Stats 111 Homework 2

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```
## Warning: package 'pROC' was built under R version 4.2.2
## Type 'citation("pROC")' for a citation.
##
## Attaching package: 'pROC'
## The following objects are masked from 'package:stats':
##
##
       cov, smooth, var
        a. H_0: Cholesterol level and CHD are independent
  1.
          H_a: Cholesterol level and CHD are dependent
  b. test statistic: 35.028 ~ chisquared(3)
    p-value: 1.202 * 10^{-7}
heart = matrix(c(307, 246, 439, 245, 12, 8, 31, 41), 4, 2)
rownames(heart) = c("low", "above normal", "high", "very high")
colnames(heart) = c("CHD no", "CHD yes")
# chi square test of independence
chisq.test(heart , correct=FALSE)
##
    Pearson's Chi-squared test
##
##
## data: heart
## X-squared = 35.028, df = 3, p-value = 1.202e-07
  c. conclusion: Cholesterol level and CHD are dependent at 5% significant level
  d. It is natural to think that higher cholesterol tends to lead to heart disease. So "low", "above normal", "high",
    "very high" comes in a natural order.
  e. H_0: Probability of CHD didn't increase with Cholesterol level.
    H_a: Probability of CHD increases with Cholesterol level.
  f. test statistic: 26.167 ~ chisquared(1)
    p-value: 3.131 * 10^{-7}
    conclusion: We reject the null and conclude that there is a trend between CHD and Cholesterol level.
# addmargins(heart)
prop.trend.test(heart[ ,2], rowSums(heart))
```

```
##
## Chi-squared Test for Trend in Proportions
##
## data: heart[, 2] out of rowSums(heart) ,
## using scores: 1 2 3 4
## X-squared = 26.167, df = 1, p-value = 3.131e-07
```

2. a. I use chi-squared of independence and got a p-value $< 2.2 * 10^{-16}$. So there is evidence that socioeconomic level is correlated with delinquent status.

```
# This is the 3 way scouts table
scout = array( c(169,43,42,11,59,196,10,10),dim = c(2, 2, 2),dimnames = list( Scout = c("No","Ye
s"),Verdict = c("Delinquet No", "Delinquet Yes"),Socioeconomic = c("Lomessw","High")))
# This is the two way table of Socioeconomc status and Scout status
socio_scout = array(c(211,69,54,206), dim=c(2,2),dimnames=list(Socioeconomic=c("Low","High"), Sc
out=c("No","Yes")))
chisq.test(socio_scout , correct=FALSE)
```

```
##
## Pearson's Chi-squared test
##
## data: socio_scout
## X-squared = 160.75, df = 1, p-value < 2.2e-16</pre>
```

b. I use odds ratio estimate and got a odds ratio of 0.314. So there is evidence that socioeconomic level is correlated with scout status.

```
# This is the two way table of Socioeconomic stats and Deliquency status
socio_deliq = array(c(212,255,53,20), dim=c(2,2),dimnames=list(Socioeconomic=c("Low","High"), De
liquent=c("No","Yes")))
prop.comp(socio_deliq)
```

```
## Warning in prop.comp(socio_deliq): Estimated probabilities represent Pr[ Deliquent | Socioeco
nomic ]. For estimates of
## Pr[ Socioeconomic | Deliquent ], change the value of 'transpose'.
```

```
## $riskdiff
##
                Deliquent
## Socioeconomic No
                             p0 Yes
                                                  riskdiff
                                             p1
                                                                 lower
                                                                              upper
##
            Low 212 0.8000000
                                53 0.20000000
                                                 0.0000000
                                                                    NA
                                                                                 NA
            High 255 0.9272727
                                 20 0.07272727 -0.1272727 -0.1880864 -0.06645901
##
                Deliquent
##
##
   Socioeconomic
                       p.value
##
            Low
                            NA
##
            High 1.531149e-05
##
## $riskratio
##
                Deliquent
   Socioeconomic
                                             p1 riskratio
##
                  No
                             p0 Yes
                                                               lower
                                                                         upper
##
                212 0.8000000
                                 53 0.20000000 1.0000000
                                                                  NA
                                                                            NA
##
            High 255 0.9272727
                                 20 0.07272727 0.3636364 0.2236909 0.5911345
##
                 Deliquent
   Socioeconomic
##
                       p.value
##
            Low
                            NΑ
            High 1.531149e-05
##
##
   $oddsratio
##
##
                Deliquent
   Socioeconomic No
##
                             p0 Yes
                                             p1 oddsratio
                                                               lower
                                                                         upper
                                53 0.20000000 1.0000000
##
                212 0.8000000
                                                                  NA
                                                                            NA
##
            High 255 0.9272727
                                 20 0.07272727 0.3137255 0.1817923 0.5414074
                Deliquent
##
   Socioeconomic
##
                       p.value
##
            Low
                            NA
##
            High 1.531149e-05
```

- c. Socioeconomic status looks like a confounder in the association between Scout status and Delinquency status. Because it is related to both Scout and Deliquency Status.
- d. OR_MH = 0.657, it's rather away from 1, so it seems that delinquet and scout status are dependent when controling for socioeconomic level.

