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Special Issue: Darwin and Evolution



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About Our Cover

Shown on this month's cover are two bonobos (*Pan paniscus*) that are part of a bonobo colony at the Jacksonville Zoo and Gardens in Jacksonville, Florida. Only nine facilities hold this endangered species in North America. Bonobos are found naturally living only in the Democratic Republic of Congo, and it is estimated that a minimum of only 15,000 to 20,000 bonobos remain in the wild.

Bonobos and chimpanzees both share ~98% of their genome in common with humans. Genomic mapping suggests that more than 4 million years ago, a common ancestor developed into humans, followed by chimps and bonobos diverging to become distinct species about 1 million years ago. It is amazing to realize that bonobos and chimpanzees are more closely related to humans than they are to gorillas!

Although bonobos and chimpanzees are ~99% genetically similar to each other, they display several important behavioral differences. Strong bonds form in bonobo society, particularly among females, and they appear to use frequent same-sex sexual activity to reinforce these bonds, resolve conflict, and calm aggression. In contrast, chimpanzees are male dominant and have demonstrated the use of physical violence to settle conflict and lethal aggression toward other chimpanzee groups. "Make love, not war" seems to be the guiding mantra of bonobo society, in contrast to chimpanzee society (and, many might say, human society as well).

The image was taken at the Jacksonville Zoo and Gardens, using a monopod-mounted Sony SLT-A77V with a Sony 70-440 GSSM lens at 360 mm. The photographer is James Ekstrom, Professor Emeritus in Science at Phillips Exeter Academy in Exeter, New Hampshire (jimekstrom8@gmail.com).

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GUEST COMMENTARY

Amanda L. Glaze

Specialties & Perspectives Intersect to Tell Us What We Know about Evolution

Our world is so complex and interconnected, it is no surprise that science is too. This essay examines the multiple lines of evidence that align to provide our modern understanding of evolution and its mechanism.

Not surprisingly, Charles Darwin is often viewed as the primary (or only) source of our knowledge of evolution. Open any biology text and you will find a photo of the grand old man, something about the voyage of the *Beagle*, and a definition of evolution. However, our modern understanding of evolution is now so much richer because of a synthesis of evidence from intersecting specialties and perspectives. Just consider the following.

Paleontology (Stories That Fossils Can Tell). Evidence in support of evolution is often found within the layers of the Earth. From shells in the Andes to hominin remains unearthed from caves, fossils suggest both the appearance of and relationships between long-dead creatures. For centuries, naturalists and field scientists used observation and detailed field notes to provide us snapshots of living things long gone but preserved in the rocks.

Geology (Stories That Rocks Can Tell). Scientists have long used geological superposition – the notion that new rock deposits form on top of older rocks – to provide relative time comparisons of fossils. In addition to suggesting relationships by relative position, technologies such as radiometric dating provide a reliable timeline for the age of fossils that are found, allowing more evidence of orders of succession of life past and present.

Biogeography (Distribution in Space & Time). Building on fossil discoveries, geographers can make comparisons between organisms around the world based on their location. Biogeography specifically looks at where we find similar fossils and maps ranges of organisms. This mapping can be used to hypothesize timelines for migrations and demonstrate that some landmasses were once connected and even suggests the order in which the landmasses may have joined and separated.

Comparative Anatomy (Homology, Analogy & Vestigial Structures). Fossils offer exemplars for comparison to known organisms. Scientists have long used comparative anatomy to explore structures in living and extinct forms. This idea of “descent with modification,” that similarities among organisms can be explained by small changes over generations, was described by Darwin, for which he is often under-credited. Close examination of structures and functions allows us to make hypotheses about relationships between organisms that have evolved within the same line (homologs) or evolved in a similar way in different lines (analogs). We can also observe remnants of traits found in ancestral species that have slowly become less useful (vestigial structures), like hind limbs in whales and the human appendix.

Comparative Embryology (Developmental Relationships). Building on our understanding of comparative anatomy, we have the ability to examine structure and function on a more intimate scale through

comparative embryology. Examination of the earliest cellular states of living things can provide evidence of evolutionary relationships and even the degrees of separation of living things based on when specific traits appear in development.

Genetics (Stories in the Genes). Darwin understood inheritance – after all, he was a pigeon breeder – but he had no knowledge of genes. The advent of genetics and related biochemistry allows us to understand the details of descent with modification and the bigger picture of diversity. Bones can suggest evolutionary history, but genetic material recovered from those bones is useful in confirming hypotheses about speciation and relationships. The ability to “look within” began with comparative anatomy and fossils, but our present understanding is confirmed on the genetic level. Evolutionary study of living organisms has demonstrated the impact of gene flow and reproductive isolation on speciation, while cladistics and “tree thinking” take us beyond comparison of homologous and vestigial structures to DNA to verify proposed relationships, ancestries, and when speciation occurred.

Cultural Anthropology (The Story That Makes Us Human). As Darwin stated in *Origin of Species*, “light will be thrown on the origin of man and his history.” As much as we learn from bones and stones, the evolutionary story of life, human and otherwise, now encompasses social elements with the scientific. Diet, culture, art, beliefs, and other elements of modern and historical human behavior greatly inform the narrative of modern humans. While physical anthropology is focused on the stories told by fossils, cultural anthropologists explore cognitive evolution by exploring behaviors such as burial practices, shared belief systems, social structures, and communication. This intersection of applied and social sciences builds our understanding of who we are.

Observations in Real Time (Evolution in Action). A principal anti-evolution argument is the notion that we can't confirm the historical record because we were not there to witness the events. While inference tells us much, the argument that evolution cannot be witnessed is false. Evolution as evidenced through descent and speciation are observable firsthand and on very modest timescales. Some groundbreaking examples of this are found in the work of Rosemary and Peter Grant with the Galápagos finches, the work of David Reznick with Trinidadian guppies, and on a long-term scale with the work of Richard Lenski on *E.coli*, just to name a few.

Synthesis: A Hallmark Trait of Science. Darwin was a man of great vision and a quintessential scientist. He moved easily between various fields of study in his quest for understanding. All who study evolution are following the same method by synthesizing evidence, data, and explanations from a wide range of fields and perspectives, thereby demonstrating that evolution is the best possible explanation for the unity and diversity of life.

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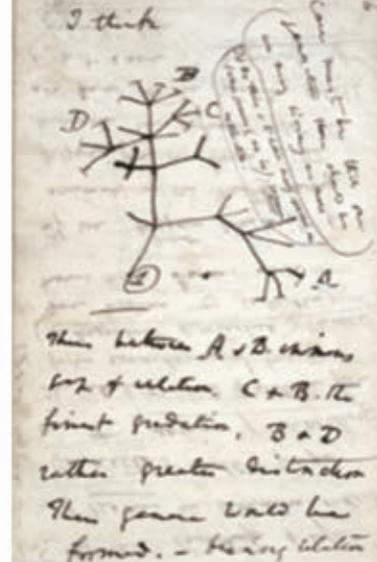
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Acceptance, Understanding & Experience: Exploring Obstacles to Evolution Education among Advanced Placement Teachers

AMANDA GLAZE, JENICE GOLDSTON



ABSTRACT

Students in the United States who wish to begin early enrollment in college-level coursework often turn to Advanced Placement (AP) secondary coursework such as AP Biology as an accelerated option. As such, it is expected that those teachers who are responsible for the AP Biology courses hold an advanced level of subject-area expertise that extends to topics that are often seen as controversial in K–12 classrooms, including evolution. We surveyed 71 AP Biology teachers in a state in the southeastern United States to see how their levels of evolution content knowledge, evolution acceptance, and understandings of the nature of science compared to results that have been found in similar studies in general biology teachers and preservice science teachers. Our results indicate that AP Biology teachers in the Southeast have understandings and levels of acceptance regarding evolution that are in line with or lower than those of fellow teachers. This suggests that in spite of the nationalized AP curriculum, there are still gaps in fundamental knowledge, understandings, and approach that need to be addressed.

Key Words: Evolution; advanced placement; teacher perceptions.

○ Introduction

Over the past two decades, science education in the United States has seen a resurgence of focus on application, scientific thinking, and process skills in research and practice. Since the development of the *National Science Education Standards* (National Academy of Sciences, 1996) and today's new focus on the *Next Generation Science Standards* (NGSS), a movement toward more uniform expectations nationally for science teaching is clear (National Research Council, 2013). The NGSS emphasize a strong focus on cross-cutting concepts, integration of engineering practices, and vertical scaffolding of content, whereby students begin learning complex concepts earlier and continue to build on them with practical applications in

It is not uncommon for biology teachers to harbor the same misunderstandings, misconceptions, and feelings of conflict with evolution that are seen in the general public.

successive years of schooling (National Research Council, 2013). Topics deemed “controversial,” such as evolution, are emphasized and included in the NGSS while continuing to be a source of conflict in the southeastern United States (Bowman, 2008; Glaze et al., 2015). In response to the NGSS, states in the Southeast that opposed the content and nature of the NGSS have refused to adopt the new standards, opting to have their respective departments of education reshape them, a right the states retain (Branch, 2015).

As a result of changing leadership in some state departments of education, several states have, or will have, new science standards in the coming years, several of which contain a stronger evolutionary biology focus than previous courses of study approved by those states (Lerner, 2000, 2012). The new standards should bring the level and depth of secondary school classwork to a higher level that more closely mirrors what has been done in Advanced Placement (AP) courses; however, standards alone are not enough to ensure the accurate teaching of evolution in classrooms (Moore & Kraemer, 2005). As a result of standards exceeding those of general biology, expectations for teachers of AP Biology courses require them to teach biological concepts at a higher level than their non-AP counterparts (Evans, 2009; College Board, 2012). AP Biology teachers can and should represent the pinnacle of biology teaching and demonstrate expertise through their knowledge of content. Their understanding and acceptance of evolution should compare favorably to that of teachers not trained to teach AP Biology.

Historically, AP courses have been indicative of high rigor and are often viewed as indicators of readiness and potential for success in college coursework (Walker, 2009; College Board, 2012). As a result, AP coursework is intentionally designed to be equivalent to university coursework (Education Commission of the States, 2006; Evans, 2009). AP Biology teachers are expected to have a level of expertise and understanding that is found in

introductory college biology courses. High expectations of expertise in AP Biology teachers include greater fluency in scientific practices, the nature of science (NOS), and content concepts including controversial concepts, like evolution that are emphasized in the standards and benchmarks for AP Biology (Musante, 2012). In undergraduate and graduate science programs, evolution is widely, if not unanimously, accepted as the scientifically valid unifying theory in biological science.

Were a university professor to refuse to address evolution in their coursework, it would most certainly be questioned by their colleagues. However, at the secondary level, biology teachers exhibit a range of inconsistent behaviors with respect to teaching evolution, often due to cultural, social, and religious pressures (Goldston & Kyzer, 2009; Glaze et al., 2015). Furthermore, research studies reveal that it is not uncommon for biology teachers to harbor the same misunderstandings, misconceptions, and feelings of conflict with evolution that are seen in the general public, which often results in the perpetuation of these same misunderstandings and misconceptions in the next generation of learners, especially when those same teachers inaccurately teach evolution or avoid it altogether (Martin-Hanson, 2006; Bowman, 2008; Cofre et al., 2017).

In an effort to improve access and rigor across AP Biology courses, the state in which this study took place, Alabama, formed an education partnership with a state-supported budget for training and incentives for teachers based on student performance in AP courses (A+ College Ready, 2017). The program was created with the largest private grant in state history, a \$13 million grant from the National Math and Science Initiative aimed specifically at increasing student enrollment and success in courses including AP Biology (College Board, 2012). While the state historically had one of the lowest rates of student success in gaining college credit for AP coursework, the past decade has seen that capital rise in response to efforts to increase access and success, and the state is being lauded as an exemplar for improvement of AP participation and success (College Board, 2007, 2012; Crain, 2017). With this in mind, AP Biology teachers in the state provide a unique lens through which we can examine the state of evolution education in an area where the teaching and learning of evolutionary theory continues to be a point of conflict, both privately and publicly (Bowman, 2008; Branch, 2015). In order to explore whether advanced scientific knowledge is approached in upper-level courses, we look carefully at the shared traits of AP Biology teachers and how their levels of acceptance and understanding compare with their AP non-trained peers in a controversial area, evolution, where there is great need of change (Moore & Kraemer, 2005). Therefore, this study examined the following questions:

1. What are the characteristics of AP Biology teachers in one state in the southeastern United States?
2. How do AP Biology teachers in one state in the southeastern United States compare to their non-AP counterparts in terms of overall acceptance of evolution, understandings of evolution, and understandings of NOS?

○ Methodology

Data Collection

For this study, potential participants were identified through their participation in a statewide program for AP Biology teachers. The state

of Alabama has 173 school districts, each of which is governed by the State Department of Education, which has endorsed the partnership program. Within those systems, 123 AP Biology teachers were registered for the program. For this study, AP program leadership forwarded an email to these members to request that they complete the survey measuring evolution acceptance and other elements; the email contained background and consent information for the study as well as a link to the Qualtrics online survey. Upon reading the initial page and consenting, participants were taken to pages associated with each of the instruments for measuring variables, including a segment addressing demographics.

Three existing surveys were included in the study to measure variables of interest. One, the Measure of Acceptance of Theories of Evolution (MATE), was used to determine levels of acceptance (Rutledge & Warden, 2000). This 20-question survey has been used extensively on students in science as well as teachers and has been validated by an expert panel (Rutledge & Warden, 2000). The survey has demonstrated reliability among teachers, with a Cronbach alpha of 0.84 (Rutledge & Warden, 2000). A second instrument, the Evolution Content Knowledge (ECK) quiz, was used to determine participant accuracy in understanding key evolution concepts based on high-school-level proficiency (Johnson, 1986). This 21-question multiple-choice quiz had validity as confirmed by an expert panel and a 0.84 Cronbach alpha level when administered to science teachers (Rutledge & Warden, 2000) and .73 Kuder-Richardson formula 20 in biology students (Johnson, 1986). For the ECK, scores were recorded as the percentage of questions correctly answered out of 100%. Finally, NOS understanding was determined by the scores obtained on the 20-question NOS instrument by Rutledge and Warden (2000). The NOS instrument employed a Likert scale to rate agreement levels with statements commonly employed in conversations about evolution, such as “The age of the earth is fewer than 20,000 years.” This survey was also validated by an expert panel and demonstrated a reliability of 0.94 when administered to science teachers (Rutledge & Warden, 2000). For the MATE and NOS instruments, the scores are traditionally grouped by range: very low (20–52), low (53–64), moderate (65–76), high (77–88), and very high (89–100) (Rutledge & Sadler, 2007). The lowest possible score on either measure is 20 and the highest 100, as there are no zero-point responses assigned and the highest point value on any one question is 5.

Limitations

The present study has a number of limitations beyond general margins of error, including questions as to whether acceptance is measurable and whether we can adequately explore understandings of NOS in Likert response forms rather than using open-ended questions. Although these measures are not without criticisms, each is used extensively with students and teachers to explore their levels of knowledge, understanding, and acceptance, and each is generally accepted as appropriate for comparing new data with existing data using the same measures. A particular limitation regarding instrumentation is that the MATE, used to measure acceptance of evolution, may be critiqued based on the nature of the questions asked, many of which focus on statements of fact in relation to evolution (“The earth is 4.5 billion years old”) and statements that are specific to Christian creationist dogma (“The earth is less than 20,000 years old”). For the purposes of this study, the MATE was selected because

it was used in a previous study in preservice teachers (Glaze et al., 2015) and in light of the fact that it is used for qualitative comparison rather than correlational analysis.

While survey scores elicit questions about the actuality of what is measured – acceptance, understanding, or belief – it is recognized that the value of using these scores for predictive research must consider at length the shallow level of understanding that is captured through the use of quick-report measures as opposed to more in-depth, open-ended probes. In addition to the measures themselves, there is always a question of accuracy on self-reported measures due to the duration of surveys and the human nature of participants. It is further noted that the size of this study, taking place in only one state and representing a small percentage of the overall population of AP teachers, therefore cannot be generalized and that the sample size itself restricted the application of additional statistical treatments to explore correlations among the variables of interest. However, over time, collecting samples across groups and locations can give us insights into the broader picture that better inform our larger efforts to improve the teaching and learning of evolution.

Data Analysis

For data analysis we transferred data from Qualtrics to SPSS/PASW 21 for analysis. We then generated descriptive statistics based on participants' responses to the demographic questions. Participant totals and percentages were generated to determine whether the sample was representative of the general population of teachers for which data were available. Next we documented other descriptive factors related to teaching, such as certification, content area, and years of teaching experience. For the purpose of answering the main question of this study, we employed a descriptive analysis of factors to allow comparison with values reported for the same measures in the existing literature. Additional statistical treatment was not conducted due to the small sample size in comparison to the number of variables of interest.

Results

Alabama has ~170 public school systems, including county systems and independent city systems. At the inception of A+, only 94 of those systems offered at least two AP classes (Southern Regional Education Board, 2017). However, in the past decade, the number of students in the state who are taking AP courses has increased from ~3000 to >11,000 (College Board, 2012). As a result of initiatives, many more systems have access to AP programs in which biology is a course option through alternative offerings such as virtual classes. In rural systems, AP Biology teachers are often shared across schools or even districts, with virtual classes developed to allow AP representation in smaller systems that lack the personnel or credentials to teach AP courses. The 42 state systems (25%) were represented in this study by 71 active AP Biology teachers of the 123 registered in the state-mandated program. The AP teacher participants represented 39% of the counties in the state and each of four major cities.

As shown in Table 1, participants in this study were mostly white females, with very few men or other racial groups. While these numbers are high, they are not surprising, as the Alabama State Department of Education (2017) reports that in the 2016–2017 school year, 79.4% of all public school teachers in the state were female and 78.5% were white—compared to 82% nationally (U.S. Department of Education, 2016). Although the sample is somewhat

Table 1. Demographics of study participants (n = 71).

Demographic	n	%
Female	56	79%
Male	11	15%
White	58	82%
Asian	1	1%
Hispanic	1	1%
African American	4	7%
Other	1	1%
Non-responding Gender	4	6%
Non-responding Race	6	8%

in line with the demographics reported statewide, there is no measure of the overall state demographics of the AP teacher subgroup for comparison. It can be pointed out from the data that AP teachers have similar gender representation, yet higher representation among white teachers than those of other races compared to the state average.

Participants in this study represented a range of backgrounds and experience. As part of the demographics, participants were asked to describe their upbringing in terms of the size of their community as either rural (<19,999) or urban (20,000+). Among the participants, 64% (45) noted that the city where they attended high school would be classified as rural, while only 36% (26) identified their background as urban. While these numbers are low in comparison to the large scale of cities in other parts of the country, it is noted that the largest city in the state represented in this study has a population of <250,000, making the qualifier for “urban” relative.

Regarding years of experience, Table 2 demonstrates that a majority of the sample in this study (60%) were considered experienced career teachers, with 43 teachers having ≥11 years of experience and 25 having ≥16 years. Of the remaining 34% of teachers who responded, 16 reported having 6–10 years of experience, while only eight reported having ≤5 years of teaching experience. In addition to years spent teaching, 69% of the teachers (49) in the study also held graduate-level certification on their teaching credentials and 13% (9) of the teachers held certifications at the highest level, which is reserved for teachers who have conducted at least half the hours required for a doctoral degree.

In terms of performance on the three primary measures – acceptance of evolution, understandings of evolution content, and understandings of NOS – participants in this sample demonstrated low to moderate mean scores in each. Table 3 shows that the mean level of acceptance among participants was 68.47 out of 100 points, which represents moderate acceptance of evolution among participants. In addition to acceptance, the participants demonstrated very low understanding of NOS, with a mean of 52.72 out of 100 points and a low understanding of the basic content concepts surrounding evolution, with an average score of 56.49%. In regard to deviation in the scores for each measure, Table 3 demonstrates the high values for standard deviation that

Table 2. Teacher certification levels and content areas (n = 71).

Demographic	n	%
B (Bachelor's)	17	24%
A (Master's)	40	56%
AA (Specialist/Doctoral)	9	13%
Biology	32	45%
General Science	34	48%
Non-responding Degree	5	7%
Non-responding Content	5	7%

Table 3. Summary of measures (n = 71).

Measure	Mean	SD
MATE-Acceptance	68.47/100 (moderate)	29.46
NOS-Understanding	52.72/100 (very low)	21.53
ECK-Content	56.49% (low)	34.72

are present in key variables, including standard deviations of 34.72 points for content knowledge, 29.46 points for acceptance of evolution, and 21.53 points for understanding of NOS.

○ Discussion

Regarding some variables, the demographics in this sample closely align to those of the larger population of teachers in the United States as well as the state where the study took place. In the sample, AP teachers appear to be well trained, highly experienced, and aptly certified in their fields, which suggests a comfort level and background that should support greater understanding and acceptance. However, in a 2009 study of science teachers as they taught evolution, Goldston and Kyzer (2009) observed changes in teacher persona during the teaching of evolution that suggest that discomfort and misunderstanding transcended years of teaching experience and background, which suggests that traditional indicators are not necessarily applicable when it comes to controversial topics (Sinatra et al., 2003). In the present study, the majority of participating teachers had a wealth of experience in the classroom – almost 90% having ≥ 6 years of experience and 60% having ≥ 11 years of experience – yet the levels of understanding and acceptance were still much lower than desired, aligning to results suggesting that experience is not an indicator of accuracy of teaching evolution (Nadelson & Nadelson, 2010). As such, it was not only in content that we saw breaks in logic between our expectations and the reality of the situation. In fact, even with lengthy teaching experience, controversial topics can override logical expectations (Sinatra et al., 2003; Boujaoude et al., 2011).

Ron Johnson (1986) noted in an early acceptance study that biology teacher performance was more in keeping with acceptance and understandings of evolution held by nonmajors in biology courses. Furthermore, Johnson (1986) characterized biology majors

as being more open in their thinking and their willingness to consider evolution than nonmajor students. Decades later, studies indicate similar results despite the implementation of standards to align practices (Rutledge & Mitchell, 2002; Bowman, 2008; Glaze et al., 2015). It stands to reason that teachers of science should be more open to scientific explanations; however, that is not always the case, and frequently teachers exhibit a willingness to divest themselves of the responsibility to accurately teach controversial topics in science (Bowman, 2008; Goldston & Kyzer, 2009).

In terms of the key measures deployed in the present study, participant teacher scores somewhat paralleled those of other science teacher samples but were notably lower in others (Rutledge & Warden, 2000; Rutledge & Mitchell, 2002; Nadelson & Sinatra, 2009; Nehm et al., 2009). Overall, acceptance of evolution in this study was moderate, with participants scoring an average of 68/100 on the MATE. This is noticeably lower than that of other teacher samples in the United States, where teacher acceptance means were documented at 77.59 in Indiana (Rutledge & Warden, 2000), 85.9 in Oregon (Trani, 2004), and 87 in Ohio (Korte, 2003). Compared with moderate to high levels of acceptance, understanding of NOS in our study was on the borderline between very low and low at a mean of 52.72/100. This is only slightly lower than what has been reported in Indiana teachers, whose average on the same NOS instrument was 59.49, also in the low range (Rutledge & Warden, 2000). Despite higher occurrence of graduate-level training and advanced certification in the sample, the level of content knowledge demonstrated among AP teachers in our study was also low, with a mean score of 56%. This is a good measure lower than the content knowledge reported on the same instrument in Indiana teachers, whose average score was 71% (Rutledge & Warden, 2000).

Each of the evolution measures in this study demonstrated a range of variability among responses, with standard deviations ranging from 21 to 35 points. The greatest variability was found in content knowledge and the least in NOS understanding. It is not uncommon in studies of evolution understanding and acceptance for there to be higher values for standard deviation as a result of both high and low outliers that must be addressed prior to statistical analysis (Trani, 2004; Glaze et al., 2015). This is often explained in terms of content knowledge by the variability in required coursework in teacher education, where courses specific to evolution are often not a part of the plan of study (Glaze & Goldston, 2015). Furthermore, existing tensions in the southeastern United States around evolution often result in teachers and students actively avoiding discussions of the subject, resulting in future teachers coming into their program with existing gaps that are not sufficiently addressed in survey courses (Goldston & Kyzer, 2009). Outlying cases in the area of acceptance are also common, as previous studies have demonstrated that there is very little correlation between actual knowledge of evolution and acceptance, which is often influenced by extrinsic and intrinsic factors (Glaze et al., 2015). It is not uncommon for a person to be wholly accepting of evolution but to reflect very little actual comprehension and understanding of the processes of evolution. Conversely, it is also possible for an individual to be highly knowledgeable of the processes and facts surrounding evolutionary theory, but to actively elect rejection of those parts that are not in alignment with their worldview (Glaze et al., 2015).

Although there were no comparable studies of in-service teachers in the same state or other states in the region, there was a comparative group of preservice science teachers who had attempted all three measures utilized in this study within a five-year window of data collection for this study. In comparing the performance of in-service AP science teachers and preservice science teachers in the same state, we see consistent measures in the acceptance of evolution, with preservice teachers in the state demonstrating an average score of 70.90/100 points on the MATE compared to the 68.47/100 of the AP teachers (Glaze et al., 2015). At the same time, we see what could be the impact of greater training and experience in the AP teacher group in terms of content, as the reported content scores in the preservice sample demonstrated an average score of 37.63% (Glaze et al., 2015) compared to the 52.72% of the AP teachers in this study. Conversely, the preservice science teacher sample demonstrated a greater understanding of NOS, with an average score of 65.45/100 points compared to 56.49/100 points in the AP teacher sample.

○ Conclusion

It has been stated that “antievolution is one of the greatest challenges for biology education” (Nehm & Schonfeld, 2007), especially in light of the role evolution plays as the unifying theory in biological sciences. Teachers in many ways represent the front lines in the battle for scientific literacy and trust in science. While a percentage of the population goes on to higher-education experiences, the other portion of the population closes the chapter of their formal education training at or before graduation from high school. As such, many in the population receive their only formal experiences with science during their grade school coursework.

In this study, we sought to determine whether AP Biology teachers have higher overall acceptance of evolution, understandings of evolution, and understandings of NOS than other science teachers. In comparing results from this study with those of other studies in the United States and one preservice study in the same state, the answer to that question is “no,” AP teachers in this sample do not have higher scores on evolution-related variables than other science teachers. Those variables include acceptance of evolution, understanding of NOS, and evolution content knowledge, factors with demonstrated patterns of influence upon one another and upon teacher choice of what, and whether, to teach evolution in the classrooms (Rutledge & Warden, 2000; Goldston & Kyzer, 2009). AP teachers demonstrated levels for each of those areas that are in keeping with existing studies among other teachers, which include moderate to high acceptance, low content knowledge, and low understanding of NOS (Rutledge & Warden, 2000; Korte, 2003; Trani, 2004; Glaze et al., 2015).

Our results add to an unfolding pattern among biology teachers with respect to understanding evolution, misconceptions about evolution concepts, and acceptance of evolution. A great deal of focus in university programs has been placed on increasing content background and practical experiences in science as a driver for improved science content teaching. However, we “can’t assume that biology teachers with extensive background in biology have an accurate working knowledge of evolution, natural selection, or the nature of science” (Nehm & Schonfeld, 2007, p. 716). In fact, research indicates that science teachers across grade levels hold misconceptions and misunderstandings that are not being addressed in their preparatory experiences (Nehm & Reilly, 2007; Nehm &

Schonfeld, 2007; Glaze & Kyzer, 2009). It is well known that common misconceptions and misunderstandings influence teaching and learning of science and can result in self-perpetuation of the very problem we are hoping to solve (McComas, 2003). As such, there is a need at all grade levels to address misconceptions, strengthen understandings of science and how scientific knowledge is generated, and target areas of science viewed publicly as “controversial.”

The responsibility for overcoming obstacles to teaching and learning of evolution falls squarely on the shoulders of professors in teacher education, who are often a single point of contact for science teachers when it comes to the pedagogical aspects of teaching so-called controversial topics. As such, teacher educators and those who provide support to in-service science teachers are tasked with finding creative and accessible ways to ensure that the impact made in those classrooms is accurate and meaningful. While AP Biology courses are held in high regard for rigor, depth, and breadth of content addressed, it is clear there is still a need to address teacher content knowledge, acceptance, and understanding with respect to evolution. If the upper echelon of our science teachers struggle with these same issues, it is clear that our work is far from complete.

○ Suggestions for Future Study

Research in science teacher preparation tells us there are a variety of approaches to certification, including alternative certification, master’s-level initiation, and others that can result in a variety of backgrounds as well as levels of training in content and pedagogy, even at the same level of teaching experience and certification. It is not clear, at this time, the role those elements may play, if any, in the range of scores found in measures surrounding evolution acceptance and understanding. Therefore, it would be beneficial in future studies to explore forms of certification as a variable of interest. Another direction building on this study would be to explore whether states with mandatory training and College Board certification for AP Biology teachers have teachers and students with higher levels of understanding and acceptance than those without. If there is existing training that can be utilized to close some of these gaps in acceptance and understanding, then we certainly should be utilizing those resources on a wider basis.

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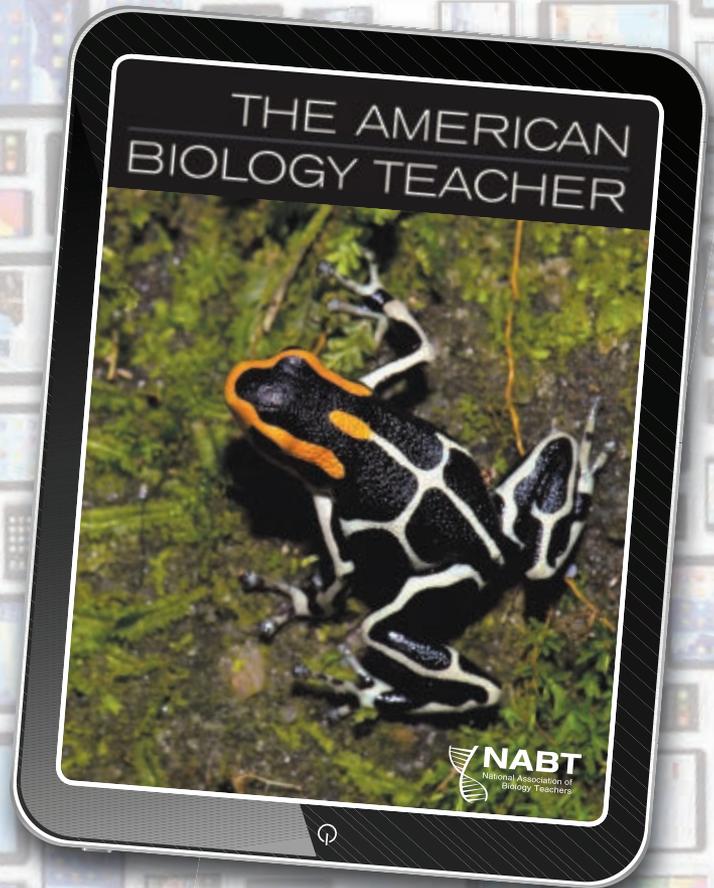
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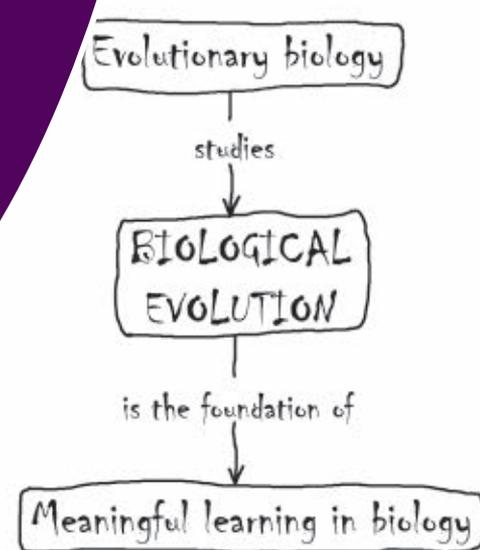
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A Concept Map of Evolutionary Biology to Promote Meaningful Learning in Biology

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ABSTRACT

Is it possible to teach biology without mentioning evolution? The answer is yes, but it is not possible for students to understand biology without the evolutionary context on which the meaning and intellectual value of biological concepts depend. Meaningful learning of evolution requires (1) that the students incorporate new knowledge into a cognitive structure linked with higher-order concepts; (2) a well-organized knowledge structure; and (3) a positive emotional attachment and identification (affective commitment) to the subject by the learner. Concept maps are useful tools in meaningful learning. We present a concept map that organizes concepts of history of life and the processes that generate it, and the hierarchical relationships among them. Biological evolution is a compelling account of life on Earth and of human origins. It constitutes a unifying explanatory framework that can generate a powerful affective commitment to the subject. The concept map provided here is tied to the Next Generation Science Standards (NGSS).

