

Written lesson

Author

October 17, 2020

Instructions: Using R start the data analysis using simple frequencies (number infected in your assigned county, hospitalized, died, etc.) and summary statistics (e.g., mean age and standard deviation). Then use chi-square analysis for bivariate associations (e.g., gender by death). When you use logistic regression, first use the unadjusted odds ratios then find the adjusted odds ratios.

Loading data

First load the data in R

```
Covid <- read.csv("Florida_COVID19_Case_Line_Data.csv")
head(Covid)
```

```
##   County Age   Age_group Gender Jurisdiction Travel_related Origin EDvisit
## 1 Broward  64 55-64 years Female   FL resident           No   <NA>     NO
## 2   Dade   40 35-44 years   Male   FL resident   Unknown   <NA> UNKNOWN
## 3 Broward  57 55-64 years   Male   FL resident           No   <NA> UNKNOWN
## 4 Broward  50 45-54 years Female   FL resident           No   <NA>     YES
## 5 Broward  81 75-84 years Female   FL resident           No   <NA>     YES
## 6   Dade   37 35-44 years   Male   FL resident   Unknown   <NA> UNKNOWN
##   Hospitalized Died Case_ Contact Case1 EventDate
## 1           NO <NA>   Yes     Yes 2020/07/19 05:00:00+00 2020/07/17 00:00:00+00
## 2     UNKNOWN <NA>   Yes   <NA> 2020/07/19 05:00:00+00 2020/07/18 23:25:02+00
## 3     UNKNOWN <NA>   Yes     Yes 2020/07/19 05:00:00+00 2020/07/18 23:24:57+00
## 4           NO <NA>   Yes     Yes 2020/07/19 05:00:00+00 2020/07/15 00:00:00+00
## 5           YES <NA>   Yes     NO 2020/07/19 05:00:00+00 2020/07/18 00:00:00+00
## 6     UNKNOWN <NA>   Yes   <NA> 2020/07/19 05:00:00+00 2020/07/18 23:25:34+00
##           ChartDate ObjectID
## 1 2020/07/19 05:00:00+00      1
## 2 2020/07/19 05:00:00+00      2
## 3 2020/07/19 05:00:00+00      3
## 4 2020/07/19 05:00:00+00      4
## 5 2020/07/19 05:00:00+00      5
## 6 2020/07/19 05:00:00+00      6
```

Filter the data, Orange COunty

Filter the data by Orange County

```

Covid <- Covid %>%
  filter(County == "Orange") %>%
  select(County, Age, Age_group, Gender, Jurisdiction, Travel_related, Hospitalized, Died, Case_)
Covid$Age_group <- as.factor(Covid$Age_group)
Covid$Gender <- as.factor(Covid$Gender)
Covid$Jurisdiction <- as.factor(Covid$Jurisdiction)
Covid$Travel_related <- as.factor(Covid$Travel_related)
Covid$Hospitalized <- as.factor(Covid$Hospitalized)
Covid$Died <- as.factor(Covid$Died)
head(Covid)

```

```

##   County Age   Age_group Gender Jurisdiction Travel_related Hospitalized Died
## 1 Orange  54 45-54 years   Male   FL resident           Unknown   UNKNOWN <NA>
## 2 Orange  16 15-24 years Female   FL resident             No     UNKNOWN <NA>
## 3 Orange  47 45-54 years Female   FL resident             No       NO <NA>
## 4 Orange  37 35-44 years Female   FL resident           Unknown   UNKNOWN <NA>
## 5 Orange  10  5-14 years Female   FL resident           Unknown   UNKNOWN <NA>
## 6 Orange  16 15-24 years Female   FL resident           Unknown   UNKNOWN <NA>
##   Case_
## 1   Yes
## 2   Yes
## 3   Yes
## 4   Yes
## 5   Yes
## 6   Yes

