

Supplementary materials for “Multiplicity adjustments for the Dunnett procedure under heteroscedasticity”

6/5/2023

This document illustrates the example in Section 6 of “Multiplicity adjustments for the Dunnett procedure under heteroscedasticity” by Tamhane and Xi. The birthweight dataset is available in the R package multcomp. R code to reproduce this document can be found at <https://github.com/xidongdxi/dunnett>.

Prepare summary input data for Table 3

```
library(multcomp)

## Loading required package: mvtnorm

## Loading required package: survival

## Loading required package: TH.data

## Loading required package: MASS

##
## Attaching package: 'TH.data'

## The following object is masked from 'package:MASS':
##
##      geyser

data("litter")
data <- subset(litter, select = c(dose, weight))
doses <- c(0, 5, 50, 500)
tab3_input <- data.frame(dose = doses, X = NA, S2 = NA, n = NA, t = NA, nu = NA)
for (i in 1:length(doses)) {
  temp <- subset(data, dose == doses[i])
  tab3_input[i, 2] <- mean(temp$weight)
  tab3_input[i, 3] <- var(temp$weight)
  tab3_input[i, 4] <- length(temp$weight)
  if (doses[i] != 0) {
    tab3_input[i, 5] <- (tab3_input[1, 2] - tab3_input[i, 2]) /
      sqrt(tab3_input[i, 3] / tab3_input[i, 4] + tab3_input[1, 3] / tab3_input[1, 4])
    tab3_input[i, 6] <- (tab3_input[i, 3] / tab3_input[i, 4] +
      tab3_input[1, 3] / tab3_input[1, 4])^2 /
      (tab3_input[i, 3]^2 / tab3_input[i, 4]^2 / (tab3_input[i, 4] - 1) +
```

```

      tab3_input[1, 3]^2 / tab3_input[1, 4]^2 / (tab3_input[1, 4] - 1))
    }
    tab3_input
  }
tab3_input$X <- round(tab3_input$X, 2)
tab3_input$S2 <- round(tab3_input$S2, 2)
tab3_input$t <- round(tab3_input$t, 2)
tab3_input$nu <- round(tab3_input$nu, 2)
print(tab3_input, row.names = FALSE) # Table 3, columns 1-6

```

```

## dose      X      S2  n      t      nu
##      0 32.31  7.26 20      NA      NA
##      5 29.31 25.93 19 2.28 27.04
##     50 29.87 14.16 18 2.28 30.51
##    500 29.65 29.21 17 1.85 22.63

```

Check for heteroscedasticity

```

k <- length(doses) - 1
x <- tab3_input$X
s2 <- tab3_input$S2
n <- tab3_input$n
t <- tab3_input$t
nu <- tab3_input$nu
nu_0 <- sum(n) - (k + 1)
nu_0 # $\nu$

```

```
## [1] 70
```

```

s2_0 <- sum((n - 1) * s2) / nu_0
round(s2_0, 3) # $S^2$

```

```
## [1] 18.754
```

```

c_Bartlett <- 1 + 1 / 3 / k * (sum(1 / (n - 1)) - 1 / nu_0)
round(c_Bartlett, 3) # Bartlett correction factor

```

```
## [1] 1.024
```

```

X2 <- (nu_0 * log(s2_0) - sum((n - 1) * log(s2))) / c_Bartlett
round(X2, 3) # Bartlett statistic $X^2$

```

```
## [1] 9.655
```

```

# p-value for the Bartlett test
round(pchisq(X2, 3, lower.tail = F), 4)

```

```
## [1] 0.0217
```

Correlation matrix for the PI method

```
lambda <- sqrt(s2[1] / n[1] / (s2[1] / n[1] + s2[-1] / n[-1]))
round(lambda, 3) # PI estimates of the  $\lambda_i$  defined in (6)
```

```
## [1] 0.458 0.562 0.418
```

```
corr_PI <- matrix(0, nrow = k, ncol = k)
for(i in 1:k) {
  for (j in 1:k) {
    corr_PI[i, j] <- lambda[i] * lambda[j]
  }
}
diag(corr_PI) <- 1
round(corr_PI, 3) # PI correlation in (5)
```

```
##      [,1] [,2] [,3]
## [1,] 1.000 0.258 0.191
## [2,] 0.258 1.000 0.235
## [3,] 0.191 0.235 1.000
```

```
eta <- s2[1] / n[1] / sqrt(n[1] - 1) /
  sqrt((s2[1]^2 / n[1]^2 / (n[1] - 1) + s2[-1]^2 / n[-1]^2 / (n[-1] - 1)))
round(eta, 3) # PI estimates of the  $\eta_i$  in (8)
```

```
## [1] 0.251 0.400 0.190
```

```
corr_U <- matrix(0, nrow = k, ncol = k)
for(i in 1:k) {
  for (j in 1:k) {
    corr_U[i, j] <- eta[i] * eta[j]
  }
}
diag(corr_U) <- 1
round(corr_U, 3) # Desired estimated correlation (10)
```

```
##      [,1] [,2] [,3]
## [1,] 1.000 0.100 0.048
## [2,] 0.100 1.000 0.076
## [3,] 0.048 0.076 1.000
```

