The cognitive role of external representations in understanding DNA structure

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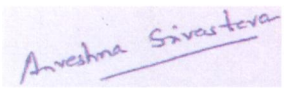
Declaration

This thesis is a presentation of my original research work. Wherever contributions of others are involved, every effort is made to indicate this clearly, with due reference and acknowledgment. This academic work was done under the supervision of Dr. Sanjay Chandrasekharan at the Tata Institute of Fundamental Research, Mumbai, India.



Anveshna Srivastava

In my capacity as the supervisor of the candidate's thesis, I certify that the above statements are true to best of my knowledge.

Dr. Sanjay Chandrasekharan

Date: 14/7/2017

Dedicated to...

The dreams of my parents!

Acknowledgment

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Abstract

Science education theorists and practitioners emphasize the need for tailoring physical learning aids in ways that support thinking about unobservable entities in science. 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 in cognitive science of the tight coupling between perception and action, and the use of physical manipulation to support learning. We hypothesized 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, multiple choice questions (MCQs) and novel methods of our own design, we were able to connect 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 - (i) we designed a simple gesture to connect a well-referenced 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 uncovers the relationship between cognitive affordances of common learning aids used in biology education, and the difficulties in students' understanding their use reveals. It contributes to the existing literature three designed 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.

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Chapter 1

Introduction

The fundamental aim of education research is to improve the practice of pedagogy (Creswell, 2002) and assessment (Black & Wiliam, 2003). While the concept of 'improvement' is influenced and determined by the shared goals of, and the desired outcomes for the society, education research has uniformly devoted itself to identifying gaps in the practice along with suggesting ways to overcome them. However, since the field of education is so diverse and complex, the task of identifying, assessing and correcting problems is huge (Lagemann & Shulman, 1999).

Another difficulty that adds to this complexity is the gap that exists between researchers and practitioners of the trade (Corey, 1952; Neumann, Pallas, & Peterson, 1999). In fact, Corey argued way back in 1952 that education researchers did not feel the responsibility of applying their findings to practical pedagogical problems. Unfortunately, this "knowing-doing gap" (Ball, 2012) has held its ground even in this century, but now it is widely acknowledged that the 'use and usability' of education research needs to be improved (Burkhardt & Schoenfeld, 2003; Levin, 2004; Broekkamp & van Hout-Wolters, 2007; Vanderlinde & van Braak, 2010; Ball, 2012).

With this background of education research, it becomes immediately clear that identifying a practical pedagogical problem which can be studied thoroughly and also responded to in a useful manner, in a limited amount of time, is a critical decision to be made by any education researcher. Therefore, the work reported in this thesis began with reviewing the wider education literature in favour of studies which highlighted practical pedagogical difficulties and the possible solutions offered by research community targeting these difficulties. Since this researcher's background is in biology, this work has a bias towards biology classrooms.

1.1 Review of literature

This section provides insight into the difficulties faced by biology teachers and students. It also highlights the various research-based solutions that were offered to these difficulties. Being mindful of the range of difficulty that one could come across while trying to make sense of immensely dynamic processes of teaching & learning, while also being aware of the temporal limitations of this dissertation work, we focus on three different aspects of pedagogical difficulties, discussed in the next section.

1.1.1 Pedagogical difficulties of biology teachers and learners

Biology is the study of life and since there are multiple processes and systems that govern the functionality of life, biology has multiple sub-disciplines which contribute to different aspects of our understanding about life and living forms. These sub-disciplines are spread out in different directions with focus varying from understanding of biomolecules (molecular biology) to applying biological understanding for the benefit of society (biotechnology). Naturally, this expanse of biological field has pushed its way into other disciplines of understanding while eroding the artificial boundary among disciplines like physics, chemistry, maths and computer science (Huang, 2000). Conversely, it has been argued that inter-disciplinarity has added value to the biological field (Cheesman, French, Cheesman, Swails, & Thomas,

2007; Garvin-Doxas, Klymkowsky, & Elrod, 2007).

Even though individual biological sub-discipline focus on specific aspects of biological understanding, there are certain unifying concepts that hold true across all biological sub-disciplines. For instance, a 'cell' is considered to be the basic structural and functional unit of all life forms and a 'gene' is considered to be the basic unit of heredity. Interestingly, as is the case with these unifying concepts- 'cell' and 'gene'- most of the biological concepts under study are not available for perception through one's sensory modalities. And this abstract nature of concepts that are to be taught becomes first of many practical problems faced in a biology class (Bahar, Johnstone, & Hansell, 1999). It is widely reported that students find it hard to understand molecules, their abstract properties being difficult for beginning biochemistry learners to grasp (Anderson & Leinhardt, 2002; Kelly & Jones, 2008; Cooper, Grove, Underwood, & Klymkowsky, 2010).

The many practical problems that emerge in a biology classroom have been captured through multiple research reports. Through the following review of literature, the aim is to gather different aspects of these difficulties. For the ease of understanding and appreciating these different aspects of difficulties, I use three diferent categories (based on (Tibell & Rundgren, 2010) - 'conceptual difficulties', 'language difficulties' and 'visualization difficulties'.

'Conceptual difficulties' captures problems with specific concepts which are prone to being misunderstood. The reasons for misunderstanding could be inherent in the concept's nature (abstract or complex). On the other hand, 'language difficulties' captures problems that emerge due to misinterpretation of the verbal medium used for communicating information about a specific concept. This misinterpretation may happen when there is an ambiguity in the usage of word(s); for instance, when a word has one meaning in conversational language and a diferent meaning in scientific language. It may also happen when the word(s) used

is(are) too complicated to be registered in the memory. Lastly, 'visualization difficulties' captures problems that emerge due to incorrect mental interpretation of a representation. This incorrectness may again be attributed to the nature of concept being represented or, to unfamiliarity with the form of representation or, to the inability to move (translate) across two or more representations pertaining to the same concept.

Conceptual difficulties

A teacher's job often entails teaching of abstract concepts which are part of complex systems following different organizational hierarchies, viz., perceivable (macro) phenomena are to be explained by abstract (molecular) events that cannot be seen or touched (Bahar et al., 1999).

Attempts to know more about biology teachers' difficulties has revealed that teaching of meiotic cell division is troubling (Cho, Kahle, & Nordland, 1985; Kindfield, 1994; Yip, 1998). In the same context, a group of Turkish teachers reported that it was hard to explain the movement of chromosomes during Prophase I of the meiotic cell division (Öztap, Özay, & Öztap, 2003). Similarly, (Dikmenli, 2010) also identified teachers' difficulties with cell cycle and cell division based on their diagrams and interviews.

When teachers face difficulty in teaching abstract concepts, it is likely that learners will also demonstrate trouble with such concepts. Hence, unsurprisingly, it has been reported that the process of cell division is also poorly understood by students of all ages (Smith, 1991; Lewis & Wood-Robinson, 2000). Connecting structural features of cell with its functional properties has also been found to be difficult (Marek, 1986; Dreyfus & Jungwirth, 1988; Westbrook & Marek, 1991; Tamir & Zohar, 1991; Flores, Tovar, & Gallegos, 2003).