```

```
str(Covid)
```

```

## 'data.frame':   43044 obs. of  9 variables:
##  $ County      : chr  "Orange" "Orange" "Orange" "Orange" ...
##  $ Age         : int  54 16 47 37 10 16 42 67 62 20 ...
##  $ Age_group   : Factor w/ 11 levels "0-4 years","15-24 years",...: 5 2 5 4 6 2 4 8 7 2 ...
##  $ Gender      : Factor w/ 3 levels "Female","Male",...: 2 1 1 1 1 1 2 1 2 1 ...
##  $ Jurisdiction : Factor w/ 3 levels "FL resident",...: 1 1 1 1 1 1 1 1 1 1 ...
##  $ Travel_related: Factor w/ 3 levels "No","Unknown",...: 2 1 1 2 2 2 1 2 1 1 ...
##  $ Hospitalized : Factor w/ 4 levels "", "NO", "UNKNOWN",...: 3 3 2 3 3 3 3 3 2 3 ...
##  $ Died        : Factor w/ 1 level "Yes": NA NA NA NA NA NA NA NA NA NA ...
##  $ Case_       : chr  "Yes" "Yes" "Yes" "Yes" ...

```

Removing NA's, UNKNOWN.

We will filter the data to remove the NA's, UNKNOWN that are not useful in our data set. First we will start with Hospitalized

```

Covid <- Covid %>% filter(Hospitalized != "" )
Covid <- Covid %>% filter(Hospitalized != "UNKNOWN")
Covid <- droplevels(Covid)
head(Covid)

```

```

##   County Age   Age_group Gender Jurisdiction Travel_related Hospitalized Died

```

```
## 1 Orange 47 45-54 years Female FL resident No NO <NA>
## 2 Orange 62 55-64 years Male FL resident No NO <NA>
## 3 Orange 16 15-24 years Male FL resident No NO <NA>
## 4 Orange 16 15-24 years Male FL resident No NO <NA>
## 5 Orange 19 15-24 years Male FL resident No NO <NA>
## 6 Orange 51 45-54 years Male FL resident No NO <NA>
## Case_
## 1 Yes
## 2 Yes
## 3 Yes
## 4 Yes
## 5 Yes
## 6 Yes
```

```
str(Covid)
```

```
## 'data.frame': 14732 obs. of 9 variables:
## $ County : chr "Orange" "Orange" "Orange" "Orange" ...
## $ Age : int 47 62 16 16 19 51 41 1 28 62 ...
## $ Age_group : Factor w/ 11 levels "0-4 years","15-24 years",...: 5 7 2 2 2 5 4 1 3 7 ...
## $ Gender : Factor w/ 3 levels "Female","Male",...: 1 2 2 2 2 2 1 2 1 1 ...
## $ Jurisdiction : Factor w/ 3 levels "FL resident",...: 1 1 1 1 1 1 1 1 1 1 ...
## $ Travel_related: Factor w/ 3 levels "No","Unknown",...: 1 1 1 1 1 1 1 1 1 2 ...
## $ Hospitalized : Factor w/ 2 levels "NO","YES": 1 1 1 1 1 1 1 1 1 2 ...
## $ Died : Factor w/ 1 level "Yes": NA NA NA NA NA NA NA NA NA 1 ...
## $ Case_ : chr "Yes" "Yes" "Yes" "Yes" ...
```

Now we will continue removing the UNKOWN from Travel_related, Gender, and Age_group

```
Covid <- Covid %>% filter(Age_group != "Unknown")
Covid <- Covid %>% filter(Travel_related != "Unknown")
Covid <- Covid %>% filter(Gender != "Unknown")
Covid <- droplevels(Covid)
str(Covid)
```

```
## 'data.frame': 12964 obs. of 9 variables:
## $ County : chr "Orange" "Orange" "Orange" "Orange" ...
## $ Age : int 47 62 16 16 19 51 41 1 28 73 ...
## $ Age_group : Factor w/ 10 levels "0-4 years","15-24 years",...: 5 7 2 2 2 5 4 1 3 8 ...
## $ Gender : Factor w/ 2 levels "Female","Male": 1 2 2 2 2 2 1 2 1 2 ...
## $ Jurisdiction : Factor w/ 3 levels "FL resident",...: 1 1 1 1 1 1 1 1 1 1 ...
## $ Travel_related: Factor w/ 2 levels "No","Yes": 1 1 1 1 1 1 1 1 1 1 ...
## $ Hospitalized : Factor w/ 2 levels "NO","YES": 1 1 1 1 1 1 1 1 1 1 ...
## $ Died : Factor w/ 1 level "Yes": NA NA NA NA NA NA NA NA NA ...
## $ Case_ : chr "Yes" "Yes" "Yes" "Yes" ...
```

Frequency tables and summary statistics

Now we can start with the frequency tables.

