

A Minimal Book Example

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Chapter 1

Prerequisites

This is a *sample* book written in **Markdown**. You can use anything that Pandoc's Markdown supports, e.g., a math equation $a^2 + b^2 = c^2$.

The **bookdown** package can be installed from CRAN or Github:

```
install.packages("bookdown")  
# or the development version  
# devtools::install_github("rstudio/bookdown")
```

Remember each Rmd file contains one and only one chapter, and a chapter is defined by the first-level heading #.

To compile this example to PDF, you need XeLaTeX. You are recommended to install TinyTeX (which includes XeLaTeX): <https://yihui.org/tinytex/>.

Chapter 2

Introduction

You can label chapter and section titles using `{#label}` after them, e.g., we can reference Chapter 2. If you do not manually label them, there will be automatic labels anyway, e.g., Chapter ??.

Figures and tables with captions will be placed in `figure` and `table` environments, respectively.

```
par(mar = c(4, 4, .1, .1))
plot(pressure, type = 'b', pch = 19)
```



Figure 2.1: Here is a nice figure!

Table 2.1: Here is a nice table!

Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
5.1	3.5	1.4	0.2	setosa
4.9	3.0	1.4	0.2	setosa
4.7	3.2	1.3	0.2	setosa
4.6	3.1	1.5	0.2	setosa
5.0	3.6	1.4	0.2	setosa
5.4	3.9	1.7	0.4	setosa
4.6	3.4	1.4	0.3	setosa
5.0	3.4	1.5	0.2	setosa
4.4	2.9	1.4	0.2	setosa
4.9	3.1	1.5	0.1	setosa
5.4	3.7	1.5	0.2	setosa
4.8	3.4	1.6	0.2	setosa
4.8	3.0	1.4	0.1	setosa
4.3	3.0	1.1	0.1	setosa
5.8	4.0	1.2	0.2	setosa
5.7	4.4	1.5	0.4	setosa
5.4	3.9	1.3	0.4	setosa
5.1	3.5	1.4	0.3	setosa
5.7	3.8	1.7	0.3	setosa
5.1	3.8	1.5	0.3	setosa

Reference a figure by its code chunk label with the `fig:` prefix, e.g., see Figure 2.1. Similarly, you can reference tables generated from `knitr::kable()`, e.g., see Table 2.1.

```
knitr::kable(
  head(iris, 20), caption = 'Here is a nice table!',
  booktabs = TRUE
)
```

You can write citations, too. For example, we are using the **bookdown** package (Xie, 2020) in this sample book, which was built on top of R Markdown and **knitr** (Xie, 2015).

Phylogenetic birth-death models

Equations from the literature to describe birth-death processes in the context of phylogenetic (time)trees.

Louca and Pennell (2020)

Number of species predicted at any point in time in a deterministic version of a birth-death process, i.e. the expected number of species over time in the stochastic process.

We note:

- λ and μ the birth and death rate resp., which can be time-dependent ($\lambda(t)$, $\mu(t)$)
- ρ the sampling fraction *at present*, such that $M_0 = N_0\rho$ is the number of species sampled in the present tree (and N_0 is the total **living** diversity)

Going backwards in time (τ is some time before present):

$$\frac{dN}{d\tau} = N(\mu - \lambda) \quad (2.1)$$

$$= N(-r) \quad (2.2)$$

The solution of which is (perform a separation of variables):

$$N(\tau) = N_0 e^{\int_0^\tau \mu(u) - \lambda(u) du} \quad (2.3)$$

i.e. the number of species alive (but not necessarily sampled in the tree) at time τ in the past.

Let's introduce $E(\tau)$, the fraction of lineages alive at time τ that won't be included in the final tree, because of either extinction or being missing from the sample. In a stochastic setting, it is also the probability that a single lineage will be missing from the final tree. $E(\tau)$ is introduced in Morlon et al. (2011), eqs. 5-7 (where it is named $\phi(t)$):

$$\frac{dE}{d\tau} = \mu - E(\lambda - \mu) + E^2\lambda \quad (2.4)$$

$$E(0) = 1 - \rho \quad (2.5)$$

Its solution is (eq. 2 in Morlon et al. (2011)):

$$E(\tau) = 1 - \frac{e^{\int_0^\tau \lambda(u) - \mu(u) du}}{\frac{1}{f} + \int_0^\tau e^{\int_0^s \lambda(u) - \mu(u) du} \lambda_s ds}$$

where s is some time before τ , and f is the probability that a lineage is sampled.

The deterministic LTT, i.e. the number of lineages present in the final tree, through time, is (by definition of M and E) given by:

$$M(\tau) = N(\tau)(1 - E(\tau))$$

Taking the derivative and replacing with (2.2) and (2.5) yields

$$\frac{dM}{d\tau} = M\lambda(E - 1)$$

which solution (taking $M(0) = M_0$ and using a separation of variables) is:

$$M(\tau) = M_0 e^{\int_0^\tau \lambda(u)(E(u)-1) du}$$

This equation fully describes the LTT expected given the birth-death model, aka **dLTT**.

Some observations:

- All terms in this equation are independent of the data! So model congruency (sharing the same dLTT) is a property of the models alone.
- Extinction does not appear in (2), but is in fact hidden in $E(\tau)$
- In @ref(eq:dltt_deriv), $0 < E < 1$, so that the rhs is negative or zero: we move backwards in time and lose lineages in the phylogeny, proportionally to rate λ . The term $\lambda(E - 1)$ ("growth" rate) can be developped into $\lambda E - \lambda$, illustrating that we are gaining lineages that would disappear later in time, and losing those that speciate later.

Analysis of dynamic equations in biology

Collection of recipes and reading notes from Otto and Day (2007).

Deriving the solution of a model

Linear models, continuous time, single variable

Theorem 2.1 (Solving Differential Equations Using a Separation of Variables).
Differential equations that can be written as $dn/dt = f(n)g(t)$ can be solved as follows:

1. Define what are $f(n)$ and $g(t)$
2. $\frac{1}{f(n)}dn = g(t)dt$
3. $\int \frac{1}{f(n)}dn = \int g(t)dt$
4. Don

Chapter 3

Applications

Some *significant* applications are demonstrated in this chapter.

3.1 Example one

3.2 Example two

Chapter 4

Final Words

We have finished a nice book.

Bibliography

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