Other difficulties related to cell metabolism has been identified. For instance, students show misunderstanding of concepts associated with photosynthesis (Wood-Robinson, 1991;

Lonergan, 2000; Özay & Öztaş, 2003; Marmaroti & Galanopoulou, 2006). Students also struggle to understand the process of respiration (Çakir, Geban, & Yürük, 2002), glycolysis (Oliveira, Sousa, Da Poian, & Luz, 2003), and coupling of reactions and inhibition of biochemical pathways (K. Schönborn & Anderson, 2003). Other reported examples include difficulty with structural and dynamic aspects of biomolecules, biophysical concepts, compartmentalization, and signalling of molecules (Roberts, Hagedorn, Dillenburg, Patrick, & Herman, 2005; Tang & Teng, 2005; Bivall Persson, Tibell, Cooper, Ynnerman, & Jonsson, 2006).

The problem with understanding of cell structure, its function and metabolism is carried over to the field of genetics and as expected, students show extreme difficulties with genetics' concepts which is both intensively studied and widely reported (Johnstone & Mahmoud, 1980; Bahar et al., 1999; Banet & Ayuso, 2000; Öztap et al., 2003; Knippels, Waarlo, & Boersma, 2005). Specifically, (Lewis & Wood-Robinson, 2000) have showed that students face difficulty with discriminating mitotic from meiotic cell division and understanding chromosomes and genetic information. In a similar vein, (D. C. Clark & Mathis, 2000) also report that students experience difficulties with discriminating chromatids, chromosomes, and the homologous parts of the chromosomes during the cell division process.

Troubles with differentiating 'germ cells' (reproductive cells which contain half the number of chromosomes in a somatic cell) from 'somatic cells' (non-reproductive body cells), and difficulties understanding the fact that different cell types in human body contain identical genetic information has also been reported (Banet & Ayuso, 2000; Lewis & Wood-Robinson, 2000).

The concept of 'gene' has also been reported to be problematic (Portin, 1993). Students have also been found to face difficulty connecting the structure and function of DNA (Deoxyribonucleic acid) molecule with genes (Marbach-Ad, 2001). A gene is operationally

defined on the basis of four of its processes: genetic transmission, genetic recombination, gene mutation, and gene function (coding proteins), and all of these processes are inter-dependent. However, it is difficult for students to appreciate the inter-dependency of these processes while developing a comprehensive understanding about the concept of gene (Portin, 1993).

Moving beyond 'genes', learning about the structure of the DNA molecule also presents itself with unique set of difficulties. The relation between genes, chromosomes and DNA, as well as the functions of DNA (replication, transcription & translation) has been identified as difficult areas to learn (Lewis & Kattmann, 2004; G. Venville & Donovan, 2007; Rotbain, Marbach-Ad, & Stavy, 2005).

Language difficulties

Language related difficulty is quite pronounced in biological sciences given that it deals with different systems and processes which involve long, cognitively taxing names, which are usually abbreviated for brevity. These names have no connection with our ordinary day-to-day conversational language. For instance, 'DNA' - a biomolecule which stands for De-oxy ribonucleic acid, or 'RT-PCR' - a technique used for replicating DNA sequences after they are generated from RNA (ribonucleic acid) - another biomolecule, and which stands for Reverse Transcriptase - Polymerase Chain Reaction. It has been observed that such domain-specific language or jargons can constitute obstacles or introduce misinterpretations of concepts (Tibell & Rundgren, 2010).

The misinterpretation may also emerge when a conceptual term is used differently in conversational language. For instance, with reference to the concept of cell cycle and cell division, it has been observed that conflicting terms, viz., 'divide', 'replicate', 'copy', 'share', 'split' used with respect to the movement of chromosomes and the genetic information is confusing for students (Lewis & Wood-Robinson, 2000).

Difficulties may also arise when the meaning of a particular concept changes, matching its pace with advancement of scientific understanding. Biological sub-disciplines like molecular biology or biotechnology have continued to develop rapidly and, hence, fundamental concepts in the field are changing their meanings as new knowledge is generated. For instance, the concept of 'gene' has evolved since it was introduced as a pure theoretical construct in 1909 by Wilhelm Johannsen (Tibell & Rundgren, 2010). In 1910, when T.H. Morgan discovered sex-linked inheritance, the concept 'gene' had a physical basis to it; still later, when the classical concept of gene came into being, 'gene' was an indivisible unit of heredity; in 1940s, the neo-classical concept of gene introduced sub-units of 'genes' as 'mutons' (units of mutation) and 'recons' (unit of recombination); in 1960s, the concept of 'gene' was expanded to include 'cistrons' (gene units which form proteins); and to this day the concept of 'gene' includes 'introns' (the non-coding gene units), overlapping genes, jumping genes etc. With such an evolution of the concept, (Portin, 1993) thinks that it has become very difficult to establish an enduring definition of the concept 'gene'.

Visualization difficulties

Visualizations play critical role in areas of understanding whose object of study are mostly imperceptible, abstract concepts. However, correct interpretation of different visualizations is a skill, referred to as 'visual literacy', which needs to be learned (K. J. Schönborn & Anderson, 2006).

It has been argued that inability to correctly visualize the relative and absolute sizes of cells, atoms and molecules interferes with development of robust understanding of processes like diffusion, and this, in turn can explain students' difficulties with the concept of cell (Westbrook & Marek, 1991).

(K. J. Schönborn & Anderson, 2006) demonstrated that several conceptual difficulties may be linked to the way content is represented and the manner in which symbolism is used.

For instance, (Cook et al., 2008) reported that some textbook illustrations related to meiosis led to development of conceptual difficulties in students.

Students often see visualizations as realistic reproductions of the phenomena they depict (Harrison & Treagust, 2000). For example, students sometimes interpret diagrams as realistic depictions of the illustrated events, rather than as schematic representations. In an interesting case of misrepresentation of visualization, it was identified that students' difficulties was linked to misleading use of arrow symbolism in textbooks (Du Plessis, Anderson, & Grayson, 2002). In a similar case, (Hull, Anderson, & Grayson, 2002) demonstrated that the arrows between the metabolites in the process of glycolysis were interpreted as a stream with a specific direction in the cytosolic solution rather than as a schematic representation of the order of reactions.

1.1.2 What makes learning some concepts hard?

A meta-view of the above literature-review spanning all the three categories (conceptual, language-related and visualization-related) identifies one common theme, i.e. - all difficulties are rooted within 'nature' of the concept in question. There are different aspects and, thereby, different interpretations of the term - 'nature' of concept. However, for the purpose of this dissertation work, we take two pragmatic routes pertaining to the way nature of a concept impacts one's understanding about it. This because the spectrum of one's understanding of a concept to lack of it, determines the degree of difficulty that one faces during the process of teaching/learning. The first route has to do with 'complexity' and the second has to do with 'abstractness' of the concept in question.

A concept is 'complex' in nature when it could be meaningfully accessed after penetrating multiple layers of understanding about other relevant concepts. For instance, the concept 'gene' could be meaningfully accessed only after penetrating layers of understanding about other concepts like cell, nucleus, chromosome & DNA.

On the other hand, a concept is 'abstract' in nature when it is beyond the purview of one's sensory modalities. Like any other complex concept, 'abstract' concept also requires understanding about other relevant concepts. For instance, the concept 'cell' requires understanding about structure and function of body system, constitutive organs, tissues etc.

