

# Infer\_ST\_GLASS Command

## Description

Infers the species tree by GLASS. The gene trees must be specified in the [Rich Newick Format](#). The generated output trees will also be generated in the rich newick format.

## Usage

```
infer_ST_GLASS (gene_tree_ident1 [, gene_tree_ident2...]) [-a taxa map] [result output file]
```

<i>gene_tree_ident1</i> [, <i>gene_tree_ident2</i> ...]	Comma delimited list of gene tree identifiers. See <a href="#">details</a> .	mandatory
<i>-a taxa map</i>	Gene tree / species tree <a href="#">taxa association</a> .	optional
<i>result output file</i>	Optional file destination for command output.	optional

Specified gene trees must have branch length. By default, it is assumed that only one individual is sampled per species in gene trees. However, the option `-a` allows multiple alleles to be sampled.

## Examples

```
#NEXUS

BEGIN NETWORKS;

Network g1 = (((a:1,b:2),c:1),d:1),e:2);
Network g2 = (((a:2,b:1),(c:1,e:1),d:2));
Network g3 = ((a:1,c:2),(b:1,e:2),d:1));

END;

BEGIN PHYLONET;

Infer_ST_GLASS (g1, g2, g3);

END;
```

## Command References

- Elchanan Mossel and Sebastien Roch. Incomplete lineage sorting: Consistent phylogeny estimation from multiple loci. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2008.

## See Also

- [List of PhyloNet Commands](#)