

NetMerger

Description

A divide-and-conquer approach to infer large network from multi-locus sequence alignments or bi-allelic markers.

Usage

To reduce the number of trinets

This mode will generate a bunch of triplets using the heuristic to reduce the number of subproblems, by covering the internal branches of gene trees.

NetMerger -mode "Triplets" [-outgroup outgroup] [-tm taxonMap] [-gts gtsFilePath] [-triplets tripletsFilePath]		
-outgroup <i>outgroup</i>	The taxon in species network designated to be the "outgroup".	required
-tm <i>taxonMap</i>	Gene tree / species tree taxa association of the full data set.	required
-gts <i>gtsFilePath</i>	The path to the text file, in which each line is a gene tree.	required
-triplets <i>tripletsFilePath</i>	The path to the file to be written with triplets. Each line of the file has three species, separated by space.	required

To divide the data set into subsets

In this mode, user can provide a "template" nexus file with regular "MCMC_SEQ" or "MCMC_BiMarkers" command. Then this mode will generate a bunch of new nexus files, under the same folder as the template, and replace the taxon mapping in the template file by a subset of that mapping. Therefore if PhyloNet uses a new nexus file as an input, a trinet will be inferred. The user can specify whether the full set or reduced set of trinets needs to be inferred.

NetMerger -mode "Nex" [-nex nexFilePath] [-tm taxonMap] [-triplets tripletsFilePath]		
-nex <i>nexFilePath</i>	The path to the "template" nexus file.	required
-tm <i>taxonMap</i>	Gene tree / species tree taxa association of the full data set.	required
-triplets <i>tripletsFilePath</i>	The path to the text file with triplets. Each line of the file has three species, separated by space. If not specified, the full set of subproblems will be generated.	optional

To merge trinets

Users can run PhyloNet with generated new nexus files. After trinets are inferred, those results generated by MCMC_SEQ or MCMC_BiMarkers can be merged by NetMerger. If the set of trinets needs to be enriched, a list of triplets will be provided, otherwise a final network is produced.

NetMerger -mode "Result" [-cl chainLength] [-bl burnInLength] [-sf sampleFrequency] [-outgroup outgroup] [-inputFolder inputFolder]		
-cl <i>chainLength</i>	The length of the MCMC chain.	required
-bl <i>burnInLength</i>	The number of iterations in burn-in period of MCMC inference.	required

-sf <i>sampleFrequency</i>	The sample frequency in MCMC inference.	required
-outgroup <i>outgroup</i>	The taxon in species network designated to be the "outgroup".	required
-inputFolder <i>inputFolder</i>	The folder where results of MCMC_SEQ or MCMC_BiMarkers locate. Each file ends in ".out" is a single inference of a subnetwork.	required

Example

```
#NEXUS

BEGIN PHYLONET;

NetMerger -mode "Triplets" -gts "/Users/zhujiafan/Documents/BioinfoData/SuperNetwork/NetMerger/gts.txt"

-triplets "/Users/zhujiafan/Documents/BioinfoData/SuperNetwork/NetMerger/triplets.txt"

-outgroup "Z"

-tm <A:A_0,A_1;B:B_0,B_1;C:C_0,C_1;D:D_0,D_1;E:E_0,E_1;F:F_0,F_1;G:G_0,G_1;H:H_0,H_1;I:I_0,I_1;J:J_0,J_1;K:K_0,K_1;L:L_0,L_1;M:M_0,M_1;N:N_0,N_1;O:O_0,O_1;P:P_0,P_1;Z:Z_0,Z_1> ;

END;
```

The above command writes triplets to file "/Users/zhujiafan/Documents/BioinfoData/SuperNetwork/NetMerger/triplets.txt" according to the gene trees in "/Users/zhujiafan/Documents/BioinfoData/SuperNetwork/NetMerger/gts.txt".

```
#NEXUS

BEGIN PHYLONET;

NetMerger -mode "Nex" -nex "/Users/zhujiafan/Documents/BioinfoData/SuperNetwork/NetMerger/newtest.nex"

-triplets "/Users/zhujiafan/Documents/BioinfoData/SuperNetwork/NetMerger/triplets.txt"

-tm <A:A_0,A_1;B:B_0,B_1;C:C_0,C_1;D:D_0,D_1;E:E_0,E_1;F:F_0,F_1;G:G_0,G_1;H:H_0,H_1;I:I_0,I_1;J:J_0,J_1;K:K_0,K_1;L:L_0,L_1;M:M_0,M_1;N:N_0,N_1;O:O_0,O_1;P:P_0,P_1;Z:Z_0,Z_1> ;

END;
```

The above command produces "newtest_0.nex", "newtest_1.nex", etc, under the folder "/Users/zhujiafan/Documents/BioinfoData/SuperNetwork/NetMerger/". The number of new nexus files equals to the number of triplets provided in "/Users/zhujiafan/Documents/BioinfoData/SuperNetwork/NetMerger/triplets.txt". Each new nexus file can be used as the input of PhyloNet.

```
#NEXUS

BEGIN PHYLONET;

NetMerger -cl 6000000 -bl 3000000 -sf 5000 -inputFolder "/Users/zhujiafan/Documents/BioinfoData/results/"
-outgroup "Z" ;

END;
```

The above command parses all files end with ".out" under the folder "/Users/zhujiafan/Documents/BioinfoData/results/", then merges those trinetts generated by Bayesian inference. The command terminates and provides additional triplets if the set of trinetts needs to be enriched, otherwise it produces the final network.

Command References

1. D.Wen and L. Nakhleh. Co-estimating reticulate phylogenies and gene trees on sequences from multiple independent loci.
2. J. Zhu, X. Liu, H.A. Ogilvie and L. Nakhleh. [A Divide-and-Conquer Method for Scalable Phylogenetic Network Inference from Multi-locus Data](#)

See Also

- [List of PhyloNet Commands](#)