

MAST Command

Description

Computes a Maximum Agreement Subtree of a pair of trees. The trees must be specified in the [Rich Newick Format](#).

The trees must be either all rooted or all unrooted. If the trees are rooted, then the rooted MAST is computed. If the trees are all unrooted, then the unrooted MAST is computed. All trees must also have at least three leaves.

Usage

```
MAST {tree1, tree2} [result output file]
```

{tree1, tree2}	The pair of trees to analyse.	mandatory
-a	A list of sets of taxa in the specified tree.	optional
result output file	Optional file destination for command output.	optional

To compute all MASTs, specify the `-a` parameter. However, since the number of MASTs may be exponential in the number of leaves in the trees, using this option can slow down the execution time (in some cases considerably).

Examples

```
#NEXUS

BEGIN TREES;

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

END;

BEGIN PHYLONET;

MAST {tree1, tree2};

END;
```

Command References

M. Steel and T. Warnow. Kaikoura tree theorems: computing the maximum agreement subtree. *Information Processing Letters*, 48:77–82, 1993.

See Also

- [List of PhyloNet Commands](#)