HOW·TO·DO·IT

Helping Students Conceptualize Species Divergence Events Using the Online Tool "TimeTree: The Timescale of Life"

NABT BioClub RECOMMENDATION

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Abstract

Misinformation, preconceptions, and the human perception of time (e.g., in seconds, minutes, days, and years) are factors that can contribute to difficulties experienced by students trying to understand evolutionary phenomena on the scale of geological or "deep" time. In addition to other approaches, the use of a simple online species-divergence estimate calculator, "TimeTree: The Timescale of Life," can add resolution and clarity to big ideas that sometimes stand in the way of students' understanding of the unifying theory in biology, evolution.

Key Words: *Evolution; phylogenetics; tree thinking; estimating species divergence times; software.*

Many writers have pointed to difficulties that students have in understanding and embracing the concepts of evolutionary biology. The rich information in phylogenetic trees present their own difficulties, requiring proficiency with "tree thinking" skills (Baum et al., 2005; Meir et al., 2007; Baum & Offner, 2008; Abraham et al., 2009; Naegle, 2009). However, it is apparent that an understanding of evolution and of the new techniques used by molecular biologists to study evolutionary processes is crucially important for ensuring that students are knowledgeable about patterns and processes in the living world (National Research Council, 2009).

In addition to other approaches for strengthening students' understanding of evolution, dating nodes on phylogenetic trees may be very useful for helping students visualize evolutionary history and processes of species divergence using an online tool, "TimeTree: The Timescale of Life" (Hedges et al., 2006; Hedges & Kumar, 2009; http://timetree.org).

TimeTree allows the user to input two species names (common or scientific) to estimate the last time those two species shared a common ancestor (Figure 1). The tool uses molecular estimates of species divergences from published, peer-reviewed literature, computes summary statistics, and presents the results, including citations of the primary literature the estimate is based on. Fortuitously, the results are broken down into results based on nuclear DNA, mitochondrial DNA, and both combined (Figure 2). This allows for discussion on why using genes from different sources can lead to differences in the divergence estimate.

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Although the tool is limited to estimates that have been reported in the literature (and not all species that a student might come up with are represented), it allows the flexibility for novice users to choose species (usually common ones, like the example comparison of cat and dog shown on the TimeTree.org homepage) and to explore the results for species they are familiar with or interested in.

The TimeTree tool allows an instructor to determine the depth to which topics in molecular evolution will be covered. For introductory students, the desired learning outcome may simply be that they recognize that nodes on phylogenetic trees symbolize the point when one ancestral species diverged into two and that those points can be dated on the basis of evidence. For more advanced students, retrieval and discussion of relevant primary literature and methods of phylogeny construction can be pursued as an extension of the node-dating exercise.

Instructors may find TimeTree a useful tool to include in their lessons on evolutionary biology (or even in general biology lessons when species are used as examples for any concept; e.g., "When do you think [example species] last shared a common ancestor with humans?") or may prefer that their students use TimeTree to explore species and examples of their own choosing, simply to gain familiarity with the relatedness of organisms and time estimates on the order of millions of years. For instructors seeking a more structured lesson plan with TimeTree for students in an introductory high school or college course, an example lesson plan modeled on the 5E Learning Cycle (Bybee et al., 1989) could include the following steps.

○ **Engage**

Start with having your students generate a list of types of evidence that could be useful in determining evolutionary relatedness, prompting with a question such as "What kind of evidence would you use to determine how closely two species are related?" This discussion will likely include categories such as the following (see, e.g., Freeman & Herron, 2007):

- The fossil record
- Appearance (morphology), including embryology and homologous anatomical structures. (Note: it is worth mentioning that not all similar structures are homologous. Depending on your specific

Figure 1. Interface for searching species divergence estimates using TimeTree.

Figure 2. Sample results from a search in TimeTree using 'cat' and 'dog' search terms.

learning objectives, you may wish to spend some time at this point in the lesson describing and discussing examples of convergent evolution.)

- Biogeography
- DNA/protein homology or "molecular homology"
- Mutations in DNA and proteins

○ **Explore**

Once the students have brainstormed a list of evidence, pose the following questions, encouraging them to use their list and to provide specific examples to support their rationale.

