Research Article

Long-Term Conceptual Retrieval by College Biology Majors Following Model-Based Instruction

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Abstract: One of the goals of college-level introductory biology is to establish a foundation of knowledge and skills that can be built upon throughout a biology curriculum. In a reformed introductory biology course, we used iterative model construction as a pedagogical tool to promote students' understanding about conceptual connections, particularly those linking genetic variation to organismal fitness. In interviews conducted 2.5 years later, we examined students' retrieval of conceptual connections emphasized during the course. Students constructed a model similar to those practiced during the course, reviewed their models with the interviewer, and answered questions about how they retrieved this knowledge conceptual understanding. Student proficiency on this task was evaluated based on the quality of their modeling and responses to questions about their models. Three distinct groups emerged: students that had an inadequate cognitive structure for the biological concepts (absent), and students that had incomplete or complete cognitive structures. Students in the Complete group were better able to verbally link genetic variation to phenotypic variation and differential fitness and successfully used relationships stored in their cognitive structure to explain gaps present in their drawn model. Students in the Incomplete group had fragmented knowledge where some concepts were connected to each other, but not to the whole model. Students in the Absent group had extensive gaps in knowledge and were unable to connect their conceptual ideas. Students who were most proficient in the task differed in their ability to access and search within their cognitive structure and verify the quality of their conceptual relationships. This allowed the most proficient students to fill in knowledge gaps and transfer their conceptual understanding to new contexts. © 2015 Wiley Periodicals, Inc. J Res Sci Teach

Keywords: undergraduate; postsecondary; modeling; cognitive structure; genetics; evolution

Retrieving knowledge from long-term memory is a cognitively intensive process consisting of global and local searches for relevant ideas and their verification. Knowing how a student in a classroom retrieves knowledge related to a discipline is essential for designing instruction that will effectively teach that knowledge.

How students search for information related to course content might be best thought of through the following analogy—imagine opening your computer file manager (e.g., Windows Explorer or Apple Finder) and sorting by the date that files were modified or created, and locating

files last accessed about 2 years ago. Those files likely contain pieces of semantic knowledge (discipline-specific or content knowledge) from that time. The knowledge may have been related to a new set of data, or knowledge formed by connections among existing data, like the construction of results for a manuscript. There are likely to be parts of these files that are nearly unintelligible upon initial inspection as you search your memory for the context that gave rise to these new data. As you glance at those files, you will probably remember how they fit into a manuscript you were writing, a research protocol, administrative tasks, etc. Some of those files may even contain pieces of knowledge that you can't remember how they are connected to anything. Two years is a long time to recall semantic knowledge when observed out of context. However, if you organize files in meaningfully named folders, you can immediately give yourself a context from which to view files within these folders. This organization of knowledge helps strengthen the coherence of the connections between the units of knowledge.

Students are regularly asked to perform this very task: recall knowledge from their distant past, possibly without context, often with mixed results. Some students may have organized their knowledge and others may have stored the knowledge in isolation. Instructors frequently assume students have effectively organized and stored knowledge they learned weeks, months, or even years ago. It is a goal for teachers, either explicitly or implicitly, to improve students' knowledge storage, subsequent retrieval, and application to new scenarios, even when the time frame for retrieval extends beyond the next course exam.

Cognitive psychologists have long investigated what knowledge students store and how they retrieve it. Our research is informed by this work and examines how students retrieve biological knowledge over long time periods. We explore students' cognitive structures (CS) which act as "building blocks for meaningful learning and retention of instructional materials" (Ifenthaler, Masduki, & Seel, 2011, pg. 41). The CS, also called a knowledge structure, represents students' organization of biological concepts stored in their long-term memory (Ifenthaler, 2011; Ifenthaler et al., 2011; Jonassen, Beissner, & Yacci, 2013).

In an interview setting, we challenged students to recall biological concepts from their CS. Our research questions focus on students' abilities to successfully navigate a retrieval cycle (Williams & Hollan, 1981), where students search for a relevant CS, search within that CS for related biological knowledge, and verify the quality of the model and relationships therein. We use model construction as a visual representation of students' CS and therefore the foundation for the exploration of students' biological knowledge.

Theoretical Framework

Cognitive Structures and How they are Stored

It is critical to understand how students store knowledge since this guides their retrieval of knowledge. The CS exists in the long-term memory and can be used as a foundation for a mental model in the working memory to be accessed during problem solving and modeling (Shell et al., 2010). As students acquire new knowledge about a concept, they attach and organize it relative to other concepts in their CS (Rumelhart & Norman, 1978). As knowledge accumulates, it may become necessary to reorganize the CS in ways that are meaningful and that enable explanation about new and changing relationships among concepts. Ifenthaler et al. (2011) suggests that learning is the expansion and connection of existing CSs with domain experts having more links and better grasp of how knowledge/concepts/schema are linked.

Students regularly store knowledge as verbal representations (Clariana, Wolfe, & Kim, 2014) which can be retrieved in formats like a written response or oral explanation. Storing knowledge as a visual representation in addition to the verbal representation (i.e., dual coding), may enhance

retrieval (Paivio, 1990) when it is advantageous for students to retrieve knowledge from both representations. Therefore, a well-defined CS comprised of both verbal and visual representations will provide multiple access points (both verbal and visual) to concepts that reside therein (Schnotz & Bannert, 2003). For example, if a student can't recall a particular concept, they may deduce it if the portion of their CS they successfully retrieve, in visual or verbal format, reveals the organization of concepts related to it. Therefore, visual representations, such as conceptual models, may enable students to use structural cues to assist in organizing, storing, and subsequently retrieving knowledge.

CSs may be domain specific (Ifenthaler, 2011) with large differences in semantic knowledge for each domain. In a comparison of the CSs of university students in biology, history, and math, Ifenthaler (2011) noted the CS for biologists was larger, more integrated, and more web-like relative to the other disciplines. The continued accumulation of biological knowledge into an already large CS may require a reorganization of the cognitive structure, which, ideally, will emphasize the critical knowledge of the field. We assume that certain CSs within biology are fundamental to a student's understanding of the discipline and will therefore be the ones most frequently accumulating knowledge due to content coverage in other biology courses. Examples of elemental CSs for biology might include central dogma, the origin and expression of genetic variation, and principles governing form and function (e.g., conservation of matter and energy).

