Introducing nanoscale phenomena to middle school learners using a DNA design activity

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Abstract

This paper summarizes the design rationale and classroom experience surrounding a middle school instructional unit on a nanoscale phenomenon: the self-assembly of DNA strands as applied to the problem of virus detection. The instructional design was motivated by a strategy for integrating new nanoscale content into an existing curricular unit, situating learner activity within a design framework, and using multiple representations of nanoscale phenomena, both as media for the design activities and as the object of student critique. Students in a middle school classroom showed significant pre-post gains both in their understandings of domain concepts and in their ability to articulate affordances and constraints of representations and models.

Objectives

It is estimated that a workforce of two million will be needed by 2015 (Roco, 2003) in the area of nanoscale science and engineering, and scientists in this area have made several calls for research in nanoscience education as they foresee the need of both to build that workforce pipeline (Chang, 2006; Foley & Hersam, 2006) and to broaden the general public understandings of the technical, social, and ethical implications of nanoscale research and development (Baird & Vogt, 2004), beginning at the middle school level.

But introducing nanoscale concepts in middle school faces at least three important challenges:

1. Nanoscale phenomena are not integrated in current middle school curricula or textbooks, nor are they represented in the educational standards and benchmarks that drive their design.
2. As nanoscale artifacts are inaccessible to middle school students due to their length scale, and because the dominant forces are different from the macroscale, students lack an experiential base that would allow them to articulate even naïve theories of their properties.
3. The use of (necessarily macroscale) models and representations of nanoscale phenomena raises the potential for the invocation of prior (macroscale) understandings that interfere with new learning.

In this paper, we offer an account of the design of, and classroom experience with, a one-week middle school unit focusing on the nanoscale phenomena of the coupling of single-strand DNA nucleotide chains. The design of the unit reflects three strategies intended to address the challenges cited above:

1. We chose a "piggyback" integration strategy, augmenting an existing curricular unit on DNA (introduced in the context of genetics) with content intended to build deeper understandings of material already "in play" within the classroom.
2. In order to foster an experiential base for learners, we adopted a design-based pedagogy, situating the learning within an activity structure in which students were asked to design a component of a "virus detection" system: a complementary DNA strand designed to catch and hold a target virus.
3. Rather than relying on a single representation or model of DNA, we employed three progressive,

complementary representations intended to highlight different aspects of the underlying phenomenon, and explicitly focused learner attention on the affordances of the different representations.

Perspectives

Adding new content to the "crowded curriculum" is a daunting task involving, ultimately, the motivation of the importance of the domain content, establishment of new standards, design of new textbooks and materials, and the development and implementation of strategies for professional development. An integration strategy for nanoscale content that demands a large, coherent segment of the school year seems unlikely to be successful (Roco, 2004); a more incremental alternative is to adopt a "back door" approach that integrates nanoscale content within the context of existing curricula and in service to existing standards. We employed a construct-centered design methodology (Krajcik, McNeill, & Reiser, 2007)—an extension of Wiggins & McTighes's backward design (1998) and Mislevy, *et al*.'s evidence-centered design (Mislevy, *et al*., 2003) frameworks—identifying and extending "foundational understandings" of nanoscale concepts already contained within middle school standards, and using these as the basis for the design of learning activities and assessments.

Self-assembly can be seen as a set of general relations that are largely instantiated in the context of specialized domains such as molecular biology or electrical engineering, where no one is an expert in self-assembly per se, but in the application of its principles. However, the spontaneous formation of patterns without direct manipulation in self-assembly is particularly useful when scientists try to build objects too small for traditional manufacturing, mainly by exploiting the ways that molecules attract or repel each other without external manipulation, and by adjusting their physical environment (Whitesides & Grzybowski, 2002).

DNA coupling is an example of nanoscale self-assembly; coupling occurs because nucleotide base pairs attract and bind when individual DNA strands come into proximity with one another. The ability to construct nucleotide chains in the laboratory has turned this natural process into an engineering opportunity; scientists can design "tethered" nucleotide strands that are capable of selectively capturing target partner strands, such as DNA strands associated with malevolent viruses (Cao, Jin & Mirkin, 2002). This affords us an opportunity to situate instruction with a design-based framework, allowing students to grapple with real world-type problems that are not typically introduced in the classroom while also developing advanced problem-solving skills (Kolodner, 1993; Fortus, *et al*., 2004). Research has demonstrated that this type of learning can also lead to substantial increases in science content knowledge and knowledge of scientific practices (Kolodner, *et al*., 2003; Mamlok, *et al*., 2001).