Key Words: Evolution; concept maps; tree of life; evolutionary processes; biology teaching.

○ Introduction

Is it possible to teach biology without mentioning evolution? The answer, unfortunately, is yes; it happens all the time, for reasons ranging from ideological opposition to teachers' discomfort with the content. It is not possible, however, for students to understand biology without the evolutionary context on which the meaning and intellectual value of biological concepts depend (Dobzhansky, 1973; McInerney, 2009). On the other hand, many introductory biology textbooks include evolution but present the information in a conceptually segregated manner (Nehm et al., 2009).

We propose a way to visualize main ideas about evolution in the context of the whole set of ideas, avoiding fragmented learning of each concept independently.

Meaningful learning, as described by Ausubel et al. (1978) and Novak (2002), requires the following elements:

- (1) The incorporation of new knowledge into a cognitive structure linked with higher-order, more inclusive concepts.
- (2) A well-organized and relevant knowledge structure.
- (3) A positive emotional attachment and identification (affective commitment) to the subject by the learner. This affective commitment is necessary because learners' feelings enhance their capacity to make sense out of their experiences.

Therefore, meaningful learning in biology is possible only with evolution as a framework, because it is the only framework that organizes all of our observations and experiments about the living world into a cohesive, conceptual whole. On the other hand, biological evolution is a great and stirring account of life on Earth and of human origins within it. Therefore, evolution is not only a unifying and explanatory element but constitutes, in itself, a powerful affective commitment and identification to the subject.

Concept maps are excellent, meaningful vehicles for learners to organize and visualize ideas or concepts and hierarchical relationships among them (requirements 1 and 2 above). They help learners clarify their thinking and organize and prioritize new information (Novak, 2010). In this article, we present in summary form a concept map (comprising three figures) that shows the central concepts of evolutionary biology and their relationships to one another in an organized, relevant knowledge structure.

This article is not an educational experiment or a replacement for a textbook. It is an educational tool for teachers and learners, to be used as an introductory road map to the main concepts of evolutionary biology and the relationship among them. Existing concept maps in biology, some of which include evolutionary biology, reside in

websites (e.g., <https://www.lucidchart.com/pages/examples/concept-map/>, <https://prezi.com/ssbyu2lvllsp/biology-concept-maps/>) and in the literature (e.g., National Academy of Sciences, 1998; Almond et al., 2015; Kong et al., 2017). Most of them, however, are too general or focus only on one topic of evolution, such as evolutionary trees or natural selection, or do not include the most recent advances in evolutionary research, such as genetic engineering. In addition, many of those concept maps were constructed by educators and not by researchers in evolution who also teach or have taught at the high school or university level. Therefore, we propose here a way to visualize main ideas about evolution in the context of the whole set of ideas, avoiding fragmented learning of each concept independently. In addition, the concept map presented here is updated with recent scientific advances in the discipline. We expect that the content of our concept map represents, in summary form, current knowledge in evolutionary biology, including the scientific controversies (e.g., the role of phenotypic plasticity in generating genetic changes) that will help students see the state of the art and the dynamics of the discipline. Also, these controversies may trigger valuable discussions in the classroom, fomenting the critical thinking of the learners.

The graphical structure will allow learners to follow the sequential flow of the patterns (history of life) and the processes that generate the patterns, as it happens in nature. We propose that the content and the graphical structure of the concept map can promote meaningful learning of evolutionary biology, because such learning occurs when relationships between concepts become more explicit, more precise, and better integrated with prior knowledge in biology (see below).

The narrative complements the map and serves as a kind of glossary with selected references. Superscript numerals relate the narrative to the most comprehensive ideas of the map.

This article is intended for precollege students and teachers. Precollege students might use the concept map to retrieve, review, or learn about evolution. Teachers could use the map for direct instruction, as a curriculum organizer, or even as an assessment tool.

○ The Scope of Evolution

The problematic expansion of bacterial resistance to antibiotics and of weeds' resistance to herbicides, the morphological and molecular similarities between different groups of organisms, the unity of all living things reflected in nucleic acids, the extraordinary and astonishing biodiversity on Earth, the past written in fossils, and the position of *Homo sapiens* in the history of life are isolated facts that one can understand and relate to each other only in the light of biological evolution (Dobzhansky, 1973).

Biological evolution¹ consists in the change of the hereditary characteristics of groups of organisms in the course of multiple generations (Futuyma & Kirkpatrick, 2017). In a long-term perspective, evolution is the descent with modification of different lineages from a common ancestor. From a short-term perspective, it is the adaptation of populations to environmental challenges and changes. Therefore, evolution has two components: the ancestor-descendant relationship of the different lineages (history of life) and the processes that produced them.

For some time, there has been controversy about the importance to evolutionary theory of four factors: nongenetic inheritance (inclusive inheritance), phenotypic plasticity, developmental processes, and niche construction. For some biologists, these factors have the potential to change our view of evolution (Laland et al., 2014, 2015;

Noble, 2015). A different group of biologists has argued that these factors already have been accounted for in modern evolutionary theory and have not yet demonstrated that their inclusion merits major changes in our current evolutionary framework (Wray et al., 2014; Charlesworth et al., 2017; Futuyma, 2017). We include these four factors in our concept map, using cautious wording about their importance, but showing that they already are part of evolutionary theory.

○ Validation of the Concept Map

We validated the concept map in three ways. First, we examined relevant literature on evolution (e.g., Darwin, 1859; Dobzhansky, 1973; Coyne, 2009; Futuyma & Kirkpatrick, 2017) and phylogenetics (e.g., Felsenstein, 2004; Baum & Smith, 2012). All the authors of this article are researchers and have published papers in high-impact journals, such as *Nature*, *Proceedings of the National Academy of Sciences*, and *Science*, on the theory and practice of biodiversity (e.g., Sala, 2001, 2003, 2016; Crisci, 2006, 2008), biogeography (e.g., Crisci et al., 2003; Crisci & Katinas, 2009; Apodaca et al., 2015b), ecology (e.g., Huxman et al., 2004; Jobbágy & Sala, 2014; Gherardi & Sala, 2015; Sala, 2016), evolution (e.g., Crisci, 1981, 1982; Barreda et al., 2010; Katinas et al., 2013), phylogenetics (e.g., Crisci & Stuessy, 1980; Katinas & Crisci, 2000; Apodaca et al., 2015a), and teaching about evolution (e.g., McInerney, 1989, 2009; Crisci et al., 1993, 2014; National Academy of Sciences, 1998; Andrews et al., 2002; Crisci & Katinas, 2011).

Second, we consulted experts in evolution (e.g., Douglas Futuyma and Edgardo Ortiz-Jaureguizar) and used our own expertise as high school and university teachers (in some cases more than 40 years of teaching) in the following subjects: biodiversity, biogeography, biology education, conservation, ecology, evolution, multivariate analysis, phylogenetics, plant morphology, plant systematics, and taxonomy. This collective expertise was very useful in the construction of the concept map, allowing us to overcome the most common difficulties (such as troubles in linking new knowledge with higher-order, more inclusive concepts in cognitive structure) and answer fundamental student questions.

Third, to validate the concept map, we aligned it with the *Next Generation Science Standards* (NGSS), as explained below.

○ Alignment of the Concept Map with NGSS

The concept map is intended for use in middle school and high school and is based on the statement that “scientific knowledge assumes an order and consistency in natural systems” (NGSS Lead States, 2013). The map also aligns with seven life-sciences core ideas of the NGSS: interdependent relationships in ecosystems, inheritance and variation of traits, biodiversity, natural selection, adaptation, evidence of common ancestry, and fossils as evidence of the history of life. Figure 1 shows grades and standards that include those seven core ideas. The standards from first to fifth grades represent the prior knowledge that anchors the concept map. The map implicitly addresses crosscutting concepts such as patterns, cause and effect, systems and systems models, and stability and change.

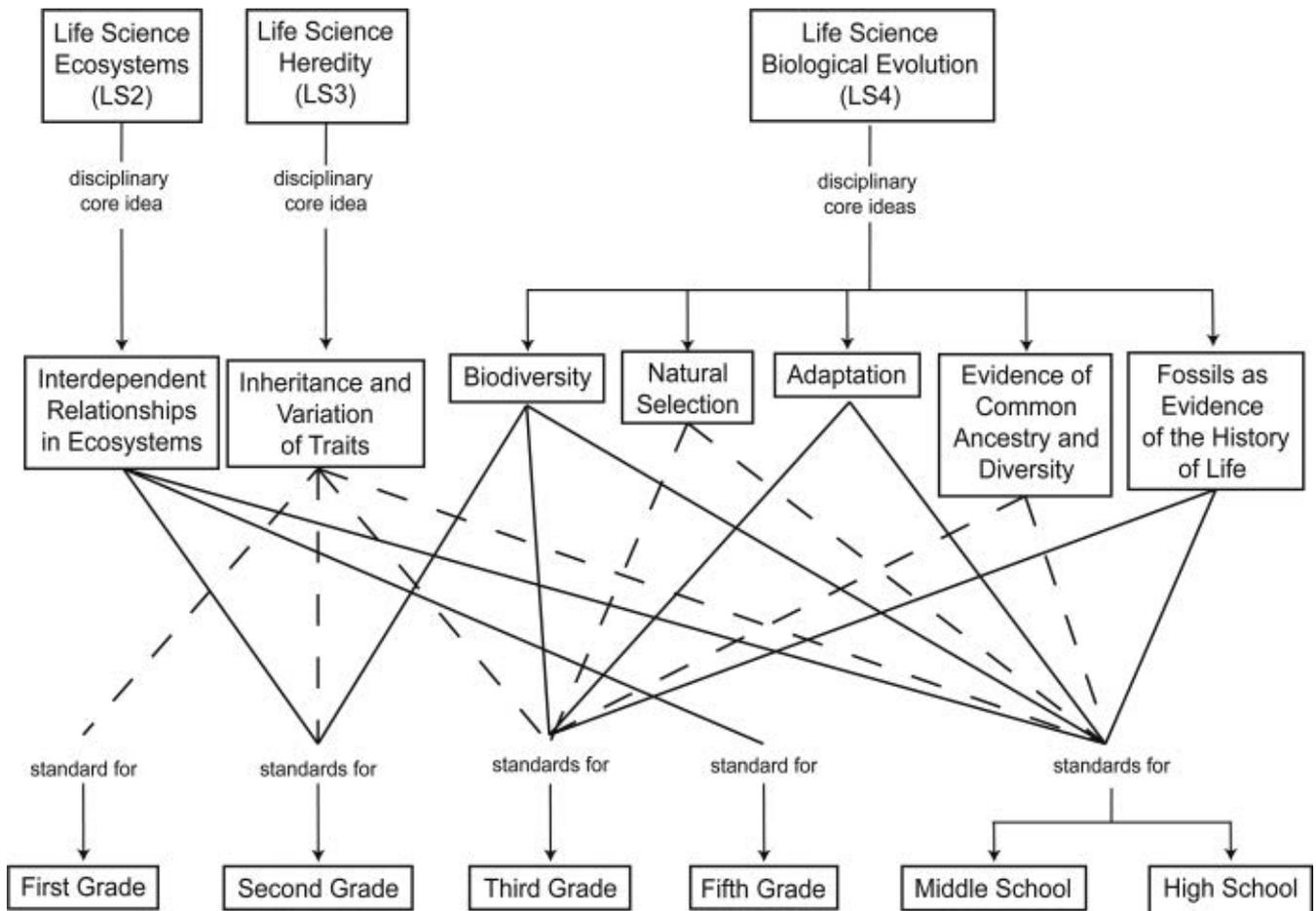


Figure 1. Life science core ideas of the NGSS that are addressed in the concept map.

○ Central Concepts of Evolutionary Biology

We built the concept map as follows:

- (1) We identified three focus questions according to the current knowledge in evolution (Futuyma & Kirkpatrick, 2017) and the idea of meaningful learning (Ausubel et al., 1978; Novak, 2002). We established as our first question, *How should students understand evolutionary biology to foster meaningful learning?* There is sound evidence that evolution has occurred and occurs now in the history of life. Among that evidence are the fossil record, the unity of life, observed evolution, vestigial structures, studies of comparative anatomy, and the spatial distribution of organisms. The evidence led us to the following two questions: *What is the history of life?* and *What processes, in mutual influence with the interaction among organisms and their environment, generated the history of life?* Most important, we wondered how students can incorporate the answers to these three questions into well-organized and relevant knowledge.
- (2) Guided by these questions, we identified what we consider the most pertinent concepts in evolution.
- (3) We established a top-down hierarchical structure, giving the concepts at the top a more inclusive category (e.g., evolutionary biology studies biological evolution, biological evolution

generates biodiversity, biological evolution is a consequence of interactions and processes) and following a sequential flow of events, as it happens in nature.

- (4) Each concept appears only once in the concept map.
- (5) We connected the concepts with a few linking words.
- (6) Although some cross-links could be specified among several concepts, for the purpose of clarity we established only the most relevant cross-links to maintain the hierarchical structure.
- (7) For learning purposes, an activity subsequent to the presentation of this concept map could include identification of cross-links among concepts to reveal a structure that is more a net than a hierarchy.

How Should Students Understand Evolutionary Biology to Foster Meaningful Learning?

Biological evolution generates biodiversity throughout the course of life's history (including the present) and as a consequence of processes at the population level in interaction with the environment (Figure 2).

What Is the History of Life?

The second question (Figure 3) is answered by reconstructing the genealogy of life (= phylogeny)². Charles Darwin was one of the first naturalists to suggest, in his notebooks in 1837 (Notebook B,

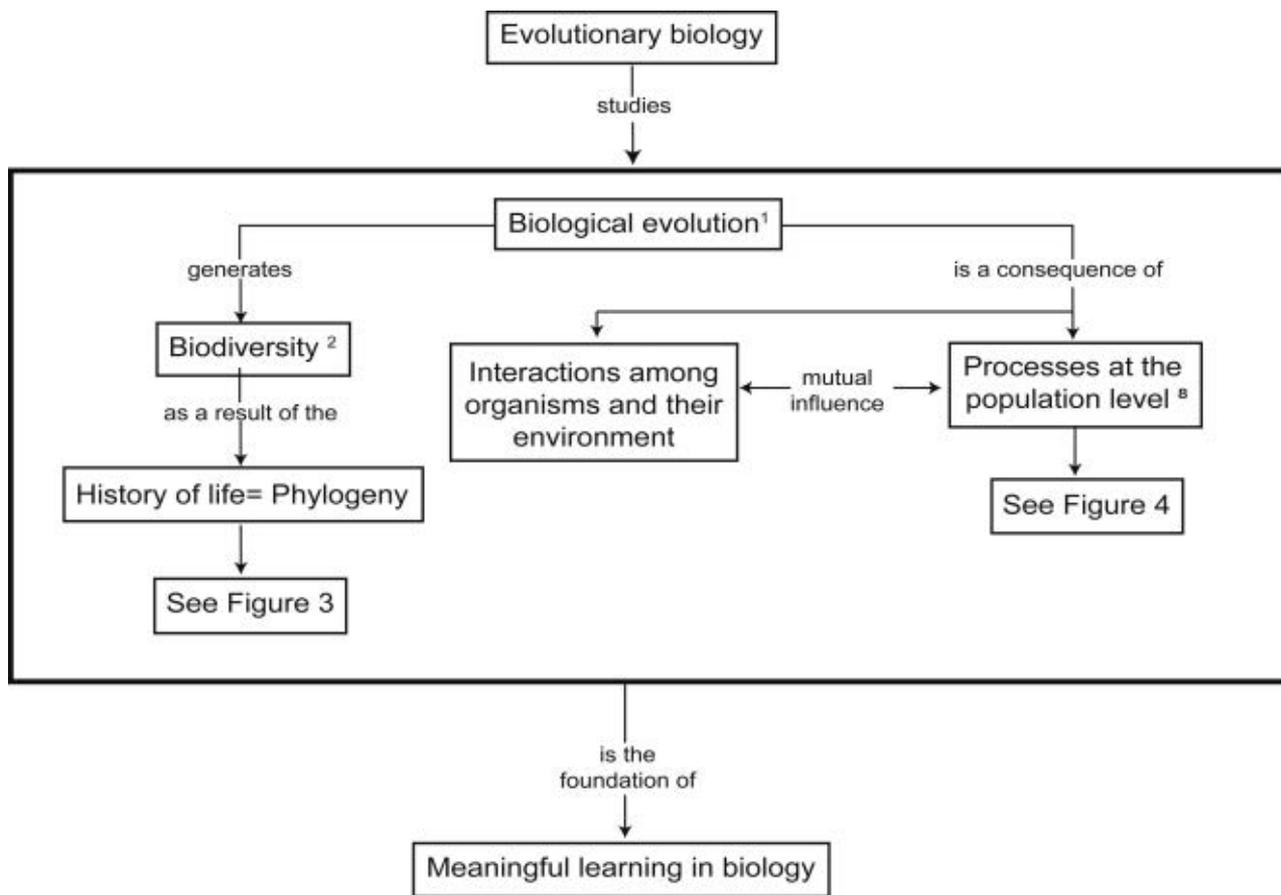


Figure 2. Concept map of evolutionary biology showing the two components of evolution: history of life and processes that generated it.

now stored in Cambridge University Library), the image of a family tree to represent the history of life. The only illustration in *On the Origin of Species* (Darwin, 1859) is a hypothetical tree of life.

Life on Earth came from a common ancestor more than 3.5 billion years ago; it then branched out over time, generating many new and diverse species reflected in the phylogeny of life (Coyne, 2009). The history of life has always been influenced by the history of the Earth³. Fossils (remains or evidence of life >5000 years old) are traces of that past and are a fundamental element for establishing the minimum age of groups and the rates of evolution of each (Pascual & Ortiz-Jaureguizar, 2007; Wyse Jackson, 2010). Fossils also reveal the phenomenon of extinction (disappearance of all members of a group of living beings), a fact common in the history of life (Lomolino et al., 2010).

Currently, scientists reconstruct the history of life by using phylogenetic methods, which are based on the character distribution of organisms and on applying homology⁴ as evidence of common ancestry. Homologous characters are those that originated, with or without modification, from the common ancestor of that group (Hall, 1994). The most widely used techniques of phylogenetic reconstruction⁵ are parsimony, maximum likelihood, and Bayesian inference (Felsenstein, 2004; Baum & Smith, 2012).

Phylogenetic trees⁶ are active hypotheses about order in nature and, as such, are refined or amended through continued research (e.g., the finding of new characters). The phylogenetic tree of the

different groups of organisms is assembled to build a hypothesis about the tree of life (Hillis, 2010).

Furthermore, phylogenetic trees are the basis of classifications⁷ that have explanatory and predictive power because they reflect the generative system responsible for the observed attributes of the organism: biological evolution (Crisci et al., 2014). These classifications provide a reference system for the whole of biology (Crisci, 2006).

What Processes, in Mutual Influence with the Interaction among Organisms and Their Environment, Generated the History of Life?

The first step in answering this third question is to investigate the mechanisms of evolution (Figure 4).

The mechanisms at the population level⁸ are subject to the interaction of organisms with their environment⁹ (Pianka, 2011). These processes generate genetic change and are due mainly to three well-settled mechanisms – mutation, genetic recombination, and gene flow (Futuyma & Kirkpatrick, 2017); and two mechanisms whose importance is still a matter of debate – nongenetic inheritance and phenotypic plasticity.

Mutation¹⁰ is the alteration of a gene whether or not it generates a change in the characteristics of the organism (Hamilton, 2009).

Genetic recombination¹¹ shuffles the genes of both parents during sexual reproduction. It does not change the frequency of genes in the

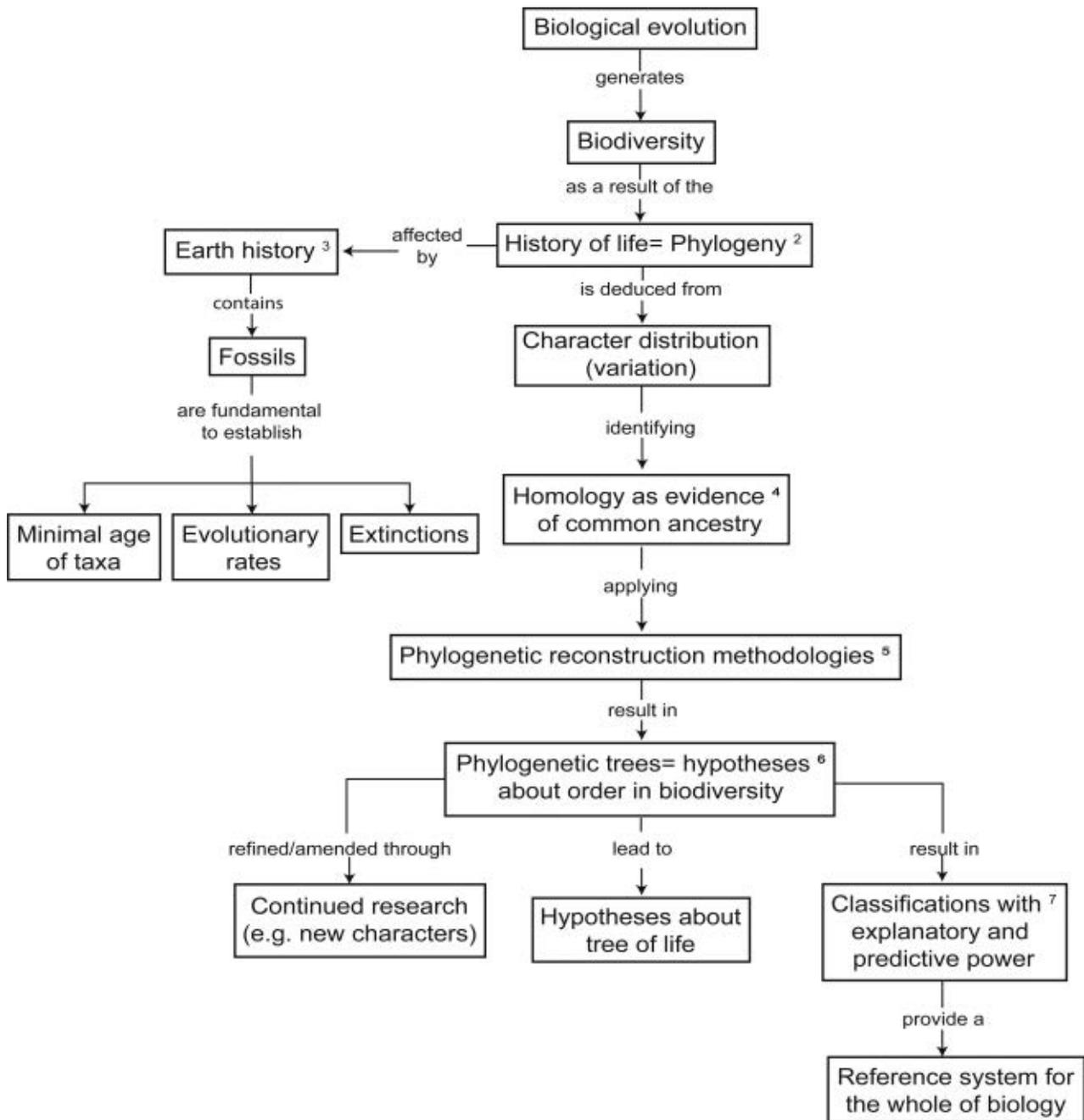


Figure 3. Part of the concept map showing the reconstruction of the history of life.

population, but it does produce new combinations of genes (Ridley, 2004). Gene mixing also occurs during crossing over in meiosis, prior to sexual reproduction (Futuyma & Kirkpatrick, 2017).

Gene flow¹² is the change in gene frequency in a population resulting from new genes introduced by the arrival of individuals from other populations (Templeton, 2006).

Nongenetic inheritance¹³ comprises changes in genetic information that do not involve alteration of the DNA (or RNA) sequence of a genome. At least three mechanisms contribute to nongenetic inheritance: (1) epigenetic inheritance, such as the DNA methylation that often reduces or eliminates gene transcription (Zenk et al., 2017); (2) parental effects that occur when the genotype or phenotype of the parents directly influences the phenotype of their offspring;

and (3) cultural inheritance that is transmitted by behavior and learning (Jablonka & Raz, 2009; Futuyma & Kirkpatrick, 2017).

Phenotypic plasticity¹⁴ is the capacity of a genotype (the set of genes possessed by an individual organism) to generate any of several phenotypes (the characteristics of an organism produced by the interaction of its genes with the environment) depending on the environment. Some evolutionary biologists hold that phenotypic plasticity can precede genetic changes (West-Eberhard, 2003; Laland et al., 2015).

These five basic processes generate heritable variation, which in turn is subject to processes that may change the frequencies of genes and phenotypes in populations. These processes include genetic drift and natural selection.

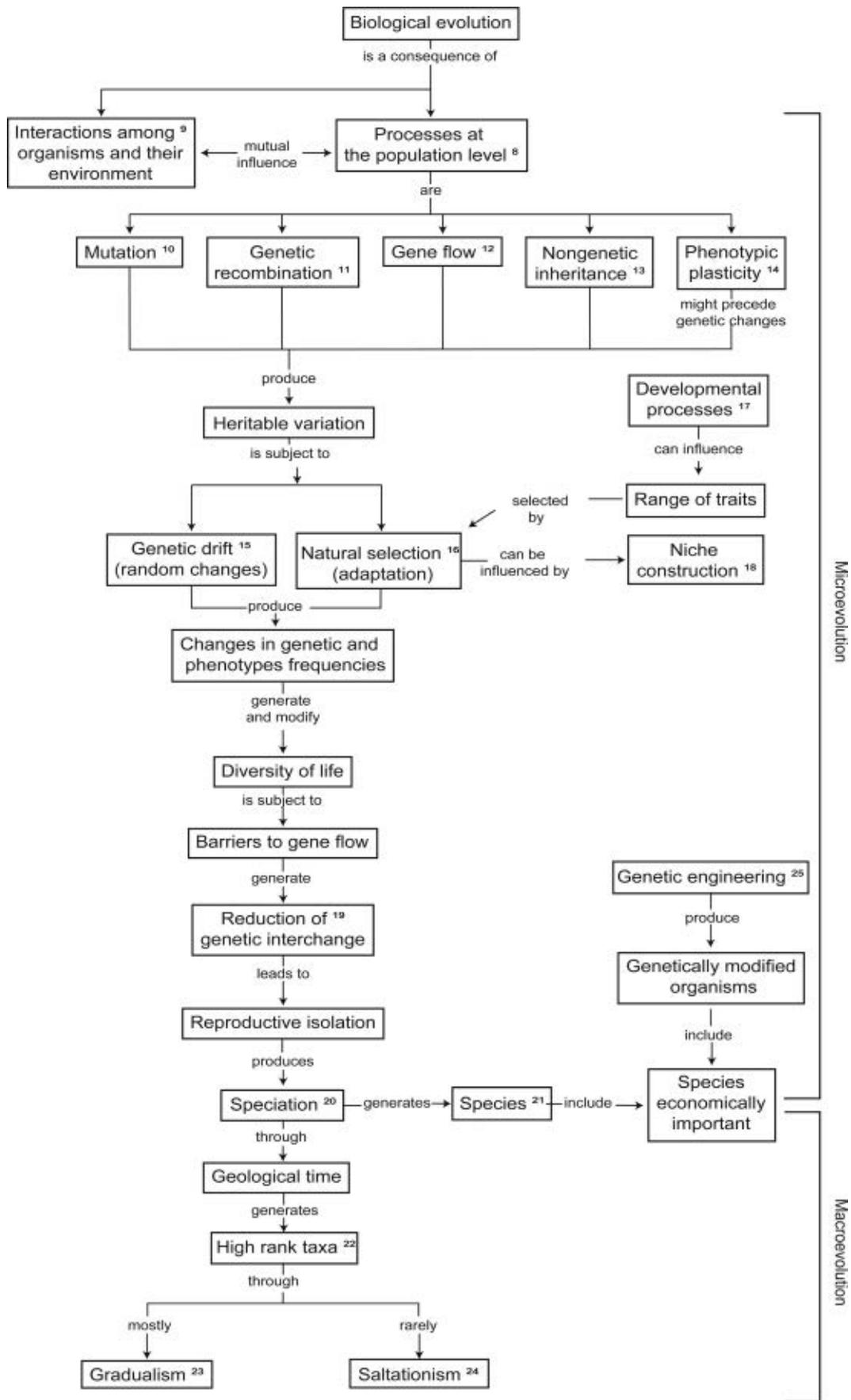


Figure 4. Part of the concept map showing what processes, in mutual influence with the interaction among organisms and their environment, have generated the history of life.

Genetic drift¹⁵ is represented by random, nonadaptive changes in the frequency of two or more genotypes within a single population because of fluctuations due to “errors of sampling” (random processes; Graur & Li, 2000). An example is the so-called “bottleneck” process (Templeton, 2006; Futuyma & Kirkpatrick, 2017), whereby a small number of individuals from a population migrate and establish themselves as settlers (founders) of a new population. Because the founders represent only a small sample of the original population, the frequencies of genotypes in the new population may differ by chance from those of the source population.

Natural selection¹⁶ reflects the fact that different phenotypes have different survival and/or reproduction capacity in the environment in which they are expressed. Differential survival generates differential perpetuation of the respective genotypes. Adaptation to that characteristic increases the survival and/or reproduction of the organism that carries it, in a determined environment. Natural selection is the only known mechanism that generates adaptations by acting on naturally occurring variation, so one might say that an adaptation is a feature that evolved by natural selection (Futuyma & Kirkpatrick, 2017). Two phenomena could influence natural selection: developmental processes and niche construction.

Developmental processes¹⁷, based on features of the genome that may be specific to a particular group of organisms, can influence the range of traits on which natural selection can act (Laland et al., 2015).

Niche construction¹⁸ is the process whereby organisms actively modify their environment and consequently modify their evolutionary niches (Odling-Smee et al., 2003).

Natural selection and genetic drift generate and modify biodiversity. That diversity is not a continuum, because a reduction of the genetic interchange¹⁹ between populations (which usually generates reproductive isolation) leads to speciation²⁰ and to the formation of new species (Coyne & Orr, 2004).

The definition of a species²¹ is very controversial (Crisci, 1981), and it has been defined in many ways for plants, animals, and microorganisms (Van Regenmortel, 1997). The most widely used, but not uncontested, criterion is the biological concept of species: a group of natural, genetically similar, interfertile populations that are reproductively isolated from other such groups (Mayr, 1970).