Retrieval of Cognitive Structures

How we search for and retrieve knowledge over long time periods is complex and impacted by many factors. Our understanding of how people obtain knowledge from their CS is guided by research on the retrieval cycle (Williams & Hollan, 1981). In this model, people generate an entry point, use this to access a CS, discriminate among similar CSs, and then recursively elaborate on the CS composition (components and relationships) (Reiser, Black, & Abelson, 1985; Williams & Hollan, 1981). Since it is a recursive process, each search for or search within a CS provides some information that further directs successive searches (Kolodner, 1983). These searches are likely to be global first (search for the CS) followed by local iterative searches (search within a CS) until the knowledge connections are exhausted (Hills, Jones, & Todd, 2012). Within this large umbrella of global then local searches, there exist myriad searching strategies like recalling the context during storage or recalling the activity that facilitated knowledge storage (Reiser et al., 1985; Williams & Hollan, 1981). While many of the early studies on retrieval focus on autobiographical or episodic knowledge, we assume semantic knowledge retrieval will be similar (Shell et al., 2010).

As students store knowledge in a CS, repetition strengthens connections among concepts within the CS (Shell et al., 2010). The strength-dependence assumption (Anderson, Bjork, & Bjork, 1994) states that the strength of relationships among concepts will be reduced within a students' CS unless they are accessed frequently (Shell et al., 2010). Remembering knowledge through repetition stabilizes the knowledge within the CS (Carpenter, 2011; Roediger & Karpicke, 2006) and also induces the forgetting of competing memories (i.e., knowledge weakly connected to the CS) (Wimber, Alink, Charest, Kriegeskorte, & Anderson, 2015). Therefore, repetition of concepts, and more importantly relationships, during learning tasks should enhance retrieval of connections over the long term.

Visual and structural cues associated with verbal knowledge may also assist in retrieval. Conjoint retention theory associated with map learning (Kulhavy, Stock, & Kealy, 1993; Verdi & Kulhavy, 2002) suggests learners develop an intact image that allows them to later retrieve that image with the structural information retained. Biology has an abundance of representational and pictorial images that must be interpreted by students for the knowledge to be stored in memory (Griffard, 2013). Griffard reports on the importance of colors and shapes and allude to the role of

spatial positioning as a way of "decoding" images. We assume students are storing at least some structural and visual knowledge along with their verbal knowledge (Schnotz & Bannert, 2003). As with other semantic knowledge, repeated storage and retrieval of this knowledge will likely strengthen the structural knowledge and facilitate retrieval of both the structural and verbal knowledge (Paivio, 1990; Verdi & Kulhavy, 2002).

Representing Cognitive Structures

Modeling emphasizes a particular way of constructing and representing knowledge where a concept is known through its connections to other concepts and the product (model) provides a visual representation of a portion of the student's CS (Nesbit & Adesope, 2006). Thus, student-constructed models provide insight into student thinking and emphasize the process by which students search for, search within, and represent their CS (Hay, Kinchin, & Lygo-Baker, 2008; Ifenthaler, 2010; Shavelson, Ruiz-Primo, & Wiley, 2005). Building models of biological systems can promote students' ecological literacy (Long et al., 2014) and systems thinking skills (Tripto, Assaraf, & Amit, 2013; Vattam et al., 2011), and serves as a foundation for accreting and connecting new biology knowledge (Dauer, Momsen, Speth, Makohon-Moore, & Long, 2013).

Structure-Behavior-Function (SBF) theory serves as a useful organizing framework (Goel & Stroulia, 1996; Hmelo, Holton, & Kolodner, 2000) for teaching, discussing, and evaluating student-constructed models of biological systems. In this framework, models are comprised of *structures* (i.e., concepts, commonly nouns) placed in boxes and connected by *behaviors* (i.e., relationships or mechanisms, commonly verbs) placed on arrows (see Figure 1). Collectively, the model describes a *function* (i.e., purpose or output). SBF-based system models resemble concept maps (Novak & Canas, 2006; Vattam et al., 2011) but are constrained by their role in describing a system function and do not require hierarchical interpretations (Jonassen, Strobel, & Gottdenker, 2005).

Prior work with models (Dauer et al., 2013), concept maps (Mintzes & Quinn, 2007), and retrieval practice (Blunt & Karpicke, 2014; Karpicke & Blunt, 2011) all show short-term improvements in students' retrieval of discipline-specific knowledge, but retention of knowledge
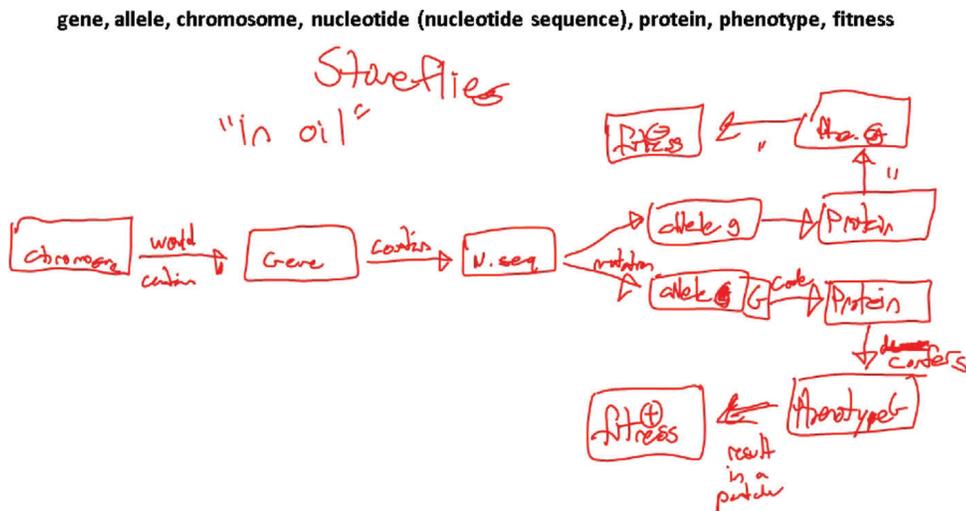