Correlation matrix for the proposed method

```
c_val <- eta^2 * nu[-1]
round(c_val, 3) #  $c$ 's
```

```
## [1] 1.699 4.882 0.820
```

```

d_val <- nu[-1] - c_val
round(d_val, 3) # d's

## [1] 25.341 25.628 21.810

round(c_val[order(c_val)], 3) # Ordered c's

## [1] 0.820 1.699 4.882

round(c(c_val[order(c_val)][1], c_val[order(c_val)][2] - c_val[order(c_val)][1],
      c_val[order(c_val)][3] - c_val[order(c_val)][2]), 3) # Ordered increments of c's

## [1] 0.820 0.879 3.184

round(d_val[order(c_val)], 3) # Ordered d's

## [1] 21.810 25.341 25.628

corr_U_approx <- matrix(0, nrow = k, ncol = k)
for(i in 1:k) {
  for (j in 1:k) {
    if (rank(c_val)[i] < rank(c_val)[j]) {
      corr_U_approx[i, j] <- eta[i]^2 * sqrt(nu[-1][i] / nu[-1][j])
    } else {
      corr_U_approx[i, j] <- eta[j]^2 * sqrt(nu[-1][j] / nu[-1][i])
    }
  }
}
diag(corr_U_approx) <- 1
round(corr_U_approx, 3) # Correlation matrix among the $U_i$'s using (9)

##      [,1] [,2] [,3]
## [1,] 1.000 0.059 0.033
## [2,] 0.059 1.000 0.031
## [3,] 0.033 0.031 1.000

```

Load functions for Methods 0-3

```

setwd(folder)
source("functions.R")

```

Adjusted p-values of Methods 0

```

library(mvtnorm)
set.seed(10000)
# Method 0
time <- proc.time()
padj0 <- homo_func(x_0 = tab3_input$X[1], x = tab3_input$X[-1],
                  s2_0 = tab3_input$S2[1], s2 = tab3_input$S2[-1],
                  n_0 = tab3_input$n[1], n = tab3_input$n[-1], direction = "lower")
time0 <- c(proc.time() - time)[3]

```

Adjusted p-values of Methods 1

```

# Method 1
time <- proc.time()
padj1 <- ind_func(x_0 = tab3_input$X[1], x = tab3_input$X[-1],
                 s2_0 = tab3_input$S2[1], s2 = tab3_input$S2[-1],
                 n_0 = tab3_input$n[1], n = tab3_input$n[-1], direction = "lower")
time1 <- c(proc.time() - time)[3]

```

Adjusted p-values of Methods 2

```

# Method 2
time <- proc.time()
padj2 <- PI_func(x_0 = tab3_input$X[1], x = tab3_input$X[-1],
                s2_0 = tab3_input$S2[1], s2 = tab3_input$S2[-1],
                n_0 = tab3_input$n[1], n = tab3_input$n[-1], direction = "lower")
time2 <- c(proc.time() - time)[3]

```

Adjusted p-values of Methods 3

```

# Method 3
time <- proc.time()
padj3 <- sim_based_func(x_0 = tab3_input$X[1], x = tab3_input$X[-1],
                      s2_0 = tab3_input$S2[1], s2 = tab3_input$S2[-1],
                      n_0 = tab3_input$n[1], n = tab3_input$n[-1],
                      direction = "lower", nsim = 1e5)
time3 <- c(proc.time() - time)[3]

tab3 <- data.frame(tab3_input,
                  Padj0 = c(NA, round(padj0, 4)),
                  Padj1 = c(NA, round(padj1, 4)),
                  Padj2 = c(NA, round(padj2, 4)),
                  Padj3 = c(NA, round(padj3, 4)))
print(tab3, row.names = FALSE) # Table 3

```

```

## dose      X      S2  n    t    nu Padj0 Padj1 Padj2 Padj3
##    0 32.31  7.26 20   NA   NA    NA    NA    NA    NA
##    5 29.31 25.93 19  2.28 27.04 0.0441 0.0455 0.0428 0.0435

```

```
##    50 29.87 14.16 18 2.28 30.51 0.1054 0.0461 0.0424 0.0441
##    500 29.65 29.21 17 1.85 22.63 0.0826 0.1104 0.1045 0.1040
```

```
time <- c(time0, time1, time2, time3)
names(time) <- paste0("Method", 0:3)
time # Computing time in seconds
```

```
## Method0 Method1 Method2 Method3
##    0.03    0.02    0.03    0.44
```

```
sessionInfo()
```

```
## R version 4.1.2 (2021-11-01)
## Platform: x86_64-w64-mingw32/x64 (64-bit)
## Running under: Windows 10 x64 (build 19044)
##
## Matrix products: default
##
## locale:
## [1] LC_COLLATE=English_United States.1252
## [2] LC_CTYPE=English_United States.1252
## [3] LC_MONETARY=English_United States.1252
## [4] LC_NUMERIC=C
## [5] LC_TIME=English_United States.1252
##
## attached base packages:
## [1] stats      graphics  grDevices  utils      datasets  methods   base
##
## other attached packages:
## [1] multcomp_1.4-18 TH.data_1.1-0  MASS_7.3-55  survival_3.3-1
## [5] mvtnorm_1.1-3
##
## loaded via a namespace (and not attached):
## [1] codetools_0.2-18 lattice_0.20-45 zoo_1.8-9      digest_0.6.29
## [5] grid_4.1.2      magrittr_2.0.2  evaluate_0.15  rlang_1.0.2
## [9] stringi_1.7.6   cli_3.3.0       rstudioapi_0.13 Matrix_1.4-0
## [13] sandwich_3.0-1  rmarkdown_2.14  splines_4.1.2  tools_4.1.2
## [17] stringr_1.4.0   xfun_0.30       yaml_2.3.5     fastmap_1.1.0
## [21] compiler_4.1.2  htmltools_0.5.2 knitr_1.37
```