Speciation, therefore, is responsible for the discontinuities we observe in the diversity of life – that is, the absence of a smooth continuum in life’s history. These discontinuities range from the species level (microevolution) to higher-ranking taxa (macroevolution) (Futuyma & Kirkpatrick, 2017). Macroevolutionary changes occur with the appearance of characteristics that distinguish large groups²², such as mammals, insects, or flowering plants. They are changes that occur on a geological timescale (Jablonski, 2007). Macroevolution includes two schools of thought: gradualism and saltationism.

Gradualism²³ proposes that macroevolution results from the accumulation of small modifications throughout geological periods. The only difference between macroevolution and microevolution would then be the amount of time in which they elapse. Macroevolution, in this view, is a simple extension in time of microevolution.

Saltationism²⁴, on the other hand, proposes that macroevolution includes processes that operate only at macroevolutionary levels. For example, large changes in chromosomes (macromutations) would give rise to very different organisms, which would adapt to new ways of life and generate differences between large groups.

One can resolve the binary distinction between gradualism and saltationism with the following argument: The evolutionary forces of microevolution work and are responsible for most of the large groups we see today. In the long history of life, however, there have been occasional occurrences of unique events that have had great consequences (Grant, 1977). An example of the last type is the evolutionary event by which a symbiotic bacterium was transformed into mitochondria of the cells of most other living beings (Margulis, 1998).

A special case of evolution is that produced by human manipulation such as genetic engineering²⁵, also called genetic modification or genome editing. It is the direct manipulation of an organism’s genome using biotechnology to produce genetically modified organisms (Vanloqueren & Baret, 2009). To the extent that those changes are transmitted to subsequent generations, the possibility exists to alter the evolutionary trajectory of the species in question. That possibility is one of the vexing challenges inherent in the now pervasive application of CRISPR-based genetic editing (Dickinson & Goldstein, 2016; Winblad & Lanner, 2017).

○ Summary

A concept map of evolutionary biology is a way to promote meaningful learning in biology. In this case, the concept map is an educational tool that generates a context of ideas around every main concept of the subject in an introductory road map to biological evolution.

Biological evolution is a great and stirring account of life on Earth and of human origins within it. It speaks of our connectedness to the rest of life on Earth and invokes our stewardship of our planet and its biodiversity. Biological evolution also can be inspirational by exposing students to the wonders of nature, such as flowers that attract pollinators by mimicking females, deep-sea fish that can swallow prey larger than themselves, and snakes that can strike mammalian prey in darkness by sensing their body heat. Exposure to evolutionary theory concerns not merely the facts of natural selection, common ancestry, homology, or speciation, but also the amazing array of things that organisms do by virtue of their adapted states (Douglas Futuyma, Stony Brook University, personal communication, June 6, 2016).

But there is something else important about the study of evolutionary theory: it causes us to engage with one of the most impressive and far-reaching achievements of the human intellect, and it is evolution itself that has provided us with the intellectual capacity to apprehend our own history and our place in the biosphere.

○ Acknowledgments

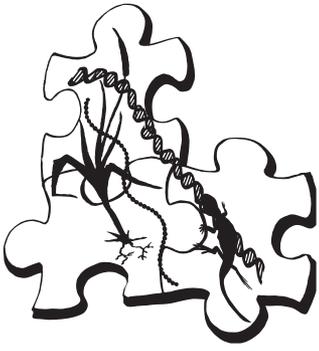
We acknowledge Douglas Futuyma, Elián Guerrero, and Edgardo Ortiz-Jaureguizar for their useful comments on a first draft of the concept map. Those faults that remain are entirely our responsibility. Piero Marchionni and Mary Rose Stoltz provided technical assistance. The reviewers are also acknowledged for their useful comments and suggestions.

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Using the I² Strategy to Help Students Think Like Biologists about Natural Selection

KAREN LUCCI, ROBERT A. COOPER

Location A



ABSTRACT

Many students have very robust misconceptions about natural selection, stemming from intuitive theories that form a child's earliest understandings of the natural world. For example, students often imagine that species evolve in response to environmental pressures that cause a need for change and that all individuals in the population simultaneously respond to this need by adapting in order to survive. While children's intuitive theories are essential for comprehending many events in their daily experience, they can make learning the counterintuitive theories of science, like natural selection, challenging. To help students develop an understanding of natural selection, teachers need to guide them through an evaluation of the intuitive theory and its well-established scientific counterpart so that they see the failure of the intuitive theory to adequately explain the evidence. In other words, it is critical for the learner to confront his or her misconceptions to break them down, rather than fail to address them. This can be done by presenting students with graphical illustrations of how natural selection works and providing the tools to interpret them. Here we illustrate how to use such a tool, the Identify and Interpret (I²) strategy.

Key Words: Data analysis; data interpretation; evolution; graphs; misconceptions; natural selection; science practices.

○ Introduction

Natural selection is one among many scientific concepts that are frequently misunderstood by students. Students tend to hold misconceptions resulting from their application of intuitive theories about the world. These misconceptions develop early in life and have consistently been found in people of all ages, across many different cultures, and throughout history (Bloom & Weisberg, 2007; Shtulman, 2017). One common student misconception about natural selection is that species evolve in response to environmental pressures that cause a need for change and that all individuals in the population simultaneously

respond to this need by adapting in order to survive. This misconception stems from the fact that students' intuitive theories cause them to focus their attention only on the individual organisms, when they should be dividing their attention between the fate of the individual organisms and the resulting changes in the make-up of the population.

Evolution by natural selection is an emergent process whereby interactions between individual organisms (e.g., herbivory, predation, and parasitism) result in changes in the population distribution over time (Ferrari & Chi, 1998; Chi, 2005; Cooper, 2017). Ernst Mayr (1982) referred to this as "population thinking." The distribution of traits in a population changes over time as a result of differences in the survival and reproductive success of the individuals. Changes in a population distribution over time can be observed by analyzing graphs that model these changes. Here, we employ an instructional strategy called Identify and Interpret (I²) that can be used for either formative or summative assessment (BSCS, 2012a, b). We illustrate how to use the strategy to guide students in their analysis of graphs that show changes in populations of rock pocket mice and Darwin's finches, two excellent examples of evolution in action.

The I² strategy can be used to scaffold students' efforts to understand any type of figure found in scientific papers and textbooks.

○ Reading & Interpreting Graphs Using I²

Reading and interpreting graphs is a skill that must be explicitly taught. The *Next Generation Science Standards* (NGSS) call for students to learn to analyze and interpret data (Science Practice 4):

Once collected, data must be presented in a form that can reveal any patterns and relationships and that allows results to be communi-

cated to others. . . . Such analysis can bring out the meaning of data – and their relevance – so that they may be used as evidence. (NGSS Lead States, 2013, p. 390)

But just how do we go about teaching students to analyze data presented in a graph? BSCS developed the I^2 strategy to scaffold students' efforts to bring out the meaning of data presented in graphs, figures, sketches, and other forms of data representation found in scientific papers and textbooks (BSCS, 2012a, b).

Students should begin their analysis of a graph by taking note of the variables on the x and y axes, making sure they understand what those variables represent. Then, using the I^2 strategy, students consider "What I see." They look for any patterns, changes, trends, or differences they can find. From each pattern, change, trend, or difference, they draw an arrow pointing to a "What I see" statement. For example, in Figure 1, students should note the upward trend in the graph – the number of chirps increases with temperature. Next the students consider "What it means." From each "What I see" statement they've written on the graph, students draw an arrow to a statement explaining the meaning of the pattern, change, trend, or difference they have identified. In Figure 1, the upward trend likely results from the fact that crickets are ectotherms and their body temperature, and therefore their metabolism, increases with environmental temperature. It can be helpful in the classroom to have students use different colors to clearly show and separate the "What I see" statements from the "What it means" statements. In addition, having students work together in small groups to interpret graphs using I^2 enables teachers to facilitate the kind of student talk that promotes learning of both content and science practices (Handelsman et al., 2004; Tanner, 2009).

After students have recorded all their "What I see" statements and explained the meaning of each with a "What it means" statement, they write a caption – a paragraph explaining the meaning of the graph. The caption begins with a topic sentence that describes what the graph shows. Each of the remaining sentences joins a description of a specific pattern, change, trend, or difference in the graph with the explanation of what it means. The following could be an appropriate caption for the graph in Figure 1:

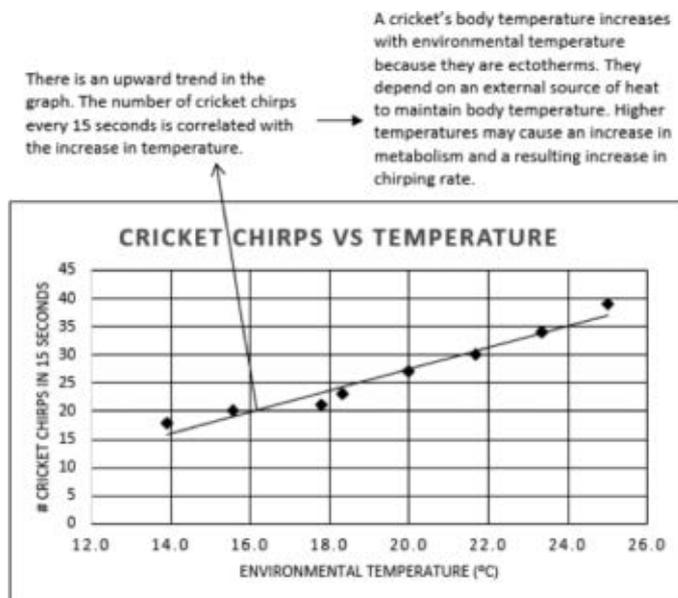


Figure 1.

Figure 1 shows the change in the number of cricket chirps during 15-second periods as environmental temperature ($^{\circ}\text{C}$) increases. The number of cricket chirps is correlated with the environmental temperature. A possible explanation depends on the fact that crickets are ectotherms, animals that depend on an external source of heat to maintain their body temperature. Higher temperatures may cause an increase in metabolism and a resulting increase in chirping rate.

Teachers should note the use of hedging language in the explanation of the cricket chirp graph ("Higher temperatures may cause an increase in metabolism and a resulting increase in chirping rate"). Students may be inclined to claim a causal relationship based on the graph. It is essential that students understand that these are observational data that only show a correlation between environmental temperature and chirping rate. Correlation is not causation. The tentative explanation provided in the caption above serves as a hypothesis that could motivate a laboratory experiment to establish causation. It would be necessary to perform a control experiment to simultaneously measure both metabolic rate and chirping rate as temperature is varied while other potential causal variables are held constant.

Students' captions can be collected and graded as either a formative or a summative assessment. Using the I^2 strategy with graphs also affords teachers the opportunity to teach, or review, basic graphing skills and basic descriptive statistical concepts like distribution, average, and variance that are essential for understanding natural selection. According to NGSS (HS-LS4-3), students who demonstrate understanding of natural selection can

apply concepts of statistics and probability to support explanations that organisms with an advantageous heritable trait tend to increase in proportion to organisms lacking this trait. [Clarification Statement: Emphasis is on analyzing shifts in numerical distribution of traits and using these shifts as evidence to support explanations.] (NGSS Lead States, 2013, p. 272)

The importance of statistical concepts for understanding natural selection has also been noted elsewhere (Endler, 1986; Gould, 1996; Petrosino et al., 2015; Cooper, 2017).

The two cases of natural selection in action presented below, the rock pocket mouse and Darwin's finches, provide graphs that clearly illustrate changes in populations over time resulting from differences in individual survival and reproductive success. The graphs come from several HHMI BioInteractive instructional resources that illustrate the fact that many organisms die during the process of natural selection, and that no individuals adapt by changing their anatomy in order to survive. By using the I^2 tool to analyze these graphs and contrasting their intuitive theories with the theory of natural selection, students begin to develop a better understanding of population thinking and the process of natural selection.

○ Changing Color Variations in Rock Pocket Mice

Our first example of evolution in action is the story of the adaptation of the rock pocket mouse to the appearance of areas of dark, black basalt rock that formed in the sandy deserts of Arizona and

New Mexico over the past one or two million years. There are two color varieties of the rock pocket mouse, a sandy-colored variety that lives predominantly on sandy-colored rock and a black variety that lives predominantly on black basalt (Figure 2). The difference in color has been linked to variation in a single gene, the melanocortin-1 receptor gene (*Mclr*), which is one of several genes involved in the synthesis of pigments in the melanocytes, specialized pigment-producing skin cells (Hoekstra & Nachman, 2003). The wild-type, sandy-colored mice produce more pheomelanin, a lighter-colored pigment, than eumelanin, the darker pigment. Mutations in the *Mclr* gene result in the production of more eumelanin in the black mice.

The mutated form of *Mclr* that produces black mice is maladaptive if the mice live in the sandy-colored desert, but it provides an advantage if the mice happen to live on the black rock. The mice are eaten by various predators, including owls, foxes, and coyotes, that rely predominantly on sight to detect their prey. Mice whose fur color does not match the substrate are at a considerable disadvantage when it comes to avoiding predators. Predators will eat either sandy-colored or black mice, but given the conditions on the lava flow, black mice are more likely to avoid predators; while on the sandy-colored desert, sandy-colored mice are more likely to avoid predators. Mutations occur randomly, providing the ultimate source of genetic variation. But more importantly, genetic recombination (random assortment and crossing over) shuffle the existing variant alleles in different combinations, resulting in the observed phenotypic variations. Natural selection then preserves those phenotypic variations that are advantageous. Once the lava flows had produced the black rock, a population of predominantly black mice could have evolved from an ancestral sandy-colored population in <100 generations (HHMI BioInteractive, 2005).

An HHMI BioInteractive activity suitable for middle school or high school provides students the opportunity to analyze data and use it as evidence to construct an explanation for the two color varieties in the rock pocket mouse (HHMI BioInteractive, 2015a). Students first watch a short film that tells the story of

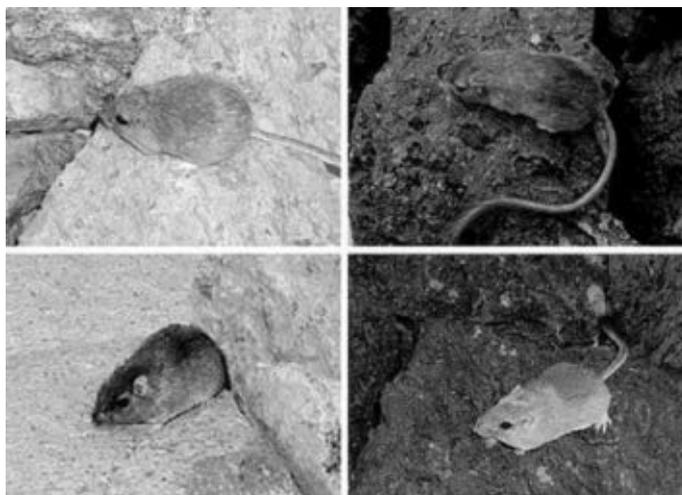


Figure 2. Used with permission from the Howard Hughes Medical Institute, © 2005. All rights reserved. <https://www.hhmi.org/biointeractive>. Original source: Nachman et al. (2003).

selection and adaptation in the rock pocket mouse (HHMI BioInteractive, 2011). After the video, they are presented with four sets of images like the one shown in Figure 3 and asked to place them in a logical sequence based on information from the video. The sets of images are snapshots showing rock pocket mouse populations at two locations over four different times. Location A is a sandy desert and remains so through all four snapshots. Location B starts out as a sandy desert but changes to dark black following a lava flow. Students sequence the images based on data collected by counting the number of mice of each color variety at each location and using information from the video. Location A has predominantly sandy-colored mice and there is little change across all four snapshots. However, when the snapshots are sequenced correctly, Location B starts out with predominantly sandy-colored mice (10 sandy, 2 black) but ends up with predominantly black mice (10 black, 2 sandy).

After sequencing the images, counting the mice, and recording the data in a table, students construct graphs like those shown in Figure 4. Working in small groups using the I^2 strategy on their graphs, students first identify the trends they see, then write “What I see” statements and “What it means” statements. Figure 5 provides examples of what students might write as they annotate the graphs.

Once students have completed their analysis of the graphs, a whole-class discussion gives them the opportunity to share what they’ve found and argue for a particular interpretation of the evidence until the class arrives at some agreement on the relevant

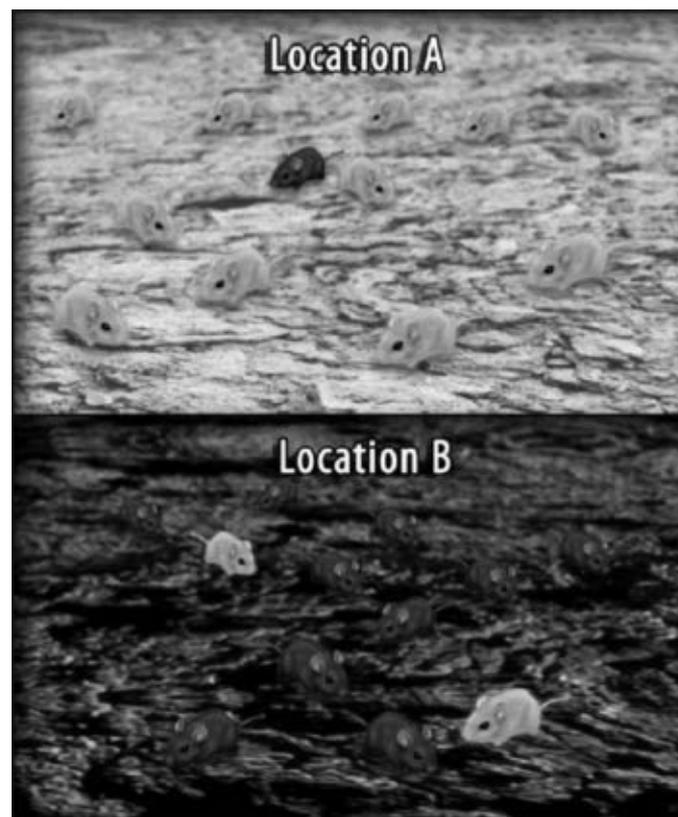


Figure 3. Used with permission from the Howard Hughes Medical Institute, © 2015. All rights reserved. <https://www.hhmi.org/biointeractive>.

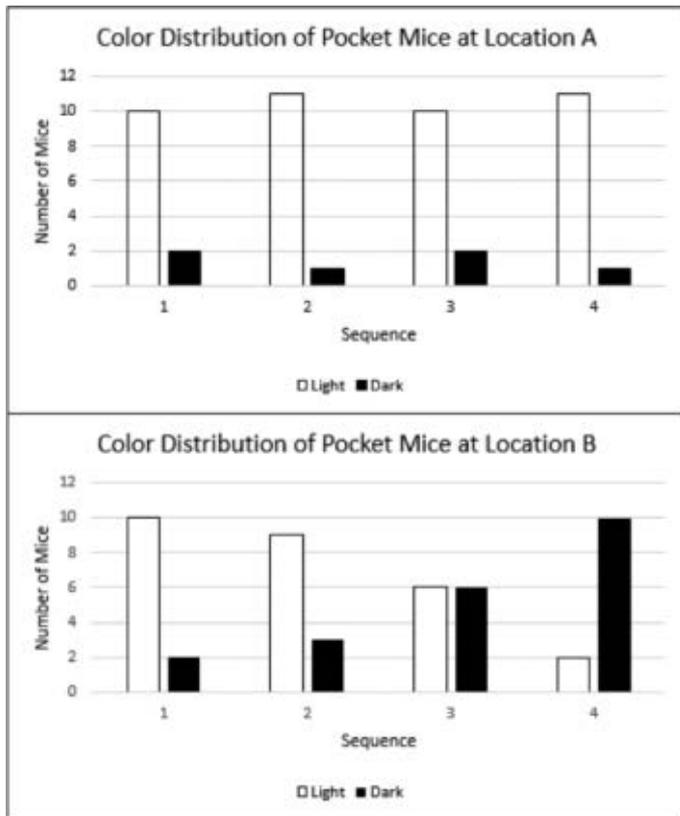


Figure 4. Used with permission from the Howard Hughes Medical Institute, © 2015. All rights reserved. <https://www.hhmi.org/biointeractive>.

features and their meaning. When the class has reached a consensus, students individually write a detailed caption for the graph by combining the “What I see” and “What it means” statements into a coherent paragraph. The following key points should be stressed with students during discussion. Darwin’s mechanism of evolutionary change is a two-step process. The first step is the production of genetic variations without any awareness of what traits might be adaptive under current conditions in the environment. This occurs during the normal process of reproduction through mutation and genetic recombination. The second step is selection, which acts on individuals differently on the basis of the traits they inherited. Those with maladaptive traits are most likely to die before reproducing successfully, while those with adaptive traits are more likely to survive and reproduce, passing on their adaptive genes to the next generation. As a result, the proportions of different genetic variations in the population may change.

It is important to stress that variations are produced by the random processes of mutation and genetic recombination that occur prior to selection. They do not arise because of a need imposed by the environment. Individuals born with maladaptive traits are simply at a disadvantage, and they cannot change their traits to become better adapted. The rock pocket mouse video (HHMI BioInteractive, 2011) makes this apparent by discussing the variety of predators that feed on the mice and by illustrating the changes in proportions of black and sandy-colored mice in the population over generations in an animation. The animation is also available as a stand-alone resource (HHMI BioInteractive, 2005).

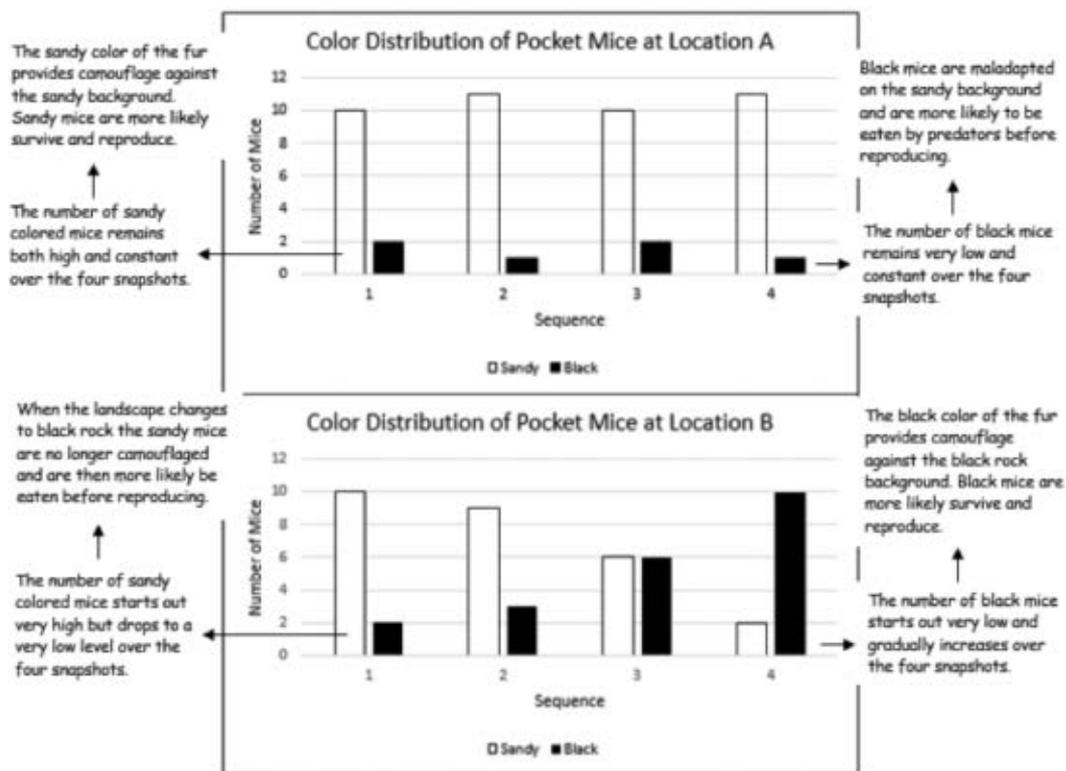


Figure 5. Used with permission from the Howard Hughes Medical Institute, © 2015. All rights reserved. <https://www.hhmi.org/biointeractive>.

○ Changes in Beak Depth of Darwin's Finches

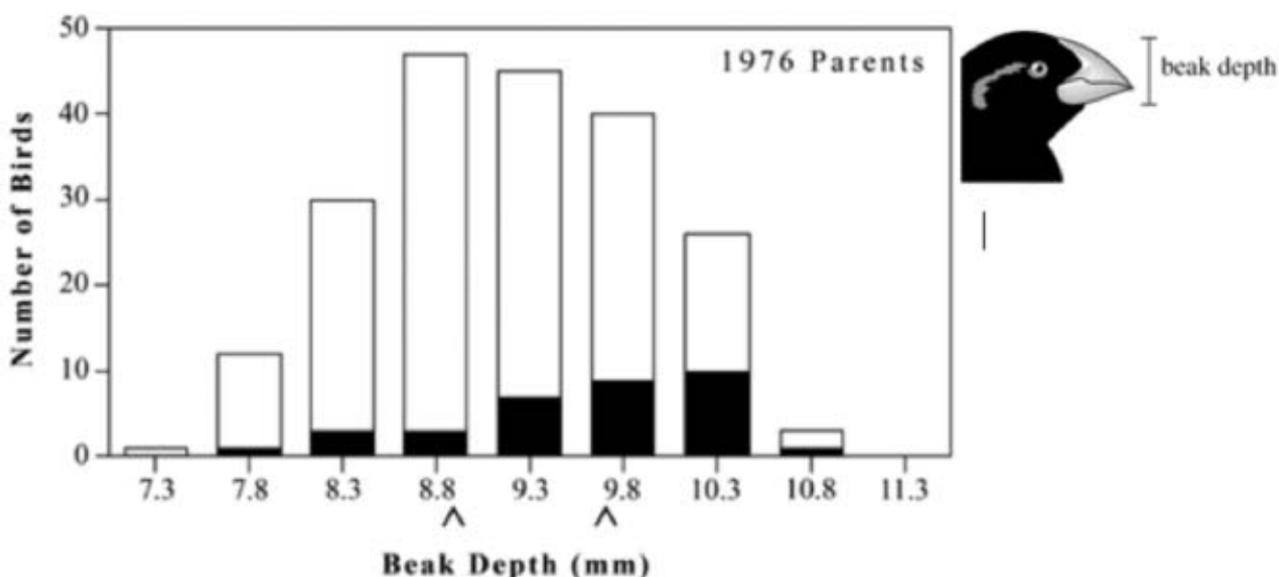
The story of the adaptation of Darwin's finches during a 1977 drought provides our second example of evolution in action. This example involves a quantitative trait, beak depth. Quantitative traits produce a continuous distribution of different phenotypes rather than a dichotomous split between two contrasting phenotypes. Variants of the trait can be displayed on a graph called a histogram that may approximate the shape of a normal distribution, and can be characterized with two numbers, the average and the standard deviation. By examining histograms from successive generations, students can see that evolution involves cumulative changes in the proportions of different variations at the population level, not changes in individual organisms.

An HHMI BioInteractive resource (HHMI BioInteractive, 2015b) presents students with the histogram in Figure 6, which displays data collected by Peter and Rosemary Grant. The histogram shows the distribution of beak depths of Darwin's finches in 1976 (white bars), with the finches that survived a drought overlain in black. In the early 1970s, the Grants selected the small island of Daphne Major in the Galápagos archipelago as a laboratory to study evolution. Since the island was small, they could manage the task of measuring all the medium ground finches on the island. During the first four years of their study, they caught, banded, and measured birds but observed little change in their traits. However, in 1977, a severe drought lasting 18 months hit the island. In May 1976, before the drought, the Grants measured an average beak depth of 9.42 mm for the population of medium ground finches. In 1978, after the drought, the average beak depth of the finches had increased to 9.96 mm, 6% larger than in 1976 (Boag & Grant, 1981).

The drought altered the food supply, creating conditions in which many of the birds from the 1976 population were ill-equipped to survive. Before the drought there was a range of seeds varying in size and hardness, but as the drought persisted the only seeds remaining were large, hard seeds from the cactus bushes that were able to weather the drought. Smaller finches were unable to crack these large, hard seeds and died at a higher rate than birds with larger beaks. The survivors that reproduced had, on average, larger beaks and produced offspring that also had, on average, larger beaks. Parents tend to produce offspring that look like themselves. The shift in the population distribution toward larger average beak depth was a result of differences in survival and reproductive success for individual birds with different beak depths. This is natural selection in action.

To begin the study of this case, students must be provided with the backstory about the Grants and their study of the finches on Daphne Major without telling them the final outcome. They need to know that the Grants were collecting data on finch beak depth, body weight, wing length, and leg length for a number of years, with little change in the finches until a drought occurred in 1977. The drought caused a change in the vegetation and a resulting change in the types of seeds available for the finches to eat. Before the drought there was a range of seeds varying in size and hardness, but following the drought there were only large, hard seeds. Ask students to predict what happened to the finches as a result of the changing conditions caused by the drought. It is likely that many will suggest that individual finches had to grow larger beaks, or produce offspring with larger beaks, in order to survive on the supply of large seeds.

Once the students have made their predictions, they can be shown the histogram in Figure 6. Working in small groups using



The histogram shows the distribution of beak depths of medium ground finches on Daphne Major in 1976 (white bars). The number of finches at each beak depth that survived the 1977 drought (black bars) are also shown. The carets mark the locations of the means for all finches (left) and the survivors (right).

Figure 6. Used with permission from the Howard Hughes Medical Institute, © 2017. All rights reserved. <https://www.hhmi.org/biointeractive>.

the I^2 technique, students take note of the variables on the axes of the histogram and make sure they understand their meaning. Then they identify any patterns or differences they see, followed by writing the corresponding “What it means” statements. One important feature for students to note is the difference in the magnitudes of the white bars and the black bars. A comparison shows that large numbers of finches died as a result of the drought. A related video (HHMI BioInteractive, 2013), which can be shown after students analyze the histograms, states that 80% of the birds died, resulting in a change in the average beak depth. Examples of “What I see” statements and their associated “What it means” statements are shown in Figure 7.

Once students have completed their analysis of the histogram showing the parents, they should be presented with the two histograms in Figure 8 comparing the beak depths of the offspring in 1976 with the beak depths of the offspring in 1978. Students use I^2 on these two histograms and relate them back to the histogram in Figure 7. Students should see that the distribution of beak depths of the 1976 offspring is similar to the 1976 parental distribution and that both have similar averages. The same can be said for parents that survived the 1977 drought and the 1978 offspring. These similarities in the respective population distributions suggest that beak depth is an inherited trait, and that selection for larger beak depth during the drought increased the average beak depth.

Once students have completed their analysis of the histograms, a whole-class discussion gives them the opportunity to share what they’ve found and argue for a particular interpretation of the evidence until the class arrives at some agreement on the relevant features and their meaning. When the class has reached a consensus, students

individually write detailed captions for the histograms by combining the “What I see” and “What it means” statements into coherent paragraphs. By examining the histograms in Figures 7 and 8 together, the two-step process of natural selection is made apparent to students. The beak depths of the 1976 parents in Figure 7 (white bars) are normally distributed, showing variation around an average beak depth of ~8.8 mm. Comparing this histogram to the 1976 offspring in Figure 8, we can see that the distribution is a very similar normal distribution with a similar average of ~8.8 mm, illustrating the fact that beak depth is inherited. Since inheritance is randomized through mutation and genetic recombination, the two distributions are not exactly identical, but they have very similar averages and standard deviations. Had the drought not occurred, it is very likely that the distribution of beak depths in the 1978 offspring would have been similar to both the 1976 parents and offspring, with an average in the neighborhood of ~8.8 mm and a similar range of variation. However, the environmental conditions during the 1977 drought caused the distribution of surviving parents to shift toward a larger average beak depth of ~9.8 mm, as shown in Figure 7 (black bars). Since beak depth is an inherited trait, when the surviving parents reproduced, the distribution of beak depths in their offspring in 1978 as shown in Figure 8 was also very similar, with an average of ~9.8 mm and a similar range of variation.

