Feedback — Module 4 Quiz **Please Note: No Grace Period**

Help Center

Thank you. Your submission for this quiz was received.

You submitted this quiz on **Thu 13 Aug 2015 11:02 PM PDT**. You got a score of **9.00** out of **9.00**.

Question 1

How many lines make up each record contained in a FASTQ file?

Your Answer		Score	Explanation
Two			
Three			
One			
Four	✔	1.00	
Total		1.00 / 1.00	

Question 2

Which of the following are components of the FASTQ format?

Your Answer		Score	Explanation
Sequence			
All of these options	✔	1.00	
Sequence identifier			

Quality score		
Total	1.00 / 1.00	

Question 3

Which of the following is NOT a type of encoding of sequence quality scores in a FASTQ file?

Your Answer		Score	Explanation
Sanger			
Solexa			
Ion torrent	✔	1.00	
Illumina 1.3+			
Total		1.00 / 1.00	

Question 4

Which of the following operations of quality control can be performed with Galaxy's NGS: QC and manipulation?

Your Answer		Score	Explanation
FastQC: Read Quality reports			
All of these options	✔	1.00	
Trim Sequences			
FASTA to FASTQ, and FASTQ to FASTA format conversion, Manipulate FASTQ			
Total		1.00 / 1.00	

Question 5

Which of the following is NOT part of the FastQC report?

Your Answer		Score	Explanation
(•) Per sequence base quality	✔	1.00	
( ) Sequence Length distribution			
( ) Per sequence quality score			
( ) Per base sequence quality			
Total		1.00 / 1.00	

Question 6

When do we filter and trim reads? Choose the correct option.

Your Answer		Score	Explanation
( ) Always filter and trim reads, we want high quality equal length reads to gain flexibility of using any tool of choice during downstream analysis.			
( ) Always trim the reads. We want only equal length reads in our data.			
(•) Depends on tools used during downstream analysis.	✔	1.00	
( ) Always filter reads. We want only high quality reads in our data.			
Total		1.00 / 1.00	

Question 7

What is ChIP sequencing most commonly used to measure?

Your Answer		Score	Explanation
Expression levels of particular proteins			
Ratios of miRNA to DNA			
The locations of protein to DNA interaction	✔	1.00	
Methylation of bases			
Total		1.00 / 1.00	

Question 8

What is MACS used for?

Your Answer		Score	Explanation
Measure RNA levels			
Peek calling/reconstruction from ChIP-seq data	✔	1.00	
Detect sequence variants using both qPCR and ChIP-seq data			
Genome assembly using suffix trees and ChIP-seq data			
Total		1.00 / 1.00	

Question 9

What is the advantage of using a control in a ChIP sequencing experiment?

Your Answer		Score	Explanation
○ Determine background expectation of the number of peaks detected.			
◉ Both options	✔	1.00	
○ Allow MACS to calculate FDR.			
○ Neither option			
Total		1.00 / 1.00	