Tangible models and haptic representations aid learning of molecular biology concepts

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Abstract

Can novel 3D models help students develop a deeper understanding of core concepts in molecular biology? We adapted 3D molecular models, developed by scientists, for use in high school science classrooms. The models accurately represent the structural and functional properties of complex DNA and Virus molecules, and provide visual and haptic feedback about biomolecular properties that are often implicit in traditional models. We investigated: 1) Can we measure conceptual growth on core concepts? 2) Do lessons with 3D models improve student outcomes on these measures?, and 3) What factors mediate learning? Model use yielded measurable gains in conceptual knowledge and the greatest gains were related to how actively models were used during a lesson and the facilitative role adopted by the teachers.

Keywords: Scientific models; science education; molecular structure; visual representations; haptic representations

Background

Molecular biology requires reasoning about molecules and processes too small to directly observe. As such, scientists use models to generate and test hypotheses about the structures of complex molecules such as proteins, viruses, and DNA (Berry & Baker, 2010). Many existing models primarily represent rigid structures of molecules. Flexible models that embed magnets into 3D-printed structures demonstrate how molecular structure relates to biomolecular functions such as DNA replication, viral assembly, protein folding, and enzyme catalysis. However learning from complex molecular models requires students to map between the model features and background knowledge about the domain. In the current study, we asked whether experience with flexible, tangible models helps students develop key conceptual knowledge in novice high school biology students and whether conceptual growth can be measured in real time. For the study, we iteratively developed and revised a series of 3D models and model-based activities. To assess conceptual knowledge, students completed identical pre/post measures organized around three targets areas: molecular structure, the relationships between structural properties and function, and the relationship between model representations and molecules.

The structurally-accurate, 3D-printed models are the product of technological development at the Scripps Research Institute (Höst, Larsson, Olson, & Tibell, 2013). The tangible models use embedded magnets to represent chemical attraction and repulsion, which allow students to "feel" bonds form in processes such as protein folding, nucleic acid synthesis, and viral self- assembly. As the structure and magnets of the 3D-printed models allow students to create “correct” models much more easily than incorrect models, the models provide formative feedback to the students, prompting them to address misconceptions, build on incomplete ideas, and confirm correct ideas.

In the field of biology, molecular models have played a critical role in transforming biochemistry from a descriptive science into a constructive one (de Chadarevian & Hopwood, 2004). We explore whether 3D physical models could be effective for promoting classroom learning by making explicit links between abstract and physical (visuospatial and haptic) representations (Bivall, Ainsworth, & Tibell, 2011). Prompting students to explore the affordances and limitations of models may scaffold students' development of metacognitive understanding of complex fields like molecular biology (Coll, France, & Taylor, 2012).

The Current Study

To examine whether interactions with flexible, 3D printed models embedded with magnets improve students conceptual understanding of molecular biology, we introduced two sets of interactive models and activities into high school biology classrooms. One set focused on DNA structure and replication, the other on the life cycle of a

virus and viral self-assembly. We were interested in three related questions:
1. Do our (pre-posttest) performance measures capture key concepts in molecular biology?
2. Do tangible models facilitate student learning of these concepts?
3. How does variation in classroom environment and model use relate to variation in learning gains?

We hypothesized that interactive models would lead to increased student learning, particularly improving students' understanding of concepts that are used regularly by working scientists but are left implicit in traditional biology curricula. Table 1 summarizes the targeted concepts. We discuss the concepts in the context of tangible models for our two featured molecular biology case studies: DNA replication and viral self-assembly. We further explored how naturally-occurring differences in classroom contexts influenced learning gains. As our models targeted concepts that are known to be challenging and typically absent from high school biology curricula, there is no clearly suitable business-as-usual condition for comparison. Thus, current aim was to establish whether our measures were reliable indicators of the concepts of interest (Table 1), and whether these newly developed models and activities improved student learning over time.

Table 1. Examples of target concepts in molecular biology

Concept	DNA replication examples	Viral assembly examples
Molecular structures	The size and structure of purines and pyrimidines forces complimentary base pairing with different numbers of H-bonds; The anti-parallel leading and lagging strands of DNA give rise to the "twist" of the double helix	The polio virus is assembled from identical pentameter subparts; Magnetic polarity (attraction bonds) allow subparts to assemble into full virus
Structure-function relationships	H-bonds between nucleotide bases are the weakest and first to break in the semiconservative process of replication	The viral replication cycle and self assembly processes are possible through repeating units and limited RNA
Model use and representations	Model component sizes and magnetic strengths are proportional to the relative sizes and bond strengths within the DNA polymer	Rate of shaking (virus assembly in a container) is analogous to the temperature of the system

Methods

Design. The study was designed as two model-based activities, described below, administered by teachers during their normal biology classes. Activities were preceded and followed by identical pre- and post-tests. Classroom observers for each activity measured students' interaction and use of models, the amount of time devoted to different parts of the activities, and teachers' roles (e.g., facilitating group discussion, answering questions, lecturing) across time points. Teacher interviews and questionnaires solicited feedback on teachers' use and perceptions of the activities and models.

