

Lab 10 Input, Output, Looping and Branching

1. Write a script `five_dirs.bash` that does these tasks:

- make a directory `five`
- make five subdirectories `five/dir1` through `five/dir5` in each subdirectory, make four files, `file1` through `file4`, such that `file1` has one line containing the digit 1, `file2` has two lines, each containing the digit 2, ..., and `file4` has four lines, each containing the digit 4

Source: Shell scripts exercise from Statistics 679: Data Science Computing Project by Professor John Gillett

2. Write a script that simulate a fasta file. The script requires three parameters 1) number of sequence to be simulated 2) the length of each sequence and 3) an output file name. Each read name begins with the word “read” follow by a read number e.g., `read1`, `read2` etc.

A script should check for the following things:

- 1) A number of parameter. If a user fails to give three parameters, the script should echo “Need three arguments: number of sequence, sequence length and output file name”.
- 2) Validity of the first and second parameter. If a user specifies a non-numeric parameter, the script should echo “First parameter must be numeric” or “Second parameter must be numeric”.
- 3) The existence of output file. If a given file name already exists, the script should echo “File already exists”

Example

```
$ ./simfasta.bash 5 10
Need three arguments: number of sequence, sequence length and output file
name
$ ls
simfasta.bash sim1.fasta
$ ./simfasta.bash 5 10 sim1.fasta
file already exists
$ ./simfasta.bash hi 10 simulates.fasta
First parameter must be numeric
$ ./simfasta.bash 5 10 simulates.fasta
$ cat simulates.fasta
>read1
TGCGATATTG
>read2
ACTGAACCAA
>read3
ACCAAGTCTA
>read4
AAAATAGTCT
>read5
ATCGTTGGCA
```