Categorical Response Variables, Marginal and Mixed Effect Models, and Review

Statistics 516, Homework 5

This homework covers regression models with categorical response variables, and marginal and mixed effects models. The homework is also serves as a kind of review of how to make inferences based on regression models (e.g., rate and odds ratios). Packages that you will need to have installed include **mice**, **SMPracticals**, **qss**, **VGAM**, **lme4**, **geepack**, **dplyr**, **tidyr**, **trtools**, and possibly **emmeans**. You may have some of these packages installed already. Note that the **qss** package requires a special command for installation which is explained in the problem that uses it. Note that you will be using the `geeglm` function from the **geepack** package to estimate marginal models, and the `lmer` and `glmer` functions from the **lmer4** package to estimate linear and generalized linear mixed models, respectively. In some problems I ask you to compare either standard errors or confidence intervals. The `contrast` function will not (by default) give you standard errors if you specify a transformation using the `tf` argument, but it will give you confidence intervals.[1] Functions from the **emmeans** package will provide both standard errors and confidence intervals.

1. This assignment is due by 8:00 AM on Monday, May 16th. Email your homework to 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

[1] The `contrast` function does have the ability to compute these standard errors using the delta method, which is what is used when you obtain them with functions from the **emmeans** package. It will report these (approximate) standard errors if you specify the argument `delta = TRUE`. However if you do this then the confidence and tests will use this standard error rather than the standard error for the un-transformed quantity. Computing the confidence interval and tests for the un-transformed quantity is generally considered to be better. The confidence interval endpoints can then be transformed which is done by default by `contrast` and functions in the **emmeans** package. The `contrast` function does not do this if `delta = TRUE` for situations where one wants to use the estimated standard error for confidence intervals and tests, but you can always omit the argument to get the confidence interval and tests the usual way.

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.

Dental Fissure Growth Data

The data frame potthoffroy in the **mice** package is from a study of the growth of the distance from the center of the pituitary gland to the pteryomaxillary fissure in boys and girls.[2] The pituitary-pteryomaxillary distance was measured four times at ages 8, 10, 12, and 14 in several boys and girls. These longitudinal data are stored in wide form.

```
library(mice)
head(potthoffroy)
```

```
  id sex   d8  d10  d12  d14
1  1   F 21.0 20.0 21.5 23.0
2  2   F 21.0 21.5 24.0 25.5
3  3   F 20.5 24.0 24.5 26.0
4  4   F 23.5 24.5 25.0 26.5
5  5   F 21.5 23.0 22.5 23.5
6  6   F 20.0 21.0 21.0 22.5
```

For plotting and modeling we need to put them into long form. This is done below. Also a quantitative age variable is created from the column labels of the wide form data.

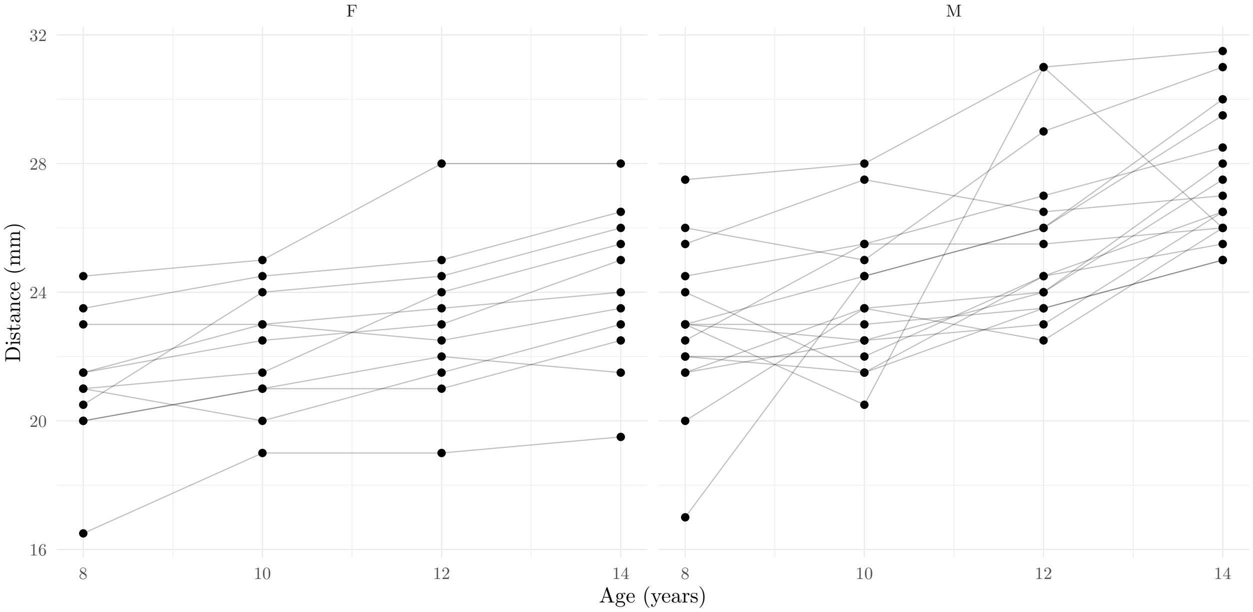
```
library(dplyr)
library(tidyr)
dental <- potthoffroy %>% rename(subject = id) %>%
  pivot_longer(cols = c(d8,d10,d12,d14), names_to = "obs", values_to = "distance") %>%
  mutate(age = as.numeric(substr(obs, 2, nchar(obs)))) %>% dplyr::select(-obs)
head(dental)
```

```
# A tibble: 6 x 4
  subject sex   distance   age
    <int> <fct>    <dbl> <dbl>
1       1 F         21       8
2       1 F         20      10
3       1 F         21.5    12
4       1 F         23      14
5       2 F         21       8
6       2 F         21.5    10
```

