

# 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 <a href="#">taxa association</a> .           | 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](#)