CalIntroRate

Description

For each reticulation branch *e* in the given phylogenetic network, quantifies the introgression probability *a(g,e)* as the probability of gene tree *g* "used" the branch *e*.

The species network and gene trees must be specified in the Rich Newick Format. The branch lengths and the inheritance probabilities in the species network need to be specified. Only topologies of gene trees are used in the method.

Usage

```
CalIntroRate network geneTreeList
```

network	The name of the network.	mandatory
geneTreeList	Comma delimited list of gene tree identifiers or comma delimited list of sets of gene tree identifiers. See details.	mandatory

Examples

```
#NEXUS

BEGIN NETWORKS;

Network net = ((((R:1.0)I12#H1:1.0::0.79)I10#H2:1.0::0.52,(((Q:1.0,I12#H1:1.0::0.21)I11:5.94,((A:1.0,(C:1.0,G:1.0)I5:1.00)I4:0.92)I6#H3:1.13::0.97)I3:0.91,(L:1.0,I10#H2:1.0::0.48)I9:0.33)I2:5.94)I1:0.84,I6#H3:0.01::0.03)I0;

END;


BEGIN TREES;

Tree geneTree1 = ((L,R),(Q,(A,(G,C))));
Tree geneTree2 = (R,(L,(A,(Q,(G,C)))));
Tree geneTree3 = (R,(L,(Q,(G,(A,C)))));

END;


BEGIN PHYLONET;

CalIntroRate net ({geneTree1,geneTree2,geneTree3});

END;
```

```
#NEXUS

BEGIN NETWORKS;

Network net = ((((R:1.0)I12#H1:1.0::0.79)I10#H2:1.0::0.52,(((Q:1.0,I12#H1:1.0::0.21)I11:5.94,((A:1.0,(C:1.0,G:1.0)I5:1.00)I4:0.92)I6#H3:1.13::0.97)I3:0.91,(L:1.0,I10#H2:1.0::0.48)I9:0.33)I2:5.94)I1:0.84,I6#H3:0.01::0.03)I0;

END;


BEGIN TREES;

Tree geneTree1 = ((L,R),(Q,(A,(G,C))));
Tree geneTree2 = (R,(L,(A,(Q,(G,C)))));
Tree geneTree3 = (R,(L,(Q,(G,(A,C)))));

END;


BEGIN PHYLONET;

CalIntroRate net (geneTree1,geneTree2,geneTree3);

END;
```

Command References

- Wen, D., Yu, Y., Hahn, M. W., & Nakhleh, L. "Reticulate evolutionary history and extensive introgression in mosquito species revealed by phylogenetic network analysis." *Molecular ecology* (2016).

See Also

- List of PhyloNet Commands