

BZ360, Sample Exam Questions (expect ~33 similar questions on the actual exam)

Name: _____

1. Which of the following is not a real 'omics' application?
 - a. Genomics
 - b. Proteomics
 - c. Transcriptomics
 - d. Blastomics
 - e. Metabolomics

2. If an allele is present in a genome as two identical copies, one on each sister chromatid, the allele is which of the following?
 - a. Hemizygous
 - b. Heterozygous
 - c. Homozygous
 - a. Tetraploid

3. The following text is in what common sequence format? _____

```
>mc1r
ACACGTAGCTATTCATCGTGATTTCGACTACGTACGACGGACTACTATCTACGGACTACTTACGGCGAGCTCAACACGTAGCTA
TTCATCGTGATTTCGACTACGTACGACGGACTACTATCTACGGACTACTTACGGCGAGCTCAACACACGTAGCTATTCATCGTG
ATTTCGACTACGTACGACGGACTACTATCTACGGACTACTTACGGCGA
```

4. What type of sequence alignment is shown below?
 - a. Local alignment
 - b. Global alignment

```
ACTGACCACGTCACAGGCTAGG
||  |  |  |||||  |||
AC---C-AGGTCAC-----AGG
```

5. The local alignment program _____ is one of the most widely used bioinformatics tools.

6. A deletion or insertion of DNA at a particular genomic locus is an example of which of the following features commonly assayed using DNA sequencing?
 - a. SNP
 - b. Indel
 - c. Both a and b are correct

7. What is a UNIX command commonly used to change directories? _____

8. Which of the following UNIX commands is used to make a new directory?
 - a. mkdir
 - b. makedir

- c. md
- d. make
- e. new

9. Which of the following UNIX commands is used to list the contents of a directory?

- a. touch
- b. ls
- c. more
- d. rm
- e. read

10. What software is needed to run the following script?

```
#!/bin/bash  
echo hello world!
```

- a. Bash shell
- b. Python
- c. Perl
- d. Python and Bash shell
- e. Perl and Bash shell

11. Using the shell below: 1) create a variable containing lowercase DNA sequence and 2) use `tr [a-z] [A-Z]` to change the sequence to uppercase and then output the uppercase sequence to a new file using no more than two lines of commands.

```
bash$
```

```
bash$
```