Question 2

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nausea <- data.frame(  
 c('A', 'B'),  
 "Yes" = c(65, 72),  
 "No" = c(15, 48),  
 row.names = 1  
)  
  
nausea

## Yes No  
## A 65 15  
## B 72 48

nausea\_table <- as.table(cbind(c(65, 72), c(15, 48)))  
nausea\_table

## A B  
## A 65 15  
## B 72 48

# Part A

# by hand  
alpha <- 0.05  
  
# risk difference  
rd <- (nausea[1, 1] / ( nausea[1, 1] + nausea[1, 2] )) - (nausea[2, 1] / ( nausea[2, 1] + nausea[2, 2]) )  
  
rd\_ci <- c(  
 rd + (  
 qnorm(1 - (alpha / 2)) \* sqrt(  
 (( nausea[1, 1] + nausea[2, 1] ) / ( nausea[1, 1] + nausea[2, 1] + nausea[1, 2] + nausea[2, 2] )) \*  
 ( 1 - ((nausea[1, 1] + nausea[2, 1]) / (nausea[1, 1] + nausea[2, 1] + nausea[1, 2] + nausea[2, 2])) ) \*  
 ( (nausea[1, 1] + nausea[1, 2])^-1 + (nausea[2, 1] + nausea[2, 2])^-1 )  
 )  
 ),  
 exp(log(rd)) - (  
 qnorm(1 - (alpha / 2)) \* sqrt(  
 (( nausea[1, 1] + nausea[2, 1] ) / ( nausea[1, 1] + nausea[2, 1] + nausea[1, 2] + nausea[2, 2] )) \*  
 ( 1 - ((nausea[1, 1] + nausea[2, 1]) / (nausea[1, 1] + nausea[2, 1] + nausea[1, 2] + nausea[2, 2])) ) \*  
 ( (nausea[1, 1] + nausea[1, 2])^-1 + (nausea[2, 1] + nausea[2, 2])^-1 )  
 )  
 )  
)  
  
# risk ratio  
rr <- ( nausea[1, 1] / ( nausea[1, 1] + nausea[1, 2] ) ) / ( nausea[2, 1] / ( nausea[2, 1] + nausea[2, 2] ) )  
  
rr\_ci <- c(  
 exp(  
 log(rr) + (  
 qnorm(1 - (alpha / 2)) \* sqrt(  
 nausea[1, 2] / ( nausea[1, 1] \* ( nausea[1, 1] + nausea[1, 2] ) ) +  
 nausea[2, 2] / ( nausea[2, 1] \* ( nausea[2, 1] + nausea[2, 2] ) )  
 )  
 )  
 ),  
 exp(  
 log(rr) - (  
 qnorm(1 - (alpha / 2)) \* sqrt(  
 nausea[1, 2] / ( nausea[1, 1] \* ( nausea[1, 1] + nausea[1, 2] ) ) +  
 nausea[2, 2] / ( nausea[2, 1] \* ( nausea[2, 1] + nausea[2, 2] ) )  
 )  
 )  
 )  
)  
  
# odds ratio  
or <- ( nausea[1, 1] \* nausea[2, 2] ) / ( nausea[2, 1] \* nausea[1, 2] )  
  
or\_ci <- c(  
 exp(  
 log(or) + (  
 qnorm(1 - (alpha / 2)) \* sqrt(nausea[1, 1]^-1 + nausea[1, 2]^-1 + nausea[2, 1]^-1 + nausea[2, 2]^-1)  
 )  
 ),  
 exp(log(or) - (  
 qnorm(1 - (alpha / 2)) \* sqrt(nausea[1, 1]^-1 + nausea[1, 2]^-1 + nausea[2, 1]^-1 + nausea[2, 2]^-1)  
 )  
 )  
)  
  
data.frame(  
 'statistic' = c('rd', 'rr', 'or'),  
 'point\_estimate' = c(rd \* 100, rr, or),  
 'lower' = c(rd\_ci[2] \* 100, rr\_ci[2], or\_ci[2]),  
 'upper' = c(rd\_ci[1] \* 100, rr\_ci[1], or\_ci[1])  
)