As stated in the rock pocket mouse section above, Darwin’s mechanism requires inheritable variation in a trait, and a specific variation of that trait must enable those individuals who possess the variation to leave more offspring than other variants. If these criteria are met, then the distribution of traits among the offspring will differ predictably from that of all the parents beyond what

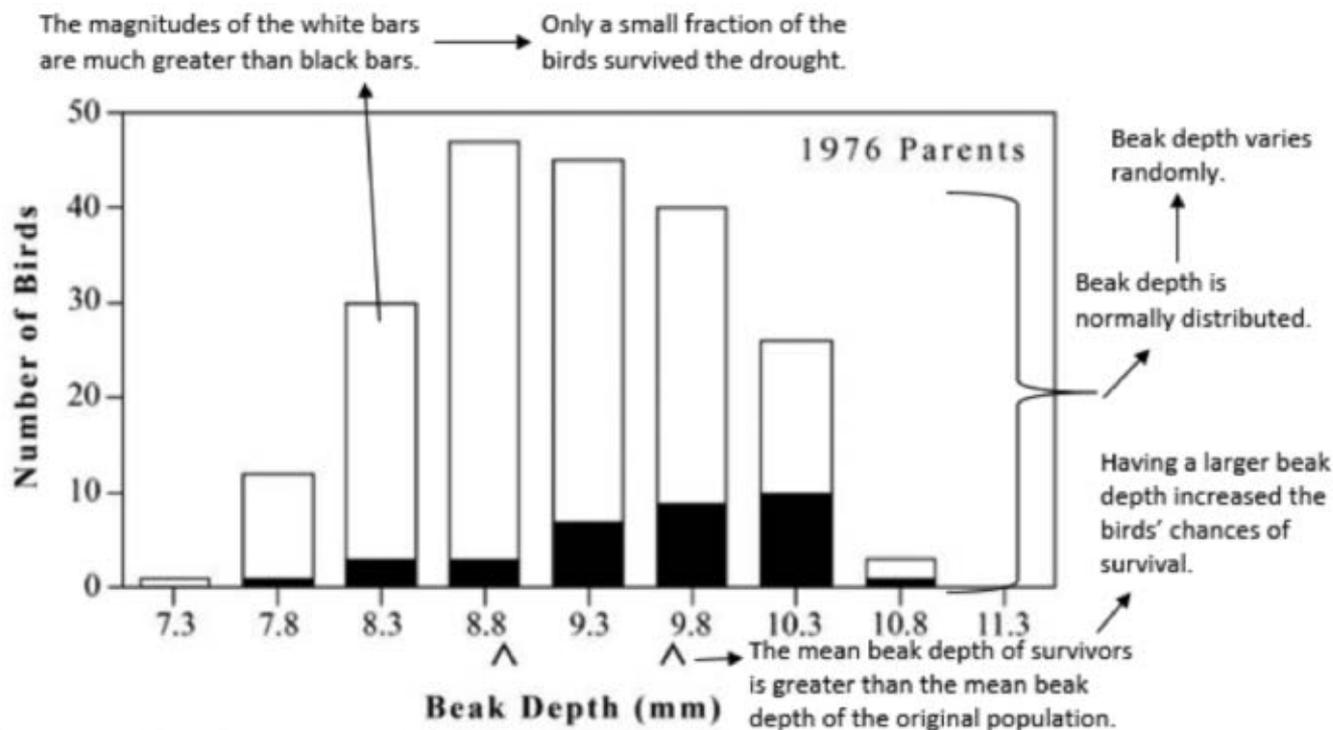


Figure 7. Used with permission from the Howard Hughes Medical Institute, © 2017. All rights reserved. <https://www.hhmi.org/biointeractive>.

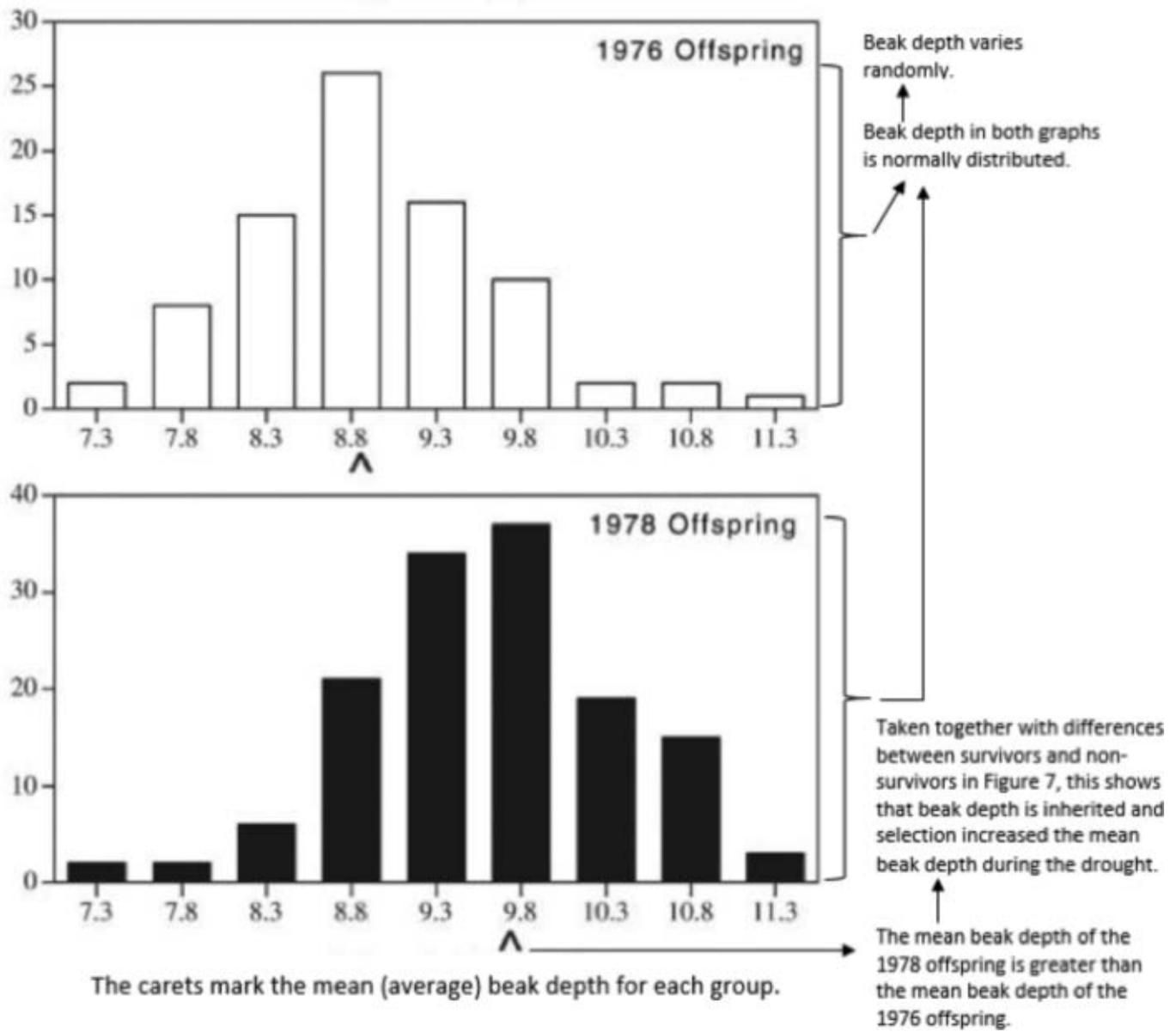


Figure 8. Used with permission from the Howard Hughes Medical Institute, © 2015. All rights reserved. <https://www.hhmi.org/biointeractive>.

would be expected from variation and inheritance alone (Endler, 1986). The survivors of the 1977 drought had, on average, larger beak depths than the nonsurvivors. As a result, they produced a new generation in 1978 that also had, on average, larger beak depths. Comparing the initial population of parents from 1976 with the offspring in 1978, students can see that there was a change in the population distribution over generations – in other words, evolution by natural selection has occurred.

Once students have written their captions, show the video describing the Grants' research (HHMI BioInteractive, 2013). A short segment of the video (5:17 minutes long; from 5:56 to 11:13) is sufficient for the students to compare their conclusions to those of the Grants. Students will see that they have arrived at the same conclusions reached by the Grants. The rest of the 16-minute video explains how natural selection contributes to the formation of new species.

○ Conclusion

Many students have very robust misconceptions about natural selection that may seem immune to instruction (Chi, 2005). The misconceptions are robust because they stem from intuitive theories that form a child's earliest understandings of the natural world (Shtulman, 2017). While these intuitive theories are essential for comprehending many events in a child's daily experience, they can make learning the counterintuitive theory of natural selection challenging, but certainly not impossible. Shtulman (2017, p. 245) writes, "Any educator who wants to help students confront and correct their intuitive theories needs to tailor his or her instruction to those theories." The key is to guide students through an evaluation of the intuitive theory and its well-established scientific counterpart. Students need a clear demonstration of how the intuitive theory fails to adequately explain the phenomenon in question,

followed by a clear demonstration of how the scientific theory adequately explains the phenomenon. The approach suggested here is to employ graphs and some basic statistical concepts to guide students through the process of population thinking. In other words, they need to be aware of the emergent and transgenerational nature of evolution by natural selection. This requires that students have an understanding of basic concepts from statistics, like the concepts of distribution, average, and variance. When the I² strategy is used on the graphs derived from the two cases of natural selection in action described here, students see that selection acts on individuals and many of them die; individual organisms do not change in order to survive. Evolutionary change emerges at the population level, in the proportions of individuals with different variations.

The I² strategy can be used to scaffold students' efforts to understand any type of figure found in scientific papers and textbooks. When students work on the I² strategy in pairs or small groups, teachers can facilitate the kind of student talk that promotes learning of both content and science practices. In short, using I² to guide students in the interpretation of data helps them learn to think like biologists (Handelsman et al., 2004; Tanner, 2009; BSCS, 2012a, b).

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- Reviews and updates of recent advances in the life sciences in the form of an "Instant Update" that brings readers up-to-date in a specific area
- Imaginative views of the future of biology education and suggestions for adjusting to changes in schools, classrooms, and students
- Other timely, relevant and interesting content like discussions of the role of the Next Generation Science Standards in biology teaching, considerations of the history of biology with implications for the classroom, considerations of the continuum of biology instruction from K-12 to post-secondary teaching environments, or contributions that consider the likely/ideal future of science and biology instruction.

Research on Learning (up to 4000 words) includes reports of original research on innovative teaching strategies, learning methods, or curriculum comparisons. Studies should be based on sound research questions, hypotheses, discussion of appropriate design and procedures, data and analysis, discussion on study limitations, and recommendations for improved learning.

Inquiry and Investigations (up to 3000 words) is the section of *ABT* that features discussion of innovative laboratory and field-based strategies. Strategies in this section should be original, engaging, focused at a particular grade/age level of student, and include all necessary instructions, materials list, worksheets and assessment tools, practical, and related to either a particular program such as AP and/or linked to standards like NGSS. The most appropriate contributions in this category are laboratory experiences that engage students in inquiry.

Tips, Tricks and Techniques (up to 1500 words but may be much shorter) features a range of suggestions useful for teachers including laboratory, field and classroom activities, motivational strategies to assist students in learning specific concepts, modifications of traditional activities, new ways to prepare some aspect of laboratory instruction, etc.

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continued

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The *Chicago Manual of Style, 14th Edition* is to be used in regards to questions of punctuation, abbreviation, and style. List all references in alphabetical order on a separate page at the end of the manuscript. References must be complete and in *ABT* style. Please review a past issue for examples. Use first person and a friendly tone whenever appropriate. Use concise words to emphasize your point rather than capitalization, underlining, italics, or boldface. Use the SI (metric) system for all weights and measures.

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Thank you for your interest in *The American Biology Teacher*. We look forward to seeing your manuscripts soon.

William McComas, Editor-in-Chief, ABTEditor@nabt.org
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Which Way Is Better? Comparison of Two Interactive Modeling Approaches for Teaching Meiosis in an Introductory Undergraduate Biology Course

RECOMMENDED
FOR AP BiologyKELSEY J. METZGER,
JOANNA YANG YOWLER

ABSTRACT

The processes of mitosis and meiosis are oft-cited and long-standing examples of concepts that are difficult for students to learn and understand. While there are many examples in the literature of “how-to-do-it,” innovative instructional approaches for teaching mitosis and meiosis, publications that include measurement of learning gains are fewer. Moreover, when measurement of learning gains are reported, the outcomes of innovative approaches are most often compared to outcomes from traditional lecture-format instruction. In contrast, this research compares two active-learning approaches to teaching meiosis through modeling in an introductory undergraduate biology course for health sciences majors. Items from the published, validated Meiosis Concept Inventory were used for pre- and post-instruction assessment. In addition, we collected data regarding student perceptions of the learning experience in each modeling scenario through two Likert-scale items and two free-response items. Overall, students demonstrated significant learning gains from pre- to post-assessment. We found no significant differences in performance on the posttest between the two modeling approaches, indicating that the selection of the modeling activity used to support student learning can be made on the basis of other criteria, such as instructor preference, physical classroom layout, or available supplies.

Key Words: Active learning; student-centered teaching; mitosis; meiosis; cell division; student performance; Meiosis Concept Inventory; modeling; curriculum design.

○ Introduction

Instruction in mitosis and meiosis is ubiquitous in biology education. However, it is well documented that students harbor misconceptions concerning these cellular processes at the middle school (Williams et al., 2011), high school (Stewart, 1982, 1983; Stewart et al., 1990; Lewis et al., 2000a, b, c; Öztap et al., 2003; Kara & Yesilyurt, 2007), and undergraduate levels (Kindfield, 1991, 1993, 1994; Smith, 1991; Quinn et al., 2009; Newman et al.,

2012; Ozcan et al., 2012). Misconceptions have also been reported in a study of prospective biology teachers (Kargöz & Çakir, 2011). Thus, learners at all levels struggle to differentiate key mechanistic differences between mitosis and meiosis – and the consequent biological differences in the cells that result from meiosis – leading to difficulty in connecting these concepts to genetic variation, Mendelian inheritance, and evolutionary processes.

The dynamics of genetic recombination and cell division are indeed quite complex, and geneticists continue to investigate the intricacies of meiosis (Page & Hawley, 2003, 2004; Mézard et al., 2015). Nevertheless, a solid grasp of these foundational genetics concepts is requisite knowledge for students to progress to a sophisticated understanding of the sources and inheritance of genetic variation across generations. Biology educators at all levels are thus well served by being familiar with common conceptual hurdles that students may need to surmount, and by evaluating instructional strategies that can be employed to facilitate student understanding of these challenging concepts.

There are many examples in the literature of “how-to-do-it,” innovative instructional approaches to teaching meiosis. In our survey of published articles, we identified three broad categories of innovative teaching practices: (1) drawing with pencil and paper (Mertens & Walker, 1992); (2) using manipulative models (Mathis, 1979; Coleman, 1986; McKean & Gibson, 1989; Oakley, 1994; Levy & Benner, 1995; Stencel, 1995; Clark & Mathis, 2000; Harrell, 2001; Lock & McDermid, 2005; Stavroulakis, 2005; Chinnici et al., 2006; Wright & Newman, 2011; Luo, 2012); and (3) students physically assuming the identity of a cellular component to act out cell division through

movement of their bodies (Chinnici et al., 2004; Kreiser & Hairston, 2007). Articles describing modeling in teaching mitosis and meiosis use a variety of materials (Table 1).

The assessment approaches taken here can serve as a general model for evaluating the effectiveness of active-learning approaches and can be applied to diverse content areas.

Table 1. Summary of published mitosis and meiosis modeling instructional approaches. Columns on the right half of the table indicate whether the article reports a measure of student performance and/or data regarding student perceptions of the instructional approach described. When such information has been included in the article, a brief description is provided.

Reference	Materials Used in Modeling Approach	Student Performance Data Included in Article?	Student Perceptions Data Included in Article?
Mathis, 1979	Audio tapes and manipulable cell models	Yes, 5 knowledge-recall items, 5 comprehension- or application-level items	Yes, Likert scale
Coleman, 1986	Wooden clothes pegs	No	No
McKean & Gibson, 1989	Paper, paper clips, and string	No	No
Oakley, 1994	Sweat socks	No	No
Levy & Benner, 1995	Ribbons	No	No
Stencel, 1995	String and paper	No	No
Clark & Mathis, 2000	Yarn, pipe cleaners, clothesline and Petri dishes	No	Yes, Likert scale and free response
Harrell, 2001	Velcro, yarn, and adhesive notes	No	No
Chinnici et al., 2004	Students as “human chromosomes”	Yes, responses to “bonus” questions on exam for extra credit	Anecdotal, two student comments from written feedback
Lock & McDermid, 2005	Pool noodles	No	Unsolicited student feedback on teaching evaluations
Stavroulakis, 2005	Sweat socks	No	Anecdotal
Chinnici et al., 2006	Sweat socks	No	Yes, course evaluation comments
Kreiser & Hairston, 2007	Students as “human chromosomes”	Yes, exam scores	No
Wright & Newman, 2011	Sweat socks	Yes, exam items and student interviews	No
Luo, 2012	Springs	No	Yes

However, publications that include measurement of learning gains using such approaches are fewer; more commonly reported are positive student responses (see Table 1), which offer limited evidence of the effectiveness of the approach. Moreover, when measurement of learning gains associated with described practices is reported, the outcomes of a single innovative approach are most often compared to outcomes from lecture-based instruction (see, e.g., Wright & Newman, 2011). As evidence for the effectiveness of student-centered, active teaching and learning approaches over traditional lecture approaches continues to mount (Freeman et al., 2015), investigations of alternative methods of active learning are needed to gauge relative efficacy, so that best practices and approaches to active learning broadly and for specific content areas can be elucidated. As such, the present study investigates and compares learning gains between two modeling approaches to teaching meiosis in two lecture sections of an introductory undergraduate biology course for health sciences majors. The goal of this investigation was to determine whether one modeling approach led to

greater learning gains compared to the other or, rather, the two approaches yielded similar outcomes for student learning and could thus be interpreted as equally appropriate alternatives for teaching the same concepts. The modeling approaches used in this study address student misconceptions regarding meiosis, especially reinforcing the particulate, physical nature of genetic loci. We hypothesized that students would demonstrate significant learning gains from pre- to post-assessment, regardless of the active-learning approach taken. Although we were interested in whether the modeling approaches produced a difference in learning gains, we had no a priori hypothesis that one approach would be more efficacious than the other. The results of this study are intended to inform instructional design choices at our institution, and to inform the biology education community more broadly. While this study focuses on evaluation of active-learning strategies for teaching meiosis through modeling, the assessment approaches taken here can serve as a general model for evaluating the effectiveness of active-learning approaches, including the use of validated instruments to

document student learning as a result of instruction, and can be applied to diverse content areas.

○ Methods

This quasi-experimental trial comparing two active-learning strategies for learning meiosis took place within the context of a health sciences undergraduate degree program (Bachelor of Science in Health Sciences, BSHS) at a small liberal arts university in the Midwest. Students entering the program are mostly traditional-aged college students. According to institutional data, ~72% of students in the program identify as female, and 20% identify as institutionally under-represented minorities (URM), a designation that includes the categories Asian, Black, and Hispanic. All participants consented to participate in this research in accordance with University of Minnesota IRB protocol no. 1008E87333.

Study subjects were students enrolled in two sections of a five-credit, first-year, foundational biology course with lab. Students enroll in this course during the second semester of their first year, which means they have completed one semester of college coursework in the program. Due to the cohort nature of enrollment in the program, students take courses in a prescribed sequence, particularly in the first and second years of the program. As such, there are very few non-degree-seeking students or students who are not in their first year of college coursework enrolled in the course. The same instructor taught all sections of the course. Instruction took place in an active-learning classroom (Dori & Belcher, 2005; Beichner et al., 2007; Dori et al., 2007; Walker et al., 2011) and using a flipped pedagogy model. The physical classroom environment and curricular design facilitated regular implementation of a variety of teaching and learning activities and classroom assessment techniques (CATs; Angelo & Cross, 1993). In preparation for classroom instruction and activities, both lecture sections were assigned pre-instruction reading with corresponding preparation questions (i.e., study guide questions). Additionally, students completed a low-stakes pre-class quiz consisting of five questions related to the material in the assigned reading. Students were allowed two attempts on the pre-class quiz and were able to see which items they answered correctly or incorrectly immediately after submitting the quiz. Supplementary materials posted on the course website included slides, links to online conceptual animations, and practice questions. In conjunction with the instruction that took place during lecture sections, all students enrolled in the lecture also completed a laboratory instruction component involving handouts for paper-and-pencil depictions of mitosis and meiosis.

During classroom instruction, lecture section A experienced a 45-minute meiosis lesson incorporating role playing, with socks held by students representing chromosomes and small beads placed on safety pins attached to the socks to represent genetic loci. This lesson incorporated elements of previously published modeling using socks (Stavroulakis, 2005; Wright & Newman, 2011), with the addition of safety pins with small craft beads placed on them to represent genetic loci (see Appendix 1; Appendices 1–3 are available as Supplemental Material with the online version of this article). Students used these materials to model provided diploid genotypes for several loci on different chromosomes and to physically act out the behavior of chromosomes during DNA replication, mitosis, and meiosis. Lecture section B experienced a 45-minute meiosis lesson utilizing manipulative modeling with pipe cleaners of varying

sizes to represent chromosomes and small craft beads placed on the pipe cleaners to represent genetic loci (see Appendix 2). Similarly, students in this treatment group used their materials to model provided diploid genotypes for several loci on different chromosomes and to physically act out the behavior of chromosomes during DNA replication, mitosis, and meiosis. Outside of this 45-minute instruction block, the students experienced identical learning scaffolding (e.g., Appendix 3).

Demographics of Lecture Sections

To determine if there were significant differences between the lecture sections with regard to demographic or incoming performance metrics, statistical analyses were conducted for all variables for which data were available. To determine if there was a significant difference between the distribution of gender (male/female) or ethnicity (non-URM/URM) in the two lecture sections, a two-tailed Fisher's exact test was used. To determine if there was a significant difference in incoming performance metrics between the two lecture sections, two-tailed t-tests were performed using comprehensive ACT scores and cumulative college GPA.

Assessment of Student Learning Gains: Meiosis Concept Inventory Subset

Items from the published, validated Meiosis Concept Inventory (MCI; Kalas et al., 2013) were used for pre- and post-instruction learning assessment. The MCI was designed as both a diagnostic tool and an assessment instrument (Kalas et al., 2013). It was implemented here to assess student learning resulting from the two modeling approaches. The 17-question MCI inventory has been validated in a population of introductory biology and genetics university students (Kalas et al., 2013). An eight-item subset (questions 1, 2, 4, 13, 14, 15, 16, and 17) of the inventory has been used for pre-/post-assessment of student learning in the university classroom (Kalas et al., 2013, p. 660). For example, learning gains (normalized change) differed among sections of students receiving different instruction. Students from sections in which active-learning techniques were used generally showed slightly higher learning gains as demonstrated by responses to the eight-item abbreviated MCI (unpublished data; K.J. Metzger & P. Kalas, personal communication). Importantly, the proportion of correct responses for each question remained the same regardless of assessment via the entire inventory or via the eight-question subset. Scores on this MCI subset were highly predictive of scores on the entire inventory ($r = 0.88$; Kalas et al., 2013, p. 660). This suggested that abbreviating the inventory did not negatively affect the construct validity of each individual question, although it may decrease the inventory's overall explained variance of meiosis conceptualization.

In our study, the MCI subset of eight items was given as a pre-/post-assessment with no feedback on performance provided to students between assessments. The posttest items were presented on the final exam of the semester, six weeks after the unit of instruction in cell division. Pre-assessment questions were administered as a low-stakes in-class completion activity preceding the mitosis and meiosis pre-class preparation and instruction. Questions were presented to students during class via projected slides, with student responses collected electronically via a quiz on the course's learning management site. Questions and responses were not available to students on the class site. Post-assessment questions were included

in the cumulative final exam, several weeks after instruction, as a more distal capture of student meiosis conceptualization. Following the method used by Kalas et al. (2013), no partial credit was given for “partially correct” responses on items for which the expert response required more than one selected choice (items 4 and 17 in our subset). Cronbach’s alpha coefficient was computed as a reliability estimate of internal consistency for the subset of MCI items using both the pretest and posttest responses. To investigate changes in performance, paired t-tests matching individual student pretest and posttest scores were used in analysis of change on average performance across all eight MCI items and also for change in performance on each of the items individually. Independent-samples t-tests were used to test for differences in performance on the MCI between lecture section A and lecture section B. Mean normalized change (c) was also used to investigate the change in performance, calculated as described by Marx and Cummings (2007). Normalized change calculates the mean of the change from pretest to posttest, rather than the change in the mean performance from pretest to posttest. Finally, scores from the unit exam for the unit that included cell division processes were also used as a metric of performance for comparison between the two lecture sections, again using an independent-samples t-test. The unit exam did not contain any items from the MCI.

Multiple regression modeling was used to investigate possible predictive variables: gender, ethnicity, incoming GPA, and comprehensive ACT, with pre-MCI score as the response variable. For multiple regression modeling with post-MCI as the response variable, pre-MCI score was also used as a predictive variable.

In addition to student performance data, we collected data regarding student perceptions of the learning experience in each modeling scenario through two Likert-scale items and two free-response items. The Likert-scale items were “Please rate how strongly you agree with the following statement: Modeling mitosis and meiosis in class helped me understand the processes of cell division” and “Please rate how strongly you agree with the following statement: Modeling mitosis and meiosis in class helped me to understand that genes are physical entities located on chromosomes.” The Likert scale used was 1 = strongly agree; 2 = somewhat agree; 3 = not sure; 4 = somewhat disagree; 5 = strongly disagree. The responses to Likert-scaled items for each lecture section were compared using independent t-test analysis. We elected to use parametric statistical tests for the Likert-scaled data following the recommendations of de Winter and Dodou (2010) for five-point Likert scale data analysis.

The free-response item prompts were “If you agreed that modeling mitosis and meiosis in class was beneficial to your learning, please explain in what ways the modeling activity was helpful” and “In what ways do you think the modeling mitosis and meiosis activity is limited, or could be improved?”

Although rigorous analysis of free-response items was not a primary goal of our investigation, we used content analysis to help contextualize Likert-scale responses. To identify emergent themes in student responses to free-response items, content analysis approaches were used. Responses were iteratively read by two reviewers and assigned a theoretical category code (Maxwell, 2008, pp. 236–238). Some responses included reference to more than one theme and were included in more than one reported category.

○ Results

Demographics of Study Population & Lecture Sections

Of 92 students enrolled in the course, 86 consented to participate in the study (participation rate = 93.5%). Of the participants, 78% identified as female and 22% identified as male; 71.18% identified as non-URM (White) and 28.34% identified as a URM (Black, Hispanic, Asian). The mean comprehensive ACT score for the study population was 24, and the mean incoming GPA was 2.87. There were 43 students in each lecture section ($N = 43$ for lecture section A, $N = 43$ for lecture section B). There was not a significant difference in gender distribution between lecture sections (two-tailed Fisher’s exact test, $p = 0.6040$). Similarly, there was no significant difference with regard to the distribution of students identified as URM between lecture sections (two-tailed Fisher’s exact test, $p = 0.1535$).

Incoming Performance Metrics

The distribution of incoming performance metrics (i.e., comprehensive ACT score and entering GPA) was analyzed using independent-samples t-tests. There were no significant differences between the two sections (sections A and B) regarding comprehensive ACT score ($t_{76} = -0.4945$, $p = 0.6224$) or start-of-term college (GPA $t_{84} = -1.72911$, $p = 0.0875$).

Item Reliability – Alpha Coefficient

Using student responses to the pretest MCI, the Cronbach’s alpha was 0.1445. Using student responses to the post-assessment MCI results in a Cronbach’s alpha of 0.5404.

MCI Pre- & Post-performance

Students improved their performance on the MCI items from pre- to post-assessment. Across both sections, there was a statistically significant increase in performance ($t_{85} = 9.837$, $p < 0.0001$) with an average normalized change of 28.85% on the posttest compared to the pretest. A comparison of performance on the MCI between the two lecture sections revealed no significant differences on the pre-assessment MCI ($t_{84} = -1.32309$, $p = 0.1894$) or post-assessment MCI ($t_{84} = -1.12013$, $p = 0.2659$). Similarly, no significant difference was found when comparing the normalized change (c) between sections ($t_{84} = -0.62974$, $p = 0.5306$).

When performance on the MCI assessment was evaluated for individual items, there was a significant increase in average performance from pre- to post-assessment for items 2, 14, 16, and 17 across the entire study population (Table 2). For item 1, there was evidence of significant decrease in performance from pre- to post-assessment (Table 2). Interestingly, this significant difference was driven by a decrease in performance on this item for section A ($t_{41} = -2.89239$, $p = 0.0061$) but not for section B ($t_{39} = -0.90243$, $p = 0.3724$). Performance for the remaining MCI items (items 4, 13, and 15) showed no significant differences between the pre- and post-assessment. Comparison of performance between lecture sections A and B on the unit exam (which addressed mitosis and meiosis concepts but did not include any MCI items) also showed no significant difference ($t_{84} = -1.50442$, $p = 0.1362$).

Table 2. Summary of Meiosis Concept Inventory (MCI) pre- and post-assessment item means across both sections.

MCI Item	Concept Addressed	Bloom's Level	Pre Score Average	Post Score Average	t Ratio	p	df
1	Ploidy	II	0.50	0.31	2.74955	0.0074**	81
2	Ploidy, what "counts" as a chromosome	III	0.16	0.33	2.99322	0.0037**	81
4	Ploidy	III	0.04	0.05	0.37598	0.7079	81
13	Changes in the amount of DNA in a cell in relation to timing of events in meiosis	II	0.29	0.35	0.896956	0.3724	81
14	Timing of events in the cell cycle and meiosis in relation to chromosomes/ chromatids	I	0.42	0.59	3.093982	0.0027**	81
15	Timing of events (segregation of sister chromatids); consequences of crossing over	II	0.33	0.49	1.834277	0.0703	81
16	Timing of events (segregation of sister chromatids); consequences of crossing over	II	0.23	0.70	7.024216	<0.0001***	81
17	Gamete formation, segregation of alleles and chromosomes	IV	0.341	0.628	4.135866	<0.0001***	81

Notes: A single asterisk (*) indicates significance at the $p < 0.05$ level, two asterisks (**) indicate significance at the $p < 0.01$ level, three asterisks (***) indicate significance at the $p < 0.001$ level. Concept(s) addressed and Bloom's level as reported in Kalas et al. (2013).

