

# Tutorial 2 – Bash & Scripting

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MICB405

# Utilities Review

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`cd` (change directory)

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

`pwd` (print working directory)

`cp` (copy)

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

`mv` (move)

`cat` (concatenate)

`echo` (print content you provide as argument)

# More Utilities...

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grep (global regular expression print)

less (less = more)

head/tail (self-explanatory)

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

sort (sort lines)

uniq (unique lines)

chmod (change mode)

mkdir (make directory)

# Advanced Utility

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**awk**

Not short for anything – does file  
processing based on lines & columns

# Special Characters

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> (redirect)

>> (append)

< (redirect, again)

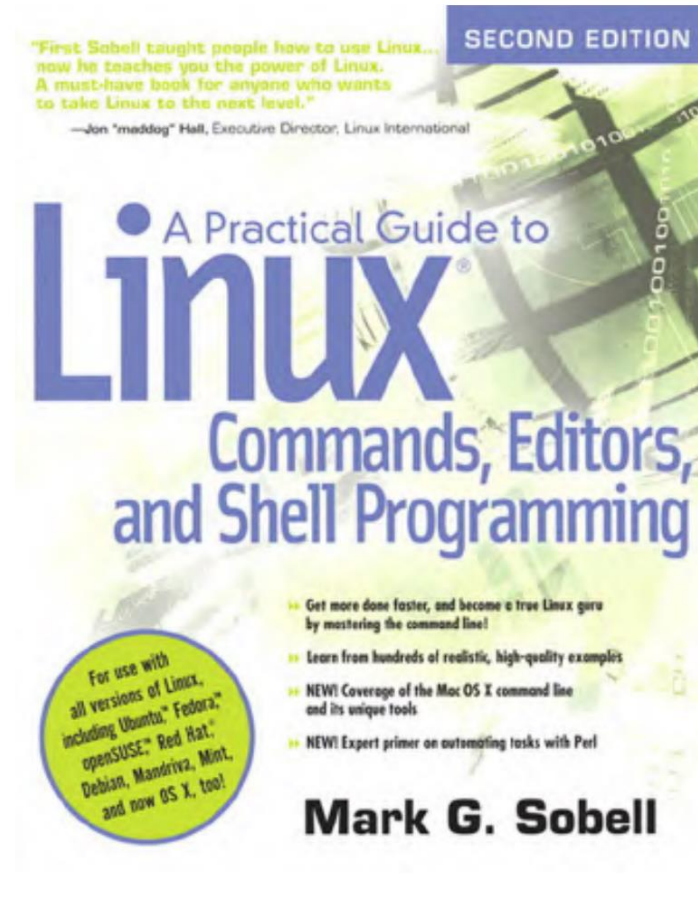
| (pipe) (not 1, 1, or I)

; (separate command)

&& (AND) || (OR)

# Review

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# In-terminal Text Editors

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**nano** = easiest

- **nano filename.txt**

**vim** = more advanced

- Rich keyboard shortcuts but steeper learning curve

These are essential for creating script text files

# Scripting Overview

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Scripts are files containing a series of directions to help automate routine or repetitive tasks

Scripts at the command line take the form of a text file somewhere in the filesystem that can be “executed”



# Headers

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

First line (“shebang”):

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

- Program should interpret following text using Bash
- Other programs = other headers

# Variables

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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

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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"

# Commandline Arguments

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Commandline arguments are assigned to the value \$1, \$2, \$3, etc...

Variables created in your Bash script will only be available for the duration of the Bash process running that script.

# Demonstration

# **if** Statements

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Bash supports the standard if conditional statement.

The basic syntax is:

```
if [commands]
then
    COMMANDS
else
    DIFFERENT COMMANDS
fi
```

# if Statement Example

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```
#!/bin/bash

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

# Return codes

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`0` = Command executed successfully

`1 or more` = Command did not execute successfully



# if Statement Example

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```
#!/bin/bash

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

# **test** statements

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

Test statements can be included at the beginning of the if program using

However **test**'s exit status indicates the return value of the test specified through its arguments, rather than exit success or error.

**test** supports numerous standard comparison operators.

# 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

# test Example

---

```
axelh@AXEL-DESKTOP:/mnt/c/Users/axelh/Linux$ ls -lth
total 0
-rwxrwxrwx 1 axelh axelh  0 Sep  8 21:26 this_is_a_file
-rwxrwxrwx 1 axelh axelh 106 Sep  8 17:20 test2
-rwxrwxrwx 1 axelh axelh 176 Sep  8 17:13 test_script.bash
drwxrwxrwx 1 axelh axelh 512 Aug 24 17:08 test
drwxrwxrwx 1 axelh axelh 512 Aug 24 14:45 awk.practice
drwxrwxrwx 1 axelh axelh 512 Aug 24 14:45 micb405
axelh@AXEL-DESKTOP:/mnt/c/Users/axelh/Linux$ test -f this_is_a_file; echo $?
0
axelh@AXEL-DESKTOP:/mnt/c/Users/axelh/Linux$ test -d this_is_a_file; echo $?
1
axelh@AXEL-DESKTOP:/mnt/c/Users/axelh/Linux$ test -f awk.practice; echo $?
1
axelh@AXEL-DESKTOP:/mnt/c/Users/axelh/Linux$ test -d awk.practice; echo $?
0
axelh@AXEL-DESKTOP:/mnt/c/Users/axelh/Linux$ [ -d awk.practice ]; echo $?
0
axelh@AXEL-DESKTOP:/mnt/c/Users/axelh/Linux$
```

Putting it all together...

# **if** Statements + **test** Statements

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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.

# for loops

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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

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```
#!/bin/bash
for (variable) in (directory/array/etc.)
do
    ACTION TO PERFORM
    ANOTHER ACTION TO PERFORM
done
```

# **for** looping through directories

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

**Summarize\_files.bash**

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

```
for foo in /home/axelh/Documents/data/*  
do
```

```
    head ${foo} > ${foo}.head.and.tail.txt
```

```
    tail ${foo} >> ${foo}.head.and.tail.txt
```

```
done
```

# for looping through directories

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```
#!/bin/bash
for foo in /home/axelh/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
```

# Breakout Groups