The use of multiple representations is a two-edged sword. On the one hand, the provision of an additional representation may compensate for inadequacies or further refine an existing representation (Ainsworth, Wood & O'Malley, 1998; Cox & Brna, 1995; diSessa, 2005); at the same time, coordination of multiple representations imposes an additional cognitive load than can interfere with learning (Tabachneck, Leonardo & Simon, 1994). Ainsworth argues that the mixed outcomes draw from the different purposes for which representations are used, and proposes a functional taxonomy for characterizing those purposes (Ainsworth, 1999); in her terms, we chose multiple representations that were intended to be both complementary and progressively extending with respect to their fidelity with the underlying nanoscale phenomena, with shared components designed to minimize the cognitive overhead of model correspondence. At the same time, the instructional unit explicitly focused on learners' critiques of representational affordances and differences, a technique that has the potential to foster learning and enhance meta-cognitive outcomes (Coll, *et al*., 2005).

Method and Data Sources

Using the construct-centered design method during the design process, we identified learning objectives and constructed open-ended assessment items in two main areas 1) DNA structure and behavior (complex chains of molecules of one of four base types: adenine, cytosine, guanine, and thymine), base pairing, attractive forces, bond strength, the design of complementary chains, and 2) the affordances of representations and models in science, worked with the classroom teacher to develop an instructional plan serving as a follow-on on an existing unit. The instruction included concepts of basic DNA structure (nucleotides, base pairs, and double helix structure) and samples of the use of different models in sciences. Concepts were introduced using static pictorial representations and dynamic models.

The assessment instrument included nine open-ended items, seven of which focused on the structure and behavior of DNA, and two of which focused on the affordances of scientific models (including one far transfer item). The DNA items included prompts to draw and label a single strand of DNA describing as many properties as possible, identify pairing between the four DNA bases, describe the base pairing process, and to find a sequence that would hold two non-trivial DNA strands together. The two other items focused on the use of models in science and asked students contrast two external representations of a car (schematics vs. radio-controlled model). The assessment was administered prior to, and following, the instructional unit.

Three representations of DNA were constructed. In the simplest, paper-and-pencil version, DNA was represented as a rigid, linear chain of nucleotides (Figure 1), with the goal of establishing the overall component structure and base pair nucleotides. A second model employed plastic "pop beads," color-coded by base type, into which we attached polarized magnets and Velcro fragments (Figure 2). This representation was intended to reflect the differential binding properties of the base pairs and the flexibility of the DNA strands. The final model was a computer graphic simulation in which DNA was depicted as large groups of strands of (color-coded) nucleotides moving in a liquid medium (Figure 3); here the purpose was to highlight the dynamism of DNA, the attractive forces governing self-assembly into paired strands and the capacity of changing an environment and without direct manipulation. (The computer simulation was implemented as a whole-class resource, projected from an overhead projector to a 6-foot diameter platform on floor of the classroom.)

Figure 1. Student proposes 'catcher' strand (T-C-C-T) that uniquely selects target strand (top) without capturing non-target strand (bottom).

