"IBS 574 - Computational Biology & Bioinformatics" Spring 2018, Tuesday (02/01), 2.00-4.00PM

# Linux shell & shell scripting - II

Ashok R. Dinasarapu Ph.D Scientist-Bioinformatics, Dept. of Human Genetics Emory University, Atlanta

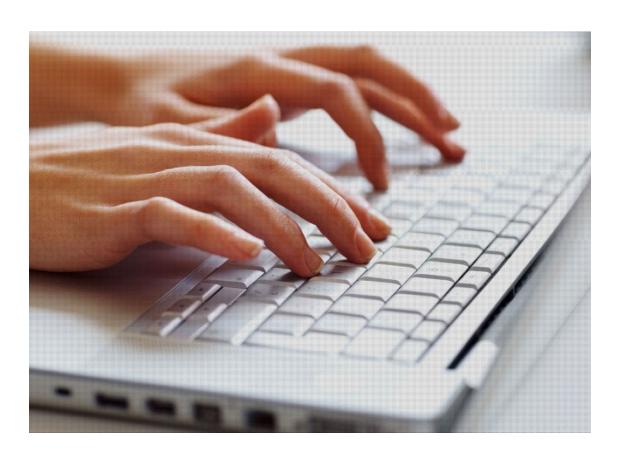
### What is Shell scripting?

- A script is a collection of commands stored in a file.
- Shell is a command-line interpreter.
- To execute a shell script, ex. "hello.sh"
   Usage:

```
./hello.sh
../hello.sh
/home/user_name/script/hello.sh
bash hello.sh (or sh hello.sh)
```

### Easiest way to do this is ...

# Start typing!



### Connecting via SSH to your server

ssh <u>user\_name@blnx1.emory.edu</u>

Alternatively, <a href="https://blnx1.emory.edu:22443/">https://blnx1.emory.edu:22443/</a>

user\_name@blnx1:~\$

~ means your home dir (/home/user\_name)

SSH allows you to connect to your server securely and perform Linux command-line operations.

# "mkdir" & directory structure

 Create directories from your home directory (i.e /home/user\_name)

```
Usage: mkdir -p project/{data,script,out,log}

project/data

project/script

project/out

project/log
```

Usage: cd project/script

Choose a text editor: emacs, Vim

Usage: vi hello.sh

**INSERT** mode:

press keys like i OR a & start typing.

"i" will let you insert text just before the cursor.
"I" inserts text at the beginning of the current line.
"a" will let you insert text just after the cursor, and
"A" will let you type at the end of the current line.

Type the following text:

```
#!/bin/sh

# My first script

echo "Hello World!"
```

"#!/bin/sh" a special clue given to the shell indicating what program is used to interpret the script.

Type the following text:

#!/bin/sh

# My first script

echo "Hello World!"

#!/bin/bash
#!/usr/bin/perl
#!/usr/bin/Rscript
#!/usr/bin/env python

View symbolic link using Is -Ia /bin/sh

"#!/bin/sh" a special clue given to the shell indicating what program is used to interpret the script.

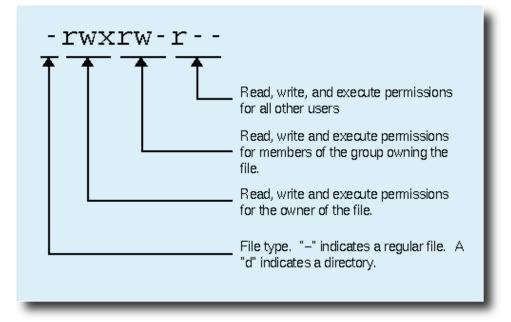
SAVE mode: press esc key AND

- :q! for not to save OR
- :x to save all typed content.

# "chmod"

- Change the permissions of files
  - Read (r), write (w), and execute (x)
  - 3 types of users (user, group & other)

Usage: ls -l



# "make file executable"

To make it executable

Usage: chmod +rwxr-xr-x hello.sh

Usage: chmod +x hello.sh

Usage: ./hello.sh

To make it un-executable

Usage: chmod -x hello.sh

# "make file executable"

To make it executable +755

Usage: chmod + rwxr-xr-x hello.sh

Usage: chmod +x hello.sh

Usage: ./hello.sh

To make it un-executable

Usage: chmod -x hello.sh

### Variables in Linux/Shell

Usage: vi hello.sh

```
#!/bin/bash
# My first script
i=22
echo "Hello, I am " $i
# echo "Hello, I am $i"
```

### Variables in Linux/Shell

Usage: vi hello.sh

```
#!/bin/bash
# My first script
i=22
j="Hello, I am "
echo $j $i
```

### Variables in Linux/Shell

Usage: vi hello.sh

```
#!/bin/bash
# My first script
i=22
j=${i}0
echo $j
```

the {} in \${} are useful if you want to expand the variable

```
Usage: ./hello.sh
```

## **Conditions** in Linux/Shell

Usage: vi hello.sh

```
#!/bin/bash
# My first script

PASS="test1234"

if [ $PASS == "test1234" ]; then
    echo "Correct pass word!!"
fi
```

Usage: ./hello.sh

Remember that the spacing is very important in the if statement.