## statistic point\_estimate lower upper  
## 1 rd 21.250000 8.109012 34.390988  
## 2 rr 1.354167 1.131024 1.621333  
## 3 or 2.888889 1.478622 5.644229

# using epiR  
library(epiR)

## Loading required package: survival

## Package epiR 1.0-15 is loaded

## Type help(epi.about) for summary information

## Type browseVignettes(package = 'epiR') to learn how to use epiR for applied epidemiological analyses

##

epi.2by2(nausea\_table)

## Outcome + Outcome - Total Inc risk \* Odds  
## Exposed + 65 15 80 81.2 4.33  
## Exposed - 72 48 120 60.0 1.50  
## Total 137 63 200 68.5 2.17  
##   
## Point estimates and 95% CIs:  
## -------------------------------------------------------------------  
## Inc risk ratio 1.35 (1.13, 1.62)  
## Odds ratio 2.89 (1.48, 5.64)  
## Attrib risk \* 21.25 (9.00, 33.50)  
## Attrib risk in population \* 8.50 (-2.38, 19.38)  
## Attrib fraction in exposed (%) 26.15 (11.58, 38.32)  
## Attrib fraction in population (%) 12.41 (4.35, 19.79)  
## -------------------------------------------------------------------  
## Test that OR = 1: chi2(1) = 10.045 Pr>chi2 = 0.00  
## Wald confidence limits  
## CI: confidence interval  
## \* Outcomes per 100 population units

There were 0.2125(0.0810901, 0.3439099) more subjects in the anesthetic group A compared to the anesthetic group B. Notice the discrepency between the hand calculation CI and the epiR function generated CI. This is due to a slightly different adjustment for the statistics at hand. Those who received anesthetic A, were 1.3541667(1.1310242, 1.6213335) times more likely to experience nausea. And, the odds of nausea in those using anesthetic A is 2.8888889(1.4786217, 5.6442288) times the odds in those using anesthetic B. All three of these estimates agree with the significants implied by their confidence intervals.

# Part B

chisq <- chisq.test(nausea\_table, correct = FALSE)  
chisq\_correct <- chisq.test(nausea\_table, correct = TRUE)  
fisher <- fisher.test(nausea\_table)  
mcnemar <- mcnemar.test(nausea\_table)  
  
df <- data.frame(  
 'approach' = c('chisq.test', 'chisq.test.corrected', 'fisher.test', 'mcnemar.nest'),  
 'test\_statistic' = c(chisq$statistic, chisq\_correct$statistic, NA, mcnemar$statistic),  
 'p\_value' = round(c(chisq$p.value, chisq\_correct$p.value, fisher$p.value, mcnemar$p.value), digits = 3)  
)  
  
iter <- 1  
for (i in df$p\_value) {  
 if (i < 0.001) {  
 df$p\_value[iter] <- '<0.001'  
 }  
   
 iter <- iter + 1  
}  
  
df

## approach test\_statistic p\_value  
## 1 chisq.test 10.045186 0.002  
## 2 chisq.test.corrected 9.084502 0.003  
## 3 fisher.test NA 0.002  
## 4 mcnemar.nest 36.045977 <0.001

# Part C

McNemar’s test was originally intended to be used for paired data. There is no indication that any pairing was done between the two groups anesthetic A and anesthetic B. Additionally, I tend to lean towards more conservative estimates, so the corrected chi-square test will be a more conservative estimate that the chi-square test with no correction, and likely a better test. At the very least we don’t need to do both.

# Part D

The most appropriate test here is likely the corrected chi-square test. While the Fisher’s exact test is a good test for low sample size, it seems as though the correction on chi-squared tests is creating a more conservative test. That being said, the chi-square test with a correction tells us that with 95% confidence we can say that the use of anesthetic A implies a significant result of nausea.