

CallIntroRate

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
```

<i>network</i>	The name of the network.	mandatory
<i>geneTreeList</i>	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)l12#H1:1.0::0.79)l10#H2:1.0::0.52,(((Q:1.0,l12#H1:1.0::0.21)l11:5.94,((A:1.0,(C:1.0,G:1.0)l5:1.00)l4:0.92)l6#H3:1.13::0.97)l3:0.91,(L:1.0,l10#H2:1.0::0.48)l9:0.33)l2:5.94)l1:0.84,l6#H3:0.01::0.03)l0;
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;
CallIntroRate 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;

CallIntroRate 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](#)