

ProcessGT Command

Description

Refines and root gene trees with respect to a rooted binary species tree under MDC criterion. The input gene trees must be specified in the [Rich Newick Format](#). Gene trees can be either rooted or unrooted. Gene losses are allowed. The generated output trees will also be generated in the rich newick format. Multiple species trees may be specified in which case the tool will run in batch mode with one execution of each species tree and set of gene trees.

Usage

```
Process_GT {species_tree_ident1 [, species_tree_ident2...]} {gene_tree_ident1 [, gene_tree_ident2...]} [-u] [-b threshold] [-a taxa map] [result output file]
```

<code>{species_tree_ident1 [, species_tree_ident2...]}</code>	Comma delimited set of species tree identifiers.	mandatory
<code>{gene_tree_ident1 [, gene_tree_ident2...]}</code>	Comma delimited set of gene tree identifiers. See details .	mandatory
<code>-u</code>	Treat gene trees as unrooted.	optional
<code>-b threshold</code>	Specifies bootstrap threshold. Edges in the gene trees that have support lower than <i>threshold</i> will be contracted.	optional
<code>-a taxa map</code>	Gene tree / species tree taxa association .	optional
<code>result output file</code>	Optional file destination for command output.	optional

By default, it is assumed that gene trees are rooted. In this case, the method refines the gene trees with respect to the species tree. If the gene trees are unrooted, users can use option `-u`. In this case, the method not only refines and but also roots gene trees.

If input gene trees have bootstrap values a 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 TREES;

Tree speceiesTree = (((a:1,b:2),c:3),d:4),e:5);
Tree geneTree1 = (((a:1,b:2,c:3),d:4),e:5);
END;

BEGIN PHYLONET;

ProcessGT {speceiesTree} {geneTree1};

END;
```

Command Refernces

- Y. Yu, T. Warnow, and L. Nakhleh. Algorithms for MDC-based multi-locus phylogeny inference. _The 15th Annual International Conference on Research in Computational Molecular Biology (RECOMB)_ , pages 531--545, 2011. LNBI 6577.

See Also

- [List of PhyloNet Commands](#)