GenST Command

Description

Generates species tree topologies based on maximal sets of compatible clusters. The input trees must be specified in the rich newick format. The generated output trees will be contained in a user specified file and also in rich newick format.

Usage

```
genst {gene_tree_ident1 [, gene_tree_ident2...]} out_file
```

gene_tree_ident1 [, *gene_tree_ident2*...]	Comma delimited set of gene tree identifiers.	mandatory
out_file	The output file destination of the generated species trees.	mandatory

Examples

```
#NEXUS

BEGIN NETWORKS;

Network net1 = ((a,b),(c,(d,(e,(f,g)))));
Network net2 = ((f,b),(c,(d,(a,(e,g)))));

END;


BEGIN PHYLONET;

genst {net1, net2} "C:\temp\genst.out.txt";

END;
```

Command References

- C. Than, R. Sugino, H. Innan, and L. Nakhleh. Efficient inference of bacterial strain trees from genome-scale multi-locus data. The *16th Annual International Conference on Intelligent Systems for Molecular Biololgy (ISMB)*. Bioinformatics, 24:i123–i131, 2008.

See Also

- List of PhyloNet Commands