Principles of Statistical Data Analysis: HW3

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1 R function: median.test(x,y)

The function median.test(x,y) calculates a permutation p-value associated with $H_0: F_x = F_y$ versus $H_A: median_x \neq median_y$. If the total amount of combinations exceeds 10000, the null-distribution is generated from 10000 random samples. The code is listed below, the include comments can guide the reader through the code.

```
# FUNCTION: calc.median.diff: -----
# Function: calculate the difference in median between two groups.
# param: ind = the indices of the first group
# param: vec = the complete list with data from group 1 and group 2
calc.median.diff <- function(ind, vec){</pre>
  # make both groups
  group1 <- vec[ind]</pre>
  group2 <- vec[!(1:length(vec)) %in% ind]</pre>
  # calculate the difference in means
  return(median(group1) - median(group2))
}
# FUNCTION: median.test: -----
# Function: calculate the p-value of the median difference between
# vector x and vector y, based on the null hypothesis F1(x) = F2(x)
# When the number of combinations is sufficiently small to do a full
# permutation test (limit at 10000), the full permutation test will
# be performed.
```

```
# param: x = vector values for group 1
  param: y = vector values group 2
median.test <- function(x, y){</pre>
  N <- 10000
  realization <- median(x) - median(y)
  len_x <- length(x)</pre>
  len_y <- length(y)</pre>
  vec \leftarrow c(x, y)
  len_vec <- len_x + len_y</pre>
  if(choose(n = len_vec, len_x) < N){</pre>
    # A limited number of combinations (< N): full permutation test
    median.diff <- combn(len_vec,</pre>
                           len x,
                           function(ind){
                             return(calc.median.diff(ind, vec))
                           })
  } else {
    # Too many (>= N) combinations - A sample test will be performed.
    median.diff <- replicate(N,</pre>
                                calc.median.diff(
                                  sample(c(1:len_vec),len_x),
    )
  # The distribution will be symmetrical. The p-value can be calculated by
  # the absolute value.
  return(mean(abs(realization) <= abs(median.diff)))</pre>
}
```

2 Comparison to other tests

The median test was compared, via simmulations, to two other commenly used tests:

- the permutation t-test
- the exact Wilcoxon-Mann-Whitney test

The three tests were compared on the basis of the Type I error and on their power (for a given sample size and delta, see below). This comparision is made for two sample sizes:

- 20 observations in each sample
- 40 observations in each sample

2.1 Power

To evaluate the power of the median test as compared to other statistical tests, the proportions of true positive outcomes of the median test, the permutation t-test and the Wilcoxon–Mann–Whitney test were acquired through Monte Carlo simulation (1000 simulations). Samples (n = 20 and n = 40) were randomly drawn from different distributions under H_a (i.e. for a given $\delta = \frac{\sqrt{Var(Y_1)}}{2}$).

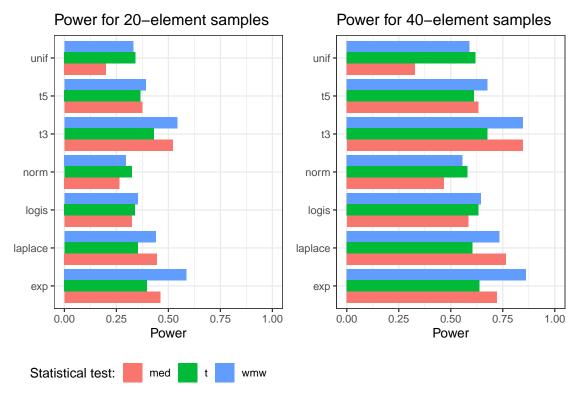


Figure 1: Relative power for different distributions and sample sizes n = 20 and n = 40.

Where $Var(Y_1)$ is based on the known variances of the respective distributions and the selected distribution parameters:

- T: $Var(Y_1) = \frac{df}{df-2}$. For df = 3, df = 5: $Var(Y_1) = 3$ and $\frac{5}{2}$, respectively.
- Standard normal: $Var(Y_1) = 1$
- Exponential: $Var(Y_1) = \frac{1}{\lambda^2}$. For rate $\lambda = 1$: $Var(Y_1) = 1$
- Uniform: $Var(Y_1) = \frac{(b-a)^2}{12}$. For distribution limits a=0, b=1: $Var(Y_1) = \frac{1}{12}$
- Laplace: $Var(Y_1) = 2b^2$. For scale parameter b = 1: $Var(Y_1) = 2$
- Logistic: $Var(Y_1) = s^2\pi^2\frac{2}{6}$. For scale parameter s=1: $Var(Y_1) = \pi^2\frac{2}{6}$

2.2 Type-I error rate

Next, the simulations were repeated under H_0 (i.e. with $\delta = 0$) to compare the type-I error rate of the median test with the permutation t-test and the Wilcoxon–Mann–Whitney test.

