The cognitive role of external representations in students' understanding of DNA structure

Synopsis

Submitted in partial fulfillment of the requirements for the degree of

Doctor of Philosophy

in

Science Education

Submitted by

Anveshna Srivastava

Homi Bhabha Centre for Science Education

Tata Institute of Fundamental Research

Mumbai, India

Thesis Advisor

Sanjay Chandrasekharan

Abstract

Both education theorists and practitioners emphasize the need for tailoring physical learning aids in ways that support thinking about the unobservable concepts being studied in useful ways. Yet, how precisely the physical structure of these aids interact with learners' mental operations is not yet well-understood. This thesis investigates the nature of this interaction. The design of the studies reported in this work capitalizes on the rapidly advancing understanding of tight coupling between perception and action in cognitive science, and also on the concept of using physical manipulation to support learning (Martin & Schwartz, 2005). We hypothesize that close observation of the process of physical interaction between the learner and the learning aid would yield insight into previously unobservable mental processes involved in learning. As a means of exploring the pedagogical implications of this hypothesis, we developed and conducted a series of studies using different learning aids for teaching and assessing pre-college/college biology students' understanding of the 3-D structure of the DNA (Deoxyribonucleic acid) molecule. Using a combination of microgenetic analysis, clinical interviews, MCQs and novel methods of our own design, we were able to connect specific pedagogical difficulties experienced by the students, as measured by their final assessments, with cognitive difficulties experienced during the intervention *process*. These analyses revealed how students' difficulties with concepts in the specific subject area – DNA structure - were sensitive to the intervention format used to teach and evaluate them. We also discovered that certain novel modifications to existing interventions considerably enhanced their pedagogical effectiveness. In particular, over the course of this research- (i) we designed a simple gesture to connect a well-cited analogy with learner's ability to visualize a particular structural concept, (ii) we designed a novel assessment instrument on top of existing concept-mapping technique that permits instructors a fine-grained view of the trajectory of learning of individual concepts associated with the subject being taught and, (iii) we designed a resource-efficient method – model 'dissection' – enabling instructors to effectively teach molecular concepts to students using 3-D models. Thus, in summary, this thesis investigates the relationship between the cognitive affordances of common learning aids used in biology education and the difficulties that their use uncovers and eliminates in students' understanding. This investigation culminated in the design of three new instruction tools, an understanding of students' difficulties with the DNA structure, and general principles for determining the effectiveness of physical learning aids for different subject areas.

Chapter 1: Introduction

One of the most prominent successes of education research is the demonstration that instructors' use of physical learning aids – *external representations*, or physical manifestations of information (Bodner & Domin, 2000), of the concepts they're trying to teach – can considerably improve students' understanding. For example, a controlled experiment by Martin & Schwartz (2005) showed that students permitted to physically manipulate number tiles were much better at interpreting fractions than students only permitted pen and paper tools. In the context of biology, Rotbain, Marbach-Ad & Stavy (2006) showed that complementary use of a 2D or 3D model of DNA (Deoxyribonucleic acid) molecule substantially enhanced students' understanding of genetics concepts beyond the understanding acquired by a control group that learned the material only through traditional classroom lectures. Across subject areas and teaching methods, students show very large differential improvements when instructed using physical learning aids, firmly establishing them as useful components of teachers' tool-sets.

Researchers have, in parallel, tried to understand what it is about such *external representations* (henceforth ER*)* that lets them improve students' understanding. Patrick et al. (2005) suggested that ERs help build understanding of structure-function relationships of concepts which are typically inaccessible to sensory modalities. Since many entities postulated and examined by contemporary science are not available for perception and action (such as atoms, molecules etc.), these entities are understood using two modes: imagination, and ERs such as models, equations and graphs. The dynamic behavior of such entities, and their complex interactions with other entities, are not directly available from the mostly static media used to represent them externally (Pande & Chandrasekharan, 2016). Thus imagination (i.e. operations on internal representations in working memory, for example mental rotation) plays a critical role in understanding the behavior of these entities. We thus take the position that there are internal and external representations, operations on these, as well as traffic between them. We take this interactive process as implicitly assumed in the standard use of the term external representations in the literature at the interface between cognitive science and education (Zhang & Norman, 1994), and this interactive process is assumed in the remainder of this work.

As an example of the problem of abstraction in pedagogy, it is observed that students find it hard to understand molecules, their abstract properties being difficult for beginning biochemistry learners to grasp (Anderson & Leinherdt, 2002; Kelly & Jones, 2008, Cooper, Grove, Underwood & Klymkowsky, 2010). It is in such situations that ERs are most useful. By presenting students with tangible attributes analogous to the underlying conceptual properties being studied, ERs can support students' intuitions precisely at those moments during the learning process where their natural physical intuitions cease to be useful. For example, designing a carbon atom with four connectors gives a very unambiguous physical interpretation for its chemical valence, the number conveying an important fact, and the physical intuition of connection mapping accurately onto the concept of chemical bonding.

Given this understanding of the mechanism by which ERs support learning, it ineluctably follows that effective use of an ER requires that there be a strong implicit analogy between the physical *affordances* of the ER, and the mental *affordances* of the concept being explained (Gibson, 1979; Harle & Towns, 2012). That is, analogies of the form -'Sodium bonds with Chlorine in the same way as this red ball is connected to this blue ball'- should be both evident from the design of the ER and veridical. At present, judgment of the implicit analogy's strength for a particular ER-concept pair is typically left to teachers' intuitions. When to use an interactive diagram, a simple comparative bar plot, a simple 2-D illustration, an intricate 3-D animation, a 3-D physical model or a combination of all or a few of them? While teachers can be expected to exercise their own judgment in many such situations, it remains an open question whether general principles to assess this correspondence can be discovered via education research.

At the same time, the set of ERs an instructor has available now to explain any given topic is continues to increase in size. Whereas earlier generations of learners primarily relied on text and illustrations, the present generation is coming of age in a technological ecosystem that promotes the use of a variety of auditory, visual and even haptic interfaces to promote learning. The size of this ER repertoire, each with its unique set of affordances and limitations, amplifies the difficulty in determining which one is best suited to any given circumstance.

Absent practical field methods, or at least actionable principles, for determining the effectiveness of ERs, an increasingly worrisome possibility presents itself. With teachers' targeting costs increasing with the number of aids available, the absence of useful mechanisms for ER selection could promote inertial reliance on outdated instruction aids due to decision fatigue, to the detriment of all concerned. Thus, the development of field-ready principles for assessing ER effectiveness is a matter of pressing concern. It is this motivation that has guided the conduct of the research reported in this thesis.

We channeled this over-arching motivation of finding general principles for assessing ER effectiveness into two distinct, though complementary, research foci:

- **ER-specific learning problems:** Identifying difficulties that students face in the use of specific ERs, as well as difficulties in understanding subject matter that are uncovered specifically by some ERs and not by others.

- **Improved ERs:** Characterizing, and where possible, improving the affordances of ERs used in our studies to enhance their pedagogical effectiveness.

We found, over the course of our work, that these two foci are naturally symbiotic. Developing better ERs allowed us greater insight into the learning difficulties of students; difficulties that students faced in using particular ERs offered clues about how to improve them.

Since our goal was to characterize the effectiveness of different ERs, we decided to focus on a single concept during instruction and assessment across all our studies. We decided to focus on the *Deoxyribonucleic acid* (DNA) molecule for this purpose. We did this because a) multiple previous reports show that learners face difficulties in understanding genetics concepts, for which DNA serves as a gateway concept (e.g.- Marbach-Ad & Stavy, 2000; Marbach-Ad, 2001; Tsui & Treagust, 2003; Lewis & Kattman, 2004; Rotbain et al., 2005; Duncan & Reiser, 2007), b) being an iconic molecule, a very large number of distinct DNA representations exist and this diversity of forms made it easier to design studies picking representations with different affordances.

We further decided to focus specifically on the *structure* of the DNA molecule. This specialization was for both pragmatic and principled reasons. Pragmatically, structural concepts are easier to externalize, quantify and track in a student's response; thus, focusing on DNA *structure* allowed us to design observationally rigorous studies. A focus on DNA structure is also particularly apposite because previous education research has documented how understanding the structure of the DNA molecule facilitates students' understanding of downstream functions like replication, transcription and translation (Marbach-Ad & Stavy, 2000). This is particularly true for pedagogical systems that superimpose knowledge of the 3D structure of the molecule over pre-existing knowledge of the 2D structure. By engendering cognitive conflict, these methods promote perspective-taking and eventually, deeper understanding (Ainsworth, 2006). Finally, by focusing on structure we can generalize our findings and analysis to other conceptual areas.

Also, for ease of comparison, the formal educational attainment of the learner sample for all these studies were held constant. We investigated first year undergraduates/Grade 12 pass biology students' understanding of the structure of the DNA molecule. In the Indian education system, the structure of the DNA molecule is introduced in Grade 11 and 12, but the detailed molecular structure is not introduced until advanced undergraduate levels. Given their familiarity with the concept, and unfamiliarity with its details, these students were perfect for our purpose.

Our methodological emphasis combined questionnaires and clinical interviews for pre-/post-pedagogical evaluation with close observation of students' interaction with our interventions, amplified and quantified appropriately on a case-by-case basis. The primary thrust of our analysis, across all our studies, lay in connecting learning difficulties uncovered by the pedagogical assessments to procedural problems posed by the intervention ERs and students' efforts to solve them.

The critical variable governing the potential value of such an analysis is the amount of information that observation of the intervention process is expected to yield about learners' pedagogical outcomes. For instance, if we simply showed students a model of DNA structure as

our intervention, the resulting data sources, no matter how closely observed, are unlikely to convey much useful information about individuals' difficulties during the intervention.

Mindful of this bottleneck, we designed our interventions and recording methods to retrieve as much of this information as possible. Kirsh and Maglio (1994) hypothesized that our actions influence our internal processes, which in turn influence our actions, i.e., our actions and cognition are closely coupled. This implies that the actions we perform on our environment can be used as a window into our mental processes. In concord with this view, we have adopted Kirsh's (2009) methodology of using physical re-arrangement as a window into corresponding mental reorganization. Whereas our studies involved a variety of external representations – including *textual* (Chapters 3 & 5), *symbolic* (Chapters 2 & 5) and *molecular* (Chapters 4 & 5) models, the unifying theme across them, central to the claims of this thesis, was the series of modifications we introduced such that students had to *physically manipulate* the representations to complete the tasks at hand. By ensuring that our interventions involved students physically *manipulating* ERs, we were able to record their pattern of physical engagement with them. As the results described in succeeding chapters attest, this method of observation provided considerable information about students' pedagogical outcomes, giving us interesting insights into the mental processes that go into the process of learning along the way. We now briefly describe these.

Study 1 (Chapter 2) made use of multiple symbolic[1] representations. Crucially, participants had to explicitly use a *physical gesture* to represent a concept. Being chronologically the first of our investigations, the process and outcomes of this study constrained the conduct of our subsequent investigations in two important ways a) we realized that biology undergraduates face multiple difficulties while dealing with DNA structure; hence, we decided to focus on DNA structure, and b) we observed that different ERs tell us different things about what students have understood; which narrowed our subsequent focus on evaluating the effectiveness of several ERs.

[1] Throughout this thesis, we differentiate between symbolic and molecular models. The defining difference between the two is that molecular models restricted their visual appearance to faithfully reproduce the structure of the DNA molecule adhering to the stylized conventions of physical chemistry whereas symbolic models reify more complex subunits of the DNA structure, e.g. strands, bases etc. in order to present a more succinct visual representation, ignoring atom-level details.

For instance, we were able to tell that students were trying to replicate the 2-D textbook diagram of DNA when they tried hard to press a 3-D *clothespin model* of DNA flat on to the table, but we could not tell the same when they interacted with the *backbone model* of DNA (a 3-D model which depicted the sugar phosphate backbone on the two strands, sans nitrogenous bases). This led us to think in terms of affordances of different representations and how we could exploit them to get a view of learners' thinking.

The findings from this study were presented at the Gordon Research Conference, 2011 and have appeared in published form as a book chapter (Srivastava & Ramadas, 2013).

Chapter 3 describes the second study, where we explored the affordances of a 'text' representation. We re-designed the usual concept-mapping task to let the learners physically manipulate the elements of the task. As reported by earlier research, we did find students' difficulties with different concepts related to DNA structure but what was most interesting about this study was that it led us to design an augmented version of concept-mapping analysis that lets educators assess the facility with which students can associate specific concepts related to DNA structure. This methodological contribution was presented as a talk at the AERA (American Educational Research Association) Conference, 2014.

Additionally, in this task we found an interesting link between students' overall competence in expressing their understanding of DNA in the task we set them, and the order in which they placed various map elements during the task. This order is readily observable to educators in practical applications of concept-mapping, and thus provides a real-time rough estimate of learners' competence levels. This work was presented at the Spatial Cognition Conference, 2016 and is currently under review as a book chapter in a Springer volume that will print selected contributions from the Spatial Cognition conference.

Chapter 4 describes the third study, where we explored the affordances of a three-dimensional molecular model of DNA structure. We divided the physical manipulation task under two heads- 'model building' and 'model dissection'. We conducted a controlled experiment to assess students' difficulties and learning in the two situations. We asked one group to 'build' DNA model and the

other group to 'dissect' the given model. We found that model dissection produces larger benefits in understanding, and is much more time-efficient than traditional model-building. These findings were presented at the European Science Education Research Association (ESERA) Conference, 2015, and have appeared in publication in the journal *Biochemistry and Molecular Biology Education* (BAMBED), 2016.

Chapter 5 describes the fourth study, where we explored the affordances of three different representations to elicit differences in students' understanding of DNA structure using a longitudinal design. Study participants were randomly assigned to one of three groups: one group received a concept-mapping intervention, the second dissected a 3-D symbolic model, and the third dissected a 3-D molecular DNA model. Not only did we find strong evidence for representation-sensitive learning, these differences persisted in a follow up study after one week, suggesting that they reflected gain in learning, and not simple testing effects. This work was presented at the annual meeting of the Society for the Advancement of Biology Education Research (SABER), 2016.

Chapter 6 describes the construction of a DNA database, where we categorize various 2-D and 3-D representations of the DNA structure. This is an outreach attempt to help educators/learners find an appropriate external representation based on specific concept(s) related to DNA structure that they intend to teach/learn. This categorization is based upon the amenability of the mentioned concept(s) to be physically dissected out from the representational model. This classification gives us a measure to equitably compare the efficacy of individual representations and gives handy information to both instructors and learners as to which representations can be used when focusing on a particular concept or a group of concepts. This open access database will be made freely available, to be modified by the audience.

Chapter 7 summarizes the findings from the four studies, and discusses its implications for both teaching and learning. The limitations are also discussed.

Chapter 2: Exploring mental visualization with gesture and analogy

In this chapter, we describe a study wherein we made use of multiple symbolic representations (both 2-D and 3-D) in conjunction with a specific gesture and a standard conceptual analogy to understand students' difficulties with the DNA structure. Using microgenetic analysis (Siegler, 2006), we were able to pinpoint changes in students' conceptual understanding. Combining this information with tracking the ERs that they were interacting with at the time, we were able to obtain information about the effectiveness of these ERs. Thus, this study documents our first exploration of the role of physical actions in making mental processes observable – via physical gestures.

