Module 3 Quiz

9/10 points (90%)

Quiz, 10 questions

~	Congra	atulations! You passed! Next Item		
	~	1/1 points		
	1. Which	of the following statements is FALSE:		
	SNVs encompass single nucleotide insertions, deletions and substitutions.			
	0	SNP refers to a Single Non-defined Polymorhism		
	Corr	ect		
		SNV refers to a Single Nucleotide Variant.		
		Structural variants include block deletions and insertions, among others.		
	~	1 / 1 points		
	2. Which	of the following statements is FALSE:		
		The BAM format is a binary compressed representation for alignments of next generation sequencing reads.		

The genotype fields in VCF provide information about the

The VCF format shows the changes in amino acid resulting

The mpileup format has either 6 or 7 columns.

from the nucleotide mutation, in column 3.

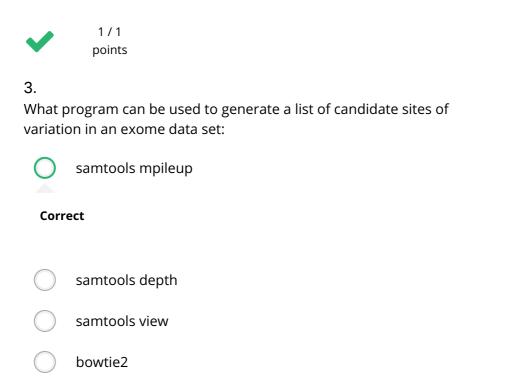
variant in each sample.

Correct

Module 3 Quiz

9/10 points (90%)

Quiz, 10 questions





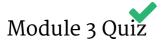
0/1 points

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:

	RNA editing can confound the detection of variants from RNA- seq data.
	RNA-seq allows detection of intronic variants.
	Exome sequencing comprehensively captures variants in the 3 and 5' UTRs of genes.
0	All of the three methods can identify variants located in the introns, albeit to different degrees.

This should not be selected



1/1 points

9/10 points (90%)

Quiz, 10 questions

5

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

0	loca

Correct

-ignore-quals
sensitive
-D



1/1 points

6.

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

```
1 ```
2 Chr3 11700316 C 8 .$...... 8C@C;CB3
3 Chr3 11951491 G 16 AAAA,.....aA..A C2@2BCBCCCAC2CC4
```

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

Correct

Only site 2 shows potential variation;
the alternate letter for site 2 is A;
the alternate allele for site 2 is supported by 9 reads
Only site 2 shows potential variation;
the alternate letter for site 2 is G;

site 1 has 8 supporting reads, and site 2 has 16

Module 3 Quiz

Only site 2 shows potential variation;

9/10 points (90%)

Quiz, 10 questions

the alternate letter for site 2 is '.';

site 1 has 8 supporting reads, and site 2 has 16



1/1 points

7.

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

- The sample contains both alleles for variant 2
- The sample contains only the alternate allele for variant 3

Correct

- The sample contains only the alternate allele for variant 1
- Average mapping quality for variant 3 is 40



8.

1/1 points

What does the following code do:

```
1 ```
2 bowtie2 -x species/species -U in.fastq | grep -v "^@" | cut -f3 | sort | uniq -c
```

 Run bowtie2 with a set of single-end reads, reporting the best alignment only; Coursera | Online Courses From Top Universities. Join for Free | Coursera

then determine the number of matches on each genomic sequence

Module 3 Quiz

9/10 points (90%)

Quiz, 10 questions

Correct

Run bowtie2 with a set of single-end reads, reporting up to 5 alignments per read;

then determine the number of matches with unmapped mates

Run bowtie2 with a set of single-end reads, reporting the top 5 alignments for a read;

then list the number of matches containing insertions and deletions, respectively

Run bowtie2 with a set of single-end reads, allowing for local matches;

then determine the number of matches with unmapped mates



1/1 points

9.

What does the following snippet of code do NOT do:

1 2 3	samtools	mpileup	-0 -f	genome.fa	in.bam	cut -f7



Report an empty column

Correct

Require a sorted BAM file
Produce a 7-column intermediate mpileup file that is piped to 'cut'

Report in the intermediate mpileup output the qualities of all read bases aligned at that position



1/1 points

10.

Module 3 Q	What does the following code do NOT do: $oldsymbol{ t UIZ}$	9/10 points (90%)
Quiz, 10 questions	1 ``` 2 bcftools call -v -c -0 z -o out.vcf.gz in.vcf.gz 3 ```	•
	Call variants in a single sample	
	Report variant sites only	
	Report output in compressed VCF format	
	Skip indels	
	Correct	