

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 Biology (ISMB)*. Bioinformatics, 24:i123–i131, 2008.

See Also

- [List of PhyloNet Commands](#)