Background

Conceptual understanding in molecular biology involves integration of the macro (genetic traits), micro (cell) and molecular (gene) levels. The student needs to comprehend the chemistry of the biomolecule, which in turn calls for understanding of the physics of atoms and molecules. Building up of the molecular structure and its location at the cellular level finally leads to its biological significance, e.g., genetic expression. Marbach-Ad and Stavy (2000) remark that the difficulty in understanding and linking these different organizational levels is "because sometimes one level (e.g., the macro level) 'belongs' to one discipline (e.g., biology), and the other level (e.g., the molecular level) 'belongs' to different discipline (e.g., chemistry)". In fact, the required integration needs to occur in several ways: one includes concepts from various disciplines, another involves the macro, micro and the molecular levels, and finally, the structure-function linkages within and across these levels.

Structural-functional linkages have been identified as a problem area in elementary genetics (Marbach-Ad, 2001; Lewis and Wood-Robinson, 2000; Lewis, 2004). Yet, in a study of major problem areas in biological sciences as identified by students, Bahar et al. (1999) reported that the structure and function of the DNA and RNA molecule was considered as one of the "least difficult" areas. We make a case here that students do have a problem in understanding the basic 3-D structure of the DNA molecule.

DNA structure

The double-helical structure of the DNA molecule can be visualized as two right-handed helices coiled around a central axis (Fig. 1). Each helix is composed of a sugar-phosphate backbone and each (deoxyribose) sugar molecule in this backbone is attached with a nitrogen base through a glycosidic bond to form a nucleoside unit. The nitrogen bases - purines (Adenine or Guanine) or pyrimidines (Thymine or Cytosine) are paired in a complementary fashion where Adenine forms two hydrogen bonds with Thymine and, Guanine forms three hydrogen bonds with Cytosine.

These hydrogen bonds along with the glycosidic bonds ensure that the nitrogen bases of the DNA molecule are planar ring structures of equal length which are perpendicular to the central DNA axis and also to their attached sugar molecules. Orientation of the nitrogenous base pairs and the specific hydrogen bonding between the complementary base pairs give rise to a basic ladder shape, which is coiled into a right handed helix of specific dimensions.

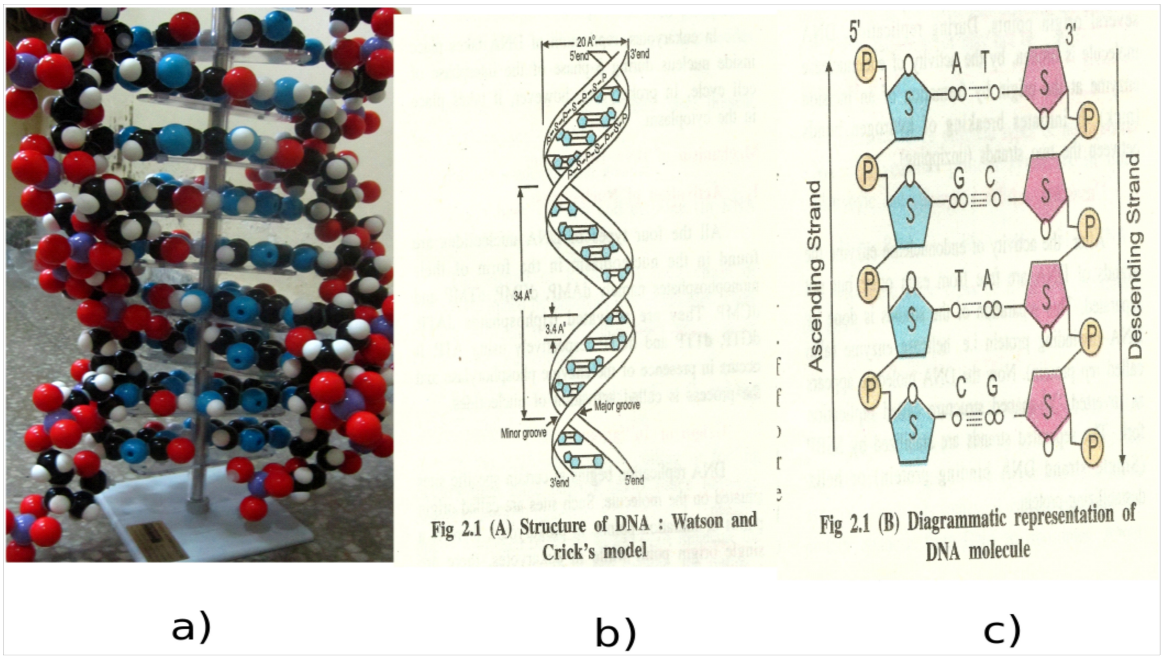


Figure 1: *a) Molecular model of the DNA structure, as used in Chapters 4 & 5; b) & c) Maharashtra State textbook (2009) representation of DNA helix and DNA ladder respectively*

The higher secondary biology textbook followed by our sample (MSB, 2009), introduces the DNA molecule by describing the components of nucleotides, the pentose sugar, phosphate group and the nitrogenous bases, with their chemical formulae. The analogy of a "twisted ladder" is

followed by two kinds of diagrammatic representations- The first (Fig. 1 b) is a schematic representation of the “DNA double helix”, depicting two criss-crossing wavy ribbon-like strands, in which are labeled the “S-P-S-P” (sugar phosphate) links in the backbone. The second diagram (Fig. 1 c) is the “detailed structure” which is a ladder structure containing skeletal outlines of the pentagonal sugar molecules connected with the phosphate groups, labeling the 3' and 5' ends.

Connecting external representation with internal representation

The question of how ERs could connect with internal mental representations is one that is important for science pedagogy to address. The embodied view of cognition suggests that our reasoning is enabled significantly by our ability to participate in actions in the world, and that our internal representations are not amodal (propositional), but linked to our sensorimotor perceptions and actions (Clark, 1997; Barsalaou, 1999). One direct implication of this view is that ERs connect to internal representations through learner's perceptions of movements and actions (Chandrasekharan, 2009).

Drawing further from the embodied view of cognition, we suggest that a possible pedagogical route from external to internal (mental) representations might be through the use of gesture. Goldin-Meadow and Beilock (2010) argue that gestures affect thinking by grounding it in action, and that gestures may even be a more powerful influence on thought than action itself. Gestures have been shown to share complementary properties with models and diagrams and, thus, to link the two representations (Padalkar and Ramadas, 2010). Gestures have also been suggested to link concrete actions with abstract representations when there is a sequential use of 'character viewpoint' gesture (reflecting actual movements) and 'observer viewpoint' gesture (goal object's movements) (Goldin-Meadow and Beilock, 2010). In context of body systems, changing observer viewpoint has shown to encourage mental visualization (Mathai & Ramadas, 2009).

Taking all the above proposals together, we suggest that: a. gestures could be used to link external and internal representations, b. gestures could be used to link together different external representations into an integrated internal representation, c. real or imagined manipulations or transformations of structure, and changing the view-point of the observer, could bring about

mental visualization of the structure, and d. character viewpoint gestures or actions could help in making a molecular, here, DNA structure, more comprehensible to students.

A complementary approach to building internal mental representations, particularly visual ones, is that of analogy. Gentner (1989) defined analogy as a mapping from a base (familiar) domain to a target (unfamiliar) one and Duit (1991) showed that the analogy relation is intrinsic to model-based reasoning and learning in science. The close relationship between visualization, mental models and analogy in the history and pedagogy of chemistry was brought out by Justi and Gilbert (2006). Analogy (like gesture) has a potential to help construct mental visual models from multiple external representations.

In this study, we use the analogy of the 'twisted ladder' for encouraging visualization of DNA structure at the physical and the chemical levels. A combination of gesture and the ladder analogy, with the device of changing observers' viewpoint and specifically, using a 'character viewpoint' simulation of DNA structure, was also possible, and fruitful.

This study

We examine students' reasoning processes in understanding the 3-D nature of the DNA molecule, through the integration of pre-requisite facts from physics and chemistry, supported by appropriate simple and low-cost external representations of DNA structure. We explore through a microgenetic study the following research questions:

1. Are students able to link the 'ladder' analogy with common 2-D diagrams of DNA structure to form a mental model of the 3-D structure of the molecule?
2. Can we use gesture to link the 2-D representations and the 'ladder' analogy with the 3-D concrete models of DNA structure?
3. Can we use mental simulation of changing observer viewpoint to link the 2-D representations and the 'ladder' analogy with the 3-D concrete models of DNA structure?

In addition to answering the above questions, we also describe students' difficulties with the DNA structure.

Methods

Sample

We worked with a convenient sample of five first year biology undergraduates (ages 17-19 years; 4 F, 1 M), who scored a first division (above 60%) in their higher secondary biology exams. The study was conducted in 2010 at HBCSE, Mumbai.

Design

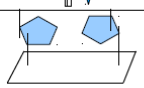
A microgenetic design was used, which is appropriate for situations that involve rapid transitions in learning. It traces the processes of learning under dynamic, 'in vivo' conditions. Three important features of a microgenetic study are: a) observations span the period of rapidly changing competence, b) within this period, the density of observations is high, relative to the rate of change and c) observations are analyzed intensively, with the goal of inferring the representations and processes that gave rise to them (Siegler, 2006).

Observations were carried out during individual sessions held on six days each, spread over a total period of 9 days. Each session involved a clinical interview-cum-teaching sequence for 1-$1^{1}/_{2}$ hour for each student per day. The pre-requisites for the sessions lay within the syllabus for secondary and higher secondary schools recommended by the State Board. Sessions on Days 1 through 4 focused on initial assessment and recall of pre-requisite concepts in biology and chemistry. Brief sequences of direct instruction were included in order to bridge some inevitable gaps in understanding. The issue of 3-dimensionality of DNA structure was addressed on Days 4 through 6 and this data was analyzed microgenetically.

Representations

We use five external representations (Models- M1-M5; Table 1) for the DNA backbone and two external representations for nitrogenous base pairs.

Table 1: External representations used for DNA backbone

Model No.	Backbone representation	
M1	Long edges of a sheet of paper (laid on the table)	
M2	Two (anti) parallel pencils (laid on table)	
M3	Two (anti) parallel pencils (held to stand erect on table)	
M4	Cardboard cutout of a sugar molecule attached with two phosphate molecules (two sets) standing on a cardboard base	
M5	Clothespin model (ladder representation of DNA which can be assembled on a table and then twisted to form a helix)	

Our first representation for the nitrogenous bases was card cutouts depicting a purine and a complementary pyrimidine molecule (Fig. 2a). Students were to use these cutouts against the M4 model to depict the orientation of the base pairs in the molecular model, while indicating the position of attachment of the base with the sugar molecule in the backbone.

Our second representation for the nitrogenous bases was the *'palm gesture*', in which the portion from the wrist till the base of fingers was considered as either a purine or a pyrimidine molecule and the straightened fingers as the complementary nitrogen base (pyrimidine or purine) (Fig. 2b). Students used this gesture to imitate the orientation of the base pairs in the ladder against the models M1-M5, as appropriate.

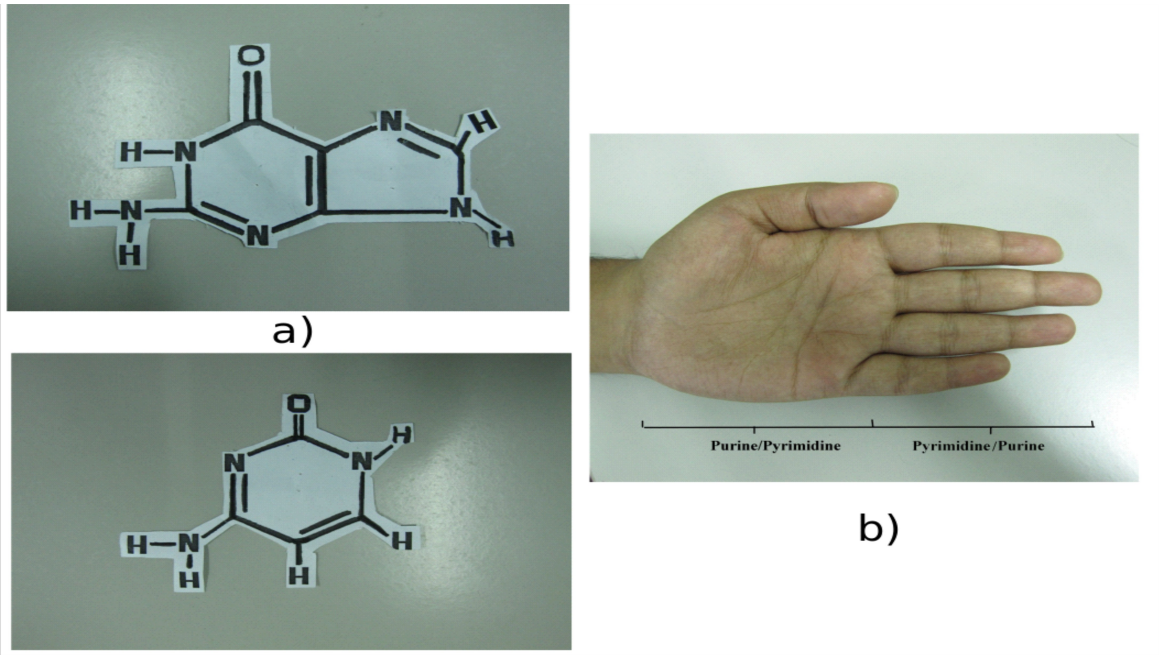


Figure 2: *a) two cut outs representing (top) purine-(down) pyrimidine N base and b) 'palm gesture' with palm representing one N base and straightened fingers representing the complementary N base*

The last type of representation was the ladder analogy, via which the backbone and the base pair representations were combined. Students were asked to visualize, first a straight ladder, and then a twisted ladder. The mental visualization (of the straight or the twisted ladder) and the simulation (of walking up the ladder) correspond respectively to the 'observer viewpoint' and 'character viewpoint' gestures/actions discussed by Goldin-Meadow and Beilock (2010). Here the actions are of course, not actually carried out, but mentally simulated.

Data analysis (Microgenetic study)

Video data from all the students was subjected to a time-sequence analysis. This time period, from between 189 and 235 minutes for the five students, was scanned for '*episodes''* consisting of continuous stretches of time during which students engaged themselves with the 3-dimensionality of the DNA molecule. An episode had either one or more 'events' where the learner made a guided or a spontaneous attempt to depict base pair orientation or twisting of the M5 backbone. The base pair orientation was indicated by their 'palm gesture', i.e. placing of the palm against the DNA backbones (M1-M5), or through similar placing of the cutouts of the base

pairs (against M4 only) (Fig. 3). The backbone models (M1-M5) in use during that episode were noted, along with the correctness ('+' event) or the incorrectness ('-' event) of placing of the base pairs. The time period was counted from the start of Day 4 as t=0.

