

Phylogenetic Inference using RevBayes

Total-evidence Dating under the FBD Model

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1 Overview

Background

1.1 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**.

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

3 Exercise: Title

3.1 Getting Started

3.2 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:              23
Number of included taxa:     23
Number of characters:        1141
Number of included characters: 1141
Datatype:                    DNA
```

References

Version dated: December 12, 2016

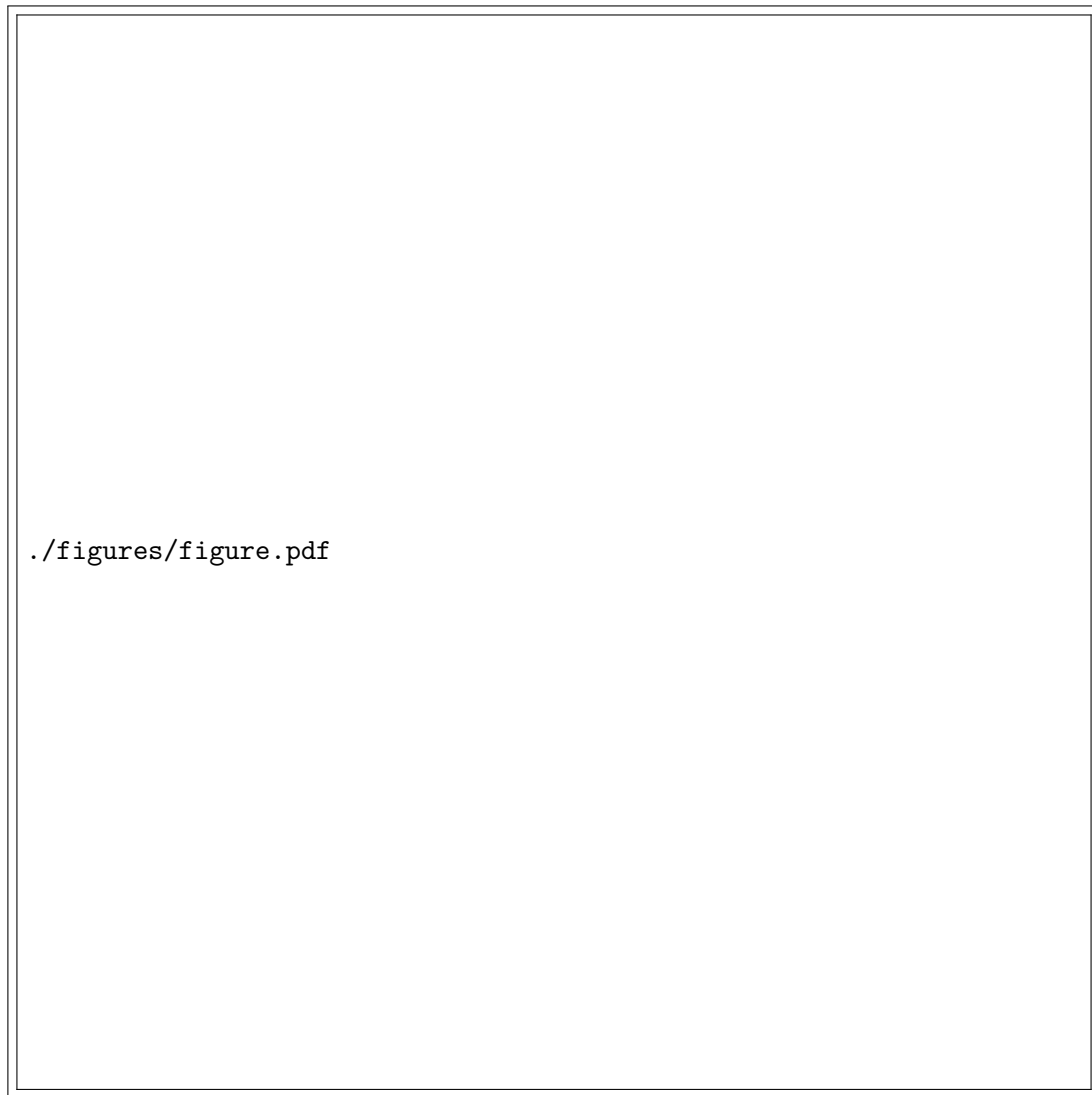


Figure 1: example figure.