Figure 1.   Example of student-constructed model that was supposed to show the origin of genetic variation, how genetic variation affects phenotypic variation, and how phenotypic variation affects fitness. Students were provided with certain concepts: gene, allele, chromosome, nucleotides, proteins, phenotype, and fitness.

and/or skills beyond the duration of the course is largely unexplored. In this study, we build upon our prior findings on short-term patterns and model attributes (Dauer et al., 2013) and examine students' long-term abilities to retrieve and represent their CS related to elemental biological concepts. We ask three questions related specifically to the retrieval cycle (Williams & Hollan, 1981):

1. How do students access their cognitive structures for focal concepts from a course 2.5 years prior?
2. How do students search within (and retrieve elements of) their cognitive structures?
3. How do students verify the quality of relationships within their cognitive structures?

We seek to extend our understanding of retrieval by situating our research in the domain-specific context of college-level biology and by exploring retrieval mechanisms over a much longer time period than most studies to date. Data that clarify how students access, search within, and verify their cognitive structures have important implications for research, instruction, and assessment in biology and across STEM. Knowing how students retrieve knowledge can inform research on how and when students stored the knowledge, how to assess the quality of a students' cognitive structure, and how students use biology cognitive structures to answer questions and make biologically sound decisions.

Methods

Population

Think aloud interviews were conducted in November 2011 and targeted students that had been enrolled 2.5 years prior (Spring semester 2009) in 1 of 3 sections of a model-based version of introductory biology ($n = 516$). This time interval captured students just prior to graduation. Participants were selected from an open solicitation, ensuring equal representation from each of three tritiles ($n = 30$, 10 per tritile) determined by students' GPA upon enrollment in introductory biology. Tritiles are defined as: Lower (L) = GPA <2.89; Middle (M) = GPA between 2.89 and 3.46; Upper (U) = GPA >3.46. Students had diverse majors at the time of the interview; 63% could be classified as Science, Technology, Engineering, or Mathematics (STEM) majors (as defined by the U.S. Immigrations and Customs Enforcement). Students were compensated for their participation.

Course Content and Emphasis on Modeling

In this study, we focus on students previously enrolled in a 1-semester (15 week) introductory biology course with content from genetics, evolution, and ecology. A primary goal of instruction was for students to develop understanding about conceptual connections linking genetics and evolution—two sub-disciplines of biology considered independently challenging. Learning genetics, for example, requires acquisition of a complex vocabulary, mathematical reasoning, and multi-level thinking (Bahar, Johnstone, & Hansell, 1999; Duncan & Reiser, 2007; Marbach-Ad & Stavy, 2000; Shea, Duncan, & Stephenson, 2014). Students' struggles with explaining evolution are similarly well-documented and typically consist of a mix of correct key concepts, naïve ideas, and cognitive biases (Bray-Speth, Long, Pennock, & Ebert-May, 2009; Catley & Novick, 2009; Morabito, Catley, & Novick, 2010; Nehm & Reilly, 2007; Nehm & Ridgway, 2011). To connect genetics and evolution requires comprehending interactions that occur across molecular, cellular, and organismal levels of hierarchy (Tsui & Treagust, 2013) and that operate on different scales of space and time. Many students in introductory biology are unable to explain, or to represent in a

model, the origin of genetic variation that is essential for mechanistic understanding of evolution by natural selection (Bray-Speth et al., 2014).

The course was explicitly designed to engage students in modeling exercises that repeatedly elicited their gene-to-evolution (GtE) CS in order to improve and strengthen relevant relationships within and between genetics and evolution (Bray-Speth et al., 2014; Kalinowski, Leonard, & Andrews, 2010). Several times throughout the course, students were asked to show, in a single model, (i) how variation arises in a genome; (ii) how variation at the molecular level has consequences for traits expressed by organisms; and (iii) how resultant variation among organisms can interact with environmental variables, resulting in population-level change. Students constructed models illustrating these three functions for multiple scenarios as a component of in-class activities, homework, quizzes, and exams. Students received feedback from instructors through online rubrics, directed discussions around sample models, and organized group activities.

Interview Protocol

Students, especially those staying in biology fields, likely further strengthened some of the relationships as they repeatedly accessed portions of their CS for particular courses, such as genetics, evolution, or ecology. However, none of the students in this study reported being asked to construct models in other courses (they were allowed to define models in their own words) resembling the ones constructed in introductory biology. It is therefore likely that interviews conducted for this study represented the first time since their introductory biology final exam where students were challenged to access the CS that connects genetics and evolution.

We conducted 30-minute think aloud interviews in which students orally communicated their thinking and reasoning throughout (Merriam, 2014; Van Someren, Barnard, & Sandberg, 1994). Interviews were video and audiotaped, and the audiotapes were later transcribed. During interviews, students used a tablet computer running Camtasia (http://www.techsmith.com) to record, in real-time, the process of constructing written or model-based responses to interview questions.

The interview had three broad student outcomes—access their CS and knowledge about model construction, create a model representing their knowledge, and compare visual and verbal representations of their knowledge. Our interview protocol was fashioned after the work of Mayer (1996) on how students learn. He suggests that students reading expository text will select relevant knowledge, organize it in working memory, and integrate it with long-term knowledge (Mayer, 1996). Students were afforded the opportunity to practice model construction and to select relevant terms from an expository text in an effort to increase the likelihood of retrieval of their memories (Nuthall, 2000; Williams & Hollan, 1981). We assume that this process initiated accessing their CS. Students then organized the new knowledge from a new scenario and integrated it with their CS pulled from their long-term memory in a visual model. To ensure students provided data that could be used to answer the research questions, we followed the model construction with detailed questioning.

Specifically, our interview protocol consisted of four independent tasks:

1. **Modeling refresher.** Students were reminded about the standards for constructing models (structures in boxes, relationships on arrows, all to show a function) and asked to create a 3-structure model (Cow, Hay, and Milk) with the function of showing how hay becomes cow's milk. No feedback was provided about the quality of student models but the interviewer did clarify directions when asked by the participant. All students remembered constructing similar models during introductory biology.

