

The default word size in FASTA is smaller than in BLAST. This makes BLAST

- (i)
- (ii)
- (iii)
- (iv)

- ☐ a. faster and more sensitive
- ☒ b. faster, but less sensitive
- ☐ c. less sensitive
- ☐ d. faster

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For two alignments with same identity score, the E-value in the BLAST program will be smaller for the larger alignment. True/False.

Select one:

- ☐ True
- ☒ False

BLAST program misses some good biological homologies below the accepted statistical cut off value. How would you identify these distant homologies?



Question 1

Not yet answered

Marked out of 1.00

Flag question

For two alignments with same identity score, the E-value in the BLAST program will be smaller for the larger alignment. True/False.

Select one:

- ☐ True
- ☒ False

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Question 2

Not yet answered

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FASTA uses exact word match, while BLAST uses a scoring scheme to look for similar words as seeds in the hashing step of the algorithm. So which is more sensitive program for database search:

- ☒ a. FASTA
- ☐ b. BLAST

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Question 3

Not yet answered

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BLAST program misses some good biological homologies below the accepted statistical cut off value. How would you identify these distant homologies?

Rich text editor toolbar with icons for undo, redo, bold, italic, bulleted list, numbered list, link, unlink, and insert image.

Question 4

Not yet answered

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Protein sequence database search is better than DNA sequence search for finding remote homologies. What are the possible reasons? [Note: List all the correct options]

- ☒ a. Because of degeneracy in the code, a change at DNA level may not always lead to a change at the amino acid level, making it possible to find distant homologies using protein database search
- ☐ b. Scoring matrices for proteins are more sensitive compared to those used for comparing DNA sequences
- ☒ c. Computationally, protein sequence is one-third the size of the corresponding DNA sequence.
- ☒ d. Only 4 characters in DNA compared to 20 in proteins, this leads to more hits by random chance at DNA level.

Question 5

Not yet answered

Marked out of 1.00

Flag question

Homology is implied if

- ☐ a. two sequences are > 50% identical
- ☒ b. both sequence and structure are similar
- ☐ c. two sequences are similar
- ☐ d. two structures are similar

Question 6

Not yet answered

Marked out of 1.00

Flag question

Computing the log odds score (match and mismatch) for comparing DNA sequences that exhibit 60% identity. Assume background frequency to be 0.25 and also assume equiprobability for mismatch.

$$\log\left(\frac{0.6}{0.25}\right) = 0.3802$$

Question 7

Not yet answered

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Which of the two scoring matrices, PAM150 and PAM125 would you use for comparing (i) closely related sequences and (ii) evolutionarily distant sequences?

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Question 8

Not yet answered

Marked out of 1.00

Flag question

Which variant of the dynamic programming algorithm would you use if the two sequences are closely related:

- ☐ a. global alignment
- ☒ b. does not matter, as both will give same results
- ☐ c. local alignment

Question 9

Not yet answered

Marked out of 1.00

Flag question

Compute the score of the following pairwise alignments:

Global alignment: Match = +1, Mismatch = 0, Gap: opening = -5, extension = -1

GAGG-TGACTGGGCA / - - -  
GTGGATG-C-GG-CAAGGG

$$+10 - 25 - 3 = -18$$

Question 10

Not yet answered

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Flag question

Give approximate values of window size and stringency (for matches) you would use for dot plot analysis when comparing two DNA sequences.

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