

# Computational Genomics: Sequences

## Homework 1

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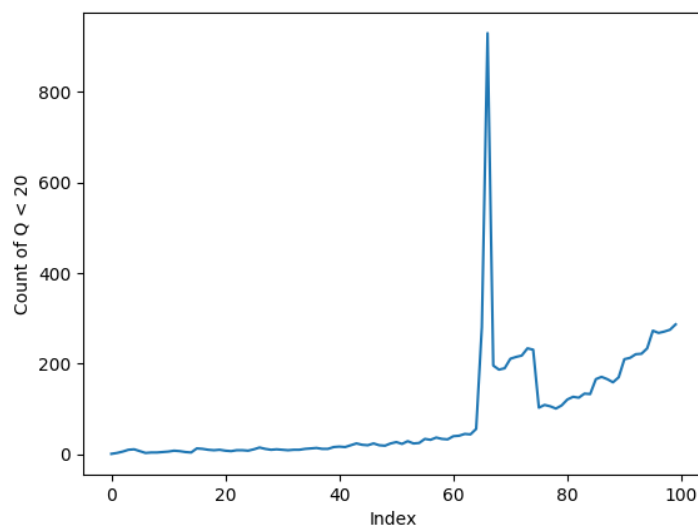
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### Answers

Some answers are instructions on how to run the associated program

1. `answer1.py > inputfile < outputfile`

- (a) Yes, the sequencer could not determine the 67th nucleotide quite often in every read



(b)

There appears to be an increase in bases with  $Q < 20$  as the index increases. This tells me that the longer the sequence the lower the quality of bases at the end

2. Winner indicated in **Bold**
  - (a) Bad Character Rule: 2 moves, 1 skip  
**Good Suffix Rule: 8 moves, 7 skips**
  - (b) **Bad Character Rule: 8 moves, 7 skips**  
Good Suffix Rule: 4 moves, 3 skips
  - (c) Bad Character Rule: 5 moves, 4 skip  
**Good Suffix Rule: 10 moves, 9 skips**
3. Winner indicated in **Bold**, the answer for case b changes
  - (a) Bad Character Rule: 2 moves, 1 skip  
**Good Suffix Rule: 8 moves, 7 skips**
  - (b) **Bad Character Rule: 8 moves, 7 skips**  
**Good Suffix Rule: 8 moves, 7 skips**
  - (c) Bad Character Rule: 2 moves, 1 skips  
**Good Suffix Rule: 11 moves, 10 skips**

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4. Send a pattern in via stdin, ensure complete works file is in same dir is in the same dir To run, call *answer4.py <pattern>*