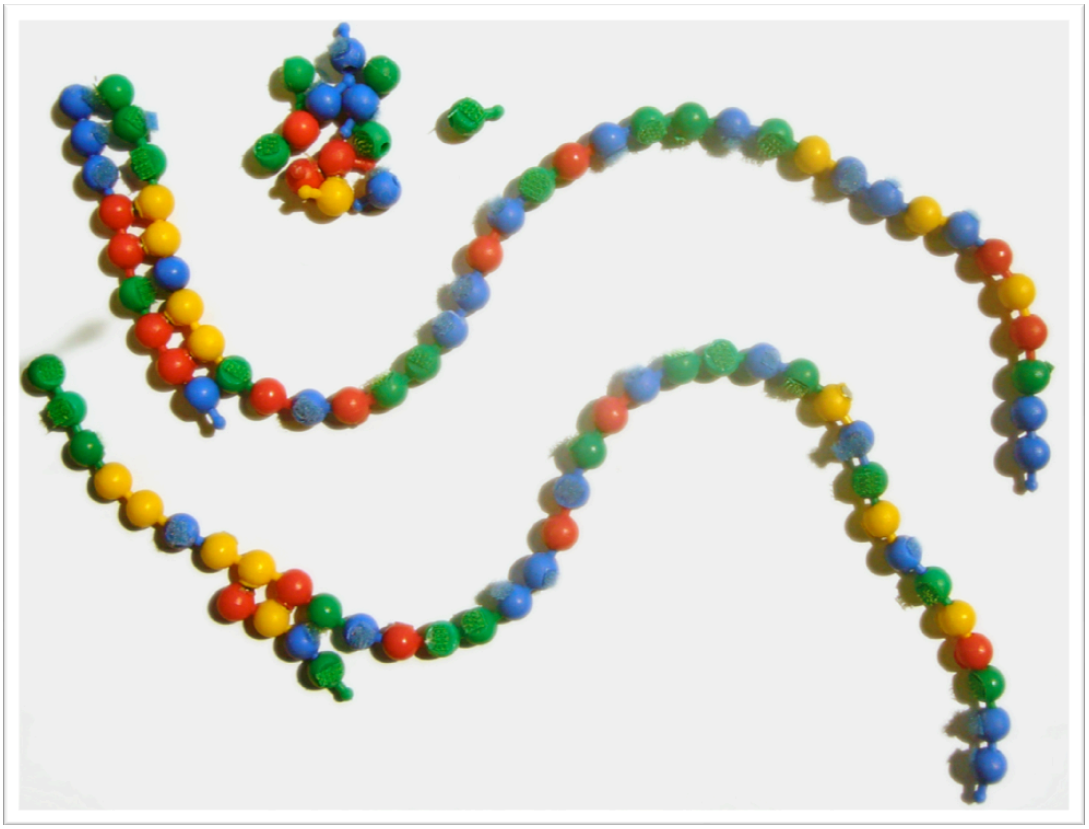

Figure 2. Pop-beads with attached polar magnets and Velcro representing nucleotide chains and base pair bonding affordances.

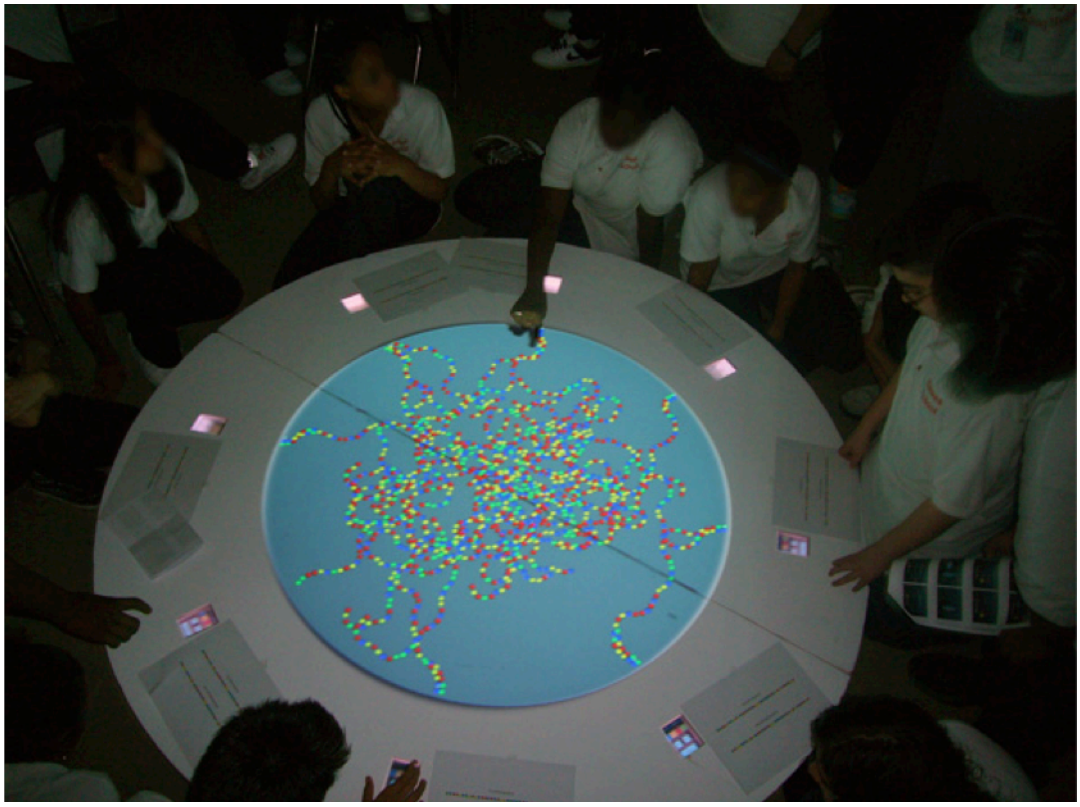

Figure 3. Students use PDAs surrounding dynamic simulated “cauldron” to design and attach candidate ‘catcher’ strands.