Exploration Exercise 1: Human–Mouse–Fish comparison

1. If you were to compare a human, a mouse, and a fish, how would you determine which species are most closely related? What kind of data would you use?

2. When thinking about the DNA of a human, a mouse, and a fish, how many differences (a lot, some, or few) would you expect to see between each pair:

    a. Number of differences between a human and a mouse

    b. Number of differences between a human and a fish

    c. Number of differences between a mouse and a fish

3. How could you graphically represent the relationship among human, mouse, and fish species?

Exploration Exercise 2: Human–Fish–Frog Comparison (questions based on Baum et al., 2005)

1. If you were to compare a human, a fish, and a frog, how would you determine which species were most closely alike? What kind of data would you use?

2. When thinking about the DNA of a human, a fish, and a frog, how many differences (a lot, some, or few) would you expect to see between the given pairs below:

    a. Number of differences between a human and a fish

    b. Number of differences between a human and a frog

    c. Number of differences between a fish and a frog

3. How could you graphically represent the relationship among human, fish, and frog species?

○ **Explain**

Using discussion format, review the students' answers to the exploration questions (above) and provide the context for using molecular data to estimate species divergence times. Instruct the students to write their predictions of species divergences, either with specific dates or more vague descriptors (longer, shorter, same time), for frog, fish, and human. Make sure that the three possible relationships between the species are represented: (1) fish and frog most closely related, with human as the outgroup; (2) fish and human most closely related, with frog as the outgroup; and (3) frog and human most closely related, with fish as the outgroup. Then have the students perform the following three comparisons with TimeTree.

- Comparison 1: frog vs. fish (suggested species: painted frog [*Discoglossus pictus*] and zebrafish [*Danio rerio*]; estimated divergence 438.0–455.1 million years ago [mya])

- Comparison 2: fish vs. human (suggested species: zebrafish [*Danio rerio*] and *Homo sapiens*; estimated divergence 438.0–455.1 mya)

- Comparison 3: frog vs. human (suggested species: painted frog and *Homo sapiens*; estimated divergence 356.1–403.8 mya)

Once the students have performed all three comparisons, they can conclude that humans and frogs shared a common ancestor more recently than frogs and humans shared a common ancestor with fish; in other words, humans and frogs are the most closely related of the three species.

○ **Elaborate**
For introductory students

Continue the discussion of phylogenetic trees and tree thinking by displaying the phylogenetic trees from "The Tree-Thinking Challenge" (Baum et al., 2005). Ask the students whether the trees show the same relationships between organisms. Use the divergence estimates from the TimeTree exercise with fish, human, and frog to date the appropriate

nodes on the phylogenetic tree (labeled as nodes x and y in Baum et al., 2005).

For advanced students

Retrieve primary literature that was used to construct the TimeTree divergence estimate. What kinds of data are reported? Are there other pieces of data (in addition to molecular sequence data) that went into the estimation of the species divergence you examined? Do the data agree, or are there some differences? If there are differences, are these differences important? What other types of data might be helpful to further clarify the evolutionary relationship between those species?

○ Evaluate

There are many possible points of evaluation during this lesson, which could include both formative and summative approaches. For example, during the brainstorming and discussion portions of the lesson, the students could be instructed to follow the "think-pair-share" process, which could then be used as a formative-assessment knowledge check. For summative assessment, the instructor can provide a pair of species and ask the students to use TimeTree to provide a species divergence estimate (using either nuclear or mitochondrial genes) and use the data to sketch a phylogenetic tree of the relationship between the species (similar to the fish, human, frog example above), complete with a date indicated at the appropriate node. This sketch could be accompanied by an essay response in which the students explain their use of the molecular data to date the node and what it tells them about the timing of species divergence.

○ Conclusions

"Timetree: The Timescale of Life" is an easy and fun, publicly accessible online tool that allows students of biology at almost any level to explore the relatedness of organisms and gain familiarity with the concept of "deep" time. Dating nodes on phylogenetic trees may be a very useful strategy for helping students acquire mastery of "tree thinking" skills, visualize evolutionary history, and understand processes of species divergence, leading to a more robust understanding of the patterns and processes of evolution.

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