

Infer_ST_MC Command

Description

Infer the species tree from gene trees using an greedy consensus which can deal with gene trees having multiple alleles in species and unrooted gene trees. 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_MC (gene_tree_ident1 [, gene_tree_ident2...]) [-u] [-a taxa map] [result output file]
```

<i>gene_tree_ident1</i> [, <i>gene_tree_ident2</i> ...]	Comma delimited list of gene tree identifiers. See details .	mandatory
-u	Specifies gene trees should be treated as unrooted.	optional
-a <i>taxa map</i>	Gene tree / species tree taxa association .	optional
<i>result output file</i>	Optional file destination for command output.	optional

By default, it is assumed that gene trees are rooted. However, the option `-u` can specify gene trees to be treated as unrooted. 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,b),c),d),e);
Network g2 = ((a,b),((c,e),d));
Network g3 = ((a,c),((b,e),d));

END;

BEGIN PHYLONET;

Infer_ST_MC (g1, g2, g3);

END;
```

See Also

- [List of PhyloNet Commands](#)