Diving deeper into these two aspects of a concept, we find that all abstract concepts are complex, given that they could be accessed only after understanding other relevant concepts. Also, all complex concepts are complex because their understanding is based upon some form of abstraction. Thus, these two aspects appear to be inter-connected.

Coming back to pedagogical difficulties, it is interesting to find that all reported difficulties are of concepts which are both complex and abstract. So, what is it about complex and abstract concepts that make them difficult to comprehend? Cognitive science presents some interlocking explanations -

1. Failure of intuitive reasoning: While dealing with abstract and complex concepts, human intuitions fail to decipher relationship across different levels of organization (Hmelo-Silver & Pfeffer, 2004; Duncan & Reiser, 2005).

2. Increased cognitive load: In order to construct a complete mental model of the concept in hand, the brain has to simultaneously process multiple events and interactions with other relevant concepts that are crucial to its understanding, along with inferring general rules that govern the conceptual relationship (Narayanan & Hegarty, 1998; Graesser et al., 1999).

3. Lack of fit with prior experience: Learners have a tendency to focus on perceptually available structures and observable patterns (Hmelo-Silver & Pfeffer, 2004), and an inclination to give simple causal explanations (Perkins & Grotzer, 2000). So, when learners encounter a concept which is perceptually not available and is also not amenable to simple explanations, it becomes difficult to comprehend.

In sum, the primary source of difficulty in dealing with abstract and complex concepts is that it requires the mastery of domain-specific rules for how things work, whereas people inevitably try to reason and understand using intuitive rules, learned informally across multiple domains, that tend to work well for concrete real-world situations. The failure of these intuitive rules necessitates that the learner take up a more structured approach to thinking within the subject area, which means that she must explicitly use the rules and algorithms the instructor asks her to use in learning about concepts in that subject area. A useful to way to approach learning of complex concepts is to let the intuitve rules play the foundation on which complex rules can be built upon. However, since these intuitive rules are too scattered in pieces, owing their origin to different experiences, they need to be re-adapted with the help of an appropriate ER to develop the understanding of the domain-specific complex rules (Disessa, 1988). Researchers have identified this gap in intuitive and taught rules and have offered pedagogical solutions that try to integrate complex rules with the intuitive ones.

Pedagogical solutions

Cognitive science's explanation for why dealing with abstractness and complexity is hard is also intuitively available to many teachers and educators, who make great efforts to ease the process of learning the formal rules of whichever system they are teaching. Consider a biology teacher explaining the process of mitosis to high school students. The rules in this setting is the list of cell components that must be duplicated. The concepts to be mastered surround the order in which the process happens - what the order is, why it has to be the way it is, etc. The perceptive teacher will, in advance of talking about mitosis, ensure that all students understand the relative positions and sizes of the cell components, perhaps by means one or more representations of a cell. In other words, the teacher will ensure that her students know the rules.

Education research heavily emphasizes the use of teaching aids, such as the scale model of the example above. To what extent are these teaching aids responses to the problem

of abstractness and complexity? Below we consider this question, in relation to the major categories of teaching solutions which specifically target pedagogical difficulties in biology education.

Using metaphors and analogies

Metaphors and analogies are known to facilitate visualization of relevant concepts and processes, which can incite conceptual change (Posner, Strike, Hewson, & Gertzog, 1982; Aubusson, Harrison, & Ritchie, 2006). For example, mitochondria are described as power-house of cells (McBride, Neuspiel, & Wasiak, 2006) or recently as the Achilles heel of tumor cells (Whitaker-Menezes et al., 2011); ATP (Adenosine triphosphate) is known as the energy currency of cell (Imamura et al., 2009) etc.

It was reported that a bookcase analogy helped grade 8 students to successfully visualize the abstract notion of energy levels of an atom (G. Venville, Bryer, & Treagust, 1994). Bean et al. (Bean, Searles, Singer, & Cowen, 1990) indicated that instruction involving a pictorial analogy of cell resembling a factory helped students appreciate cell parts and functions.

It is also reported that students often relate to anthropomorphic views of cellular processes (Zohar & Tamir, 1993), such as the cell knowing what to take in and what to discard (Dreyfus & Jungwirth, 1988). This strategy often works when processes are described by imputing human characteristics (anthropomorphisms) or intentional (teleological) behavior, such as explaining the action of antibodies as attacking an invader (Tibell & Rundgren, 2010) , or the entry of antigens as entry of foreigners.

Using role-play

Chinnici et al. (2004) reported that procuring students to act as human chromosomes through role playing is an effective method to enhance learning about the process of mitosis and meiosis.

Using drawings

Students can present a broad spectrum of ideas through drawings (Rennie & Jarvis, 1995). Drawings have been broadly used in science education more like a diagnostic tool to identify students conceptual understanding (Assaraf & Orion, 2005) . For instance, Reiss et al., (Reiss et al., 2002), with the help of several biology educators, asked a total of 586 students (ages 7-15) from 11 countries to draw what is inside their body. They analysed the drawing based on the criterion of anatomical accuracy and, unsurprisingly, found that 15 year olds had a better understanding about their internal organs.

In a similar demonstration of drawing as a diagnostic tool, (Köse, 2008) analysed 156 diagrams of biology students which uncovered multiple students misconceptions on the process of photosynthesis and respiration. Also, Dikmenli (Dikmenli, 2010) analysed diagrams on cell cycle and division, collected from 124 biology student teachers. The findings suggested that student teachers showed a series of misconceptions pertaining to cell division and structuring of events like the replication of DNA molecule.

In a case that enhances the value of diagrams from a diagnostic tool to a pedagogical tool responsible for conceptual change, Rotbain et al., (2010) demonstrated that when diagram-based activity was integrated with regular lecture in a molecular genetics classroom, students showed statistically significant achievements on a written questionnaire against the control group who did not undergo the diagram-based activity.

Using models

In practice, "scientists use models to represent aspects of the world for various purposes" (Giere, 2004). Models can be used to describe complex phenomena, be manipulated to represent core ideas and dynamicity of a system and facilitate communication of ideas (Svoboda & Passmore, 2013). In science education there is an extensive literature about models and modeling (S. W. Gilbert, 1991; Van Driel & Verloop, 1999; Boulter & Buckley, 2000; J. K. Gilbert, Boulter, & Elmer, 2000; Harrison & Treagust, 2000). As a paradigmatic ex-

ample demonstrating the role of both visualization and embodiment (Kirsh, 2009) in how physical models help students learn, a controlled experiment showed that students permitted to physically manipulate number tiles were much better at interpreting fractions than students only permitted pen and paper tools (Martin & Schwartz, 2005). Since the literature on models in education is very diverse, this review focuses on the use of physical models in biology education, the most directly relevant subset of models for the work reported in this dissertation.

