

Phylogenetic Inference using RevBayes

Total-evidence Dating under the FBD Model

Tracy A. Heath, April Wright, and Walker Pett

1 Introduction

[Ronquist et al. \(2012\)](#)

1.1 Models

1.1.1 Sequence Evolution

Point to other tutorials (e.g., GTR stuff)

1.1.2 Morphological Character Change

Mk models and ascertainment bias

1.1.3 Lineage-Specific Substitution Rates

Clocks ([Zuckerkandl and Pauling 1962](#)) and relaxing them

1.1.4 Lineage Diversification and Sampling

Birth-death processes and FBD

2 Prerequisites

What do you need to know before doing this?

2.1 Requirements

We assume that you have read and hopefully completed the following tutorials:

- `RB_Getting_Started`
- `RB_Basics_Tutorial`

Note that the `RB_Basics_Tutorial` introduces the basic syntax of `Rev` but does not cover any phylogenetic models. You may skip the `RB_Basics_Tutorial` if you have some familiarity with `R`. We tried to keep this tutorial very basic and introduce all the language concepts on the way. You may only need the `RB_Basics_Tutorial` for a more in-depth discussion of concepts in `Rev`.

3 Data and files

We provide the data file(s) which we will use in this tutorial. You may want to use your own data instead. In the **data** folder, you will find the following files

- **bears_extant_cytb.nex**: description of file/data (we also need more descriptive file names).

4 Exercise: Title

4.1 Getting Started

We will complete this analysis in **RevBayes** by entering the **Rev** code interactively.

4.2 Loading the Data

→ Download data and output files (if you don't have them already) from:
<http://revbayes.github.io/tutorials.html>

First load in the sequences using the **readDiscreteCharacterData()** function.

```
data <- readDiscreteCharacterData("data/bears_cytb.nex")
```

Executing these lines initializes the data matrix as the respective **Rev** variables. To report the current value of any variable, simply type the variable name and press enter. For the **data** matrix, this provides information about the alignment:

```
data
DNA character matrix with 23 taxa and 1141 characters
=====
Origination:                bears_cytb.nex
Number of taxa:              10
Number of included taxa:     10
Number of characters:        1000
Number of included characters: 1000
Datatype:                    DNA
```

References

Ronquist, F., S. Klopstein, L. Vilhelmsen, S. Schulmeister, D. L. Murray, and A. P. Rasnitsyn. 2012. A total-evidence approach to dating with fossils, applied to the early radiation of the Hymenoptera. *Systematic Biology* 61:973–999.

Zuckerkandl, E. and L. Pauling. 1962. Molecular disease, evolution, and genetic heterogeneity. Pages 189–225 *in* Horizons in Biochemistry (M. Kasha and B. Pullman, eds.) Academic Press, New York.

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