Participants. Nine high-school biology teachers from three different California schools used the models and activities in their classrooms. Teachers received 4 hours of training on background content, features of the models and activities, and strategies for integrating the models into existing biology curricula and for giving student feedback. Class sizes ranged from 22 to 31, yielding final sample sizes of 850 for DNA models and activities and 675 for virus models and activities. The student sample was 59% female and included 33% 9th, 49% 10th, 8% 11th, and 10% 12th grade students.

Models and Activities

Model-based activities typically spanned two class periods. During this time, students interacted with the models with the goal of learning about specific phenomena. For each activity, teachers introduced the models and activities with a series of discussion questions designed to engage students with the relevant phenomena. Students were then given the opportunity to explore the models in small groups and to work through activity worksheets. After working in small groups, students shared their observations, evaluated their responses to the worksheet questions, and revisited the introductory questions in more detail. Finally, teachers elaborated on the properties and use of the models themselves, and helped students make connections between model representations and the structures, functions, and processes underlying the phenomena.

DNA model. A significant challenge for physical models of DNA is the representation of flexibility (that allows sections of DNA to be available for replication) and bonding that allows of both pairing and mis-pairing (that results in for sequences of DNA to code for different proteins). The multi-component DNA model (Figure 1) consists of multiple nucleotides, each with a base, sugar and phosphate. Hydrogen bonds on the bases set in plastic "plungers" that allow for a certain degree of rotation and accurately represent the Watson-Crick hydrogen bonding capacity. Individual bases have attachment sites for the sugars and the phosphates that make up of the backbone of DNA. Finally, the covalent bonds that hold the nucleotides together are represented by a flexible strand of plastic string. The model features a snap bead design so students can create strands of DNA with different lengths. In the current version of the model, one strand is fully connected, representing a template strand of DNA, whereas the other strand could be constructed nucleotide-by-nucleotide so students could engage in the process of replication. The 3D tangible DNA model allows students to investigate several challenging

concepts including the molecular structure of DNA and the semiconservative nature of replication.

DNA Labeling and Replication activities. After group discussion of DNA, students identified and labeled different parts of the DNA models on a worksheet and provided brief explanations of the evidence that they used to identify each part. Students discussed the component parts that make up DNA's structure; the ways in which different types of bonds and spatial configurations enable important functions of DNA; the advantages and limitations of models (including comparing tangible DNA models to a folded paper model that was distributed); and the ways in which the structure of DNA allow cells to replicate genetic information.

On the second day, students completed a DNA replication activity, building complementary strands for the DNA double-helix from the 3D model components. Students added components (e.g., nucleotides) to the model one at a time and, after each component was added, responded to a question on a worksheet. Students discussed: What processes occur during replication? How is DNA structure related to function in the process of replication? How does the process of replication ensure exact copies are created? And, how do the models help explain the relationship between structure and function?

Figure 1. Assembled interactive DNA model

Poliovirus model. The 3D model of the poliovirus (Figure 2), developed at Scripps Research Institute, highlights the dynamic process of self-assembly and the role of temperature. In self-assembly, subunits come together to form larger structures as a result of random motion and local attractions. Most biomolecular processes rely on self-assembly for the formation of complex molecules. However, self-assembly is a challenging concept because there are few analogs in everyday life. In the model, molecular interactions are represented by magnets on the edges of each viral subunit. When pieces are put into random motion, by shaking, the pieces collide and the magnetic attraction causes them to assemble into various intermediate structures and finally into a complete model of the viral capsid. The rate of shaking represents the temperature of the system and students can use the model to investigate the role of temperature on the formation of particles. The ability of the model to self-assemble emerges because the local structures and attractive forces of the poliovirus sub-units were used to design the model; this process of self-assembly was not specifically designed.

Viral life cycle and self-assembly activities. After a group discussion of viral replication, students demonstrated their understanding of the replication process by arranging steps starting with the virus binding to a cell and ending with many newly-formed viruses bursting from the cell. Students next discussed virus structure and replication (with a focus on correct vocabulary - e.g., *capsid, RNA*); the viral cycle compared to other cycles in biology; and the steps in the viral cycle represented by the cards and 3D model.