2. **Extraction.** Students read a short passage that was patterned after cases used during the course. The case described an oil spill that took place 1 year prior to the interviews and had severely contaminated a major river located 1 hour from the university (see Supplemental Appendix A). In this case study, stoneflies (insects) were negatively affected by crude oil released into the river. Some stoneflies were able to survive because they had a genetic mutation that affected the permeability of their exoskeleton. In this way, genetic variation results in different proteins that can affect the phenotype and the organisms' response to a selective agent, the oil. Students were asked to identify and list the important concepts from the description that would allow them to describe how genes can affect organism fitness in the case of the oil spill. This task provided students an opportunity to access their CS and prepared them for the model-building task to follow. We did not ask students to expand on their knowledge of the concepts or ask the student to connect them during this portion of the interview.

3. **Model construction.** Participants were instructed to build a box-and-arrow model specific to the oil spill scenario that included seven genetics and evolution concepts: gene, allele, chromosome, nucleotides, protein, phenotype, and fitness (see Supplemental Appendix A). In their model, students were asked to show the effect of genetic variation on phenotypic variation and effect of phenotypic variation on stonefly fitness. These three functions of the model were also verbally reiterated by the interviewer to reinforce the goal of the task.

4. **Review and reflection.** During this part of the interview, students answered questions about both their procedural and their relational knowledge. Procedural questions were directed at understanding the process students used in assembling their models and included questions such as, "Can you explain why you started with 'gene'?" and "I noticed that you arranged your boxes first, then went back to add arrows. Can you tell me more about that strategy?" Relational questions probed students' conceptual knowledge, for example, "Were you unfamiliar with any of the provided words or relationships among these words?" and "Can you tell me how genes are different from alleles?"

Analysis

Student models were evaluated for biological correctness using a correctness rubric that rated model relationships on a 3-point scale: incorrect (1), plausible but lacking technical clarity (2), and scientifically accurate (3) (Dauer et al., 2013). Complexity was measured using the web-like causality index (Plate, 2010), which is the percent of structures with multiple effects (out-arrows) plus the percent of structures with multiple causes (in-arrows). Model complexity varies from 0 (linear) to 2 (completely interconnected).

In addition to an *a priori* categorization of students by academic achievement (tritile), we also used a constant comparison approach to classify students on the basis of their ability to provide evidence of a correct and coherent understanding of the genetic basis of evolution (see Table 1). Students were classified into one of three groups according to their procedural and relational knowledge in the review task. "Complete" students provided explanations that demonstrated complete understanding of all elements in their constructed GtE model, were able to adapt their explanations to the oil spill scenario, and described how their model represented the prescribed functions. Students were classified as "Absent" if they were unable to verbally produce a coherent explanation of the prescribed functions, poorly defined most or all of the concepts, and were unable to adapt their thinking to the scenario. Students in the "Incomplete" group were able to describe some aspects of the functions but lacked a complete understanding. Students were classified solely on their verbal responses and independent of students' model correctness or complexity, or their tritile in the course. For the purposes of this study, we use the Complete,

Table 1

Categorization of students by completeness of cognitive structure and performance during Introductory Biology

| | Category | | |
	Absent	Incomplete	Complete
Tritile			
Lower	4	4	2
Middle	0	6	4
Upper	5	2	3

Completeness of students' cognitive structures did not align with their performance in the course. Students in Introductory Biology were post hoc binned into tritiles based on performance and ten students per tritile were selected for the interviews.

Incomplete, and Absent categorization to better capture the range of students' skills and knowledge exhibited during the interview and because we observed these categories to be unrelated to measures of prior achievement (i.e., grades or Lower, Middle, and Upper tritiles; see Table 1).

Results and Discussion

Knowledge retrieval consists of both directed and random components (Unsworth, Brewer, & Spillers, 2013). The directed component is the retrieval cycle is searching for a CS, searching within the CS, and verifying the quality of relationships within the CS (Williams & Hollan, 1981). Within the retrieval cycle, there is a random component that is the uncertainty associated with each stage. For example, did I locate the correct CS? Did I locate the correct connections among concepts? Did I determine the relationship that best describes that connection? We report generalized results from the directed component to characterize how Absent, Incomplete, and Complete groups retrieved knowledge similarly within a group. We include examples of variations in responses to show the random component inherent to any student of memory retrieval.

How do students search for a cognitive structure?

The retrieval cycle is initiated when students search for and connect with an appropriate CS to serve their needs. We identified three access points that may support or inhibit the search for the CS. Students may have started with (i) the provided *scenario* to link to their previous understanding of known biological systems; (ii) the *task* of model construction to access procedural knowledge about constructing a model; or (iii) the model *structures* provided in the task (i.e., concepts such as allele, fitness, phenotype, etc.) that link to known content knowledge.

Our data suggest the scenario did not likely facilitate students' search for a relevant CS. During interviews, we asked students to read the scenario quietly, then allowed them to ask any clarifying questions. Only 8 of 20 students indicated that they had heard of the spill (10 were inadvertently not asked, as this question was not part of our original protocol). Of the students explicitly asked, students that were familiar with the oil spill created equally correct ($p = 0.83$) and complex ($p = 0.94$) models compared to those who were unfamiliar. Students' variable knowledge about the oil spill scenario was probably similar to that of students during the course, where some scenarios provided were familiar to some students, but not others. Research by Nehm and Ha (2011) indicates that problem context can affect students' performance, but we are unable

to determine the extent to which familiarity with the provided scenario influenced students' performance on the task or their abilities to retrieve elements of their CS.

Retrieval of the process of modeling (how to represent structures, relationships, and functions) did not contribute to differences in accessing the CS. We asked students about their construction of box and arrow type models in other courses. None reported this as a requirement for other courses suggesting the final exam in introductory biology was the last time they practiced this skill as a summative assessment. All students remembered modeling during introductory biology and most interviewees correctly applied the modeling rules to connect Hay–Cow–Milk. Given the pervasiveness of the modeling practice throughout the course, we were not surprised that students were able to retrieve most or all of the procedural aspects of modeling. In a similar longitudinal study of concept mapping in college-level geology, Mintzes and Quinn (2007) found differences in quality of students' concept maps, but did not suggest students fail to remember the process of concept map construction. Overall, the modeling skill appeared to be largely retained, suggesting this component was not a limiting factor in retrieving their CS or representing it visually during the interview.