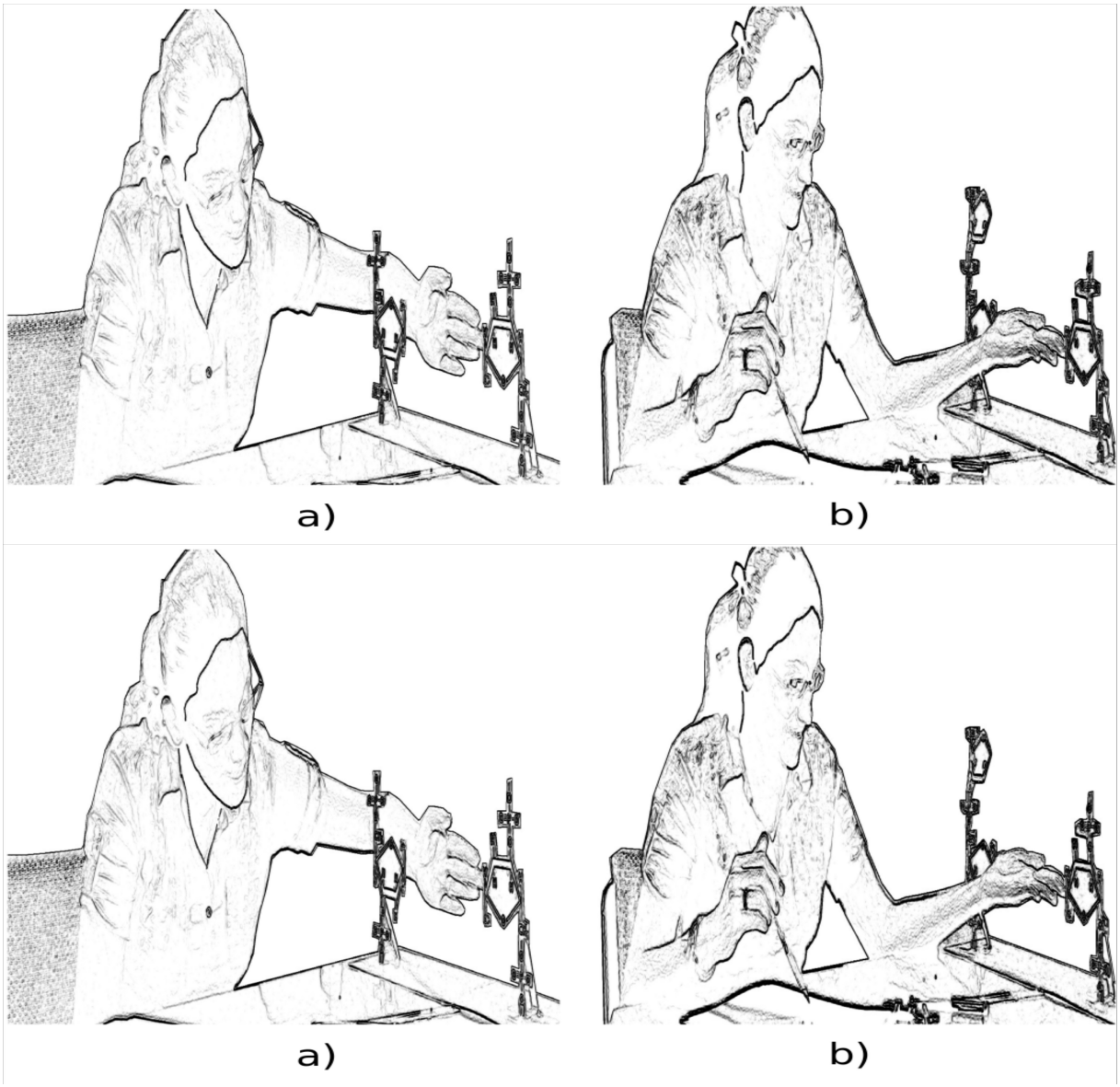


Figure 3: *Palm gesture used with M4 model – a) Incorrect (-) gesture and b) Correct (+) gesture*

Results

Students' difficulties with the ladder structure

At the beginning of Day 4 it was clear to us that all the students were visualizing the 'steps' of the DNA ladder to be 'flat'. The first event on Day 4 for every student was a '-' event, referring to a

straight ladder structure where students depicted the base pair orientation in the plane of the backbones. This turned out to be a strongly held misconception, probably reinforced by the common textbook diagram.

The initial incorrect palm gesture in Episode I on Day 4 was followed up by between 30-55 minutes of questions-cum instruction related to the formation of the nucleoside and bonding of the DNA base pairs, after which the students were asked to repeat the palm gesture (Episode II). Although all the students began with the incorrect 'in the plane of the backbone' gesture, they quickly changed to the correct gesture (in Episode II or Episode III). We refer to this as a '+' ve transition, indicating a realization of the 3-dimensionality of the ladder structure. Strikingly, however, the correct response was not stable in any of the students. As the interviews proceeded, all the students showed a series of '-'ve and '+'ve transitions, that is, they kept switching between the correct and incorrect response. This was notwithstanding the fact that the correct response was often accompanied by an 'Aha!' moment and positive encouraging feedback (a broad shared smile, and 'good!' or 'very good!') from the interviewer.

Students' difficulties with the helical structure

Here, a '+' or '-' event indicates that the base pair is shown perpendicular (correct) or parallel (incorrect) to the axis of the helix. The palm gesture was used with models M1-M4 to represent the fact that the base pairs were planar (of equal lengths), parallel to each other, and perpendicular to the two backbones, just like the steps of a ladder. _The DNA ladder being a helical one, the next task for the students was to depict the base pairs orientation in a helical ladder. For this they had to maintain the base pairs locally perpendicular to the two backbones and to the axis of the helix, but show that each base pair was twisted (by 36º) with respect to its adjacent base pair. This could be indicated by the student positioning their two palms in parallel planes, but angularly displaced with respect to each other, either in the air, or against the M5 (clothespin) model.

Before the M5 model was constructed, students were asked whether the base pair orientation would change if the straight ladder was twisted to form a helical one. Interestingly, only two

students said that the base pair orientation would change in the helix while the other three students said that the bases would remain parallel, exactly as in the straight ladder structure.

All students (except 1) remembered that there were 10 base pairs in one helical turn, and there was a 36^{o} angle involved somewhere, but none guessed that 36^{o} was the constant angle between the base pairs.

All our students had great difficulty in visualizing the 3-D structure of the DNA molecule, with most of them trying to force the three-dimensional model to conform to a flattened 2-D representation they thought to be veridical.

Context of the '+’ve transitions

Throughout the Days 4-6 when students were questioned about the orientation of the base pairs, they frequently switched between a '-' (incorrect) response (base pairs locally in the plane of the backbone) and a '+' (correct) one (base pairs locally perpendicular to the plane of the backbone). The '-'ve ('+' to '-') transitions were all unconscious ones, whereas the '+'ve ('-' to '+') transitions, symbolic of a learning episode, were usually the result of an interjection or a hint by the interviewer. The first '+'ve transition for each student occurred after they were given the ladder analogy: “Have you seen a ladder?” Initially, for 3 students, the ladder analogy by itself did not help. So the interviewer followed it up with an instruction to the student to (mentally): “Try to climb the ladder. Where will you step? How will you place your foot?” This instruction to mentally simulate walking up the ladder immediately led to an 'Aha!' moment and a quick correction of the gesture or the cutout orientation.

Visualizing the 3-D structure of DNA

We were not too surprised when all the students in our sample initially thought that the DNA base pairs (the 'steps' of the ladder) were in the plane of the backbone. This was a natural misconception following from the common textbook diagrams. Most available visuals, physical models and videos on DNA structure do not emphasize this particular feature, though it is significant enough that Watson and Crick's (1953 a) original paper mentions it.

What surprised us was the difficulty that students had in correcting their apparently simple misconception. All of them had one or more 'Aha!' moments when they realized that the base

pairs were 'really' like the steps of a ladder, i.e., planar and perpendicular to the backbone. But, especially while dealing with the molecular (M4 and M4 (c)) or the helical (M5) models, they rapidly and repeatedly forgot this simple fact. The difficulty here probably lay in a limitation of working memory. In the case of M4, students were not able to simultaneously hold in their mind the molecular structure, the bonding, and the base pair orientation. In the case of M5, they had to keep in mind the twisting of the base pairs along with their perpendicularity to the backbone. The second surprise came when three of the students constructed the DNA 'helix' as two crisscrossing backbones with base pairs between them, forcibly flattening them to lie flat on the table! Despite considerable curricular and extra-curricular exposure, students in our sample had not realized the essential 3-dimensionality of DNA structure.

In the framework of Goldin-Meadow and Beilock (2010), the ladder analogy by itself is observer-centric, and the palm gesture is an 'observer viewpoint' gesture. We found that these were not sufficient in most cases to bring about learning. We had to ask students to imagine themselves actually stepping on the ladder, i.e., getting 'inside' the model. This could be seen as the equivalent of 'character viewpoint' gestures or actions, which may have provided for the students a bridge between an imagined concrete action and the abstract representation of base pair orientation. Our results show that, though students did not spontaneously link the ladder analogy with their textbook diagrams, gestures could be used to link 2-D representations with multiple 3-D models of DNA structure. Mental simulation, involving changing the observer viewpoint, to one from 'inside' the molecule, could effectively link the ladder analogy with the molecular structure of DNA.

While this study clearly documented the difficulties students face in relying upon mental imagination to appreciate the three-dimensional complexity of DNA structure, it could characterize this difficulty broadly in functional terms, without pinpointing the specific *conceptual* misunderstandings that contributed to the difficulty. We turned next to designing a study that would allow us to do this.

Chapter 3: Tracking the process of concept-mapping to assess learners' conceptual understanding

After developing a holistic sense of students' difficulties with DNA structure, we decided to identify specific concepts that were particularly difficult to comprehend. To this end, we adopted a different external representation to investigate - concept maps. We asked subject area experts to identify concepts relevant to the structure of DNA molecule and asked students to design a conceptual network. Rather than simply evaluate finished concept maps, as is traditionally done, we wanted to operationalize our over-arching goal of tracking mental processes by observing physical actions by tracking the actual process of concept-map building. Since there were no extant methods for making such observations quantitatively, a major component of this project involved designing and testing observation methods and metrics that could feasibly and usefully characterize important elements of the concept-map building process. We report these novel contributions in this chapter.

Augmenting concept-mapping analysis

Concept maps were originally developed for assessment, not teaching (Novak & Gowin, 1984). They have since been used for both purposes in a variety of pedagogical settings (Novak & Cañas, 2008; Cañas, A. J. et al., 2015). For instance, Kharatmal and Nagarjuna (2008) showed how in the final built concept map, experts differed from novices in their choice of linking phrases. However, there is a fundamental constraint on the ability of concept maps to identify problem areas in students' understanding. Existing research in this area primarily restricts itself to assessing finished versions of students' maps, although see Cañas (2015) for a review of some alternative approaches. Quantitative assessments, therefore, are limited to holistic judgments about students' proficiency in the overall subject area, as shown by Ruiz-Primo and Shavelson (1996). A more nuanced understanding of individual concept-level proficiency is necessary for designing useful interventions, extending concept-mapping's ability to provide such understanding would greatly improve its utility as an assessment tool.

The principal contribution of this work is the empirical demonstration of novel procedural analyses that allow concept-level assessments of proficiency using concept maps. Static map

scoring methods elide interesting information about the *processes* that underpin concept-map construction. This work provides a novel methodology for quantitative assessment of concept maps that includes procedural aspects of concept-map construction, and empirically substantiates it by connecting procedural statistics concretely with established static measures of conceptual understanding in a particular biology education concept-map building exercise.

The methodological improvements presented in this paper improve the capabilities of concept-mapping as an assessment tool, and advance the larger project of identifying points where the process of building/linking concepts is difficult, so that interventions may subsequently be targeted specifically to these points.

Materials

After briefly introducing an existing concept-map on 'animal cell' (DiCarlo, 2006), each student was briefed on the task and given a Styrofoam sheet (to use as the working surface), 37 printed cardboard concept cards, unlimited unidirectional chart-paper arrows (to show connections between concept cards), and pin-up labels (to write down specific links between concepts alongside the arrows). Students were also provided with push-pins to pin map elements to the working sheet.

Sample

12 biology undergraduate students (5 male, 7 female) responded to a general call for a concept-mapping study. All were previously exposed to the basic structure of DNA (Deoxyribonucleic acid) molecule in high school (Grade 12). Sessions with students were conducted individually at HBCSE, Mumbai, in 2012.

Instruction

There were no special instructions given to the students regarding rules of concept-mapping technique. Each student was simply asked to build a concept map, focusing on the structure of the DNA molecule with the provided materials.

Data sources and research design

All sessions were videotaped, and the final concept-map was photographed. All videos were transcribed, and formed the major data source for analysis. A two-phased analysis was performed on the data to a) obtain map level performance statistics using static map scoring methods and, b) obtain concept-level performance statistics using novel procedural analysis methods. We used a microgenetic research design (Siegler 2006; Aalsvoort, Geert & Steenbeek, 2009), appropriate for tracing the processes of learning under dynamic conditions.

Methods

Static map scoring

We adapted a method for scoring non-hierarchical maps from the research of (McClure, Sonak & Suen, 1999), who used the number of valid propositions identified in a concept map as a measure of its overall validity, which they called relational scoring. Note, though, that this method penalizes subjects that make smaller, more accurate concept maps, over subjects that make larger, less accurate ones. A modification that would only consider the ratio of propositions judged valid to propositions observed would suffer from the opposite problem – it would favor small accurate maps over larger, less accurate ones.

We improved on this existing method by borrowing a test statistic from information retrieval theory – the *'F-measure'* (van Rijsbergen, 1986). The F-measure is the harmonic mean of the precision and recall of a test, where '*precision'* in our case is simply the ratio of propositions judged valid to total propositions made, and '*recall'* is the ratio of propositions judged valid to the total number of valid propositions *possible*. It is immediately evident that precision in our case corresponds to the traditional propositional accuracy measured by standard scoring schemes.

As is standard, we define a *proposition* as occurrences of *concept-linking phrase-concept* sequences. Three graduate students independently scored the propositions. These scores were submitted to an inter-rater reliability test. The inter-rater reliability was quite high ($\kappa = 0.94$), in line with reliability measures of similar scoring schemes seen in the literature (Novak & Gowin, 1984; Lomask, Baron, Greig and Harrison, 1992). We approximated recall as the ratio of number

of concept cards used to the total number of concept cards available. We finally combine precision and recall scores obtained from students' concept maps as,

$$F = \frac{2 \times precision \times recall}{precision + recall}$$

This calculation gives us a scalar measure of the accuracy of the completed concept map for each student. As we discuss above, the subjective elements of this computation, assigning validity to students' propositions, are statistically reliable (κ = 0.94). All other elements are observable, leading us to believe that this scoring method is a reliable indicator of final map quality.

Procedural concept scoring

We compute two measures on a per concept basis: (i) a measure of concept-specific accuracy, and (ii) a measure of '*uncertainty*' for the use of the concept.