Regression Modeling

Multiple regression modeling was completed with predictor variables of gender, ethnicity, comprehensive ACT, college GPA at the start of term, and lecture section (Table 3). In pretest performance, the only variable that was a significant predictor of performance on the MCI subset was ethnicity, with URM students scoring, on average, 12 percentage points lower than non-URM students (non-URM pre-assessment mean score = 27.664, URM pre-assessment mean score = 15.625). The adjusted power for this variable was 0.7134 (Wright & O'Brien, 1988), and the Cohen's f effect size (defined as the square root of μ/μ^2) was 0.333, which is a medium effect (Cohen, 1988).

In the multiple regression for posttest MCI performance, the same predictor variables were used, with the addition of pretest MCI to the model. In that model, college GPA at the start of term and comprehensive ACT were significant predictors of performance (see Table 3), with adjusted power of 0.810 and 0.921, respectively. Cohen's f was 0.359 for ACT and 0.306 for GPA, both of which are a medium effect (Cohen, 1988). In posttest response

data, ethnicity was no longer a predictor variable (non-URM post-assessment mean score = 50.717, URM student post-assessment mean score = 41.406).

Student Perceptions of Modeling Activities

Students who participated in the pipe-cleaner version of the modeling exercise (section B) reported a significantly higher agreement with the item "Modeling mitosis and meiosis in class helped me understand the process of cell division" as compared to students who participated in the sock modeling activity ($t_{72} = -2.31788$, $p < 0.023$). Mean agreement was 2.18 for section B, compared to a mean agreement of 2.83 for section A (1 = strongly agree). However, there was no significant difference in student responses to the item "Modeling mitosis and meiosis in class helped me to understand that genes are physical entities located on chromosomes" ($t_{72} = -1.01645$, $p > 0.31$). Mean agreement with this item was 2.54 for section A and 2.23 for section B.

Content analysis of student responses from both sections (summarized in Table 4) indicated a positive response to being able to

Table 3. Multiple regression modeling predicting student pre- and post-assessment MCI scores.

	t	p	B	β	F	df	p	R ²
MCI Pre								
Overall model					2.799	76	0.023	0.165
Gender (F)	-0.94	0.349	-2.195	-0.106				
Ethnicity (URM)	-2.79	0.007	-5.803	-0.313				
ACT	0.85	0.396	0.528	0.106				
GPA	0.59	0.85	2.289	0.074				
Lecture section (A)	0.50	0.619	0.945	0.056				
MCI Post								
Overall model					8.433	76	<0.0001	0.420
Gender (F)	-0.63	0.053	-0.120	-0.060				
Ethnicity (URM)	-0.17	0.865	-0.030	-0.017				
ACT	3.61	0.0006	0.181	0.378				
GPA	3.09	0.0029	0.967	0.327				
Lecture section (A)	0.74	0.463	0.113	0.070				
MCI pre score	0.93	0.353	0.112	0.093				

Notes: Significant predictors are in bold. Ethnicity was coded as under-represented minority (URM) or non-URM. ACT is comprehensive ACT score. GPA is the student's university GPA at the beginning of the term (spring semester, first year). Lecture section was coded as A (sock modeling) or B (pipe-cleaner modeling).

physically represent the processes of mitosis and meiosis, whether with pipe cleaners or socks. In particular, student responses from both sections suggested that the use of small craft beads to represent physical genetic loci was an especially effective approach in solidifying student understanding of genes as physical entities with a fixed location. Further, the use of different colored beads to represent different alleles at a single locus in a heterozygous individual was especially helpful in being able to demonstrate the outcomes of crossing over during meiosis I. When students were asked how the modeling exercise could be improved, students in lecture section A (sock modeling) suggested more explanation and instructor guidance accompanying the modeling activity to reduce confusion much more frequently than students in lecture section B (pipe-cleaner modeling) (Table 4).

○ Discussion

In this study, two active-learning approaches involving modeling were assessed and compared for their effectiveness in supporting student learning of the cellular division processes of mitosis and meiosis. Using a subset of the validated MCI as a pretest and post-test instrument, we found that regardless of the active-learning

modeling approach used during instruction, students demonstrated significant learning gains pre- to post-assessment. This result is consistent with other studies that demonstrate significant learning gains following instruction. Although Kalas et al. (2013) report Bloom's taxonomy levels for MCI items, too few items were included in our study to robustly determine whether students performed differently on MCI items of different cognitive levels. The greatest learning gains occurred for MCI items 16 and 17, which both address segregation of alleles. Cronbach's alpha for the pre-assessment was quite low, indicating a high degree of randomness in student responses. The Cronbach's alpha for the post-assessment increased to 0.5404, indicating greater internal consistency among student responses on the posttest. While lower than the 0.78 reported by Kalas et al. (2013, p. 659) for the entire concept inventory, we used only a subset of the MCI in our assessments. Additionally, multiple concepts were represented in the items that comprised the subset used here, which could contribute to the lower alpha we observed.

No significant differences in student performance were found between treatment groups in posttesting as determined through t-test and multiple regression analysis. Multiple regression analysis of pre-assessment responses revealed ethnicity to be a significant predictor of performance on the pre-assessment. In contrast, no

Table 4. Qualitative analysis of student responses regarding the helpfulness and limitations of the modeling activities.

Prompt & Total Number of Student Responses (Section A; Section B)	Theme	Percentage of Student Responses in Theme: Total (Section A, Section B)	Example Student Response
<p>"If you agreed that modeling mitosis and meiosis in class was beneficial to your learning, please explain in what ways the modeling activity was helpful." N = 69 (38; 31)</p>	Visual representation	49.3% (44.74%, 54.84%)	"Visualizing the alleles and how they actually switched over. As well as realizing that they duplicate then proceed with the meiosis or mitosis."
	Physical manipulation	28.99% (26.32%, 32.26%)	"I love having a physical component to the ideas we talk about in class. I can memorize what you say in a lecture but I actually learn what happens when it is physically happening."
	Compare mitosis and meiosis	14.50% (18.42%, 9.68%)	"It was helpful in showing how the chromosomes line up compared to meiosis and mitosis, as well as some of the phases."
	Physical nature of genetic loci and exchange of genetic information	14.50% (18.42%, 9.68%)	"The beads helped me to understand that genes are located on the chromosomes and that they are exchanged during crossing over."
<p>"In what ways do you think the modeling mitosis and meiosis activity is limited, or could be improved?" N = 74 (48, 31)</p>	Instructions introduced confusion	40.54% (58.14%, 16.12%)	"The directions were confusing to follow, and waiting around to figure out what was going on made me more confused. I would recommend being more clear about the parental and maternal strand, and emphasizing that one bead goes on each pin for each sock."
	Additional instructor explanation	16.22% (23.26%, 6.45%)	"I think it could be helpful if we went over this activity as a class first so that we knew what was supposed to be happening, and then did the activity as small groups to get a better understanding."
	Large-group activity	9.46% (16.28%, 0%)	"I think it should have been done in one big group, and then the rest of the class watched it. I feel like it would have been easier to have [the instructor] explain everything while it was going on, too."

significant difference was found between the average post-assessment performance of URM students compared with that of non-URM students. This result suggests that the instruction that occurred between the pre- and post-assessment may have disproportionately and positively affected URM students, which resulted in reduction of the performance gap that existed between URM and non-URM students prior to instruction. In post-assessment regression modeling, only comprehensive ACT score and college GPA at the beginning of term emerged as predictive variables of post-assessment performance. These variables were not significant predictors on the pre-assessment. This result indicates that students with stronger incoming academic performance metrics outperform their relatively academically less successful peers, regardless of the instructional approach used.

Given that the two treatment groups in this study were well matched with regard to sample size, incoming performance metrics, and known demographics, we conclude that both modeling exercises were equally effective in supporting student learning. Since there is no difference in performance due to instruction, the selection of the modeling activity used to support student learning can be made on the basis of other criteria, such as instructor preference, physical classroom layout, or available supplies. While our pretest and posttest assessments were separated by several weeks, our study is limited in that we were not able to assess whether the learning gains persisted over a longer period (i.e., a semester or more after instruction). Therefore, we cannot eliminate the possibility that one of these approaches may result in greater longitudinal retention.

While the performance data did not support a difference in learning gains between the two instructional approaches implemented, the Likert-scale student perception data we collected indicated a significant difference in student-perceived helpfulness: students who participated in the pipe-cleaner modeling (section B) indicated higher agreement with the statement “Modeling mitosis and meiosis in class helped me understand the process of cell division” as compared to students who experienced the sock modeling (section A). Content analysis of student responses to free-response items suggest that the modeling activity using socks would benefit from additional structure, as students in section A more frequently cited being confused by the instructions for the modeling activity and also more frequently reported a desire to perform the modeling as a class demonstration rather than in small groups. Because our study included only one semester of data, the greater perceived helpfulness of the pipe-cleaner modeling, while significant, may not be generalizable.

In conclusion, this study provides evidence of the equal effectiveness of two active-learning approaches to the teaching of mitosis and meiosis. As such, our findings support flexibility for individual instructors to determine which active-learning approach is the best fit for their class and their learners. However, in spite of concentrated effort to focus instruction on improved understanding of meiosis, student misconceptions still persisted after instruction, as evidenced by student responses to items on the post-assessment MCI, especially item 1. Hence, although students improved in their knowledge of meiosis from the instructional activities described in our study, students may require multiple exposures to focused learning opportunities to fully ameliorate misconceptions regarding this complex, yet pedagogically crucial, cellular process. Future research questions of interest are to investigate (1) whether the significant difference in perceived helpfulness of the modeling approaches is consistent in a subsequent offering

of the same course (or other populations of students); and (2) whether combining the two modeling approaches in one population of students would result in greater learning gains than what we observed from either of the modeling approaches applied singly.

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Appendix 1.

Sock Mitosis and Meiosis Modeling Activity

Adapted from Wright and Newman, 2011 (1).

Instructor Preparation/Modifications to Wright et al, 2011 for implementation at UMR:

Instructions will include directive to model mitosis as well as meiosis

All students will participate in modeling, rather than only 6 students acting as chromosomes with socks and 2 students acting as centrosomes (8 students total). Rather, we will utilize 4 groups of students, all modeling. We will use $N=4$, $2N=8$ to involve all students. This will affect the correct responses for items in Wright et al., 2011 table II.

1. Instructor will divide students into 4 groups of 11 students each. There will not be parity among males and females (as male students are outnumbered by female students). For each group, 8 students will be given the number 1-4 to represent different chromosomes in the hypothetical genome. Two students with the same number will act as homologous pairs of chromosomes. Two students in each group of 11 will be assigned the role of centrosomes (C). The final student in each group of 11 will serve as the “Reader” and will read the instructions to the group members.
2. Each student with a number 1-4 is given a unique solid-colored sock (with its mate hidden inside) in one of four sizes (adult large, adult small, child, and infant). Students will be directed by their group’s Reader to hold up the sock in one hand. Student volunteers will then “replicate” their DNA by pulling the hidden sock out and will then be instructed to hold both socks in the same hand. Pins with colored beads will be used to represent alleles. Maternal and paternal alleles will be represented by different colored beads for the same gene. Students will be asked to pin a bead of the same color as the parental sock on the newly replicated sock.
3. Students will count the number of chromosomes present in the hypothetical cell.

Instructions here will diverge depending on if students are modeling mitosis or meiosis.

4. For mitosis, students will be asked to form alignment along the metaphase plate. The 2 students role playing centrosomes will “rope” the sister chromatids and pull them apart to opposite poles of the cell. Students will count how many chromosomes are present in the daughter cells.

End Mitosis role playing

For meiosis, Student “chromosomes” are then asked by the “Reader” to find their homologous pair.

5. Students will be asked to participate in crossing over between the two homologous chromosomes, involving only one chromatid from each replicated homologous chromosome. Specifically, the “Reader” for the group will instruct students representing homologous chromosomes to link arms to represent the formation of a synaptonemal complex, and perform an exchange of genetic material represented by the beads pinned on the socks.
6. The “Reader” will instruct homologous pairs of chromosomes to align along the metaphase plate. The 2 students role playing centrosomes will “rope” the homologous chromosomes and pull them apart to opposite poles of the cell. Students will be asked to count the number of chromosomes present in each daughter cell, and whether the daughter cells are diploid or haploid.
7. Individual students representing replicated chromosomes (sister chromatids) with 2 socks being held in one hand will be instructed to align along metaphase plate for meiosis II division.

End meiosis role playing

1. Wright LK, Newman DL. 2011. An interactive modeling lesson increases students’ understanding of ploidy during meiosis. *Biochem Mol Biol Educ* 39:344–351.

Modeling Mitosis and Meiosis: Reader Handout

A. Mitosis Modeling

1. Before you begin modeling, consider a diploid organism that has four chromosomes, numbered 1, 2, 3, 4. What is a normal karyotype for a **somatic cell** of this organism?
2. Students in your group either have a chromosome number or a “C.” Students with a chromosome number will need to find their appropriately sized sock (*remember, chromosomes are numbered from largest to smallest*). Students who are assigned a “C” are acting as the centrosomes and will each need a length of yarn.
3. Students who are assigned a chromosome: Hold up your sock in one hand.
4. “Replicate” your DNA chromosome by pulling the hidden sock out and then hold both socks in the same hand. Pins with colored beads will be used to represent alleles. Maternal and paternal alleles will be represented by different colored beads for the same gene. Pin a bead of the same color as the parental sock on the original and newly replicated socks according to the genotype information below:
 - i. **On chromosome 1 reside genes A and B:**
Gene A alleles: black/white (black is dominant to white)

Gene B alleles: dark blue/light blue (dark blue is dominant to light blue)

Genotype: Your organism is heterozygous for gene A and heterozygous for gene B. Assume the maternal copy of chromosome 1 has dominant alleles for both genes.

ii. On chromosome 2 reside genes C and D.

Gene C alleles: green/yellow (alleles have codominant relationship)

Gene D: Red (This gene is monomorphic: it only comes in one form!)

Genotype: Your organism is heterozygous for gene C, homozygous for gene D.

iii. On chromosome 3 resides gene E

Gene E alleles: pink/purple (Pink is dominant to purple)

Genotype: Your organism is homozygous for the recessive allele

5. As a group, count the number of chromosomes present in the hypothetical cell.
6. Form alignment along the metaphase plate. How are the replicated chromosomes (sister chromatids) aligned?
7. The 2 students role playing centrosomes will “rope” the sister chromatids and pull them apart to opposite poles of the cell.
8. As a group, count how many chromosomes are present in the daughter cells.

End Mitosis role playing

B. Meiosis Modeling

1. Before you begin modeling, consider a diploid organism that has four chromosomes, numbered 1, 2, 3, 4. What is a normal karyotype for a **somatic cell** of this organism?
2. “Replicate” your DNA chromosome by pulling the hidden sock out and then hold both socks in the same hand. Pins with colored beads will be used to represent alleles. (*This will be the same as above, you do not need to pin again*)
3. Pairs of homologous chromosomes will need to form a tetrad (or bivalent) to participate in crossing over (also known as homologous recombination). Students holding replicated chromosome 1s will indicate the formation of a bivalent by linking arms.
4. Perform crossing over for one of the genes on chromosomes 1 and 2.
5. Are there any new allele combinations present after recombination that were not present before recombination? Explain.
6. What does alignment look like for metaphase of meiosis I?
7. Complete meiosis I by having student centrosomes separate bivalents (paternal and maternal homologous chromosomes) to 2 daughter cells.
8. As a group, count the number of chromosomes present in the hypothetical cell.
9. Complete meiosis II by having student centrosomes separate sister chromatids to daughter cells.
10. As a group, count the number of chromosomes present in the hypothetical cell.

End Meiosis role playing

Appendix 2.

Modeling Mitosis and Meiosis

A. Modeling Karyotypes and Genotypes

1. Consider a diploid organism that has four chromosomes, numbered 1, 2, 3, 4. What is a normal karyotype for a **somatic cell** of this organism? To begin, model a normal karyotype of a somatic cell with the appropriate pipe cleaners.
2. Placing genes on chromosomes:

- a On chromosome 1 reside genes A and B.
 - i. Gene A alleles: black/white (black is dominant to white)
 - ii. Gene B alleles: dark blue/light blue (dark blue is dominant to light blue)

Genotype: Your organism is heterozygous for gene A and heterozygous for gene B. Assume the maternal copy of chromosome 1 has dominant alleles for both genes.
- b On chromosome 2 reside genes C and D.
 - i. Gene C alleles: green/yellow (alleles have codominant relationship)
 - ii. Gene D: Red (This gene is monomorphic: it only comes in one form!)

Genotype: Your organism is heterozygous for gene C, homozygous for gene D.
- c On chromosome 3 resides gene E
 - i. Gene E alleles: pink/purple (Pink is dominant to purple)

Genotype: Your organism is homozygous for the recessive allele

B. Modeling Mitosis and Meiosis

For #4, each person should select one pair of homologous chromosomes.

4. Model mitosis with your materials. What do the chromosomes look like in metaphase?
Share your answers for #4 in your group.

For # 5, work in pairs to model meiosis for either chromosome 1 or chromosome 2.

5. Model meiosis with your materials. What are possible outcomes of crossing over for each gene? What do the chromosomes look like in Anaphase I? Metaphase II?

Share your answers for #5 in your group.

Appendix 3.

Mitosis and Meiosis Discussion Questions

1. What are homologues, sister chromatids, and bivalents? When do sister chromatids separate during mitosis? When do sister chromatids separate during meiosis?
2. Describe the arrangement of chromosomes at metaphase of mitosis. How is this different from the arrangement of chromosomes at metaphase I of meiosis I?
3. What are the differences in the cells produced by mitosis and meiosis?

Mitosis vs. Meiosis Defining Features Matrix: Complete the following table with information about the listed feature in mitosis and meiosis.

Feature	Mitosis	Meiosis I	Meiosis II
Preceded by DNA replication? (Yes/No)			
When is formation of bivalents?			
Crossing over during prophase? (Yes/No)			
Describe alignment at metaphase plate			
Describe separation at anaphase			
Genetically identical daughter cells produced? (Yes/No)			
Haploid daughter cells produced? (Yes/No)			

Pancake Evolution: A Novel & Engaging Illustration of Natural Selection

D. ANDREW CRAIN, MATTHEW HALE



ABSTRACT

Understanding the theory of natural selection is crucial for any student of biology, but many secondary and postsecondary students struggle with the concepts. We present a novel, engaging exercise to illustrate natural selection through making pancakes. After students make pancakes (representing offspring) with various ingredients (illustrating genetic diversity and allelic variation), other students (representing the environment) judge the pancakes on the basis of taste. Only the highest-ranking pancakes are made in a second generation (illustrating population change over time), and new ingredients are added. After several generations of pancakes, with each generation exposed to ever-changing “environments,” students understand the fundamental concepts associated with the theory of natural selection.

Key Words: Evolution; natural selection; pancakes.

○ Introduction

Despite the primacy of evolutionary theory in the field of biology, a minority of individuals in the United States accept this fundamental concept (Miller et al., 2006). Educators have developed numerous methods to teach the concept of natural selection (e.g., Heim, 2002; Kalinowski et al., 2013; Hildebrand et al., 2014; Hongsermeier et al., 2017), but misconceptions among high school and college students are rampant (Gregory, 2009; Yates & Marek, 2015).

While no pedagogical technique is universal in its ability to promote scientific literacy, analogies are particularly helpful in explaining abstract scientific concepts because they promote higher-level thinking and the understanding of the new concepts (Gardner, 2016). One example of this is the use of familiar foods to illustrate complex scientific concepts. The use of food to illustrate scientific concepts has been shown to be more effective than standard science curricula for primary school students (Duffrin et al., 2010; Hovland et al., 2013), but few secondary and postsecondary science curricula utilize food. Here, we present a novel method to teach fundamental

tenets of evolution through natural selection using pancakes and familiar food ingredients (see Table 1). These biology core ideas are requirements for meeting High School Next Generation Science Standards LS4B/LS4C and for all introductory college biology courses. All analogies have the potential for fostering misconceptions, so Table 1 also shows potential misconceptions.

Briefly, pancake batter is used to represent a shared genotypic background, to which variations (i.e., novel alleles or phenotypic traits) are introduced in the form of added ingredients. These novel “food alleles” – ingredients like chocolate, paprika, pickles, and bacon bits – represent variation at a food “gene.” Students first make pancakes with a single random ingredient, representing acquisition of the first novel “food allele.” The pancakes are then eaten, judged, and scored on the basis of their palatability, using the students’ taste preferences as environmental selective pressures. Particularly delicious pancakes persist, representing an adaptive benefit of the novel allele, while unpalatable pancakes, given low scores, are abandoned (representing death without reproduction). Thus, the most delicious alleles in the first generation are perpetuated to the next generation, where new food genes similarly acquire novel alleles. This represents subsequent acquisition of new diversity at different genes. And by perpetuating this process of adding novel ingredients, tasting, and judging palatability across multiple rounds (i.e., generations), students illustrate the process of selection for adaptive combinations of alleles in a given environment and selection against maladaptive combinations.

○ Materials & Procedure

After preparation of pancake batter and ingredients, this laboratory can be completed in 60–90 minutes, making it conducive to both class and laboratory time periods. For each student group, materials needed include a portable electric hot-plate burner, small frying pan, spatula, pancake batter, and various ingredients (student food allergies and dietary restrictions influence selection of ingredients).

Table 1. Representation of major components of natural selection, corresponding components in the laboratory exercise, and potential for misconceptions from the analogy.

Component of Selection & Evolution	Lab Component	Potential for Misconceptions
Shared genotypic background	Pancake batter	The origin of variation appears to be in the addition of elements (genes) to the organism, rather than in mutation and genetic recombination of existing genes.
Trait variation, de novo genetic diversity, alleles	Added ingredients	
Selective environmental pressure	Taste preferences, scoring	In nature, genotypes and phenotypes that are more likely to be eaten are less likely to increase in frequency in the population. The opposite is true in this activity.
Traits positively affecting survival are reproduced and thus are more common in the population	Ingredient perpetuation after generation 1	One common misconception is that individuals, rather than populations, evolve. With only two or three pancake generations, this misconception may be reinforced.
Distribution of traits in a population can change when conditions change	Generation 2 results from scoring	
Species and trait extinction/elimination	Low scoring results in not using the ingredient in subsequent generations	

Table 2. Example ingredients used to illustrate how alleles can create different phenotypes.

"Gene"	"Allele 1"	"Allele 2"
Spice	Cumin	Paprika
Dairy	Cheddar cheese	Blue cheese
Vegetable	Kale	Pickles
Candy	Chocolate chip	Caramel
Condiment	Hot sauce	Mustard
Candy bar	Reese's Cup	Milky Way
Meat	Bacon bits	Vienna sausage

A food-safe space is needed; we have used a physics laboratory and an outdoor classroom, but numerous other campus options are available.

First, students are divided into two large groups: "Pancake Producers" (with each pancake produced representing an offspring) and "Pancake Judges" (representing the environment in which offspring are born and, therefore, the selective pressure shaping population traits).

Pancake Producers are divided into groups of two or three students. Identical pancake batter is provided for all groups, representing similar genetic composition, and each group is then given a unique ingredient (for examples, see Table 2). Clear instructions are given to each Pancake Producer group and each Judge (see Tables 3 and 4). Once a single large pancake with

Table 3. Instructions for "Pancake Producers" (i.e., reproductive pairs).

Step 1	Prepare your batter with the assigned ingredient.
Step 2	Cook a single, large pancake (your offspring) in the provided pan on the burner with a setting of medium low.
Step 3	Cut your pancake into enough pieces for each Judge and distribute.
Step 4	Clean your pan and cooking area.
Step 5	You will now become a "Pancake Judge" for the next generation of pancakes.

the novel ingredient is made, the pancake is sliced into small pieces and distributed to the Judges for a "blind" rating on a scale from 1 (completely inedible) to 10 (delicious); instructors can create their own taste scale. A high score represents successful reproductions of the recipe (or the offspring, following the analogy; for an example, see Table 5, generation 1).

After tabulating the results of generation 1, the previous Judges become the new Pancake Producers, and the two top-ranking pancake ingredients are used in the next batch. Half of the newly assigned Pancake Producers will use winning ingredient 1 from generation 1, and the other half winning ingredient 2. Each producer group is also assigned a new ingredient at random (via coin flip or use of a random number generator; see Table 5, generation 2). Thus, during the second generation, each pancake will have two ingredients, and the

Table 4. Instructions for “Pancake Judges” (i.e., the environment).

Step 1	With a blindfold on, taste each pancake piece and, without input from others, rate it from 1 to 10 (think about a “9” being a pancake you would definitely make again, a “6” being one you might make again, and a “3” being one you would not make).
Step 2	Input your data on the provided worksheet for each pancake.
Step 3	You will now become a “Pancake Producer” for the next generation of pancakes.

Table 5. Example results from “Pancake Judges” after generation 1 and generation 2. After generation 1, Reese’s Cups and cheddar cheese pancakes were remade in generation 2, each with another additional ingredient. Unexpected results often occur after generation 2 (such as cheese + oregano, which students said tasted like pizza), illustrating that evolution often results in unpredictable results based on the environment.

Generation 1	Reese’s Cup	Cheddar Cheese	Vienna Sausage	Kale	Pickle	Mustard
Student 1	8	9	4	3	4	2
Student 2	9	7	5	1	3	1
Student 3	7	8	3	2	3	4
Student 4	7	9	4	1	3	3
Student 5	9	9	4	3	4	3
Student 6	9	8	4	5	6	2
Student 7	9	7	8	5	6	3
Student 8	8.5	7	5	2	2	2
Student 9	8.5	6	5	2	2	1
Student 10	8	7	4	3	2	2
Gen. 1 Average	8.3	7.7	4.6	2.7	3.5	2.3
Generation 2	Reese’s + Curry	Reese’s + Oregano	Reese’s + Hot Sauce	Cheese + Curry	Cheese + Oregano	Cheese + Hot Sauce
Student 1	9	9	8	9	9	8
Student 2	10	5	4	8	8	1
Student 3	8	8	9	1	9	1
Student 4	8	8	6	8	9	1
Student 5	9	6	4	5	6	1
Student 6	8	7	8	9	9	2
Student 7	9	7	9	9	9	5
Student 8	5	5	7	4	9	4
Student 9	6	5	8	5	4	8
Student 10	4	4	3	4	7	1
Student 11	7	3	8	4	7	1
Student 12	6	5	3	5	5	1
Gen. 2 Average	7.4	6	6.4	5.9	7.6	2.8

environment has changed. If time allows, a third generation of pancakes can be produced using the same method.

For advanced learners, modifications to this laboratory can easily be made to illustrate more complex evolutionary concepts. Table 6 presents alterations to the protocol that can be used as analogies for genetic drift, neutral theory, evidence for evolution, and cladistics, and instructors are encouraged to develop other modifications.

○ Assessment of the Pancake Demonstration

Two methods were used to assess the ability of this laboratory to improve student understanding of natural selection: (1) evaluation of scores on natural selection questions on examinations, compared to scores on other topics on the same examinations; and (2) evaluation of student lab reports in which students were asked to write a

Table 6. Example modifications of the standard lab protocol to teach advanced evolutionary concepts.

Advanced Concept	Modification of Standard Procedure
Genetic drift after bottleneck	During the second generation of pancake production, a “surprise” power loss is applied to all but one burner. As a result, the only pancake produced and, thus, reproduced will be the one from the functional burner.
Neutral theory	Neutral theory of molecular evolution suggests that for some alleles there is no selective advantage in variants; this can be illustrated by shifting from one form of a food to another, very similar, one. For instance, the change from a Reese’s Cup to a Reese’s Egg or Tree in a blindfolded taste test shows no difference. Students are then challenged to think about this in the context of human traits with questions such as “Are there traits that vary from person to person or population to population that do not have any impact on fitness?” This is a springboard for considerations of how these traits might change over time without the constraints of fitness on frequencies.
Evidence for evolution	After several generations of creating and judging pancakes, students are asked to imagine that the pancakes they made are preserved in an anaerobic environment for millions of years. Students are then asked what could be analyzed to reconstruct the evolutionary history of the pancakes. Appearance of ingredients (phenotype of fossils), chemical analysis of the ingredients (genotype of fossils), and ingredient geographic distribution through geological time (biogeography) are examples of answers.
Clades and monophyletic groups	After two rounds of making and judging pancakes, introduce the concept of cladistics and guide the students in constructing clades based on similarities in ingredients.

Table 7. Representative quiz and examination questions, showing the percentage of students answering the question correctly (n = 78).

Question	% Students Correct
During the pancake lab, you illustrated natural selection. Match the following components with the correct natural selection term in questions 1–4: a. ingredients, b. Pancake Judges, c. pancake batter, d. winning pancakes.	
1. Allele variation	94
2. Environment	86
3. Ancestral organism	85
4. Surviving population	100
5. All of the following are correct descriptions of the way that natural selection occurs, except that a. populations are composed of individuals that have variation in traits b. individuals change traits during their lifetime, passing on these traits to offspring c. populations have more offspring than can survive in the environment d. individuals more suited to the environment survive, passing on their traits to offspring	78
6. <i>Evolution</i> is a term that is often misinterpreted. Which of the following is the unit that evolves, or changes, over time? a. An element b. An atom c. An individual d. A population	90

paragraph describing how the activity illustrated the theory of natural selection using the following terms: *adaptation*, *selection*, *genetic variation*, *trait variation*, *environment*, and *population*.

Table 7 shows that, depending on the question, between 78% and 100% of students correctly answered natural selection questions. The total quiz and exam averages (covering topics other than evolution) were 58% and 73%, respectively, showing greater understanding of natural selection. A paired t-test (alpha level 0.05) indicated that students answered more natural selection questions correctly ($M = 88.4$, $SD = 16.2$) than non-natural selection questions ($M = 71.4$, $SD = 13.7$) on the same examination ($t_{68} = 2.0$, $p < 0.001$). In addition, 100% of students attempting the lab report assignment at the conclusion of the activity correctly explained how the lab illustrated natural selection ($n = 75$).

○ Conclusions

We have found this short laboratory exercise to be an engaging method to teach fundamental principles of natural selection. This interactive activity uses an analogy to assist student learning by building on students' own relevant knowledge, a pedagogically supported technique (Glynn, 1994).

Such noncontroversial activities are particularly needed in regions where lack of acceptance of evolution is founded in identity-protective cognition. In such areas, simply providing scientific information fails to foster acceptance of scientific conclusions, and other means of teaching the concepts are necessary (Walker et al., 2017). Our students truly enjoy the pancake-making exercise, and evidence shows that they learn much from this demonstration. Many common misconceptions, such as "survival of the fittest" and "individual evolution," are easily identified and articulated by students after completing this lab.

○ Acknowledgments

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A Simplified Bioenergetics Model of a Hammerhead Shark for Teaching Natural Selection

JAY Y. S. HODGSON

Evolutionary Results (Automatically Calculated)		
Life or Death?	Reproduction?	
Dead	No Reproduction	
Rostrum Drag (N per s)	Body Drag (N per s)	
7.78	3.45	
The Values Below Cannot Be User Edited		
Rostrum Measurements		
Surface Area (m ²)	Rostrum Mass (Kg)	Total Shark Mass (Kg)
0.69	5.00	10.00
Foraging Effects		
Volume Sampled (m ³ per day)	Prey Encounters (per day)	Consumption (KJ per day)
1250.29	12.50	1300.0
Bioenergetics Values		
Basal Metabolism (KJ per day)	Rostrum Drag Loss (KJ per day)	Body Drag Loss (KJ per day)
650.0	671.8	298.1
		Waste (KJ per day)
		351.0

ABSTRACT

Students often have difficulty understanding the underpinning mechanisms of natural selection because they lack the means to directly test hypotheses within the classroom. Computer simulations are ideal platforms to allow students to manipulate variables and observe evolutionary outcomes; however, many available models solve the scenario for the users without revealing the evolutionarily significant calculations. I developed a simplified bioenergetics model of a hammerhead shark for teaching natural selection that allows the users to manipulate variables and see the impacts of modeling while solving for the evolutionary consequences. Students generate variation within the population by controlling cephalofoil widths and swimming speeds of an individual, which affect its ability to detect and capture prey at the expense of energy lost as drag from swimming. The trade-off between energy gained from successful predation and energy lost from metabolic expenditures dictates rates of reproduction. By manipulating a subset of factors that influence differential reproductive success, students gain an improved understanding of natural selection.