Early research on molecular structures relied heavily on physical models. For instance, Linus Pauling used his newly-invented space-filling models to predict the basic folding units of protein structures, while Watson and Crick used brass-wire molecular models to determine the structure of DNA. In biology education, many studies suggest that the use of models greatly enhances student understanding of cell division (D. C. Clark & Mathis, 2000; Pashley, 1994). Brown (C. R. Brown, 2014) recommends building chromosome models for improved conceptual understanding. Rotbain et al. (Rotbain, Marbach-Ad, & Stavy, 2006) have demonstrated that using a 3-D bead model along with regular lecture in a molecular genetics classroom (for high-schoolers) showed significant improvement in students understanding over two control groups, one that just had the regular lecture and the other who used an illustration model along with the lecture.

Using graphical tools

Graphical or visual tools, such as conceptual maps, conceptual networks, and conceptual change strategies, such as conceptual change texts, are the methods more likely to reduce or eliminate misconceptions of students (Novak & Cañas, 2008; Tekkaya, 2003). Kinchin, Hay & Adams (Kinchin, Hay, & Adams, 2000) analysed concept maps to develop a qualitative method to categorize students progression in understanding of biology concepts. Laight (Laight, 2004) reported that working with concept maps could potentially assist motivation, engagement and deep learning in medical and biomedical science education when

used as a supplement to more traditional teaching/learning activities.

Using computer-based technologies

Computer-aided educational materials for biology classes are recommended for removing students misconceptions (Çepni, Taş, & Köse, 2006; Kara & Yeşilyurt, 2008). Computer-generated visualizations are also increasingly used in molecular biology to promote more effective learning of visually and spatially complex topics (Tibell & Rundgren, 2010).

McClean et al. (McClean et al., 2005) tested animations of molecular and cellular processes (like transcription, translation, gene expression, protein transport etc.) developed by World Wide Web Instructional Committee at North Dakota State University, and found that when integrated with regular lecture module, students showed significant retention of content material over control group who did not see the animations. Similarly, Rotbain et al. (Rotbain, Marbach-Ad, & Stavy, 2008) found that instruction with computer animation (LogalTM Molecular Biology) for simulation of the structure of DNA, RNA, DNA replication, and protein synthesis led to significantly improved performance of students on a written questionnaire over control group who just had the regular instruction minus animation.

Using virtual-reality

Recent advances in virtual reality present opportunities for students to be immersed in complex, dynamic, and three-dimensional structures and relationships via sensory aids such as haptics (Bivall Persson et al., 2006; Minogue & Jones, 2006; Wiebe, Minogue, Jones, Cowley, & Krebs, 2009). Other studies indicate that animations are superior for visualizing spatial aspects and dynamic processes (Williamson & Abraham, 1995; Pallant & Tinker, 2004; Marbach-Ad, Rotbain, & Stavy, 2008).

Notable is the evolving technology of computer auto-fabrication (3D printing) that has now made it possible to produce physical models for complex molecular assemblies. For instance, Gillet et al. (Gillet, Sanner, Stoffler, & Olson, 2005) have demonstrated that with

Python Augmented Reality ToolKit (PyARTK), they could assemble proteins like HIV Protease and Superoxide Dismutase.

Nicholson et al. (Nicholson, Chalk, Funnell, & Daniel, 2006) recreated a fully interactive model of the middle and inner ear from a magnetic resonance imaging scan of a human cadaver ear. To test the model's educational usefulness, they conducted a randomized control study in which 31 medical students completed a web-based tutorial on ear anatomy that included the interactive model, while a control group of 30 students took the tutorial without exposure to the model. Their results revealed that the intervention group demonstrated significantly better understanding about ear anatomy than the control group.

The above review does not provide a comprehensive list of pedagogical difficulties or the proposed solutions in biology education. However, it gives a broad sense of difficulties faced by both biology instructors and students and a large array of solutions that education research has to offer. This dissertation focuses on a subset of pedagogical solutions which are characterized as being *'shareable object of thought'* (Kirsh, 2010), or *external representations*, henceforth ERs. While there is a multiplicity of philosophical positions one can take regarding the distinction between internal and external representations of knowledge, in this dissertation, we take the position that there are distinct internal and external representations, with the latter characterized as representations of knowledge perceptually available to multiple observers simultaneously. We further assume the possibility of mental operations on both kinds of representations, as well as interaction between them. The gist of this interaction is that actions on external representations affect internal representations by making different physical concepts perceptually salient, and internal representations affect external representations through our actions that are governed by changes in the internal representations (Kirsh & Maglio, 1994). The existence of this interactive process is implicit 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.

1.1.3 How do 'external representations' (ERs) work?

The rich literature partially summarized above provides substantial evidence 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. 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 (ERs) that lets them improve students' understanding. In this section, we briefly discuss the reasons behind the apparent success of ERs in improving learning outcomes.

1. ERs enhance cognitive strength: Kirsh (Kirsh, 2010) discusses seven ways in which ERs enhance cognitive strength. These are - a) ERs change the cost structure of the inferential landscape; b) they provide a structure that can serve as a shareable object of thought; c) they create persistent referents; d) they facilitate re-representation; e) they are often a more natural representation of structure than mental representations; f) they facilitate the computation of more explicit encoding of information; g) they enable the construction of arbitrarily complex structure; h) and they lower the cost of controlling thoughtthey help coordinate thought. Kirsh further argues that it is because of the above functions that ERs support thinking through and sense-making of a situation. In a similar vein, Pande & Chandrasekharan (Pande & Chandrasekharan, 2017) explore the role of ERs and argue that ERs support mental operations in working memory (for instance, via 'mental rotation'), and, thus, aid 'imagination' during the interaction process.

2. ERs help build S-F relationships: Patrick et al., (Patrick, Carter, & Wiebe, 2005)

suggest that ERs work by building understanding of structure-function relationships of concepts which are typically inaccessible to sensory modalities.

3. ERs provide access to different information: (Koedinger & Nathan, 2004) have argued that differences in external representations affect performance and learning when one representation is easier to comprehend than another or when one representation elicits more reliable and meaningful solution strategies than another. For instance, (Schwonke, Berthold, & Renkl, 2009) used eye-tracking to assess differences in processing strategies for text, equations and diagrams presenting the same pedagogical information. They showed that students inspected equations and diagrams with substantially longer fixations, but for lesser durations overall. This suggested to the authors that equations and diagrams provide either quicker access to the same information, or that they promote the sampling of information in smaller chunks than text.

4. ERs anchor learners' intuitions: 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 (Clement, 1993). 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.

The list above is not exhaustive, but does indicate that explanations for how ERs work are rather general and can prove difficult to ground for specific instuctional aids in a specific learning context. As we discuss next, this gap between theory and practice presents a major opportunity for new work in this area, and is the motivation behind the research reported in this dissertation.

1.2 Research Motivation

We have reviewed above both literature discussing problems in pedagogy and an array of possible solutions. We now suggest that much work remains to be done to map these two lists onto each other, such that instructors can find optimal ERs for teaching specific concepts effectively. We describe below why this task is increasingly urgent and important.

1. The choice problem: We have seen above that several major categories of learning aids aim, explicitly or implicitly, to concretize the abstract primitives that would let students understand a particular subject area correctly. Viewed from the prism of cognitive science, a more general insight emerges. Differences in ER efficacy for learning are caused by differences in the implicit congruence between the model and the phenomenon being explained. At present, judgment of the implicit congruence for a particular model-phenomenon 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.

