

# Intro to Bash, In Class Exercises

## QBS Bootcamp

- 1) RA\_OA\_RNA\_seq.xls. Download the RA\_OA\_RNA\_seq.xls file to your desktop (sent in email last night).
- 2) In your terminal window, print out the contents of the file.
- 3) Use "head" and "tail" to print out the first and last 10 lines of this file.
- 4) How many genes are in this file?
- 5) Create a directory on your desktop called QBS\_Bootcamp\_IntrotoBash. Copy the RA\_OA\_RNA\_seq.xls file from your desktop to the QBS\_Bootcamp\_IntrotoBash directory.
- 6) Rename the RA\_OA\_RNA\_seq.xls file in your QBS\_Bootcamp\_IntrotoBash directory to qbs\_bootcamp\_data.xls.
- 7) Move the RA\_OA\_RNA\_seq.xls on your desktop into your QBS\_Bootcamp\_IntrotoBash directory and remove the qbs\_bootcamp\_data.xls file.
- 8) Write the first and last 20 lines of the RA\_OA\_RNA\_seq.xls file to a file called RA\_OA\_RNA\_seq\_subset.xls.
- 9) Count the number of genes beginning with the letter "A" that appear in this data file.