

Introduction

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INTRODUCTION

Vragen: hoe juist kunnen we fylogenieen construeren?

Diversiteit Soortvorming Verwantschap Fylogenie DNA Bayesiaanse analyse Priors

SPECIATION is the process that creates new species, connecting all of life to one shared common ancestor. It is a process that has resulted in the millions of species on Earth nowadays, as well as in the many species that have gone extinct. Some speciation events happened earlier than others, from hundreds of millions of years ago (so-called 'long-enduring species', or, informally, 'living fossil') to more recent ones. See figure 1.1 shows an example of each.



Figure 1.1 | An long-enduring species (left) and a young species (right). The species at the left is a preserved specimen of *Latimeria chalumnae*, estimated to exist for hundreds of millions of year. The species at the right is the *Homo sapiens*, existing for around a third of a million years.

Within the field of biology, it is a very basic question to ask which species are closest related to one another. If you think that's an easy question, try to apply it, for example, on the 8 crocodilian pictures in figure 1.2. You may come up with one or more pairs of hypothesized closest-related species, but you will probably get stuck on which ancestors of these pairs are most closely related. Note that doing the other way around, to use morphology to classify species, is tricky: how to decide when the morphology between two specimens is different enough to classify these as two species?

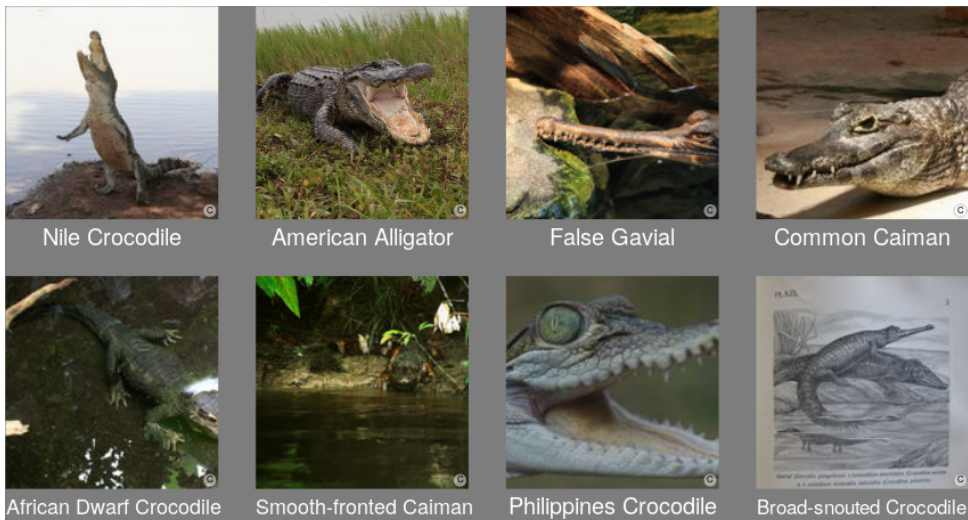


Figure 1.2 | Eight members of the order of crocodylians

The second very basic biological question, is to ask *when* these speciation events took place. This question cannot be answered based on morphologies of the present-day species alone.

A classical way to answer this second question is using the morphology of fossils. This approach can only be used if the species *can* fossilize, and those fossils are found in multiple points in time. Even if this is the case, there are caveats. Using morphology on extinct species is even trickier, as species change their appearance in time. Also an imaginary time machine would not help us out: we could try to determine the number of species in each timepoint, but that would only work if we could confidently define what a species is. We cannot, because speciation is usually a gradual process.

A modern approach to answer the second question is using the DNA sequences of extant species. DNA is inherited from parent to offspring and carries the species' evolutionary histories within it. Using DNA, we can find the closest related species by measuring the similarity in DNA sequences. When a speciation event took place can be approximated by counting the differences between DNA sequences: the more differences, the more independent mutations have occurred, thus the longer time it was when the two species speciated.

The way to depict evolutionary relationships, is using a phylogeny.

The main question of this thesis is: how well can we construct a phylogeny from an alignment? What is the error we make when we construct a 'tree without birds'?

