

University of Pennsylvania
BIOL4536 Fall 2023
Professor: Gregory R. Grant
QUIZ#4
(BLAST/DNA-Seq)

October 23rd, 2023

Name: _____

Question 1. (2 pts.) BLAST is (circle all that apply)

- (A) Global Aligner
- (B) Local Aligner
- (C) Protein Aligner
- (D) DNA Aligner
- (E) Low homology aligner

Question 2. (2 pts.) True or False: The BLAST E -value of a score is the expected number of alignments with that score (or higher) against a database of random sequence.

Question 3. (2 pts.) Suppose the scoring scheme for a BLAST DNA search is +1 for match and -1 for mismatch. The expected score for an ungapped alignment of two *random* sequences (background probability $1/4$ per nucleotide) of length N is:

- (A) 0
- (B) $-\frac{1}{4}N$
- (C) $-\frac{1}{2}N$
- (D) $-\frac{3}{4}N$
- (E) $-N$

Question 4. (1 pt.) A fastQ file has how many rows per read?

- (A) One
- (B) Two
- (C) Three
- (D) Four

Question 5. (1 pts.) True or False. In paired-end data, we get the sequence of an entire fragment whenever the length of the fragment is less than three times the length of the reads.

Question 6. (2 pts.) In your own words, in high throughput sequencing, what's the difference between single-end and paired-end data?