Some tables between categorical variables The table below show that we have some missing values for Hospitalized, and we can remove them but its up to you to remove those NA's in the variables, I do

recommend because we are just interested in those who answered something meaningful, we might lose a lot of information about variables and observations but we will have more accurate results. We can see that the majority of observations didn't go to a hospital, and the most observations fall between 15-24 years and 25-34 years.

```
table(Covid$Age_group, Covid$Hospitalized)
```

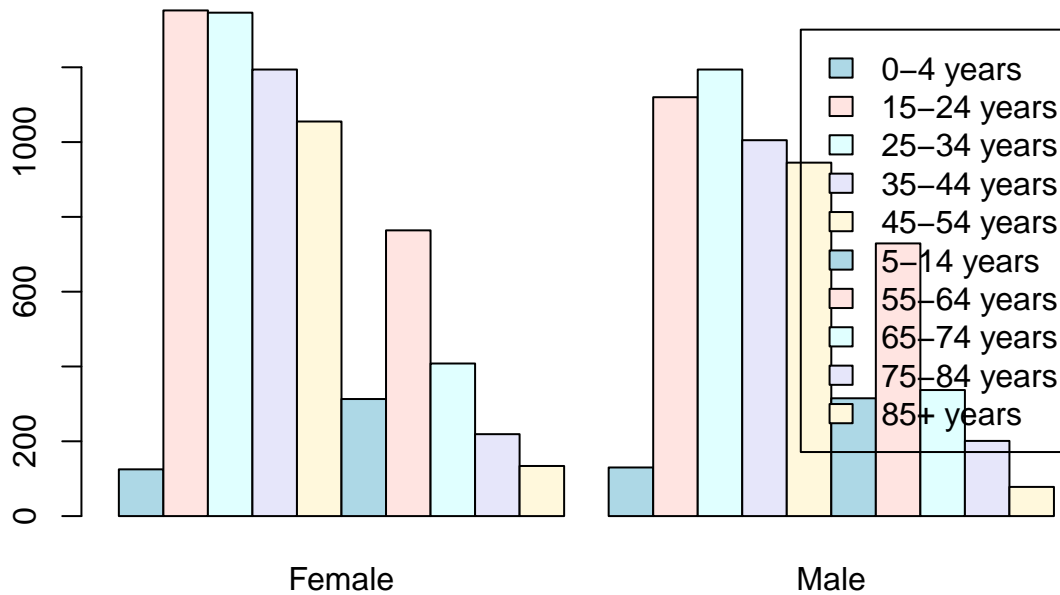
```
##
##           NO  YES
## 0-4 years  248   7
## 15-24 years 2436  36
## 25-34 years 2448  92
## 35-44 years 2047 152
## 45-54 years 1813 187
## 5-14 years   621   7
## 55-64 years 1214 279
## 65-74 years  514 231
## 75-84 years  213 207
## 85+ years    78 134
```

In this table we can see that the observations for female and male are similar for each age group category. We can also make a bar plot so you can see how it looks like the table.

```
table1 <- table(Covid$Age_group, Covid$Gender)
table1
```

```
##
##           Female Male
## 0-4 years    125  130
## 15-24 years  1352 1120
## 25-34 years  1346 1194
## 35-44 years  1194 1005
## 45-54 years  1055  945
## 5-14 years    313  315
## 55-64 years   764  729
## 65-74 years   408  337
## 75-84 years   219  201
## 85+ years    134   78
```

```
barplot(table1,
        col = c("lightblue", "mistyrose", "lightcyan",
                "lavender", "cornsilk"),
        legend = rownames(table1), beside=TRUE)
```



