

Referring gene trees

Formats

Many commands use a list of gene trees, which are contained in TREE block, as input. There are two formats.

- One is comma delimited list of gene tree identifiers, as below, which indicates each tree is from a different locus.

```
(gene_tree_ident1 [, gene_tree_ident2...])
```

This format is valid for all commands that require a list of gene trees as input.

- One is delimited list of sets of gene tree identifiers, as below, where gene trees in the same set are from one locus.

```
({gene_tree_ident1, [, gene_tree_ident2...]} [, {gene_tree_ident3, [, gene_tree_ident4...]}])
```

It is usually used when gene trees are reconstructed from Bayesian method. For example,

```
#NEXUS

BEGIN TREES;

Tree gt1 = [&W 0.9] ((C,((B,D),A)),E);
Tree gt2 = [&W 0.1] (B,(D,(C,(A,E))));
Tree gt3 = [&W 0.6] (D,(B,((C,E),A)));
Tree gt4 = [&W 0.4] (D,((B,E),(C,A)));

END;

BEGIN PHYLONET;

InferNetwork_ML ({gt1,gt2},{gt3,gt4}) 1;

END;
```

where gt1 and gt2 (and gt3 and gt4) are trees from one locus with posterior probabilities.

Or bootstrapping.

```
#NEXUS

BEGIN TREES;

Tree gt1 = ((C,((B,D),A)),E);
Tree gt2 = (B,(D,(C,(A,E))));
.....
Tree gt200 = (D,((B,E),(C,A)));

END;

BEGIN PHYLONET;

InferNetwork_ML ({gt1-gt100},{gt101-gt200}) 1;

END;
```

where gt1 to gt100 (and gt101 to gt200) are 100 bootstrap replicates from one locus.

Note that this format is only valid for command [InferNetwork_ML](#) and [CalGTProb](#).

Abbreviation

- using '-' : trees are named continuously with the same prefix

```
#NEXUS

BEGIN TREES;

Tree gt1 = ((C,((B,D),A)),E);
Tree gt2 = (B,(D,(C,(A,E))));
.....
Tree gt200 = (D,((B,E),(C,A)));

END;

BEGIN PHYLONET;

InferNetwork_MP (gt1-gt200) 1;

END;
```

- using 'all' : all trees in TREES block will be used

```
#NEXUS

BEGIN TREES;

Tree gt1 = ((C,((B,D),A)),E);
Tree gt2 = (B,(D,(C,(A,E))));
.....
Tree gt200 = (D,((B,E),(C,A)));

END;

BEGIN PHYLONET;

InferNetwork_MP (all) 1;

END;
```