

Bash Exercises

These exercises should be completed in the terminal with access to the folders created in the previous exercises.

Exercise 1: Your first bash script

Using nano, write an executable shell script (called myfirst.sh) that prints the statement "I am alive".

Hints: echo is what Bash uses to print lines. Remember the shebang line.

Exercise 2: Variables

Define four variables named: NAME1, NAME2, NAME3, and EVENT.

Using echo, print the sentences below in the myfirst.sh script. The variables are not written correctly and are missing the \$ character.

"NAME1, NAME2, and NAME3 are going on a trip. It is going badly because NAME1 and NAME2 are fighting over EVENT. NAME3 has been really quiet because they are the reason EVENT happened, and they don't want NAME1 and NAME2 to know."

Exercise 3: Positional arguments

Create a new script called icecream.sh Using positional arguments and echo, make icecream.sh print out this sentence: "Why do people like X when Y is superior?"

Here X and Y marks where the two positional arguments should be placed.

Exercise 4: Count sequences with variables

Using grep, '>' and '|', count the fasta sequences in MRSA1.fasta in BTG_intro/Bacteria_MRSA_Illumina/. Do this by creating a new script count_fasta.sh using variables.

Exercise 5: Count sequences with positional arguments

Update count_fasta.sh to use positional arguments instead of using variable names.

Advanced exercises

Exercise 6: IF statements

Create a script called greaterthan.sh. Using an *if statement* and positional arguments, see if a number is greater than 60. Hint: Use echo for the command that triggers if TRUE.

Exercise 7: Else statements

Add an *elif statement* to the above *if statement* to see if the variable is precisely 60. Add an *else statement* if the above isn't TRUE.



Extra exercises

Exercise 8:

Create a script called check_fasta.sh. Loop over all fasta files in the BTG_intro/Bacteria_MRSA_Illumina/ directory and print the file names.

Exercise 9:

Make a script called array.sh. Make an array with things that should be on a pizza and print all strings in that array using a for loop.

Exercise 10:

Update check_fasta.sh. Using the word count function from before, loop over all fasta files in the BTG_intro/Bacteria_MRSA_Illumina/ directory. Print the number of sequences and the file name for each file.

Manipulating strings with Bash

Here is a link to a guide for different string manipulations in Bash:

https://tldp.org/LDP/abs/html/string-manipulation.html

This is <u>not</u> a thing you are expected to know. But this might be interesting for those who will work extensively with Bash.