

Multilocus Data

Formats

Multilocus data is a list of sequence alignments, which is contained in DATA block of a nexus file. Commands use multilocus data are listed:

- [MCMC_SEQ](#): Co-estimation of reticulate phylogenies (ILS & hybridization) and gene trees from multiple independent loci.

Here is an example:

```
#NEXUS
Begin data;
    Dimensions ntax=5 nchar=80;
    Format datatype=dna symbols="ACTG" missing=? gap=-;
    Matrix
[YAL053W, 25, ...]
Scer TCTTTATTGACGTGTATGGACAATT
Spar TCTTTGTTAACGTGCATGGACAATT
Smik TCCTTGCTAACATGCATGGACAATT
Skud TCTTTGCTAACGTGCATGGATAATT
Sbay TCTTTACTAACGTGCATGGATAACT
[YAR007C, 30]
Scer ATGAGCAGTGTTCAACTTTCGAGGGGCGAT
Spar ATGAGCAGCGTTCAACTTTCGAAGGGCGAC
Smik ATGAGCAGCGTGCAACTATCAAAGGGCGAC
Skud ATGAGCAGTGTTCAACTTTCGAAGGGCGAC
Sbay ATGAGCAGCGTTCAACTTTCGAAGGGCGAC
[YBL015W, 25]
Scer TCTAATTTGTTAAAGCAGAGAGTTA
Spar TCTAATTTGTTAAAGCAGAGAGTTA
Smik TCTAATTTGTTAAACAGAGAGTTT
Skud TCTAATCTGTTGAAGCAGAGAGTTA
Sbay TCTAATCTGTTGAAGCAAAAAGTCA
;End;
BEGIN PHYLONET;
MCMC_SEQ -loci (YBL015W,YAR007C) -cl 550000 -bl 50000 -sf 5000;
END;
```

Mandatory info:

- number of taxon in the sequence alignments: "ntax=#numTaxon"
- the name and the length of sequences of the locus: "[#locusName, #seqLen]" or "[#locusName, #seqLen, #extraInfo]"
- the sequence alignment: "#speciesName sequence"