Biological concepts were likely the most influential factor promoting students' search for their CS. During interviews, students had two opportunities to interact with concepts as a way of eliciting their CS: first, when asked to extract biological concepts from the prompt, then later when provided with the list of seven concepts they had previously learned and were required to include in their models. During extraction from the prompt, students identified and wrote down the concepts from the scenario that helped them understand how genes could affect fitness. Concepts that were written first included dominant/recessive (referring to gene [$n = 2$], allele [$n = 14$], or genotype [$n = 7$]), permeability (referring to phenotype [$n = 2$]), and the oil spill (referring to the environmental conditions that selected for a phenotype [$n = 3$]). Students more frequently referred to dominant ($n = 12$) than recessive ($n = 2$) while some mention both ($n = 3$). Four students referred to dominant and recessive genes despite dominant and recessive being appropriated to alleles in the prompt, indicating a lack of attention to wording or misappropriation of adjectives in their CS.

Additional evidence further clarifies how students used biological concepts to access their CS. During the review task, we asked students to reflect on the moment when they first encountered the list of concepts and searched for the context for each word. Words that students have repeatedly heard or used in other science courses can likely be recalled easily while unfamiliar words may highlight weak or non-existent connections (Shell et al., 2010). Students reported a diverse set of unfamiliar concepts such as nucleotides ($n = 6$), chromosomes ($n = 5$), and proteins ($n = 5$). More students in the Incomplete group (8 of 13 students) reported unfamiliar terms, followed by the Absent group (3 of 8), and the Complete group (2 of 9). As might be expected, there were different metrics for culling unfamiliar terms that highlights the students' ability to fill in knowledge gaps and deduce the meaning of unfamiliar words. The two students from the Complete group reporting unfamiliar terms (chromosome and nucleotide) proceeded to not only use these terms first in their models, they also correctly connected them into their models. On the surface these terms seemed unfamiliar, but the Complete students were able to actively re-familiarize themselves with the concepts. In contrast, although the Absent students reported a similar number of unfamiliar terms, they were never able to correctly integrate them during model construction or the review task. One of these students never included phenotype in their model, another added fitness second to last, and the third one incorrectly connected chromosome and allele. It is likely that these terms were never connected or weakly connected to the Absent students' CSs. With a single exception, students in the Incomplete group more closely matched the Absent group, incorrectly connecting

their unfamiliar terms or leaving them out altogether. The Complete students report fewer unfamiliar terms, suggesting a more cohesive CS for the provided concepts.

How do students search within their cognitive structure?

After locating the CS in their long-term memory, students begin the process of mental model construction in the working memory by trying to retrieve connected portions of their CS (i.e., retrieve a "chunk" of knowledge; Greca & Moreira, 2000; Johnson-Laird, 1983). An intact CS will allow students to narrow the search for relevant details and focus on the relationships among the concepts that will allow them to describe the prescribed functions (Hmelo-Silver, Marathe, & Liu, 2007). One student described what we believe generally occurs: "[I] have to identify the terms as best I could and try to see which ones I could associate with each other. This is the way I did it when I actually took the class. I never started at the beginning, I picked the terms that I knew and associated them with one another" (stu. 510).

Students appear to build their model in pieces and connect the pieces according to some image or plan in their long-term memory. They reported trying to "organize in my head" (stu. 98), "trying to piece it together in my head" (stu. 119), and "trying to remember my order of hierarchy" (stu. 208). These students hint at having a visual representation of their CS. Others were more explicit about the visual representations that they were drawing upon, "when I think about gene I get the picture of chromosome first. . . I mean it's just the first thing that comes to mind when I think about genes, you see the structure of chromosome" (stu. 443), "in my mind I see how this goes together" (stu. 514), "I am trying to think of the pictures of the nucleotide sequence and what they stand for" (stu. 475). Again, there is not a clear distinction among categories reporting a visual representation of their CS, with two Absent students, four Incomplete students, and two Complete students. Despite arguments that conceptual models do not result in the same dual coding of visual and verbal representations (van Meter & Garner, 2005), responses from college students in our study suggested they were accessing visual representations that took the shape of drawings, textbook visualizations, maps, or representations of boxes connected with arrows as generated during introductory biology (Kulhavy et al., 1993; Nesbit & Adesope, 2006). Whether a drawing or a map, students likely begin by relating a subset of concepts, then use this information to generate progressively more specific information towards the target context or scenario (Halamish, Goldsmith, & Jacoby, 2012; Jacoby, Shimizu, Daniels, & Rhodes, 2005). As their thoughts become more specific to the context, they must decide which relationships have the greatest relevance to their task and what words, from all possible relationships, correctly describe each connection.

