Birth Weight

Team C

11/03/2021

Needed Packages

```
if(!require(FSA)){install.packages("FSA")}
if(!require(ggplot2)){install.packages("ggplot2")}
if (!require("mosaic")) install.packages("mosaic", dep=FALSE)
if (!require("nortest")) install.packages("nortest", dep=TRUE)
if (!require("epitools")) install.packages("epitools", dep=TRUE)
if (!require("prettyR")) install.packages("prettyR", dep=TRUE)
if (!require("rms")) install.packages("rms", dep=TRUE)
library(tidyverse)
# add other as needed
```

Problem – Infant Birth Weight Data

Read data into R

```
# this data came from SASHELP.BWEIGHT
bw <- read.csv('bwgt.csv')
bw <- data.frame(bw)
#summary(bw)
bw = transform(bw, AgeGroup.f = as.factor(AgeGroup))
bw = transform(bw, Race.f = as.factor(Race))
bw = transform(bw, Drinking.f = as.factor(Drinking))
bw = transform(bw, Death.f = as.factor(Death))
bw = transform(bw, Smoking.f = as.factor(Smoking))
bw = transform(bw, SomeCollege.f = as.factor(SomeCollege))
bw = transform(bw, LowBirthWgt.f = as.factor(bw$LowBirthWgt))
```

Code 1 - Data Summary

```
summary(bw)
```

```
##   LowBirthWgt          Married             AgeGroup        Race          
##   Length:3089        Length:3089        Min.   :1.000   Length:3089       
##   Class :character   Class :character   1st Qu.:2.000   Class :character  
##   Mode  :character   Mode  :character   Median :2.000   Mode  :character  
##                                         Mean   :2.021                     
##                                         3rd Qu.:2.000                     
##                                         Max.   :3.000                     
##     Drinking            Death              Smoking           SomeCollege       
##   Length:3089        Length:3089        Length:3089        Length:3089       
##   Class :character   Class :character   Class :character   Class :character  
##   Mode  :character   Mode  :character   Mode  :character   Mode  :character  
##                                                                              
##                                                                              
##                                                                              
##   AgeGroup.f      Race.f     Drinking.f Death.f    Smoking.f  SomeCollege.f
##   1: 357     Asian   : 145      : 197   No :2483      : 197       : 245    
##   2:2310     Black   : 518   No :2493   Yes: 606   No :2191   No :1526     
##   3: 422     Hispanic: 624   Yes: 399              Yes: 701   Yes:1318     
##              Native  :  32                                                 
##              White   :1770                                                 
##                                                                            
##   LowBirthWgt.f
##   No :2476    
##   Yes: 613    
##               
##               
##               
##               
```

```
summary(bw$LowBirthWgt)
```

```
##    Length     Class      Mode 
##      3089 character character
```

```
summary(bw$Smoking)
```

```
##    Length     Class      Mode 
##      3089 character character
```

```
mytab <- tally(~ Race.f | AgeGroup.f, data=bw)
addmargins(mytab)
```

```
##           AgeGroup.f
## Race.f        1    2    3  Sum
##   Asian       8  101   36  145
##   Black      91  375   52  518
##   Hispanic   83  475   66  624
##   Native      6   22    4   32
##   White     169 1337  264 1770
##   Sum       357 2310  422 3089
```

```r
mytab1 <- tally(~ Married | AgeGroup.f, data=bw)
addmargins(mytab1)
```

```
##        AgeGroup.f
## Married    1    2    3  Sum
##     No    61 1533  351 1945
##     Yes  296  777   71 1144
##     Sum  357 2310  422 3089
```

```r
mytab2 <- tally(~ LowBirthWgt.f | Race.f, data=bw)
addmargins(mytab2)
```

```
##              Race.f
## LowBirthWgt.f Asian Black Hispanic Native White  Sum
##           No    117   342      523     26  1468 2476
##           Yes    28   176      101      6   302  613
##           Sum   145   518      624     32  1770 3089
```