For this part the majority of observations are in the FL resident group, no matter the age group they are.

```
table(Covid$Age_group, Covid$Jurisdiction)
```

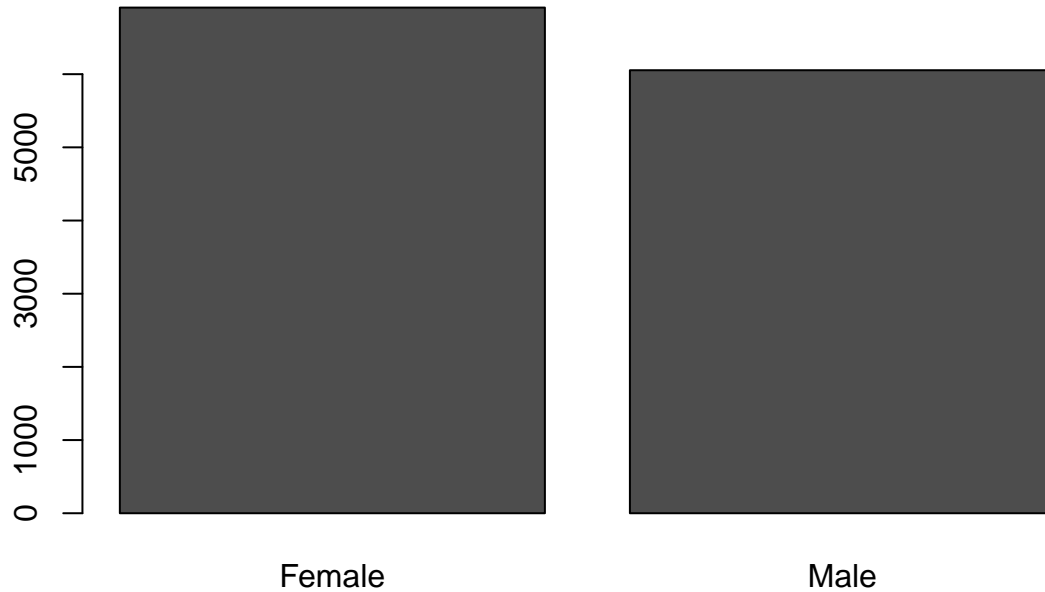
```
##
##           FL resident Non-FL resident Not diagnosed/isolated in FL
## 0-4 years           254             1             0
## 15-24 years        2455            17             0
## 25-34 years        2529            11             0
## 35-44 years        2189            10             0
## 45-54 years        1988            12             0
## 5-14 years          628             0             0
## 55-64 years        1484             9             0
## 65-74 years         730            14             1
## 75-84 years         409            11             0
## 85+ years          211             1             0
```

All the cases in the data are positive and the majority of positive covid-19 cases are females but the difference is not huge, its a small difference.

```
table(Covid$Case_, Covid$Gender)
```

```
##
##      Female Male
## Yes   6910 6054
```

```
barplot(table(Covid$Case_, Covid$Gender))
```



The majority of positive cases of covid-19 are between 15-24 years, 25-34 years and 35-44 years.

```
table(Covid$Age_group, Covid$Case_)
```

```
##
##           Yes
## 0-4 years  255
## 15-24 years 2472
## 25-34 years 2540
## 35-44 years 2199
## 45-54 years 2000
## 5-14 years   628
## 55-64 years 1493
## 65-74 years  745
## 75-84 years  420
## 85+ years   212
```

Summary statistics for Age The median age is 37 which means that 50% of the observations have an age below 36 and 50% of the observations have an age above 36.

```
summary(Covid$Age)
```

```
##   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   0.00  24.00   37.00   39.26  52.00  106.00
```

