

Module 2 Quiz

10/10 points (100%)

Quiz, 10 questions

✓ **Congratulations! You passed!**

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points

1.

Which of the following strings cannot denote a DNA sequence:

- ☐ TACNATTCG
- ☐ GACTACGAGCGATTACAGCGAGCATT
- ☐ GGTACGAGC
- ☒ MASLLRG

Correct1 / 1
points

2.

How many lines does it take to specify:

i) one fasta sequence? and ii) one fastq sequence?

Select the best answer.

- ☐ Both fasta and fastq can take any number of lines
- ☒ Fasta – a fasta header followed by any number of sequence lines; fastq – 4 lines

Correct

- ☐ Fasta – 3 lines; fastq – 4 lines

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Fasta – 2 lines, including a fasta header; fastq – 4 lines

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points

3.

Which of the following is incorrect:



Information on primary and secondary alignment can be represented in the FLAG field in SAM records.



BEDtools can be used to align sequences to the genome.

Correct



SAMtools flagstats reports the total number of alignments.



BEDtools can be used to extract alignments within a certain range.



1 / 1
points

4.

Which of the following is NOT an alignment operation:



Cut and paste

Correct



Deletion



Substitution



Insertion



1 / 1
points

5.

What is the minimum number of columns that are sufficient to specify a BED format?

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☐ 7

☒ 3



Correct

☐ 5

☐ 6



1 / 1
points

6.

Which of the following represents the most accurate conversion into BED of the GTF record:

```
1  '''
2  chr1  CLASS  exon  516 811 100 + . gene_id "genA"; transcript_id "genA.1";
3  chr1  CLASS  exon  1001 1115 100 + . gene_id "genA"; transcript_id "genA.1";
4  chr1  CLASS  exon  3010 3312 100 + . gene_id "genA"; transcript_id "genA.1"
5  '''
```

☐

```
1  '''
2  chr1  516 3312 genA + 516 3312 0 2 296,303 0,2494
3  '''
```

☐

```
1  '''
2  chr1  516 3312  genA.1  100 + 800 900 0 3 296,115,303 0,485,2494
3  '''
```

☒

```
1  '''
2  chr1  515 3312  genA.1  100 + 515 3312  0 3 296,115,303 0,485
3  ''' ,2494
```



Correct

☐

```
1  '''
2  chr1  515 811 genA 100 + . 800 811 0 1 296 0
3  '''
```



1 / 1
points

7.

Determine the number of genes, transcripts, exons per transcript, gene orientation (strand), and the length of 5' most exon(s) from the GTF

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Shippit below. Select the correct answer.

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```
1  ...
2  chr1 HAVANA gene 3205901 3671498 . - . gene_id "MUSG51951.5";
3  chr1 HAVANA transcript 3205901 3216344 . - . gene_id "MUSG51951.5";
4  transcript_id "MUST162897.1";
5  chr1 HAVANA exon 3213609 3216344 . - . gene_id "MUSG51951.5"; transcript_id
6  "MUST162897.1";
7  chr1 HAVANA exon 3205901 3207317 . - . gene_id "MUSG51951.5"; transcript_id
8  "MUST162897.1";
9  chr1 HAVANA transcript 3206523 3215632 . - . gene_id "MUSG51951.5";
10 transcript_id "MUST159265.1";
11 chr1 HAVANA exon 3213439 3215632 . - . gene_id "MUSG51951.5"; transcript_id
12 "MUST159265.1";
13 chr1 HAVANA exon 3206523 3207317 . - . gene_id "MUSG51951.5"; transcript_id
14 "MUST159265.1";
15 ...
```

- ☐ Genes: 2; Transcripts: 2; Exons: 3,2; Strand: -; Length of 5' exon(s): 2736, 2194.
- ☒ Genes: 1; Transcripts: 2; Exons: 2,2; Strand: -; Length of 5' exon(s): 2736, 2194.

Correct

- ☐ Genes: 2; Transcripts: 2; Exons: 2,2; Strand: -; Length of 5' exon(s): 2500, 2000.
- ☐ Genes: 2; Transcripts: 4; Exons: 1,1,1,1; Strand: -; Length of 5' exon(s): 2736,1417, 2194,795.



1 / 1
points

8.

Which of the following is FALSE for the following read alignments:

```

1   ...
2   R1 83 chr12 9232390 255 50M = 9232180 0
3   ATGGCAGAGCCTAATATGTCCTCTAGAGAATGGGAGAGATGGGAAGTCAT
    HGHGHHHHHHHHHHHHHHHHHHHHHHHHHIGIIIIHHHHHHHHHHHGHHFH NM:i:0 NH:i:1 HI:i:0
4   R2 97 chr12 9232391 255 28M278N22M = 9242529
5   0 TGGCAGAGCCTAATATGTCCTCCAAACTGAGACAGAAGCTCGGCAGAT D
    >DDDHGHHHHHHHHHHIHHHHHHHHHHHIGFFGGGHHHHHHHHHHF.B FM:i:4 NH:i:3 HI:i:0 XS:A
    :+ NS:i:2
6   R3 77 * 0 0 0 * * 0 0 CTGATATGAGGAAGAGAGATTGCTTAAGCCCGAGGAGTAGAGGCTGTACC
    @@@@FFDFHFHJJJJJJJEGFGIGHHHHHHHIIGCDE?D?FGGCBHDGGG
7   ...

```

- ☐ R2's alignment is spliced and contains a 278 bp intron.
- ☐ R1's alignment starts at position 9232390 and ends at position 9232439.
- ☒ R1, R2 and R3 all map to chromosome 12.

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9.

```
1  ...
2  R2_97_chr12_9232391_255_28M278N22M = 9242529
3  0 TGGCAGAGCCTAATATGCTCCCCAAACTGAGACAGAAGCTCGGGCAGAT D
   >DDDDHHHHHHHHHHHHHHHHHHHHHHHHHHIIGFFGGGHHHHHHHHHHHHF.F NM:i:4 XS:A:+ NS:i:2
4  ...
```

☐

Correct

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points

10.

Files 'A.bed' and 'B.bed' contain the following sets of intervals:

```
1  ````
2  File A           File B
3  chr1  100 400      chr1  300 500
4  chr1 1000 1400      chr1  900 1600
5  chr1 2000 2400      chr12 2000 2200
6  ````
7  What would be the answers for the following sequence of commands:
8  ````
9  bedtools intersect -wao -a A.bed -b B.bed | sort -u | wc -l
10 bedtools intersect -wo -a A.bed -b B.bed | cut -f1-3 | sort -u | wc -l
11 bedtools intersect -wo -a A.bed -b B.bed | cut -f4-6 | sort -u | wc -l
12 ````
```

☐ 9, 3, 6☐ 5, 5, 5☒ 3, 2, 2

Correct

☐ 9, 3, 4