

SymmetricDifference Command

Description

Computes the symmetric difference, also known as the Robinson-Foulds (RF) distance, between two trees. The trees do not need to be rooted. The trees must be specified in the [Rich Newick Format](#). The tool reads in two trees. It outputs the number of False Negative edges, the number of False Positive edges, the number of internal edges in the experimental tree and finally the number of internal edges in the model tree.

Usage

```
SymmetricDifference model_tree_ident experimental_tree_ident [result output file]
```

<i>model_tree_ident</i>	The name of the model tree to analyse.	mandatory
<i>experimental_tree_ident</i>	The name of the experimetnal to analyse.	mandatory
result output file	Optional file destination for command output.	optional

Examples

```
#NEXUS

BEGIN NETWORKS;

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

END;

BEGIN PHYLONET;

SymmetricDifference tree1 tree2;

END;
```

Command References

- D.R. Robinson and L.R. Foulds. Comparison of phylogenetic trees. *Mathematical Biosciences*, 53:131â147, 1981.

See Also

- [List of PhyloNet Commands](#)