2. Proliferation of education technology tools: Amplifying the choice problem, the set of ERs an instructor has available now to explain any given topic 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.

3. Using multiple external representations is challenging: While correct use of multiple external representations (MERs) has been argued to promote more robust and general-

izable learning (Ainsworth, 1999), it is often found in practice that students find using MERs challenging."Knowledge acquisition from multiple representations requires that the learner create referential connections between corresponding elements and corresponding structures in different representations. As this process is usually difficult, learners frequently fail to construct coherent mental representations and, thus, do not sufficiently understand the subject matter" (Seufert, 2003). Students frequently find the cognitive demands of integrating information from multiple external representations too challenging, resulting not only in ineffective learning, but also at times learning deficits induced by the use of MERs (Bodemer & Plötzner, 2004). These deficits are especially exacerbated for novices unaccustomed to extracting information from novel representations, who often end up erroneously focusing on surface features of the representation, to their conceptual detriment (Lowe, 1996).

For these and other reasons, researchers are unanimous in prescribing that students' use of ERs be supported, both when they are being used individually (Lewalter, 2003; Lowe, 2003) and when they are used in combinations (Gutwill, Frederiksen, & White, 1999; Seufert, 2003). Omission of such support is seen to turn ERs into sources of confusion rather than clarity for students. However, how precisely such support is to be provided is left unspecified in most of this literature.

As we anticipate above, the general view at the intersection between cognitive science and education research is that effective use of an ER requires that there be a strong implicit correspondence 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 visually evident from the design of the ER and conceptually veridical.

But 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. For the most part, teachers are expected to identify possible areas of confusion in their classroom on their own, and devise mitigation strategies on their own. 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. Figure 1.1, depicts this difficulty in a schematic form and illustrates how that motivates the design of this study.

1.3 Research foci

Our work seeks to find a middle path between the two extremes - a grand unified theory of ER versus every teacher to themselves. By narrowly focusing on a specific biology topic, and investigating the efficacy of different ERs in teaching it, we attempt to make precise and effective prescriptions specific to this topic, but hopefully generalizable across classrooms and teaching styles. By restricting the conceptual scope of our inquiry, we aim to offer empirically grounded suggestions.

The focus of this work is to characterize the functional scope of existing ERs. Earlier efforts in this direction have borne encouraging results. Specific to molecular biology and chemistry, a number of authors have presented computer simulation tools that afford deep and accurate 3D visualizations of molecular structure (Bottomley, Chandler, Morgan, & Helmerhorst, 2006). Others have used psychophysical testing to identify critical cognitive skills essential for visual literacy, and used these insights to develop more effective test instruments for conducting biochemistry assessments (Mnguni, Schönborn, & Anderson, 2016). More generally, systematic efforts have been made to identify the key characteristics of digital resources that promote more effective learning (Littlejohn, Falconer, & Mcgill, 2008). The research reported in this thesis contributes to this active area of research.

We channel our over-arching motivation of mapping structural affordances of ER onto

cognitive affordances of learners into two complementary research foci:

a) **Finding 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.

b) **Designing 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 focused on the instruction of a single concept during instruction and assessment across all our studies. Figure 1.2 gives this overall structure of the research design and how it served to meet our twin research foci.

1.3.1 Area of interest

We decided to focus on the biological molecule - Deoxyribonucleic acid (DNA) - for the purpose of this dissertation work. Our choice was governed by multiple factors:

1. Several previous reports show that learners face difficulties in understanding concepts in genetics, for which DNA serves as a gateway concept ((Marbach-Ad & Stavy, 2000; Marbach-Ad, 2001; Tsui & Treagust, 2003; Lewis & Kattmann, 2004; Rotbain et al., 2005; Duncan & Reiser, 2007))

2. 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.

3. Pragmatically, structural concepts are easier to externalize, quantify and track in a students response; thus, focusing on DNA structure allowed us to design observationally rigorous studies.

4. 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).

5. Finally, by focusing on (DNA) structure, we can generalize findings/analysis to other conceptual areas.

Next, we were to decide what sample of the student population should we work with for our study.

1.3.2 Sample

For ease of comparison, the formal educational attainment of the learner sample for all the studies reported in this work were held constant. We investigated first year undergraduates/Grade 12 passed 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 just right for our purpose. This because being exposed to basics and not to biochemical details, these students were ready to learn new concepts and this ensured that on exposure to designed ERs, there would be learning 'pauses' which would help researcher

to make intense observations to capture both the *process* of learning and interaction with ERs. The intense observations would also help us identify their difficulties corresponding to both structural affordances of ER and the specific conceptual difficulties that the particular ER would reveal.

1.3.3 Method & Design

Our methodological emphasis combined clinical interviews, questionnaires, self-reports 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 individual's 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 & Maglio, 1994) hypothesized that our actions influence our internal processes, which in turn influences our actions, i.e., our action 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 (Kirsh, 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 [1], 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.

1.4 Thesis organization

This thesis is organized into 7 different chapters. Chapters 2-5 describe four studies that were conducted as part of this dissertation work. In each of these studies, we focus on the *process* with which a learner interacts with one specific ER. This interaction process was intensively analysed using dense observations made during the course of the study-tasks, and each study was able to advance our knowledge about students' understanding and difficulties about concepts related to the the structure of the DNA molecule in particular, and about the nature of the ER used in general. Chapter 6 describes the construction of a database on ERs of DNA structure. Chapter 7 discusses the implications of this dissertation work in light of the findings of the four studies and it also talks about the limitations of this work and the way forward.

Study 1 (Chapter 2) uses multiple symbolic representations. However, the focus of this study was a specific physical *gesture* that was used in conjunction with a well-referenced *analogy*. Being chronologically the first of our investigations, the process and outcomes of

[1]Throughout this thesis, we differentiate between 'symbolic' and 'molecular' models. The defining difference between the two is that 'molecular' models restrict 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 succint visual representation, ignoring atom-level details.

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, its contribution to our initial focus on DNA structure, and b) we observed that different ERs give us different information about students' understanding and difficulty; hence, its contribution to our focus on evaluating the effectiveness of different forms of ERs, viz., textual, symbolic and molecular.

As an example of the latter point, 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.

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 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) (Srivastava, 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 now made freely available in a coupleof weeks.

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

1.5 Publications based on this dissertation

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.

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.

