Identifying affordances of 3D printed tangible models for understanding core biological concepts

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Abstract: 3D models derived from actual molecular structures have the potential to transform student learning in biology. We share findings related to our research questions: 1) what types of interactions with a protein folding kit promote specific learning objectives?, and 2) what features of the instructional environment (e.g., peer interactions, teacher involvement) affect learning? We provide a framework for categorizing ways of using the models that can be used as evidence for whether and how physical models promote molecular understanding.

Introduction

Many studies have reported that core ideas in molecular biology are difficult for students to understand (e.g., Hildebrand 1991; Longdon, 1982). Molecular biology requires students to understand processes at multiple levels from the sub-microscopic (e.g., atoms) to microscopic (e.g., proteins, genes, chromosomes) to larger structures (e.g., organelles, cells, and organs). Because students have no direct experience with molecular components or processes, the coordination of these levels is particularly challenging (Kindfield, 1994). Students have difficulties mapping structure, function, and emergent processes, fail to make important connections, and develop misunderstandings of the mechanisms involved in biological processes (e.g., Duncan et al., 2009; Lewis & Wood-Robinson, 2000; Marbach-Ad & Stavy, 2000).

Tangible models that allow researchers to "think with their hands" play an essential role in many significant scientific findings. In molecular biology, Pauling used models to predict the basic folding units of protein structure, and Watson and Crick used models to identify the structure of DNA and reconcile decades of genetic data. In the current project we investigate whether and how an innovative protein folding model developed at the Scripps Research Institute promotes understanding of core concepts in molecular biology, including handedness and how structure determines the function of a protein.

The protein folding kit has numerous advantages over traditional "ball and stick" models (see Figure 1). Typical models are limited to simple chemical structures, making them unsuitable for modeling complex biological molecules, and cannot be easily used to represent dynamic processes such as protein folding. In contrast, the protein folding kit realistically models features of biological molecules such as their shape and flexibility for function and interaction. Typical "ball and stick" models have no affordances for assembling "correct" molecules as they have generic slots for fitting together atoms or molecules. Students can create erroneous models as easily as accurate models. Finally, typical models require students to follow complex directions to assemble structures. The protein folding kit has affordances that allow the models to assist in their own assembly, guiding students to create models based on natural interactions. Forces between embedded magnets represent molecular attraction and repulsion. The magnets allow students to use these forces to engage in the process of folding a protein from the primary structure, a long chain of amino acids. Students are able to observe the model's emergent properties as they discover the nature of the folding process.

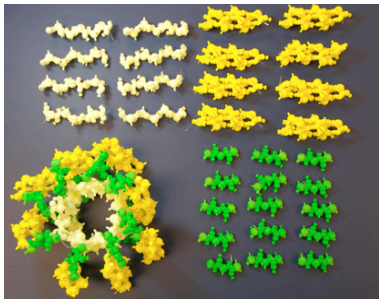

Figure 1. The protein folding kit. Top left and bottom right show primary structures of chains of amino acids. Top right shows secondary structure of helices. Bottom left shows tertiary structure of complete folded protein.

In the current study we explore the affordances of the innovative protein-folding model and focus our investigation on two research questions: 1) what types of interactions with the model promote learning?, and 2) what features of the instructional environment (e.g., peer interactions, teacher involvement) affect learning?

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Data Sources and Analyses

To explore the affordances of the protein-folding model, we carried out observations in a graduate course in structural biology at The Scripps Research Institute. Researchers videotaped two sections of the course, in which 14 students participated in a lab practical to explore and build a model of a folded protein. Students worked in groups of 3-6 students while instructors circulated to ask and answer questions and ensure students were on task. Students started with the primary structure, the backbone of a strand of amino acids, then built secondary structures (helices and beta sheets), and finally built the tertiary structure, the folded TIM barrel protein (see Figure 1). The learning objectives were: 1) to understand how the handedness of the primary structure influenced the handedness at the other levels of structure, and 2) to understand how hydrogen bonds allow for stability in common secondary structures (beta sheets and helices).

All video recordings were transcribed. Preliminary coding identified which features of the tangibles students attended to (e.g., the magnets, the peptide chains), what concepts were mentioned (e.g., molecular structure and self-assembly), what processes were carried out (e.g., how students attempt to fold the protein, what strategies they use to complete the task), and what explanations were generated (e.g., "those proteins don't fit together because they have different shapes").

Preliminary Findings

All student groups were successful in ultimately building the completed protein model. Preliminary coding identified three main types of interactions with the model that appeared to help students make connections between the model building exercise and fundamental concepts in molecular biology. The interaction types identified were labeling, building, and testing. This first activity, labeling, is the process by which students map the parts or structures of the model to scientific terminology. E.g., the force between magnets represents a hydrogen bond. Labeling allowed students to make connections between the model and course content. Building is the process of students using the model to learn about the interactions between pieces and the resulting spatial structures. For instance, students made bonds to form three types of helices. The activity of building provided a deeper encoding of the structures of molecules as students learn using multiple modes of processing (auditory, visual, and touch). Finally, testing refers to using the tangible model for conducting scientific inquiry and generating explanations. E.g., students tested how folding secondary structures impacted the overall stability of the protein. We postulate that the activity of testing helps students develop a schematic understanding of the science system as they generate causal inferences from their interactions with the models.

Preliminary findings of classroom features suggest engagement with instructors who provided prompting questions significantly contributed to learning, as interactions with instructors generated a greater number of relevant questions than students working alone. We anticipate our continued analyses will reveal additional features of the instructional environment that affected learning. Though our results are in the context of this particular model, we expect that the findings will generalize to other domains and provide important insights into when and how tangible models can be used to promote conceptual understanding in science.

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