

Tutorial 2 – Bash & Scripting

MICB405 – BIOINFORMATICS – 2021W-T1

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The Unix Philosophy

1. Make each program do one thing well. To do a new job, build a new program rather than complicate old programs.
2. The output of any program should easily become the input for another.

Utilities review

cd (change directory)

ls (list files) (-l) (long)

pwd (print working directory)

cp (copy)

rm (remove) (-r) (-recursive)

mv (move)

cat (concatenate)

echo (print content you provided as argument)

More utilities...

grep (global regular expression print)

less (read text files)

head/tail (print first/)

wc (wordcount) (-l, -w, -m) (-lines, -word, character)

sort (sort lines)

uniq (return unique lines)

chmod (change mode a.k.a. permissions)

mkdir (make directory)

awk command

Less Unix-y than previous commands

- More of a multi-tool for dealing with data files
- Not short for anything – does file processing based on lines & columns
- Follows the format:
 - `awk 'yourFilter { yourAction }' yourFile`
 - `awk 'NR >= 2 { print $0 }' mtcars.tsv`

Special characters

> (redirect)

>> (append)

| (pipe) (not `l`, `l`, or `I`)

; (separate command)

&& (AND) **||** (OR)

***** (wildcard)

In-terminal text editing

nano = easiest to use & sufficient for most purposes

- Example: **nano filename.txt**
- This makes a new file, or edits an existing one of that name

Ctrl + o = overwrite (save)

Ctrl + x = exit

Scripting

Helps repeat repetitive tasks

Scripts the form of a text file that can be “executed” when you need them

Script headers

All script files need a header to indicate how the script file should be run

First line specifies the program that will interpret the rest of the script

`#!/bin/bash`

- Program should interpret following text using Bash
- Other programs = other headers, if run by calling the script directly

Script variables

We can create a variable and assign it a value with

RESULTS_DIR="results/"

- Note that spaces matter when setting Bash variables. Do not use spaces around the equal sign

Variables

To access a variable's value, we use a dollar sign in front of the variable's name.

Suppose we want to create a directory for a sample's alignment data, called <sample>_aln/, where <sample> is replaced by the sample's name.

```
SAMPLE="Individual_2A"
```

```
mkdir "${SAMPLE}_data/"
```

This will create a file with the name "Individual_2A_data"

Command line arguments

```
grep -c "string" yourFile
```

```
bash mySearchScript.bash ./folder/file
```

Arguments added after calling a script are assigned to the default variables \$1, \$2, \$3, and so forth... within the script

for loops

In bioinformatics, most of our data is split across multiple files.

Many processing pipelines need a way to apply the same workflow on each file, taking care to keep track of sample names.

Looping over files with Bash's for loop = simplest way to accomplish this

Three essential parts to creating a pipeline to process a set of files:

1. Selecting which files to apply the commands to
2. Looping over the data and applying the commands
3. Keeping track of the names of any output files created

for loops

```
#!/bin/bash
```

```
for A_FILE in /home/username/*  
do  
    ACTION on $A_FILE  
    ANOTHER ACTION on $A_FILE  
done
```

for looping through directories

Creating **for** loops that loop through an entire directory

```
#!/bin/bash
for FOO in /home/ahauduc_mb20/test_directory/*
do
    head $FOO > ${FOO}.head.and.tail.txt
    tail $FOO >> ${FOO}.head.and.tail.txt
done
```

if statements

Use if you want to perform commands on a subset of files, or only if an action meets certain conditions.

The basic syntax is:

```
if [command is true]  
then  
    DO THIS  
else  
    DO THAT  
fi
```


if statements

```
#!/bin/bash

if cat $1
then
    echo "The file exists!"
else
    echo "The file doesn't exist!"
fi
```

Return codes

0 = Command executed successfully

1+ = Command did not execute successfully

- There can be many different error types denoted by specific numbers

Return codes are invisible

```
#!/bin/bash

if cat $1
then
    echo "The file exists!"
else
    echo "The file doesn't exist!"
fi
```

test statements: `[[statement]]`

Like other programs, **test** exits with either 0 or 1.

Test statements can be included at the beginning of the if program to make producing the right return code easier

test supports numerous helpful comparisons you might need

test summary

String/integer	Description
<code>-z str</code>	String str is null
<code>str1 = str2</code>	str1 and str2 are identical
<code>str1 != str2</code>	str1 and str2 are different
<code>int1 -eq -int2</code>	Integers int1 and int2 are equal
<code>int1 -ne -int2</code>	int1 and int2 are not equal
<code>int1 -lt -int2</code>	int1 is less than int2
<code>int1 -gt -int2</code>	int1 is greater than int2
<code>int1 -le -int2</code>	int1 is less than or equal to int2
<code>int1 -ge -int2</code>	int1 is greater than or equal to int2

test summary for files/directories

File/directory expression	Description
-d dir	dir is a directory
-f file	file is a file
-e file	file exists
-r file	file is readable
-w file	file is writable
-x file	file is executable

if Statements + **test** Statements

Combining test with if statements is simple:

```
#!/bin/bash
if [[ -f some_file.txt ]]
then
    ACTION TO PERFORM
else
    ACTION TO PERFORM
fi
```

- Note the spaces around and within the brackets: these are required.

Putting it all together...

for looping through directories

```
#!/bin/bash
for foo in /home/axel/Documents/data/*
do
    if [[ -f ${foo} ]]
    then
        head ${foo} > ${foo}.head.and.tail.txt
        tail ${foo} >> ${foo}.head.and.tail.txt
    else
        echo "${foo} is not a file to summarize!"
    fi
done
```