DNA sequences of different species may vary in length, due to insertions and deletions in genetic sequences. Usually, we use a procedure (a software tool, for example) to align the sequences, as shown in figure 1.3:

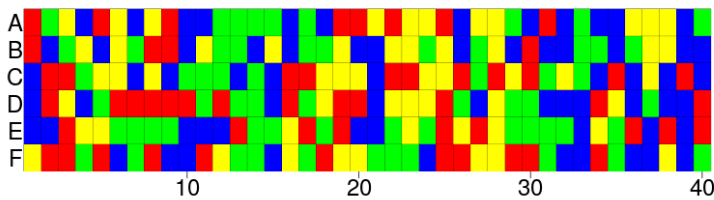


Figure 1.3 | A 40-nucleotide DNA alignment of the six species

Speciation at the species level simplifies a species to a horizontal line (also called a 'branch') in a phylogeny, answering basic questions like 'Which species lived when?', 'When did a speciation event take place?' (depicted by the vertical lines) and 'Who is the ancestor of which species?'. Figure 1.4 shows an example phylogeny:

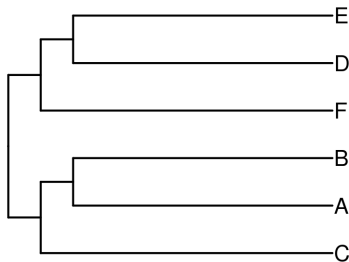


Figure 1.4 | A phylogeny with six species

Figure 1.4 shows a phylogeny (also called 'phylogenetic tree', or simply 'tree') with six hypothetical species and their evolutionary relationships. Going from left to right, we travel through time from the past to the present. The leftmost vertical line indicates the first speciation event, which gave rise to the first two ancestral species. This first split in the tree is called the crown, the moment in time this occurred is called the crown age.

Each of these ancestral species gives rise to its own evolutionary history, resulting in a tree with two clades: the ABC and the DEF clades. Sure, we could equally well have started the phylogeny with one ancestral species at the utmost left, going further back in time from the crown age to, what is called, the stem age, but in the context of this thesis, we do not.

It is impossible to go out in the field and measure a phylogeny, as they depict which species lived when *in the past*.

Figure 1.3 shows an alignment of our six hypothetical species that we actually could have found in nature. From this alignment, we can *infer* a phylogeny, which basically means 'best guess following a rational procedure'. There are multiple ways to infer a phylogeny, for example, using maximum likelihood or Bayesian inference. In this thesis, I focus on the latter.

With Bayesian inference, we use an alignment and our model assumptions to infer a posterior (more precise: 'a joint posterior distribution of phylogenies and model parameters'). We do so, by first creating a random phylogeny. Using a likelihood equation, we can calculate how likely it is. For that, we use a Markov Chain Monte Carlo algorithm, which is n

A posterior contains multiple inferred phylogenies, in which the more likely ones are present more often. This distribution of phylogenies shows the (un)certainty of the inference. Figure 1.5 shows the posterior phylogenies we obtain from our alignment:

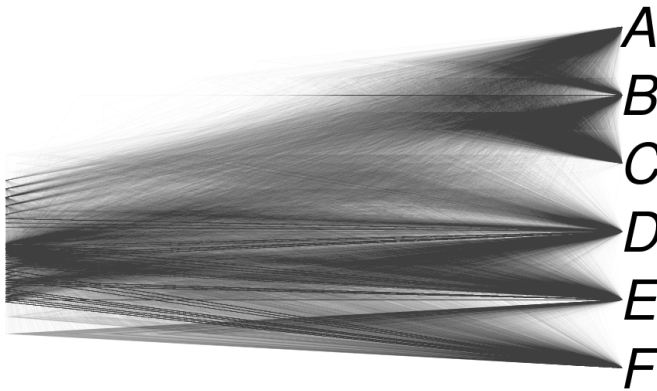


Figure 1.5 | The posterior phylogenies of the six species, from a DNA alignment of 40 nucleotides

Figure 1.5 shows a high degree of uncertainty, as the inferred phylogenies vary widely in shape. The inference only weakly distinguishes between the ABC and DEF clades.

The inference described so far is unsatisfactory, as we can only draw weak conclusions. We can improve the inference by using a longer DNA sequence or by picking a better inference model. In a simulation study, we can easily increase the number of nucleotides, figure 1.6 shows the posterior phylogenies we obtain from our longer alignment:

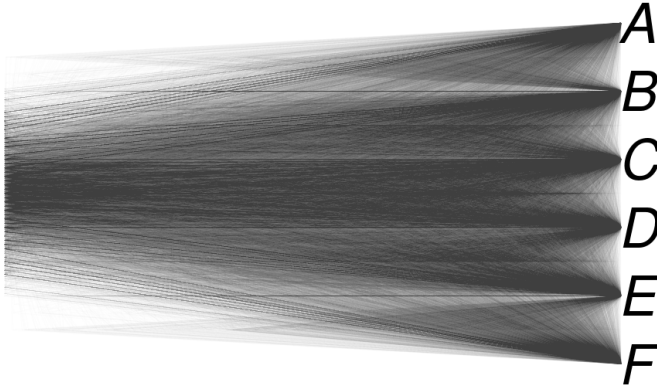


Figure 1.6 | The posterior phylogenies of the six species, from a DNA alignment of 400 nucleotides

Figure 1.6 shows that in this example, with more information, we can only show our uncertainty more clearly.