After the students have accessed their CS and begun to form a mental model, they begin to draw their model on the tablet. Students' selection of their first word to include in their model appears to set the tone for the rest of their model construction. We observed students connecting terms they reported as "familiar" in the first proposition (structure-behavior-structure), likely because these concepts had the greatest primacy in their CS (Unsworth, 2008). Most commonly, chromosome and nucleotides ($n = 10$ each) were written on the tablet first, while gene ($n = 6$), protein ($n = 3$), and fitness ($n = 3$) were also added first on some models (see Figure 2). Students in all categories used chromosome as the initial word. Students in the Complete and Incomplete groups also commonly started with nucleotides and students in the Absent group also commonly started with gene. The most common connections for the first proposition were chromosome-nucleotides ($n = 7$) followed by chromosome-gene, ($n = 5$), gene-allele ($n = 5$), and nucleotides-gene ($n = 4$). When gene was the first structure in the first proposition, it was always connected to allele (average correctness of 1.8). Overall, there was considerable proposition diversity and few patterns associated with categories.
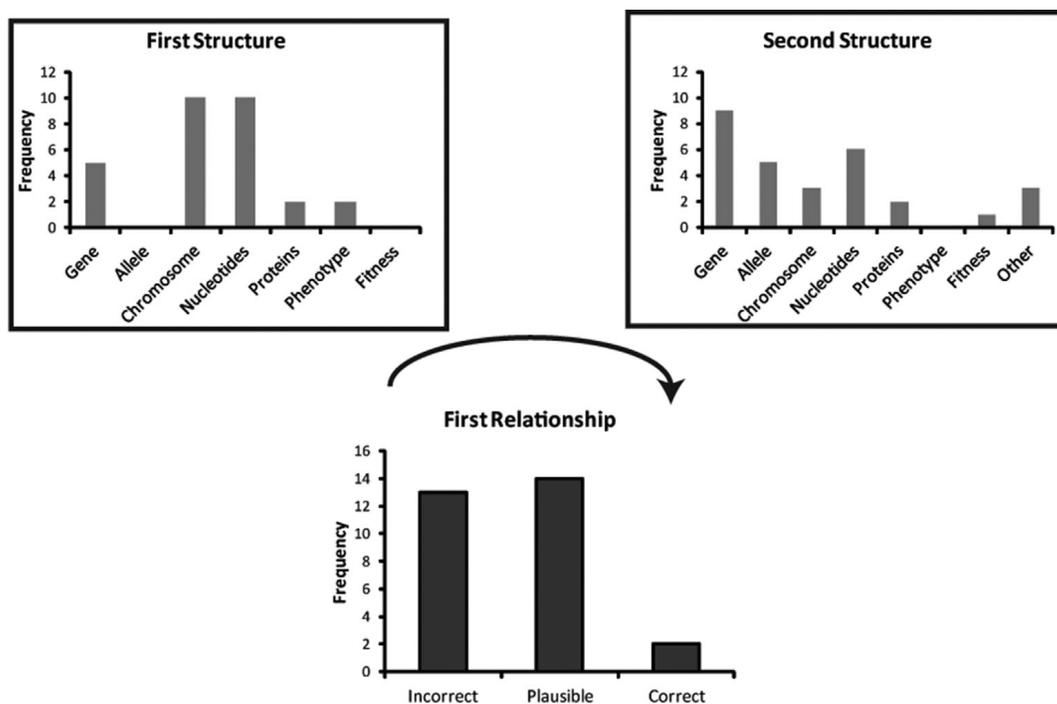
Figure 2. Frequency of combining possible structures in the first proposition of the student-constructed models. The first relationship was rated as incorrect, plausible if the relationship was correct but unclear if the student clearly understood the relationship or scientifically correct.

When prompted to explain why they began with these concepts, eight students specifically started with the smallest concept (usually nucleotides), calling them the "building blocks," "most basic" component, and "smallest piece of the puzzle." Others ($n = 3$) started with chromosome because it was "the largest component," possibly referring to the other micro-scale concepts included in the prompt. A small subset of students reported creating the model with consideration of how their initial word related to the overall function instead of piecing together two or three concepts in isolation. These students were from all of the categories ($n = 7$; A/I/C 2:2:3).

> "I started with nucleotide sequence because to me that's what causes the difference. You know and that's were talking about. The main issue here is the difference in phenotype, and differences in genotype cause differences in phenotype" (stu. 342)

Hmelo-Silver and Azevedo (2006) showed experts were more likely than novices to discuss or show the function of the model, that is, how a structure affects the outcome. While these seven students briefly described a model function during the review task, we would not classify them as expert responses. In our interviews, there were few differences in students discussing the functions of the model, but the differences emerged in verifying the quality of the relationships as they constructed and remembered the models.

How well do students verify relationships within their models?

As the process of model-construction proceeds, students repeatedly access their CS from long-term memory to support their mental model in working memory (Lewis-Peacock & Postle,

2008). One of the hallmarks of the retrieval cycle is that students will repeat the process of accessing their CS and verifying the order and quality of the relationships among the concepts (Williams & Hollan, 1981). We consider how students verify their models in three phases: globally, specifically (at the level of propositions), and retrospectively. Globally, we consider the quality of students' models as a first glimpse into the quality of their cognitive structure in their working memory. Since students create a visual representation of this model, they would need to verify the overall connectedness and relevance to the new scenario. When considering the propositions more specifically, we examine how students verify the quality of relationships before adding them to their visual model. Retrospective verification occurs as students receive feedback to their working memory from the visual model they created. In the context of interviews, students verify the organization and quality of their model as they explain and respond to questions from the interviewer.

One broad approach to measure the adeptness of how students verify their relationships is to quantify students' overall model quality. Students created models with an average relationship correctness of $C = 1.8$ (sd $= 0.75$). This average score is below the "2" value that represents a model with relationships that would be deemed plausible (i.e., correct but vague). In addition, students' models were largely linear, and therefore could not show variation in phenotype or fitness (see Figure 3). Students in the Absent group created predominantly incorrect models ($C = 1.5$) while students in the Complete group created significantly more correct models ($C = 2.0, p < 0.05$), with an average correctness of plausible. Students in Absent group created the least connected models (see Figure 3) while students in the Complete and Incomplete group created similarly connected models with more relationships than the Absent group.

A more in depth measure of verification is to examine students' ability to correctly connect individual words or concepts (see Figure 4). The average correctness values for most relationships were incorrect, although some relationships, allele->gene, allele->protein, and phenotype->fitness, had an average correctness, across all students, above "2," the level of plausible. Complete students were most likely to start their models with a correct first proposition (68% compared to 58% (Incomplete) and 50% (Absent), and constructed models with a greater than mean correctness for most relationships (see Figure S1). We are particularly interested in students' use of the concept allele. We consider allele as a bridge concept, helping tie together micro-scale and macro-scale concepts (Bray-Speth et al., 2014; Marbach-Ad & Stavy, 2000). Twelve students connected gene to allele AND allele to protein or phenotype. The students that correctly interconnected allele into their models were from the Complete ($n = 3$) and Incomplete ($n = 6$) groups, while the students in the Absent group ($n = 3$) used incorrect relationships when integrating allele. Seven students connected gene to allele but didn't connect allele to proteins or phenotypes, all from the Absent and Incomplete groups. Students recognized the importance of allele to the scenario, but students with incomplete or absent CSs couldn't clearly articulate the appropriate relationship.

