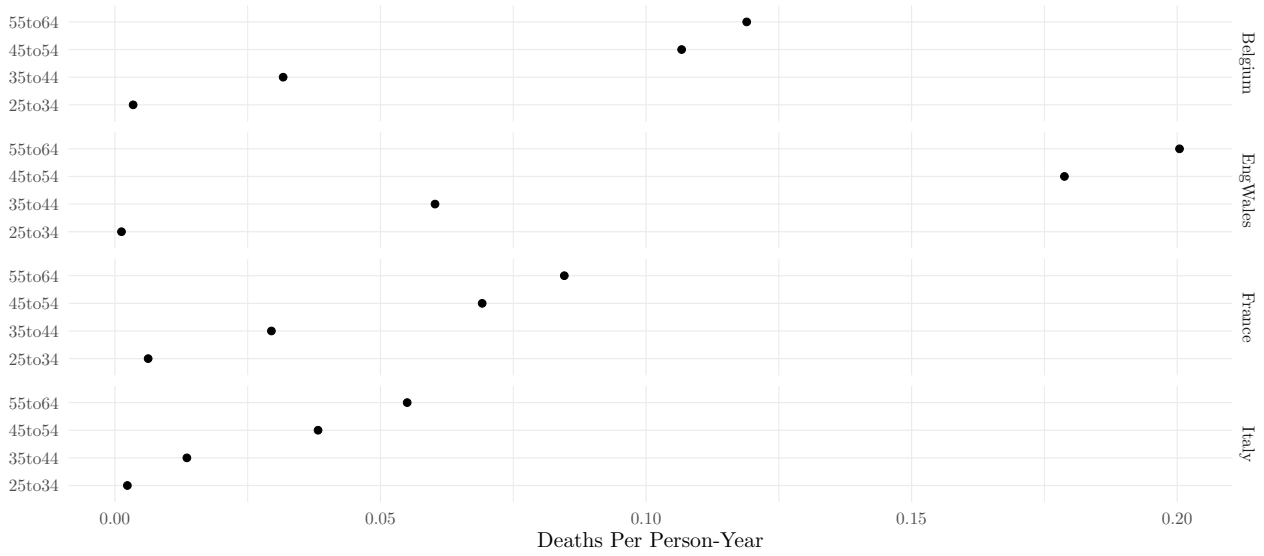


Alternatively we could plot the observed rates by grouping them by country.

```
p <- ggplot(cervical, aes(x = Deaths / Wyears, y = Age)) +
   theme_minimal() + geom_point() + facet_grid(Country ~ .) +
   labs(y = NULL, x = "Deaths Per Person-Year")
```

[10] We can use the more common gender-neutral term "person-year" here with the understanding that the rate is among people that have a cervix and thus are susceptible to cervical cancer.

```
plot(p)
```



The goal here is to model the rate of deaths due to cervical cancer to compare the rates between countries/regions and also between age groups.

1. Estimate a Poisson regression model for the rate of deaths due to cervical cancer that produces the following output when using `summary`.

   ```
                   Estimate Std. Error z value  Pr(>|z|)
   (Intercept)      -6.7040    0.06859 -97.744 0.000e+00
   CountryEngWales   0.5105    0.04267  11.964 5.481e-33
   CountryFrance    -0.3119    0.04518  -6.904 5.071e-12
   CountryItaly     -0.8704    0.04730 -18.400 1.318e-75
   Age35to44         3.3888    0.05990  56.574 0.000e+00
   Age45to54         4.4201    0.05651  78.223 0.000e+00
   Age55to64         4.5905    0.05625  81.612 0.000e+00
   ```

   Note that since the number of person-years varies by country/region and age group you will need to use an offset variable. Report the parameter estimates and their standard errors using `summary`.

2. Using either `contrast` or functions from the **emmeans** package, estimate three ratios that compare the expected death rate for the three older age groups with the youngest age group. Summarize each rate ratio in a sentence that describes clearly how the age groups compare with respect to the death rate.