Key Words: Evolution; computer simulation; drag; foraging; differential reproduction.

Introduction

Vision and Change in Undergraduate Biology Education (AAAS, 2011) identified *evolution* and *structure and function* as the two most important core concepts for biological literacy. Assessments, however, have frequently shown poor student proficiency in evolutionary topics (Alters & Nelson, 2002; Anderson et al., 2002). Furthermore, in traditional classroom settings, where students do not have the ability to test hypotheses experimentally, student comprehension and retention of evolution is low (Gardiner, 1998; Alters & Nelson, 2002; Johnson & Lark, 2018). Several authors have proposed that students move beyond the terms *know* and *understand* when assessing competency and advance to higher-level outcomes, including *analyze*, *compare*, *predict*, and *model* (Fu et al., 2009; AAAS, 2011; National Research Council, 2012). AAAS (2011) further identifies *ability to use quantitative reasoning* and *ability to use modeling and*

simulation as two of the top three core competencies students must learn about scientific inquiry. Johnson and Lark (2018) call for selection experiments with digital organisms as guided investigations of evolutionary mechanisms.

Computer simulations allow students to simplify complex systems by manipulating variables, making comparisons and predictions, and testing hypotheses within the classroom. Several simulations for evolution are available for purchase or free download. While they may be effective in showcasing evolutionary concepts, and are often based on classic studies, they often lack transparency when calculating the evolutionary consequences or outcomes. For example, it is a common technique to let the user manipulate an organism's color or habitat, and then the computer solves which variants have higher fitness without revealing the assumptions of the model or the mathematical calculations that mimic life. This "black box" approach has the potential to minimize quantitative reasoning and prevent the student from using simulated data to predict, analyze, and test evolutionary concepts directly.

I developed a simplified model of hammerhead shark bioenergetics for demonstrating opposing evolutionary constraints and natural selection that is transparent in its assumptions, calculations, intermediate steps, and results. A fundamental assumption of fish bioenergetics models is that the calculations are performed on an individual because they give a more accurate response to environmental variables than population-level models (Kitchell et al., 1977); simulations can be repeated and results can be interpreted to represent the population. Here, the user is able to generate variation within the population by altering head widths (structure) and swimming speeds of an individual, which affect its ability to locate and capture prey (function). Although increasing head width and swimming speed improve prey detection, they cause an increase in drag that escalates the energy required to swim. Students are able to apply quantitative reasoning while making predictions about how changing these variables alter both prey detection and metabolic demands. As the students incrementally alter these variables, the model continuously updates and reveals the results, allowing the students to evaluate their predictions

and investigate opposing constraints. Using the bioenergetics approach, the shark can reproduce only if there is remaining energy after the metabolic demands of producing a head and pushing it through water have been paid. These variations within the population result in differential reproductive success, which is the driving force in natural selection.

○ The Hammerhead Shark

Hammerhead sharks are charismatic megafauna characterized by their laterally widened rostrum, called the cephalofoil. The cephalofoil is dense with ampullae of Lorenzini, which allow the shark to detect the electromagnetic fields of its prey. Mello (2009) hypothesized that the widened cephalofoil aids in prey detection by allowing the shark to scan a larger electromagnetic field. Additionally, the elongation of the rostrum provides wide eye spacing, producing acute binocular vision for visual detection of prey (McComb et al., 2009). Furthermore, the wide spacing of nostrils on the rostrum allows the shark to determine the direction of scent trails (Kajiura et al., 2005).

I chose to model the winghead (*Eusphyra blochii*) because it is the most basal of the hammerhead species (Lim et al., 2010) and has the highest rostrum-to-body ratio, ranging from 0.4 to 0.5. In contrast, that of the great hammerhead (*Sphyrna mokarran*) ranges from 0.20 to 0.25. Hammerhead evolution has incrementally reduced cephalofoil width in the more derived species (Lim et al., 2010). By investigating the upper limits of cephalofoil widths and associated costs, students will understand the opposing evolutionary constraints that give natural selection direction, and they can see why “bigger is not always better.” Wingheads eat a variety of fishes and cephalopods. Once sexual maturity is achieved at ~1.0 m in length, an average female winghead gives live birth to 6–25 pups/year.

○ Suggested Teaching Narrative

Instructors are recommended to give the students background context before using the bioenergetics model. Particular attention should be paid to the equations that calculate the energy budget. I distribute a “pre-lab” exercise of these concepts and equations that students must complete before using the computer model. The following narrative is the basis of the one I assign and may serve as a starting point.

○ Opposing Constraints

If the widened rostrum aids in prey detection, is a wider rostrum better? A wider rostrum should allow the shark to survey larger volumes of water per unit time than narrower rostrums. So, why is the rostrum-to-body ratio limited to 0.4–0.5 for wingheads?

Phenotypic performance is limited because every form is a balance of strengths and weaknesses. Water is 775 times denser than air; therefore, moving through it requires considerably more energy than moving through air. Since wingheads are constantly swimming in search of prey, the energy gained from digesting prey must exceed the energy spent pursuing and capturing the prey. Every object that moves through a fluid, such as air or water, is met with resistance, called drag. The drag equation for all objects is

$F_D = \frac{1}{2}\rho\mu^2C_D A$ (Equation 1), where F_D is drag force measured in Newtons (N), ρ is the mass density of the fluid (kg/m^3), μ is the flow velocity (m/s), C_D is the drag coefficient, and A is the area of the object (m^2).

The combined surface areas of the cephalofoil and body directly contribute to the total drag the shark experiences while swimming. The widened rostrum protrudes laterally off the head of the shark, adding to the drag the shark encounters when swimming. Subsequently, a trade-off exists between gains from the rostrum during prey detection and the drag generated during prey pursuit. Therefore, there is a compromise of not being too small and limiting foraging success but not being too large and risking massive expenditures; this concept is known as *opposing constraints*.

○ Bioenergetics Modeling

Bioenergetics is the study of energy movement and transformation through biological systems. This concept is modeled for fish in the equation $C = R + W + G$ (Equation 2), where C is consumption, R is respiration, W is waste, and G is growth. A typical carnivorous fish, such as a winghead, has a baseline bioenergetics budget of 1 unit consumed = 0.44 units of respiration + 0.27 units of waste + 0.29 units of growth (Kitchell et al., 1977).

As soon as food enters the digestive tract, a flat percentage is lost as waste. Respiration sustains the organism, which includes basal metabolism, movement, prey capture, and the action of digesting the meal. Basal metabolism is fixed, based on shark size, but the others are variable, depending on swimming speed and number of prey consumed. After the costs of waste and respiration have been calculated, remaining energy can be invested in growth. Reproduction comes out of the growth budget because gonads have to develop and the developing young require energy. If the organism cannot balance metabolic demands, it cannot reproduce and may die.

The energy trade-off of energy gained from prey and metabolic expenses will determine the amount of energy available for reproduction. Sharks with higher drag have less energy left over for reproduction, so they will have lower differential reproduction. Sharks with decreased prey detection will also have less energy for reproduction. Natural selection will favor the shark body plans that maximize the energy gained to energy lost because, all other things being equal, those individuals within the population should have the greatest reproductive success.

○ Using the Bioenergetics Model

Distribution

The model (Figure 1) is a Microsoft Excel file that has been tested on several versions of Excel for both Windows and Macintosh. It is not compatible with mobile apps and other spreadsheet applications. It is provided “as is” and is free to download and distribute from <https://goo.gl/jnPUJ9> (through Weebly.com). I will also share the model when contacted by email. The model has three spreadsheet tabs: Bioenergetics Model, Model Assumptions, and an optional Graph Builder. The first two tabs are locked to prevent user alterations to the equations and source code, but I will distribute an unlocked version upon direct request.

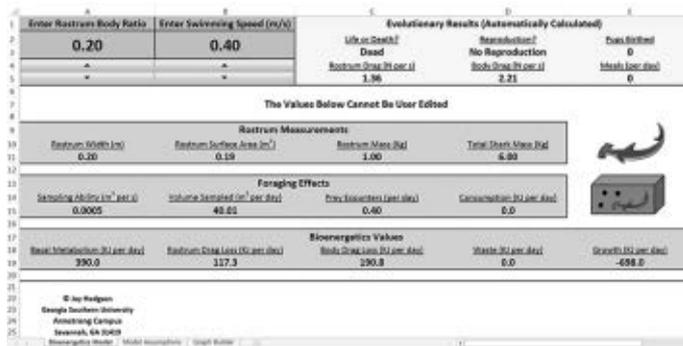


Figure 1. The winghead bioenergetics model (first tab) viewed from within Microsoft Excel for Windows.

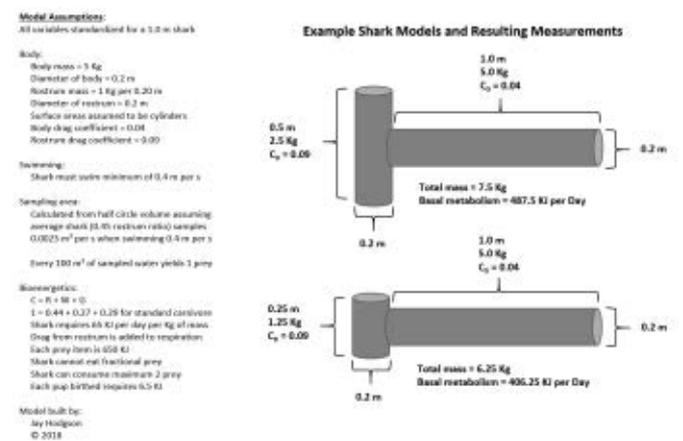


Figure 2. Model assumptions (second tab) used when calculating bioenergetics output and evolutionary consequences.

Model Assumptions

While the model is based on values published in the literature, certain parameters have been simplified to aid student understanding of the core concepts (Figure 2). The adaptive peak the model solves for reflects the actual predominant phenotype and average birthrate in the natural population. Deviations from this represent phenotypes with lower fitness.

All variables have been scaled for a shark with a body length of 1.0 m. To minimize confounding variables and variation, the body and cephalofoil of the shark are assumed to be cylinders without fins and with diameters of 0.2 m when calculating surface area; however, the drag calculated from their movement reflects the actual shape of the shark. The shark body has the drag of a fusiform body with a drag coefficient of 0.04 and the cephalofoil has the drag of a wing with a drag coefficient of 0.09. Drag is calculated according to Equation 1. Since drag is often calculated as N/s , the model transforms the values into KJ to fit into the bioenergetics equation. Basal metabolic requirements of 65 KJ/day per kilogram of mass are extrapolated from Lowe (2002), Dowd (2006), and Bouyoucos et al. (2017). The basal metabolism of a 5.0 Kg body (sans head, 1 Kg/m) remains fixed, but as the cephalofoil widens at 1.0 Kg per every 0.20 m (scaled to one-fifth of the body mass), the shark's total basal metabolism will increase accordingly. Swimming speed, prey sampling

area, and prey detection of wingheads are based on the work of Barousse (2009) and Mara (2012). For simplicity, the model assumes that every 100 m^3 of water sampled yields one prey item, and the shark cannot eat more than two prey per day. Each prey item yields 650 KJ , and fractional prey cannot be consumed. The bioenergetics model of $C = R + W + G$ (Equation 2) from Kitchell et al. (1977) has been modified to assume that respiration (R) is the sum of both basal metabolism and energy lost to drag. As either or both the cephalofoil size and swimming speed change, the model adjusts prey detection, prey consumption, basal metabolism, waste, body drag, cephalofoil drag, and growth. The shark can survive and reproduce only if the growth values are positive; the more positive the growth values are, the more pups it will birth. Each pup birthed requires 6.5 KJ , and fractional pups cannot be produced.

Data Entry & Results

The user enters values for Rostrum:Body Ratio and Swimming Speed using clicker arrows in the orange box in the Bioenergetics Model tab found in columns A and B, rows 1–5. The smallest ratio allowed is 0.20 and the slowest swimming speed is 0.40 m/s ; upper limits beyond reasonable biological measurements are possible, and students are encouraged to try them. After these values are input, all other values in the model are automatically populated using Equations 1 and 2.

As the user manipulates Rostrum:Body Ratio, values in the gray Rostrum Measurements boxes will change, including Rostrum Width, Rostrum Surface Area, Rostrum Mass, and Total Shark Mass (rows 9–11). Once Swimming Speed is altered, values in the gray Foraging Effects boxes will change, including Sampling Ability, Volume Sampled, Prey Encounters, and Consumption (rows 13–15). These foraging values are synergistic with rostrum size because changes in rostrum width will influence prey detection and consumption. As both Rostrum:Body Ratio and Swimming Speed are manipulated, values in the gray Bioenergetics Values change (rows 17–19). Specifically, Rostrum Drag Loss and Body Drag Loss adjust as differently sized cephalofoils swim at varying speeds, and Growth changes synergistically on the basis of energy gains from prey capture and losses from drag. Basal metabolism changes only according to total shark mass and is independent of swimming speed. Waste is a fixed rate based on total prey consumption and does not change with swimming speed or varying drag.

Final results are shown in the yellow Evolutionary Results boxes (columns C–E, rows 1–5). Students will learn how their manipulations of Rostrum:Body Ratio and Swimming Speed ultimately influence prey capture and total energy expenditures. If the shark runs an energy deficit, the shark will ultimately die. If the shark harvests sufficient energy, it will be possible to reproduce with differing total offspring. Drag calculations from Equation 1 are also listed so that students can compare the drag between the cephalofoil and body while assessing the cost and benefit of the sensory investment. Students may also use the optional Graph Builder tab to visualize changes in their variables (Figure 3). They can enter Rostrum:Body Ratio and Pups Birthed into columns A and B, respectively, and then plot other values of their choosing, including drag and other metabolic expenditures. The graph will automatically populate.

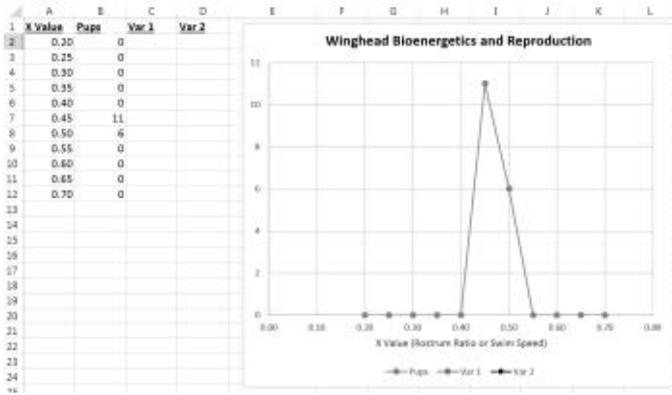


Figure 3. An optional graph builder (third tab) that instructors may assign when students use the model.

○ Learning Outcomes

After using the winghead bioenergetics simulation, students should be able to use modeling to analyze, compare, and predict the following:

- **Variation within populations.** By changing cephalofoil size (morphology) and swimming speed (behavior), individuals vary within the population. Each variant incurs different energy expenditures and gains.
- **Inheritance.** Sharks in this model have the potential to reproduce if energy gains exceed energy expenditures. The successful parental phenotype will be inherited by its offspring.
- **Natural selection.** Not all individuals survive, and those that do will have differential reproductive success reflective of the number of pups birthed. Traits are passed on in unequal rates, and this is a nonrandom process. Individuals that maximize energy gain to energy loss in their environment, in terms of prey detection and drag, will have the highest reproduction. The phenotype with the greatest reproductive success will be the most common in the population.

○ Student Reasoning While Using Models

Computer simulations are often complex and need scaffolding to enhance student reasoning (Löhner et al., 2005; Sins et al., 2005). To guide student reasoning, Sins et al. (2005) outlined five steps in the process: *analyze, use inductive reasoning, quantify, explain, and evaluate*. The hammerhead model was intentionally made to be simplistic, in terms of only manipulating rostrum size and swimming speed, to reduce confounding variables and enhance student comprehension of the most essential concepts while exploring opposing evolutionary constraints. When using this shark model, instructors should guide students how to deconstruct the model into its individual variables of rostrum size, swimming speed, prey detection, energy gained, energy spent, and pups birthed. Then students should hypothesize how those variables interact and ultimately dictate energy budgets for growth and reproduction. As students manipulate the model variables, they will see quantitatively how each parameter changes. From those data, they should explain how phenotypic variation affects the

opposing constraints of prey detection and drag, especially the upper and lower limits of each. Moreover, they should connect how all of the model variables are related and drive differential reproduction, which is central to natural selection. Finally, students should extrapolate the model results and apply them to concepts of natural selection, including comparing the model results to observed results in nature and applying them to other organisms and systems. Ultimately, these align with the AAAS (2011) core concepts of *evolution* and *structure and function* and the core competency of *ability to use quantitative reasoning*. Furthermore, the use of this model could be assessed as skills-based learning, meeting the core competency of *ability to use modeling and simulation*.

○ Student Reception

This model has been used during five separate terms, to date, in a college course that was recently revised with funding by the National Science Foundation. Students in this class also used other evolutionary models. On two separate occasions, the overall course was independently assessed per National Science Foundation mandate. When compared to the commercial models, ~75% of the students ranked this shark model as of similar quality. Anonymous student comments about the shark model were overwhelmingly favorable and complimented the model's ability to reinforce concepts of natural selection.

○ Alternative Models

While the model I produced is free to use and distribute, instructors may wish to build their own. To do so, at minimum a similar model must contain applications of Equation 1, Equation 2, and simulated prey detection and capture. Fish bioenergetics is an extensive field, and data are widely available. Jørgensen et al. (2016) provide a contextual overview.

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Teaching Evo-Devo with Legos: It's Not the Genes You Have, It's How You Use Them

● MICHAEL I. DORRELL

ABSTRACT

Evolution is a central principle of biology. However, key aspects of evolution can be very difficult to model in a classroom setting. Two such key principles are (1) how the accumulation of small, relatively minor modifications can lead to the diversity of life over extended periods of time; and (2) how closely related genomes between different organisms can yield such dramatic differences in patterning and phenotype. The second aspect is explained largely by evolutionary developmental biology (“evo-devo”), whereby tiny modifications in when, where, and how much the same genes are used during development can lead to dramatic differences in the adult. Developmental construction, using similar building tools, can lead to the formation of a large variety of forms. Here, I describe fun, inexpensive, and simple methods using drawings and Legos by which students can actively generate understanding of descent by modification and evo-devo. Specifically, students learn how the same genes, used in different ways, can lead to “endless forms most beautiful” as originally phrased by Darwin himself. With the accompanying guided discussion, these activities also illustrate other key principles of evo-devo such as combinatorial and modular enhancers, Von Baer’s principles, and genetic and morphological homology.

Key Words: Evo-devo; evolutionary developmental biology; enhancers.

○ Introduction

Evolution takes millions of years, and thus it is neither an easily observable phenomenon nor a readily tangible concept. Even rapid selective events, such as those occurring in viruses or prokaryotic cells, are not easily accessible to students. The mechanism of evolution relies on small, random mutations in the genome, which lead to gradual phenotypic changes that, if advantageous within the environmental context, may become more prominent in the population (Davidson & Erwin, 2006). The divergence of individuals within populations, let alone speciation from these incremental changes, can be difficult to model. Here, I describe a simple drawing activity that allows students to participate in generating small incremental changes, ultimately seeing how these can lead to divergence of phenotypes from a common ancestor while retaining evidence of

underlying homology. These concepts of descent with modification and underlying homology are difficult for students to visualize, and especially difficult to connect. By witnessing divergence of images that all begin from a simple structure like a heart drawing, students are better able to conceptualize and accept this as a key aspect of evolution. This activity, with appropriate follow-up and discussion, can also be used to demonstrate (1) homology, (2) co-option (these small iterations are built by using the same preexisting genes in different ways, with the preexisting genes repurposed for a new function by altering the way those genes are used; Werner et al., 2010; Jiggins et al., 2017; Van Belleghem et al., 2017), and (3) Von Baer’s principles of development occurring from general toward more specific features (Abzhanov, 2013).

Another key aspect of evolutionary mechanisms is the ability of similar genomes to result in dramatically different phenotypes. Why do organisms that look so different have such similar genomes? How can mutations of key genes lead to changes without major negative effects on phenotype? The answer to both of these questions lies within the field of evolutionary developmental biology (“evo-devo”; Akam, 1998; Carroll, 2005). While lagging behind its counterparts of physiology and ecology with regard to understanding biology and evolution, evo-devo has emerged as a field that is critical for understanding the mechanism of evolution. Advances in our understanding of genetics, particularly the non-coding regions of the genome, have revealed much of the mechanism by which changes in gene expression, rather than changes in the genes themselves, can lead to dramatic phenotypic changes without necessarily altering the function of the key proteins, especially if changes happen early in the organism’s embryonic developmental cascade (Rebeiz & Tsiantis, 2017). In early development, there are many key genes that organize the body structure. These developmental control genes are often referred to as “tool kit genes” in that they are the tools that can be used to build an organism (Akam, 1998; Carroll, 2005). These are highly conserved throughout evolution, largely because they play such a critical role in development of an organism. The fact that these genes are so important means that mutations to their

coding regions, resulting in modified versions of the proteins, are often detrimental or even lethal to the developing organism. However, if the non-coding regions of these genes are altered, such as the modular enhancers that control when and where these genes are activated, this allows nonlethal changes to occur. Just as a hammer can be used in many different ways to help build a wide variety of objects from a chair to a table to a bicycle, a tool kit gene can be used in many different ways to construct different organismal structures. If you destroy the hammer, nothing can be built. However, use the hammer in a different way and something new emerges. In the same way, a mutation in a tool kit gene that causes a change in the way that gene is used, rather than destroying the gene product itself, can lead to emergence of new organisms. As Sean Carroll puts it in his wonderful book *Endless Forms Most Beautiful*, “it’s not the genes that you have, it’s how you use them” (Carroll, 2005). Small changes in where, when, and how much a tool kit gene is used, rather than changes in the protein coding region of the gene, can lead to diversity without lethality. This also explains why genomes of dramatically different organisms are so similar, especially within the coding region of genes. Just as two people can have the exact same set of construction tools in their tool box, but build completely different objects, two organisms with similar tool kit genes can build very different phenotypes based on how those tool kit genes are used during development (Carroll et al., 2008).

Here, I describe an activity using Legos that models how similar genomes can be used to make the diversity of life that we recognize on Earth. This activity can be modified in several ways to make it appropriate for students ranging from elementary to undergraduate. Again, with the appropriate follow-up discussion, this hands-on activity can be used to model key aspects of evo-devo. With the Legos acting as tool kit genes, students can use the exact same set of Legos to construct, or “develop,” a multitude of different structures similarly to how the same genes can be used to construct dramatically different organisms during development. The differences in phenotypes do not lie in differences in the genes, but rather in how those genes are used during the construction (development) of that organism. Teachers are encouraged to use and adapt the included PowerPoint discussion slides for their own classroom purposes. Together with the drawing activity, students actively learn how descent with modification, combined with changes in the gene expression of key tool-kit genes during embryonic development, can lead to what Darwin called “endless forms most beautiful.”

○ The Activity

What You Need

For the drawing activity, you will need three sheets of regular-sized paper, each with the same simple shape drawn on the front. I used a heart, but any basic shape will work fine as long as they are all the same. For the Lego activity, students can work individually or in small groups, depending on the size of the class. You will need a small set of Legos for each of the students or groups. Each set must be adequate to build something small yet substantial, and each MUST contain very similar, if not the exact same, set of Lego pieces. I purchased four large buckets of Legos and then separated them evenly into 25 different sets, each containing the same number and shapes of blocks (I didn’t worry about color; for a picture of a

standard set of Legos, see Figure 2). These sets can be used for years as long as it is emphasized to the students that they are not allowed to swap Legos and that, at the end of the activity and discussion, the sets must be put back into their bags exactly as they got them.

Getting Started

I use this as a culminating lecture for my undergraduate Developmental Biology course after we have discussed enhancer regions, gene regulation, and how evo-devo explains key mechanisms of evolution whereby small changes in the genome (usually in the enhancers) can have profound effects on phenotype. Even for advanced students, this simple activity is highly effective in helping them tie together these key concepts in a more tangible and clear manner. However, with any appropriate level of pre-instruction, these simple activities can be used to help explain difficult concepts like how humans and apes (or even humans and more distant organisms) can have such similar genomes and vastly different phenotypes.

As part of my college course, I have the students read *Endless Forms Most Beautiful* by Sean Carroll (2005). Students then perform these activities (playing with Legos and doodle drawing) while watching the video “What Darwin Never Knew” in lab (PBS, 2011). I strongly encourage teachers to use some of the many great resources available, such as the NOVA interactive websites on evo-devo (PBS, 2009), gene switches (Patel, 2007), the “zoo of you” (Shubin, 2009), and “guess the embryo” (VanCott, 2009) to help supplement teaching and to build understanding of these key topics. The activities described here can then be used as an active-learning, concrete visual of how these concepts emerge to help explain evolution and are effective as an introduction to the concepts of evo-devo, or as a culminating experiential activity to help solidify those same concepts. “What Darwin Never Knew” is very good at explaining key concepts of evo-devo and can be appropriate for high school or undergraduate students.

Instructions

I do not tell the students ahead of time why I am having them “play” with Legos or draw. Rather, I have them think that it is a treat while they watch the video. Having no anticipation of the purpose, the outcome where students truly grasp the concept, which I call the “lightbulb” or “aha” moment, is dramatic. For the drawing exercise, arbitrarily divide the students into three sections. I group them by rows of desks that are near each other so that the drawings can be easily passed from student to student in intuitive circles of around 10 students each. Students are told that they can only add or erase within a 1 cm² section of the drawing at a time, at which point they must pass the picture on to the next person, who will alter another small section of the drawing before passing it further down the row. I usually include an example of the size of the limited area that they can modify during each iteration at the top of the drawing. Any alteration (additional drawing or erasing) must be connected to the preexisting image. Students cannot start a new drawing area out in empty space, but must connect their drawing to a preexisting part of the image, which will expand as the activity progresses. This is a key point in evo-devo, as new structures do not emerge out of nothing, but rather as modifications of preexisting structures. Note that some aspects of the image may end up looking like they are unconnected if the students choose to erase a connecting line later. However, as Williston’s law points out, the loss of structures is just as

key to evolution as the gain of structures (Carroll, 2005). Other than these two simple rules, there are no explicit instructions and so each change is “random,” although depending on the maturity level of the class, teachers may want to emphasize “appropriate” drawings only. Each drawing gets passed around within its specific group (no passing between groups) repeatedly over the course of a couple of hours. In doing so, the three drawings repeatedly get modified in small increments over the course of a reasonable amount of time. If you have relatively limited time, you may wish to expand the area to about one square inch per iteration so that adequate divergence between the drawings can emerge. I have the students do this drawing activity, along with the Lego activity described next, while watching the video. College students are able to multitask in this manner, and I have found that the majority of their focus on the Legos and drawing is during the first hour of the video, which is more of a review for them anyway. By the time the evo-devo-heavy portion of the video comes around, students’ focus on the video is strong. In some ways, I’ve found that having the students multitask in this manner actually helps keep them focused rather than dozing off. However, each teacher should plan the activity however works best for their class, bearing in mind students’ maturity and attention levels.

For the Lego activity, students are explicitly instructed to build using their own Lego set (no swapping). Remember that each set contains basically the same number and shapes of Legos. Other than that, there are no restrictions. Although students are able to use all of the Legos in their set, they do not have to use them all, just as not all genes are used in any given organism; there are vestigial genes or pseudogenes that are not used by certain organisms (Chandrasekaran & Betrán, 2008). Structures that are built without use of all the pieces or “genes” can also be used to discuss the classic experiment whereby a mouse mesenchyme is used to stimulate development of teeth in the chick oral epithelium. That experiment demonstrates that the chicken genome must have genes that encode tooth development, remnants from the last common ancestor with mice, even though those genes are no longer used or induced under the normal chick developmental program (Harris et al., 2006). Once students have built something they like, they should save it to share with the class at the end.

○ Outcome & Discussion

At the end of the activity, the three drawings will have become highly diverse (see Figure 1). These drawings can be used to demonstrate four main concepts: (1) that small, random, incremental changes over time can lead to diversification, especially between separated populations; (2) that underlying homology still remains – the heart can still be seen underlying all the details that have progressively emerged, just as the underlying homology of physiological structures like organismal limbs are apparent beneath the more detailed phenotypical differences that have evolved; (3) that these changes are based on relatively simple changes in how the same “genes” (in this case the pencil graphite and the eraser) are used rather than the *de novo* synthesis of new genes; and (4) the order of development from simple (general) structures to more specific and complex aspects of an organism’s morphology.

The only rules that the students were given regarding the drawing were that they were to alter only a small region at a time (small incremental changes), that their changes must attach to a preexisting structure on the picture (modifications can only be made on preexisting

structures), and that they could use only the provided pencils and erasers (limited to preexisting pseudogenes). During discussion, I emphasize that the small, random incremental changes that lead to diversification are normally selected for in the context of natural selection. While a strong understanding of natural selection is also a key aspect of understanding evolution and should not be addressed as a passing comment, I am assuming that the students have previously been taught natural selection, and therefore this discussion can be used to bridge the concepts of incremental change, natural selection, and descent with modification. A minor modification that can be used to add a natural selection component to the model activity is described below. In addition, the modification from a general image (heart) to much more diverse and specified structures demonstrates how development occurs. The more general parts (e.g., the homologous bone structure of limbs) develop first, and the evolutionary “modifications” develop later. This is why it is very difficult to discern the species of very different organisms from their early embryos; the early embryos look remarkably similar and the specific features appear later (VanCott, 2009). This is a result of developmental necessity in relation to common ancestry; descent with modification requires that the underlying general commonalities develop first, and very similarly between organisms (Abzhanov, 2013). Students often modify the additions made by other students by further drawing or erasing parts of the new structures, demonstrating how continued incremental changes can modify structures that have already evolved from the original form (Figure 1A).

After the students have finished building with their Legos, I have them briefly describe their creations. Each will be unique and often vastly different, despite starting with the exact same set of pieces (see Figure 2). Based on their construction (their choices of when and where to use each piece), the vast differences emerge. This is analogous to organisms that have very similar genomes yet very different phenotypes. Based on when, where, and how much those genes are used during development, or how those genes are used to “construct” the organism, “endless forms most beautiful” can emerge. To further strengthen the point and visualize the concept, I put up a slide of all the different animals built out of Legos at Legoland. In order to make a giraffe out of Legos, it is not necessary to develop a new “giraffe neck piece.” To make an elephant, an “elephant trunk piece” is not required. Instead, these animals are built using the same, standard Legos in a new way (see slides 6–8 in the PowerPoint discussion file). The same genes, used in different manners (timing and location) during development, can result in dramatically different phenotypes.

These concepts fit perfectly into what the video “What Darwin Never Knew” discusses. I then work to tie it all together with a short PowerPoint guided discussion about how enhancer regions and mutational alterations therein provide the framework for evo-devo. These slides can be accessed as Supplemental Material with this article (see Figure 3). Teachers are encouraged to download and modify the slides for their own discussion purposes.

