

DeepCoalCount_AlloppNet

Description

Counts the minimum number of extra lineages required to reconcile a list of gene trees within the branches of an allopolyploid 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_AlloppNet network_ident (gene_tree_ident1 [, gene_tree_ident2...]) [-a taxa map] [-b threshold]
[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>-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

Examples

```
#NEXUS

BEGIN NETWORKS;

Network net = (((((X,Y)I5,Z)I4)I7#H1,B)I6,A)I1,(D,(I7#H1,C)I3)I2)I0;

END;

BEGIN TREES;

Tree geneTree1 = (((a,b),(x1,y1)),(c,((x2,z2),d)));
Tree geneTree2 = (((((x1,y1),z1),b),a),(((x2,y2),z2),c),d));

END;

BEGIN PHYLONET;

DeepCoalCount_AlloppNet net (geneTree1,geneTree2) -a < A:a; C:c; B:b; D:d; X:x1,x2; Y:y1,y2; Z:z1,z2>;

END;
```

Command References

- Yan, Z., Cao, Z., Liu, Y., and Nakhleh, L. Species Network Inference in the Presence of Polyploid Complexes Using PhyloNet. Manuscript in preparation.
- Yu, Y., Barnett, R., and Nakhleh, L. 2013. [Parsimonious inference of hybridization in the presence of incomplete lineage sorting](#). Systematic Biology, 62(5): 738–751.

See Also

- [List of PhylNet Commands](#)