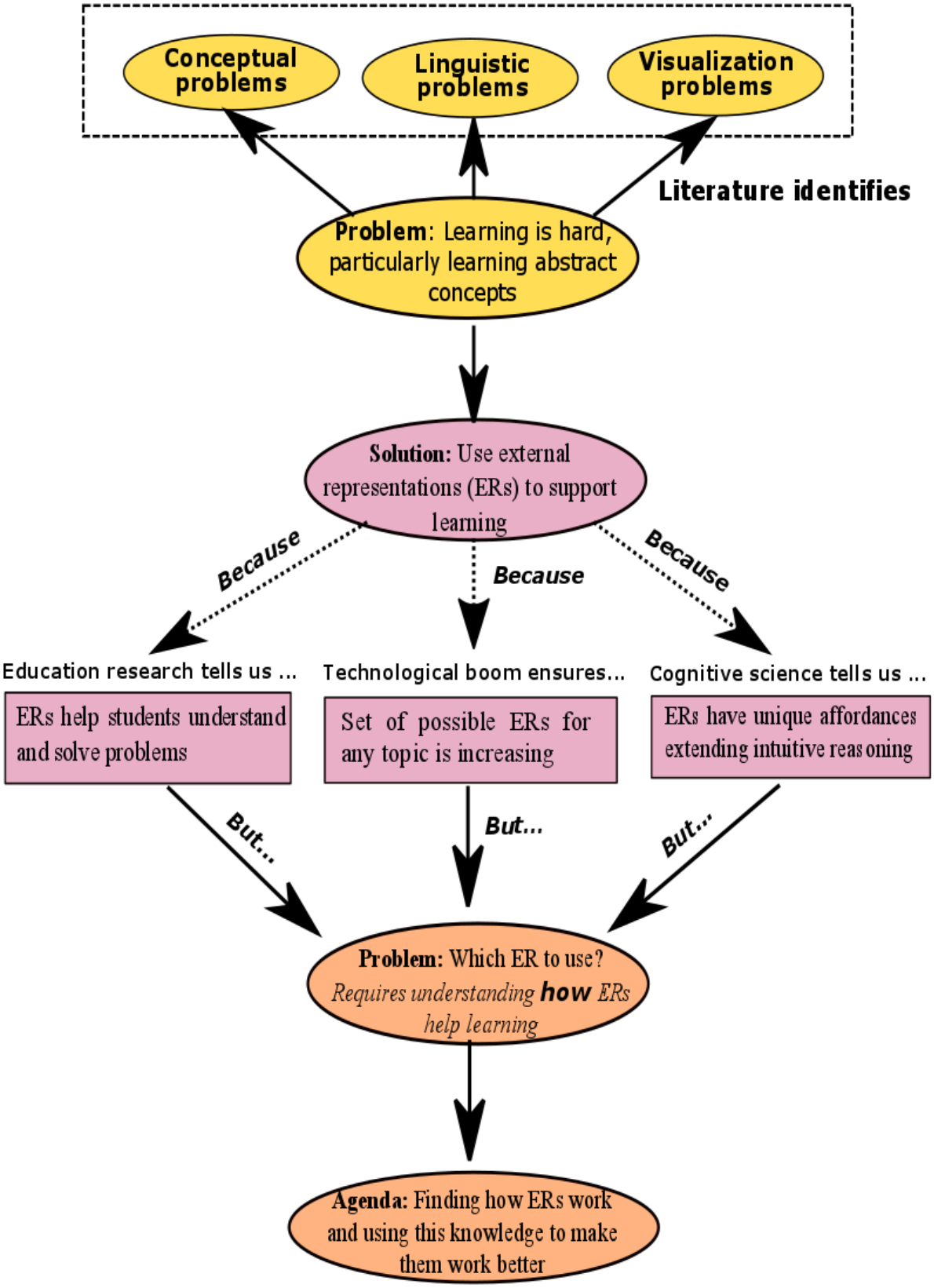


Figure 1.1: Motivation behind designing the research agenda

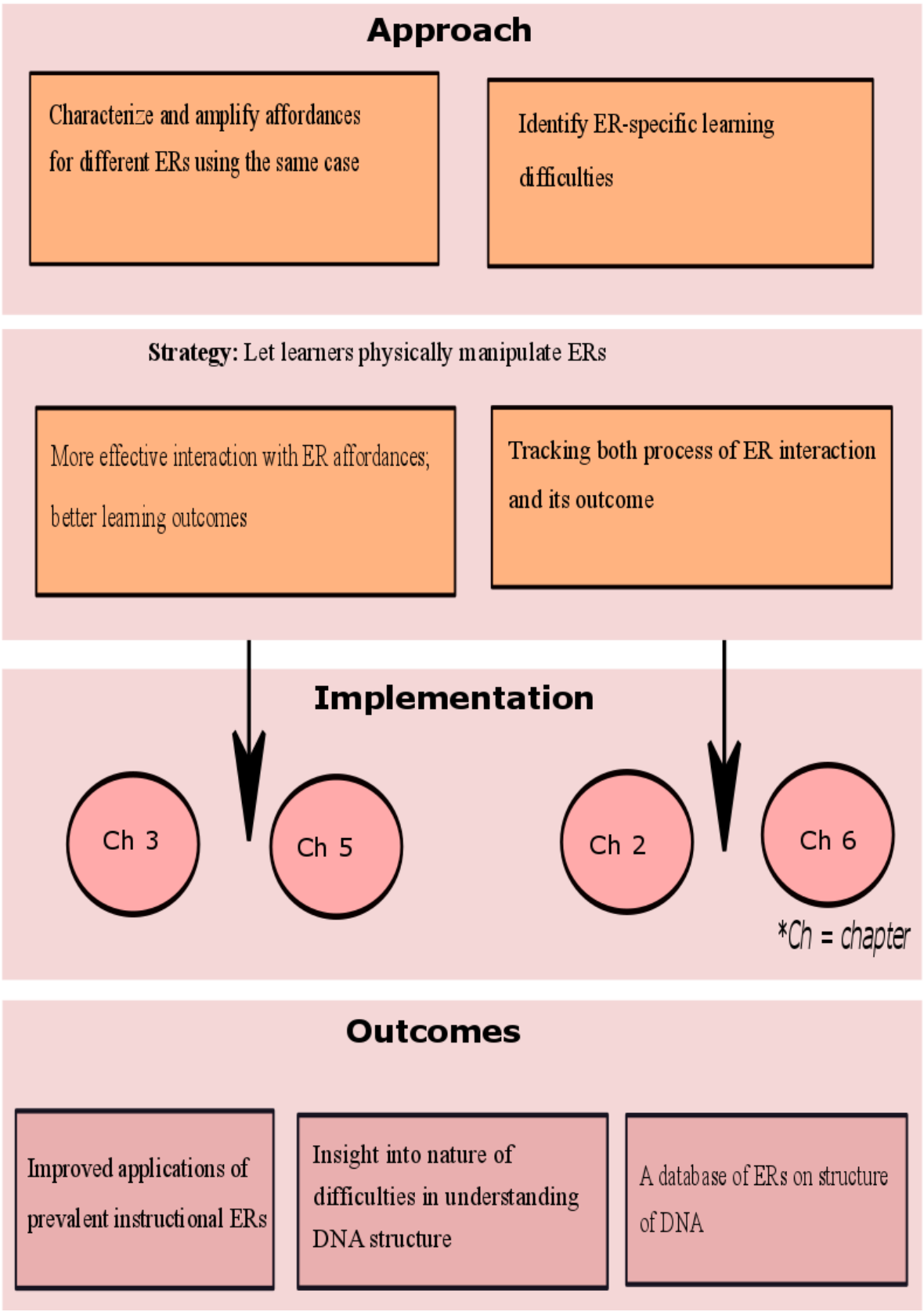


Figure 1.2: Research overview: Process & deliverables

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.

The birth of molecular biology was significantly marked by the discovery of the double helical structure of the DNA molecule by (J. D. Watson & Crick, 1953). The general correctness of this structure was gradually proven in subsequent years by substantial research on the structural as well as functional aspects of the molecule. The structure of DNA had immediate functional implications: It follows that in a long molecule many different permutations are possible, and it therefore seems likely that the precise sequence of the bases is the code which carries the genetical information) (J. Watson & Crick, 1953)(p. 965).