By this time in my undergraduate course, we have extensively discussed the modular and combinatorial nature of enhancers, as well as co-option. The main concepts can be presented to students at all levels, with varying levels of detail as appropriate. The drawing and Lego activities should be accessible to all and will help explain (1) that small incremental changes can lead to diversity and (2) that the same genes (Legos) can result in many different phenotypes based on how they are used to construct the organism during development (when, where, and how much those genes are used).

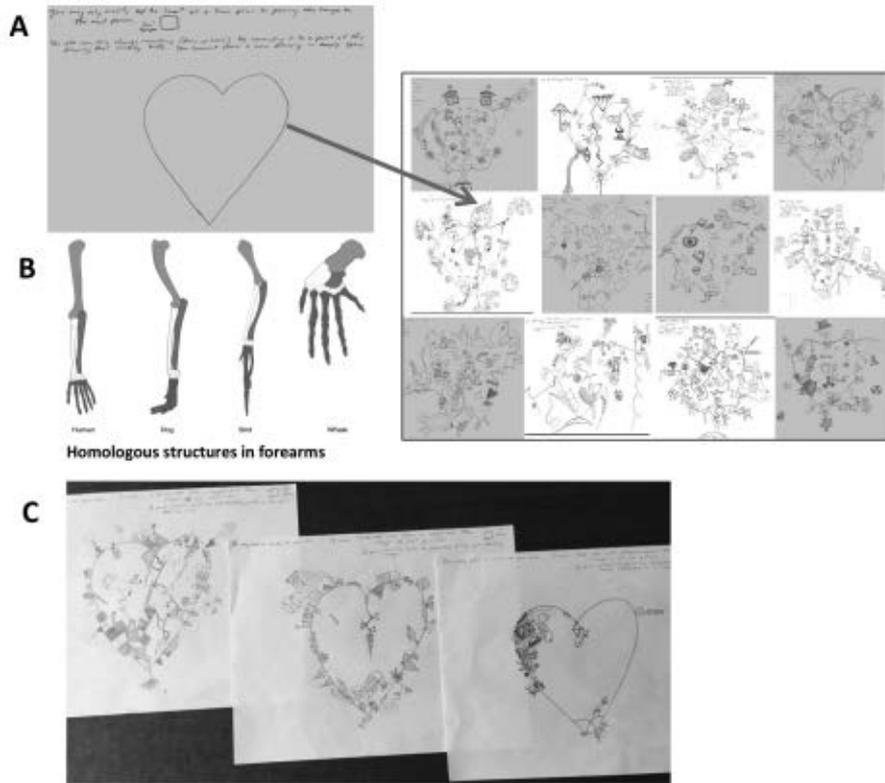


Figure 1. Drawing activity. **(A)** Simple heart structures were passed around within three separate groups of about 10 students each, with the simple instructions that students could modify them only by adding to the existing structure (drawing) or subtracting from it (erasing) within an area $<1 \text{ cm}^2$, with alterations required to be attached to the preexisting image. After each person's modification, the picture was passed on to the next person and thus continuously modified in small increments over the course of a couple of hours. Complex and diverse pictures emerge, but the underlying homology of the original heart remains. **(B)** This is similar to how limbs or other homologous structures can evolve highly distinct, detailed structures while the underlying homology of the bone structure remains as evidence of common ancestry and similar developmental construction. **(C)** While the images can become quite intricate within a couple of hours, sometimes the drawings are less elaborate, depending on the creativity and interest of the students. However, even less intricate designs still model the diversification that occurs from small, random, incremental changes; these can be used to demonstrate that not all species evolve comparably.

Potential Modification of the Incremental Drawing Activity

I have also tried to include a “natural selection” component to the heart drawings by periodically removing sharp edges specifically in one drawing, specifically removing soft edges in another drawing, and leaving the third drawing untouched as they are continuously passed around the group. This can be done by having an instructor and teaching assistant (if available) sit within a group and erase hard vs. soft edges each time the drawing comes to them, thus modeling selective pressure against specific phenotypic changes. The third group would have no such selective pressure and thus the image would emerge completely as modified by students. If it is not possible to have the instructor or teaching assistant perform these modifications, the instructor can enlist the help of a trusted student within each group to be given that same job. This shows the importance of environmental selection of certain traits in determining the evolutionary phenotypic outcome, as the drawings can become quite distinct based on the selection of hard or soft edges. The concept can be exemplified well with this slight modification, but the results have varied with regard to the extent of relevant differences in the final drawings. The teacher should be prepared to adjust on the fly if

the differences are not dramatic. Similarly, not all images change evenly, often depending on the level of excitement you've managed to generate in the class regarding the images (Figure 1C). In that case, the teacher can also emphasize that not all species evolve. Many are still very similar to the original common ancestor while other branches may have evolved quite extensively. I do try to make the drawing activity a “friendly competition” between the groups to help motivate them to be creative and take the drawing activity seriously. This can sometimes help to ensure its success.

Summary

Using this hands-on activity, paired with an associated video and PowerPoint slides (see Figure 3), can successfully help students understand key aspects of evolution, including descent with modification, and the key aspect of evo-devo whereby the same genes can be used to generate dramatically different phenotypes, depending on how those genes are used during development. Students come away from these activities having a better grasp of how species such as humans and apes, or even more distant animals, can have very similar genomes, yet with a few small modifications to the enhancer regions that control when, where, and how much a gene is expressed, “endless

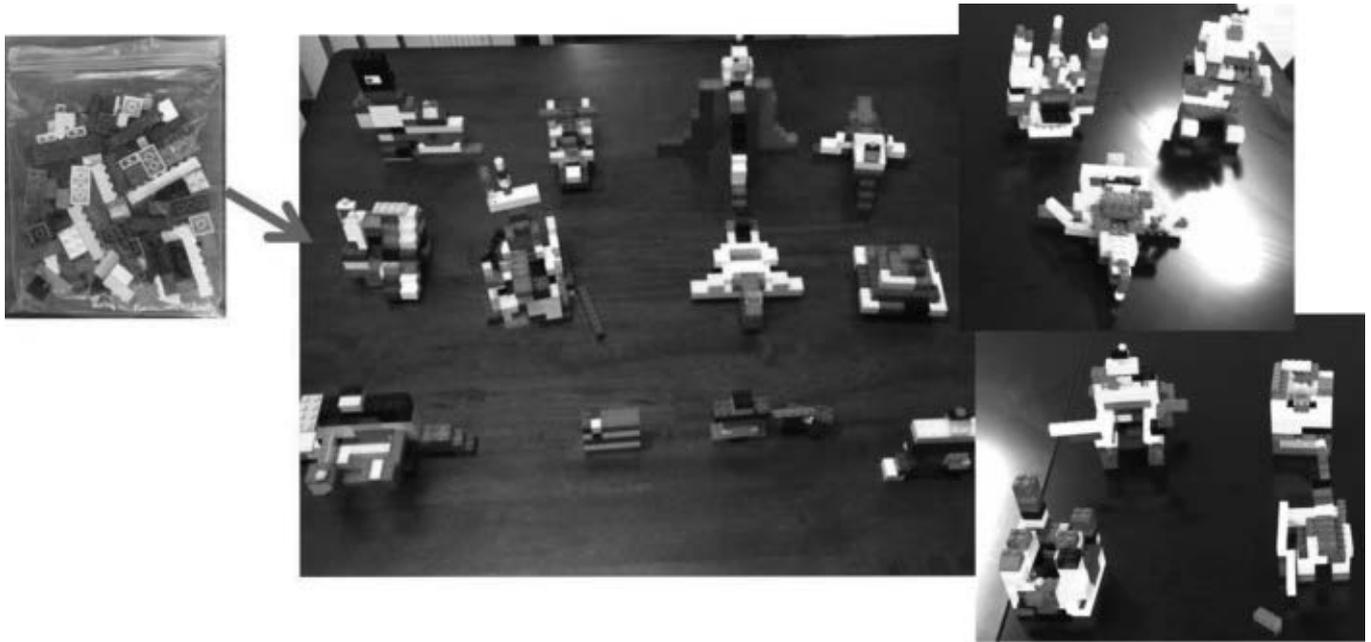


Figure 2. Lego activity. Using the same set of Legos (left image), students create many different designs demonstrating how the same building tools can be used to create highly different phenotypes depending on construction. In the same manner, very similar sets of genes can yield highly distinct organisms based on when, where, and to what extent each gene is used during development.

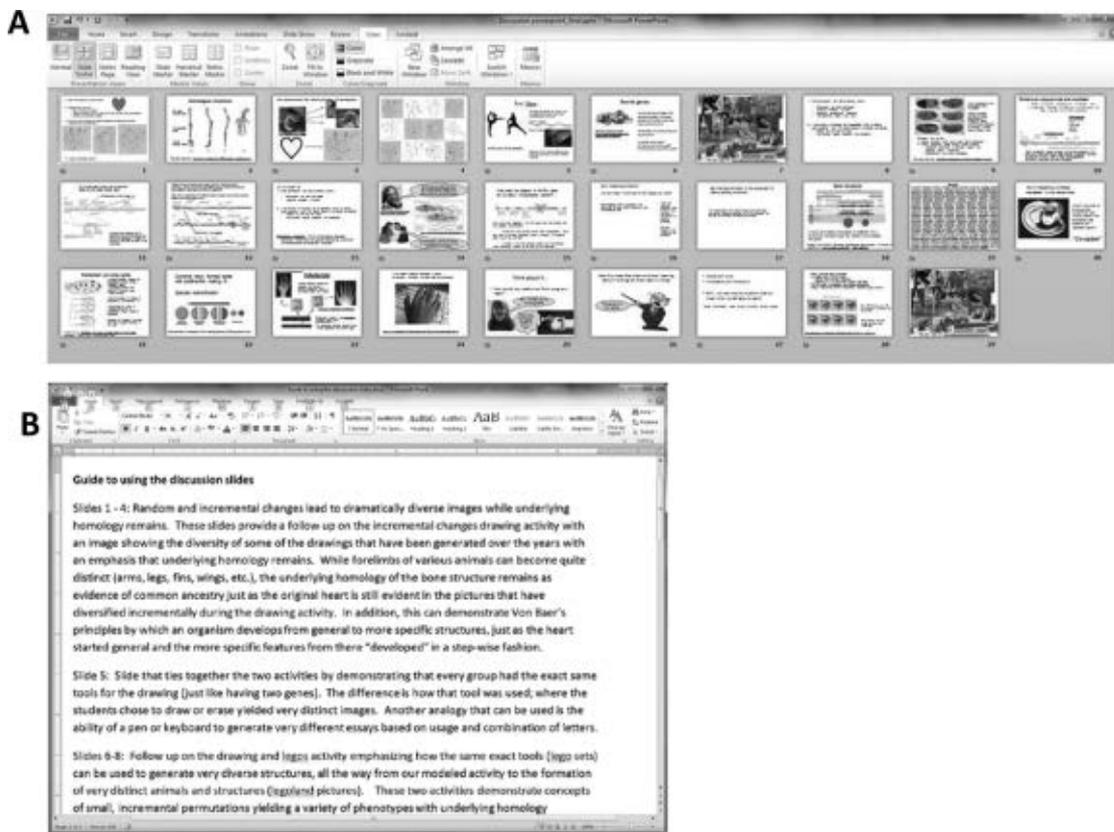


Figure 3. Discussion slides and description. These slides and their description have been made available for download and use at the following site online. They are designed to be used as a follow-up discussion with students to help them understand the relationship of the activities to enhancer regions, developmental biology, and evo-devo. **(A)** Slides: https://www.dropbox.com/s/2xcfxhqdekb2j6l/Discussion%20powerpoint_final.pptx?dl=0. **(B)** Word description file: https://www.dropbox.com/s/n0qtqftyjoriaa0/slides_guide.docx?dl=0.

forms most beautiful” can emerge. Teachers are encouraged to use and adapt these activities and the associated discussion slides – which include human examples of polydactyly (Gilbert & Barresi, 2018) and eye color (White & Rabago-Smith, 2011) to demonstrate the roles of enhancers in causing phenotypic changes.

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ABSTRACT

Active-learning approaches can improve understanding of core biological concepts. We describe a revised hands-on simulation for teaching evolution by natural selection, which focuses on prey–predator coevolution in escape/pursuit speed. It illustrates how selection pressure on individual speed increases average population speed through differential survival, while also reducing variation in speed among individuals. A simulated beneficial mutation helps differentiate the generation of individual traits from the process of natural selection and illustrates the effects of a beneficial mutation on immediate and subsequent generations. Overall, this exercise addresses several common misconceptions and allows students to collect and assess their own data, quantitatively. We report results from pre- and post-assessments in an introductory, undergraduate biology class, which indicate significantly improved understanding associated with the simulation.

Key Words: Active learning; card game; coevolution; math anxiety; mutation; natural selection; predation; sorting process.

○ Introduction

Evolution—one of five core concepts for biological literacy (AAAS, 2011)—presents a teaching challenge because it requires conceptual understanding of a long-term process (Catley & Novick, 2009). Many students also harbor preconceptions or personal beliefs that hinder understanding of underlying mechanisms (Alters & Nelson, 2002; Bardapurkar, 2008; Gregory, 2009). An important breakthrough for students is to recognize natural selection as a sorting process separate from mutation (Price, 2013). They should also realize that (1) “need” does not drive adaptation, (2) variation among individuals is raw material

for selection, and (3) adaptation does not necessarily change all members in a population (Bishop & Anderson, 1990; Gregory, 2009). Consequently, instructors have both devised active-learning approaches to engage students with the process of natural selection (e.g., Lauer, 2000; Riechert et al., 2011; Weber et al., 2016) and applied basic statistical techniques to increase conceptual understanding and reduce math anxiety (Stuckert & Vance-Chalcraft, 2016; Lee et al., 2017).

Tatina (2007) proposed a playing-card exercise to simulate a coevolutionary “arms race.” It focuses on comparative running speeds between predators and prey, demonstrating natural selection as a sorting process, highlighting the significance of variation among individuals, and revealing the mechanism of adaptation. Here, we present a revised, quantitative version of this simulation, suitable for introductory undergraduate or advanced high school courses.

Tatina (2007) emphasized that (1) coevolution changes mean running speed in prey and predator populations, (2) variation among individuals induces differential survival within each population, (3) only traits in the reproducing population can compose the next generation, and (4) average, not individual, running speed changes between generations. Our revised simulation adds (5) calculation of standard error for mean running speeds to represent intrapopulation variation, (6) simulation of a beneficial mutation within the coevolution process, and (7) increased emphasis on quantitative skills. We also modify the number of prey vs. predators to illustrate a somewhat more natural scenario. We provide before-and-after data for

four semesters from 18 laboratory sections to show that the simulation improved student understanding.

The game and accompanying calculations clearly illustrate how natural selection and beneficial mutation are separate but interacting mechanisms of evolution.

○ Materials

- The simulation requires regular, numbered UNO cards (or any numbered cards) with a range of five consecutive numbers (e.g., 1–5).
 - Each prey–predator combination requires 60 cards (50 prey, 10 predators).
 - Each simulation requires spare cards of the higher numbers in the sequence (e.g., 4 and 5) for constructing subsequent generations.
- We provide students with tables for data entry and accompanying worksheets for all data summaries and calculations.
- Students provide writing utensils and calculators.

○ Simulation

Laboratory sections of our introductory biology course, Principles of Zoology, hold 20–30 students, whom we divide into five or six prey–predator combinations. Each prey–predator group receives an envelope with numbered cards presorted into prey and predators. Each card represents an individual. Each number represents its flying, running, or swimming speed. Card-number frequency distributions overlap between prey and predators (e.g., Table 1). Prey outnumber predators in a 5:1 ratio. We label envelopes to represent real-world prey–predator scenarios such as (1) gazelle vs. cheetah, (2) snowshoe hare vs. Canada lynx, (3) fur seal vs. white shark, (4) eastern cottontail vs. ermine, (5) mallard vs. peregrine falcon, and (6) blue sheep vs. snow leopard.

○ Rules of Play

1. Starting with the provided cards, prey and predator teams calculate the beginning mean and standard error of running speed for their populations (Table 1).

Table 1. Example starting card distribution for a prey–predator group with starting means and standard errors of card numbers (i.e., running speeds). Card numbers can be any consecutive sequence of five.

Team 1 Card Numbers (Running Speeds)	Snowshoe Hare (Prey): Number of Cards	Canada Lynx (Predator): Number of Cards
3	5	1
4	10	2
5	20	4
6	10	2
7	5	1
Total card count	50	10
Mean ± SE	5 ± 0.2	5 ± 0.4

2. Each team shuffles its cards and places them in a pile face down between itself and the opposing team.
3. Play begins as the prey team turns over the first five cards while the predator team turns over one card.
4. The outcome of each interaction depends on the relative speeds of prey vs. predator.
 - a. Prey with an equal or higher speed (i.e., card number) than the opposing predator outrun that predator and escape to contribute to the next generation.
 - i. Prey win ties based on the rationale that predators must both catch *and* subdue prey, giving equally fast prey an advantage (this oversimplifies reality but provides a framework for simulation).
 - b. Predators subdue all opposing prey with lower speeds.
 - c. Each predator must subdue at least two prey to avoid starvation and contribute to the next generation.
 - i. This modification of Tatina (2007) provides increased “realism” because
 - (1) A predator does not have to subdue every prey it encounters to survive.
 - (2) A predator that ultimately starves can still subdue some prey.
5. Teams retain cards of survivors to determine the next generations.
6. Teams discard cards of subdued prey or starved predators.
7. The game continues with each team revealing its cards five prey to one predator at a time until all interactions are decided.
8. We assume that all survivors are reproductive equals. Thus, each team simulates reproduction by rebuilding the population to the original carrying capacity of 50 prey or 10 predators based on the proportions of each speed (i.e., card number) that survived (Table 2).

Table 2. Example first-round results for predator group based on a simulation using the starting card distribution in Table 1. Calculation of the next predator generation is illustrated.

Team 1 Predator Card Numbers (Running Speeds)	Canada Lynx: Starting Number of Cards	Canada Lynx: Surviving Cards	Canada Lynx: Next Generation of Cards
3	1	0	0
4	2	1	2
5	4	1	2
6	2	2	4
7	1	1	2
Total card count	10	5	10
Mean ± SE	5.0 ± 0.37	–	5.6 ± 0.34

Table 3. Mean (\bar{X}) and standard error (SE) of running speed for each generation based on a simulation run using the starting populations in Table 1. Generations with an “m” notation (e.g., 3m) are those in which a beneficial mutation occurred for one prey individual (in this case, a mutation converted a 5 to an 8).

Generation	Prey		Predator	
	\bar{X}	SE	\bar{X}	SE
1	5.0	0.16	5.0	0.37
2	5.4	0.14	5.6	0.34
3	5.8	0.12	6.4	0.16
3m	5.9	0.13	6.4	0.16
4m	6.7	0.08	6.6	0.16
5m	7.1	0.03	7.0	0.00

- a. Each team also calculates the mean and standard error of the speed of their new generation for comparison with the parent generation (Table 2).
9. Using their second generations, teams play the second round of the simulation like the first (steps 3–8).
10. Once the third generation is established, one individual from the prey population receives a **beneficial mutation** that increases its speed to one number above the highest number in the population.
 - a. To simulate this, the prey team haphazardly pulls one card from their third generation and replaces it with a “wild” UNO card or a card with a number one higher than the highest in the population.
11. Following the simulated mutation, the prey team recalculates the mean and standard error of the speed of their population in the third generation, which now includes one mutant.
 - a. The predator team does not experience a mutation, so their mean speed and standard error remain constant (Table 3).
 - i. It is best if members of the predator team participate in the mutation process with the prey team.
12. Thereafter, a third and (if time allows) fourth round of the simulation are run.
13. After the fourth simulation, students also calculate the characteristics of the fifth generation.

○ Practical Considerations

Our lab periods are 110 minutes, and the majority of student groups complete four rounds and calculate speeds of a fifth generation within that time. If less time is available, the main trends are visible in fewer rounds (Tatina, 2007), but at least four rounds are needed to include the mutation simulation (Table 2 and Figure 1). It is also possible to play the game in stages (say, from one class period to another), until several rounds are completed.

The analytical results are means and standard errors of running speeds per generation (Table 3). However, students also report card-number frequencies as part of their calculations, which helps

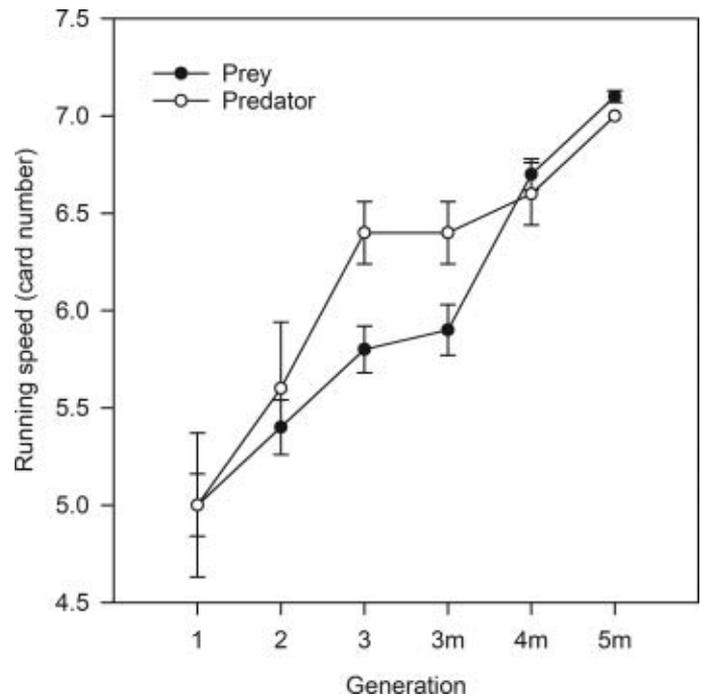


Figure 1. Graphed results from Table 3 showing mean running speed with standard error as required for homework. Students graph their own results. Results vary depending on play.

clarify the mechanism of natural selection. The calculations slow some student groups at first, but once they master them in the first round, groups typically are proficient in subsequent rounds. This meets our goal of strengthening quantitative skills and reducing math anxiety.

We suggest that students form groups of four or five so that at least two students collaborate on each prey and predator team. Teamwork allows students with more confidence to coach and assist others needing help. Students can also cross-check each other’s calculations within and among teams to reduce the errors.

As increased engagement is one goal of active-learning pedagogies (Nelson, 2008), it is important to note that students generally enjoy this simulation. It consistently keeps students engaged for an

entire lab period. It also succeeds in getting students working together and interacting throughout the learning process.

○ Homework Assignment & Follow-up Discussion

As homework, each student plots the mean and standard error of speed for each prey and predator generation in their simulation. They transcribe data from their opposing team during lab and graph both results together. This makes use of in-lab calculations and employs graphing skills introduced during previous lab assignments completed earlier in the semester.

Students see several trends in their graphs (Figure 1), which we discuss as a class in the subsequent lab period. First, they see coevolution in the parallel increase in speed for both populations (Tatina, 2007). They also see shrinking genetic diversity in the standard error, and they see the limitation that the traits of individuals within the population set on the potential to increase population speed. They further see that a beneficial mutation has a limited immediate population-level effect but influences subsequent generations. In the case shown for predators (Tables 2 and 3), strong selection eliminated all speeds below 7, demonstrating negative or “purifying” selection (Loewe, 2008). In addition, the beneficial mutation in the third generation of the prey population allowed mean speed to exceed 7—the maximum speed of the predator population—by the fifth generation. Overall, the game and accompanying calculations clearly illustrate how natural selection and beneficial mutation are separate but interacting mechanisms of evolution.

For further class discussion, the data and analyses demonstrate natural selection as a process of sorting among varied individuals. For instance, students quickly see that selection pressure favors faster individuals, especially as selection eliminates the slowest predators, which cannot encounter two catchable prey (Table 2). Students also see that adaptation and coevolution change population averages through differential survival, but that natural selection is not “all or nothing” because a predator with average speed sometimes encounters slower prey. Further, students can see that although natural selection affects the reproductive success of individuals, the results of natural selection become evident across subsequent generations.

If desired, students can calculate survival probabilities for different speeds or track the changing proportions of specific speeds

across generations. Calculating the percentage of each number surviving each generation illustrates higher survival for faster individuals (i.e., higher numbers) and that for individuals having average speed in the starting population, survival decreases by generation, as the overall population gets faster. Similarly, calculating the percentage of the population comprised by each number, by generation, illustrates the disappearance of low numbers, the decrease of average numbers, and the increase of high numbers. Students can tabulate or graph these results to see the trends, which are also excellent fodder for in-depth class discussions.

○ Assessment of Student Learning

To assess student learning, we administered pretests and posttests, available to students online in the week preceding and the week following simulations, respectively. These tests were voluntary and received approval from the Institutional Review Board of Weber State University (protocol nos. 2016-COS-3 and 2017-COS-6) prior to implementation. We asked students to complete an informed-consent form about this study before responding to the pretest. We excluded students from the analysis if they elected not to participate in the study. We also excluded students who only responded to either the pretest or posttest. With these caveats, we accumulated data for 298 students from 18 lab sections over four successive semesters.

For the assessment, we used the same questions in pretests and posttests within each semester and for all lab sections. We held nine multiple-choice questions constant across all semesters for long-term analysis of student learning. Paired t-tests using these long-term data indicated that posttest scores exceeded pretest scores each semester, with average improvement from 11% to 13.8%, depending on semester (Table 4).

To discern the simulation’s relative effectiveness for students with different levels of prior understanding, we classified students into one of three groups based on pretest scores: (1) $\leq 50\%$, (2) 51–79%, and (3) 80–99% (excluding students earning 100%). Paired t-tests showed significantly higher posttest scores for all three groups (Table 5). Students in the first group showed greatest improvement (~27%), possibly reflecting higher potential for improvement. It is nevertheless encouraging both that the simulation most benefited students with poorest prior understanding

Table 4. Paired t-test comparisons of students’ overall performance (percentage) on pretests and posttests, by semester.

	Fall 2016	Spring 2017	Fall 2017	Spring 2018
Pretest percentage ($\bar{X} \pm SE$)	77 \pm 2	66 \pm 2	67 \pm 2	71 \pm 2
Posttest percentage ($\bar{X} \pm \pm SE$)	91 \pm 1	77 \pm 3	80 \pm 3	84 \pm 2
n	107	55	65	71
t	8.878	3.786	5.504	7.439
p	<0.001	<0.001	<0.001	<0.001
Cohen’s d	0.858	0.511	0.683	0.883

Table 5. Paired t-test comparisons of percentage improvement on pretests and posttests for students grouped by level of prior understanding, based on pretest scores (excludes students earning 100% on the pretest).

Groups (Pretest Percentage Earned)	One ($\leq 50\%$)	Two (51–79%)	Three (80–99%)
Pretest percentage ($\bar{X} \pm SE$)	44 \pm 1	65 \pm 1	84 \pm 1
Posttest percentage ($\bar{X} \pm SE$)	71 \pm 3	80 \pm 2	92 \pm 1
n	51	113	108
t	7.952	9.969	8.252
p	<0.001	<0.001	<0.001
Cohen's d	1.114	0.938	0.794

Table 6. Chi-square goodness-of-fit comparison, by semester, between pretest and posttest percentages of students correctly responding to the question “If no mutation occurs to affect the running speed, what will most likely happen to the running speed of predator and prey populations over time?”

	Spring 2017	Fall 2017	Spring 2018
Pretest percent	18	28	23
Posttest percent	49	52	59
n	55	65	71
χ^2	11.77	8.21	19.7
p	<0.001	0.004	<0.001
Cramer's V	0.462	0.355	0.527

and that almost all students gained some benefit. We are confident that students also benefited from completing the calculations and working in teams.

Importantly, after the simulation, students better distinguished natural selection from mutation (Table 6). Over three semesters, we asked the additional question “If no mutation occurs to affect the running speed, what will most likely happen to the running speed of predator and prey populations over time?” In the pretest, only 18–28% chose the correct answer, “The average running speed of both predator and prey populations will first increase and then remain the same.” Many chose “The average running speed of predator and prey populations will never change due to lack of mutation.” Encouragingly, 49–59% (depending on semester) identified the correct answer in the posttest. A chi-square goodness-of-fit comparison indicated that improvements were statistically significant every semester (Table 6).

○ Conclusion

In summary, this simulation exposes mechanisms of natural selection that are commonly misunderstood. It also allows students to work as teams, practice and apply quantitative skills, and draw their own conclusions. Ideally, an active-learning exercise that distinguishes genotype from phenotype by calculating separate allele

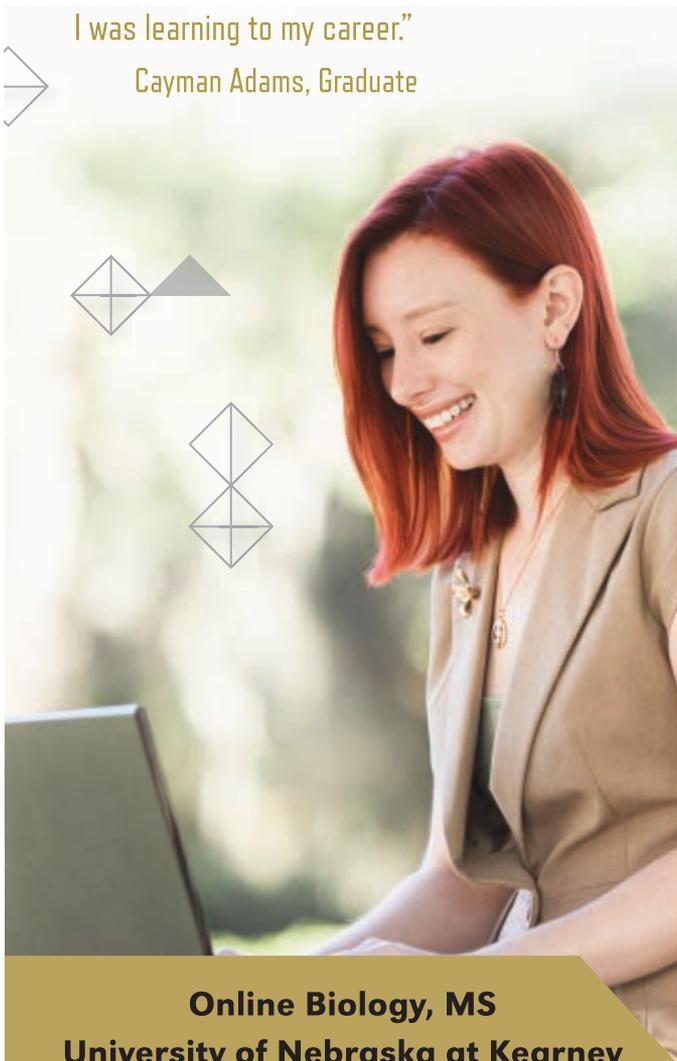
and phenotype frequencies (e.g., Lee et al., 2017; Jördens et al., 2018) would follow this simulation. However, we find that this simulation is ideal for initial exposure to the theory of natural selection.

