# Instructions to BASH Shell Scripts

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### BASH Shell Script

- Why use BASH script?
  - Wrap Linux commands and tools together
  - Write a pipeline
  - Submit jobs
- Create a BASH script:
  - Use a text editor such as vi to create a text file containing Linux commands
  - First line contains the magic "shbang" sequence: #!/bin/bash
  - Comments start with "#" except for the first "shbang" line
  - Use "\" at the end of a line to break one command into multiple lines
  - Make the script executable: chmod 755
    - 7 is the combination of permissions 4+2+1 (read, write, and execute), 5 is 4+0+1(read, no write, and execute)
    - Order of permission for: user, group, others
- Run a BASH script: ./example\_bash.sh or bash -x example\_bash.sh

## BASH Shell Script

- Cons: have very little built-in math (consider using other Tools: R, Python)
- Back quotes ``and \$() mean executing the command inside the quotes or parenthesis first and then assign the output as values for the variable on the left-hand-side
  - some\_variable=`some Unix command`
  - some\_variable=\$(some Unix command)
- Each source code line is printed prior to its execution when specify option -x
  - Either in the header (first line, i.e., shebang, in the script): #!/bin/bash -x
  - Or on the command line: bash -x example bash.sh

# Common Syntax in BASH Script

• if/else (Here [] is part of the command, and the space is important around []) if [ condition ] ; then commands fi if [condition]; then commands else commands fi if [condition]; then commands elif [condition]; then commands

## Logic Syntax

- Numeric comparison: -eq, -ne, -gt, -ge, -lt, -le
- String comparison: =, !=, <, >, -z, -n
- Directory exist: if [ -d \$dir ]; then ...
- File exist: if [ -f \$myfile ]; then ...
- File exist and nonempty: if [ -s \$myfile ]; then ...
- Executable file: if [ -x \$myfile ]; then ...
- || and && operands inside if [condition] (i.e. between round parentheses) are logical operands (or/and)
- || and && operands outside if [ condition ] mean then/else ([\$a-eq 1] || [\$b-eq 2]) && echo "ok" || echo "nok"
- Practically the statement says: if (a=1 or b=2) then; print "ok"; else; print "nok";

# Logic Syntax

```
    Loop:

            for var in bash-list; do commands
            done

    while [condition]; do commands
    done
```

#### AWK: Useful Tool in BASH

- The word awk is derived from the names of its inventors!!!
- awk is actually Aho Weinberger and Kernighan.
- From the original awk paper published by Bell Labs, awk is
  - "Awk is a programming language designed to make many common information retrieval and text manipulation tasks easy to state and to perform."
- Simply put, awk is a programming language designed to search for, match patterns, and perform actions on files.

# AWK: Useful Tool in BASH for handling text files

awk options program file

- Options:
  - To specify a file separator: -F fs
  - To declare a variable: -v var=value
- Program:
  - To define an awk script, use braces surrounded by single quotation marks like this:

```
awk '{print "Welcome to awk command tutorial "}'
```

- pattern { action }
  - awk -F"\t" 'NR==1{print \$0}' file
  - BEGIN {...} pattern {...} pattern{...}END{...}
  - Commands in {...} are separated by semicolons ";"

#### **AWK**

- Built-in Variables: \$0, \$1, NR, FNR, NF
- Built-in Math Functions: sin(x), cos(x), sqrt(x), exp(x), log(x)
- C operators like: ++, --, +=, -=
- More information:
  - https://likegeeks.com/awk-command/
  - https://www.ibm.com/developerworks/library/l-awk1/

# Example 1: run FastQC on a single file

- Step 1: Create a folder to hold all files related to the task/project
  - Recommended folder structure
    - \${HOME}/project
    - \${HOME}/project/scripts
    - \${HOME}/project/data
    - \${HOME}/project/refs
    - \${HOME}/project/logs
    - \${HOME}/project/output
- Step 2: Create the job submission script in \${HOME}/project/scripts
  - Recommend to create one script per step, e.g. FastQC, mapping, calling variants, etc.
  - Give a descriptive name to your scripts e.g. step01\_fastqc.sh

# Example bash script: run FastQC on a single file

```
#!/bin/sh
     # This script requires a single parameter when
     # called - the portion of the file name
     # preceding .fastq.gz or .bam. This is usually
     # the <sample name>
6.
     # The output directory (OUTDIR) needs to exist
     module load FastQC
     PRJDIR="${HOME}/project"
     DATADIR="${PRJDIR}/data"
    OUTDIR="${PRJDIR}/output/FastQC"
12. if [ -e /bin/mktemp ]; then
           TMPDIR=`/bin/mktemp -d /scratch/XXXXXX`
13.
     elif [ -e /usr/bin/mktemp ]; then
15.
           TMPDIR=`/usr/bin/mktemp -d /scratch/XXXXXX`
16. else
17.
           echo "Error. Cannot find program to create tmp directory"
18.
           exit
19. fi
```

```
18. cp ${DATADIR}/$1.fastq.gz ${TMPDIR}

19. fastqc -o ${TMPDIR} --no-extract ${TMPDIR}/$1.fastq.gz

20. /bin/rm ${TMPDIR}/$1.fastq.gz

21. rsync -av ${TMPDIR}/ ${OUTDIR}/$1

22. /bin/rm -fr ${TMPDIR}

23. module unload FastQC
```

#### Line numbers are not part of the script!

- Line 8 load the FastQC module
- Lines 9-11 defines some variables to use in the script
- Lines 12-19 create the unique folder in /scratch
- Line 18 copies data to the unique folder
- Line 19 runs the fastqc program
- Line 20 deletes the data copied in line 18
- Line 21 copies results back to the project folder
- Line 22 removes the unique scratch folder
- Line 23 unload the FastQC module