

Infer_ST_MDC_Time Command

Description

Infer the species tree using MDC criterion but considering time. The input gene trees must be specified in the [Rich Newick Format](#). Gene trees must be rooted and have branch length. Gene losses are allowed. The generated output trees will also be generated in the rich newick format.

The resulting species trees are displayed with the number of extra lineages in each branch. For example, consider the following inferred species tree:

```
((a:0,b:0):2,(c:0,d:0):1):0
```

In this species tree, there are two extra lineages in branch between node (a, b) and the root, and one extra lineage in branch between node (c, d) and the root. All other branches have 0 extra lineages.

Usage

```
infer_ST_MDC_TIME (gene_tree_ident1 [, gene_tree_ident2...]) [-b threshold] [-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
<i>-b threshold</i>	Specifies bootstrap threshold. Edges in the gene trees that have support lower than <i>threshold</i> will be contracted.	optional
<i>-a taxa map</i>	Gene tree / species tree taxa association .	optional
<i>result output file</i>	Optional file destination for command output.	optional

A bootstrap threshold can be set with the *-b* option.

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:5,b:5):4,c:9):3,d:12):3,e:15);
Network g2 = ((a:6,b:6):11,((c:12,e:12):2,d:14):3);
Network g3 = ((a:8,c:8):7,((b:14,e:14):1,d:15));

END;

BEGIN PHYLONET;

Infer_ST_MDC_Time (g1, g2, g3);

END;
```

See Also

- [List of PhyloNet Commands](#)