The instructional unit was enacted in an urban 7th grade classroom; 29 students completed the unit and both pre- and post-tests. The first two days of the unit were devoted to introductory didactic lessons about DNA, viruses and the use of representations/models in science (using multiple models of the Solar system as the prompt for discussion). The last three days of the unit were devoted to the challenge of designing "catcher strands" capable of selectively capturing target single strand viral DNA while avoiding the capture of non-target strands using the three models (in succession).

The teacher posed a fictional scenario that required the students to use their knowledge in order to save the adjacent class who drank water that contained a virus. Students were introduced to the representations and asked to work in small groups to find the viral DNA strand. They had to pay special attention to the differences between the "good DNA" strands and the viral ones, since they were very similar, and if the "catcher" was not designed carefully, there was a risk to catch the good DNA. This is a non-trivial task requiring the identification of unique subsequences of bases that appear only in the target strand; in addition, the sequences must be long enough so that the aggregate attractive force is sufficient to overcome entropic forces that would pull the strands apart. (The minimum sequence length was stipulated for the first two models, but students were required to determine the minimum length empirically in the simulation.)

Each representational form afforded a different technique for constructing and testing candidate 'catcher' strands. In the paper version, students specify catcher strand components by inscribing them adjacent to the target strand and comparing them with corresponding elements of non-target strands to ensure their selectivity. In the case of the pop-beads, students assembled catcher strands by physically connecting the beads, then holding them up against the target to see if the magnetic poles and Velcro strips permitted adhesion. In the simulation, students designed their catcher strands one nucleotide at a time on a handheld PDA, then "attached" their candidate to the perimeter of a large "cauldron" full of target (and non-target) strands, observing whether their design was successful by seeing if it captured the "right" kind of strand.

As a capstone activity, students were asked to complete a table describing the strengths and limitations of the three DNA representations employed during the unit.

Results

A scoring rubric was developed for coding student responses based on the evidence of understanding reflected in item responses; items were scored using a consensus coding process and the results normalized to a unit value for each item. Table 1 shows the results of the pre-post assessments for the clusters of items relating to DNA structure and behavior, those probing understandings of representation and modeling, and overall performance.

Table 1. Learning outcomes of instructional unit

	# Items	Pre-test M (*SD*)	Post-test M (*SD*)	t (28)	Cohen's *d*
DNA structure/behavior	7	0.27 (*.37*)	3.64 (*1.36*)	14.43**	3.36
Representation/modeling	2	0.53 (*.33*)	0.81 (*.37*)	4.68**	0.80
Overall performance	9	0.81 (*.55*)	4.46 (*1.56*)	14.15**	3.12

***p<.01*

The pre-test indicated that the students were somewhat prepared to compare model affordances, but had little prior understanding of DNA structure or behavior. Pre-post differences were significant for the assessment as a whole, as well as for the two item clusters. The magnitude of the pre-post performance gain was substantial, with mean overall scores rising from 9% to 50%, scores on the DNA items from 4%

to 52%, and on scores on the representation/modeling items from 27% to 40%. Students exhibited the largest performance improvements on items probing understanding of DNA component elements (complex molecules) and the "information structure" (i.e., C-G, T-A attraction) aspects of the base-pair attraction, with weaker outcomes on items relating to nucleotide chain structure, nanoscale forces, and vocabulary. Prior experience with scientific models resulted in a smaller but still strong effect of the intervention on the representation and modeling items. Anecdotally, students evidenced strong engagement in the unit, with a clear preference for the computer simulation model, citing its dynamism as having greater fidelity with the modeled phenomenon, and its interactivity as a motivating factor for participation.

Significance

The study provides tentative support for the three-pronged strategy outlined in the introduction: introducing nanoscale concepts as an extension to existing curriculum content, employing a design-based activity structure as a vehicle for students to develop an experiential base, and utilizing complementary representational forms during design activities and as the objects of critique. It is important, however, to circumscribe the results; the research design does not allow to us attribute outcomes to any single element of that strategy. Moreover, the learning gains, while significant, leave ample overhead for improvement; we will be using the data obtained in this study to guide the next development iteration of our materials and instructional plan. Finally, while none of these research-based strategies are original to the current work, their combination and application, particularly in the domain of middle school learning, provides a new data point in the area of nanoscience education.

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