There was also evidence of students' ineffective verification process because of missing or weak connections among concepts. Without a comprehensive CS, students were unable to define a concept through its relationship to other concepts and they struggled to verify the quality of the relationships. The most striking examples were those students who memorized relationships without any context: "I know that 'code for' is in there and 'express' is in there" (stu. 444) or "codes like codes... I don't know how to explain it... it is just something I learned hahaha" (stu. 244). These relational words are treated as another "item" required in the model rather than a word to describe how concepts connect. It may reflect students' shallow learning strategies employed during introductory biology that would limit these words' connections to other concepts (Tomanek & Montplaisir, 2004). Generally, students misappropriated (rated as a 1 on the
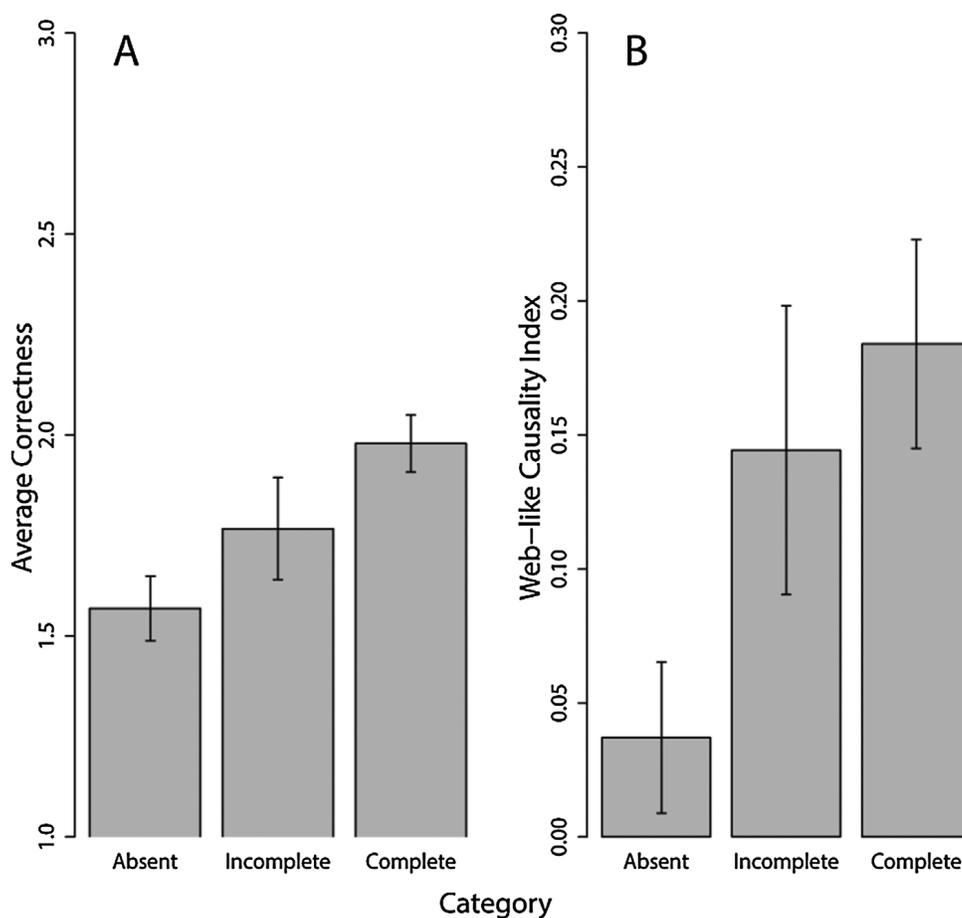
Figure 3. Rating of student-constructed models for biological correctness (A) of the relationships and the interconnectedness of student models. (B) Students in the Complete category created significantly more correct models than the Absent students ($p < 0.05$).

correctness scale) commonly known verbs like made (17 of 41 uses of made), contain (5 of 9 uses), determine (5 of 30 uses), and biological jargon relationships like codes (17 of 35 uses) and express (5 of 15 uses). Instances of misappropriating language for relationships were rampant among the Absent students: "alleles depend on the variance of the genes themselves" (stu. 208), "genes are expressed on DNA? Or DNA codes for at the gene" (stu. 405), fitness is "whether gene variation is efficient" (stu. 510). While Absent students generally found pieces of their CS, clearly some of these students were not able to verify the quality of their language.

Once the model was constructed on the tablet, students were able to "see their thinking" and consider how their mental model may have been different than the model they constructed. At this point in the interview, students were not allowed to re-construct parts of their model, but could verbally revise or refine what they meant. Schwarz et al. (2009) developed a learning progression for understanding models as changeable entities. The Schwarz et al. progression encompasses both how the student changes the model and why. They suggest that as students engage in modeling activities they are able to build increasingly explanatory models about biological phenomena and make revisions that improve clarity and explanatory power. As students in our study were asked about each relationship, they were provided with an opportunity to be
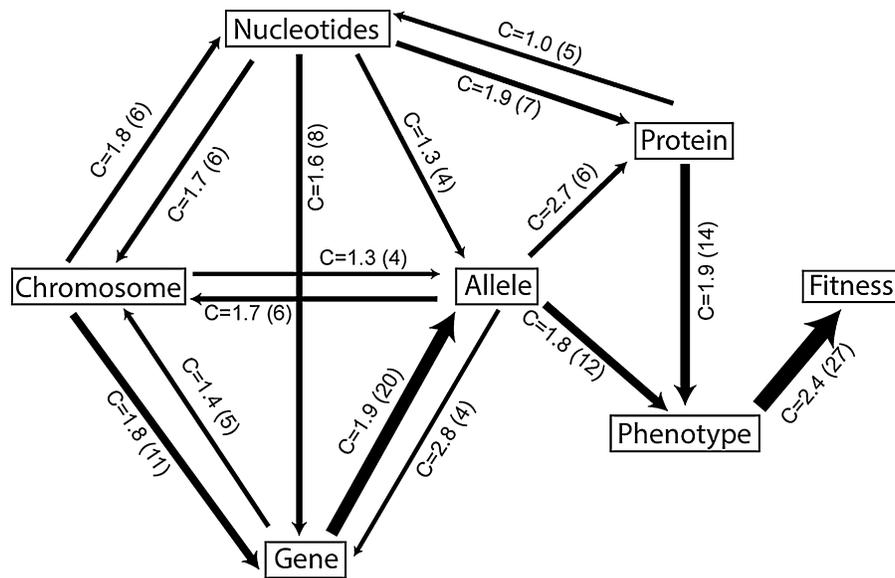
Figure 4.   A map of student models representing the frequency of connections (in parentheses and arrow thickness) among structures on the interview. When fewer than four students connected two concepts, the arrow was omitted. The average correctness (C) was calculated based on relationships rated as 1 (incorrect), 2 (plausible), 3 (biologically correct).

