Feedback — Module 3 Quiz

Help Center

Thank you. Your submission for this quiz was received.

You submitted this quiz on **Tue 22 Sep 2015 9:58 PM PDT**. You got a score of **10.00** out of **10.00**.

Question 1

Which of the following statements is FALSE:

Your Answer		Score	Explanation
○ Different versions of a gene resulted from genomic mutations are called alleles.			
○ Differences in the genomes of individuals are strong contributors to their phenotypic variations.			
○ SNV refers to a Single Nucleotide Variant.			
◉ SNP refers to a Single Non-defined Polymorhism	✔	1.00	
Total		1.00 / 1.00	

Question 2

Which of the following statements is FALSE:

Your Answer		Score	Explanation
○ The VCF FORMAT lines specify the format used for the genotype data.Option text			
○ The BAM format is a binary compressed representation for			

alignments of next generation sequencing reads.		
○ The mpileup format produced by SAMtools can be used to represent sites of variation.		
◉ The VCF format shows the changes in amino acid resulting from the nucleotide mutation, in column 3.	✔	1.00
Total		1.00 / 1.00

Question 3

What program can be used to generate a list of candidate sites of variation in an exome data set:

Your Answer		Score	Explanation
○ bwamem			
○ samtools view			
○ bowtie2-build			
◉ samtools mpileup	✔	1.00	
Total		1.00 / 1.00	

Question 4

In a comprehensive effort to study genome variation in a patient cohort, you sequence and call variants in the exome, whole genome shotgun and RNA-seq data from each patient. Which of the following is FALSE when comparing these three types of resources:

Your Answer	Score	Explanation
○ RNA editing can confound the detection of variants from RNA-seq data.		
○ RNA-seq will only capture variants in the expressed genes.		

Exome sequencing comprehensively captures variants in the 3' and 5' UTRs of genes.	✔	1.00
Exome sequencing can capture variants in a pre-defined set of coding exons and their immediate surrounding area.		
Total		1.00 / 1.00

Question 5

Which of the following options can be used to allow bowtie2 to generate partial alignments?

Your Answer		Score	Explanation
-N			
--local	✔	1.00	
--sensitive			
-S			
Total		1.00 / 1.00	

Question 6

Select the correct interpretation for the snippet of 'mpileup' output below.

```
Chr3    11700316        C       8       .$.......      8C@C;CB3
Chr3    11951491        G       16      AAAA,......aA..A        C2@2BCBCCCA
C2CC4
```

Your Answer	Score	Explanation

◉ Only site 2 shows potential variation; the alternate letter for site 2 is A; site 1 has 8 supporting reads, and site 2 has 16	✔	1.00
○ Both sites show potential variation; the alternate letter for site 1 is $, and for site 2 is A; site 1 has 8 supporting reads, and site 2 has 16		
○ None of the sites shows potential variation; site 2 has support from 1 forward and 15 reverse reads		
○ Only site 2 shows potential variation; the alternate letter for site 2 is '.'; site 1 has 8 supporting reads, and site 2 has 16		
Total		1.00 / 1.00

Question 7

Given the set of variants described in the VCF excerpt below, which of the following is FALSE?

```
##INFO=
##INFO=
##FORMAT=
##FORMAT=
Chr3    11966312        .       G       A       15.9    . DP=5;MQ=15    GT:PL   1/1:43,9,0
Chr3    11972108        .       TAAAA   TAAA    32.8    .       INDEL;IDV=7;IMF=0.636364;DP=11;MQ=22    GT:PL   0/1:66,0,2
Chr3    13792328        rs145271872     G       T       5.5     .       DP=1;MQ=40      GT:PL   0/1:32,3,0
```

Your Answer		Score	Explanation
○ The sample contains both alleles for variant 2			
◉ The sample contains only the alternate allele for variant 3	✔	1.00	
○ The alternate allele for variant 1 is A			

○ Variant 1 has read depth 5		
Total		1.00 / 1.00

Question 8

What does the following code do:

```
bowtie2 -x species/species -U in.fastq | grep -v "^@" | cut -f3 | sort | uniq -c
```

Your Answer		Score	Explanation
○ Run bowtie2 with a set of single-end reads, reporting the best alignment only; then list the total numbers of forward and reverse complemented reads, respectively			
◉ Run bowtie2 with a set of single-end reads, reporting the best alignment only; then determine the number of matches on each genomic sequence	✔	1.00	
○ Run bowtie2 with a set of single-end reads, reporting up to 5 alignments per read; then determine the number of matches on each genomic sequence			
○ Run bowtie2 with a set of paired-end reads, allowing up to 10 matches per read; then report the number of matches on each genomic sequence			
Total		1.00 / 1.00	

Question 9

What does the following snippet of code do NOT do:

```
samtools mpileup -O -f genome.fa  in.bam | cut -f7
```

Your Answer		Score	Explanation
○ Produce a 7-column intermediate mpileup file that is piped to 'cut'			
◉ Generate intermediate output in uncompressed BCF format	✔	1.00	
○ Take in the input BAM file in.bam			
○ Generate intermediate output in mpileup format			
Total		1.00 / 1.00	

Question 10

What does the following code do NOT do:

```
bcftools call -v -c -O z -o out.vcf.gz in.vcf.gz
```

Your Answer		Score	Explanation
○ Report output in compressed VCF format			
○ Report variant sites only			
○ Call variants in a single sample			
◉ Skip indels	✔	1.00	
Total		1.00 / 1.00