

Shell scripting - 07/05/2020

Programming for Bioinformatics - Module 3

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Consider the following data, saved into the space-separated file `fastq.txt`.

```
1 @SRR5109807.811 811/1
2 GGCCTTGGAGGATGCATGGTTCTGGCATCTGCTTCTGGTGAGAGCCTCAGGAAACATTTATTCA
3 +
4 AAAA?C11BC?AB1B1B3F1BAG1EHH1AA13DADDDG1AGHHFHHGEBAA0FA0FGHFGFGFGB
5 @SRR5109807.812 812/1
6 GGCCTTGTAGGATGCATGGTTCTGGCATCTGCTTCTGGTGAGAGCCTCAGGAAACATTTATTCA
7 +
8 @BBABFFFFFFFFFGGFGGGGGGGGHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHGHHGGHHHHHHFGHHF
9 @SRR5109807.813 813/1
10 GGCCTTGTAGGATGCATGGTTCTGGCATCTGCTTCTGGTGAGAGCCTCAGGAAACATTTATTCA
11 +
12 BB@?AF4FFFBBGGGGGDCGGGFGHBFEHFHHHHHCFHHCF25BGHGGEC3FHGHHHGHFFGEG
13 @SRR5109807.814 814/1
14 GGCCTTGTAGGATGCATGGTTCTGGCATCTGCTTCTGGTGAGAGCCTCAGGAAACATTTATTCA
15 +
16 AAABBBFFFFFFFFFGGGGGGGGGGHHHHHHHHHHGHHHHHGBGHHGHHHHHHHHHHHHHHHHHHHHGHHH
17 @SRR5109807.815 815/1
18 GGCCTTGTAGGATGCATGGTTCTGGCATCTGCTTCTGGTGAGAGCCTCAGGAAACATTTATTCA
19 +
20 ABBCCFFFFFFFFFFGGGGGGGGGGHHHHHHHHHHHHHHHHHHHHGHHHHHHHHHHHHHHHHHHHHGHHHHHHH
```

1. (2 points) What is the output of the following two commands?

- (a) `cat fastq.txt | cut -c 1-2 | sort -u | tail -5 | wc -l`
- (b) `cat fastq.txt | cut -c 1-2 | tail -5 | sort -u | wc -l`

2. (2 points) What is the output of the following command?

```
cat fastq.txt | grep "^A" | wc -l
```

3. (3 points) What is the output of the following command?

```
cat fastq.txt | awk 'BEGIN{n=0} $1 ~ /^A/ {if($1 ~ /\?/) n++}END{print n}'
```

4. (3 points) What is the output of the following command?

```
cat fastq.txt | sed -e '/^A/d' | sed -e '/\?/d' | wc -l
```