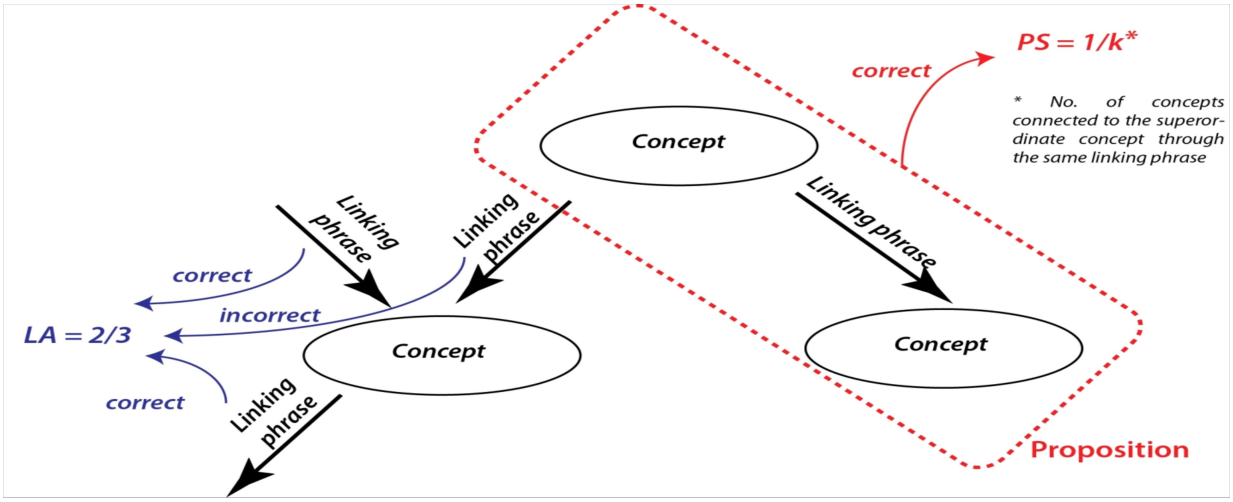


Figure 4: *This diagram illustrates the calculations underlying our two different measures of accuracy. Map-level propositional accuracy is obtained by averaging proposition scores computed for all propositions in the map. Proposition scores are binary, except when a parent concept links to multiple children, in which case the 1 is divided equally across the number of correct subordinate concepts. Concept-level link accuracy is computed as the ratio of the number of correct incoming and outgoing links for a concept to the total number of incoming and outgoing links. Whereas propositional accuracy gives us a big picture view of students' map-building capability, link accuracy affords us a more granular understanding of which concepts they generally get right, and which they get wrong.*

We measure uncertainty using the number of moves a student makes with a concept card. We use the term *'move'* for actions which change the position of a concept-card, viz., picking, dropping, placing, shifting. Measuring uncertainty using number of moves follows from the intuition that a concept card that a student can confidently place will be moved sparingly, while cards that the student is unsure about will be moved around frequently, as the student revises and/or

backtracks. Hence, we assume that the more a concept is moved, the greater concept-uncertainty it reflects, and vice-versa. The number of moves is documented from the video transcripts, where all moves made on the working sheet were coded by the first author during the transcription process.

We measure concept-specific accuracy using a measure we call '*link accuracy'* – measured by the number of correct propositions divided by total number of propositions formed by the concept in focus. Figure 4 illustrates how link accuracy differs from standard propositional accuracy used in previous scoring schemes, including our own static scoring scheme described above.

Results

A joint plot of concept accuracy and concept uncertainty helps identify subject-specific learning problem areas.

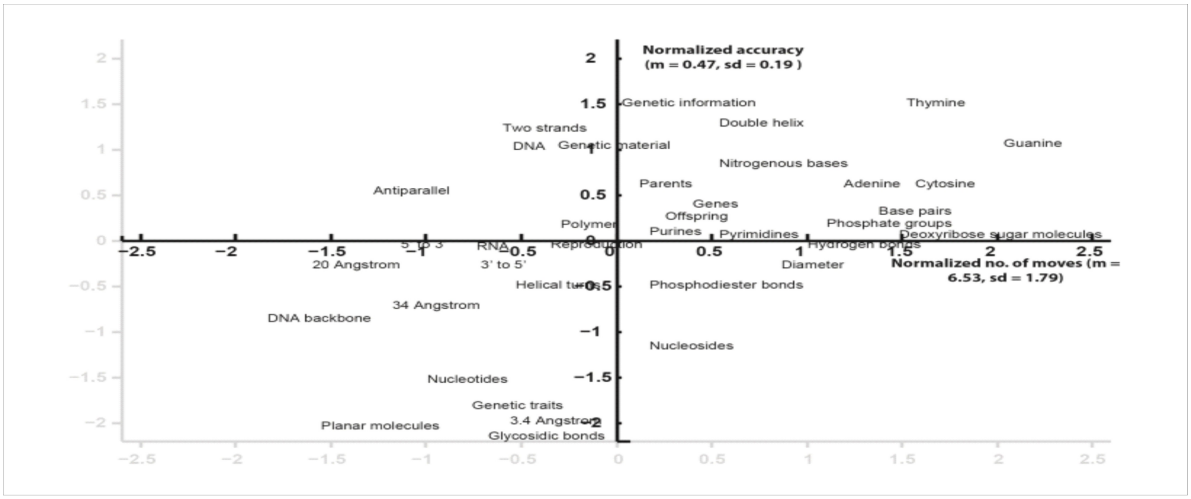


Figure 5: *Plotting concept uncertainty against concept accuracy averaged across all 10 subjects for each concept used in the concept map building exercise*

Figure 5 plots the normalized number of moves against the normalized accuracy associated with each concept averaged across all students in our study. Concept-uncertainty is measured using the number of moves per concept, normalized across all concept moves by all subjects. Concept-accuracy is measured using the ratio of correct propositions associated with each concept, normalized across all propositions made by all subjects. This plot visualizes the relative facility with which students can use individual concepts (facility decreases clockwise from quadrant II). This visualization strategy gives us a plethora of information about students' relative facility in using each of these concepts during map-building.

To the extent that we see an over-arching theme in problem areas and poorly understood concepts about DNA in our study sample, we see that students can more or less accurately place simple concepts, viz., concepts that clearly relate functionally to one, or a small number of other concepts (e.g. anti-parallel, parents, offspring etc.), but are less fluent in handling structurally complex concepts that actually require a deeper understanding of the subject (e.g. planar molecules, DNA backbone etc.).

Procedural analysis yields an alternative holistic measure of concept-map building performance. What is the relationship between static map accuracy and our proposed two-dimensional assessment of facility with concepts? In order to compare, we need a holistic summary of the concept-level information we have obtained from procedural analysis. We hypothesize that the relative number of concepts populating each of the 4 quadrants of the graph we plot in Figure 5 contains useful information about the level of subject-area understanding. Rather than try to shoehorn this information into a number, we suggest that it might be more intuitive to depict it in the form of *understanding contours* – closed shapes drawn around the origin such that the area covered within each quadrant is proportional to the relative number of concepts within it. A comparison between the understanding contours plotted for the best 3 (mean F-measure = 0.92) and worst 3 (mean F-measure = 0.68) performers, as measured by static map-scoring (Figure 6) reveals stark differences.

In general, the contour for better performers (Figure 6A) predominantly covers quadrant I, suggesting that they tend to move concepts around a number of times, but are relatively successful in forming accurate connections. On the other hand, the contour for the worst performers (Figure 6B) predominantly covers quadrants III and IV, showing that they either know they don't know about specific concepts (leading to sparse movements of concepts seen in quadrant III) or try to move them around, but fail, possibly due to mistaken understanding of concepts in quadrant IV.

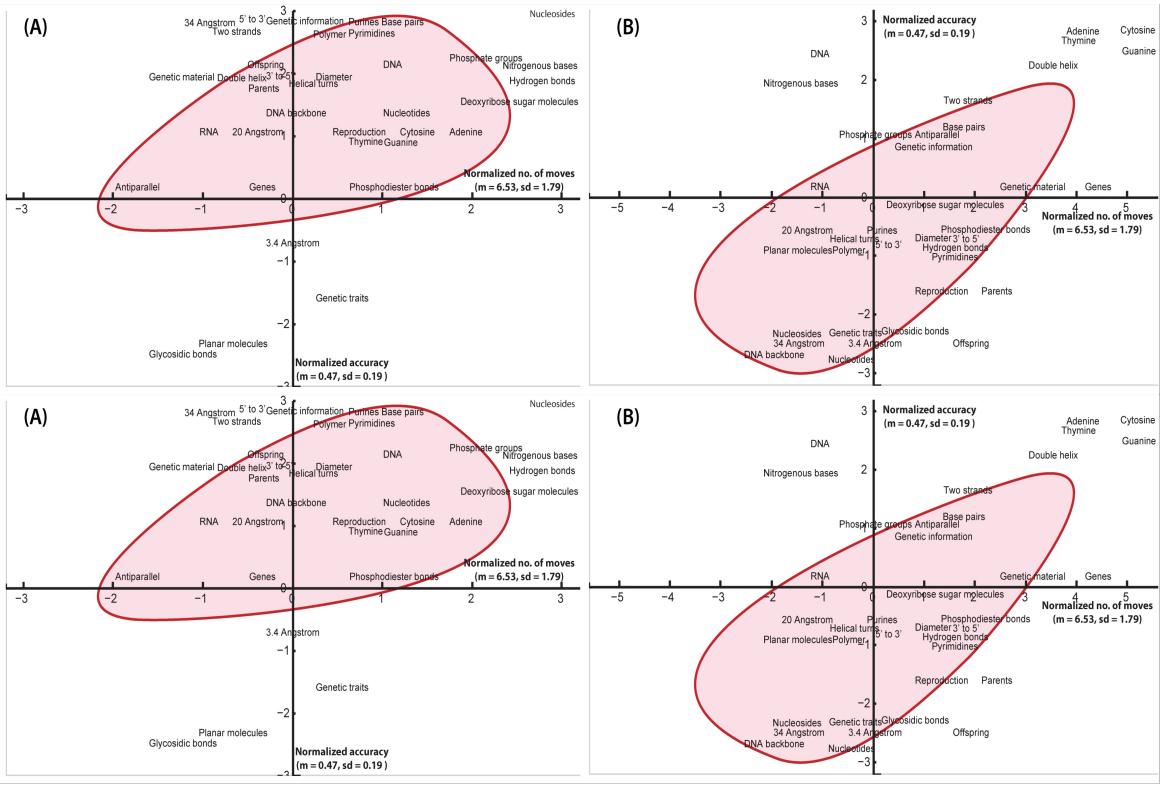


Figure 6: *This figure illustrates conceptual certainty and accuracy for (A) the best three performers of the task, and (B) the worst three performers of the task. We drew contours for respective plots on the basis of number of concepts falling in each quadrant. The area occupied by the contour curve is drawn proportional to the number of concepts lying in the quadrant.*

This analysis suggests that better performers explore the concept space more effectively, which in turn suggests that concept maps are effective ways of eliciting partial and nebulous understanding of concepts. At the same time, it supports the viability of our hypothesis that understanding contours might be used as alternative holistic markers to measure students' subject-area understanding.

Weak comprehension and element placement

Element placement trends were identified through a time-sequence analysis, where the video recording was broken into a series of snapshots taken every minute, for every student. For each snapshot, the number of cards (C), arrows (A) and phrases (P) were recorded. Graphs generated to visually capture the process showed four types of processes,

- C-AP: Most cards placed first on the workspace, followed by alternate arrow and linking phrase placement, typically assigning a linking phrase to each arrow as soon as it is placed.
- CA-P: Cards and arrows placed on the workspace together, followed by linking phrase placements.
- CAP: Map elements placed in systematic propositional order. Two cards, an arrow and its linking phrase, then the next concept pair and its arrow and linking phrase, and so on.
- C-A-P: First all cards, then all arrows, then all linking phrases. These subjects displayed the most reorganization of the map during the arrow placement stage.

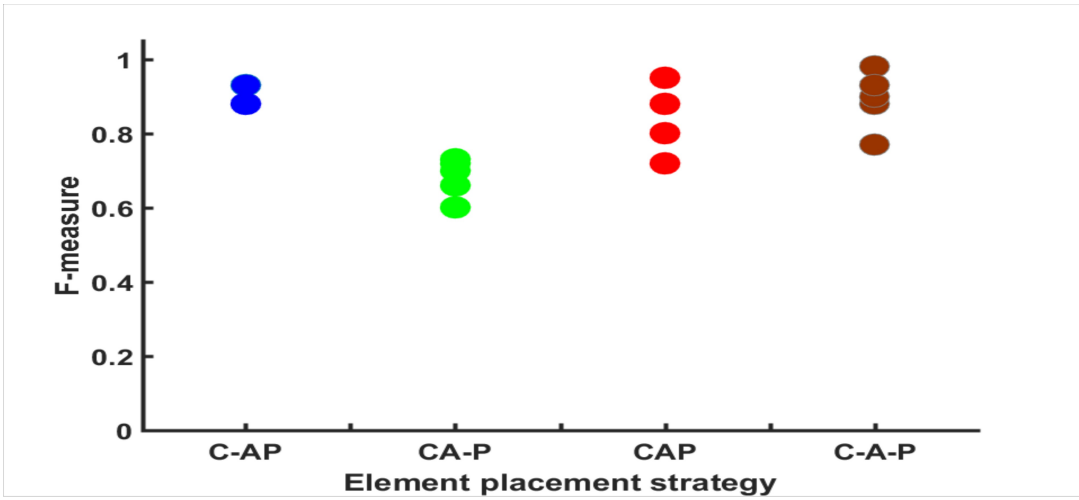


Figure 7: *Plot of map-building strategy vs final competence score*

Strikingly, we found no mixtures of map placement strategies within subjects. Subjects quickly converged to one of these four strategies very early in their building process and maintained it exclusively till the end of their map-building. This suggests that (a) use of a particular strategy likely primes subjects to think of the map-building task in a mental *frame* in which the chosen strategy is the most natural one, and/or (b) how natural a strategy appears to a subject likely depends on the content and strength of her internal representations of concept-associations related to the subject.

Subjects with lower F-measures are uniquely characterized by adoption of the CA-P building strategy (Fig. 7), wherein cards and arrows were placed on the workspace together, and linking phrases were added in afterward. In fact, 5 of the 6 lowest F-measure scores recorded in our

sample belong to the 5 subjects recorded using the CA-P strategy. A one-way ANOVA test excluding the CA-P cohort shows insignificant differences in the mean F-measure for the remaining population ($F_2 = 1.17$, $p = 0.35$); a one-way ANOVA including this cohort shows extremely significant difference ($F_3 = 7.75$, $p = 0.0027$), substantiating the statistical significance of the discrepancy.