3. Using either `contrast` or functions from the **emmeans** package, estimate three ratios that compare the expected death rate in England and Wales with the three other countries. Summarize each rate ratio in a sentence that describes clearly how the countries/regions compare with respect to the death rate.[11]

Toxicity of Trans-Cypermetrin for Tobacco Budworm

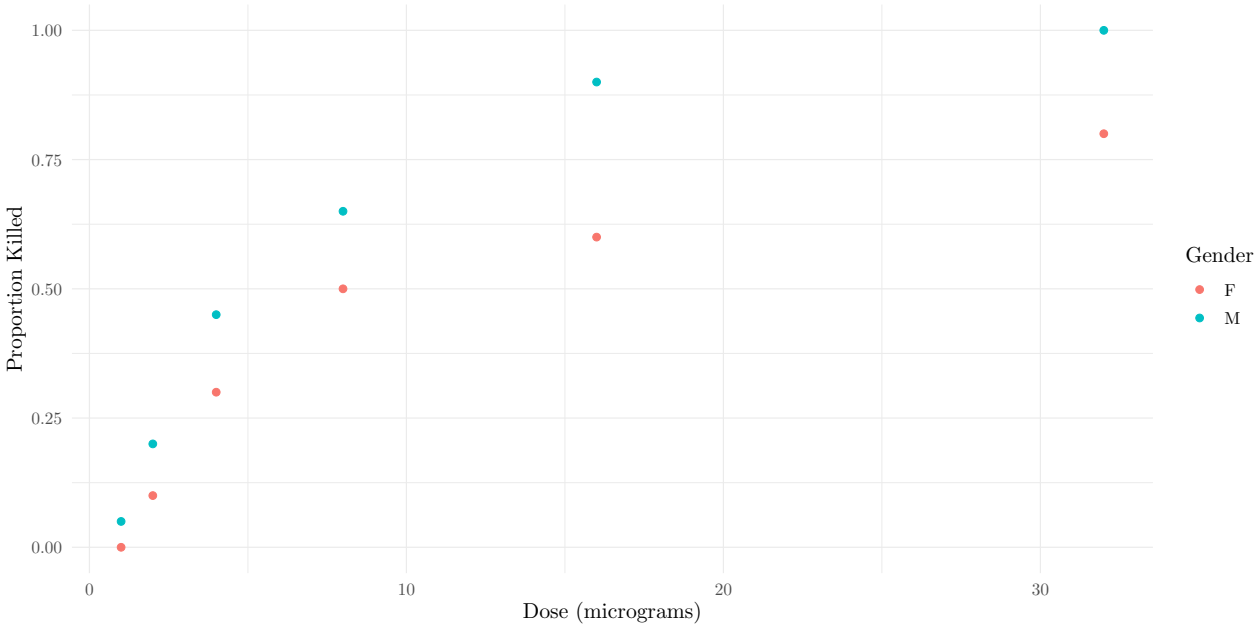
The data frame `budworm` in the **GLMsData** package is from a study of the toxicity of the pyrethroid trans-cypermethrin in tobacco budworm (*Heliothis virescens*) which are responsible for considerable damage to cotton crops in North and South America.[12]

[11] Not too much should be made of these rate ratios. The paper that reported these data pointed out that there was evidence that death rates due to cervical cancer were under-reported in some countries.

[12] Holloway, J. W. (1989). A comparison of the toxicity of the pyrethroid trans-cypermethrin, with and without the synergist piperonyl butoxide, to adult moths from two strains of *Helios virescens*. Final year dissertation, Department of Pure and Applied Zoology, University of Reading, UK. Batches of twenty male or female moths were exposed to each of six doses of the pyrethroid,

```
library(ggplot2)
library(GLMsData)
data(budworm)

p <- ggplot(budworm, aes(x = Dose, y = Killed/Number, color = Gender)) +
  theme_minimal() + geom_point() +
  labs(x = "Dose (micrograms)", y = "Proportion Killed")
plot(p)
```



In this problem you will use logistic regression to investigate the effect of dose on mortality.