Students used the 3D poliovirus model to explore self-assembly: students were instructed to place the virus pieces into a closed container and continuously shake the container. As they observed the effect of the rate and force of shaking and the success of the viral self-assembly process, they answered questions about the model structure, stability, and the effect of increasing the energy to the system. Students also observed the interactions between the viral subunits and answered worksheet questions that prompted them to make inferences about the relationship between viral structure (multiple identical pentameter pieces) and function (replication and self-assembly).

Figure 2. Assembly process for Poliovirus model.

Measures

Pre/post tests. Students' understanding of content was measured before and after the activities with identical pre- and posttests designed separately for DNA and virus activities. Test items were designed to tap into core concepts, reasoning skills and spatial understandings that are central to molecular biology. Items were either researcher-developed, designed to directly address problem solving and model use, or sourced from AAAS (MLSCI:Wright & Hamilton, 2008) and other educational research studies related to molecular biology (e.g., Stieff, 2007). Tests aligned with the key concepts in Table 1. Sample items from the DNA and virus test are presented below in (1) and (2), respectively:

(1) Two major functions of DNA are replication and transcription. Name three ways these processes are the same and three ways they are different.

Explain how the following structures of DNA enable it to replicate: a. Hydrogen bonds between pairs; b. Covalent bonds between sugars and phosphates.

(2) Describe one way that self-assembly is needed for gene expression.

Describe how the following affect self-assembly:
a. The shapes of the parts that self-assemble; b. The energy available for self-assembly; c. The positive and negative charges on proteins

Classroom observations. Researchers observed each activity and recorded the amount of time spent using the models, the depth of model use, ranging from highly

interactive use to passive observation; and the teacher's role, (e.g., addressing the entire class, individually interacting with students, or doing unrelated activities.)

Teacher interviews. Teachers completed a brief questionnaire after each activity and participated in a one-on-one interview with researchers at the end of the study. These measures addressed teachers' implementation and perceptions of the activities and use of the models.

Results

1. Do our (pre-posttest) performance measures capture key concepts in molecular biology?

We identified three critical cross-cutting concepts as learning goals: Molecular Substructures, Structure-Function Relationships, and Model Understanding, (see Table 1). These concepts were used to design both sets of activities and the pre/post measures. To determine whether the items we developed tapped into the hypothesized targets, we computed Confirmatory Factor Analysis (CFA) models to test whether these three critical concepts were latent variables around which students' posttest performance on the pre/post measures could be organized (loading strength for the DNA and Virus concept models are shown in Figures 3 and 4, respectively). Specifically, we tested a model with factor loadings for our three concept-based factors against other two three-factor models, which were based on item type (e.g., multiple choice, diagram, open response) and on science curriculum content and objectives (e.g., providing information and constructing explanations), as well as an exploratory three-factor model in which the factors were not specified *a priori*. Models were computed using the `TAM` package in R (Kiefer, Robitzsch & Wu, 2015) and we compared BIC values as an index of model fit, with lower values indicating better fit. For both DNA and virus activities, the concept-based CFA model yielded the lowest BIC values of the four. Model fit BIC differences ranged from 65 to 120 in favor of the concept-model, strongly indicating a better fit to the posttest data (Rafferty, 1995). These models support the hypothesis that our models and activities target complex underlying concepts in molecular biology and not simply, for example, improving students' abilities to provide information or select the correct response on a multiple choice question.

2. Do tangible models facilitate student learning of these concepts?

After establishing organizing conceptual factors for the pre and post measures, we examined student responses to determine whether their proficiency had changed from pre- to posttest. For both the DNA and virus activities, we fit separate Rasch models to students' pre and posttest responses to compare gains in estimated student proficiency from pre- to post. We first used posttest scores to generate item difficulty estimates, the odds of students incorrectly answering an item vs. correctly answering the item, and Expected A Posteriori (EAP) estimates of student proficiency, the odds of answering an item correctly vs. incorrectly. We then used the posttest item difficulty estimates as fixed item parameters to estimate student proficiency at pretest, while equating item difficulty between pre- and posttest. Histograms of students' proficiency estimates are displayed in Figure 5 for DNA and Figure 6 for virus activities.

Figure 3. Loading strengths for the concept-based CFA model of DNA posttest items (on y-axis).

