

## Description of R output from the Mantel-Haneszel Method (Need to install **lawstat** and **metafor** packages)

### R Code for Mentel-Haneszel Method

```
> # Mantel-Haneszel Method with Odds Ratio Estimation

> library("lawstat") #load lawstat package for M-H Method

> boymatrix <- matrix(c(20,100,15,150),nrow=2,byrow=TRUE, #set table for boy
+   dimnames = list("Sleep" = c("Low","High"), # label column variable
+   "Result" = c("Fail","Pass"))) # label row variable
> print(boymatrix) # Print the table
      Result
Sleep Fail Pass
Low     20  100
High    15  150

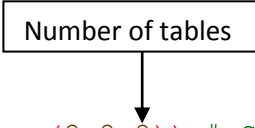
> girlmatrix <- matrix(c(30,100,25,200),nrow=2,byrow=TRUE, #set table for girl
+   dimnames = list("Sleep" = c("Low","High"), # label column variable
+   "Result" = c("Fail","Pass"))) # label row variable
> print(girlmatrix) # Print the table
      Result
Sleep Fail Pass
Low     30  100
High    25  200

> myarray <- array(c(boymatrix,girlmatrix),dim=c(2,2,2)) # Set matrix for HM

> cmh.test(myarray) # Run the Mantel-Haneszel Method

      Cochran-Mantel-Haenszel Chi-square Test

data: myarray
CMH statistic = 12.477, df = 1.000, p-value = 0.000, MH Estimate =
2.229, Pooled Odd Ratio = 2.188, Odd Ratio of level 1 = 2.000, Odd
Ratio of level 2 = 2.400
```



### R Code for Tarone's Test for Homogeneity of Odds Ratios (Need R version 2.12.2 and after)

```
> #Tarones Test for Homogeneity of Odds Ratios

> library("metafor") # Load metafor package

> calcTaronesTest <- function(mylist,referencerow=2) # R Tarones test function
+ {
+   numstrata <- length(mylist)
```

```

+   # make an array "ntrt" of the number of people in the exposed group, in
each stratum
+   # make an array "nctrl" of the number of people in the unexposed group,
in each stratum
+   # make an array "ptrt" of the number of people in the exposed group that
have the disease,
+   # in each stratum
+   # make an array "pctrl" of the number of people in the unexposed group
that have the disease,
+   # in each stratum
+   # make an array "htrt" of the number of people in the exposed group that
don't have the
+   # disease, in each stratum
+   # make an array "hctrl" of the number of people in the unexposed group
that don't have the
+   # disease, in each stratum
+   ntrt <- vector()
+   nctrl <- vector()
+   ptrt <- vector()
+   pctrl <- vector()
+   htrt <- vector()
+   hctrl <- vector()
+   if (referencerow == 1) { nonreferencerow <- 2 }
+   else { nonreferencerow <- 1 }
+   for (i in 1:numstrata)
+   {
+     mymatrix <- mylist[[i]]
+     DiseaseUnexposed <- mymatrix[referencerow,1]
+     ControlUnexposed <- mymatrix[referencerow,2]
+     totUnexposed <- DiseaseUnexposed + ControlUnexposed
+     nctrl[i] <- totUnexposed
+     pctrl[i] <- DiseaseUnexposed
+     hctrl[i] <- ControlUnexposed
+     DiseaseExposed <- mymatrix[nonreferencerow,1]
+     ControlExposed <- mymatrix[nonreferencerow,2]
+     totExposed <- DiseaseExposed + ControlExposed
+     ntrt[i] <- totExposed
+     ptrt[i] <- DiseaseExposed
+     htrt[i] <- ControlExposed
+   }
+   # calculate Tarone's test of homogeneity, using the rma.mh function from
the
+   # "metafor" package
+   tarone <- rma.mh(ptrt, htrt, pctrl, hctrl, ntrt, nctrl)
+   pvalue <- tarone$TAp
+   print(paste("Pvalue for Tarone's test =", pvalue))
+ }

> mylist <- list(boymatrix,girlmatrix) # Set up matrices for Tarone's Test

> calcTaronesTest(mylist)
[1] "Pvalue for Tarone's test = 0.69852363197761"

```