Module 3 Quiz

9/10 points (90%)

Quiz, 10 questions

Congratulations! You passed!

Next Item

1 / 1 points

1.
Which of the following statements is FALSE:

- Different versions of a gene resulted from genomic mutations are called alleles.
- SNP refers to a Single Non-defined Polymorhism

Correct

- SNV refers to a Single Nucleotide Variant.
- Differences in the genomes of individuals are strong contributors to their phenotypic variations.

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1 / 1 points

2.
Which of the following statements is FALSE:

- The VCF format shows the changes in amino acid resulting from the nucleotide mutation, in column 3.

Correct

- VCF stands for Variant Call Format.
- The BCF format is a binary compressed version of VCF.
-

The VCF INFO lines describe characteristics of the variant, included in column 8.

Module 3 Quiz

9/10 points (90%)

Quiz, 10 questions

✔ 1 / 1 points

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

- samtools mpileup

Correct

- samtools depth
- samtools view
- bowtie2

✖ 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:

- Whole genome sequencing can comprehensively identify variants in all protein-coding genes.
- RNA-seq will only capture variants in the expressed genes.

This should not be selected

- RNA-seq can systematically identify variants in gene regulatory regions.
- RNA-seq allows detection of intronic variants.

1 / 1

1 / 1 points

Module 3 Quiz

9/10 points (90%)

Quiz, 10 questions

5.
Which of the following options can be used to allow bowtie2 to generate partial alignments?

- [x] --local

Correct

- [ ] -l
- [ ] --very-fast
- [ ] –ignore-quals

---

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  ```
```

- [x] 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 1 shows potential variation;

  the alternate letter for site 1 is $;

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

- [ ] Only site 1 shows potential variation;

  the alternate letter for site 1 is C;

  site 1 has 9 supporting reads, and site 2 has 16

Both sites show potential variation;

Module 3 Quiz

Quiz, 10 questions

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

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site 1 has 9 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?

```
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 alternate allele for variant 1 is A

The alternate allele for variant 3 is T

The quality values for the three calls are 15.9, 32.8 and 5.5

✔ 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  ```
```

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;

Module 3 Quiz

Quiz, 10 questions

9/10 points (90%)

then report the number of 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 paired-end reads, allowing for local matches;

  then report the numbers of alignments containing insertions and deletions, respectively;

---

1 / 1 points

9.
What does the following snippet of code do NOT do:

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

- Generate intermediate output in uncompressed BCF format

Correct

- Generate intermediate output in mpileup format
- Take in the input BAM file in.bam
- Require a sorted BAM file

---

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
```
```

Module 3 Quiz

Quiz, 10 questions

9/10 points (90%)

- Report output in compressed VCF format
- Call variants in a single sample
- Skip indels

Correct

- Report variant sites only