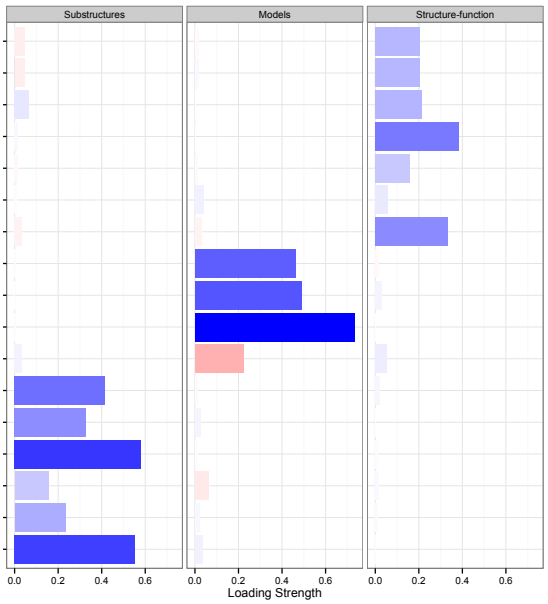

Figure 4. Loading strengths for the concept-based CFA model of Virus posttest items (on y-axis).

For both activities, student proficiency increased from pre- to posttest, following the model activities. The increase was deemed statistically reliable through Chi-square goodness of fit tests (DNA: $\chi 2(1, N=850) = 26.2$, $p<.01$; Virus: $\chi 2(1,$

N=675) = 40.1, p<.01). We take these findings as preliminary evidence that students using the tangible models make measurable and reliable gains in their understanding of key concepts in molecular biology.

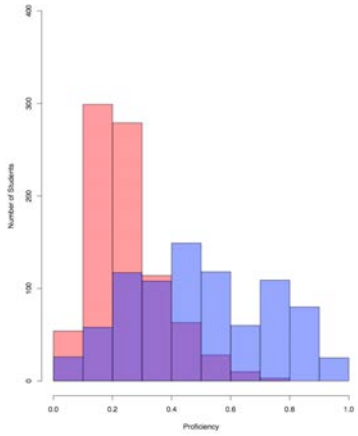

Figure 5. DNA activity student proficiency gains, evident as a distributional shift from pretest (pink) to posttest (blue).

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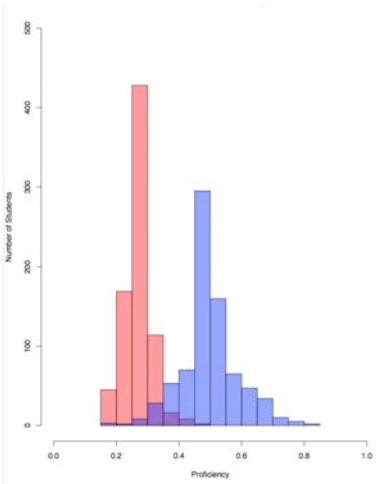

Figure 6. Virus activity student proficiency gains, evident as a distributional shift from pretest (pink) to posttest (blue).

3. What kind of instructional context and model usage leads to the greatest gains in learning?

Preliminary analyses (not reported here) revealed that, for both DNA and virus activities, item difficulty and teacher, together, predicted gains from pre- to posttest: test gains vary considerably by item and by teacher. We explored this variation further by examining classroom observations collected in each classroom for each activity. Specifically, we used mixed effects logistic regression models to test whether differences in gains from pre- to posttest were related to differences in aspects of classroom model use and the facilitating role adopted by teachers in the classroom

We fit separate models for DNA activities and virus activities. Each model included item and classroom random effects on the intercept as well as several fixed effects, explained in turn. The best fitting models for both DNA and virus test gains included item difficulty, the amount of time students spent engaging with the models in different ways, and the amount of time teachers spent actively facilitating students' activity use.

Students in the DNA activities made greater gains for more difficult items (β =0.2, p<.05) and several observed aspects of the classroom environment were also related to test gains, as shown in Figure 7. The amount of time spent using the models was not predictive of gains (β= 0.03, *ns*), however students who spent long periods of time passively using models showed smaller test gains (β= -0.31, p<.01). Additionally, the amount of time that teachers spent systematically monitoring and assisting students during the activities predicted greater test gains (β=0.22, p<.01).