1. Estimate *two* logistic regression models: one using dose and gender as explanatory variables, and a second using the *logarithm* of dose and gender as explanatory variables. For the model using the logarithm of dose as an explanatory variable, include the transformation within the model formula as `log(dose)` rather than creating a new variable in the data frame. Both models should include an interaction between dose (or log of dose) and gender. Report the parameter estimates and their standard errors for both models using the `summary` function, and plot both models by adding curves to the plot above to show the estimated expected proportion of dead budworms as a function of dose and gender. You can either make one plot showing both models, or one plot for each model.

2. For the model without the log transformation of dose, estimate the odds ratio for each gender for the effect of increasing dose by one unit (i.e., one microgram), and for the model with the log transformation of dose, estimate the odds ratio for each gender for the effect of doubling the dose. Use the `contrast` function to estimate the odds ratios. Summarize each odds ratio in a sentence that describes clearly the effect of increasing the dose for a given gender of tobacco budworm.

3. The plots show that the estimated probability of mortality is higher for male tobacco budworms (except perhaps at very low doses). Use either the `contrast` function or functions from the **emmeans** package to estimate the odds ratio for the effect of gender (i.e., comparing males to females) at a dose of five micrograms, and again at a dose of 10 micrograms. Summarize each of the four odds ratios in a sentence that describes clearly the comparison between male and female budworms at those two doses.

and the number that were killed after 72 hours of exposure was observed. The plot below shows the proportion of moths killed by gender and dose.

4. In the previous problem you estimated odds ratios to compare male and female tobacco budworms at five and 10 micrograms of dose. Use either the `contrast` function or functions from the **emmeans** package to estimate the *probability* and the *odds* of death of male and female tobacco budworms at doses of five and 10 micrograms.

5. The two models you estimated and used in the previous problems are not equivalent. We might want to assess which model is a better fit to the data. There are several ways that this could be done. One is to inspect the plots you made earlier to compare the estimated expected proportions to the observed proportions. A second approach is to inspect a residual plot of the predicted values against standardized or studentized residuals. And a third approach is to look at the residual deviance of each model, noting that the residual deviance can be viewed as a measure of the "lack of fit" relative to a hypothetical best-fitting model. Use all three methods to compare the three models and decide which of the two models would be a better fit to the data and explain your decision.

6. The models with an interaction allow the odds ratio for one explanatory variable to depend on the value of the other explanatory variable (i.e., the odds ratio for the effect of dose can depend on gender, and the odds ratio for the effect of gender can depend on dose). The *estimated* odds ratio for one explanatory variable does depend on the value of the other, but suppose we want to know if this is *statistically significant*. This can be tested using a likelihood ratio test or a Wald test. Using the model you selected in the previous problem, estimate the same model except *without* the interaction and use this model with the original model with the interaction to conduct a likelihood ratio test of the interaction. Also conduct a Wald test of the interaction using `summary`. You should be able to identify the parameter responsible for the interaction relatively easily. For each test report the test statistic and the p-value as well as the decision assuming a significance level of 0.05.

Case-Control Study of Peptic Ulcers and Aspirin Use

The data frame `ulcer` in the **dobson** package contains data from a study of the relationship between peptic ulcers and aspirin use.[13] There is evidence that non-steroidal anti-inflammatory drugs (NSAID) like aspirin are risk factors for peptic ulcers. This study used a retrospective case-control design. This design involves identifying a sample of "cases" (e.g., people with a peptic ulcer) and a sample of "controls" (e.g., people without a peptic ulcer) and then comparing them with respect to prior risk factors (e.g., regular use of aspirin). This particular study formed case and control groups for two different kinds of cases corresponding to two different kinds of peptic ulcers: *duodenal* ulcers (i.e., ulcers in the first part of the upper intestines), and *gastric* ulcers (i.e., ulcers in the stomach).