Implications

Based on our results, an intuitive interpretation of the four quadrants in Figure 5 emerges, as shown in Figure 8A. Additionally, we can further postulate a relationship between stages of learning and the relative number of concepts we expect to see in each of the four quadrants, as outlined in Figure 8B. Our proposal is supported by empirical studies of skill acquisition, which find an inverse-U relationship between training magnitude and uncertainty and a sigmoid relationship between training magnitude and accuracy in multiple learning tasks (Gallistel, Fairhurst & Balsam 2004). Clearly, only a learning progression that traverses the quadrants in the order III→IV→I→II proposed in Figure 8B is compatible with both these observations.

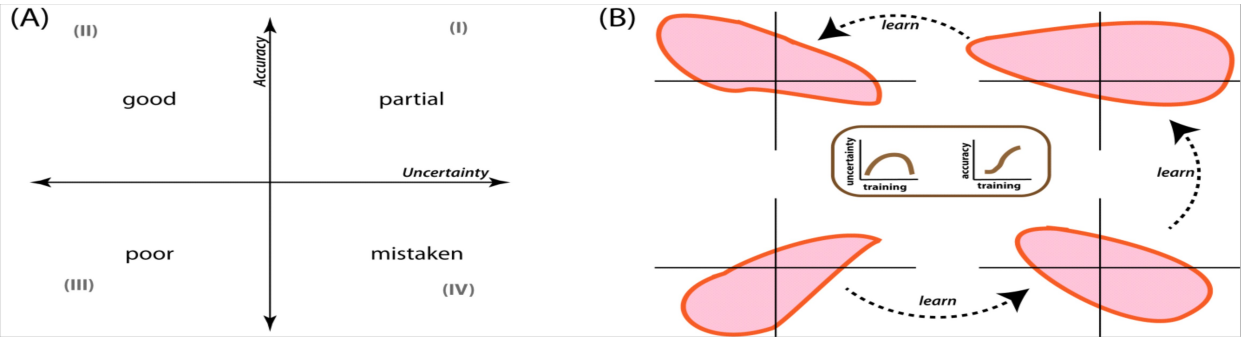


Figure 8: *An illustration of the learning zones defined through our analyses. (A) Students' understanding of concepts can be visualized on a 2-D plot showing how the accuracy with which they can contextually place concepts within a concept network interplays with their uncertainty about these interconnections. While the learning-based identification of the four quadrants is not rigorous, it should prove to be a useful visualization for both educators and students. (B) We can draw understanding contours using the number of concepts falling in each of the four quadrants. Larger numbers cause the contour lines to shift away from the origin. The understanding contours of different students and student populations can compactly represent information about the level of subject understanding (as in Figure 6). Insight from prior literature on the individual relationships between learning, accuracy and uncertainty (see inset) suggest that subjects will follow a progression through the quadrants III→IV→I→II as they progressively understand the concept space better. Tracking understanding contours across a student's educational career would allow educators to track her progressive understanding quantitatively.*

This methodological contribution has straightforward practical applications. Designing understanding contours from procedural statistics yields a compact and intuitive visualization of a student's holistic understanding of a subject area. We envisage such contours being generated on a per-student basis *ad libitum* for remedial student evaluations and periodically on a classroom basis (say every semester) for teacher evaluations and curriculum design.

Chapter 4: Dissecting physical models to improve mental models

The studies reported in chapters 2 & 3 helped us develop, respectively, a general and specific sense of students' difficulties and fluency with different concepts of DNA structure. The next step was to try to identify useful physical models that could improve students' understanding of difficult concepts in DNA structure. Before we could consider deploying such a study, we ran into a practical problem - building intricate models as a pedagogical exercise is time-consuming and effort-intensive for both learner and instructor. We anticipated considerable difficulty in scaling up such dyadic interactions to a large enough samples to draw statistically meaningful conclusions from. In response to this challenge, we hit upon the idea of having students dissect previously built models as a pedagogical exercise instead. However, since this had not been previously validated as a valid teaching approach, we decided to conduct a controlled experiment to validate it ourselves. Our experiment showed that, modulo concerns over sample sizes, model dissection is as good, and likely better, at helping students understand specific concepts about DNA structure. The principal advantage of this new approach is that it reduces the demarcation problem students inevitably face when handling complex biochemical systems. This chapter describes the details of our experiment validating model dissection as a viable pedagogical technique.

Background

As we anticipate above, an important practical concern in having learners build physical models from pre-fabricated components is an implicit trade-off between the physical degrees of freedom in building the model and the intensity of instructor supervision needed. Models that are too flexible, permitting multiple possible constructions, require greater supervision to ensure focused learning; models that are too constrained require less supervision, but can be constructed mechanically, with little to no conceptual engagement. This work proposes 'model-dissection' as an alternative to 'model-building', whereby instructors could make efficient use of supervisory resources, while simultaneously promoting focused learning. We report empirical results from a study conducted with college students, where we demonstrate that asking them to 'dissect' out specific conceptual structures from an already built 3-D model, leads to a significant improvement in conceptual understanding than asking them to build the 3-D model from smaller

components. Using questionnaires to measure understanding both before and after model-based interventions for two cohorts of students, we found that that both the 'builders' and the 'dissectors' improved in the post-test, but it was the latter group who showed statistically significant improvement. These results, in addition to the intrinsic time-efficiency of 'model dissection', suggest that it could be a valuable pedagogical tool.

Research suggests that physical manipulation of models facilitates cognitive processes of learner (Gabel & Sherwood, 1980; Martin & Schwartz, 2005). Physically manipulable models help learner to visualize complex ideas, processes and systems. Learning with models is particularly useful in context of concepts which are not directly perceptible to senses, viz., organic molecules. Model-building, where students build physical models themselves, leads to improved spatial understanding and the ability to translate that understanding from known to unknown problem situations (Dori & Barak, 2001).

A practical concern about model-building as an instructional aid is that one has to trade off degrees of building freedom with the intensity of instructor supervision. Using a completely open-ended kit for building allows for maximum exploration of possibilities, but requires a lot of instructor supervision to ensure everyone builds the right structure. On the other hand, using pre-fabricated kits with low degrees of building freedom permit instructors to be more hands-off, since very few deviations from the canonical structure are possible, but simultaneously permit students to put components together purely as a mechanical task – with little conceptual engagement.

We offer a solution to this problem – we suggest that students will learn better by breaking models than building them. To be more precise, we propose that getting students to '*dissect'* 3-D models is a more efficient way of teaching them about related concepts than having them build such models from kits. For understanding biological systems, which are inevitably complex, modular and intricate, dissection has historically proved to be a very powerful pedagogical device. How does one element of the system relate to its neighbors? What components connect to this one? How does the structure of this element support its biological function? Observing biological organs in situ creates a natural setting for studying such questions, and allows students

to figure out many such answers by the simple task of observation. Now, we propose that the benefits of dissection as a study method can also translate to learning-by-doing activities like physical model manipulation.

With a small empirical study, we explore the relative efficacy of model-building and model dissection in improving students' understanding of DNA structure. The DNA molecule is a very popular benchmark for such a comparative study, since it is an important concept that serves as an entry point to vast areas of molecular biology and biochemistry for pre-college biology students. It is also particularly apt for studying model-based pedagogical methods, because details of its 3D structure are best understood using models and a deep understanding of its 3D structure causes fewer misconceptions about its function later on in more advanced classes.

Method

Sample

Eighteen biology undergraduate students (6 males; 12 females) responded to a general call for a workshop on understanding DNA structure using 3-D physical model. Students were randomly assigned into two cohorts of 'model builders' and 'model dissectors'. Further, within each cohort, two groups were formed. Thus, in effect, there were two groups who were 'building' models and two groups who were 'dissecting' models. The two groups, in both the cohorts, had 5+4 students. The study was conducted as part of a workshop organized at HBCSE, Mumbai in 2014.

Study Design

The basic design of the experiment sandwiched model-related activity between a pre- and a post-test, administered using a set of MCQs (4 choices/1 correct) to each student individually. Questions for both pre- and post- sets were common for all students, but differed between themselves. Thus, a total of 32 questions were designed drawing upon common Grade 12 biology textbook resources.

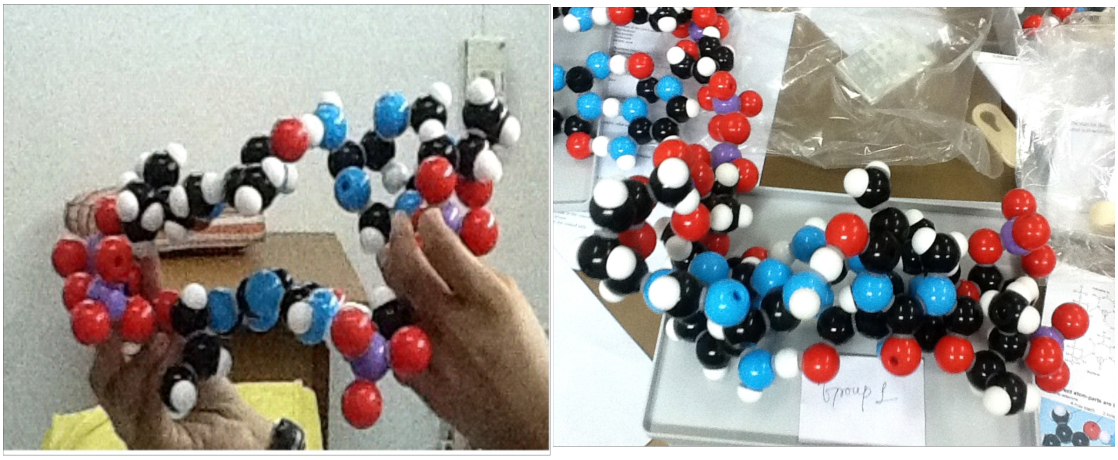


Figure 9: *Photographs depicting nucleotide base pairs (left) built by model builders from component atoms and (right) given as starting element to model dissectors*

Model-building intervention: The two groups were given a 2-D printed diagram of DNA structure, giving molecular details. Also given was differentially colored atomic component of 3-D DNA physical model (Fig. 9). Students in each group were asked to build the physical model using the components, while referring to a 2-D blueprint.

Model-dissecting intervention: The two groups were also given the 2-D printed diagram of DNA structure, giving molecular details. They were then given two nucleotide base pairs and were asked to successively dissect them to show the instructor, in order, (i) nucleotide, (ii) nucleoside, (iii) deoxyribose sugar molecule, (iv) nitrogenous base (ATGC) and (v) phosphate group.

Results

Physical manipulation leads to improved performance:

In line with previous research literature, our results suggest that an opportunity to physically manipulate the 3-D model led to improvement in conceptual understanding. Measuring conceptual understanding via response accuracy on a 16 question questionnaire, we found a 25% improvement overall in our study, with the difference between pre- and post-test scores statistically significant $t(34)= -2.5$, $p = 0.017$ (Fig. 10). While some of this improvement could

be attributed to mental priming during the re-test, this is unlikely to be a big effect, since the questions used during pre- and post-testing were different.

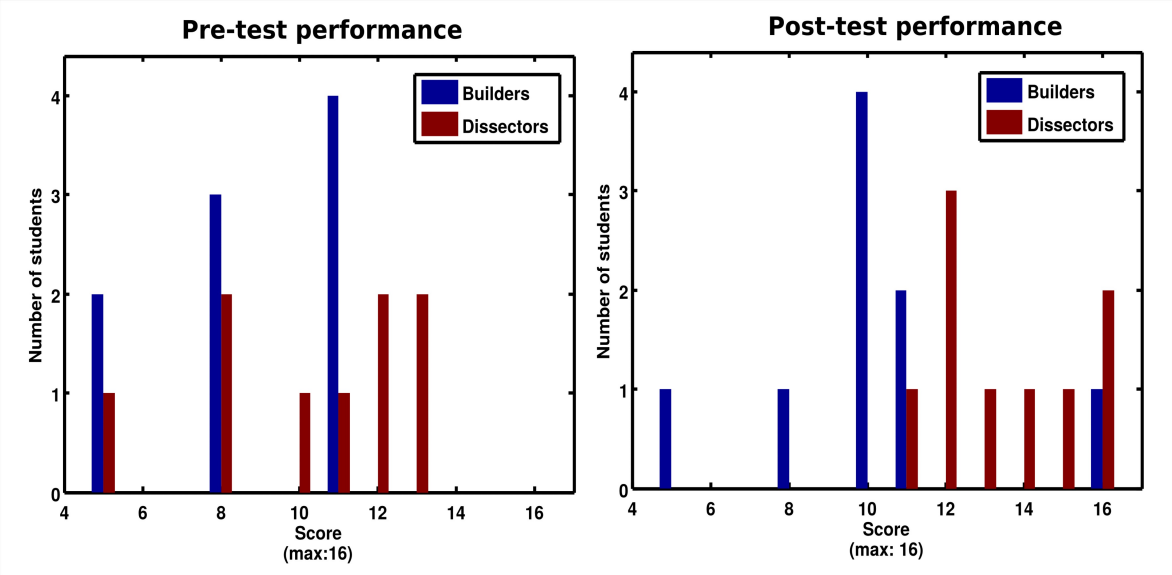


Figure 10: *Comparing pre- vs post-test performance for both our cohorts as measured by the number of questions (out of 16) each student got correct. While both groups showed improvement on the post-test, the 'dissector' group showed greater improvements than the 'builder' group, with nearly all students in the dissector group scoring above 75% on the post-test.*

Model dissection leads to significantly improved performance than model building:

While the overall sample showed improvement in test scores, this increase was larger for the dissector group, as illustrated in Figure 11. The difference between the performance of the two groups on the post test was statistically significant, $t(16)= -2.9$, $p= 0.01$. In contrast, the pre-test performance difference between the two groups was statistically insignificant, $t(16)= -1.26$, $p= 0.22$. These observations together demonstrate that, *ceteris paribus*, model dissection promotes performance to a greater degree than model building.

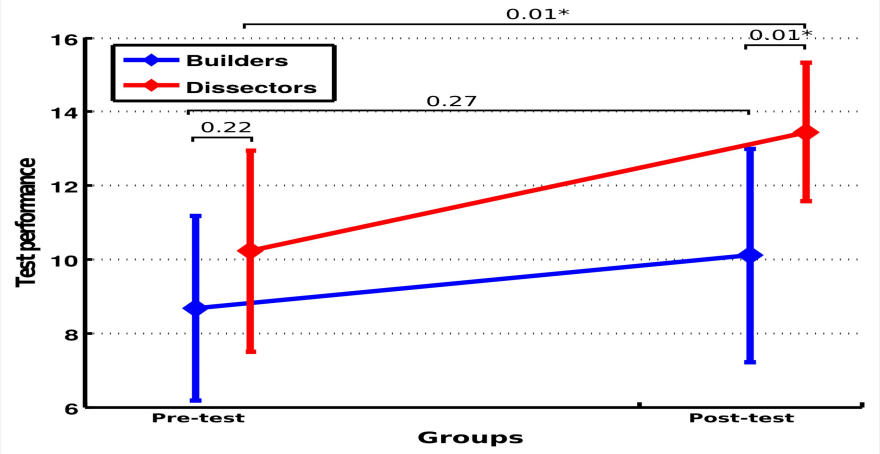


Figure 11: *Illustrating performance improvement in pre- vs post-tests of knowledge about DNA structure. All results are sample averages. Error bars represent +/- 1 SD. P-values are derived from two sample T-tests in all cases.*

Implications

(1) Model dissection can be more effective as a teaching aid than model-building.

