**Easy**

**What is a pairwise sequence alignment used to compare?**

A. Three sequences

B. Two sequences

C. A sequence and a structure

D. An entire genome

**What is the purpose of pairwise sequence alignment?**

A. To compare multiple sequences simultaneously

B. To find regions of similarity that may indicate functional, structural, or evolutionary relationships between two sequences

C. To determine the three-dimensional structure of a protein

D. To analyze gene expression levels

**What type of sequences can be aligned using pairwise alignment?**

A. Only DNA sequences

B. Only protein sequences

C. DNA, RNA, and protein sequences

D. Only RNA sequences

**Which type of alignment aligns the entire length of two sequences?**

A. Local alignment

B. Global alignment

C. Semi-global alignment

D. Multiple sequence alignment

**The length of a sequence and the ratio of similarity it achieves are considered measures of similarity in DNA and protein, respectively ?**

A. More than 100 nu, 50% similarity and more than 100 aa, 35% similarity

B. More than 100 nu, 55% similarity and more than 100 aa, 25% similarity

C. More than 100 nu, 70% similarity and more than 100 aa, 25% similarity

D. More than 100 nu, 80% similarity and more than 100 aa, 50% similarity

**How many BLAST forms are available from NCBI?**

A. 2

B. 3

C. 4

D. 5

**Which of the following statements about gaps in pairwise alignments is FALSE?**

A. Gaps can be introduced into either sequence.

B. Gaps indicate insertions or deletions in the original sequences.

C. A longer gap penalty discourages frequent gaps.

D. Gaps always receive positive scores.

**In sequence alignment, what is a "match"?**

A. A pair of different nucleotides or amino acids

B. A pair of identical nucleotides or amino acids

C. An inserted gap

D. The end of the sequence

**What does BLAST stand for?**

A. Basic Local Alignment Search Tool

B. Best Local Alignment Search Technique

C. Basic Long Alignment Search Tool

D. Best Long Alignment Search Technique

**What is the main function of a scoring matrix in sequence alignment?**

A. To store the sequences being aligned

B. To visualize the alignment results

C. To assign scores to aligned pairs of residues

D. To count the number of gaps in the alignment

**Medium**

**The result from the blast tool returns an E-value of 0.01, is that result significant?**

A. Yes

B. No

**What is the primary difference between global and local alignment?**

A. Global alignment aligns sequences end-to-end, while local alignment finds the best matching subsequences within the sequences.

B. Local alignment aligns sequences end-to-end, while global alignment finds the best matching subsequences within the sequences.

C. Global alignment is faster than local alignment.

D. Local alignment can only be used for DNA sequences, while global alignment can be used for both DNA and protein sequences.

**What is the main advantage of using local alignment over global alignment?**

A. Local alignment is faster than global alignment.

B. Local alignment can find conserved regions within sequences that may not align well end-to-end.

C. Local alignment does not use gap penalties.

D. Local alignment always produces longer alignments than global alignment.

**In pairwise sequence alignment, what does a gap represent?**

A. A region where the sequences are identical.

B. A mismatch between the sequences.

C. A region where one sequence has extra nucleotides or amino acids that the other sequence does not have.

D. An alignment error.

**In which situation is local alignment preferred over global alignment?**

A. When comparing sequences of similar length and overall similarity.

B. When the sequences have regions of high similarity embedded within larger regions of low similarity.

C. When aligning very short sequences.

D. When aligning sequences without gaps.

**Which factor is not typically considered when creating a scoring scheme for sequence alignment?**

A. The biological function of the sequences.

B. The evolutionary relationship between residues.

C. The frequency of residue substitutions.

D. The computational complexity of the alignment algorithm.

**How can evolutionary information be integrated into pairwise sequence alignments?**

A. By using only nucleotide sequences

B. By applying a uniform scoring matrix

C. By utilizing substitution matrices derived from multiple sequence alignments and phylogenetic analyses

D. By ignoring gaps in the alignment

**In comparative genomics, what role does pairwise alignment play in the identification of orthologous and paralogous genes?**

A. It identifies only orthologous genes

B. It helps in identifying orthologous genes (genes in different species that evolved from a common ancestral gene) and paralogous genes (genes related by duplication within a genome) by highlighting regions of similarity and divergence

C. It cannot distinguish between orthologous and paralogous genes

D. It focuses solely on non-coding regions

**What challenges arise when aligning sequences that contain highly repetitive regions, and how can these challenges be addressed?**

A. The alignment becomes trivial and requires no special handling

B. Repetitive regions can cause alignment ambiguity and errors; using algorithms that can handle repeats or masking repetitive regions before alignment can address these challenges

C. Repetitive regions are always ignored in alignments

D. There are no challenges with repetitive regions

**How does the presence of pseudogenes complicate pairwise sequence alignments?**

A. Pseudogenes are not found in any genomes

B. Pseudogenes improve alignment accuracy

C. Pseudogenes have no effect on sequence alignment

D. Pseudogenes can introduce false alignments due to their similarity to functional genes, potentially misleading evolutionary and functional analyses; distinguishing true genes from pseudogenes using additional annotation data can mitigate this