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18/MHS05/010

Physiology

CSC 262

1. (a) List and discuss any three criterion of database searching.
2. Keyword / Basic search
3. Advanced search

Keyword: It searches ones field and is useful to determine how big the connection of articles related to the topic is. It is also helpful when doing a known item search.

Advance: It is a more refined search. Multiple search terms in multiple fields can be searched for simultaneously. It is used when the collection of interested articles is large and needs to be narrowed.

(b) Explain briefly basic social alignment search tool (BLAST) as used in database similarity searching.

BLAST: It is an algorithm and program for comparing primary biological sequence information such as the amino acid sequence of protein or the nucleotides of DNA / RNA sequences. It enhances researchers to compare a subject protein or nucleotide sequence (called a query) with a database of sequences and identity library sequences that resemble the query sequence above a certain threshold.

1. (a) Briefly discuss the differences between Dayhoff PAM Matrices and BLOSUM Matrices
2. PAM: Are used to score alignment between closely related protein sequences, they are based on global alignment, their mutation in global alignments are very significant, their alignment have higher similarity than BLOSUM , also higher numbers in the PAM matrix naming denotes greater evolutionary distance.
3. BLOSUM: Are used to score alignment between evolution divergent protein sequences, they are based on local alignment ,their alignments have two similarity than PAM, they are based on highly conserved stretches of alignment, also higher numbers in the BLOSUM matrix naming denotes higher sequences similarity and smaller solution.

(b) Explain briefly Heuristic Database Searching

It refers to a search strategy that attempts to optimize a problem by interactively improving the solution based on a given heuristic function or a cost measure. It does not always guarantee to find an optimal or the best solution, but may instead find a good or acceptable solution within a reasonable amount of time and memory space.

1. (a) Define the following (i) Sequence Homology (ii) Sequence Similarity (iii) Sequence Identity (i) Homology: Is the biological homology between DNA, RNA or protein sequences defined in terms of shared ancestry in the evolutionary history of life.
2. Similarity: Is a measure of an empirical relationship between sequences.
3. Identity: Is the amount of characters which match exactly between two different sequences.

(b) (i) Give any three (3) methods of Alignment Algorithm (ii) Discuss briefly Pairwise Sequence Alignment

(i) (a) Dot-matrix

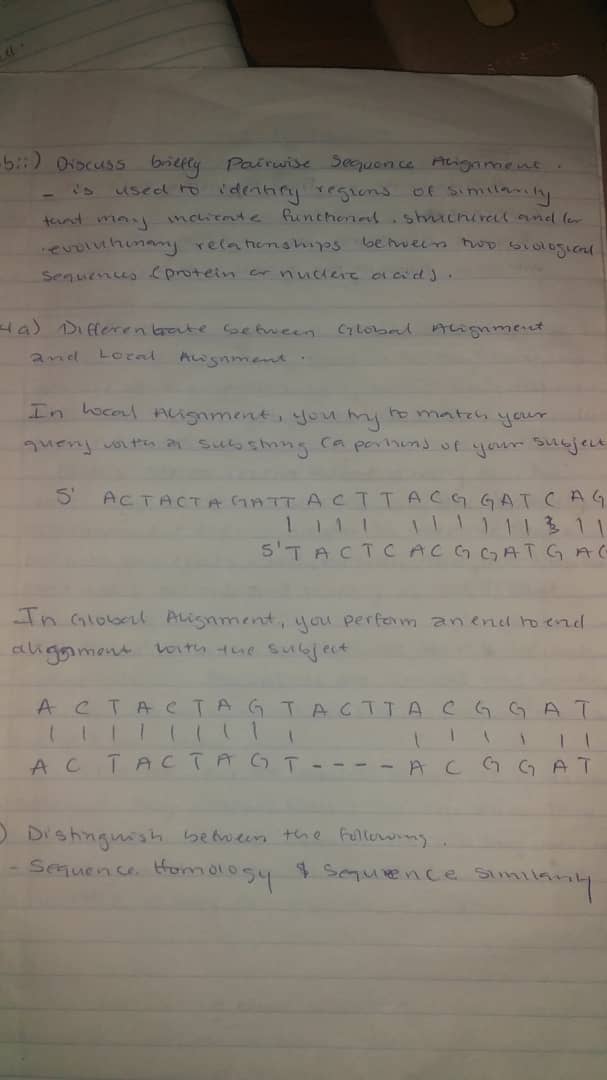
(b)Dynamic programming

(c)Word

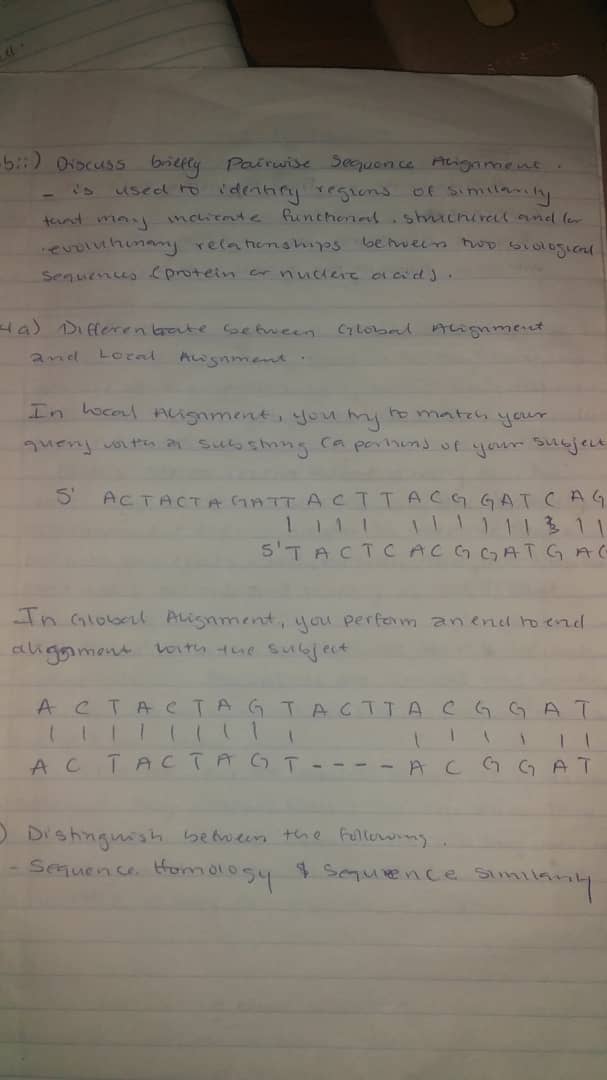
(ii) It is used to identify regions of similarity that may indicate functional, structural and evolutionary relationships between two biological sequences (protein or nucleic acids).

1. (a) Differentiate between Global Alignment and Local Alignment

In local alignment, you try to match your query with a substring (a portion) of your subject.



In global alignment, you perform an end to end alignment with the subject.



(b) Distinguish between the following (i) Sequence Homology and Sequence Similarity (ii)Sequence Similarity and Sequence Identity

(i) Sequence homology is the biological homology between DNA,RNA or protein sequences define in terms of shared ancestry in the evolutionary history of life while Sequence similarity is a measure of an empirical relationship between sequences.

(ii) Sequence similarity is a measure of an empirical relationship between sequences while Sequence identity is the amount of characters which match exactly between two different sequences.