Code 2

```r
bw <- read.csv('bwgt.csv')
# Create a new smaller data set of size 2500
set.seed(1568)
ssize <- sample(1:nrow(bw),round(nrow(bw) * .8092))
new_bwgt <- bw %>% slice(ssize)
new_bwgt <-new_bwgt  %>% na_if("") %>%  na.omit

# Make the following columns
new_bwgt <- new_bwgt %>% mutate( AgeGroup.f = factor(AgeGroup), Race.f = factor(Race),
Drinking.f = factor(Drinking), Death.f = factor(Death),Smoking.f = factor(Smoking),
SomeCollege.f = factor(SomeCollege), LowBirthWgt.f = factor(LowBirthWgt))
```

Test for Association between Low Birth Weight and smoking

```r
#Risk ratio
RR1<-riskratio(x=new_bwgt$Smoking.f, y=new_bwgt$LowBirthWgt.f)
RR1$measure
```

```
##          risk ratio with 95% C.I.
## Predictor estimate     lower    upper
##       No   1.00000        NA       NA
##       Yes  1.13645 0.9433483 1.369078
```

```r
RR1$p.value
```

```
##          two-sided
## Predictor midp.exact fisher.exact chi.square
##       No          NA           NA         NA
##       Yes  0.1838204    0.1963432  0.1814622
```

Since 95% C.I. does contain the value of 1, which is the value of no smoking. So, there is insufficient evidence to conclude that the two groups are statistically significantly different. Also, the p.values can confirm our found.

```r
#chisq test
chisq.test(new_bwgt$Smoking.f,new_bwgt$LowBirthWgt.f)
```

```
##
##  Pearson's Chi-squared test with Yates' continuity correction
##
## data:  new_bwgt$Smoking.f and new_bwgt$LowBirthWgt.f
## X-squared = 1.625, df = 1, p-value = 0.2024
```

The chi-squared result shows that there is not enough evidence to say the low birth weight is causing by the smoking.

```r
#oddsratio
oddsratio(new_bwgt$Smoking.f, new_bwgt$LowBirthWgt.f,rev=c("b"),method="wald")$measure
```

```
##          odds ratio with 95% C.I.
## Predictor estimate     lower    upper
##       Yes 1.000000        NA       NA
##       No  1.174036 0.9276977 1.485787
```

Even though the odd ratio of the non-smoking group is greater than one, the value is just 1.17. Also, the 95% C.I. does include 1, so our conclusion will be the same as above. We cannot say when women is smoking, it is more likely to deliver a low birth weight baby.

```
# Fisher's Exact Test
tab22<- table(x=new_bwgt$Smoking.f , y=new_bwgt$LowBirthWgt.f)
tab22<- as.matrix(tab22)

# Two-sided alternative hypothesis
fisher.test(tab22)
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  tab22
## p-value = 0.1963
## alternative hypothesis: true odds ratio is not equal to 1
## 95 percent confidence interval:
##  0.9190588 1.4931839
## sample estimates:
## odds ratio
##   1.173928
```

```
# One-sided less than alternative hypothesis
fisher.test(tab22,alternative="less")
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  tab22
## p-value = 0.918
## alternative hypothesis: true odds ratio is less than 1
## 95 percent confidence interval:
##  0.000000 1.438835
## sample estimates:
## odds ratio
##   1.173928
```

```
# One-sided greater than alternative hypothesis
fisher.test(tab22,alternative="greater")
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  tab22
## p-value = 0.1019
## alternative hypothesis: true odds ratio is greater than 1
## 95 percent confidence interval:
##  0.955358      Inf
## sample estimates:
## odds ratio
##   1.173928
```

All these three will lead to the same conclusion as we mentioned above, that is, there is no significant association at $\alpha = 0.5$ between smoking and low birth weight.

```r
# MH test:
mantelhaen.test(new_bwgt$Smoking.f, new_bwgt$LowBirthWgt.f, new_bwgt$Drinking.f,correct=T)
```

```
##
##  Mantel-Haenszel chi-squared test with continuity correction
##
## data:  new_bwgt$Smoking.f and new_bwgt$LowBirthWgt.f and new_bwgt$Drinking.f
## Mantel-Haenszel X-squared = 5.9382, df = 1, p-value = 0.01482
## alternative hypothesis: true common odds ratio is not equal to 1
## 95 percent confidence interval:
##  1.089772 2.005459
## sample estimates:
## common odds ratio
##          1.478341
```

