

Question 1

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```
snp_bonferroni <- p.adjust(snp, method = "bonferroni")
snp_fdr <- p.adjust(snp, method = "fdr")

counter1 <- 0

for(i in 1:length(snp_bonferroni)) {
  if(i == 1){
    print("After a bonferroni correction for multiple comparisons:")
  }
  if(snp_bonferroni[i] <= alpha) {
    print(c("P-value", i , "was significant"), quote = FALSE)
    counter1 <- counter1 + 1
  }
}

## [1] "After a bonferroni correction for multiple comparisons:"
## [1] P-value      7          was significant
## [1] P-value     10          was significant

counter2 <- 0

for(i in 1:length(snp_fdr)) {
  if(i == 1){
    print("After a false discovery rate correction for multiple comparisons:")
  }
  if(snp_fdr[i] < alpha) {
    print(c("P-value ", i, " was significant."), quote = FALSE)
    counter2 <- counter2 + 1
  }
}

## [1] "After a false discovery rate correction for multiple comparisons:"
## [1] P-value      7          was significant.
## [1] P-value      8          was significant.
## [1] P-value     10          was significant.
```

A total of 2 p-values were significant after a bonferroni correction. And a total of 3 p-values were significant after a false discovery rate correction.