```
OR_MH = (169*11/(169+42+43+11)+59*10/(59+10+196+10))/(43*42/(169+42+43+11)+196*10/(59+10+196+10))
```

e. H0: OR_MH = 1 Ha: OR_MH != 1 p-value: 0.1843 conclusion: we fail to reject the null => ie. delinquet and scout status are uncorrelated when controling for socioeconomic levels.

```
mantelhaen.test(scout)
```

```
##
## Mantel-Haenszel chi-squared test with continuity correction
##
## data: scout
## Mantel-Haenszel X-squared = 1.7622, df = 1, p-value = 0.1843
## alternative hypothesis: true common odds ratio is not equal to 1
## 95 percent confidence interval:
## 0.3635458 1.1874379
## sample estimates:
## common odds ratio
## 0.6570297
```

- f. The effect of being delinquent on scout status differs across different socioeconomic levels. So socioeconomic level is a effect modifier.
- 3. a. If the person doesn't drink and smoke, then the expected BP is beta 0. It is a meaningful interpretation because it is a plausible condition.
- b. If the person Smoke, then drink brings additional beta 3 effect on BP.
- c. The effect of drinking on BP for smokers is beta2 hat + beta3 hat more than nonsmokers.
- d. H0: beta2 = beta3 = 0

Ha: H0 is not true

Reduced Model: y = beta0 + beta1xDrink

Full Model: y = beta0 + beta1xDrink + beta2xSmoke + beta3xDrinkxSmoke

- 4. a. BMI reasonably correlates with blood pressure and the prevalence of CHD.
- b. Both p-values are way below 0.05 significant level. That means BMI is a confounder.

H0: SBP and BMI are independent.

Ha: SBP and BMI are dependent.

H0: CHD and BMI are independent.

Ha: CHD and BMI are dependent.

```
# Framingham Data
framingham = read.table("C:\\Users\\Owen\\Downloads\\Framingham copy.txt")
        Recode sex to something obvious (sex=1 -> male)
framingham$sex = framingham$sex - 1
names( framingham )[1] = "female"
        Create SBP and BMI groups
framingham$sbphi = cut( framingham$sbp, breaks=c(min(framingham$sbp),146, max(framingham$sbp)),
include.lowest=TRUE )
framingham$bmigrp = cut( framingham$bmi, breaks=c(min(framingham$bmi, na.rm=TRUE),20, 25, 30, ma
x(framingham$bmi, na.rm=TRUE)), include.lowest=TRUE, right=FALSE)
bmisbp.table = xtabs( ~ bmigrp + sbphi, data=framingham )
epitab( bmisbp.table, pvalue="chi2" )
n.hisbp = bmisbp.table[,2]
n.strata = rowSums(bmisbp.table)
chisq.test(bmisbp.table)
prop.trend.test( n.hisbp, n.strata )
#####
        Compute test of independence and test for trend for BMI and CHD
bmichd.table = xtabs( ~ bmigrp + chdfate, data=framingham )
epitab( bmichd.table, pvalue="chi2" )
n.chd = bmichd.table[,2]
n.strata = rowSums(bmichd.table)
chisq.test(bmichd.table)
prop.trend.test(n.chd, n.strata)
```