(2) It is also more time-efficient, and standardizable, since dissection concepts can be determined beforehand.

Discussion

The primary conclusion of our study is that model dissection provides considerable pedagogical benefits. At least in our study, it outperforms model building in improving performance in context of understanding a complex and imperceptible molecular structure. The benefit of the model-dissecting intervention is not restricted to only those concepts that are explicitly probed in the dissection intervention. A more generalized benefit is also seen, so our results cannot be explained away by the trivial difference that model-building does not target specific concepts while dissection does.

Model-dissection naturally takes less time per student than building, although building requires less interactivity and so can be performed in parallel for multiple students. Overall, the greater efficiency of the dissection method in promoting understanding, even in our small study, suggests that it is a viable alternative to model-building as an instructional aid.

Chapter 5: Learning difficulties within and across different external representations

In the preceding chapters, we identified students' difficulties in understanding the DNA concept and its associations, and devised a new way of using physical models to teach students that might potentially ameliorate these difficulties. Along the way, by experimenting with concept maps and physical models, we modified their standard presentations to make them more effective for our purpose. These advances finally put us in the position to answer the main question of this thesis: how do different ERs amplify or reduce specific conceptual difficulties for students? We operationalized this question via a comparative evaluation of the efficacy of multiple external representations in promoting learning of the same concept for different cohorts of students. This is what we undertook in the study described in this chapter.

Study design

We investigated how interventions based on three different external representations of DNA structure influence the internal representations of pre-college biology students. The study followed a case study design, where individual sessions were video recorded. As differential interventions, three groups of five students each were asked to either 1) construct a concept map using preset concepts related to DNA structure, 2) dissect a symbolic 3-D model or 3) dissect a 3-D molecular model of DNA structure into simpler components.

The difference between *symbolic* and *molecular* models, from the standpoint of our experiment, was that molecular models restricted their visual appearance to faithfully reproduce the structure of the DNA molecule adhering to the stylized conventions of physical chemistry whereas symbolic models reify more complex subunits of the DNA structure, e.g. strands, bases etc. in order to present a more succinct visual representation, ignoring atom-level details.

To understand how students' internal representations changed, we asked them to draw a diagram of the DNA structure both pre- and immediately post-intervention, and after a one week interval. Further, clinical interviews were done both pre- and post-intervention, to track changes in each student's reasoning process, her understanding of the task, and the changes in her diagrams.

A rich body of literature guided the design of our study. Cox (1999) has suggested that the effectiveness of a particular external representation in a particular pedagogical context depends upon a complex 3-way interaction between – a) properties of representation, b) demands of the task & c) within subject factors such as prior knowledge & cognitive style. Since we hold task demands constant, and expect to pool outcomes across subjects given the same external representation to work with, we expect that differences in process and outcome during the task will reflect the influence of the affordances of these representations.

The overall workflow of the study follows the principles of 'descriptive synthesis' proposed by Schonborn & Anderson, (2009). Their experiment protocol was conducted in three phases a) eliciting conceptual understanding- prior to exposure of a model, b) eliciting reasoning based on their interpretation of the ER, c) eliciting evaluation & critique of the ER used. The pre-intervention diagram was our source for eliciting pre-exposure conceptual understanding; within task performance was assessed using observable markers of performance during the task and from differences between the post- and pre-task diagrams (see results below). Evaluation and critique of the representation was directly probed during the post-task clinical interview.

We rely strongly on the power of student-drawn diagrams as windows into their existing conceptual understanding and the shifts therein our interventions generate. This reliance is justified theoretically by multiple existing research programs that also use student-generated diagrams to measuring thought processes & way of reasoning (Beilfuss et al., 2004; Reiss & Tunnicliffe, 2001; Gobert, 2000; Gobert & Clement, 1999; Schonborn & Anderson, 2009).

Sample

Fifteen pre-college and college biology students participated in this study; we reimbursed their travel costs. Studies were conducted in 2015 at Aligarh, Uttar Pradesh. All participants provided written consent for participation in the study.

Analysis & Findings

A. Tracking internal representation: Diagrams

There were two separate analyses conducted quantitatively, one focused on tracking improvements in understanding using the progression of three diagrams (D1, D2, D3) generated

by each participant, one on their performance in the individual interventions themselves, measured using the variables we identified as appropriate in previous chapters. We report both below.

I Diagram analysis

Diagrams were analyzed for concepts that were elucidated either verbally, spatially or both. Note that 4 students (2 each in symbolic and molecular model group) did not turn up for the post week meet and, hence, we do not have D3 for them. We categorized elements drawn inside diagrams into three categories:

i) Spatial where, elements are located (symbolically or in molecular details) within the diagram without being labeled as a term.

ii) Verbal where, elements are not located within the diagram but are verbally mentioned and/or elaborated upon the sidelines of the diagram.

iii) Spatial-Verbal where, elements are both spatially located within the diagram and are also labeled verbally

From these element categorizations, we computed a summary quantitative indicator of diagrammatic competence – a verbal-spatial score. Verbal-spatial scores were calculated per diagram by dividing the number of concepts represented spatial-verbally divided by the total number of concepts represented in the diagram. The total number of concepts was determined by combining the number of concepts represented only spatially, only verbally and spatial-verbally.

1. Almost every participant improved on the verbal-spatial scores post-task

Student	**Verbal-Spatial Scores**		**Diagrammatic pattern in D1-D2**
	D1	**D2**	
Aditi	0.67	0.83	H--H
Kajal	0.86	0.83	H--H
Femina	0.3	0.8	L—L
Kush	0.8	0.83	H—L
Love	0.57	0.89	H--L
Harendra	0.38	0.5	H—L
Pushkar	0.82	0.89	H—L
Deeksha	0.5	0.7	L—L
Atul	0.5	0.5	H--H

Pramod	0.17	0.33	H—L
Ozair	0.89	0.86	H—L
Arshad	0.22	0.86	H—H
Shashank	0.25	0.88	H--L
Kushagra	0.78	0.75	H—L
Devendra	0.29	0.5	H--L

Notes:

a) In the above table, the first 5 students did the concept map task; second five did the skeletal model dissection and the last five did the molecular model dissection.

b) 11 out of 15 students showed increase in verbal-spatial scores post task; 3 decreased and 1 remained the same. It is to be noted that the 3 students who showed decrease did not label a term in D2 which they had already labeled in D1 and hence, we cannot say that the representations had a negative impact on them. It is just that they focused on new concepts. This is reflected by the difference between the scores which is 0.03 in all three cases.

Overall, the interventions led to enhanced verbal-spatial performance in 73% of students in the post-test diagrams. More striking, though, was the finding that there were substantial differences in performance improvement between the three interventions. Students who interacted with the diagram-like symbolic model showed consistent, small improvements in performance. Students who interacted with the other two representations showed either extremely high or low improvements in performance. Given the large size of variability relative to average performance improvement itself, this finding supports pedagogical theories that suggest that difficulties in translating information across multiple representations is a critical bottleneck in pedagogical interventions.

2. Ladder representation of the DNA structure dominated the post-task diagrams

11 students made L (ladder) representation of DNA in D2. No one went back from Ladder to Helical (L--H). Ladder (L) representation suggests that students are narrowing their focus on a small area of DNA and are sharing the details. When H (Helical) representation is made, the idea is to give a broad overview of the DNA structure and it is not convenient to show the detailed molecular structures of DNA elements within the constraints of the helix and, hence, we can say

that 'L' representations give a more detailed picture of the molecule and 'H' representations give more detailed overview (like pitch of the helix, grooves etc.)

Hence, moving to L representation suggests that there is something that is getting transferred from the external representations (concept map, skeletal model or molecular model) that is enabling students to focus on the detailed aspect. Here's the break-up of activity in the 3 groups:
Concept map: 2/5 students went from H--L in D2
Skeletal model: 3/5 students went from H--L in D2
Molecular model: 4/5 students went from H--L in D2

Students' diagrams systematically changed in visual format and emphasis, sensitive to task demands. Whereas 87% students drew diagrams emphasizing the double helical structure of the DNA molecule before the intervention, 69% of them switched to drawing ladder-like two-dimensional cross-sections of DNA after intervention, and persisted with this format in the 1 week post-test, suggesting long-term effects as a consequence of the intervention.

B. Tracking overt behavior: interaction with external representation

1. Concept-map

Map-builder	Total propositions	Valid propositions	F-measure
Femina	28	22	0.88
Love	28	22	0.88
Kush	24	19	0.88
Kajal	20	15	0.77
Aditi	24	13.5	0.70

2. Symbolic-model dissection

Dissector	Concept to be dissected				
	Nucleotide	Nucleoside	Deoxyribose sugar molecule	4 nitrogenous bases	Phosphate group
Atul	X*	X	X	√!	-
Pramod	X	X	-	√	-
Deeksha	X	√	√	√	-
Pushkar	√	√	√	√	√
Devendra	X	√	X	√	-

***Concepts that were not dissected; !Concepts that were dissected**

3. Molecular-model dissection

Dissector	Concept to be dissected				
	Nucleotide	**Nucleoside**	**Deoxyribose sugar molecule**	**4 nitrogenous bases**	**Phosphate group**
Harendra	X	X	√	X	√
Shashank	√	√	√	X	√
Kushagra	√	√	√	X	√
Ozair	√	√	√	X	√
Arshad	X	X	√	X	√

As the tables above demonstrate, most of the students in our sample were quite knowledgeable about DNA structure. For example, the mean F-measure for the concept card sample was 0.822, compared to the average F-measure of 0.69 in the sample of students used in the move count study described in Chapter 3. It is even more interesting, therefore, to document the pattern of mistakes they make, since generalizable patterns seen therein should indicate concepts that are of particular difficulty to all learner, demonstrating failures of pedagogy, not student effort – the high baseline competence of our sample reduces the possible impact of latent individual learning deficiencies.

The multiple representation-based design of our study allowed us to discover both sources of conceptual errors, viz. concepts that students across all our representations are susceptible to, and representation-specific errors, errors seen more often in particular representations, either because the cognitive affordances of that representation made the apperception of that concept particularly difficult, or because they probed an aspect of the students' understanding that the other representations were insensitive to.

C. Tracking internal representation: Clinical interview

Critiquing the external representation

ER	Interactor	Advantages of the ER	Disadvantages of the ER	Suggestion for improvement
	1. Femina	(Makes it) easy to understand	Time consuming; not easy to make	Should be used in conjunction with

				diagram.
Concept map	2. Love	(Helps to) remember concepts for a longer time	Gives a broad overview but fails to give a finer picture.	Bigger arrows (to show links between concepts) may be used.
	3. Kush	I liked it and I enjoyed it; I'll likely remember it forever	-	-
	4. Kajal	Helps to clearly understand; It enhances one's interest (in learning) and (helps to) remember and recall conceptual links.	Multiple concepts may lead to confusion.	-
	5. Aditi	Like a graph, it (helps) figure out the conceptual links of the DNA in the brain	The link breaks when you do not know about it	-
Symbolic-model				
	1. Atul	Easy model; not time-taking; easy to explain others	-	I'll use spring to show (helical) turns; also make it a little bigger
	2. Pramod	Clarifies nucleotide, nucleoside & N bases	You cannot know it completely (sugar & phosphate group)	-
	3. Deeksha	Makes it easy to visualize and,	Insufficient to explain concepts	Will represent the bonds and also

		hence, to represent & understand; easy to make	like formation of phosphodiester bond, or the 5'- 3' running strands.	name the elements
	4. Pushkar	Color coding makes it easy to recognize and differentiate and also dissect.	-	Will use different shapes and colors for different elements; bonds could be differentiated; may use magnets and metals; may be bulky but will be good.
	5. Devendra	Gives a 3-D view of what is attached with what	A small representation; not very clear.	Will make it bigger; show helical turns and clearly represent the bases
Molecular-model dissector				
	1. Harendra	The 3-D structure of sugar-phopshate backbone, N-bases-purines, pyrimidines were clearly visible.	Can't tell from where it gets started; won't know if learning for the first time; small unit	Will add more nitrogen bases (to extend the model)
	2. Shashank	Big (prominent) Po4 group & N bases; looks very nice	It has balls; you need to remember the color of the ball first and then	Will wrap paper around these balls and name carbon, nitrogen etc.; also

			recognize.	show bonds through strips
	3. Kushagra	Shows structure of elements which cannot be drawn so in a 2-D diagram; tells about arrangement of base pairs	Not easy to handle; if dissected, will take a long time to join it.	Will add more base pairs (to extend) and will include bigger balls for all atoms and smaller for H atoms.
	4. Ozair	This is a luxury (3-D model)	So many balls can mess up with your thoughts	-
	5. Arshad	An interesting model; clarifies concepts	Confusing at times	-

The clinical interview on critiquing the representation presents an interesting insight about learner's point of view. The disadvantages and the suggestions for improvement prominently reflected their own points of difficulties that they faced while completing the task.

Discussion

As an example of purely conceptual errors, all participants of the concept map task either did not use the 'planar molecule' card or linked it incorrectly on the map (the problem was noted in Chapter 2). Possible reasons – they either do not understand the meaning of the term 'planar', or they understand the meaning of the word 'planar' but they do not recall exactly which molecule is planar. This in turn is connected, in the model-handling students with misunderstanding of the orientation of the nitrogenous bases in a base pair.

As an example of errors likely enforced by properties of a particular representation, consider the case of modelers dissecting out the four nitrogenous bases. All the symbolic modelers got the four nitrogenous bases correct, while all the molecular modelers got it wrong. The problem, as anticipated, lies in the affordances of the model accessible to the dissector. In the symbolic model, participants do not need to know the molecular details of the bases but this information

becomes significant when they have to dissect out molecules from a sea of colored atoms in the molecular model. This is a clear example of a demarcation problem, caused by inadequate symbol grounding, wherein participants failed to identify the points where the molecules had to be broken.