Chi square test

Chi square for bivariate analysis Now by doing the chi square test we can see if 2 categorical variables are related or not, by using chi square for gender and died, we can see that p value is smaller than alpha 0.05 so we can conclude that the gender and died variables are dependent, that means one of the 2 gender is more likely to die.

```
table(Covid$Gender, Covid$Died)
```

```
##
##           Yes
## Female 136
## Male   188
```

```
chisq.test(table(Covid$Gender, Covid$Died))
```

```
##
## Chi-squared test for given probabilities
##
## data:  table(Covid$Gender, Covid$Died)
## X-squared = 8.3457, df = 1, p-value = 0.003866
```

By doing the chi square test between age group and hospitalization, the p value is smaller than alpha 0.05 so we can say that age and hospitalization are related, in other words depending in your age it is more likely to be hospitalized.

```
table(Covid$Age_group, Covid$Hospitalized)
```

```
##
##           NO  YES
## 0-4 years   248   7
## 15-24 years 2436  36
## 25-34 years 2448  92
## 35-44 years 2047 152
## 45-54 years 1813 187
## 5-14 years   621   7
## 55-64 years 1214 279
## 65-74 years  514 231
## 75-84 years  213 207
## 85+ years    78 134
```

```
chisq.test(table(Covid$Age_group, Covid$Hospitalized))
```

```
##
## Pearson's Chi-squared test
##
## data:  table(Covid$Age_group, Covid$Hospitalized)
## X-squared = 2231.7, df = 9, p-value < 2.2e-16
```

Here we did a chi square test between age and gender, where we found a p value lower than alpha 0.05, so age and gender are related.

```
table(Covid$Age_group, Covid$Gender)
```

```
##
##           Female Male
## 0-4 years      125  130
## 15-24 years   1352 1120
## 25-34 years   1346 1194
## 35-44 years   1194 1005
## 45-54 years   1055  945
## 5-14 years     313  315
## 55-64 years    764  729
## 65-74 years    408  337
## 75-84 years    219  201
## 85+ years     134   78
```

```
chisq.test(table(Covid$Age_group, Covid$Gender))
```

```
##
## Pearson's Chi-squared test
##
## data:  table(Covid$Age_group, Covid$Gender)
## X-squared = 19.985, df = 9, p-value = 0.018
```

Here the p value is lower than 0.05, so we can say that Travel related depends on Hospitalized.

```
table(Covid$Travel_related, Covid$Hospitalized)
```

```
##
##           NO  YES
## No  11033  1230
## Yes   599   102
```

```
chisq.test(table(Covid$Travel_related, Covid$Hospitalized))
```

```
##
## Pearson's Chi-squared test with Yates' continuity correction
##
## data:  table(Covid$Travel_related, Covid$Hospitalized)
## X-squared = 14.212, df = 1, p-value = 0.0001633
```

In this chi square the p value is smaller than alpha 0.05 so we can conclude that Jurisdiction and age are related.

```
table(Covid$Age_group, Covid$Jurisdiction)
```

```
##
##           FL resident Non-FL resident Not diagnosed/isolated in FL
## 0-4 years           254             1             0
## 15-24 years        2455            17             0
## 25-34 years        2529            11             0
```



```
## 35-44 years      2189      10      0
## 45-54 years      1988      12      0
## 5-14 years        628       0      0
## 55-64 years      1484       9      0
## 65-74 years       730      14      1
## 75-84 years       409      11      0
## 85+ years        211       1      0
```

```
chisq.test(table(Covid$Age_group, Covid$Jurisdiction))
```

```
## Warning in chisq.test(table(Covid$Age_group, Covid$Jurisdiction)): Chi-squared
## approximation may be incorrect
```

```
##
## Pearson's Chi-squared test
##
## data:  table(Covid$Age_group, Covid$Jurisdiction)
## X-squared = 65.836, df = 18, p-value = 2.258e-07
```

