# Stats 506 F20, Final Project

## Zhihao Xu, xuzhihao@umich.edu

December 07, 2020

# **Topic**

Performance of Benjamini-Hochberg Adjustment in an atypical situation. Click here to view the Github Repo of this project.

## Introduction

In the multiple hypothesis testing problem, usually we care about the False Discovery Rate(FDR) instead of Type 1 Error. Benjamini-Hochberg procedure is commonly used to control the FDR in multiple hypothesis testing.

#### Benjamini-Hochberg procedure:

Begin by ordering the p-values in ascending order.

$$p_{(1)} \le p_{(2)} \le \dots \le p_{(n)},$$

Fix a significant level  $q \in [0,1]$ . Let  $i_0$  be the largest i for which

$$p_{(i)} \leq \frac{i}{n}q.$$

Reject all  $H_{(i)}$  with  $i \leq i_0$ . This procedure is proved in Benjamini & Yekutieli (2001). If the joint distribution of the statistics (or joint dist. of the p-values) is PRDS(positive regression dependency on each one from a subset) on the set of true nulls  $H_0$ , then the Benjamini-Hochberg procedure BH(q) controls the FDR at level q. However, in practise, we do not always know the precise correlation structure. In Benjamini & Yekutieli (2001), it also introduced a BY-Adjust procedure, which use rejection threshold  $q = q / \sum_{i=1}^{n} \frac{1}{i}$  to control the FDR at level q regardless of correlation structure. However, this procedure is quite conservative. In this project, I want to demostrate the performance of original BH procedure on various correlation structure.

#### Experiment Setting

Consider n i.i.d. samples  $x_t$ , t = 1, ..., n,  $x_t = [x_{t1}, ..., x_{tm}] \in \mathbb{R}^m$ . Suppose  $x_{ti} \sim N(\mu_i, 1)$ . We want to test the null hypothesis  $H_{0,i}: \mu_i = 0$  for i = 1, ..., m. Consider the following setting:

- (a) **i.i.d.**:  $x_{ti}$  for i = 1, ..., m are i.i.d.
- (b) **Positive Correlated**:  $Cov(x_{ti}, x_{tj}) = 0.8$  for  $i \neq j$ .
- (c) **Negative Correlated**:  $Cov(x_{ti}, x_{tj}) = 0.8$  for  $1 \le i < j \le m/2$ ,  $x_{t,i+m/2} = -x_{t,i}$  for  $1 \le i \le m/2$ .

Here we apply the BH-Adjust and BY-Adjust at level q=0.1 by conducting B=1000 simulations with n=200 and m=100 in each setting, and compare the FDR and power of these adjustment procedure. We will try the following cases:

- 1. Global Null:  $\mu_i = 0$
- 2. Sequential True Alternatives:  $\mu_1 = \mu_2 = 0.2, \mu_3 = \mu_4 = 0.4, \mu_5 = \mu_6 = 0.6, \mu_7 = \mu_8 = 0.8, \mu_9 = \mu_{10} = 1,$  and  $\mu_i = 0$  for 10 < i < 50.

Here we test  $H_{0,i}: \mu_i = 0$  at significance level  $\alpha = 0.05$ , compute p-value by

$$p = 2\left[1 - \Phi\left(\left|\frac{\bar{X}_{\cdot,i} - 0}{1/\sqrt{n}}\right|\right)\right]$$

## Simulation Result

1. Global Null:  $\mu_i = 0$ 

Method	Correlation Structure	FDR
ВН	Independent	0.036
BY	Independent	0.013
BH	Positive Correlation	0.029
BY	Positive Correlation	0.005
BH	Negative Correlation	0.030
BY	Negative Correlation	0.004

**2.** Sequential True Alternatives:  $\mu_1 = \mu_2 = 0.2, \mu_3 = \mu_4 = 0.6, \mu_5 = \mu_6 = 1, \text{ and } \mu_i = 0 \text{ for } 6 < i \le 50.$ 

```
result_sig = cbind(adj, col1, sprintf("%5.3f", result_sig[,1]), sprintf("%5.3f", result_sig[,2]))
colnames(result_sig) = c("Method", "Correlation Structure", "FDR", "power")
row.names(result_sig) = NULL
knitr::kable(result_sig, align="c")
```

Method	Correlation Structure	FDR	power
ВН	Independent	0.045	0.813
BY	Independent	0.009	0.752
BH	Positive Correlation	0.032	0.816
BY	Positive Correlation	0.002	0.747
BH	Negative Correlation	0.027	0.844
BY	Negative Correlation	0.004	0.775

## Conclusion & Discussion

Through the above simulation result, we can see that although the negative correlation structure does not satisfy the PRDS assumption, we can also use BH method to control FDR in some cases. BY method can always control FDR successfully but will also leads to conservative rejection. In the above simulation, the FDR got by the BY-method is only 1/10 of our target, which will also cost the decrease in power. Hence, if the correlation structure is unknown, it is also reasonable to use BH method, and we can also use BY-method as a base line method.