3 Conclusion

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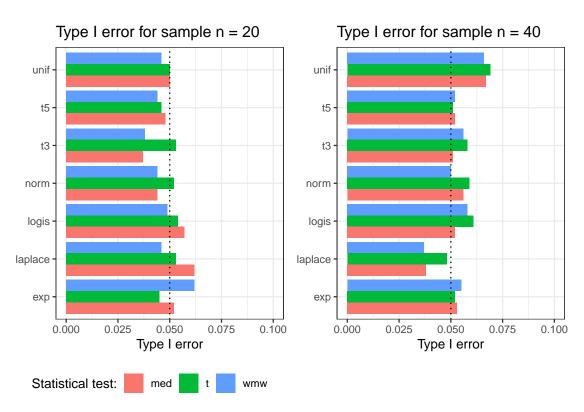


Figure 2: Type I error for different distributions and sample sizes n=20 and n=40. The dotted line represents the significance level alpha

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4 Addendum: full code

Additionally to the function median.test, we use a function calc.rejection to evaluate the proportion of tests where H_0 is rejected. If $\delta = 0$ (then H_0 is true), this represents the type I error proportion.

```
calc.rejection <- function(N, dist, dist_arg, shift, p.val = 0.05){</pre>
    # perform N tests on randomly drawn samples Y1 and Y2
    p.med <- p.wmw <- p.t <- c()
    for(j in 1:N) {
      Y1 <- do.call(what = dist,
                      args = dist_arg)
      Y2 <- do.call(what = dist,
                     args = dist_arg) + shift
      df \leftarrow data.frame(rep(c('A', 'B'), each = n), c(Y1, Y2))
      colnames(df) <- c("group", "Y")</pre>
      p.med[j] \leftarrow median.test(x = Y1, y = Y2)
      p.wmw[j] <- wilcox.test(Y1, Y2, exact = TRUE) $p.value
      p.t[j] <- pvalue(oneway_test(Y~group, data = df,</pre>
                                      distribution =
                                        approximate(nresample = 10000)))
    }
  # calculate the proportion of HO rejections
  return(c( mean(p.med < p.val),</pre>
             mean(p.wmw < p.val),</pre>
             mean(p.t < p.val)</pre>
          )
}
calc.df_power <- function(N, n, delta, p.val = 0.05){</pre>
  distributions <- c('rt',
                       'rt',
                       'rexp',
                       'rlogis',
                       'rnorm',
                       'runif',
                       'rlaplace')
  dist_names <- c('t3', 't5', 'exp', 'logis', 'norm', 'unif', 'laplace')</pre>
  dist_var \leftarrow c(3, 5/3, 1, pi^2/6, 1, 1/12, 2)
  dist_args <- list(list(n, 3),</pre>
                      list(n, 5),
                      list(n),
                      list(n),
                      list(n),
                      list(n),
                     list(n))
  for(i in 1:length(distributions)) {
    cat(paste('power calculation for distribution : ',
```

```
distributions[i], '\n'))
  res <- calc.rejection(N,
                          distributions[i],
                          dist_arg = dist_args[[i]],
                          delta * (dist_var[i])^(1/2) / 2,
                          p.val = 0.05)
  power.med[i] <- res[1]</pre>
  power.wmw[i] <- res[2]</pre>
  power.t[i] <- res[3]</pre>
df_power <- data.frame(Distribution = dist_names,</pre>
                         med = rep(x = 0.0, length(distributions)),
                         wmw = rep(x = 0.0, length(distributions)),
                         t = rep(x = 0.0, length(distributions)))
df_power$med <- power.med
df_power$wmw <- power.wmw</pre>
df_power$t <- power.t</pre>
df_power <- melt(df_power, id.vars = 'Distribution')</pre>
return(df_power)
```

Using the above defined formulas, the simulation can be performed with the following code:

```
# Simulations
N <- 1000
power.med <- power.wmw <- power.t <- c()

for(n in c(20, 40)){
# For simulations under HO (delta = 0) and Ha (delta = 1)
    for(delta in 0:1) {
        if(delta) {
            title <- pasteO('Power_', n, '_', N) }
        else{
            title <- pasteO('TypeI_error_', n, '_', N) }

        df_power <- calc.df_power(N, n, delta)

        write.csv(df_power, paste(title, '.csv', sep=''))
    }
}</pre>
```

In this report, the number of random permutations to construct the null-distribution was set at 10000 and, in order to keep the computational time somewhat manageable, the number of Monte Carlo simulations was set at 1000. This is - however - an arbitrary choice. In order to have some idea on the effect of the number of Monte Carlo simulations on the stability of the relative statistical power, we ran simulations for a different number of tests under H_a . The samples (n = 40) were drawn from a standard normal distribution. The result (see below) indicate that - for the given distribution, amount of permutations and sample size - the result of the Monte Carlo simulation is relatively stable at 500 simulations or more, suggesting that the increased

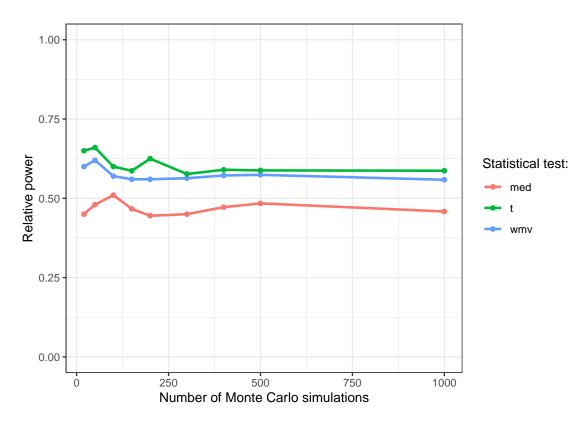


Figure 3: The relative power for an increasing number of Monte Carlo simulations

computational demand that is associated with an additional increase in the number of Monte Carlo simulations does not substantially increase the robustness of the result.