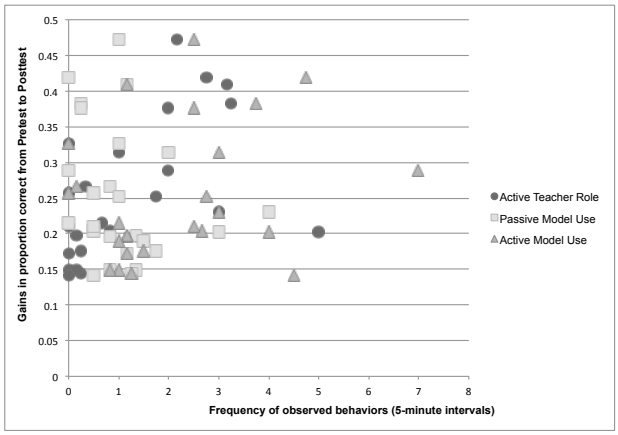

Figure 7. Relationships between DNA test gains (y-axis) and frequency of observations of active and passive model use and active teacher role predictors (x-axis). Passive model use and active teacher roles were reliable predictors.

In contrast to the DNA activities, students in the virus activities made greater gains for *less* difficult items (β =-0.28, p<.05). This reversal may be due to the fact that the virus test items were more difficult, overall, compared to the DNA items, leaving more room for improvement on easier items. Similar to the results from the DNA activities, the quantity of overall model use did not predict test gains. However, the amount of time students spent actively and passively using the model had opposite effects on test gains, as shown in Figure 8. Longer periods of active model use predicted greater test gains (β =-0.61, p<.01), while long periods of passive model use predicted smaller test gains (β =-0.12, p<.01). Finally, teachers' facilitative role during the virus activities was not related to students' test gains: the amount of time that teachers spent systematically monitoring and assisting students during the activities was not a reliable predictor of test gains (β=0.08, *ns*).

We also examined teachers' open-ended interview responses as qualitative evidence for the potentially facilitating effects of active model use and teacher role in student performance. Responses from teachers whose students showed the highest gains revealed common themes in the ways they structured the activities and used the models with their students. These teachers all reported starting their biology unit with the activities and structuring their class time to maximize model use.

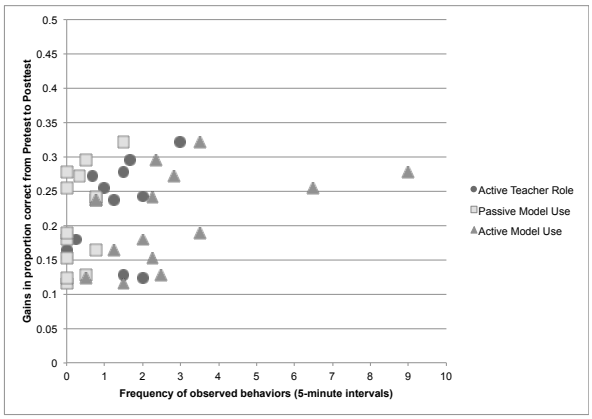

Figure 8. Relationships between virus test gains (y-axis) and frequency of observations of active and passive model use and active teacher role predictors (x-axis). Active and passive model use were reliable predictors.

Teachers used the models and activities to reinforce vocabulary, synthesize concepts learned across biology units and, especially, to highlight properties of molecules that are otherwise difficult to observe, as a quote from one teacher's interview reveals:

> *"[I think] having the models there allowed students to connect a physical shape and structure to something incredibly small that they don't really understand."*

Across high school classrooms, the conceptual gains were sensitive to students' opportunity to actively engage with the models and how teachers linked the interactive models to complex concepts and vocabulary. The 3D DNA and virus models offer spatial and haptic affordances that highlight important structural and functional features. Our data suggest that using these novel models leads to learning gains over the course of a few lessons.

Conclusions

In this study, we asked whether valid measures of key science concepts could be created and whether high school students that use flexible 3D models better understand key concepts in molecular biology. The tangible molecular models accurately represent the structural and functional properties of complex DNA and virus molecules. Model use helped high school students understand critical biology concepts that are often implicit in current DNA and viral assembly instruction. Active model use and teacher scaffolding were related to increased pre- to posttest gains. Our findings demonstrate that non-expert high school students benefit from model use in reasoning about molecular structures and processes: concepts that motivate experts' use of models in the lab.

Our results also suggest a role for modality-specific, grounded representations in conceptual learning (Barsalou et al., 2003; Mahon & Caramazza, 2008). We suggest that visuo-spatial and haptic representations of the models aid students in specifically encoding and understanding complex 3D molecular structure, and haptic representations of the forces and bonds between components enable students to further reason about how these structures influence biomolecular processes (Morris et al, 2007; White, 2012). This work highlights the role of learning tools that allow students to see 3D molecular structure and to use haptic feedback to "feel" molecular processes through models that accurately represent both 3D structure as well as chemical attraction and stability.

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