Homework 7

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1. Multiple comparisons.

We discussed several methods for multiple comparison adjustment, all of which can be implemented from scratch. In particular, the built-in `p.adjust` function returns "adjusted" p-values, which may not be what you want as an analyst. One way to improve the utility is to create "wrapper" functions around `p.adjust`.

- Implement a Bonferroni-Holm correction function that takes a vector of p-values `p` and a value for `alpha` and returns a logical vector indicating which elements of `p` are statistically significant. Construct this as a "wrapper" around the built-in `p.adjust` function. **(1/2 point)** Create a similar function for FDR. **(1/2 point)**
- Revise the function from part 1 so that you calculate adjusted p-values manually. **(1 point)**
- Revise the function from part 2 so that you calculate adjusted p-values manually. **(1 point)**

Test your function on the following vector of p-values. *NB: be sure that the functions work with unordered inputs!*

```
## Test A Test B Test C Test D Test E Test F Test G Test H Test I Test J
##  0.0025  0.0050  0.0075  0.0100  0.0125  0.0150  0.0175  0.0200  0.0225  0.0250
```

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2. Analysis of variance.

There is a set of CSF biomarker data available here (https://jlucasmckay.bmi.emory.edu/global/bmi510/csf.csv). Implement an ANOVA on the variable `Ab42` using the grouping variable `Group`. You should perform a "complete case" analysis; e.g., delete any observations with missing values for `Ab42`.

- Calculate SS_{GROUP}. **(1 point)**
- Calculate SS_{TOT}. **(1 point)**
- Calculate SS_{ERROR}. **(1 point)**
- Calculate MS_{GROUP}. **(1 point)**
- Calculate MS_{ERROR}. **(1 point)**
- Calculate the F-statistic. **(1 point)**
- Calculate the p-value **(1/2 point)** and check it against the result of `anova`. **(1/2 point)**