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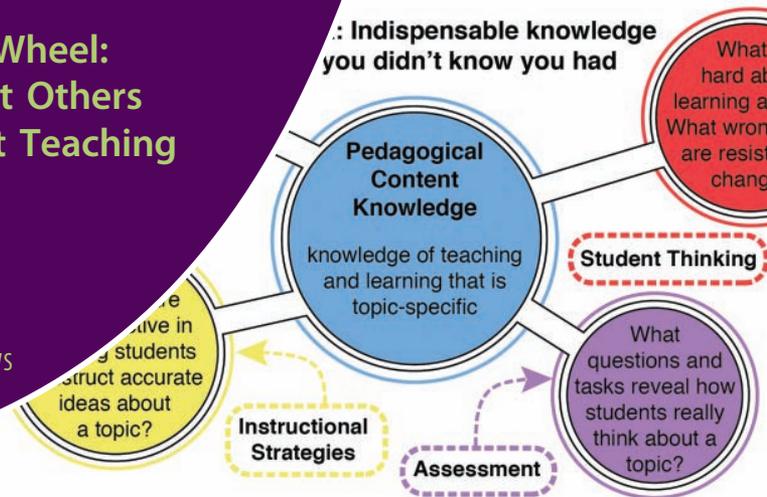
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Don't Reinvent the Wheel: Capitalizing on What Others Already Know about Teaching Topics in Evolution

MICHELLE A. ZIADIE, TESSA C. ANDREWS



ABSTRACT

What knowledge do you need to be an effective instructor? One key type of knowledge is pedagogical content knowledge (PCK), which includes awareness of how students are likely to think about a topic and where they will struggle as they learn that topic. We propose PCK as a valuable framework for reflecting on your own knowledge for teaching topics in evolution. We have created a searchable file that uses PCK as a framework to organize over 400 peer-reviewed papers from 40+ journals to give you better access to relevant resources for teaching evolution to undergraduates and advanced high school students. None of us have time to read 400 papers to inform our teaching, so we provide tips to maximize your use of this collective knowledge in the time you have available. We have written these to be useful to instructors across career stages.

Key Words: Evolution education; undergraduate; teaching evolution; PCK; pedagogical content knowledge; student thinking; instructional strategies; teaching strategies; assessment; learning objectives.

Take a moment to reflect on the knowledge that you use when you teach evolutionary topics. Most obviously, you use knowledge of the discipline of evolutionary biology. You also use pedagogical content knowledge (PCK). PCK combines content knowledge of a specific topic with knowledge about how students will interact with that topic as they learn (Magnussen et al., 1999; Park & Oliver, 2008; Gess-Newsome, 2015). Most often we build PCK through teaching experience, but could we also benefit from the published work of veteran evolution instructors and education researchers? We think so. Our aim in this article is to guide you to recognize the PCK that you may already have and to encourage you to capitalize on collective knowledge to continue to build PCK for teaching topics in evolution.

You have been using and building PCK since you started learning to teach. For example, imagine you pose this question to your students and they write down their thoughts: “A species of fish lacks fins. How would biologists explain how a species of fish without fins evolved from an ancestral fish species with fins?” (Nehm et al., 2012). Now reflect: What kinds of answers do you

expect from your students? Could you predict a difficulty your students would have with this question? Maybe you predicted that undergraduates would have a much harder time answering this question accurately than one about how traits become common through natural selection (Nehm & Ha, 2011). Or maybe you thought about how students would be likely to explain that fins evolved away because the fish didn’t “need” them anymore (Bishop & Anderson, 1990). If so, you were relying on PCK for teaching natural selection.

PCK is central to many parts of teaching. We use PCK when we decide what learning objectives for a topic are important and reasonable for students to achieve and what objectives are less crucial and can be cut if we run out of time. We employ PCK when predicting what makes a topic particularly hard to learn and where students might get stuck. During instruction we use PCK when drawing on specific analogies, visual representations, or activities that we know are useful in helping students construct accurate understandings. Additionally, we rely on PCK when writing in-class questions and exam questions that reveal what students actually know about a topic. Importantly, what is challenging about learning (and therefore teaching) one topic is often entirely different than what is challenging about learning the next topic, so we depend on distinct PCK for each topic we teach.

As a result, the body of PCK we need as evolution instructors is staggering! What if we could supplement our personal PCK by drawing on the collective knowledge others have already built through experience and research? This knowledge can be referred to as “collective PCK.” Collective PCK is generated by researchers and instructors and made publicly available for others. We have taken steps to make collective PCK in peer-reviewed literature more readily available. We hope this makes it more useful to college and AP Biology instructors at all career stages.

We created a searchable file that organizes over 400 peer-reviewed papers about undergraduate and high school evolution instruction from over 40 different journals (see <https://www.lifescied.org/doi/suppl/10.1187/cbe.17-08-0190>). You can read more

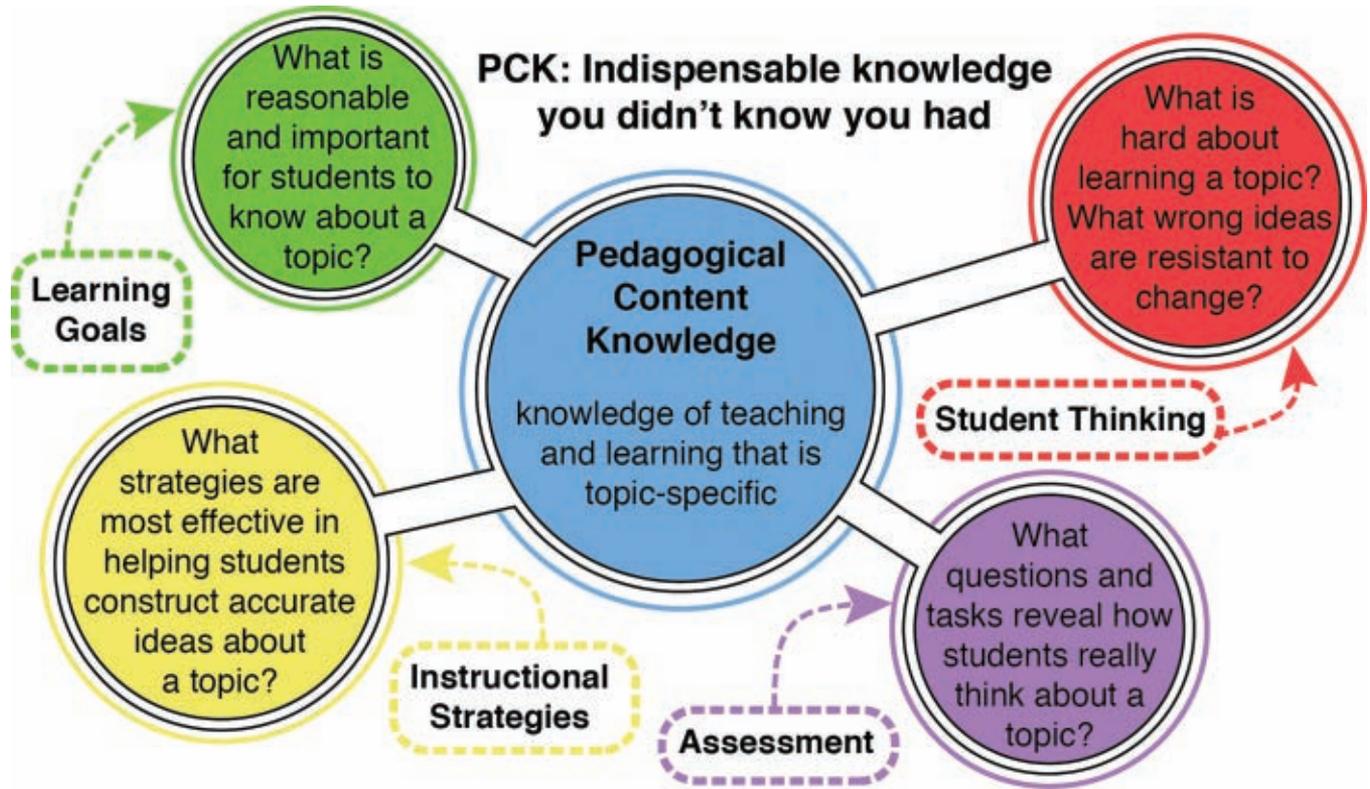


Figure 1. Pedagogical content knowledge: the indispensable knowledge you didn't know you had.

about how we identified, screened, and analyzed these papers in Ziadie & Andrews (2018). None of us have time to read 400 papers to inform our teaching, so here are some tips to maximize your use of this collective knowledge in the time you have available.

○ **Tip 1: Use the Searchable File to Strategically Identify Peer-Reviewed Papers That Meet Your Specific Needs**

The searchable file organizes each paper by several characteristics so that you can find just what you are looking for. Papers are organized by the area of instruction (student thinking, instructional strategy, assessment, learning goals), the type of work (empirical, descriptive, author's perspective, literature review), evolution topic(s) (e.g., genetic drift, speciation, population genetics, human evolution), publication year, and journal. For example, if you are preparing to teach a lesson about phylogenetics and you want an evidence-based activity to challenge your students, you can sort the file by "phylogenetics," "type," and "instructional strategies." You would find eight papers that describe empirical investigations (i.e., type = empirical) of an instructional strategy for teaching phylogenetics to undergraduates and another 24 papers that describe instructional strategies but do not investigate their effectiveness (i.e., type = descriptive). This searchable file is freely available as a supplemental material with Ziadie and Andrews (2018) at <https://www.lifescied.org/doi/10.1187/cbe.17-08-0190>.

○ **Tip 2: Prioritize Papers about Student Thinking**

An awareness of how students are likely to think about a topic is central to all facets of teaching. Knowing what prior ideas students will have and what difficulties they may experience as they learn a topic will help you design student-centered learning objectives, assessments, and instruction. There are different types of work that present collective PCK about student thinking. We recommend starting with literature reviews, which condense what researchers have discovered and thus provide high return on invested time. For many evolutionary topics, there have been too few empirical investigations of undergraduate thinking to warrant a literature review (Ziadie & Andrews, 2018). In those cases, there is significant value in reading a single study that describes in detail the ideas students commonly have about a topic.

○ **Tip 3: Not Sure Where to Start? Here Are Five Papers That We Highly Recommend**

- *Gregory (2009)*. Though natural selection seems logical – even intuitive – to a biologist, it is consistently challenging for undergraduates to learn. Many students retain major misconceptions about natural selection, even after carefully planned instruction

(e.g., Nehm & Reilly, 2007; Andrews et al., 2011). This literature review summarizes the specific difficulties students encounter in learning natural selection. This is particularly useful because the misconceptions that students invoke as they think about other topics, such as genetic drift and evolutionary development, are often rooted in misunderstandings of natural selection (Andrews et al., 2012; Hiatt et al., 2013; Price & Perez, 2016).

- *Gregory (2008)* and *Meisel (2010)*. Being able to read phylogenetic trees is a key step in developing understanding of evolutionary relationships. It is also very hard. Without targeted instruction many students leave college courses unable to interpret even simple trees (e.g., Novick & Catley, 2007). For example, students often think that the order of terminal nodes in a tree indicates relatedness and so assume that two nodes that are physically closer to each other are more closely related (Baum et al., 2005; Meir et al., 2007). Gregory (2008) reviews accurate and inaccurate ways to read phylogenetic trees and describes common misconceptions. Meisel (2010) focuses on the two most common misconceptions and suggests approaches to helping students overcome these challenges.
- *Mead & Scott (2010a)* and *Mead & Scott (2010b)*. Terms used in evolutionary biology often have different meanings in everyday life. For example, scientists use the term *random* to refer to unpredictability of a given event but students often interpret *random* to mean purposeless or meaningless. In fact, it is common for students to think that random processes are not important in biological systems (Garvin-Doxas & Klymkowsky, 2008). This two-part essay series highlights problematic terms in teaching evolution and suggests research-based solutions. Keeping in mind how the terminology we use might be heard by students prevents inadvertently promoting inaccurate ideas.

○ Tip 4: Create Opportunities to Learn from Your Students

What topics are particularly difficult for your students? Do you know why they struggle? Pick a topic that you expect to be challenging and that you would like to rethink in your teaching, and use your students as confidential informants to learn how they think about this topic. You can learn about student thinking in class by asking all students to write a response to an open-ended question on notecards (Angelo & Cross, 1993). A quick read through these cards will reveal a wide variety of thinking and some patterns that you might not anticipate. You can learn even more in conversations with students. Invite students with a range of performance to office hours and ask them probing questions with the goal of uncovering their thinking. Some prompts that we find useful are “What do you mean when you say...?” and “Tell me more about that.” It is also informative to ask students to discuss how one concept relates to another. Try to get a complete picture of what a student is thinking before giving any feedback. You may be surprised by how much you learn!

○ Conclusion

Our work focused on cognitive components of evolution education rather than work related to students’ beliefs, acceptance, and attitudes

regarding evolution. We recognize that such work can be highly valuable to instructors, but it was outside the scope of the research that produced the searchable file. We recommend a recent essay that presents a framework, reviews relevant research, and recommends teaching practices to reduce perceived conflict between evolution and religion and increase acceptance of evolution among students (Barnes & Brownell, 2017).

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The NABT Nominating Committee is looking for your recommendations for our next leaders.

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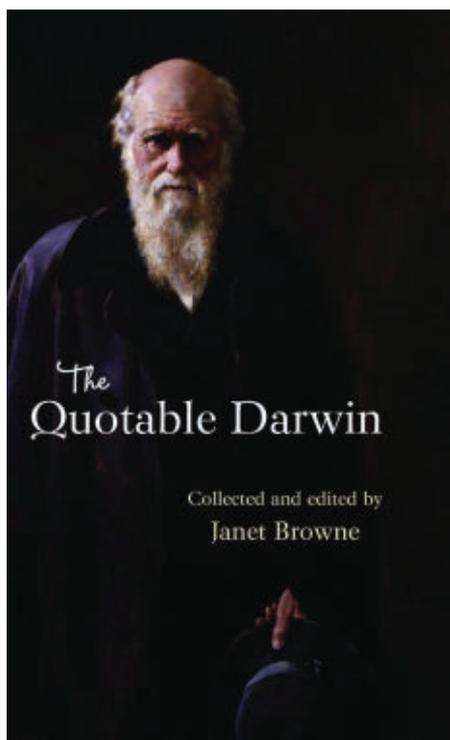
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EVOLUTION SPECIAL EDITION

Editor's Note: For our special issue on Evolution commemorating the birth month of Charles Darwin, this column features several recent publications centered on evolution, Darwin, and related topics.



A DEEPER PERSPECTIVE ON DARWIN

The Quotable Darwin. Collected and edited by Janet Browne. 2018. Princeton University Press. (ISBN 9780691169354). 348 pp. Hardcover, \$24.95.

This book is an essential addition to the collection of any person who studies evolution or takes an interest in the history of evolutionary study or Darwin himself. A somewhat small and

pleasantly unassuming text, it represents the life of Darwin through his own words, from writings, publications, correspondences, and other sources. Following him from the earliest days of his life to his explorations on the *Beagle* and through his later years in research and the synthesis of his positions, Browne has captured the essence of Darwin in a way that few besides hardcore Darwin scholars could.

Appropriate for scholar and casual reader alike, the book presents Darwin in all his many roles – young man, student, family man, adept scholar, and conscientious thinker. While many of us speculate about Darwin's thinking from an exterior perspective, he comes to life in these pages as we view his concerns, troubles, joys, excitement, and considerations of science through his own lens.

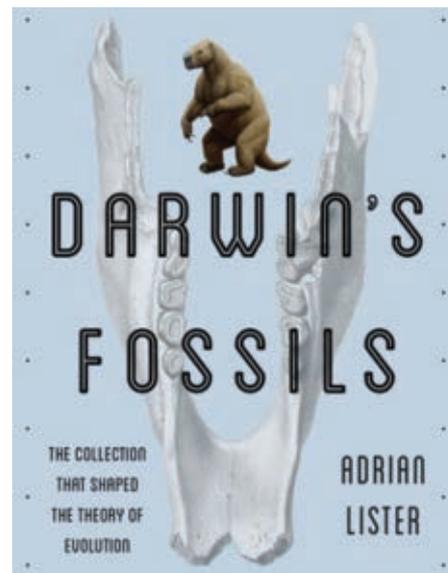
The structure of the book itself is useful, gathering the chapters into six sections: “Early Life and Voyage of the *Beagle*,” “Marriage and Scientific Work,” “Origin of Species,” “Mankind,” “On Himself,” and “Friends and Family.” Each section contains a number of subdivided chapters that address contributing elements to those areas of his life. I personally found this layout to be both easy to navigate and useful, in that I have read through the book as a whole but also have moments when I like to peruse specific sections, according to my thoughts that day or my preparations for class. The format lends itself equally well to either approach.



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DARWIN'S SUPPORTING EVIDENCE

Darwin's Fossils: The Collection That Shaped the Theory of Evolution. By Adrian Lister. 2018.



Smithsonian Books. (ISBN 978-1588346179). 160 pp. Softcover, \$19.95.

Adrian Lister's new book offers an excellent account of the thrust of scientific discovery as it developed within Darwin during his formative years, complete with ample and detailed photographs and artwork of fossil specimens collected by the eminent scientist during the voyage of the *Beagle*. These fossils, collected over a span of five years, were pivotal in the argument for natural selection and the writing of *On the Origin of Species by Means of Natural Selection* (Darwin, 1859). Lister also offers insight into the process and the adventure of scientific thinking and discovery.

In the chapter “The Making of a Naturalist,” the reader learns about the training Darwin received that led to his position aboard the *Beagle*. Upon arrival in South America, he set upon a series of excursions focused on geological inquiry and fossil collection. The book's detailed maps of the *Beagle*'s voyage are magnificent, and the photographs of Darwin's colleagues and mentors are crisp.

Lister discusses several significant finds of extinct mammals, discovered by Darwin during extensive, rigorous, and grueling hiking excursions. Of all the mammal specimens, the giant ground sloth *Megatherium* and the giant hoofed mammal *Toxodon platensis* take precedence, not only due to their size and preservation but for the impact on Darwin's acceptance of transmutation.

A section on petrified forests describes Darwin's hike through the Andes to Agua de la Zorra, where he discovered a gigantic fossilized forest: *Agathoxylon* stumps up to 6½ feet (1.98 m) tall spanning a large area, dating to the Middle Triassic, were well preserved and far predated the formation of the Andes. The position, angle, and location of the stumps solidified Darwin's awareness of past environments and geological change over time. He also collected numerous leaf impressions, imperfect coal, and other petrified wood gathered from South America and Oceania, all consistently found in locations that were clearly inhospitable to supporting such biota at the time.

Darwin was also inspired by the ample marine fossils found in shell-bed elevations far from present coastlines. The variety of invertebrates and vertebrates at stratified positions allowed him to understand the former uplift of the land at various points in South America. One of the many notable examples is when he found marine sedimentary rock and bivalves at the top of Piuquenes pass, over 13,000 feet (3962 m) in elevation. This awareness of geological movement and fossil specimen location heavily influenced his appreciation for geological change over time.

Upon his return from the voyage, Darwin spent time presenting his findings at scientific organizations in London. Indicative of his thought processes at the time were cautious declarations of biological diversity and extinction in relation to environmental pressure. Lister presents quotations that illustrate the development of the theory of evolution, with respect to the dialogue between Darwin and Alfred Russel Wallace in the 1850s. The publication of *On the Origin of Species* in 1859 solidified the foundation of the theory, reinforced in following years by many key fossil finds by others. This collection of fossils by Darwin and others offered prima facie evidence for evolution and supported the formation of the theory of evolution by means of natural selection.

As Lister's book illustrates, Darwin created a model for scientific discovery, a process that we continue to emulate nearly two centuries later. His impact stretches beyond a greater understanding of the world around us, creating a standard for how to conduct research through rigorous immersion in fieldwork and judicious discovery. Lister also shows the importance of the collaborative

efforts of Darwin's colleagues and their debates over his finds.

This book is perfect for casual reading and is an important resource, particularly when paired with Darwin's account of the voyage (Darwin, 1840). The text is peppered with the right amount of insets regarding geological and historical information. The book would also be an excellent companion to introductory biology coursework. The combination of a low price, superb organization, effective writing, and excellent illustrations offers students new to the field of evolution insight into the workings of scientific processes, the foundation of evolutionary theory, and the excitement of scientific discovery. Instructors of introductory biology and/or evolution would prompt student engagement and success by adding this book to their course.



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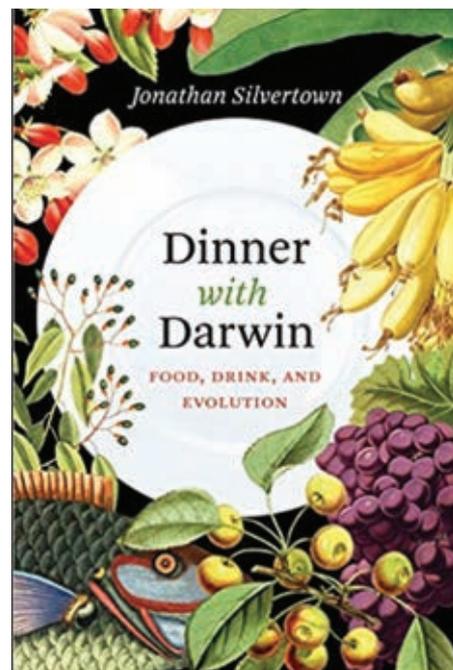
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EVOLUTION IN OUR EVERYDAY LIVES

Dinner with Darwin: Food, Drink, and Evolution. By Jonathan Silvertown. 2017. University of Chicago Press. (ISBN 978-0-226-24539-3). 232 pp. Hardcover, \$27.50.

Nothing brings people together these days quite like good food and good company. *Dinner with Darwin* does an incredible job of inviting the reader to dinner but with a heavy side of science, specifically evolution, and does so in such a way as to invite Darwin himself to your table for

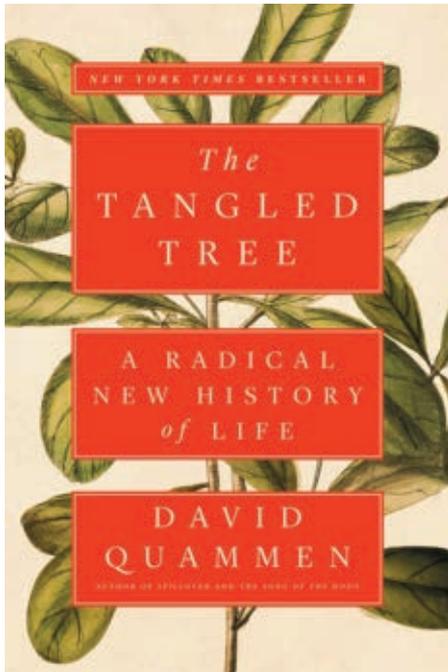


a deeper conversation. While the book is not a collection of recipes and aperitifs, it weaves a story line through the evolutionary history of much of the food and drink we enjoy. The chapters run like courses at the table, addressing the cook and guests ("A Cooking Animal," "Feasting") as well as the courses that have become staples at the modern table (shellfish, bread, soup, desserts, wine, etc.). Each is written through an evolutionary lens of discovery and development, answering the questions of where our tastes for these elements originated, the pathways by which we have learned our trades in food, and the mechanisms that drive some of the traits that make our choices unique.

I love the concept of "evolutionary gastronomy" because food truly is something that brings people together. As I was reading this book, I was able to share a good deal of it with my two sons (self-proclaimed foodies), talking about the scientific background of the things we ate as we traveled, and about how humans have changed along with our diet and command of elements in nature through breeding, domestication, and habits. In those interactions (my boys are seven and 17) I could really see the application of the chapters to conversations with my students across the spectrum of ages and how each part tells a little bit of our story as well as the role of science in our history and daily lives. I must also add that as a person who frequently has these wandering scientific conversations with colleagues and friends over dinner, this book has greatly expanded my own repertoire of topics!



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REVISITING OUR EVOLUTIONARY UNDERSTANDINGS

The Tangled Tree: A Radical New History of Life. By David Quammen. 2018. Simon & Schuster. (ISBN 978-1476776620). 420 pp. Hardcover, \$30.00.

As a biology teacher and an evolution educator, I needed this book. For those of us who teach in the K–12 universe, our understanding and consequently our teaching of evolution can tend to be slow to evolve as the resources we use to teach

evolutionary concepts are themselves slow to embrace new advances in the field. In the world of teaching introductory evolution, a comprehensive view of evolutionary thinking is likely to include an overview of classic Darwinism followed by a connection to the Modern Synthesis and a mention of modern DNA sequencing as it lends support to ideas of species' common ancestry as part of the tree of life.

In *Tangled Tree*, David Quammen tells the next chapter in the development of evolutionary theory as he relates the groundbreaking work of Carl Woese and a wealth of other microbiologists. Woese is best known for his work describing and placing the Archaea into the updated three-domain, six-kingdom system of taxonomy, but he remains largely unknown to the vast majority of biology students. This deeply researched and richly written book seeks to change that and make sure that readers never forget this seemingly overlooked biologist from Urbana, Illinois.

Quammen gives his readers valuable background about the early days of evolutionary theory and the development of the “tree of life” metaphor. He provides us with strong historical descriptions of how “tree thinking” came to dominate evolutionary thought, which sets the stage for Woese and colleagues' discoveries that in addition to the verticality of nuclear gene transfer from generation to generation, there is also a mechanism that allows genes to move horizontally *between* species. This horizontal gene transfer serves to modify the metaphorical tree into more of a web, with both vertical and horizontal phylogenies for many species. This conceptual revolution gives *Tangled Tree* its name.

In addition to its detailed presentation of the science behind horizontal gene transfer and a new phylogenetic view of the tree of life, *Tangled Tree* illustrates the ways in which modern biology now works. Quammen's storytelling does a

stellar job of showing us that current research is more than mundane lab work. He details the relationships and inspirations not only of Woese, but of his extended community of collaborators and colleagues who encouraged and challenged each other to expand our understanding of this new field of evolutionary thought. Indeed, this book is a great reminder that science, as a way of knowing, is influenced greatly by the human strengths and weaknesses of those doing the science.

All of us who teach evolution in our classes would do well to read *Tangled Tree* so that we update and deepen our understanding of both the history of evolutionary thought and the diversity of all current life on Earth. This is a fine work that addresses both the *natural* and the *history* in natural history.



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CourseSource: Evidence-Based Teaching Resources for Undergraduate Biology Education
(<https://www.coursesource.org/>)

Inspired by national reports like *BIO 2010* and *Vision and Change*, which call for reformation in undergraduate biology education, *CourseSource* provides tools for faculty teaching life sciences who want to increase student learning. The developers of *CourseSource* recognize the tremendous time and effort it takes to change a biology curriculum. Moreover, they understand that some faculty want the freedom and flexibility to modify aspects of their course rather than changing everything all at once. Designed with these concerns in mind, *CourseSource* offers a variety of useful resources that allow you to improve your teaching style your way and at your own pace. More importantly, the resources hosted on the website have been peer reviewed by real faculty working in a variety of contexts.

Whether you teach introductory biology, genetics, or bioinformatics, *CourseSource* has materials that will help you grow your communication skills, engage your students, and inoculate excitement into the content. Faculty can browse the resources using a variety of categories that include class size, *Vision and Change* core concepts, lesson length, and pedagogical approach. These categories can also be used as filters to narrow down resources. Included are everything from simulations to education essays, and even unexpected materials like a guide for using Wikipedia in the classroom, tips for teaching biology in prisons, and a “how to” guide for producing recorded interviews.

Clicking on a resource, like “A First Lesson in Mathematical Modeling for Biologists: Rocs,” reveals a follow-up page that presents an “At a Glance” overview of the activity. Tabs along the top of the page give the user the freedom to look at the materials

themselves, and to access supporting materials, information about the authors, comments from other users, and additional references and resources. Metadata can also be found, including the number of times each particular resource has been downloaded. For the experienced reformers, faculty are invited to register on the site and upload their materials for others to use.

Other life sciences education websites exist, with archives of resources that sit useless and used less over time, but *CourseSource* differs from all these in one very important way: curation. The resources offered have been carefully vetted, curated, and tailored by practicing faculty who understand the day-to-day challenges of teaching in higher education. These down-to-earth materials will empower you to transform the lives of your students, setting them up for success in future courses and ultimately in their careers.

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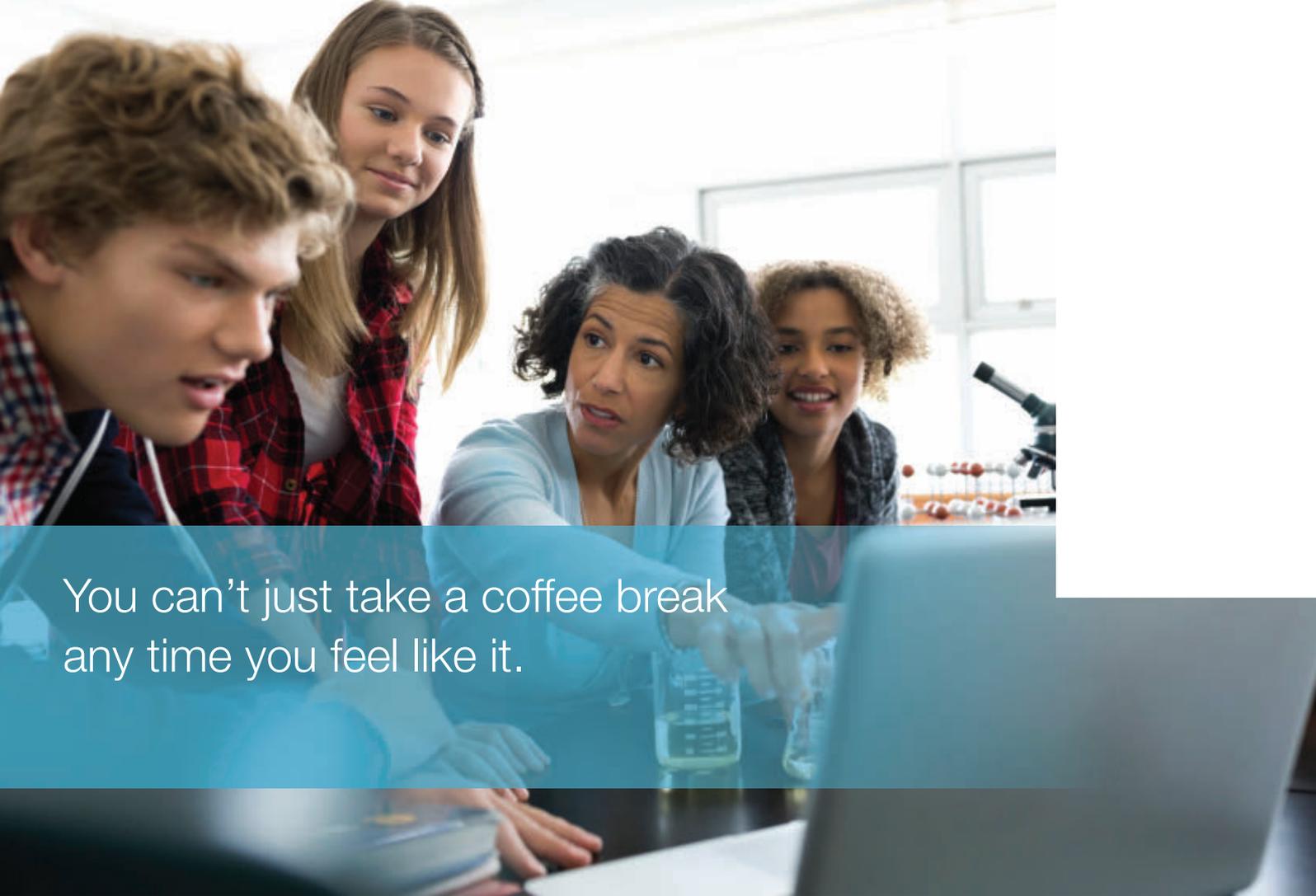
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