hw1_program

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```r
library(vcdExtra)
```

```
Warning: package 'vcdExtra' was built under R version 3.5.3

Loading required package: vcd

Warning: package 'vcd' was built under R version 3.5.3

Loading required package: grid

Loading required package: gnm

Warning: package 'gnm' was built under R version 3.5.3
```

```r
data("Abortion")    #loads the Abortion data
Abortion
```

```
, , Support_Abortion = Yes

        Status
Sex       Lo  Hi
  Female 171 138
  Male   152 167

, , Support_Abortion = No

        Status
Sex       Lo  Hi
  Female  79 112
  Male   148 133
```

Note that, current data is in a format of 2x2 table with *Sex* and *Status* as row and column, while *Support_Abortion* as layer. However, we need to restructure the data in a way so that *Sex* and *Support_Abortion* to be row and column variable respectively, while *Status* is layer variable.

```r
Abortion2 = aperm(Abortion, c(1,3,2))
dimnames(Abortion2)
```

```
$Sex
[1] "Female" "Male"

$Support_Abortion
[1] "Yes" "No"

$Status
[1] "Lo" "Hi"
```

Now, to test the null hypothesis H_0 : row||column|Layer we use **Cochran-Mantel-Haenszel Chi-Squared Test**;

```r
mantelhaen.test(Abortion2)
```

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

data:  Abortion2
Mantel-Haenszel X-squared = 7.9435, df = 1, p-value = 0.004826
alternative hypothesis: true common odds ratio is not equal to 1
95 percent confidence interval:
 1.117674 1.808322
sample estimates:
common odds ratio
       1.421659
```

Note that, we get an p-value of 0.004826, which is extremely lower than the significance level of $\alpha = 0.05$. Hence, we reject the null hypothesis that the variables *Sex* and *Support_Abortion* are independent given the layered variable *Status* in the light of *Abortion* data.