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]
```

species_tree_ident1 [, *species_tree_ident2*...]	Comma delimited set of species tree identifiers.	mandatory
gene_tree_ident1 [, *gene_tree_ident2*...]	Comma delimited list of gene tree identifiers. See details.	mandatory
-u	Gene trees should be treated as unrooted.	optional
-b *threshold*	Gene tree bootstrap threshold. Edges in the gene trees that have support lower than *threshold* will be contracted.	optional
-a *taxa map*	Gene tree / species tree taxa association.	optional
resultOutputFile	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)::.5;
Tree geneTree3 = ((a::.5,c::.5)::.5,((b::.5,e::.5)::.5,d::.5)::.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