Test for Association between Low Birth Weight and drinking

```r
#Risk ratio
RR1<-riskratio(x=new_bwgt$Drinking.f, y=new_bwgt$LowBirthWgt.f)
RR1$measure
```

```
##          risk ratio with 95% C.I.
## Predictor  estimate     lower   upper
##       No  1.0000000        NA      NA
##       Yes 0.9057919 0.7032788 1.16662
```

```r
RR1$p.value
```

```
##          two-sided
## Predictor midp.exact fisher.exact chi.square
##       No          NA           NA         NA
##       Yes  0.4434666    0.4896086  0.4393742
```

```r
#chisq test
chisq.test(new_bwgt$Drinking.f,new_bwgt$LowBirthWgt.f)
```

```
##
##  Pearson's Chi-squared test with Yates' continuity correction
##
## data:  new_bwgt$Drinking.f and new_bwgt$LowBirthWgt.f
## X-squared = 0.48508, df = 1, p-value = 0.4861
```

```r
#oddsratio
oddsratio(new_bwgt$Drinking.f, new_bwgt$LowBirthWgt.f,rev=c("b"),method="wald")$measure
```

```
##          odds ratio with 95% C.I.
## Predictor estimate     lower    upper
```

```
##       Yes 1.000000        NA       NA
##       No  0.885103 0.6494903 1.206188
```

```r
# Fisher's Exact Test
tab23<- table(x=new_bwgt$Drinking.f, y=new_bwgt$LowBirthWgt.f)
tab22<- as.matrix(tab23)

# Two-sided alternative hypothesis
fisher.test(tab22)
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  tab22
## p-value = 0.4896
## alternative hypothesis: true odds ratio is not equal to 1
## 95 percent confidence interval:
##  0.6372546 1.2133958
## sample estimates:
## odds ratio
##   0.885151
```

```r
# One-sided less than alternative hypothesis
fisher.test(tab22,alternative="less")
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  tab22
## p-value = 0.2449
## alternative hypothesis: true odds ratio is less than 1
## 95 percent confidence interval:
##  0.000000 1.157093
## sample estimates:
## odds ratio
##   0.885151
```

```r
# One-sided greater than alternative hypothesis
fisher.test(tab22,alternative="greater")
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  tab22
## p-value = 0.8015
## alternative hypothesis: true odds ratio is greater than 1
## 95 percent confidence interval:
##  0.6714868       Inf
## sample estimates:
## odds ratio
##   0.885151
```

```r
# MH test:
mantelhaen.test(new_bwgt$Drinking.f, new_bwgt$LowBirthWgt.f, new_bwgt$Smoking.f,correct=T)
```

```
##
##  Mantel-Haenszel chi-squared test with continuity correction
```

```
##
## data:  new_bwgt$Drinking.f and new_bwgt$LowBirthWgt.f and new_bwgt$Smoking.f
## Mantel-Haenszel X-squared = 4.4378, df = 1, p-value = 0.03515
## alternative hypothesis: true common odds ratio is not equal to 1
## 95 percent confidence interval:
##  0.4277696 0.9516248
## sample estimates:
## common odds ratio
##         0.6380252
```

All 5 tests' outputs give the same result, at $\alpha = 0.5$,there is no strong evidence to conclude the relation between having a low birth weight baby and drinking is significant.

