**HomeWork 4.2** Student: Shang-Fu Chen

**::ERROR #1: Remove a directory in bash::**

$ rm grch38

rm: grch38: is a directory

**Correction: Add flag “-r” (recursive)**

$ rm -r grch38

**REFERENCE:** [**https://goo.gl/kJfapB**](https://goo.gl/kJfapB)

**::ERROR #2: Send variables to sed::**

$ A=\_genotype.vcf

$ cat test.log

/rpt\_1/sample\_001\_genotype.vcf

/rpt\_1/sample\_002\_genotype.vcf

/rpt\_2/sample\_003\_genotype.vcf

$ cat test.log | sed 's/${A}//g’

/rpt\_1/sample\_001\_genotype.vcf

/rpt\_1/sample\_002\_genotype.vcf

/rpt\_1/sample\_003\_genotype.vcf

**Correction: Use double quote instead of single quote.**

$ $ cat test.log | sed "s/${A}//g"

/rpt\_1/sample\_001

/rpt\_1/sample\_002

/rpt\_1/sample\_003

**REFERENCE:** [**https://goo.gl/UtasY6**](https://goo.gl/UtasY6)

**::ERROR #3: Send variables containing slash to sed::**

$ B=/rpt\_1/

$ cat test.log | sed "s/${B}//g"

sed: -e expression #1, char 10: unknown option to `s'

**Correction: Use alternative delimitator.**

$ cat test.log | sed "s~${B}~~g"

sample\_001\_genotype.vcf

sample\_002\_genotype.vcf

sample\_003\_genotype.vcf

**REFERENCE:** [**https://goo.gl/i7KRbd**](https://goo.gl/i7KRbd)

**::ERROR #4: basic grep syntax::**

$ grep test.vcf chr9

grep: chr9: No such file or directory

**Correction: Follow the command line as *“grep [options] [pattern] [input\_file\_names]”***

$ grep chr9 test.vcf

chr9 5423103 9-5423103 A G . . rs10491647 GT 1/1

chr9 5318770 9-5318770 C A . . rs10491649 GT ./.

**REFERENCE:** [**https://goo.gl/6ffB2h**](https://goo.gl/6ffB2h)

**::ERROR #5: grep for special characters::**

$ grep ".\/." test.vcf

chr9 5423103 9-5423103 A G . . rs10491647 GT 1/1

chr9 5318770 9-5318770 C A . . rs10491649 GT ./.

**Correction: Add flag “-F” instead of backslash**

$ grep -F "./." test.vcf

chr9 5318770 9-5318770 C A . . rs10491649 GT ./.

**REFERENCE:** [**https://goo.gl/AFMaAy**](https://goo.gl/AFMaAy)

**::ERROR #6: Sequence of numbers in bash::**

$ echo {5:20}

{5:20}

**Correction: Use seq or {n..m}**

$ echo $(seq 5 20)

5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20

$ echo {5..20}

5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20

**REFERENCE:** [**https://goo.gl/3gyKxf**](https://goo.gl/3gyKxf)

**::ERROR #7: Use seq in echo::**

$ echo (seq 20)

-bash: syntax error near unexpected token `seq'

**Correction: Add dollar sign to specify the function**

$ echo $(seq 20)

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20

**::ERROR #8: For-loop structure::**

$ for i in {5..20} do

echo ${i}

done

-bash: syntax error near unexpected token `echo'

**Correction: Add semicolon.**

$ for i in {5..20}; do

echo ${i}

done

5

6

7

8

9

10

11

12

13

14

15

16

17

18

19

20

**REFERENCE:** [**https://goo.gl/Uy9UFQ**](https://goo.gl/Uy9UFQ)

**::ERROR #9: integer comparison in if-loop operator::**

$A=0

$B=1

$ if ["$A"<"$B"]; then echo "a<b"; else echo "a>=b"; fi

-bash: 1]: No such file or directory

a>=b

**Correction: Use comparison operator**

$ if ["$A" -lt "$B"]; then echo "a<b"; else echo "a>=b"; fi

-bash: [0: command not found

a>=b

**Correction: The space is necessary**

$ if [ "$A" -lt "$B" ]; then echo "a<b"; else echo "a>=b"; fi

a<b

**REFERENCE:** [**https://goo.gl/PVBWTo**](https://goo.gl/PVBWTo)

**::ERROR #10: off-by-one error::**

$ for ((RPT = 0; RPT < 10; RPT++)); do echo $RPT; done

0

1

2

3

4

5

6

7

8

9

**Correction: Check the end condition of the loop.**

$ for ((RPT = 1; RPT <= 10; RPT++)); do echo $RPT; done

1

2

3

4

5

6

7

8

9

10

**REFERENCE:** [**https://goo.gl/2oxq5e**](https://goo.gl/2oxq5e)

**::ERROR #11: Cleaner way to create folder structure::**

$ mkdir myProject

$ cd myProject

$ mkdir src

$ mkdir doc

$ cd doc

$ mkdir api

$ mkdir system

$ cd ../

$ mkdir tools

**Correction: Use recursive syntax to create nested directory structure and subfolders**

$ mkdir -p myProject/{src,doc/{api,system},tools}

**REFERENCE:**

[**https://goo.gl/LuWjP7**](https://goo.gl/LuWjP7)

[**https://goo.gl/Vy94UV**](https://goo.gl/Vy94UV)