The plot below shows the observations with line segments connecting the observations from the same subject.

```
library(ggplot2)
p <- ggplot(dental, aes(x = age, y = distance)) + theme_minimal() +
  geom_line(aes(group = subject), alpha = 0.25) + geom_point() +
  facet_wrap(~ sex) + labs(x = "Age (years)", y = "Distance (mm)")
plot(p)
```

[2] Potthoff, R. F., & Roy, S. N. (1964). A generalized multivariate analysis of variance model useful especially for growth curve problems. *Biometrika*, *51(3)*, 313–326.



These data were featured in the lecture on fixed effects models.[3] The fixed effects approach is not useful here for making inferences regarding sex, so you will consider some other approaches that are more useful. When using the `geeglm` and `lmer` functions you might find it useful that these data are very similar in structure to the `Sitka` data featured in lecture where we have `age` instead of `Time`, `sex` instead of `ozone`, and `subject` instead of `tree`. Note that unlike the `Sitka` data we do not need to transform the response variable or the time/age variable. For each of the problems below report the `summary` output so that I can verify that you specified and estimated the model correctly.

1. Estimate a linear model using the `lm` function with distance as the response variable and age and `sex` as the explanatory variables, with an interaction. Note that this is arguably not an appropriate model here as it does not account for the lack of independence of observations from the same subject, but you will use it for comparison. Using either the `contrast` function or functions from the **emmeans** package, estimate (a) the difference in the expected distance between boys and girls at ages of 8, 10, 12, and 14, (b) the rate of change in the expected distance per year for boys and for girls, and (c) the difference in the rate of change in the expected distance per year between boys and girls.

2. Estimate a *marginal* linear model using the `geeglm` function from the **geepack** package with `distance` as the response variable and age and sex as the explanatory variables, with an interaction. Note that subject is your `id` variable and your correlation structure should be specified as exchangeable as was done in lecture. Using this model make the same inferences that you did in the previous problem using the `contrast` function or the **emmeans** package. Note that the syntax for these inferences should be the same as what you used in the previous problem.

3. Estimate a linear *mixed effects* model using the `lmer` function from the **lme4** package with distance as the response variable and age and `sex` as the explanatory variables, with an interaction. Specify a random "main effect" for subject. Using this model make the same inferences that you did in the previous problems using the `contrast` function or the **emmeans** package. Note that the syntax for these inferences should be the same as what you used in the previous problem.

4. Compare the inferences you obtained in the three problems above, paying particular attention to the estimates and their standard errors. Discuss briefly the similarities and differences in the inferences for the three approaches.

[3] These data have appeared in many articles and books, and are included in several R packages. In lecture I used the data frame form the **heavy** package, but this package requires compilation of some C code which may not be able to do if you do not have a compiler installed.