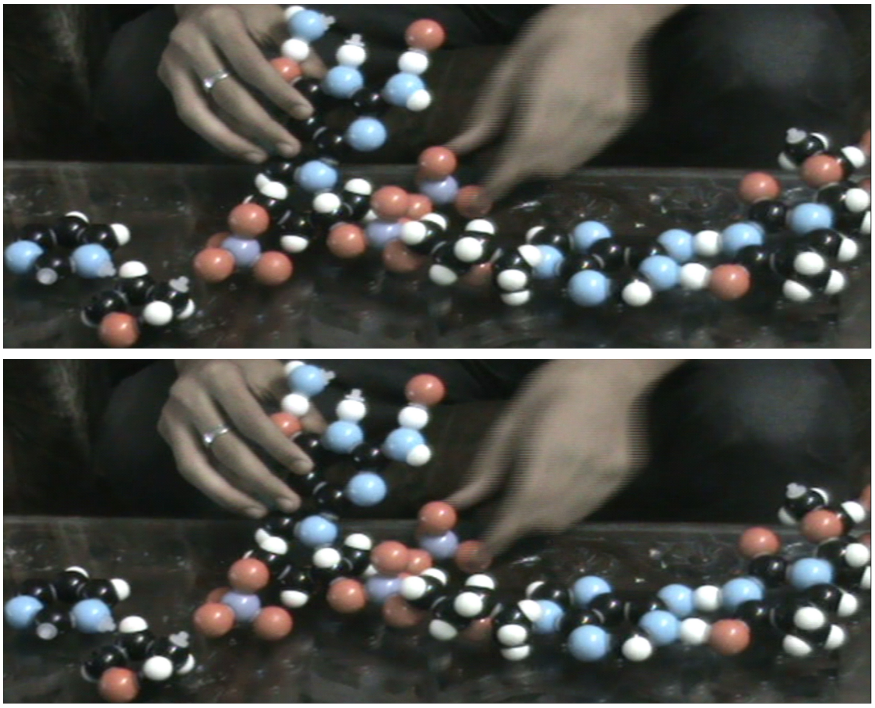


Figure 12: *A molecular modeler struggles to identify the limits of the nitrogenous base*

As a complementary example, the phosphate group (PO_4) was difficult to identify in the symbolic model but easy to recognize in the molecular model. There are possibly twin reasons for this. One, in standard textbooks, the shorthand PO_4 is commonly used for phosphate group and two, the P atom is used only in the backbone and hence, identifying a purple color surrounded by four red atoms was a relatively easy task. On the other hand, in the symbolic model, all the molecules were represented by different colored blocks, making the recognition task much harder.

For an example of errors caught by the subtlety of a particular model, consider the specific difficulty faced by multiple students in identifying where the sugar molecule is attached in the structure. Is the base directly attached with the sugar molecule or to the phosphate group?

Figure 13: *A symbolic modeler incorrectly points to denote the position of deoxyribose sugar molecule*

In the image above, a dissector points at the middle of two bases to represent the position of the deoxyribose sugar molecule. While concept-mapping or a written test might have missed the fact that the student is hazy about the precise location of the sugar molecule, the symbolic model leaves no such room for uncertainty.

A related example: concept mapping identified situations wherein students know there was a general relationship between two concepts but were not sure about the causality. This happened most prominently when all participants used the linking phrase 'contain' to signify the relationship between 'genes' and 'DNA/Double helix' but the directionality of the arrow was not uniform.

Thus, this study shows that concept maps are most efficient when the focus is on establishing links between different concepts and the flow of relationships, symbolic models are best suited when focus is on spatial organization, and molecular models are favorable when the focus is on acute understanding about the spatial and structural organizations.

Chapter 6: Construction of the DNA database

Context

One of the major motivations behind this dissertation project was the awareness about the 'integration gap' – a large divergence between the biology which is known to researchers and the biology which is experienced in schools (Yager, 1983). There are two ways to lower this integration gap - a) researchers simplify their work and share it with instructors and students, or b) instructors and students come to researchers with the difficulties that they face in making sense of new developments in the field. The first option is likely more efficient – it entails that researchers keep up with pedagogical research documenting the difficulties faced by teachers and students in understanding previous material, and develop resource materials which could be easily integrated with regular pedagogical practice.

Through the course of this project, we've tried to understand learners' difficulties with DNA structure. Through this chapter we want to extend that understanding by reaching out to biology teachers and students, in the form of a publicly accessible database of models of DNA structure. The database is created on the basis of the findings in Chapter 4 of this dissertation where we found that model-dissection showed considerable pedagogical benefits. Capitalizing on these findings, we have organized around 100 structural representations of DNA to create the database.

Sources

The internet and biology textbooks formed the major sources of the vast array of representations used in the database.

Basis of organization

The scheme for organizing these structural representations involves the identification and dissection/demarcation of the following five elements of the DNA structure – a) Nucleotide b) Nucleoside c) Deoxyribose sugar d) The 4 nitrogenous bases (Adenine, Thymine, Guanine & Cytosine) d) Phosphate group and e) Bonds (Hydrogen, Glycosidic and the Phosphodiester).

Ideally, had the representation been physically manipulable, learner could have benefited by 'dissecting' out the above five elements from it. Since physically manipulable models are not easily available, we have modified the feature of 'dissection' to 'demarcation' of the elements of

DNA structure, where, the limits of the individual elements need to be marked. In the database, a representation occupies higher position in the hierarchy when all the aforementioned five elements can be identified and demarcated.

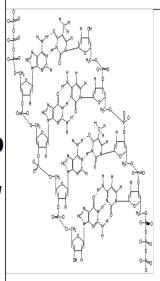
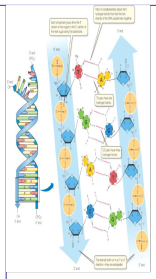
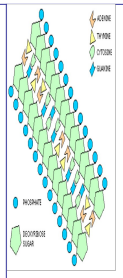
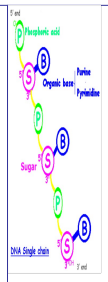
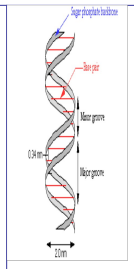
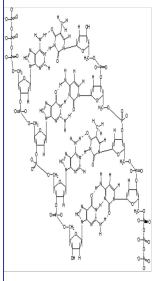
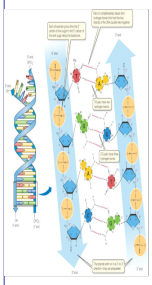
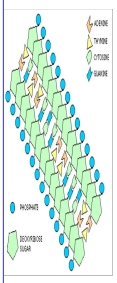
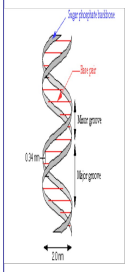
Structural elements to be 'dissected' or 'demarcated'	**External representation**				
					
					
Nucleotide	√	√	√	√	X
Nucleoside	√	√	√	√	X
Deoxyribose sugar	√	√	√	√	X
4 N bases	√	√	X	√	X
Phosphate group	√	√	√	√	X
Bonds **Hydrogen**	√	√	X	X	X
Glycosidic	√	√	√	X	X
Phospho-diester	√	√	√	X	X

Table: *Sample organization of 5 external representations of DNA structure on the basis of identification & 'demarcation' of the five elements.*

In the above table, one can easily demarcate the five elements in the first two representations and, hence, these two will lie higher in the hierarchy, whereas the last representation gives the overview of the DNA helical structure and one cannot identify & demarcate any of the five structural elements and, hence, it will lie lower in the hierarchy.

Implications

We believe that this collation of multiple representations of the DNA structure will be an efficient pedagogical tool for both biology teachers and students for the database offers a range of choice. The choice gives the freedom to focus on particular concepts and leave the rest. So, for instance, when instructors choose to move from building generic conceptual understanding to specific conceptual understanding, they can use representations from the lower hierarchy (viz., helical representations) first and then move up in the hierarchy (towards molecular representations).

In the database, a few external representations have found the same level in the hierarchy, owing to the possibility they offer to demarcate similar elements. This gives freedom to instructors and learners to choose representations from within the same hierarchy.

This database will also allow audience to add other structural representation of the DNA structure to the existing list of representations corresponding to their hierarchical position. This will encourage teachers and learner to actively engage with the tool and, thus, also enrich the repository.

Chapter 7: Discussion & Implications

The overarching aim that guided the four studies described in this dissertation was to understand how external representations influence the process of learning. To capture this process, we made learners interact with different ERs in a controlled manner. Specifically, we designed physical manipulation tasks for different ERs and intensively observed this process of interaction. The density of our observations gave us rich information about students' conceptual and representational difficulties and it also gave us an opportunity to improve the efficiency of existing tools to capture these difficulties.

Even though we focused on a specific biological concept – DNA structure – several generalizable conclusions emerged. Primarily, the process of learning was observed to be punctuated by episodes of conceptual difficulties triggered by interaction with the external representation(s). These conceptual difficulties were elucidated, for instance, when learners used incorrect 'palm gesture' to represent the orientation of the nitrogenous base pairs, when they tried to press the 3-D model of the DNA so hard on the table that it became flat, closely resembling the 2-D representation in the textbook (Chapter 2) or, when learner showed lower facility with concepts like, 'planar molecules' or 'glycosidic bonds' during the concept-map building task (Chapter 3) or, when learner found it difficult to 'dissect out' different elements of the DNA structure because they could not identify the boundaries of these elements (Chapters 4 & 5).

Such representation-specific conceptual difficulties arise because interactions with the external representations lead to the creation of cognitive 'hurdles' in the learner's mind (Thompson, 1994). These 'cognitive hurdles' are, in fact, markers of learning and their presence re-affirms the constructivist position that learners' minds are not *tabula rasa* and that they come with their prior knowledge (Limo´n, 2001). Critically, these difficulties are driven entirely by students' prior knowledge of DNA *structure.* These are conceptually distinct from difficulties in parsing details about DNA structure as a consequence of prior incomplete knowledge about DNA function. For instance, the common attribution of trait inheritance to genes often cause naïve students to think of DNA strands being made up of genes as distinct physical blocks (Shaw et al., 2008). While

our work has focused on identifying difficulties associated only with structure, future extensions must necessarily engage with the additional complexity generated by students' misconceptions about the structure-function mapping.

Secondarily, we also observed that students across the four studies manipulated the external representations extensively, and used the affordances of these models to develop and/or amend their knowledge considerably. This supports the stance of Schwartz (2005) that such interactions play an important constitutive role in developing understanding and justifies our choice of physical manipulation as our conduit to students' mental operations.

At the same time, the large role of manipulating external representations in the trajectory of students' understanding strongly highlights the importance with which questions regarding the design of effective ERs must be answered. Which ER to use for which concept? Allow free-form discovery or guided manipulation? Which sequence of models to use to best explain a particular series of concepts? The large effect sizes seen in some of our controlled studies accentuate the urgency with which these questions must be addressed. While we could not have presumed to answer them comprehensively in this dissertation's span, our focus on answering them for one specific subject area – DNA structure – could help construct a blueprint for other such efforts. Our specific contributions to biology education emerged as particularized answers to these general questions, and can be broadly categorized into the following three themes.

One, by reporting on the range of conceptual difficulties that students face while learning about the DNA structure (Chapters 2, 3 & 5), we equipped biology instructors with the information that could help them tailor their classroom practices and address learners' concerns, and also make informed choices regarding the use of simplified external representations.

Two, by proposing simplified pedagogical tools for specific representation-driven difficulties, viz., the 'palm gesture' (for orientation of the base pairs; Chapter 2) or for general structure, viz., 'dissection' of 3-D models (Chapters 4 & 5) , we provided direct assistance to making instruction using these representations more effective going forward. Many of our suggestions, like model-

dissection, are straightforwardly generalizable to other learning areas, further amplifying their impact.

Three, by providing an organized list of external representations on DNA structure (Chapter 6), we provide biology instructors with a handy menu for selecting models to use in their teaching practice, sensitive to the representation-specific concerns we have highlighted alongside.

Additionally, our understanding of the affordances of different ERs can be translated into a useful sequence of tools that can be used in a classroom. Pedagogical transaction usually proceeds by giving a general idea about the area of interest to giving specific insights about relevant concepts. This flow of information goes from generic to specific. Mirroring this trajectory, we recommend that these tools be used in the following sequence-

Concept maps → Symbolic models → Molecular models

This sequence could be exploited in learning about various concepts across different subjects where spatial relations are critical to understanding function. An interesting example to consider within biology is the structure of chlorophyll molecule which is vital for photosynthesis. The biomolecule is composed of a central porphyrin ring and a phytol chain. Based on the type of side chain attached to the central ring, chlorophyll is either 'a' (with -CH3 or methyl group) or 'b' (with -CHO or aldehyde group). This structural difference between the two types is critical to their absorption of light of different wavelengths. Based on our proposed sequence, a concept map exercise can first be used to let learners identify and connect relevant structural and functional concepts and then a symbolic model may be used to spatially locate the different structural components, and finally the molecular model may be used to understand how the relative locations of different atoms and the series of single and double bonds in the phytol chain contribute to the role played by the two chlorophyll photo-receptors.

Similar lesson plans can be constructed for a variety of biochemistry concepts. Using the refined variations of ERs developed in our thesis in such plans would benefit both instructors and students. Since molecular models are useful primarily for biochemistry concepts, instructors may

use only concept maps and symbolic models to develop deeper understanding for other non-biochemistry concepts.

Apart from contributions to the education community, this work also uncovered multiple future research directions. The tools we have designed and the methodological improvements we have suggested could be made more efficient over a period of time. For instance, we recognize the labor-intensive nature of our concept map assessment and believe that improved methods for calculation of moves, possibly leveraging touchscreens, could significantly enhance its pedagogical value. The novel process analyses proposed in this work also presents an opportunity to be applied in various other contexts, both to characterize students' difficulties and to improve existing pedagogical tools.

Publications

Journal

- **Srivastava, A.** (2016). Building mental models by dissecting physical models. *Biochemistry and Molecular Biology Education*, *44*(1), 7-11.

Book Chapter

- **Srivastava, A.**, & Ramadas, J. (2013). Analogy and Gesture for Mental Visualization of DNA Structure. In D. Treagust & C. Tsui (Eds.), *Multiple Representations in Biological Education* (Vol. 7, pp. 311-329). Netherlands: Springer Netherlands.

- **Srivastava, A**., Srivastava, N., & Chandrasekharan, S. (under review). Order of element placement in physical concept-mapping reveals differences in subject matter comprehension. In Thomas Barkowsky, Heather Burte, Christoph Hölscher & Holger Schultheis (Eds.) *Lecture Notes in Artificial Intelligence: Spatial Cognition X*.

Conference

- **Srivastava, A.**, & Ramadas, J. (July, 2011). *Using Analogy and Gesture for Mental Visualization of DNA Structure*. Poster presented at Gordon Research Conference on Visualization in Science and Education. Bryant University, RI, USA.

- **Srivastava, A**., Srivastava, N., & Chandrasekharan, S. (April, 2014). *Measure concept-mapping, not concept-maps: Procedural analysis elucidates stages in students' understanding of biology concepts*. Paper presented at the Annual Meeting of the American Educational Research Association (AERA). Philadelphia, USA.

- **Srivastava, A.** & Chandrasekharan, S. (September, 2015). *Building mental models by dissecting physical models*. Paper presented at the Biennial Conference of the European Science Education Research Association (ESERA). Helsinki, Finland.

- **Srivastava, A.** & Chandrasekharan, S. (July, 2016). *How external representations of a biological concept change learner' internal representations*. Paper presented at the National Meeting of Society for the Advancement of Biology Education Research (SABER). University of Minnesota, MN, USA.

- **Srivastava, A**., Srivastava, N., & Chandrasekharan, S. (August, 2016). *Order of element placement in physical concept-mapping reveals differences in subject matter comprehension*. Poster presented at the Spatial Cognition conference. Philadelphia, USA.

References

Anderson, K. C., & Leinhardt, G. (2002). Maps as representations: Expert novice comparison of projection understanding. *Cognition and Instruction*, *20*(3), 283-321.