Code 3

Test for Association between Low Birth Weight and Smoking controlling for Death

```
new_bwgt1<-table(new_bwgt)
tab1<-margin.table(new_bwgt1, c(15,13,12))
d_yes<-tab1[, , Death.f = "No"]
d_no<-tab1[, , Death.f = "Yes"]
```

```
#Risk ratio for Death= Yes
RR1<-riskratio(d_yes)
RR1$measure
```

```
##              risk ratio with 95% C.I.
## LowBirthWgt.f estimate     lower    upper
##           No  1.000000        NA       NA
##           Yes 1.162103 0.8812414 1.532478
```

```
RR1$p.value
```

```
##              two-sided
## LowBirthWgt.f midp.exact fisher.exact chi.square
##           No          NA           NA         NA
##           Yes  0.2991542    0.3191694  0.2964308
```

```
#Risk ratio for Death= No
RR1<-riskratio(d_no)
RR1$measure
```

```
##              risk ratio with 95% C.I.
## LowBirthWgt.f  estimate     lower   upper
##           No  1.0000000        NA      NA
##           Yes 0.8456945 0.6186096 1.15614
```

```
RR1$p.value
```

```
##              two-sided
## LowBirthWgt.f midp.exact fisher.exact chi.square
##           No          NA           NA         NA
##           Yes  0.3015446    0.3031373  0.2982256
```

```
#chisq test for Death= Yes
chisq.test(d_yes)
```

```
##
##  Pearson's Chi-squared test with Yates' continuity correction
##
## data:  d_yes
## X-squared = 0.89219, df = 1, p-value = 0.3449
```

```
#chisq test for Death= No
chisq.test(d_no)
```

```
##
##  Pearson's Chi-squared test with Yates' continuity correction
##
## data:  d_no
## X-squared = 0.8562, df = 1, p-value = 0.3548
```

```r
#oddsratio for Death= Yes
oddsratio(d_yes,rev=c("b"),method="wald")$measure
```

```
##              odds ratio with 95% C.I.
## LowBirthWgt.f estimate     lower    upper
##           Yes 1.000000        NA       NA
##           No  1.220403 0.8392721 1.774614
```

```r
#oddsratio for Death= No
oddsratio(d_no,rev=c("b"),method="wald")$measure
```

```
##              odds ratio with 95% C.I.
## LowBirthWgt.f  estimate     lower    upper
##           Yes 1.0000000        NA       NA
##           No  0.7904843 0.5073498 1.231626
```

```r
# Fisher's Exact Test for Death=Yes
# Two-sided alternative hypothesis
fisher.test(d_yes)
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  d_yes
## p-value = 0.3192
## alternative hypothesis: true odds ratio is not equal to 1
## 95 percent confidence interval:
##  0.8174221 1.7929076
## sample estimates:
## odds ratio
##   1.220293
```

```r
# One-sided less than alternative hypothesis
fisher.test(d_yes,alternative="less")
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  d_yes
## p-value = 0.8728
## alternative hypothesis: true odds ratio is less than 1
## 95 percent confidence interval:
##  0.00000 1.69251
## sample estimates:
## odds ratio
##   1.220293
```

```r
# One-sided greater than alternative hypothesis
fisher.test(d_yes,alternative="greater")
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  d_yes
## p-value = 0.172
## alternative hypothesis: true odds ratio is greater than 1
## 95 percent confidence interval:
```

```
##  0.8708259       Inf
## sample estimates:
## odds ratio
##   1.220293
```

```r
# Fisher's Exact Test for Death=No
# Two-sided alternative hypothesis
fisher.test(d_no)
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  d_no
## p-value = 0.3031
## alternative hypothesis: true odds ratio is not equal to 1
## 95 percent confidence interval:
##  0.4968447 1.2674330
## sample estimates:
## odds ratio
##  0.7909397
```

```r
# One-sided less than alternative hypothesis
fisher.test(d_no,alternative="less")
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  d_no
## p-value = 0.1772
## alternative hypothesis: true odds ratio is less than 1
## 95 percent confidence interval:
##  0.000000 1.178722
## sample estimates:
## odds ratio
##  0.7909397
```

```r
# One-sided greater than alternative hypothesis
fisher.test(d_no,alternative="greater")
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  d_no
## p-value = 0.8756
## alternative hypothesis: true odds ratio is greater than 1
## 95 percent confidence interval:
##  0.532999      Inf
## sample estimates:
## odds ratio
##  0.7909397
```

```r
# MH test:
mantelhaen.test(tab1,correct=T)
```

```
##
##  Mantel-Haenszel chi-squared test with continuity correction
##
```

```
## data:  tab1
## Mantel-Haenszel X-squared = 0.0010773, df = 1, p-value = 0.9738
## alternative hypothesis: true common odds ratio is not equal to 1
## 95 percent confidence interval:
##  0.7604251 1.3570002
## sample estimates:
## common odds ratio
##          1.015823
```