Logistic Regression

Making the logistic regression... Lets say you want to predict the probability that you will be hospitalized based on gender, age , Jurisdiction and Travel related

```
logic <- glm(formula=Hospitalized ~ Gender+Age+Jurisdiction+Travel_related, data=Covid, family = binomial)
summary(logic)
```

```
##
## Call:
## glm(formula = Hospitalized ~ Gender + Age + Jurisdiction + Travel_related,
##      family = binomial, data = Covid)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.8802  -0.4488  -0.2747  -0.1844   3.3170
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -5.497316   0.111697 -49.216 < 2e-16
## GenderMale    0.319895   0.064058   4.994 5.92e-07
## Age           0.065048   0.001784  36.460 < 2e-16
## JurisdictionNon-FL resident  1.656781   0.280018   5.917 3.28e-09
## JurisdictionNot diagnosed/isolated in FL 12.482674 196.967726   0.063  0.949
## Travel_relatedYes  0.157407   0.133104   1.183  0.237
##
## (Intercept)          ***
## GenderMale           ***
## Age                  ***
## JurisdictionNon-FL resident ***
## JurisdictionNot diagnosed/isolated in FL
```

```
## Travel_relatedYes
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 8584.1 on 12963 degrees of freedom
## Residual deviance: 6805.6 on 12958 degrees of freedom
## AIC: 6817.6
##
## Number of Fisher Scoring iterations: 10
```

By looking the p values ($Pr > z$) you can see that all the variables are significant, but JurisdictionNont diagnosed/isolated in FL, and Travel_relatedYes have p values greater than 0.05, so we will say that these 2 variables are not significant in the model.

The model to predict the probability of being hospitalized is:

$$P(\text{Hospitalized}) = \frac{e^{-5.497+0.319(\text{Male})+0.065(\text{Age})+1.657(\text{JurisdictionNon-Flresident})+12.483(\text{JurisdictionNotdiagnosed/isolatedinFL})}}{1 + e^{-5.497+0.319(\text{Male})+0.065(\text{Age})+1.657(\text{JurisdictionNon-Flresident})+12.483(\text{JurisdictionNotdiagnosed/isolatedinFL})}}$$

We can check how our model can predict accuracy the probability of being hospitalized

```
hosp_predict <- predict(logic, newdata=Covid, type="response")
length(hosp_predict)
```

```
## [1] 12964
```

```
head(hosp_predict)
```

```
##      1      2      3      4      5      6
## 0.08016974 0.24150939 0.01572511 0.01572511 0.01904912 0.13470841
```

We will recode the prediction variable, if the probability is greater than 0.5 then it will be hospitalized, if not then it will not be hospitalized

```
hosp_predict <- ifelse(hosp_predict < 0.5, "NO", "YES")
head(hosp_predict)
```

```
##      1      2      3      4      5      6
## "NO" "NO" "NO" "NO" "NO" "NO"
```

Now we will make the confusion matrix that is the predicted hospitalized and the observed hospitalized

```
confusionmatrix <- table(Covid$Hospitalized, hosp_predict)
confusionmatrix
```

```
##      hosp_predict
##      NO  YES
## NO 11504 128
## YES 1120 212
```

The misclassification are those where you predict No but the Observed is Yes, those are 1120, and those where you predict Yes but the Observed is No, 128 divided by the total.

```
misclass <- (1120+128)/length(hosp_predict)
misclass
```

```
## [1] 0.09626658
```

Adjusted Odds Ratio Before we calculated the model with unadjusted odds ratio, now we can make the logistic regression model using adjusted Odds Ratio Unadjusted Odds Ratio

```
logic$coefficients
```

```
##                (Intercept)
##                -5.49731596
##                GenderMale
##                0.31989547
##                Age
##                0.06504836
##                JurisdictionNon-FL resident
##                1.65678136
## JurisdictionNot diagnosed/isolated in FL
##                12.48267371
##                Travel_relatedYes
##                0.15740718
```

Adjusted Odds Ratio

```
or <- exp(logic$coefficients)
round(or,2)
```

```
##                (Intercept)
##                0.00
##                GenderMale
##                1.38
##                Age
##                1.07
##                JurisdictionNon-FL resident
##                5.24
## JurisdictionNot diagnosed/isolated in FL
##                263728.04
##                Travel_relatedYes
##                1.17
```