

DeepCoalCount_tree Command

Description

Counts the number of extra lineages contributed by a species tree and a set of gene trees. The trees must be specified in the [Rich Newick Format](#). Specifying more than one species tree will run the command multiple times with one execution per species tree.

Usage

```
DeepCoalCount_tree {species_tree_ident1 [, species_tree_ident2...]} (gene_tree_ident1 [, gene_tree_ident2...])  
[-u] [-b threshold] [-a taxa map] [resultOutputFile]
```

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

The command assumes that the trees are rooted. Gene trees may be reinterpreted as unrooted with the [-u] flag.

By default, it is assumed that only one individual is sampled per species in gene trees. However, the option [-a [taxa map](#)] allows multiple alleles to be sampled.

Examples

```
#NEXUS  
  
BEGIN TREES;  
  
Tree speceiesTree = (((a,b),c),d),e);  
Tree geneTree1 = (((a,b),c),d),e);  
Tree geneTree2 = ((a,b),((c,e),d));  
Tree geneTree3 = ((a,c),((b,e),d));  
  
END;  
  
BEGIN PHYLONET;  
  
DeepCoalCount_Tree {speceiesTree} (geneTree1, geneTree2, geneTree3);  
  
END;
```

```
#NEXUS

BEGIN TREES;

Tree speceiesTree = (((x,y),w),m),n);
Tree geneTree1 = (((a::.5,b::.5)::.5,c::.5)::.5,d::.5)::.5,e::.5)::.5;
Tree geneTree2 = ((a::.5,b::.5)::.5,(c::.5,e::.5)::.5,d::.5)::.5;
Tree geneTree3 = ((a::.5,c::.5)::.5,(b::.5,e::.5)::.5,d::.5)::.5;

END;

BEGIN PHYLONET;

DeepCoalCount_tree {speciesTree} (geneTree1, geneTree2, geneTree3) -u -b .5 -a <x:a; y:b; w:c; m:d; n:e>;

END;
```

Command References

- C. Than and L. Nakhleh. Species tree inference by minimizing deep coalescences. *PLoS Computational Biology*, 5(9):e1000501, 2009.
- Y. Yu, T. Warnow, and L. Nakhleh, "Algorithms for MDC-based multi-locus phylogeny inference." *Proceedings of the 15th Annual International Conference on Research in Computational Molecular Biology (RECOMB)*, LNBI 6577, 531-545, 2011.
- Y. Yu, T. Warnow, and L. Nakhleh, "Algorithms for MDC-based multi-locus phylogeny inference: Beyond rooted binary gene trees on single alleles." *Journal of Computational Biology*, 18(11): 1-18, 2011.

See Also

- [List of PhyloNet Commands](#)