## **Conditions** in Linux/Shell

Usage: vi hello.sh

```
#!/bin/bash
# My first script
PASS="test123"
if [$PASS=="test1234"]; then
   echo "Correct pass word!!"
else
   echo "enter correct pass word!!"
```

# "for" loop in Linux/Shell

Usage: vi hello.sh

```
#!/bin/bash
# My first script

for i in {1..10}; do
    echo $i
    # echo ${i}a
done
```

# "Array" in Linux/Shell

Usage: vi hello.sh

```
#!/bin/bash
arr=('A' 'B' 'C' 'D' 'E')
for i in {0..4}; do
    echo $i
    echo ${arr[$i]}
done
```

# "for" loop in Linux/Shell

Usage: vi hello.sh

```
#!/bin/sh
# My first script
for i in 1 2 3 x y z
do
     echo $i
done
```

loop indices doesn't have to be just numbers!!!

```
{1..3} x y z
Use bash
```

Usage: ./hello.sh

# "while" loop in Linux/Shell

Usage: vi hello.sh

```
#!/bin/bash
# My first script
i=0
while [ $i -le 5 ]; do
   # echo "before $i"
   i=$(($i+1))
   echo "after $i"
done
```

## Functions in Linux/Shell

Usage: vi hello.sh

```
#!/bin/bash
# function definition
add_user()
   USER=$1
   PASS=$2
   echo "Passwd $PASS created for $USER on $(date)"
# function call
echo $(add_user bob letmein)
```

# Functions in Linux/Shell

Usage: vi hello.sh

```
#!/bin/bash
# function definition
add_user()
   # USER=$1
   # PASS=$2
   echo "Passwd $1 created for $2 on $3"
# function call
echo $(add_user bob letmein "$(date)")
```

### download a fastq file

Usage: cd project/data

#### wget

https://github.com/CGATOxford/UMI-tools/releases/download/v0.2.3/example.fastq.gz

View

Usage: zcat example.fastq.gz|head

Check file size

Usage: Is -Ih example.fastq.gz

Count number of sequences in a fastq file

Usage: grep -c "^>" example.fastq.gz

## "Calculate the length of reads"

Create the following executable file at project/script

Usage: vi fastq.sh

```
#!/bin/bash
# cd project/log (to run this script from log directory)
zcat ../data/example.fastq.gz | \
awk '{if(NR%4==2) print length($1)}' > ../out/length.txt
```

Usage: ../script/fastq.sh

### "Plot - Histogram"

Create the following executable file at project/script

Usage: vi hist.R

```
#!/usr/bin/Rscript
# cd project/log (to run this script from log dir)
t.dat <- read.table('../out/length.txt')
jpeg('../out/rplot.jpg')
hist(t.dat[,1])
dev.off()</pre>
```

26

Usage: ../script/hist.R

## "Calculate the length of reads"

Create the following executable file at project/script

Usage: vi fastq.sh

```
#!/bin/bash
# cd project/log (to run this script from log directory)
zcat ../data/example.fastq.gz | \
awk '{if(NR%4==2) print length($1)}' > ../out/length.txt
# include R script and run
../script/hist.R
```

Usage: ../script/fastq.sh

## "Calculate the length of reads"

Create the following executable file at project/script

Usage: vi fastq.sh

```
#!/bin/bash
# cd project/log (to run this script from log directory)
zcat ../data/example.fastq.gz | \
awk '{if(NR%4==2) print length($1)}' > ../out/length.txt
# include R script and run
../script/hist.R
```

Usage: ../script/fastq.sh 2>error.log

Redirect error output to a file

# Open/View Image

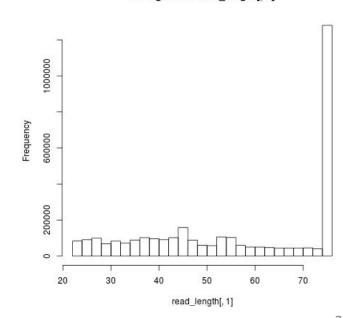
Login as interactive mode

Usage: ssh -Y user\_name@blnx1.emory.edu

Usage: xdg-open rplot.jpg

- -X Enables X11 forwarding
- -Y Enables trusted X11 forwarding

X11 is the X Window System



Histogram of read length[, 1]

### **AWK**

 AWK is an interpreted programming language & designed for text processing.