Swedish Speed Limit Study — Revisited, Again

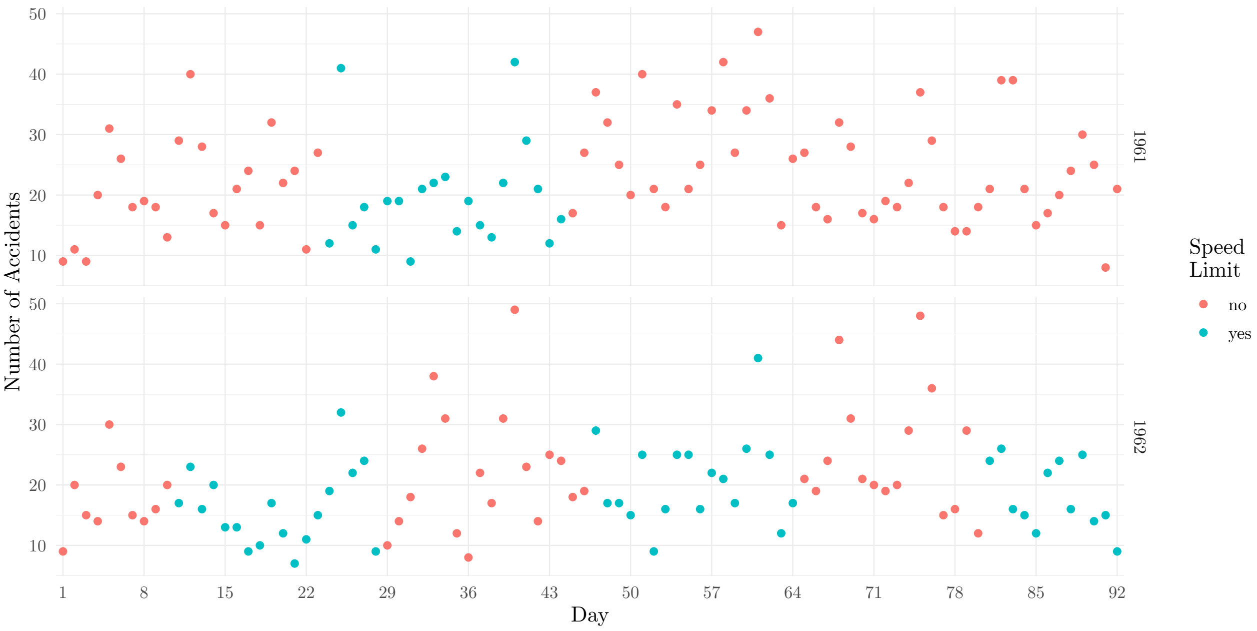
Once again consider the data from the third and fourth homework assignments (review the study description given in the third homework assignment).

```
library(SMPracticals)
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
```

Here is a plot of the number of accidents for each year and day.

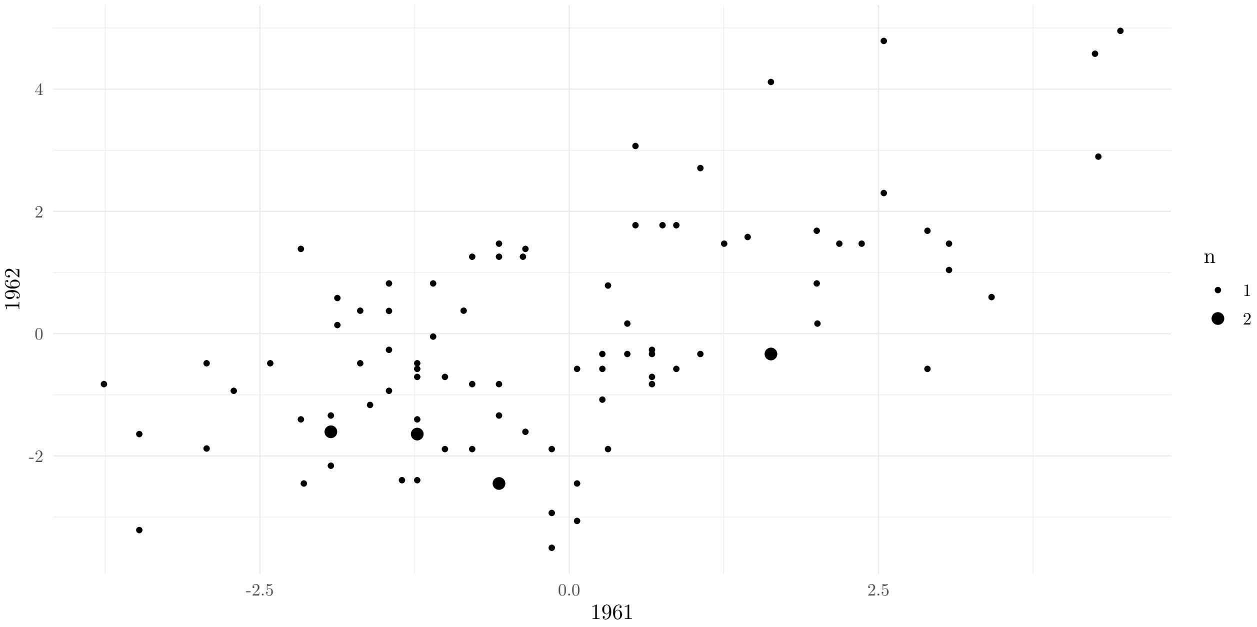
```
library(ggplot2)
p <- ggplot(limitstudy, aes(x = day, y = y, color = limit)) +
  theme_minimal() + geom_point() + facet_grid(year ~ .) +
  scale_x_discrete(breaks = seq(1, 92, by = 7)) +
  labs(x = "Day", y = "Number of Accidents", color = "Speed\nLimit")
plot(p)
```



