

QBS 103 Introduction to Bash In Class Exercises

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1. Navigate to our class GitHub page at this address: <https://github.com/kosarekn/QBS103/tree/main>. In the "data" folder you will find a file called RA_OA_RNA_seq.xls. Download this file to your desktop on your local machine.
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_103_IntrotoBash. Copy the RA_OA_RNA_seq.xls from your desktop to the QBS_103_IntrotoBash directory.
6. Rename the RA_OA_RNA_seq.xls file in your QBS_103_IntrotoBash directory to QBS103_data.xls.
7. Move the RA_OA_RNA_seq.xls on your desktop into your QBS_103_IntrotoBash directory and remove the QBS103_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_sub.xls. Hint: You can use to group commands together. Make sure to separate your commands by a ;!
9. Count the number of genes beginning with the letter "A" that appear in this data file.