

HmmCommand

Description

Uses a hidden markov to assign a species tree to each loci in data coming from a species network.

Usage

Before using this command, you need to get [lib.zip](#). Assuming it is then unzipped to *LocalPath* where the unzipped folder is located,

- Mac: use `-Djava.library.path=LocalPath/lib`, when launching PhyloNet from command line.
- Linux: add *LocalPath/lib* to your `LD_LIBRARY_PATH`, before launching PhyloNet from command line.
- Windows: please contact us.

```
HmmCommand species_network [-gtr] [-allelemap taxaMap] [-iterations numIterations] [-threads numThreads] [-numberofruns numRuns] [-noplots] [-outputdirectory outputLocation]
```

<i>species_network</i>	The species network topology of the data. Branch lengths are not needed.	mandatory
<code>-gtr</code>	Changes the mutation model from the default JC to GTR.	optional
<code>-allelemap taxaMap</code>	Gene tree / species network taxa association .	optional
<code>-iterations numIterations</code>	The number of hill climbing iterations to use for each run.	optional
<code>-threads numThreads</code>	The number of threads to use when processing.	optional
<code>-numberofruns numRuns</code>	The number of times to restart the hill climbing process.	optional
<code>-noplots</code>	Stop showing plots when finished.	optional
<code>-outputdirectory outputLocation</code>	The directory to store the output of the run.	optional

Examples

```
#NEXUS

BEGIN NETWORKS;
Network net = ((A:3,ANC#H1:2.25):2,((B:.75)ANC#H1:0,C:.75):4.25);
END;

Begin DATA;
  dimensions ntax=3 nchar=6;
  format datatype=dna symbols="ACTG" missing=? gap=-;
  matrix
1   AGGTGG
2   AACCTT
3   ACCTGT
;
END;

BEGIN PHYLONET;
HmmCommand net -allelemap <A:1; B:2; C:3> -outputdirectory "foo" -threads 4 -iterations 300;
END;
```

Command References

- Liu KJ, Dai J, Truong K, Song Y, Kohn MH, and Nakhleh L (2014) An HMM-Based Comparative Genomic Framework for Detecting Introgression in Eukaryotes. PLoS Comput Biol 10(6): e1003649.
- Liu KJ, Steinberg E, Yozzo A, Song Y, Kohn MH, and Nakhleh L (2014) Interspecific Introgressive Origin of Genomic Diversity in the House Mouse. Under review.

See Also

- [List of PhyloNet Commands](#)