

BB512/BB612 - Homework II

Apr 7, 2022

Use the `montpick` eset to perform the required analyses:

```
con <- url("http://bowtie-bio.sourceforge.net/recount/ExpressionSets/montpick_eset.RData")
load(file = con)
close(con)

pdata <- pData(montpick.eset)
edata <- exprs(montpick.eset)
fdata <- fData(montpick.eset)
```

1. [20 pt] Transform, remove lowly expressed genes, and normalize the expression data
2. [30 pt] Perform t-tests to compare the expressions of all genes between the two populations (“CEU” and “YRI”). Obtain the p-values. Adjust the p-values. How many genes have $FDR < 0.1$?
3. [50 pt] Perform permutation tests to compare the expressions of all genes between the two populations (“CEU” and “YRI”). Obtain the p-values. Adjust the p-values. How many genes have $FDR < 0.1$?