Test for Association between Low Birth Weight and Drinking controlling for Death

```r
tab2<-margin.table(new_bwgt1, c(15,11,12))
d_yes1<-tab2[, , Death.f = "No"]
d_no1<-tab2[, , Death.f = "Yes"]
```

```r
#Risk ratio for Death= Yes
RR1<-riskratio(d_yes1)
RR1$measure
```

```
##              risk ratio with 95% C.I.
## LowBirthWgt.f estimate     lower    upper
##           No  1.000000        NA       NA
##           Yes 1.121268 0.7618986 1.650145
```

```r
RR1$p.value
```

```
##              two-sided
## LowBirthWgt.f midp.exact fisher.exact chi.square
##           No          NA           NA         NA
##           Yes  0.5566217    0.5458626  0.5644661
```

```r
#Risk ratio for Death= No
RR1<-riskratio(d_no1)
RR1$measure
```

```
##              risk ratio with 95% C.I.
## LowBirthWgt.f  estimate     lower    upper
##           No  1.0000000        NA       NA
##           Yes 0.7852063 0.4619528 1.334658
```

```r
RR1$p.value
```

```
##              two-sided
## LowBirthWgt.f midp.exact fisher.exact chi.square
##           No          NA           NA         NA
##           Yes   0.377272    0.4237677  0.3729685
```

```r
#chisq test for Death= Yes
chisq.test(d_yes1)
```

```
##
##  Pearson's Chi-squared test with Yates' continuity correction
##
## data:  d_yes1
```

```
## X-squared = 0.20717, df = 1, p-value = 0.649
```

```r
#chisq test for Death= No
chisq.test(d_no1)
```

```
##
##  Pearson's Chi-squared test with Yates' continuity correction
##
## data:  d_no1
## X-squared = 0.53419, df = 1, p-value = 0.4648
```

```r
#oddsratio for Death= Yes
oddsratio(d_yes1,rev=c("b"),method="wald")$measure
```

```
##              odds ratio with 95% C.I.
## LowBirthWgt.f estimate     lower    upper
##           Yes 1.000000        NA       NA
##           No  1.143486 0.7244916 1.804796
```

```r
#oddsratio for Death= No
oddsratio(d_no1,rev=c("b"),method="wald")$measure
```

```
##              odds ratio with 95% C.I.
## LowBirthWgt.f  estimate     lower    upper
##           Yes 1.0000000        NA       NA
##           No  0.7591707 0.4135274 1.393717
```

```r
# Fisher's Exact Test for Death=Yes
# Two-sided alternative hypothesis
fisher.test(d_yes1)
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  d_yes1
## p-value = 0.5459
## alternative hypothesis: true odds ratio is not equal to 1
## 95 percent confidence interval:
##  0.6922058 1.8217709
## sample estimates:
## odds ratio
##   1.143438
```

```r
# One-sided less than alternative hypothesis
fisher.test(d_yes1,alternative="less")
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  d_yes1
## p-value = 0.7611
## alternative hypothesis: true odds ratio is less than 1
## 95 percent confidence interval:
##  0.000000 1.702521
## sample estimates:
## odds ratio
##   1.143438
```

```r
# One-sided greater than alternative hypothesis
fisher.test(d_yes1,alternative="greater")
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  d_yes1
## p-value = 0.3177
## alternative hypothesis: true odds ratio is greater than 1
## 95 percent confidence interval:
##  0.7501199       Inf
## sample estimates:
## odds ratio
##   1.143438
```

```r
# Fisher's Exact Test for Death=No
# Two-sided alternative hypothesis
fisher.test(d_no1)
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  d_no1
## p-value = 0.4238
## alternative hypothesis: true odds ratio is not equal to 1
## 95 percent confidence interval:
##  0.398984 1.479963
## sample estimates:
## odds ratio
##   0.759641
```

```r
# One-sided less than alternative hypothesis
fisher.test(d_no1,alternative="less")
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  d_no1
## p-value = 0.2304
## alternative hypothesis: true odds ratio is less than 1
## 95 percent confidence interval:
##  0.00000 1.33571
## sample estimates:
## odds ratio
##   0.759641
```

```r
# One-sided greater than alternative hypothesis
fisher.test(d_no1,alternative="greater")
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  d_no1
## p-value = 0.8531
## alternative hypothesis: true odds ratio is greater than 1
## 95 percent confidence interval:
```

```
##  0.4386242       Inf
## sample estimates:
## odds ratio
##   0.759641
```

```r
# MH test:
mantelhaen.test(tab2,correct=T)
```

```
##
##  Mantel-Haenszel chi-squared test without continuity correction
##
## data:  tab2
## Mantel-Haenszel X-squared = 0.0060663, df = 1, p-value = 0.9379
## alternative hypothesis: true common odds ratio is not equal to 1
## 95 percent confidence interval:
##  0.6800377 1.4286344
## sample estimates:
## common odds ratio
##         0.9856598
```