Bahar, M., Johnstone, A.H., & Hansell, M.H. (1999). Revisiting learning difficulties in biology. *Journal of Biological Education*, 33 (2), 84-86.

Barsalaou, L.W. (1999). Perceptual symbol systems. *Behavioral and Brain Sciences*, 22, 577- 560.

Beilfuss, M., Dickerson, D., Boone, W., & Libarkin, J. (2004). Exploring conceptual understandings of groundwater through student's interviews and drawings. In *Proceedings of the 77th Annual Meeting of the National Association for Research in Science Teaching, Vancouver*.

Bodner, G. M., & Domin, D. S. (2000). Mental models: The role of representations in problem solving in chemistry. *University Chemistry Education*, *4*(1).

Cañas, A. J., Novak, J. D., & Reiska, P. (2015). How good is my concept map? Am I a good Cmapper?. *Knowledge Management & E-Learning: An International Journal (KM&EL)*, *7*(1), 6-19.

Chandrasekharan, S. (2009). Building to discover: a common coding model. *Cognitive Science*, *33*(6), 1059-1086.

Clark, A. (1997). *Being there: Putting brain body and world together again*. Cambridge, MA: MIT Press.

Cooper, M. M., Grove, N., Underwood, S. M., & Klymkowsky, M. W. (2010). Lost in Lewis structures: An investigation of student difficulties in developing representational competence. *Journal of Chemical Education*, *87*(8), 869-874.

Cox, R. (1999). Representation construction, externalised cognition and individual differences. *Learning and instruction*, *9*(4), 343-363.

DiCarlo, S.E. (2006). Cell biology should be taught as science is practised. *Nature Reviews Molecular Cell Biology*, 7, 290-296.

Duncan, R. G., & Reiser, B. J. (2007). Reasoning across ontologically distinct levels: Students' understandings of molecular genetics. *Journal of Research in Science Teaching*, *44*(7), 938-959.

Dori, Y. J., & Barak, M. (2001). Virtual and physical molecular modeling: Fostering model perception and spatial understanding. *Educational Technology & Society*, 4(1), 61-74.

Duit (1991). On the role of analogies and metaphors in learning science. *Science Education*, 75 (6), 649-672.

Gabel, D., & Sherwood, R. (1980). The effect of student manipulation of molecular models on chemistry achievement according to Piagetian level. Journal of Research in Science Teaching, 17(1), 75-81.

Gallistel, C. R., Fairhurst, S., & Balsam, P. (2004). The learning curve: Implications of a quantitative analysis. *Proceedings of the National Academy of Sciences of the United States of America*, 101(36), 13124-13131.

Gentner, D. (1989). The mechanisms of analogical learning. In Vosniadou, S and Ortony, A. (1989). *Similarity and Analogical Reasoning* (pp. 199-24). Cambridge: Cambridge University Press.

Gibson, J. J. (1979). The ecological approach to visual perception.

Gobert, J. D. (2000). A typology of causal models for plate tectonics: Inferential power and barriers to understanding. *International Journal of Science Education*, *22*(9), 937-977.

Gobert, J. D., & Clement, J. J. (1999). Effects of student-generated diagrams versus student-generated summaries on conceptual understanding of causal and dynamic knowledge in plate tectonics. *Journal of research in science teaching*, *36*(1), 39-53.

Goldin-Meadow, S., Beilock, Sian L. (2010). Action's Influence on Thought: The case of gesture. *Perspectives on Psychological Science*, 5 (6), 664-674.

Harle, M., & Towns, M. H. (2012). Students' understanding of external representations of the potassium ion channel protein, part I: Affordances and limitations of ribbon diagrams, vines, and hydrophobic/polar representations. *Biochemistry and Molecular Biology Education*, *40*(6), 349-356.

Justi, R. and Gilbert, J. (2006). The role of analog models in the understanding of the nature of models in Chemistry. In Aubusson, P.J. and Harrison, A. G. and Ritchie, S.M. (2006). *Metaphor and Analogy in Science Education* (pp. 119-130). Dordrecht: Springer.

Kelly, R. M., & Jones, L. L. (2008). Investigating students' ability to transfer ideas learned from molecular animations of the dissolution process. *J. Chem. Educ*, *85*(2), 303.

Kharatmal, M., & Nagarjuna, G. (2008). Exploring roots of rigor: A proposal of a methodology for analyzing the conceptual change from a novice to an expert. In *Concept Mapping: Connecting Educators. 3rd International Conference on Concept Mapping* (pp. 391-398).

Kirsh, D, & Maglio, P. (1994). On distinguishing epistemic from pragmatic action. *Cognitive science*. 31;18(4):513-49.

Kirsh, D. (2009). Interaction, external representation and sense making. Unpublished manuscript. Retrieved from *adrenaline.ucsd.edu* on 17th July, 2016

Lewis, J., & Wood-Robinson, C. (2000). Genes, chromosomes, cell division and inheritance-do students see any relationship?. *International Journal of Science Education*, *22*(2), 177-195.

Lewis, J. (2004). Traits, genes, particles and information: re-visiting students' understandings of genetics. *International Journal of Science Education*, 26 (2), 195-206.

Lewis, J., & Kattman, U. (2004). Traits, genes, particles and information: re-visiting students' understandings of genetics. *International Journal of Science Education*, 26 (2), 195-206.

Limón, M. (2001). On the cognitive conflict as an instructional strategy for conceptual change: A critical appraisal. *Learning and instruction*, *11*(4), 357-380.

Lomask, M., Baron, J. B., Greig, J., & Harrison, C. (1992, March). *ConnMap: Connecticut's use of concept mapping to assess the structure of students' knowledge of science*. In Annual Meeting of the National Association of Research in Science Teaching. Cambridge, MA.

Maharashtra State Board of Secondary and Higher Secondary Education. (2009). Biotechnology. In *Standard XII 'Biology'*, Chapter 2 (pp. 13-33). Pune: MSBSHSE.

Marbach-Ad, Gili (2001). Attempting to break the code in student comprehension of genetic concepts. *Journal of Biological Education*. 35(4), 183-189.

Marbach-Ad, Gili and Stavy, Ruth (2000). Students' cellular and molecular explanations of genetic phenomena. *Journal of Biological Education*. 34 (4), 200-205.

Martin, T., & Schwartz, D. L. (2005). Physically distributed learning: Adapting and reinterpreting physical environments in the development of fraction concepts. Cognitive science, 29(4), 587-625.

Mathai, S. and Ramadas, J. (2009). Visuals and visualization of human body systems. *International Journal of Science Education*, 31 (3), 439-458.

McClure, J. R., Sonak, B., & Suen, H. K. (1999). Concept map assessment of classroom learning: Reliability, validity, and logistical practicality. *Journal of Research in Science Teaching*, 36(4), 475-492.

Novak, J.D., & Gowin, D.B. (1984). *Learning how to learn*. Cambridge: Cambridge University Press.

Patrick, M. D., Carter, G., & Wiebe, E. N. (2005). Visual representations of DNA replication: Middle grades students' perceptions and interpretations. *Journal of Science Education and Technology*, *14*(3), 353-365.

Padalkar, S. and Ramadas, J. (2010). Designed and spontaneous gestures in elementary astronomy education. *International Journal of Science Education*, first published on: 15 November 2010 (iFirst), 1-37.

Pande, P., & Chandrasekharan, S. (2016). Representational competence: towards a distributed and embodied cognition account. *Studies in Science Education*, 1-43.

Reiss, M. J., & Tunnicliffe, S. D. (2001). Students' understandings of human organs and organ systems. *Research in Science Education*, *31*(3), 383-399.

Rotbain, Y., Marbach-Ad, G., & Stavy, R. (2005). Understanding molecular genetics through a drawing-based activity. *Journal of Biological Education*, 39 (4), 174-178.

Rotbain, Y., Marbach-Ad, G., & Stavy, R. (2006). Effect of bead and illustrations models on high school students' achievement in molecular genetics. *Journal of Research in Science Teaching*, 43 (5), 500-529.

Ruiz-Primo, M. A., & Shavelson, R. J. (1996). Problems and issues in the use of concept maps in science assessment. *Journal of Research in Science Teaching*, 33(6), 569-600.

Schönborn, K. J., & Anderson, T. R. (2009). A model of factors determining students' ability to interpret external representations in biochemistry. *International Journal of Science Education*, *31*(2), 193-232.

Shaw, K. R. M., Van Horne, K., Zhang, H., & Boughman, J. (2008). Essay contest reveals misconceptions of high school students in genetics content. *Genetics*, *178*(3), 1157-1168.

Siegler, R. S. (2006). Microgenetic analyses of learning. *Handbook of child psychology*.

Srivastava, A., & Ramadas, J. (2013). Analogy and Gesture for Mental Visualization of DNA Structure. In D. Treagust & C. Tsui (Eds.), *Multiple Representations in Biological Education* (Vol. 7, pp. 311-329). Netherlands: Springer Netherlands.

Srivastava, A., Srivastava, N., & Chandrasekharan, S. (April, 2014). *Measure concept-mapping, not concept-maps: Procedural analysis elucidates stages in students' understanding of biology concepts*. Paper presented at the Annual Meeting of the American Educational Research Association (AERA). Philadelphia, USA.

Thompson, P. (1994). Students, functions, and the undergraduate curriculum. In E. Dubinsky, A. Schoenfeld, & J. Kaput (Eds.), Research in collegiate mathematics education. (Vol. 1, pp. 21-44). Providence, RI: American Mathematical Society.

Tsui, C.-Y., & Treagust, D.F. (2003). Genetics reasoning with multiple external representations. *Research in Science Education*, 33, 111-135.

Van der Aalsvoort, G. M., Van Geert, P., & Steenbeek, H. W. (2009). Microgenetic methodology: Possibilities with regard to research on learning and instruction. *Investigating Classroom Interaction: Methodologies in Action; K. Kumpulainen, CE Hmelo-Silver, & M. César (Eds.)*, 203-229.

Van Rijsbergen, C. J. (1986, September). (invited paper) A new theoretical framework for information retrieval. In *Proceedings of the 9th annual international ACM SIGIR conference on Research and development in information retrieval* (pp. 194-200). ACM.

Watson, J.D., & Crick, F.H.C. (1953 a). Molecular structure of nucleic acids: A structure for deoxyribose nucleic acid. *Nature*, 171 (4356), 737-738.

Yager, R. E. (1983). The importance of terminology in teaching K‐12 science. *Journal of Research in Science Teaching*, *20*(6), 577-588.

Zhang, J., & Norman, D. A. (1994). Representations in distributed cognitive tasks. *Cognitive science*, *18*(1), 87-122.

Appendix- A

Pre-test questionnaire (Study 3)

Instruction: Circle the most appropriate response.

1. DNA is a -----
a) Polymer
b) Polysaccharide
c) Base
d) Protein

2. The 'D' in the DNA stands for ---
a) De-hydroxy
b) De-oxy
c) De-carboxy
d) Di-carboxy

3. If DNA is like a ladder, what makes the step? ---
a) Base
b) Base pair
c) Sugar

d) Hydrogen

4. The backbone of the DNA is made up of ---
a) Sugar units
b) Phosphate units
c) Sugar-phosphate units
d) Sugar-base units

5. The building block of DNA is ---
a) Nucleoside
b) Nucleotide
c) Glycoside
d) Phosphate

6. The sugar-base units together form the ---
a) Phosphodiester bonds
b) Hydrogen bonds
c) Nucleosides
d) Nucleotides

7. The sugar-phosphate units together form the ---
a) Nucleoside
b) Nucleotide
c) Backbone
d) Hydrogen bond

8. The large sized nitrogenous bases present in DNA are ---
a) Purines
b) Pyrimidines
c) Ribose
d) Pentose

9. The small sized nitrogenous bases present in DNA are ---
a) Purines b) Ribose c) Pyrimidines d) Hexose

10. The two strands of DNA are connected through ---
a) Hydrogen bonds b) Glycosidic bonds c) Phosphodiester bonds d) Covalent bonds

11. The bond that connects phosphate group with nitrogenous base ---
a) Hydrogen b) Glycosidic c) Phosphodiester d) None

12. This holds the key to DNA replication ---
a) Complementarity of bases b) Attachment with sugar molecule c) Helical structure d) None of the above

13. DNA is a double stranded molecule in

a) Parallel form b) Anti-parallel form c) Clockwise form d)Anti-clockwise form

14. Which base is not present in RNA but found in DNA
a) Adenine b) Thymine c) Uracil d) Guanine

15. The number of base pairs in one nucleotide
a) 0
b) 1
c) 2
d) 3

16. The distance between adjacent base pairs is
a) equal
b) unequal
c) changes with change in temperature
d) depends on their chemical composition

Appendix- B

Post-test questionnaire (Study 3)

Instruction: Circle the most appropriate response

1. The 3' end of the DNA signifies:
a) Position of H atom in a base molecule
b) Position of H atom in sugar molecule
c) Position of C atom in a base molecule
d) Position of C atom in sugar molecule

2. The 5' end of the DNA signifies:
a) Position of H atom in a base molecule
b) Position of H atom in sugar molecule
c) Position of C atom in a base molecule
d) Position of C atom in sugar molecule

3. Purines are:

a) Two ringed structure
b) Adenine-Thymine
c) Single ringed structure
d) Guanine-Cytosine

4. The number of hydrogen bonds seen between Guanine and Thymine
a) 3
b) 2
c) 0
d) 1

5. Glycosidic bond is the bond between
a) Sugar and base molecule
b) Sugar and sugar molecule
c) Base and base molecule
d) Sugar and phosphate molecule

6. In the sugar phosphate backbone, the phosphorus atom is attached to
a) 4 oxygen atoms
b) 3 oxygen atoms
c) 3 carbon atoms
d) 4 carbon atoms

7. The number of hydrogen bonds seen between Guanine and Cytosine
a) 3
b) 0
c) 2
d) 1

8. In the DNA structure, how many base pairs form one helical turn?
a) 2
b) 5
c) 9
d) 10

9. Monomer of the DNA molecule:
a) Nucleobase
b) Nucleotide
c) Nucleoside
d) Nucleic acid

10. Phosphodiester bond is a bond between
a) Sugar molecule-Phosphate group
b) Phosphate group-Nitrogenous base
c) Sugar molecule-Phosphate group-Sugar molecule
d) Two nitrogenous bases.

11. The large sized nitrogenous bases present in DNA are ---
a) Purines
b) Pyrimidines
c) Ribose
d) Pentose

12. This holds the key to DNA replication ---
a) Complementarity of bases
b) Attachment with sugar molecule
c) Helical structure
d) None of the above

13. If DNA is like a ladder, what makes the step? ---
a) Base
b) Base pair
c) Sugar
d) Hydrogen

14. The number of hydrogen bonds between Adenine and Thymine
a) 2
b) 3
c) 1
d) 0

15. The backbone of the DNA is made up of ---
a) Sugar units
b) Phosphate units
c) Sugar-phosphate units
d) Sugar-base units

16. The base pairs of DNA are placed
a) Parallel to the central axis
b) Perpendicular to the central axis
c) in the backbone
d) diagonal to the central axis