InferNetwork_ML_Bootstrap

Description

Infers a species network from a collection of gene trees with parametric bootstrap.

Usage

```
InferNetwork_ML_Bootstrap (gene_tree_ident1 [, gene_tree_ident2...]) numReticulations [-sr samplingRound] [-bl]
[-ms MSCommand] [-em softwired|hardwired] [-a taxa map] [-b threshold] [-s startingNetwork] [-h {s1 [,s2...]}]
[-w (w1,...,w7)] [-x numRuns] [-m maxNetExamined] [-md moveDiameter] [-rd reticulationDiameter] [-o] [-p (rel,
abs)] [-r maxRounds] [-t maxTryPerBr] [-i improveThreshold] [-l maxBL] [-pl numProcessors] [-di]
[resultOutputFile]
```

gene_tree_ident1 [, *gene_tree_ident2*...]	Comma delimited list of gene tree identifiers. See details.	mandatory
numReticulations	Maximum number of reticulations to added.	mandatory
-sr *samplingRounds*	Number of sampling processes repeated in parametric bootstrap. Default value is 100.	optional
-bl	Include the branch lengths of the gene trees in the inference. The gene trees need to be ultrametric and branch lengths need to be in coalescent units.	optional
-ms *MSCommand*	The path of the executable of MS software. Must be specified if -bl above is used.	optional
-em *softwired* | *hardwired*	The method that is used for evaluate the support of the branches in the inferred network. Options include softwired and hardwired cluster-based method. By default, softwired is used.	optional
-b *threshold*	Gene trees bootstrap threshold. Edges in the gene trees that have support lower than *threshold* will be contracted.	optional
-a *taxa map*	Gene tree / species tree taxa association.	optional
-s *startingNetwork*	Specify the network to start search. Default value is the optimal MDC tree.	optional
-h *{s1 [, s2...]}*	A set of specified hybrid species.	optional
-w *(w1, ..., w7)*	The weights of operations for network arrangement during the network search. Default value is (0.1,0.1,0.15,0.55,0.15,0.15,2.8).	optional
-x *numRuns*	The number of runs of the search. Default value is 5.	optional
-m *maxNetExamined*	Maximum number of network topologies to examined. Default value is infinity.	optional
-md *moveDiameter*	Maximum diameter to make an arrangement during network search. Default value is infinity.	optional
-rd *reticulationDiameter*	Maximum diameter for a reticulation event (the distance between two parents of a reticulation node). Default value is infinity.	optional
-o	If specified, after the search the returned species networks will be optimized for their branch lengths and inheritance probabilities.	optional
-p *(rel, abs)*	The original stopping criterion of Brent's algorithm. Default value is (0.01, 0.001).	optional
-r *maxRound*	Maximum number of rounds to optimize branch lengths for a network topology. Default value is 100.	optional
-t *maxTryPerBr*	Maximum number of trial per branch in one round to optimize branch lengths for a network topology. Default value is 100.	optional

-i *improveThreshold*	Minimum threshold of improvement to continue the next round of optimization of branch lengths. Default value is 0.001.	optional
-l *maxBL*	Maximum branch lengths considered. Default value is 6.	optional
-pl *numProcessors*	Number of processors if you want the computation to be done in parallel. Default value is 1.	optional
-di	Output the Rich Newick string of the inferred network that can be read by Dendroscope .	optional
resultOutputFile	Optional file destination for command output.	optional

In parametric bootstrap, the sampling process is repeated 100 times. Users can change this number using option *-sr*.

By default, only topologies of the gene trees are used in the computation. However, users can use option *-bl* to include the branch lengths of the gene trees in the computation. If so, the input gene trees must be
ultrametric and the branch lengths need to be in coalescent units. By specifying option *-bl*, users need to have MS software (Hudson R.R. 2002) downloaded (http://home.uchicago.edu/~rhudson1/source/mksamples.html),
and then provide the executable including its path through option *-ms*. For example, if having the executable locally at /tools/MS/ms, then "-ms /tools/MS/ms" needs to be specified. Note that it is not necessary if only topologies of the gene trees are used (not using *-bl*).

See command InferNetwork_ML for all other parameters.

Examples

```
#NEXUS

BEGIN TREES;

TREE gt0 = (D:7.07072,((C:3.56753,B:3.56753):1.76822,A:5.33575):1.73497);
TREE gt1 = (((B:1.97661,C:1.97661):2.23864,A:4.21524):1.77987,D:5.99511);
TREE gt2 = ((C:4.31675,(B:3.14621,A:3.14621):1.17054):2.09695,D:6.4137);
TREE gt3 = ((D:5.83927,A:5.83927):0.566624,(B:1.80987,C:1.80987):4.59603);
TREE gt4 = ((D:5.77537,(B:1.77451,C:1.77451):4.00086):0.810136,A:6.58551);
TREE gt5 = (D:6.80413,(A:3.82444,(C:2.31671,B:2.31671):1.50773):2.97969);
TREE gt6 = (D:7.61541,(C:4.41986,(A:2.52336,B:2.52336):1.8965):3.19554);
TREE gt7 = ((A:4.99068,(C:3.03372,B:3.03372):1.95696):0.782212,D:5.77289);
TREE gt8 = (D:5.95232,((C:1.86462,B:1.86462):3.20304,A:5.06765):0.88467);
TREE gt9 = ((A:3.84332,(C:3.74007,B:3.74007):0.103251):4.82743,D:8.67075);
TREE gt10 = ((A:4.19291,(C:1.73235,B:1.73235):2.46056):2.60752,D:6.80043);
TREE gt11 = (A:7.35563,((B:1.7592,C:1.7592):4.0683,D:5.8275):1.52813);
TREE gt12 = (((B:3.14432,A:3.14432):0.613233,C:3.75755):1.95882,D:5.71638);
TREE gt13 = (((C:2.6677,B:2.6677):2.66994,A:5.33764):4.71766,D:10.0553);
TREE gt14 = ((C:4.00286,(B:3.0957,A:3.0957):0.907165):1.94607,D:5.94893);
TREE gt15 = (D:5.89168,(A:3.77037,(B:2.13754,C:2.13754):1.63283):2.12131);
TREE gt16 = (D:6.43412,(A:3.85214,(B:2.6542,C:2.6542):1.19794):2.58198);
TREE gt17 = (D:6.27103,((B:1.80021,C:1.80021):1.91286,A:3.71307):2.55796);
TREE gt18 = (((C:1.72131,B:1.72131):4.04022,A:5.76154):2.49476,D:8.25629);
TREE gt19 = (((B:1.8262,C:1.8262):2.49809,A:4.32429):3.80882,D:8.13311);
TREE gt20 = (D:6.95436,((B:2.60072,C:2.60072):1.85771,A:4.45842):2.49594);

END;


BEGIN PHYLONET;

InferNetwork_ML_Bootstrap (gt0,gt1,gt2,gt3,gt4,gt5,gt6,gt7,gt8,gt9,gt10,gt11,gt12,gt13,gt14,gt15,gt16,gt17,gt18,
gt19,gt20) 1;

END;
```

Command References

- Y. Yu, J. Dong, K. Liu, and L. Nakhleh, Maximum Likelihood Inference of Reticulate Evolutionary Histories, Proceedings of the National Academy of Sciences, vol. 111, no. 46, pp. 16448-16453, 2014

See Also

- List of PhyloNet Commands