

# Assignment: Process RNA-seq files

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DUE: Friday 7/31 by 9AM

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Using the count files you created for your two different tissues, you'll find the differences between the tissues. Everything should be in/backed up to the same GitHub repository as your processing code.

1. Analyze the RNA-seq. You need to have an `.Rmd` file showing all your code and it must include:
  - PCA
  - differential expression table
  - volcano plot and/or MA plot
  - pathway analysis
2. 10 minute presentation for Friday at 12PM explaining your figures/results. The presentation should include:
  - Any figures you made during the course of the analysis (PCA, volcano plot, MA plot, pathway visualization)
  - Anything interesting you want to mention about the top genes or pathways