BIOSTAT 238: Homework 1

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Main function:

We must simulate data many times from a population with a standard normal distribution, 10 observations at a time for the intervention group (A), 10 at a time for the control group (B), and then check to see if the difference between groups is significant at each "look" k.

The function has the following arguments:

K: the number of looks, defaults to 5;

m: the number of subjects added to each group before another look occurs, defaults to 10;

delta: the mean of the intervention group relative to the control group, defaults to 0;

signif_thres1: the critical value that is compared with the Z-statistics at the intermediate looks to determine statistical significance, defaults to 1.96;

signif_thres2: the critical value that is compared with the Z-statistic at the final look to determine statistical significance, defaults to 1.96;

n_tests: the number of tests to simulate, defaults to 100000;

show_avg_term_ss: outputs the expected terminating sample size for each group, defaults to FALSE.

```
group_seq <- function(K = 5, m = 10, delta = 0,
                      signif_thres1 = 1.96, signif_thres2 = 1.96,
                      n_tests = 100000, show_avg_term_ss = FALSE){
 results <- c() # Tracks reject or accept for each test
 reject_tally <- c() # Tracks the k value at which the first rejection occurs
 for(test in 1:n_tests){ # Each iteration carries out a complete test
    # Regenerate data vectors for each test:
   A <- rnorm(m*K, mean = delta, sd = 1)
   B \leftarrow rnorm(m*K, mean = 0, sd = 1)
    # Create temporary vector to store Z-statistics for each test:
   temp <- c()
    for(k in 1:K){ # Generate Z-statistics
      # Calculate Z-statistic for the specific k and store in temp vector:
      Z_k \leftarrow (1/sqrt(2*m*k*1))*(sum(A[1:(k*m)])-sum(B[1:(k*m)]))
      temp[k] \leftarrow Z_k
   } # end for
    # For each test, compare with significance thresholds imposed;
    # If any of the K groups are rejected, put 1; else 0:
    if((any(abs(temp[1:(K-1)]) > signif_thres1)) | ((abs(temp[K]) > signif_thres2))){
     results[test] <- 1
      # For part c, tally the k at which the first rejection occurs:
```

```
reject_tally[test] <- ifelse(any(abs(temp[1:(K-1)]) > signif_thres1),
                                    min(which(abs(temp[1:(K-1)]) > signif_thres1)), K)
    } else {
      results[test] <- 0
      reject_tally[test] <- NA
  } # end for
  # Print proportion of tests rejected when delta = delta:
  power <- paste0("Pr(reject null | delta = ", delta, ") = ",</pre>
                  round(length(results[results==1])/n tests, 4))
  # Print expected terminating sample size for each group:
  if(show_avg_term_ss == TRUE){
    freq <- as.numeric(table(reject_tally))</pre>
    avg_term <- 0
    for(k in 1:K){
      avg_term <- avg_term + (freq[k]*k*m)</pre>
    avg_term_sample <- paste0("The average terminating sample size for each group when delta is ",
                               delta, " is ", ceiling(avg_term/n_tests))
    list(power = power, avg_term_sample_size = avg_term_sample)
  } else {
    list(power = power)
}
```

Problem 1.

Part 1.

Conduct a simulation study to find the type I error rate of the above group sequential test, the probability under the null that $|Z_k| > 1.96$ for at least one k = 1, ..., 5.

Solution.

Call the above function with default arguments. When delta is 0, power to detect a difference is alpha.

```
group_seq()
## $power
## [1] "Pr(reject null | delta = 0) = 0.1426"
```

Part 2.

Find the power of the above group sequential test when $\mu_A - \mu_B = 0.1, 0.5, 1.0, 1.5, 2.0$.

Solution:

Call the above function with varying deltas.

```
group_seq(delta = 0.1)
## $power
## [1] "Pr(reject null | delta = 0.1) = 0.1776"
group_seq(delta = 0.5)
## $power
## [1] "Pr(reject null | delta = 0.5) = 0.7728"
group_seq(delta = 1.0)
## $power
## [1] "Pr(reject null | delta = 1) = 0.9992"
group_seq(delta = 1.5)
## $power
## [1] "Pr(reject null | delta = 1.5) = 1"
group_seq(delta = 2.0)
## $power
## [1] "Pr(reject null | delta = 2) = 1"
```

Part 3.

Find the expected terminating sample size for the above group sequential test when $\mu_A - \mu_B = 1.0$.

Solution:

Call the above function with delta = 1; additionally, show the expected termination sample size.

group_seq(delta = 1.0, show_avg_term_ss = TRUE)

```
## $power
## [1] "Pr(reject null | delta = 1) = 0.9992"
##
## $avg_term_sample_size
## [1] "The average terminating sample size for each group when delta is 1 is 16"
```

Since looks in this case are done once for every 20 subjects (10 in each group), the minimum terminating sample size for each group when delta = 1 is best to be rounded up to 20.

Problem 2.

Repeat problem 1 except change the first threshold to 3 instead of 1.96.

Part 1.

Find the type I error rate.

Solution:

Call the above function with default arguments, but change the first threshold.

```
group_seq(signif_thres1 = 3, signif_thres2 = 1.96)
## $power
```

```
## $power
## [1] "Pr(reject null | delta = 0) = 0.0533"
```

We see that this type 1 error rate is very similar to the type 1 error of a standard test without any intermediate looks.

Part 2.

Find the power of the above group sequential test when $\mu_A - \mu_B = 0.1, 0.5, 1.0, 1.5, 2.0$.

Solution:

Call the above function with varying deltas, making sure that the first threshold is set to 3.

```
group_seq(delta = 0.1, signif_thres1 = 3, signif_thres2 = 1.96)

## $power

## [1] "Pr(reject null | delta = 0.1) = 0.0832"

group_seq(delta = 0.5, signif_thres1 = 3, signif_thres2 = 1.96)

## $power

## [1] "Pr(reject null | delta = 0.5) = 0.7088"

group_seq(delta = 1.0, signif_thres1 = 3, signif_thres2 = 1.96)

## $power

## [1] "Pr(reject null | delta = 1) = 0.999"

group_seq(delta = 1.5, signif_thres1 = 3, signif_thres2 = 1.96)

## $power

## [1] "Pr(reject null | delta = 1.5) = 1"

group_seq(delta = 2.0, signif_thres1 = 3, signif_thres2 = 1.96)

## $power

## [1] "Pr(reject null | delta = 2) = 1"
```

Part 3.

Find the expected terminating sample size for the above group sequential test when $\mu_A - \mu_B = 1.0$.

Solution:

Call the above function with delta = 1; additionally, show the expected termination sample size.

```
group_seq(delta = 1.0, signif_thres1 = 3, show_avg_term_ss = TRUE)
```

```
## $power
## [1] "Pr(reject null | delta = 1) = 0.9989"
##
## $avg_term_sample_size
## [1] "The average terminating sample size for each group when delta is 1 is 25"
```

Since looks in this case are done once for every 20 subjects (10 in each group), the minimum terminating sample size for each group when delta = 1 is best to be rounded up to 30.