Conceptual understanding in molecular biology involves integration of the macro (genetic traits), micro (cell) and molecular (gene) levels. A student needs to enter into the chemistry of the biomolecule, which in turn calls on 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 & 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 integration occurs in several ways, one that includes concepts from various disciplines, another that 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 & Wood-Robinson, 2000) (Lewis & Kattmann, 2004). Yet, in a study of major problem areas in biological sciences as identified by students, Bahar et al., (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.

2.1 Structure of the DNA molecule

The double-helical structure of the DNA molecule can be visualized as two right-handed helices coiled around a central axis (Figure 2.1). 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. The chemistry of the constituents of DNA, including the details of atomic structure, electronic configuration, chemical bonds, etc., is consequential to the integrity of the overall physical structure of the molecule.

2.2 Textbook representations of DNA structure

In Indian schools, the chemical prerequisites for learning the biology of the DNA molecule are built up from middle school till the higher secondary level (age 17), as part of the chemistry curriculum. The higher secondary biology textbook followed by our sample (Board, 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.

Figure 2.1a 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. Also labeled are the major groove, minor groove and the 3' and 5' ends. Connecting the backbone are the skeletal structures of the nitrogenous base pairs with the respective number of hydrogen bonds. The dimensional details: diameter of the helix (20 Å), one helical turn (34 Å), and distance between adjacent nitrogenous base pairs (3.4 Å), are indicated. The accompanying text mentions the angle between successive base pairs, or pitch angle to be 36° and also that each spiral turn contains 10 pairs of nucleotides (Board, 2009, pg. 15).

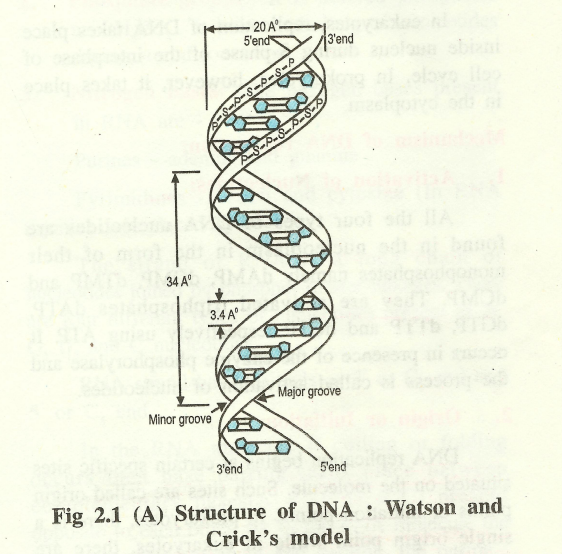


Fig 2.1 (A) Structure of DNA : Watson and Crick's model

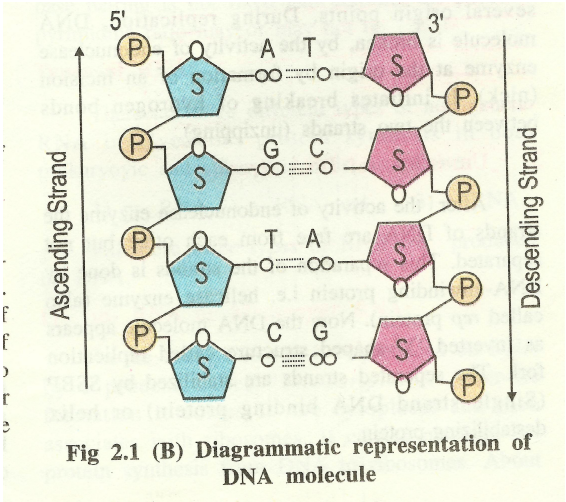


Fig 2.1 (B) Diagrammatic representation of DNA molecule

Figure 2.1: Maharashtra State textbook (2009) representation of a) DNA helix and, b) DNA ladder respectively

Figure 2.1b is the detailed molecular 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. The sugar molecules are shown attached with purines (two joined circles) or pyrimidines (one circle). The hydrogen bonds between the complementary bases are represented through either two (for AT) or three (for GC) dotted lines. Thus, by the end of high school, students are introduced to standard diagrams of the DNA molecule. The twisted ladder is an analogy for DNA structure which has considerable potential to help students mentally visualize the structure at both the gross physical and the detailed chemical levels. Our interest was in seeing that whether they are able to sustain the analogy at both of these levels in order to form a mental image of the 3-D molecular structure of DNA.

2.3 Connecting external representation with internal representation

The role of multiple external representations (MERs) in supporting students' learning has been explored by Ainsworth (Ainsworth, 1999) and Tsui and Treagust (Tsui & Treagust,

2003). Multiple representations are believed to support complementary information or processes, by having a familiar representation help to understand the information carried by, or constrain the interpretation of, a new representation. Ainsworth's analysis, and Tsui and Treagust's applications of it to genetics reasoning, are done in the context of computer-aided learning. Both of these papers however refer to MERs in more general terms, and further assume a link between external representations and internal mental representations. Ainsworth suggests that MERs support abstraction, extension and relations among representations while Tsui and Treagust carry out a detailed analysis of students' learning and reasoning in genetics as they use multiple representations (Ainsworth, 1999) (Tsui & Treagust, 2003) (Tsui & Treagust, 2007).

The question of how MERs could connect with internal mental representations is one that is important for science pedagogy to address. Recent research on embodied and spatial cognition provides a possible answer. 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 (A. Clark, 1997) (Barsalou, 1999). One direct implication of the embodied view is that MERs connect to internal representations through the learner's perceptions and actions.

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 (Goldin-Meadow & 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. They see gesture as a form of simulated action, in which there is no direct manipulation of the world, but the result of it is a rich internal representation that incorporates the sensorimotor properties required to act on the world.

This insight from cognitive science was used by Padalkar and Ramadas (Padalkar & Ramadas, 2011) to propose a pedagogical purpose for deliberately designed gestures in science. Gestures might be used to internalize a natural phenomenon, a model, or properties of space. Models are three dimensional and visually realistic but are limited by the fact that they are not transformationally flexible and hence are less amenable to analytical thought. Diagrams on the other hand are visually economical and precise in capturing analytical relationships, but their two-dimensional, static and abstract nature poses difficulty. Gestures are shown to share complementary properties with both models and diagrams, and thus used to link models with diagrams. Importantly, the gestures in this study serve not only to link external representations with internal mental ones, they are also designed to link two types of external representations (concrete models and diagrams).

Mental models are transformationally flexible, and hence can be used to simulate phenomena. The intuitive notion of transformational reasoning was developed in Ramadas (Ramadas, 2009) and applied in the context of structure and function of human body systems by Mathai and Ramadas (Mathai & Ramadas, 2009). They proposed that tasks calling for imagined manipulation of structure, or changing the viewpoint of an observer, would encourage mental visualization of body systems. The idea of changing observer viewpoint ties in well with Goldin-Meadow and Beilock's (Goldin-Meadow & Beilock, 2010) discussion of hierarchies of gestures and actions. In their analysis of McNeill's (McNeill, 1992) classification, 'character viewpoint' gestures reflect actual movements, 'observer viewpoint' gestures capture the goal object or its trajectory, and 'metaphoric' gestures represent abstractions. They suggest that character and observer viewpoint gestures, if used in sequence, could provide a bridge between concrete actions and more abstract representations.

