LCA Command

Description

Computes the least common ancestor of a group of nodes in a tree. The tree must be specified in the [Rich Newick Format](#).

Usage

```
LCA tree_ident ({taxon1, taxon2, [, taxon3...]} [{taxon4, taxon5, [, taxon6...]}]) [result output file]
```

tree_ident	The name of the network to analyse.	mandatory
({taxon1, taxon2, [, taxon3...]} [,{taxon4, taxon5, [, taxon6...]}])	A list of sets of taxa in the specified tree.	mandatory
result output file	Optional file destination for command output.	optional

The tool prints the given tree with all internal nodes labeled. If a node is not labeled in the original tree, then the node receives a generated name. Then the tool reads sets of nodes. For each node set read, the command prints their least common ancestor.

Examples

```
#NEXUS

BEGIN TREES;

Tree tree1 = ((1,4,3),2);
Tree tree2 = ((1,2),(4,3));


END;


BEGIN PHYLONET;

LCA tree2 ({1,4}, {2,3});

END;
```

See Also

- [List of PhyloNet Commands](#)