## Homework 6

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2022-08-08

```
1a)
x = rnorm(1000, mean = 0, sd = 1)
for (i in 1:100)
  x[i] = x[i] + 1
pvalue = 2* pnorm(-abs(x))
1b)
discovery = pvalue < 0.05
type2Error = sum(pvalue[1:100] > 0.05)
type1Error = sum(pvalue[101:1000] < 0.05)</pre>
paste0("Number of Type I errors: ", type1Error)
## [1] "Number of Type I errors: 49"
paste0("Number of Type 2 errors: ", type2Error)
## [1] "Number of Type 2 errors: 82"
paste0("False Discovery Proportion: ", type1Error/sum(discovery))
## [1] "False Discovery Proportion: 0.73134328358209"
1c)
BH<-function(p,alpha = 0.05){
    pw<-na.omit(p)</pre>
    n<-length(pw)</pre>
    pw<-sort(pw)</pre>
    comp < -(pw < (1:n)*alpha/n)
    outcome<-sum(comp==TRUE)</pre>
    if(outcome>0){
      last<-max((1:n)[comp==TRUE])</pre>
      pcut<-pw[last]</pre>
      shr<-p*0
      shr[p \le pcut] \le -1
      out<-list(shr,sum(shr>0,na.rm=T),pcut)
      names(out)<-c("Reject", "Total.Rej", "Pcut")</pre>
    }
    else
        shr<-p*0
        out<-list(shr,outcome,0)</pre>
        names(out)<-c("Reject", "Total.Rej", "Pcut")</pre>
```

```
return(out)
}

Id)
bh = BH(pvalue)

# false positive -> reject null when null hypothesis is true (H1 when should be H0)
# false negative -> accept null when null hypothesis is false (H0 when should be H1)

bh_type1 = sum(bh$Reject[101:1000] == 1)
bh_type2 = sum(bh$Reject[1:100] == 0)

paste0("Number of Type I errors: ", bh_type1)

## [1] "Number of Type 2 errors: ", bh_type2)

## [1] "Number of Type 2 errors: 100"

paste0("False Discovery Proportion: ", bh_type1/sum(bh$Reject == 1))
```

1e) The BH method had more type 2 errors than the standard method but less type 1 errors. The FDP for the BH method is also NaN as it had no rejections, but the standard method had an FDP of 73.8%. This indicates that in this case, the standard method is preferable because it has less type 2 errors than the BH method and was able to produce an FDP.

## [1] "False Discovery Proportion: NaN"