Another way to improve our inference is using a better inference model. An inference model embodies our assumptions on how we think evolution works, and consists of (1) how nucleotides mutate to others (also called 'the site model'), (2) how often mutations occur (also called 'the clock model'), and (3) how speciation works (also called 'the tree prior' or 'the speciation model'). Theory predicts that usually the inference model becomes less important if there is more information in an alignment. The example shows here, however, shows one of the exceptions.

Ideally, we pick an inference model identical to the actual way things work (or: 'the true model'), be it in nature or *in silico*. In practice, the true model that nature uses is unknown. Due to this, scientists came up with many models to explain the DNA (RNA, protein, morphological and fossil) data best.

In a theoretical study, when can simply pick how nature works; that is, how it is simulated. Theoretical studies are useful, as these explore how well we will ever be able to explain nature. To do so, a 'true' speciation model is picked to generate 'true' phylogenies. From these phylogenies, a 'true' site model and clock model are used to simulate a 'true' alignment. From that 'true' alignment, which is the data we can gather from nature, we can then see how close our inferred phylogenies are to the 'true' phylogeny.

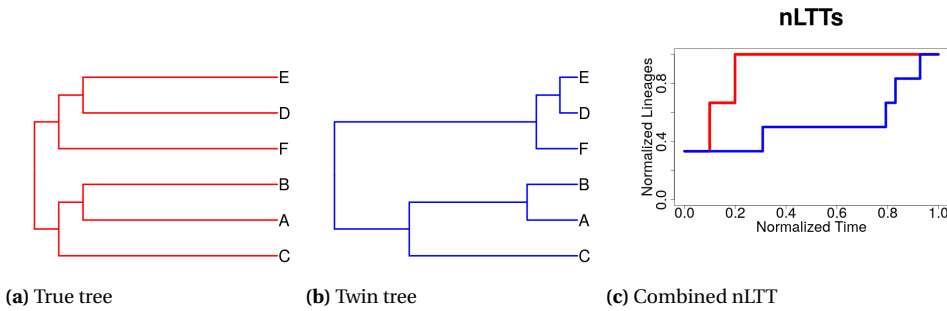


Figure 1.7 | nLTTs

There are many ways to quantify how similar two phylogenies are. The normalized lineages-through-time (nLTT) statistic (¶) simplifies a phylogeny to a number of lineages (the number of branches) in time. Both number of lineages and time are normalized to have a maximum of one, which allows us to compare two trees of any number of tips of any crown age. The difference between two phylogenies is simply the surface between the two phylogenies' nLTT plots. If two phylogenies are identical in normalized shape, the nLTT difference between them is zero, else the value will be higher, with a maximum of one. Because the value of the nLTT increases with increasing difference between the trees, the nLTT statistic is a measure of difference, or error.

In this thesis, I quantify the errors we make in our phylogenetic inference:

- In chapter 2, I show an R package I developed to do Bayesian inference from the command-line
- In chapter 3, me and Giovanni Laudanno describe an R package we developed to quantify the error we make in phylogenetic inference
- In chapter 4, Giovanni Laudanno and I quantify the error we make in phylogenetic trees when speciation can co-occur
- In chapter 5, I quantify the error we make in phylogenetic trees when speciation takes time
- In chapter 6, I show which conclusions can be drawn from these chapters

1.0.1. PHOTO ATTRIBUTION

Figure 1.1, the left image, Preserved specimen of *Chalumnae* by Alberto Fernandez Fernandez is licensed under CC BY-SA 3.0. the image at the right, Akha couple in northern Thailand by Weltenbummler84 is licensed under CC BY-SA 2.0 DE.

For figure 1.2, the selection of these eight images was done by OneZoom. These images, from top-left to bottom-row, row-first: Nile Crocodile by Marco Schmidt is licensed under CC-BY-SA 3.0. American Alligator by NASA Kennedy. False Gavia by Yinan Chen is

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