The word "AWK" is derived from the initials of the language's three developers: A. Aho, B. W. Kernighan and P. Weinberger.

- Following are the variants of AWK
  - AWK the (very old) original from AT&T
  - NAWK A newer, improved version from AT&T
  - GAWK It is GNU AWK. The Free Software foundation's version

### Basic Structure of AWK

### pattern { action }

- The pattern specifies when the action is performed.
- By default, AWK execute commands on every line.
- AWK reads a line from the input stream (file, pipe, or STDIN)
- This process repeats until the file reaches its end.

### Basic Structure of AWK

```
pattern { action } __
```

 Two other important patterns are specified by the keywords "BEGIN" and "END"

```
BEGIN { print "START" }
pattern { print }
END { print "STOP" }
```

- **BEGIN block** executes only once. This is good place to initialize variables.
- The body block applies AWK commands on every input line.
- The END block executes at the end of the program.

### File processing/Printing records

Choose a text editor: emacs, Vim

### Usage:

vi marks.txt

```
1 Amit Physics 80
2 Ralf Maths 90
3 Shyam Biology 87
4 Kedar English 85
5 Ashok History 89
```

```
awk '{print}' < marks.txt</pre>
```

awk 'BEGIN{printf "SNo\tName\tSub\tMarks\n"}{print}' < marks.txt

### Printing Fields (Columns)

### Choose a text editor: emacs, Vim

### Usage:

vi marks.txt

```
1 Amit Physics 80
2 Ralf Maths 90
3 Shyam Biology 87
4 Kedar English 85
5 Ashok History 89
```

```
awk '{print}' < marks.txt
awk '{print $0}' < marks.txt
awk '{print $1,$2,$3,$4}' < marks.txt (space)
awk '{print $1"\t"$2"\t"$3"\t"$4}' < marks.txt (tab)</pre>
```

### Printing Columns by Pattern

### Choose a text editor: emacs, Vim

### Usage:

vi marks.txt

```
1 Amit Physics 80
2 Ralf Maths 90
3 Shyam Biology 87
4 Kedar English 85
5 Ashok History 89
```

```
awk '/E/ {print}' < marks.txt
awk '/E/' < marks.txt
awk '/A/ {print $2"\t"$4}' < marks.txt (tab)</pre>
```

### Count by Pattern match

### Choose a text editor: emacs, Vim

### Usage:

vi marks.txt

```
awk
'BEGIN{i=0}
/A/ {i+=1}
END{print i}
' < marks.txt
```

```
1 Amit Physics 80
2 Ralf Maths 90
3 Shyam Biology 87
4 Kedar English 85
5 Ashok History 89
```

awk 'BEGIN{i=0} /A/ {i+=1} END{print i}' < marks.txt

# Count by Pattern match

#### Choose a text editor: emacs, Vim

#### Usage:

vi marks.txt

```
awk \
'BEGIN{i=0} \
/A/ {i+=1} \
END{print i} \
' < marks.txt
```

```
1 Amit Physics 80
2 Ralf Maths 90
3 Shyam Biology 87
4 Kedar English 85
5 Ashok History 89
```

awk is one-liner

awk 'BEGIN{i=0} /A/ {i+=1} END{print i}' < marks.txt

# Count by Pattern match

#### Choose a text editor: emacs, Vim

## Usage:

vi marks.txt

```
#!/bin/bash
awk \
'BEGIN{i=0} \
/A/ {i+=1} \
END{print i} \
' < marks.txt</pre>
```

```
1 Amit Physics 80
2 Ralf Maths 90
3 Shyam Biology 87
4 Kedar English 85
5 Ashok History 89
```

./marks.sh

# Count by Pattern match

#### Choose a text editor: emacs, Vim

## Usage:

vi marks.txt

```
#!/usr/bin/awk -f
BEGIN{i=0} \
/A/ {i+=1} \
END{print i}
```

```
1 Amit Physics 80
2 Ralf Maths 90
3 Shyam Biology 87
4 Kedar English 85
5 Ashok History 89
```

awk -f marks.awk < marks.txt

#### env

```
XDG_SESSION_ID=38
TERM=xterm-256color
SHELL=/bin/bash
SSH_CLIENT=10.110.52.30 28952 22
SSH_TTY=/dev/pts/8
USER=adinasarapu
```

