

# Tutorial using BEAST v2.4.2

## Tutorial template

*Author I. Name*

Template for an empty tutorial

### 1 Background

This is a template tutorial and style guide to help formatting Markdown tutorials.

Please start the tutorial by adding some background about the tutorial in this section, clearly explaining the question/problem and the type of analysis that the methods in the tutorial should be used for. In the next section please add a short description of all the programs or packages used in the tutorial. The tutorial exercise should follow this part. Please add a short explanation on the dataset used in the tutorial before starting with the exercise. Please also add a section after the exercise interpreting the results. End your tutorial with some useful links.

Some of the text in this tutorial template is just dummy filler text. Please do not try to understand it.

## 2 Programs used in this Exercise

### 2.0.1 BEAST2 - Bayesian Evolutionary Analysis Sampling Trees 2

BEAST2 is a free software package for Bayesian evolutionary analysis of molecular sequences using MCMC and strictly oriented toward inference using rooted, time-measured phylogenetic trees (Bouckaert et al. 2014). This tutorial uses the BEAST2 version 2.4.2.

### 3 Practical: Exercise title

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### 3.2 This is another subsection

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## 4 Tutorial style guide

### 4.1 Text styling

This is how to write *italic text*.

This is how to write **bold text**.

This is how to write ***bold and italic text***.

Do text superscripts like this  $7^{th}$ ,  $x^{2y}$  or  $x^{2y+3z}$ .

### 4.2 Lists

#### 4.2.1 Unnumbered lists

- Lorem ipsum dolor sit amet, consectetur adipiscing elit.
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### 4.3 Figures

## 5 Code

A bit of inline monospaced font can be made `like this`. Larger code blocks can be made by using the code environment:



Figure 1: This figure is 25% of the page width.



Figure 2: This figure is only 10% of the page width.

Java:

```
public class HelloWorld {

    public static void main(String[] args) {
        // Prints "Hello, World" to the terminal window.
        System.out.println("Hello, World");
    }

}
```

XML:

```
<BirthDeathSkylineModel spec="BirthDeathSkylineModel" id="birthDeath" tree="@tree" contemp="↵
true">
  <parameter name="origin" id="origin" value="100" lower="0."/>
  <parameter name="R0" id="R0" value="2" lower="0." dimension="10"/>
  <parameter name="becomeUninfectiousRate" id="becomeUninfectiousRate" value="1" lower="↵
0." dimension="10"/>
  <parameter name="samplingProportion" id="samplingProportion" value="0."/>
  <parameter name="rho" id="rho" value="1e-6" lower="0." upper="1."/>
</BirthDeathSkylineModel>
```

R:

```
> myString <- "Hello, World!"
```

```
> print (myString)
[1] "Hello , World!"
```

## 6 Equations

Inline equations:  $\dot{x} = \sigma(y - x)$

Displayed equations:

$$\left(\sum_{k=1}^n a_k b_k\right)^2 \leq \left(\sum_{k=1}^n a_k^2\right) \left(\sum_{k=1}^n b_k^2\right) \quad (1)$$

### 6.1 Instruction boxes

Use block-quotes for step-by-step instruction that the user should perform (this will produce a framed box on the website):

The data we have is not the data we want, and the data we need is not the data we have.

We can input **any** formatted text in here:

- Even
- Lists

or equations:

$$(x_1, \dots, x_n) \begin{pmatrix} \phi(e_1, e_1) & \cdots & \phi(e_1, e_n) \\ \vdots & \ddots & \vdots \\ \phi(e_n, e_1) & \cdots & \phi(e_n, e_n) \end{pmatrix} \begin{pmatrix} y_1 \\ \vdots \\ y_n \end{pmatrix} \quad (2)$$

## 7 Hyperlinks

Add links to figures like this:

- Figure [1](#) is 25% of the page width.
- Figure [2](#) is 10% of the page width.

Add links to external URLs like [this](#).

Links to equations or different sections within the same document are a little buggy.

## 8 Useful Links

- Bayesian Evolutionary Analysis with BEAST 2 (Drummond and Bouckaert 2014)
- BEAST 2 website and documentation: <http://www.beast2.org/>
- BEAST 1 website and documentation: <http://beast.bio.ed.ac.uk>
- Join the BEAST user discussion: <http://groups.google.com/group/beast-users>





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## Relevant References

- Bouckaert, R, J Heled, D Kühnert, T Vaughan, C-H Wu, D Xie, MA Suchard, A Rambaut, and AJ Drummond. 2014. Beast 2: a software platform for bayesian evolutionary analysis. *PLoS computational biology* 10: e1003537.
- Drummond, AJ and RR Bouckaert. 2014. *Bayesian evolutionary analysis with BEAST 2*. Cambridge University Press,