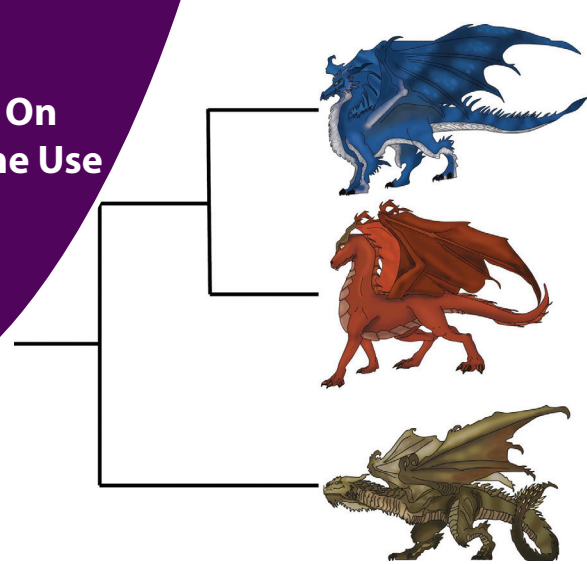


How to Classify Your Dragons: On Teaching Tree-Reading with the Use of Fantastical Creatures

● Thilo Schramm, Anika Jose, Philipp Schmiemann



ABSTRACT

We present material and instructions to teach the construction of phylogenetic trees using specifically designed images of dragons. Using fictional creatures, we can control the number and properties of characteristics, as well as present students with a context they might consider interesting. Besides creating evolutionary trees from data, students can learn that trees based on morphological characteristics might contradict and trees based on genetic analysis are a more reliable tool in classification. The material used in this learning environment is freely available, so educators can use and customize it freely.

Students working with this material declared a high motivation to work with the fictional animals and engaged in very active discussions about different classifications of the dragons.

Key Words: evolutionary tree; tree-thinking; evolution.

There is a kind of tradition of teaching modern concepts of evolution using fictitious creatures, and probably most well-known are the *Caminalcules* (Gendron, 2000), but there are also activities including aliens (Cruz, 2013) or other fantastical creatures (Cruz, 2017). There are multiple advantages in using invented organisms in teaching students the first steps in basically any context of biology, as it allows educators to have full control over the physiology, ecology, and any other kind of information (Gendron, 2000). Therefore, the learning environment can be tailored to specifically target certain misconceptions or clearly highlight concepts or connections. Furthermore, students are typically not able to base their assumptions on prior knowledge and are therefore forced to rely only on the information given in the exercise.

Especially the field of taxonomy and the field of reading and interpreting evolutionary trees (typically called tree-thinking, subdivided into tree-reading and tree-building) can greatly profit from using fictional organisms, as characters can easily be defined and a “true” phylogeny can be used as a basis. Numerous studies showed that students struggle in reading evolutionary trees (e.g., Bokor et al., 2014; Catley et al., 2013; Halverson et al., 2011) and teaching this aspect of evolution is very important (Meisel, 2010), especially,

as there are numerous well-known misconceptions reported (Gregory, 2008; Schramm & Schmiemann, 2019)

Working with evolutionary trees is either working with abstract diagrams, where the nodes are labeled with numbers or letters, or working with a selection of creatures, be it existing plants or animals or fictitious ones. There is probably no fantastic type of creatures more iconic for fantasy settings than the dragon. Portrayed as ancient powers, wise entities, terrifying wild beasts, or as mounts for kings and powerful leaders, dragons play important roles in the stories they appear in. They have been part of human myths from all around the world for centuries, or even millennia (Blust, 2000), and people are fascinated by these creatures. Previous other learning environments used the context of dragons to great success (Cruz, 2017; McElroy-Brown & Reichsman, 2019; Tsui & Treagust, 2003).

In this learning environment we are using pictures of different types of dragons to teach students the first steps of creating their own evolutionary trees based on characters as well as simplified genetical data. Furthermore, we bring up the topic that identifying morphological characteristics can easily be biased by subjectively choosing characteristics or putting more weight on certain traits, and that genetical data therefore typically acts as the basis for modern evaluations of evolutionary relationships.

○ Material & Methods

Eleven pictures of different kinds of dragons or dragon-like creatures were created following the painting instructions of William O'Connor (2011). As these images are specifically designed for this learning environment, there are no restrictions in reproducing or changing them. The represented types of creatures were chosen to display a variety of characteristics and therefore a diversity of phenotypes. Based on this selection of species, a phylogeny was created that is then regarded as the “true” phylogeny of the selected dragons.

Basing a phylogeny on the characteristics of the dragons can lead to multiple possible trees, as some traits can be interpreted in different ways and there is no information given about age of fossils or similar means of dating. Based on an underlying phylogenetic tree (included in the Supplemental Material), simplified fictional gene

sequences were designed to allow students to assess the relative relationship by genetic information and compare these findings to the ones from phylogenetic inference. The presented material is based on the idea of the botanical phylo-cards (Gibson & Cooper, 2017).

When working with these materials, students are meant to develop two phylogenetic hypotheses, one based on the phenotypical data and another one based on genetic information. The idea of this learning environment is, on the one hand, that students can take their first steps in creating evolutionary trees from data and, on the other hand, to convey the idea that genetic and morphological information can contradict and that modern biologists typically rely on genetic data.