. . .

awk 'BEGIN {print ENVIRON["USER"]} '
awk 'BEGIN {print ENVIRON["SHELL"]} '
awk 'BEGIN {print ENVIRON["HOSTNAME"]}'

awk 'END { print FILENAME }' marks.txt
(Please note that FILENAME is undefined in the BEGIN block)

FS, OFS, RS, ORS, NR and NF

FS: Input Field Separator (default is space)

**OFS**: Output Field Separator (default is space)

```
env | awk 'BEGIN{FS="=";}{print $1}'
env | awk 'BEGIN{FS="="; OFS=":"}{print $1,$2}'
```

FS, OFS, RS, ORS, NR and NF

**FS**: Input Field Separator (default is space)

**OFS**: Output Field Separator (default is space)

```
awk '{print $1,$2,$3,$4}' < marks.txt (space) 
awk '{print $1"\t"$2"\t"$3"\t"$4}' < marks.txt (tab) 
awk 'BEGIN{FS="\t"; OFS="\t"}{print $1,$2,$3,$4}' < marks.txt
```

FS, OFS, RS, ORS, NR and NF

FS: Input Field Separator (default is space)

**OFS**: Output Field Separator (default is space)

```
awk '{print $1,$2,$3,$4}' < marks.txt (space) 
awk '{print $1"\t"$2"\t"$3"\t"$4}' < marks.txt (tab) 
awk 'BEGIN{FS="\t"; OFS="\t"}{print $1,$2,$3,$4}' < marks.txt
```

awk - $F'\t'$  'BEGIN{OFS="\t"}{print \$1,\$2,\$3,\$4}' < marks.txt

FS, OFS, RS, ORS, NR and NF

RS: Input Record Separator (default is Newline)

**ORS**: Output Record Separator (default is Newline)

```
awk '{print $1,$2,$3,$4}' < marks.txt (space) awk '{print $1"\t"$2"\t"$3"\t"$4}' < marks.txt (tab) awk 'BEGIN{FS="\t"} (print $2,$4}' < marks.txt
```

awk 'BEGIN{OFS=":"; ORS=";"}{print \$2,\$4} END{print "\n"}' < marks.txt

FS, OFS, RS, ORS, NR and NF

NR: Record number

NF: Number of Fields in a Record

```
cat marks.txt | wc -l (Number of lines/rows) cat marks.txt | wc -w (Number of words)
```

```
cat marks.txt | awk '{print NR,"->",NF} '
cat marks.txt | awk 'NR<4' (get first 3 records)
cat marks.txt | awk '{print NR}' | tail -1 (number of records)
cat marks.txt | awk '{ total = total + NF } END { print total }'
```

02/02/17 45

 AWK provides conditional statements to control the flow of a program

#### if or if else

```
#!/bin/bash
awk 'BEGIN {
  num =10;
  if (num % 2 == 0)
    printf "%d is even number.\n", num;
  else
    printf "%d is odd number.\n", num
}'
```

 AWK provides conditional statements to control the flow of a program

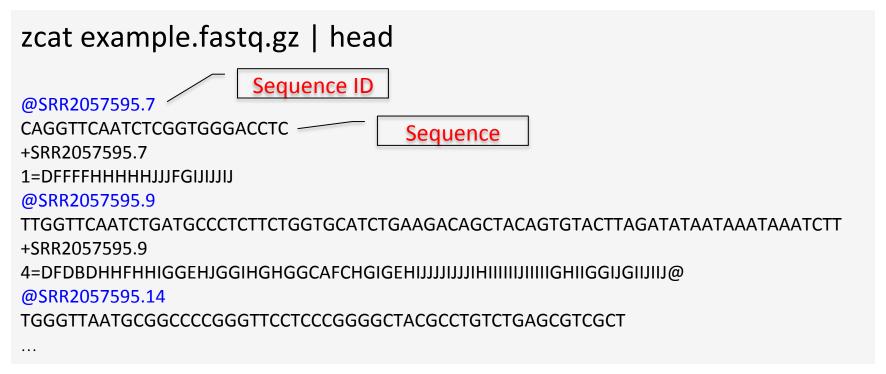
#### for loop

in is used while accessing
array elements

```
#!/bin/bash
awk 'BEGIN {
    arr[0] = 11;
    arr[1] = 22;
    arr[2] = 33;
    for(i in arr) printf "%d is a number.\n", arr[i]
}'
```

awk 'BEGIN { arr[0]=11; arr[1]=22; for(i in arr) printf "%d is a number.\n", arr[i] }'