```
## $tab
##
              sbphi
## bmigrp
               [80,146]
                                p0 (146,270]
                                                    p1 oddsratio
                                                                     lower
##
     [16.2,20)
                   231 0.06292563
                                          24 0.0235525 1.000000
                                                                        NΑ
                   1685 0.45900300
##
     [20,25)
                                         283 0.2777233 1.616543 1.042364
##
    [25,30)
                   1399 0.38109507
                                         467 0.4582924 3.212920 2.083356
##
     [30,57.6]
                    356 0.09697630
                                         245 0.2404318 6.623947 4.220519
##
              sbphi
## bmigrp
                   upper
                              p.value
##
     [16.2,20)
                      NA
##
     [20,25)
                2.507005 3.048828e-02
##
    [25,30)
                4.954915 2.938902e-08
     [30,57.6] 10.396037 1.606474e-19
##
##
## $measure
## [1] "wald"
##
## $conf.level
##
  [1] 0.95
##
## $pvalue
## [1] "chi2"
##
##
##
   Pearson's Chi-squared test
##
## data: bmisbp.table
  X-squared = 225.24, df = 3, p-value < 2.2e-16
##
##
##
   Chi-squared Test for Trend in Proportions
##
##
## data: n.hisbp out of n.strata,
   using scores: 1 2 3 4
## X-squared = 214.6, df = 1, p-value < 2.2e-16
##
## $tab
##
              chdfate
## bmigrp
                                           p1 oddsratio
                                                            lower
                                                                     upper
                            p0
                                 1
     [16.2,20) 220 0.06836544 35 0.02377717 1.000000
##
                                                               NΔ
                                                                        NA
##
     [20,25)
             1465 0.45525171 503 0.34171196 2.158167 1.489560 3.126885
##
     [25,30)
               1180 0.36668738 686 0.46603261 3.654237 2.526936 5.284444
##
     [30,57.6] 353 0.10969546 248 0.16847826 4.416026 2.984212 6.534820
              chdfate
##
## bmigrp
                    p.value
##
     [16.2,20)
                         NA
##
    [20,25)
              3.307489e-05
##
     [25,30)
               3.227521e-13
##
     [30,57.6] 4.767196e-15
##
## $measure
## [1] "wald"
```

```
##
## $conf.level
## [1] 0.95
##
## $pvalue
## [1] "chi2"
##
##
##
   Pearson's Chi-squared test
##
## data: bmichd.table
## X-squared = 120.25, df = 3, p-value < 2.2e-16
##
##
   Chi-squared Test for Trend in Proportions
##
##
## data: n.chd out of n.strata,
   using scores: 1 2 3 4
## X-squared = 114.14, df = 1, p-value < 2.2e-16
```

- c. OR for CHD against BMI in the level of [20,25) is 2.16 with a 95% CI of (1.49, 3.13) OR for BMI in the level of [25,30) is 3.65 with a 95% CI of (2.53, 5.28). OR for BMI in the level of [30,57.6] is 4.42 with a 95% CI of (2.98, 6.53).
- d. The MH common odds ratio is 1.66 with a 95% CI of (1.43,1.92). Because 1 is not in the CI, so CHD and sbp are related while adjusting for the level of BMI.

```
##### Compute relevant counts
n.sbplo = xtabs( ~ sbphi + bmigrp, data=framingham )[1,]
n.sbphi = xtabs( ~ sbphi + bmigrp, data=framingham )[2,]
lo.chd = xtabs( ~ chdfate + sbphi + bmigrp, data=framingham )[2,1,]
hi.chd = xtabs( ~ chdfate + sbphi + bmigrp, data=framingham )[2,2,]

# Just to show the 3 way table that is being used above for the MH and BD tests
sbphi.chd.table = table(BP=framingham$sbphi, CHD=framingham$chdfate, BMI=framingham$bmigrp)

##### Compute M-H estimate of adjusted OR and test for heterogeneity
mh.rslt = meta.MH(n.sbphi, n.sbplo, hi.chd, lo.chd, names=levels(framingham$bmigrp))
summary( mh.rslt )
```

```
## Fixed effects ( Mantel-Haenszel ) meta-analysis
## Call: meta.MH(ntrt = n.sbphi, nctrl = n.sbplo, ptrt = hi.chd, pctrl = lo.chd,
       names = levels(framingham$bmigrp))
##
##
##
               OR (lower 95% upper)
## [16.2,20) 3.78
                     1.48
                                9.66
                                2.40
## [20,25)
            1.84
                    1.41
## [25,30)
            1.55
                    1.25
                                1.92
## [30,57.6] 1.57
                    1.13
                                2.18
## Mantel-Haenszel OR =1.66 95% CI ( 1.43,1.92 )
## Test for heterogeneity: X^2(3) = 4.03 (p-value 0.2579)
```

```
# MH test using 3 way table mantelhaen.test(sbphi.chd.table)
```

```
##
## Mantel-Haenszel chi-squared test with continuity correction
##
## data: sbphi.chd.table
## Mantel-Haenszel X-squared = 45.864, df = 1, p-value = 1.268e-11
## alternative hypothesis: true common odds ratio is not equal to 1
## 95 percent confidence interval:
## 1.433431 1.924566
## sample estimates:
## common odds ratio
## 1.660943
```

```
e. H0: OR_{MH}=1
Ha: OR_{MH} 
eq 1
p-value: 1.268*10^{-11}
```

conclusion: We reject the null and conclude that CHD and sbp are dependent while adjusting for BMI.