As I discussed in the third homework assignment, there may be an effect of the factor `day`. This is because the days are matched in the sense that a given day in 1961 is the same day of the week and month as the day with the same level in 1962 (e.g., if a given day is a Sunday in 1961 it is also a Sunday in 1962). The accident rate may vary by day due to differences in, for example, traffic (e.g., work days versus weekends and holidays). Plotting the residuals from a Poisson regression model shows some evidence of an association between days that is not captured by the model.

```
m <- glm(y ~ limit + year, family = poisson, data = limitstudy)
limitstudy$residuals <- rstudent(m)

d <- limitstudy %>% dplyr::select(day, year, residuals) %>%
  pivot_wider(names_from = year, values_from = residuals)
p <- ggplot(d, aes(x = `1961`, y = `1962`)) + theme_minimal() +
  geom_count() + scale_size_continuous(breaks = 1:2, range = c(1,2.5))
plot(p)
```



Here you will extend your Poisson regression model to account for the lack of independence of observations made on the same day in 1961 and in 1962. For each model report the output of `summary` so that I can verify that you specified and estimated the model correctly.

1. Estimate a *marginal* Poisson regression model using the `geeglm` function with the number of accidents as your response variables, and limit and year as explanatory variable (with no interaction). Note that day will be your `id` variable and you should specify an exchangeable correlation structure.

2. Estimate a *mixed effects* Poisson regression model using the `glmer` function with the number of accidents as your response variables, and limit and year as explanatory variable (with no interaction). Specify your model with a random main effect for day.

3. For each of the two models you estimated above, use either the `contrast` function or functions from the **emmeans** package to estimate (a) the expected number of accidents with and without a posted speed limit each year and (b) the rate ratio describing the relationship between whether or not a speed limit was posted and the expected number of accidents (like you did in the previous two homework assignments). Compare your estimates and standard errors to what you got when you used a Poisson regression model in the third homework assignment (using `family = poisson`, not `family = quasipoisson`) in terms of the estimates and either standard errors or confidence intervals for the rate ratios. Briefly discuss similarities and differences between the three models.

Audit Study of Discrimination in Hiring

The data frame `resume` in the **qss** package are from an audit study of hiring discrimination based on perceived gender and race.[4] Resumes were sent in response to job advertisements, and the researchers recorded whether or not the job application resulted in a call-back. The applicants were fictitious with randomly-assigned names that were selected so that they would be likely identified as white or African-American, and as female or male.[5] Use the command

```
devtools::install_github("kosukeimai/qss-package", build_vignettes = TRUE)
```

to install the **qss** package. Note that you will need to have the **devtools** package installed to do this, but you should have it installed already since it is necessary to install **trtools**.

```
library(qss)
data(resume)
head(resume)
```

```
  firstname    sex  race call
1   Allison female white    0
2   Kristen female white    0
3   Lakisha female black    0
4   Latonya female black    0
5    Carrie female white    0
6       Jay   male white    0
```

For plotting and modeling it is useful to aggregate the data to show the number of call backs and the total number of resumes for each combination of name, sex, and race.

```
library(dplyr)
resumeagg <- resume %>% group_by(firstname, sex, race) %>%
  summarize(callbacks = sum(call), applications = n()) %>%
  mutate(sexrace = interaction(sex, race, sep = " and "))
head(resumeagg)
```

```
# A tibble: 6 x 6
# Groups:   firstname, sex [6]
  firstname sex    race  callbacks applications sexrace
  <chr>     <chr>  <chr>     <int>        <int> <fct>
1 Aisha     female black         4          180 female and black
2 Allison   female white        22          232 female and white
3 Anne      female white        20          242 female and white
4 Brad      male   white        10           63 male and white
5 Brendan   male   white         5           65 male and white
6 Brett     male   white         4           59 male and white
```