metacognitive about the concepts, the relationships, and how it fits into the model function. While the students in the Schwarz et al. study were provided with additional empirical data to assist in their model revision, we believe the students in our interview were collecting the data about ordering of structures and relationship quality from their long-term memory. Based on this continued retrieval from their long-term memory, many students changed the ordering of concepts and reconsidered how they would describe the relationships.

> "I think this is wrong now... so a chromosome, which is what you think of as two pieces connected together. And then the DNA is wound around them, or that's what it is, a chromosome, strands of DNA." (stu. 357)

> "I started with proteins because it is the absolute smallest thing on the list, oooh, it isn't, is it? Uhh... nucleotide, gene. Yaa, it's all coming back to me now." (stu. 498)

> "genes are not made up of alleles, alleles are variants of genes" (stu. 26)

> "the protein determines the nucleotide sequence, but I think it's the other way around, the nucleotide sequence determines the protein, and then so on" (stu. 430).

In the Schwarz et al. progression, students improve in their ability to use the model as an explanatory tool. We found little evidence that students in our interviews considered their models as explanatory of the three prescribed functions. One student did revisit the entire model and specifically considered how he had showed the three functions: "I have the origin of genetic variation of gene g and then I have how the genetic variation results in phenotypic variation, and then the impacts of phenotypic variation on stone flies" (stu. 98). Unfortunately, this student's perception of showing the prescribed functions was largely incorrect. Although we did not ask

questions about this during this study, it is possible that students would choose to alter their models if the interviewer asked the student to identify how the model explains the three functions.

Implications for Research and Instruction

Our study suggested that neither problem context, nor task familiarity were limiting factors in students' performance during interviews. However, we are not willing to exclude either as potentially important variables in students' abilities to construct accurate and meaningful CSs and subsequently retrieve them. Students in this study took an introductory biology course that used frequent and iterative conceptual modeling as a way to promote understanding about the genetic underpinnings of natural selection—namely, how variation originates and is expressed. Our instructional design purposefully engaged students in model construction across a range of cases and biological scenarios in order to promote their ability to abstract and apply foundational principles about genetics and evolution, regardless of context (i.e., to construct a generalized CS and transfer it). However, Nehm and Ha (2011) and Nehm, Beggrow, Opfer, and Ha, 2012 demonstrated that students' responses on short-essay assessments of natural selection are particularly sensitive to contextual features of the problem itself. For example, explaining trait gain versus loss can generate different patterns of response, as can use of plants versus animals, or familiar versus unfamiliar organisms. To date, the role of such contextual features on students' model-based explanations has not been explored, nor is there evidence to inform us about the role of context in influencing students' abilities to subsequently retrieve that information over short or long terms. Studies that explore the role of context on model-based representations of phenomena are warranted in order to better understand its potential impact on both short and long-term retrieval.

Although we did not observe an influence of the task (rules and operations associated with model construction) on students' retrieval abilities, we do know from personal experience that the model-building task can be problematic for students, particularly early in instruction. Students commonly report that although they understand a phenomenon, they struggle to represent their knowledge in the form of a model. Our data indicate that task familiarity did not impede students' performance in interviews 2.5 years following completion of an immersive, model-based introductory biology. However, we cannot speak to the level of immersion required during instruction to achieve fluency with the model construction task, nor the length of time one could reasonably expect familiarity with the task to be retained. Such data will be important in informing instructional designs that are both effective and efficient.

As students progress through a college biology curriculum, they are regularly confronted with volumes of concepts that seemingly have no connection to information or ideas learned in previous courses. By definition, modeling shifts attention away from knowing concepts in isolation and toward understanding concepts through their relationships with others. Although drawing (and likely, modeling) requires additional cognitive load during learning (Schwamborn, Thillmann, Opfermann, & Leutner, 2011), the creation of a second modality of knowledge storage appears to help some students re-access conceptual frameworks (van Meter, Zecevic, Schwartz, & Garner, 2006). Recent work has shown that modeling biological phenomena can help students organize concepts in ways that generate more parsimonious explanations (Dauer et al., 2013) and create frameworks that increase students' potential for future learning (Sinha et al., 2013). It follows that instruction that regularly engages students in modeling conceptual connections may be useful in promoting development of more connected and robust cognitive structures that can be more readily retrieved and used to scaffold new knowledge, whether over a course or a curriculum.

Our current study provides insight into how students retrieve and interact with portions of their CS related to the origin and expression of genetic variation that was a focus of instruction 2.5

years earlier. While our findings are some of the first to report retrieval patterns over time frames corresponding to curricula (years) rather than courses (weeks, months), we cannot speak to the generalizability of our findings for CSs associated with other knowledge domains, nor whether the model-based learning employed during introductory biology promoted learning in other biology courses. Increasingly, college biology educators are being called upon to design instruction that develops students' proficiency with core disciplinary practices in conjunction with their conceptual knowledge (AAAS, 2011). Knowing how students organize, store, and retrieve their biology conceptual knowledge will assist in the design of this instruction to help foster development of robust cognitive structures throughout their college curriculum.

Acknowledgments

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