A FASTQ file normally uses four lines per sequence



Line 1 begins with a '@' character and is followed by a sequence identifier Line 2 is the raw sequence letters

Line 3 begins with a '+' character and is *optionally* followed by the same sequence identifier Line 4 encodes the quality values for the sequence in Line 2

A FASTQ file normally uses four lines per sequence

```
zcat example.fastq.gz | head
                   Sequence ID
@SRR2057595.7
CAGGTTCAATCTCGGTGGGACCTC
                                Sequence
+SRR2057595.7
1=DFFFFHHHHHJJJFGIJIJJIJ
@SRR2057595.9
+SRR2057595.9
4=DFDBDHHFHHIGGEHJGGIHGHGGCAFCHGIGEHJJJJJJJJJHIIIIIJJIIIIIGHIIGGIJGIJJIJJ@
@SRR2057595.14
TGGGTTAATGCGGCCCCGGGTTCCTCCCGGGGCTACGCCTGTCTGAGCGTCGCT
zcat example.fastq.gz | awk '{if(NR%4==2) print}' | head -20
zcat example.fastq.gz | awk '{if(NR%4==2) print $1}' | head -20
zcat example.fastq.gz | awk '{if(NR%4==2) {print substr($0,1,10)}}' | head -20
zcat example.fastq.gz | awk 'END{print NR/4}'
```

02/02/17 49

#### # Separate (filter) FASTQ reads based on their length

```
#!/bin/bash
zcat example.fastq.gz | \
    awk 'NR%4 == 1 {ID=$0}
        NR%4==2 {SEQ=$0}
        NR%4==3 {PLUS=$0}
        NR\%4==0 \{QUAL=\$0\}
            seqlen=length(SEQ)
            qualen=length(QUAL)
            if(seqlen==qualen&&seqlen>=75)
            print ID"\n"SEQ"\n"PLUS"\n"QUAL | \
            "gzip > filtered.fastq.gz"
```

#### # Separate (filter) FASTQ reads based on their length

```
#!/bin/bash
                                                    echo $((1%4)) 1
zcat example.fastq.gz | \
                                                    echo $((2%4)) 2
    awk 'NR%4 == 1 {ID=$0}
                                                    echo $((3%4)) 3
        NR%4==2 {SEQ=$0}
                                                    echo $((4%4)) 0
        NR%4==3 {PLUS=$0}
                                                    echo $((5%4)) 1
        NR\%4==0 \{QUAL=\$0\}
                                                    echo $((6%4)) 2
                                                    echo $((7%4)) 3
                                                    echo $((8%4)) 0
            seqlen=length(SEQ)
             qualen=length(QUAL)
             if(seqlen==qualen&&seqlen>=75)
            print ID"\n"SEQ"\n"PLUS"\n"QUAL | \
             "gzip > filtered.fastq.gz"
```

# Practice Makes Perfect



# **String Comparison Operators**

Operator	Description	Example
= or ==	Is Equal To	if [ "\$1" == "\$2" ]
!=	Is Not Equal To	if [ "\$1" != "\$2" ]
>	Is Greater Than (ASCII comparison)	if [ "\$1" > "\$2" ]
>=	Is Greater Than Or Equal To	if [ "\$1" >= "\$2" ]
<	Is Less Than	if [ "\$1" < "\$2" ]
<=	Is Less Than Or Equal To	if [ "\$1" <= "\$2" ]
-n	Is Not Null	if [ -n "\$1" ]
-Z	Is Null (Zero Length String)	if [ -z "\$1"]

# **Integer Comparison Operators**

Operator	Description	Example
-eq	Is Equal To	if [ \$1 -eq 200 ]
-ne	Is Not Equal To	if [ \$1 -ne 1 ]
-gt	Is Greater Than	if [ \$1 -gt 15 ]
-ge	Is Greater Than Or Equal To	if [ \$1 -ge 10 ]
-lt	Is Less Than	if [ \$1 -lt 5 ]
-le	Is Less Than Or Equal To	if [ \$1 -le 0 ]
==	Is Equal To	if (( \$1 == \$2 ))
!=	Is Not Equal To	if (( \$1 != \$2 ))
<	Is Less Than	if (( \$1 < \$2 ))
<=	Is Less Than Or Equal To	if (( \$1 <= \$2 ))
>	Is Greater Than	if (( \$1 > \$2 ))
>=	Is Greater Than Or Equal To	if (( \$1 >= \$2 ))