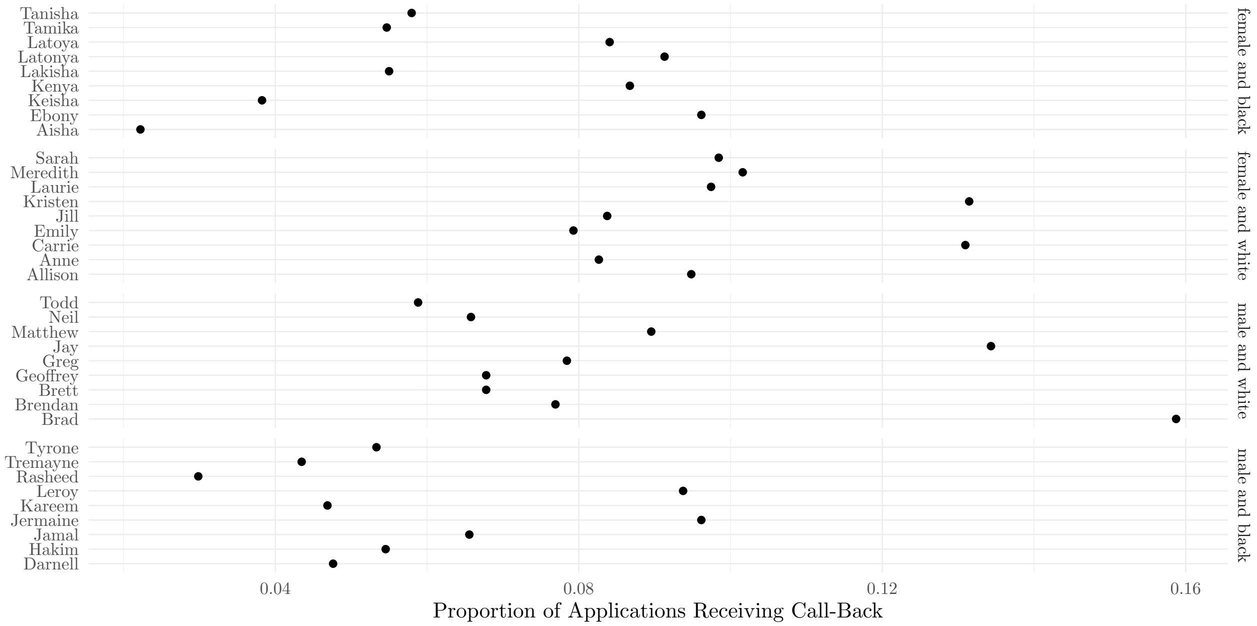
Note the use of the `interaction` function here to create a new variable `sexrace` for every combination of the variables `sex` and `race`. This is used in the plot below. The plot shows the proportion of job applications that received a call-back for each name.[6]

[4] Bertrand, M. & Mullainathan, S. (2004). Are Emily and Greg more employable than Lakisha and Jamal? A field experiment on labor market discrimination. *American Economic Review*, *94*, 991–1013.

[5] This study is actually a bit more complicated because the researchers also manipulated other characteristics of the resumes such as education, experience, awards, and other information that was included or omitted from the resume. Also the data include information about the jobs for which the "candidates" applied such as skill and experience requirements, and the type of industry. For the purpose of this exercise we will ignore these other variables.

[6] The `scales = "free_y"` argument lets the scale of the variable (here `firstname`) to be "free" for each facet. If it was omitted then every name would be listed for every value of `sexrace`, but that is not necessary here since only certain names go with each value of `sexrace` (i.e., the name factor is *nested* within the combinations of the sex and race factors). Try removing the argument and see what happens to the plot to better understand what it does.

```
library(ggplot2)
p <- ggplot(resumeagg, aes(x = firstname, y = callbacks/applications)) +
  theme_minimal() + coord_flip() + geom_point() +
  facet_grid(sexrace ~ ., scales = "free_y") +
  labs(y = "Proportion of Applications Receiving Call-Back", x = NULL)
plot(p)
```



The focus here would be on the relationship between the probability (or odds) of a call-back as a function of the likely perceived race and gender of the applicant. But there may be an effect of the *name* as well. The name may have an effect because (a) some names may be more or less likely to be perceived as from an applicant of a certain race or gender, and (b) names may differ in terms of other perceptions such as social class. Here you will consider some methods for accounting for the effect of name while making inferences about the effect of (likely perceived) gender and race. Be sure to report the output of `summary` for each model so that I can verify that you specified and estimated the model correctly.

