

Bioinformatics Assignment - LLLL76

QUESTION ONE

A - 25 MARKS

- given a tree
- given lineage constraints
- in the form $(i, j) < (k, l)$ where (i, j) is the lowest common ancestor of i and j
- using this algorithm a tree will be created such that all lineage constraints are observed
- if no tree can be created then Null will be returned
- this is done by splitting the set of leaf nodes into the number of sets created by removing the root nodes
- and observing a set of rules that are to be followed if a tree is to exist
- 1 - for each constraint i and j are in the same set
- if they are not then the lowest common ancestor is the root node which cannot be a descendent of anything so we have an issue
- 2 - for each constraint if k and l are in the same set the i, j, k, l are in the same set
- if they are not in the same set then they cannot be compared as they are not in the same descendent line.
- 3 - No to leaves are in the same block unless it follows from rules 1 and 2

This is done recursively.

given a set of non empty leaf nodes and the set constraints

if the set contains a single node then return the a tree consisting of only that node

if the set contains more than a single node

remove the root node of the current set

splitting the leaf nodes set into a set of sets

if the number of sets is one then return the null tree

else

for each of the sets

restrict the set of constraints to those that contain any relevant leaf nodes

calculate the tree that satisfies this altered set of leaf nodes and constraints recursively

if the tree returned is the Null tree then return the Null tree

if for every subset in cN no null tree is returned then a tree does exist

let T be the tree with a new node for its root and whose children are the roots of $T_i, 1 \leq i \leq m$
return T

B - 20 MARKS

C - 25 MARKS

D - 25 MARKS

E - 30 MARKS

QUESTION TWO

A - 15 MARKS

B - 10 MARKS