Data from case-control studies are often modeled using logistic regression where the status (i.e., case or control) is used as the response variable. It is actually the *wrong* model for the design. The likelihood function for logistic regression assumes that the individual binary observations are independent, but this cannot be true in a retrospective case-control design where the number of cases and controls are determined by the researchers. It can be shown, however, that using logistic regression will result in consistent estimators for all parameters *except* β_0.[14] The β_0 parameter in a retrospective case-control design depends also on the probabilities of cases and controls being included in the study (which are generally unknown) so what is being estimated by β_0 in a logistic regression model for a retrospective case-control study is not the same as what is being estimated by β_0 for a prospective study where, for example, subjects were first classified based aspirin use and then we waited to see who developed peptic ulcers. This implies that the model for the retrospective case-control design *cannot* produce valid inferences for the *probability* of an event since the number of cases and controls are determined *by design*. But it can be shown that the inferences for the *odds ratio* for any explanatory variable are valid. Retrospective case-control designs are often used for fairly rare events (e.g., ulcers) where it is easier to identify a sample of subjects with the condition *after* it has happened.[15]

[13] Duggan, J. M., Dobson, A. J., Johnson, H., & Fahey, P. P. (1986). Peptic ulcer and non-steroidal anti-inflammatory agents. *Gut*, *27*, 929–933.

[14] The property of consistency is quite technical, but what it essentially means that as the sample size increases the estimator will have a tendency to produces estimates that are closer to the parameter being estimated.

[15] Because probabilities and odds are very similar for very small probabilities, an odds ratio for a model for a rare event (like an ulcer) can be viewed as a good approximation to the relative risk which is a ratio of probabilities instead of odds. So if the

The data from this study are stored in terms of frequencies of each combination of ulcer type, case or control status, and aspirin use.

```
library(dobson)
ulcer
```

```
# A tibble: 4 x 4
  ulcer    aspirin  control  case
  <chr>    <chr>      <dbl> <dbl>
1 gastric  non-user      62    39
2 gastric  user           6    25
3 duodenal non-user      53    49
4 duodenal user           8     8
```

For modeling it is useful to reshape the data so that each row gives the number of cases and controls.

```
library(dplyr)
library(tidyr)
ulcer <- dobson::ulcer %>%
  pivot_wider(names_from = `case-control`, values_from = frequency)
ulcer
```

```
# A tibble: 4 x 4
  ulcer    aspirin  control  case
  <chr>    <chr>      <dbl> <dbl>
1 gastric  non-user      62    39
2 gastric  user           6    25
3 duodenal non-user      53    49
4 duodenal user           8     8
```

We can also compute the proportion of regular users of aspirin and non-users that are cases for each type of ulcer — i.e., the proportion of participants in the study for each combination of ulcer type and aspirin use that have an ulcer.

```
ulcer %>% group_by(ulcer, aspirin) %>%
  mutate(proportion = case / (case + control))
```

```
# A tibble: 4 x 5
# Groups:   ulcer, aspirin [4]
  ulcer    aspirin  control  case proportion
  <chr>    <chr>      <dbl> <dbl>      <dbl>
1 gastric  non-user      62    39      0.386
2 gastric  user           6    25      0.806
3 duodenal non-user      53    49      0.480
4 duodenal user           8     8      0.5
```

This illustrates why a logistic regression model for a retrospective case-control design cannot be used to infer probabilities. For example, the percent of regular aspirin users that have a gastric ulcer is over 80%, but certainly the probability of a regular aspirin user having a gastric ulcer is not that high. As stated earlier, a logistic regression model for a retrospective case-control design can be used to estimate odds ratios, but not (interpretable) probabilities.

1. Estimate a logistic regression model for the proportion of subjects that are cases using ulcer type and aspirin use as explanatory variables. Include an interaction in your model. Report the parameter estimates and their standard errors using the `summary` function.

2. Using either the `contrast` function or functions from the **emmeans** package, estimate the odds ratio for the effect of regular use of aspirin for gastric and duodenal ulcers (i.e., one odds ratio for each type

odds ratio is, say, two, then this means that the odds are twice as high but also the probability is nearly twice as high.

of ulcer). Report the odds ratios and their confidence intervals. Interpret each odds ratio in writing to explain what it means about the relationship between having a particular type of ulcer and regular aspirin use.

3. A test of the interaction is a test of whether or not the odds ratios are different for the two types of ulcers. Conduct either a likelihood ratio test or a Wald test of the interaction. Report your test statistic, p-value, and decision using a significance level of 0.05.