**ADEKANYE UTHMAN AYOTUNDE**

**16/MHS03/003 < CARRY OVER>**

CSC 262 ASSIGNMENT

**ANATOMY**

**400L**

1a

1. Search criteria
2. Query criteria
3. Search criteria means data which meets Idearc’s search element and other requirements (including, without limitation, its Technical Requirements) and which is either (i) entered or selected on, and submitted through, a Search Form by a user, (ii) coded into the applicable Search Form (e.g., a Search Form in the form of a submission button) to be automatically submitted to Idearc in connection with the user’s initiation of a SF Search, and reasonably related to the page of the Local Network on which such submission button appears, or (iii) submitted by a user through a Search Engine. Sample 1 Based on 1 documents
4. query criterion is an expression that Access compares to query field values to determine whether to include the record that contains each value

1b.

BLAST is the most commonly used sequence similarity searching tool. It allows users to construct and perform a blast search with a custom which helps find distant evolutionary relationship.

2a

|  |  |
| --- | --- |
| PAM matrice1. It is used to score alignment between closely related protein sequences
2. Based on global alignment
3. Alignment have high similarity than BLOSUM alignments
4. Mutation in global alignment are very significant
 | BLOSUM matriceIt is used to score alignment between evolutionary divergent protein sequences.Based on local alignment.It has low similarity than PAM alignment.It is based on high conserved stretches of alignment |

2b

 **heuristic**  databasesearching is from a Greek εὑρίσκω "I find, discover") is a technique designed for solving a problem more quickly when classic methods are too slow, or for finding an approximate solution when classic methods fail to find any exact solution. This is achieved by trading optimality, completeness, accuracy, or precision for speed. In a way, it can be considered a shortcut.

A **heuristic function**, also called simply a **heuristic**, is a function that ranks alternatives in search algorithms at each branching step based on available information to decide which branch to follow. For example, it may approximate the exact solution.

3a

1. Sequence homology is the interference or a conclusion about a common ancestral relationship drown from sequence similarity.

ii. sequence similarity is the comparison between two sequences share a high enough degree of similarity or it is the measure of an empirical relationship between sequences.

iii. sequence identity is the amount of characters which match exactly between two different sequences.

3bi. 3 methods of alignment algorithm

1. Dot Matrix Method
2. The dynamic programming method
3. The word method

3bii.

Pair wise sequence alignment; the main applicaton of pairwise sequence alignment is retrieving biological sequences in data bases based on similarity. Pairwise sequence alignment methods are used to find the best-matching piecewise (local or global) alignments of two query sequences. Pairwise alignments can only be used between two sequences at a time, but they are efficient to calculate and are often used for methods that do not require extreme precision (such as searching a database for sequences with high similarity to a query). The three primary methods of producing pairwise alignments are dot-matrix methods, dynamic programming, and word methods.

4ai

|  |  |
| --- | --- |
| Global alignment1. Two sequences are aligned and area assumed to be generally similar over their entire length.
2. It starts at the beginning of the two sequences and add gaps to each until the end of one is reached.
 | Local alignmentTwo sequences are aligned but does not assume that the two sequences in question have similarity over their lengthIt finds the region of highest similarity between the two sequences and build the alignment outward from there. |

4bi

|  |  |
| --- | --- |
| Sequence homology1. It refers to shared encestry, sequences
2. The two sequence are homologous if they are derived from a common ancestral sequence
3. It usually implies similarity
 | Sequence similarityIt refers to the likeness of percentage identity between the two sequencesSharing of statistically sigbificant number of bases of amino acidIt does not imply similarity |

4bii

Sequence similarity refers to the percentage of aligned residues that have similar physiochemical characteristics and can bemore readily substituted for each other

While

Sequence identity refers to the percentage of matches of the same amino acid residues between two designed sequences