

DeepCoalCount_network

Description

Counts the minimum number of extra lineages required to reconcile a list of gene trees within the branches of a phylogenetic network. The species network and gene trees must be specified in the [Rich Newick Format](#).

The input gene trees can be gene tree distributions inferred from Bayesian methods like MrBayes.

Usage

```
DeepCoalCount_network network_ident (gene_tree_ident1 [, gene_tree_ident2...]) [-a taxa map] [-b threshold] [-m ac|mul] [resultOutputFile]
```

<i>network_ident</i>	The name of the network.	mandatory
<i>gene_tree_ident1</i> [, <i>gene_tree_ident2</i> ...]	Comma delimited list of gene tree identifiers. See details .	mandatory
<i>-m ac or mul</i>	Specify the algorithm used for computation (see reference). The default value is <i>ac</i> .	optional
<i>-a taxa map</i>	Gene tree / species tree taxa association .	optional
<i>-b threshold</i>	Specifies gene trees bootstrap threshold. Edges in the gene trees that have support lower than <i>threshold</i> will be contracted.	optional
<i>resultOutputFile</i>	Optional file destination for command output.	optional

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.

The *-m* option is used to specify the algorithm for computation, where *mul* stands for the algorithm based on MUL-trees (Yu Et. Al, under review) and *ac* stands for the algorithm based on ancestral configurations (Yu and Nakhleh, under review). They produce exactly the same result, but the latter one is more efficiently in general cases.

Examples

```
#NEXUS

BEGIN NETWORKS;

Network net = ((A:2,((B:1,C:1):1)X#H1:0::0.3):1,(D:2,X#H1:0::0.7):1);

END;

BEGIN TREES;

Tree geneTree1 = (C,((B,D),A));
Tree geneTree2 = (B,(D,(C,A)));
Tree geneTree3 = (D,(B,(C,A)));

END;

BEGIN PHYLONET;

DeepCoalCount_network net (geneTree1,geneTree2,geneTree3);

END;
```

Command References

- Y. Yu, R.M. Barnett, and L. Nakhleh. Parsimonious inference of hybridization in the presence of incomplete lineage sorting. Under review.
- Y. Yu and L. Nakhleh. Fast algorithms for reconciliation under hybridization and incomplete lineage sorting. Under review.

See Also

- [List of PhyloNet Commands](#)