LINUX WORKSHOP

04 Shell Scripting

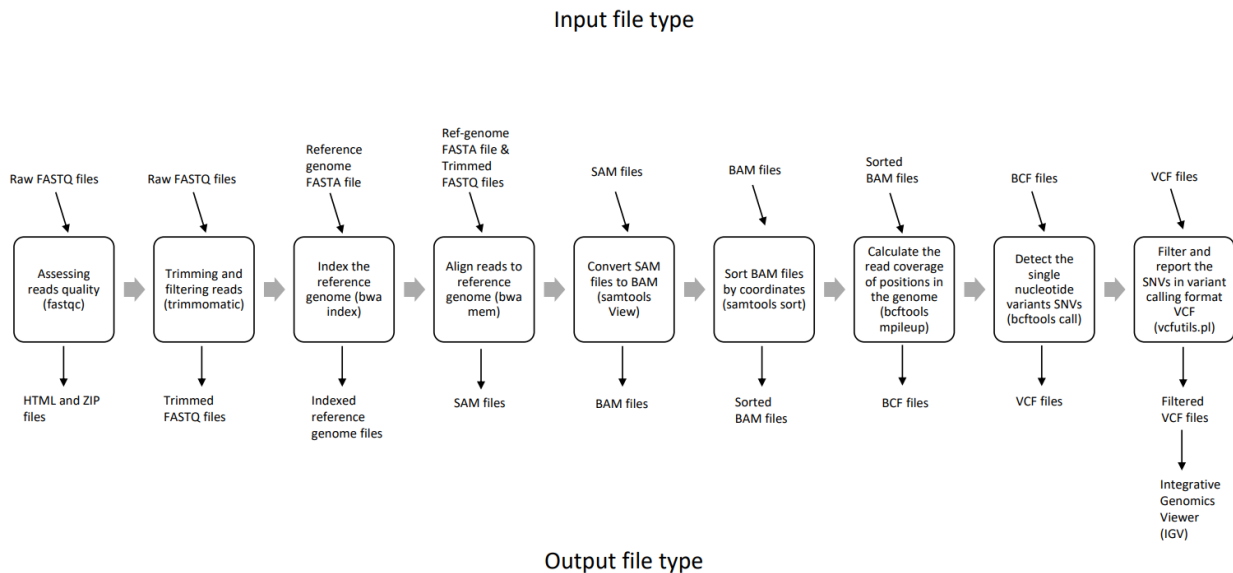*By Jiajia Li (ANU Biological Data Science Institute)*

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Learning Objectives

In this session, we will learn how to write a shell script with for loops to run all the steps in the workshop together at once.

The variant calling workflow for short reads

Shell script

A shell script is a text file that allow you to combine your sequence of commands together and run it all at once.

First, let's write a simple shell script and run it.

```
cd ~/workshops/variant-calling
nano first_script.sh
```

```
echo "Hello!"
sleep 1
echo "I'm Ubuntu. What's your name?"
sleep 1
read NAME
sleep 1
echo "Hello $NAME, nice to meet you!"
```

```
sh [/path/to/file]
```

Practise

Write every step in the variant calling workflow in a shell script and run it.

Use for loop to loop through all three sample.

Here is a for-loop example:

```
for i in *_1.fastq
do
base=$(basename $i _1.fastq)

fastq1=${base}_1.fastq
fastq2=${base}_2.fastq
trim1=${base}_1.trim.fastq
trim2=${base}_2.trim.fastq
untrim1=${base}_1un.trim.fastq
untrim2=${base}_2un.trim.fastq

trimmomatic PE $fastq1 $fastq2 \
            $trim1 $untrim1 \
            $trim2 $untrim2 \
            SLIDINGWINDOW:4:20 MINLEN:25 ILLUMINACLIP:NexteraPE-PE.fa:2:40:15

done
```

THANK YOU

Contact Us

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