Module 3 Quiz

8/10 points (80%)

Quiz, 10 questions

Congratulations! You passed!

Next Item

1 / 1 points

1.
Which of the following statements is FALSE:

- SNV refers to a Single Nucleotide Variant.
- SNP refers to a Single Non-defined Polymorhism

Correct

- Structural variants include block deletions and insertions, among others.
- SNVs encompass single nucleotide insertions, deletions and substitutions.

---

1 / 1 points

2.
Which of the following statements is FALSE:

- The mpileup format has either 6 or 7 columns.
- The VCF format shows the changes in amino acid resulting from the nucleotide mutation, in column 3.

Correct

- The BAM format is a binary compressed representation for alignments of next generation sequencing reads.

The genotype fields in VCF provide information about the variant in each sample.

Module 3 Quiz

8/10 points (80%)

Quiz, 10 questions

0 / 1 points

3.
What program can be used to generate a list of candidate sites of variation in an exome data set:

- mkdir
- samtools

This should not be selected

- bedtools
- bcftools

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:

- Exome sequencing comprehensively captures variants in the 3' and 5' UTRs of genes.
- Exome sequencing can capture variants in a pre-defined set of coding exons and their immediate surrounding area.
- Exome sequencing cannot determine variants in novel polymorphic alternative splicing events.

This should not be selected

- Exome sequencing captures fewer variants than whole genome sequencing.

4. Whole genome sequencing can potentially detect all variants that can be found with either exome sequencing or RNA-seq.

Module 3 Quiz

8/10 points (80%)

Quiz, 10 questions

✔ 1 / 1 points

5.

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

- ◯ --local

Correct

- ◯ –ignore-quals
- ◯ -D
- ◯ --sensitive

✔ 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
4  ```
```

- ◯ Both sites show potential variation

  the alternate letter for site 1 is $, and for site 2 is G;

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

- ◯ 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

Both sites show potential variation;

Module 3 Quiz

Quiz, 10 questions

8/10 points (80%)

the alternate letter for site 1 is $, and for site 2 is A;

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

Both sites show potential variation;

the alternate letter for site 1 is C, and for site 2 is G;

site 1 has 8 supporting reads, and site 2 has 7

---

1 / 1 points

7.

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

```
1  ```
2  ##INFO=<ID=DP,Number=1,Type=Integer,Description="Raw read depth">
3  ##INFO=<ID=MQ,Number=1,Type=Integer,Description="Average mapping quality">
4  ##FORMAT=<ID=GT,Number=1,Type=String,Description="Genotype">
5  ##FORMAT=<ID=PL,Number=G,Type=Integer,Description="List of Phred-scaled genotype
     likelihoods">
6  Chr3  11966312   .  G A 15.9  . DP=5;MQ=15    GT:PL   1/1:43,9,0
7  Chr3  11972108  . TAAAA TAAA  32.8  .  INDEL;IDV=7;IMF=0.636364;DP=11;MQ=22 GT
     :PL 0/1:66,0,2
8  Chr3  13792328  rs145271872 G T 5.5 . DP=1;MQ=40  GT:PL 0/1:32,3,0
9  ```
```

The sample contains only the alternate allele for variant 3

Correct

The sample contains both alleles for variant 2

Average mapping quality for variant 3 is 40

The sample contains only the alternate allele for variant 1

---

1 / 1 points

8.

What does the following code do:

```
1  ```
2  bowtie2 -x species/species -U in.fastq | grep -v “^@” | cut -f3 | sort | uniq -c
3  ```
```

Module 3 Quiz

Quiz, 10 questions

8/10 points (80%)

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

then determine the number of exact matches on each genomic sequence

Run bowtie2 with a set of single-end reads, reporting the best alignment only;

then determine the number of matches on each genomic sequence

Correct

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

then determine the number of reads mapped reverse complemented

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:

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

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

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

Require a sorted BAM file

Report an empty column

Correct

Module 3 Quiz

Quiz, 10 questions

8/10 points (80%)

1 / 1 points

10.

What does the following code do NOT do:

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

- [x] Skip indels

Correct

- [ ] Use the 'consensus caller' model to call variants
- [ ] Report output in compressed VCF format
- [ ] Report variant sites only