1. Estimate a logistic regression model using the `glm` function that you can use to obtain odds ratios for the effect of gender and race on the odds that an application will get a call-back. Include an interaction between gender and race. Note that this model may not be appropriate since it does not account for an effect of name, but it will be used for comparison.

2. Estimate a *marginal* logistic regression model using the `geeglm` function that you can use to obtain odds ratios for the effect of gender and race on the odds that an application will get a call-back. Include an interaction between gender and race. Use first name as your `id` variable and specify an exchangeable correlation structure. The data will first need to be sorted by `firstname` for using with the `geeglm` function. You can do this using

   ```
   resumeagg <- resumeagg %>% arrange(firstname)
   ```

   before estimating the model.

3. Estimate a *mixed effects* logistic regression model using the `glmer` function that you can use to obtain odds ratios for the effect of gender and race on the odds that an application will get a call-back. Include an interaction between gender and race. Specify a random main effect for first name in your model. Report the output of `summary` for this model.

4. Use either the `contrast` function or functions from the **emmeans** package to estimate the odds ratios for the effects of gender and race for each of the three models you estimated. Note that since there is an interaction you should have two odds ratios for each explanatory variable (i.e., the odds ratios for the effect gender will be computed for each race, and the odds ratio for race will be computed for each gender). Focusing on the estimates and either the standard errors or confidence intervals for the odds ratios, briefly describe how these odds ratios compare across the three models.

A Sequential Model for Vaccine Efficacy

An article published on covid-datascience.com discussed some misunderstandings about data on the efficacy of the COVID-19 vaccine in Israel.[^efficacy] One issue was that the apparent efficacy of the vaccine is underestimated if one fails to account for age. The reason is that older people were much more likely to be vaccinated, but older people are also more likely to develop a severe infection requiring hospitalization. Here the variable age is an example of what is sometimes called a *suppressor variable* because it reduces the apparent effect of another explanatory variable if it is not also included as an explanatory variable. For this problem I have created a fictional data set that demonstrates this phenomenon.

```
vaccine <- data.frame(
  age = c("<50","<50","50+","50+"),
  vaccine = c("n","y","n","y"),
  uninfected = c(7932, 9635, 800, 8516),
  infected = c(1817, 514, 193, 456),
  hospitalized = c(96, 6, 19, 15)
)
vaccine
```

```
  age vaccine uninfected infected hospitalized
1 <50       n       7932     1817           96
2 <50       y       9635      514            6
3 50+       n        800      193           19
4 50+       y       8516      456           15
```

These data are in aggregated form, showing the number of subjects for each combination of age (less than 50 or 50 or more years in age) and vaccination (yes or no) classified as uninfected, infected with COVID-19, and hospitalized due to COVID-19. Note that people who are hospitalized are also infected, so the infected category is only for people who are infected but not hospitalized. For each model you estimate below, report the output of `summary` so that I can verify that you specified and estimated the model correctly.

1. Estimate *two* logistic regression models using the `glm` function: one model for the probability that someone will get COVID-19 (i.e., classified as `infected` or `hospitalized` versus `uninfected`) and another for the probability that someone who gets infected will be hospitalized (i.e., `hospitalized` versus `infecteced`). Use only whether or not someone was vaccinated as your explanatory variable. Note that since the data are in aggregate form you can specify the "response variable" in `glm` as `cbind(infected + hospitalized, uninfected)` for the first model, and `cbind(hospitalized, infected)` for the second model. Estimate the odds ratio for the effect of vaccine for each model, and write a sentence that summarizes how to interpret each odds ratio.

2. Estimate a *sequential* regression model using the `vglm` function from the **VGAM** package with the status as your three-category response variable (i.e., uninfected, infected, or hospitalized, in that order) and vaccine as your only explanatory variable. You should find that the parameter estimates correspond to what you obtained with the two logistic regression models in the previous problem.

3. Estimate the sequential regression model but now including age as a second explanatory variable (do not include an interaction between vaccine and age). Report and interpret in a sentence the odds ratios for the effect of vaccination on (a) infection, and (b) hospitalization of an infected person. [^efficacy]: Vaccine efficacy is an example of what we could a *marginal effect* in a binomial regression model. It is the (estimated) percent reduction in the probability of an infection from vaccination.