○ Assignments

In the first step of working in this learning environment, students are asked to investigate the cards in Supplemental Material A (see Figure 1). Taking a closer look at the characteristics and properties of the different species of dragons, they are expected to form pairs or groups of dragons that they think are closely related. These groups are again ordered following their relatedness. In the next step, they compare their organization with the ones of other classmates and argue why they arranged the dragons the way they did.

In the second step, the students are given Supplemental Material B, the simplified genetic codes of the different species of

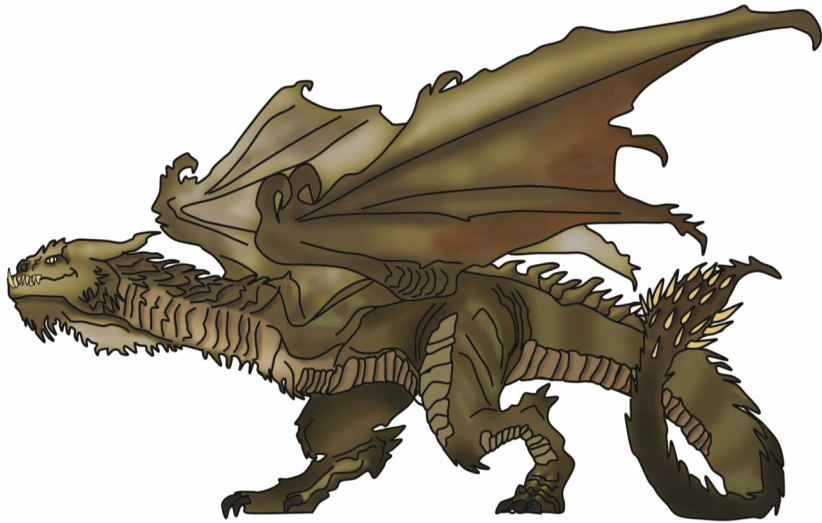
American Wyvern	
<i>Wyvernus morcaudus</i>	
	
<p>Wyverns are seen as the most ferocious hunters of all dragons. With their long legs, spiny tail and the pair of wings, they can run with astounding speed and if needed, fly for short distances, even though they are not able to swiftly change their direction of movement.</p> <p>They take down their prey using poisonous stingers at the end of their tail, combined with their razor-sharp teeth they are fearsome hunters and can take down prey much larger than themselves.</p>	
Characteristics:	
Legs: 2	Size: ≈ 50 ft / 15 m
Wings: 2	Breath Attack: none
Wingtype: Batlike	Intelligence: Mediocre
Wingspan: ≈ 25 ft / 7.5 m	Other: Poisonous Stinger

Figure 1. Example of a card from supplemental material A. Characteristics and a short description are presented along with the name and a picture of the creature.

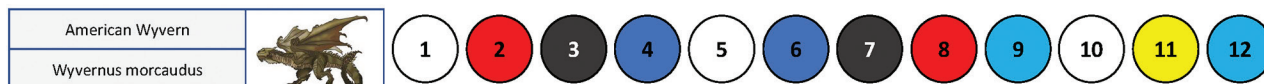


Figure 2. Example of the genetic code of a dragon from supplemental material B. The name of the creature, a picture, and the simplified genetic code are presented.

dragons (see Figure 2). The code consists of 12 colored bands per dragon. Two dragons showing the same color in the same spot indicates almost identical gene sequences. Again, students are asked to organize the dragons based on their relative relationship, this time arguing with the genetic data. In the third step, they compare their genetic organization with the morphological organization of the first step and argue why the two might differ.

The tasks can be extended by creating circle-in-circle diagrams or simple phylogenetic trees in both phases. Furthermore, students can be asked to create a table of traits in the first phase, to simplify the organization of species and the creation of diagrams.

○ Students' Feedback

The material was applied in the German equivalent to A-level biology courses. As expected, students came up with multiple ways of organizing the dragons. One prominent approach was to base the tree mostly on the number of legs, and another approach was the use of intelligence as a main criterion, or the development of wings. Participants discussed their results actively, realizing that multiple approaches can be seen as equally correct. After analyzing the genetic data, it became clear that phenotypical traits are only of limited use for inferring phylogenies.

Students reported a high motivation to work with the material due to the interesting topic. Furthermore, they argued that the use of fictional creatures is very helpful to concentrate on the biological concepts and not be distracted by fractional prior knowledge. Despite these positive points, they criticized how the extensiveness of the material required strong focus to deduce the phylogenetic tree. Additionally, multiple students reported that the material was challenging. In some cases, students were basing the organization of the dragons based on the Latin names given. Omitting the Latin names could therefore put a stronger focus on analyzing morphological and genetic data. Furthermore, this could allow students to discuss to what extent the different dragon species could form different taxonomic groups, like family and order. Extending this idea, the students could choose suitable Latin names for the species, which could further increase their motivation.

○ Conclusion

The idea of this work was twofold. We wanted to make learning material available that can be used to teach students how to create evolutionary trees with fictional organisms. Approaches by other authors were based on material that is not freely available (Cruz, 2013, 2017), thus limiting the usability of the exercises. We also wanted to present material that can be used to support college students in creating evolutionary trees and give them insights into how modern phylogenetics is practiced. As A-level students were able to use the material, despite reporting challenging difficulty, we expect

the material to be applicable to high school students as well. If the difficulty needs to be reduced, we advise reducing the number of presented species.

Supplemental Material

Supplemental Material is available at https://duepublico2.uni-due.de/receive/duepublico_mods_00074842_

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