According to the tests results shows above, we conclude the association between low birth weight and drinking controlling for death is not statistical significant.

Code 4

Test for Association between Low Birth Weight and Death

```r
#Risk ratio
RR1<-riskratio(x=new_bwgt$Death.f, y=new_bwgt$LowBirthWgt.f)
RR1$measure
```

```
##          risk ratio with 95% C.I.
## Predictor estimate    lower    upper
##       No  1.000000       NA       NA
##       Yes 8.201933 6.962315 9.662259
```

```r
RR1$p.value
```

```
##          two-sided
## Predictor midp.exact  fisher.exact    chi.square
##       No          NA            NA            NA
##       Yes          0 2.342608e-146 4.397064e-176
```

According to the risk ratio, since the 95% confidence interval does not contain 1, the association between the low birth weight and death is statistical significant.

```r
#chisq test
chisq.test(new_bwgt$Death.f,new_bwgt$LowBirthWgt.f)
```

```
##
##  Pearson's Chi-squared test with Yates' continuity correction
##
## data:  new_bwgt$Death.f and new_bwgt$LowBirthWgt.f
## X-squared = 796.62, df = 1, p-value < 2.2e-16
```

```r
#oddsratio
oddsratio(new_bwgt$Death.f, new_bwgt$LowBirthWgt.f,rev=c("b"),method="wald")$measure
```

```
##          odds ratio with 95% C.I.
## Predictor estimate    lower    upper
##       Yes  1.00000       NA       NA
##       No  23.64956 18.22641 30.68632
```

```r
# Fisher's Exact Test
tab24<- table(x=new_bwgt$Death.f , y=new_bwgt$LowBirthWgt.f)
tab22<- as.matrix(tab24)

# Two-sided alternative hypothesis
fisher.test(tab24)
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  tab24
## p-value < 2.2e-16
## alternative hypothesis: true odds ratio is not equal to 1
## 95 percent confidence interval:
##  18.06601 30.93969
## sample estimates:
## odds ratio
```

```
##   23.58755
```

```r
# One-sided less than alternative hypothesis
fisher.test(tab24,alternative="less")
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  tab24
## p-value = 1
## alternative hypothesis: true odds ratio is less than 1
## 95 percent confidence interval:
##   0.00000 29.65712
## sample estimates:
## odds ratio
##   23.58755
```

```r
# One-sided greater than alternative hypothesis
fisher.test(tab24,alternative="greater")
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  tab24
## p-value < 2.2e-16
## alternative hypothesis: true odds ratio is greater than 1
## 95 percent confidence interval:
##  18.82176      Inf
## sample estimates:
## odds ratio
##   23.58755
```

```r
# MH test:
mantelhaen.test(new_bwgt$Death.f, new_bwgt$LowBirthWgt.f, new_bwgt$Drinking.f,correct=T)
```

```
##
##  Mantel-Haenszel chi-squared test with continuity correction
##
## data:  new_bwgt$Death.f and new_bwgt$LowBirthWgt.f and new_bwgt$Drinking.f
## Mantel-Haenszel X-squared = 794.75, df = 1, p-value < 2.2e-16
## alternative hypothesis: true common odds ratio is not equal to 1
## 95 percent confidence interval:
##  18.20822 30.65360
## sample estimates:
## common odds ratio
##          23.62515
```