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 MERs 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 (Gentner, 1989) defined analogy as a mapping from a base (familiar) domain to a target (unfamiliar) one. Duit (Duit, 1991) showed that the analogy relation is intrinsic to model-based reasoning and learning in science. Justi and Gilbert (Justi & Gilbert, 2006) brought out the close relationship between visualization, mental models and analogy in the history and pedagogy of chemistry. Harrison and Treagust (Harrison & Treagust, 2006) argued that analogy is a powerful way to think, construct ideas and test new knowledge. Analogy (like gesture) has a potential to help construct mental visual models from multiple external representations. We used 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 observer viewpoint and specifically, using a 'character viewpoint' simulation of DNA structure, was also possible, and fruitful.

2.4 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 (MERs) of DNA structure. We explored 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?

Table 2.1: Demographic Information of Participants in this Study

Name*	Age	Gender	Mother Tongue	Degree pursuing	Courses**
Anuja	18	F	Marathi	Microbiology	MPC
Sharada	18	F	Oriya	Biotechnology	BMC
Nitin	19	M	Marathi	Microbiology	MPC
Sandhya	17	F	Telugu	Biotechnology	BMC
Aakriti	18	F	Hindi	Microbiology	MPC

*Names are changed to preserve anonymity
**MPC: Microbiology, Physics, Chemistry; BMC: Biotechnology, Microbiology, Chemistry

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?

2.5 Methods

Participants

We worked with a convenient sample of five first year biology undergraduates (ages 17-19 years; 4F, 1M). These students (details in Table 2.1) were selected based on their scores in their higher secondary biology exams (above 60%) for we wanted to ensure that the participants had some basic understanding of the DNA structure.

2.6 Research Design

We used a microgenetic research design (Siegler & Crowley, 1991) (Siegler, 2006) (Flynn & Siegler, 2007) which is appropriate for situations that involve rapid transitions in learning by tracing the processes of the students learning under dynamic, in vivo conditions. The three important attributes 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)(p. 469).

Students are observed very closely during the period of learning and then these observations are revisited again and again for a finer understanding of the patterns that depict change in real-time as how it occurs (Van der Aalsvoort, Van Geert, & Steenbeek, 2009)(p.9).

In our study, observations were carried out during six individual sessions held over nine days. Each session involved a clinical interview-cum-teaching sequence for 1 to 1.5 hours for each student per day. The language of the interview was English except for some occasions when Marathi and occasionally Hindi were used for two of the interviewees: Nitin and Aakriti. The prerequisites 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 prerequisite 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 these data were analyzed microgenetically.

2.7 Representations of the DNA backbone and the nitrogenous base pairs

Students were asked to draw the textbook diagrams (the ladder and helical structures of Figures 2.1a and 2.1b), and recall the well-known ladder analogy for DNA structure. The DNA backbone was represented by five simple models (M1 to M5 in Table 2.2). M1 comprised

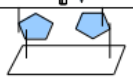
Model No.	Backbone representation	
M1	Long edges of a sheet of paper (laid on the table)	
M2	Two (anti) parallel pencils (laid on table)	
M3	Two (anti) parallel pencils (held to stand erect on table)	
M4	Cardboard cutout of a sugar molecule attached with two phosphate molecules (two sets) standing on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

Table 2.2: External representations used for DNA backbone

of a sheet of paper laid on the table and the students were asked to consider its long edges to represent the two DNA backbones. M2 was two (anti) parallel pencils laid 6 on the table and considered as the two DNA backbones. M3 was a variant of M2 where the two anti-parallel pencils (the backbones) were made to stand erect on the table. M4 was a cutout model depicting the two backbones, each consisting of two phosphate groups attached with one sugar molecule at its 3' and 5' positions, fixed on a cardboard base. M4 thus showed the molecular details of the two sugar-phosphate backbones.

M5, or the 'clothespin model,' was adapted from Venville (G. J. Venville, 2008). Students were provided with two plastic tubes along which could be strung interlocking clothespins of four different colors (green, yellow, blue and pink) to represent the complementary DNA bases. Students were asked to construct the M5 model to depict first the ladder structure and then the helical representation of the DNA molecule.

In combination with models representing the DNA backbone, two types of representations of the nitrogenous base pairs were introduced. The first representation consisted of card cutouts of the different N-bases (Figure 2.2a) & 2.2b)) which was suggested by Watson's own account of his discovery of base-pairing, as recounted in a beautiful video produced by the Cold Spring Harbor Laboratory. Students were to use these cutouts against the M4

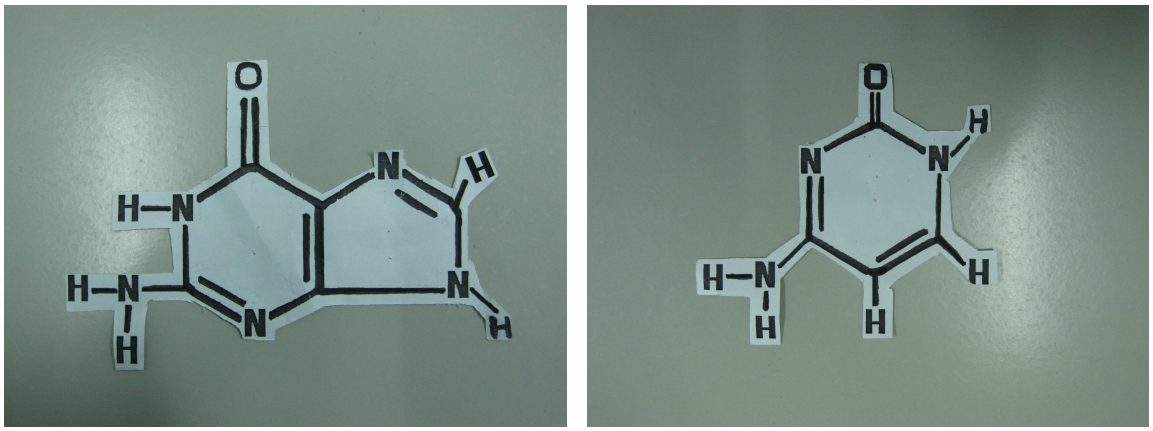


Figure 2.2: Two cut outs representing a)(left) purine and b)(right) pyrimidine nitrogenous base

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.

The other base pair representation comprised of 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) (Figure 2.3). Students used the gesture to imitate the orientation of the base pairs in the ladder against the models M1-M5, as appropriate.

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 ladder analogy was used as a reminder to students while they attempted to show the base pair orientation with the help of the palm gesture or the cutouts. If the analogy by itself did not work then the students were instructed to mentally simulate the action of walking up the straight ladder, and in that situation consider how the steps of the ladder would be oriented. The gesture and mental simulation device were also used for the helical ladder structure in model M5. The mental visualization (of the straight or the twisted ladder) and the simulation (of walking up the ladder) correspond

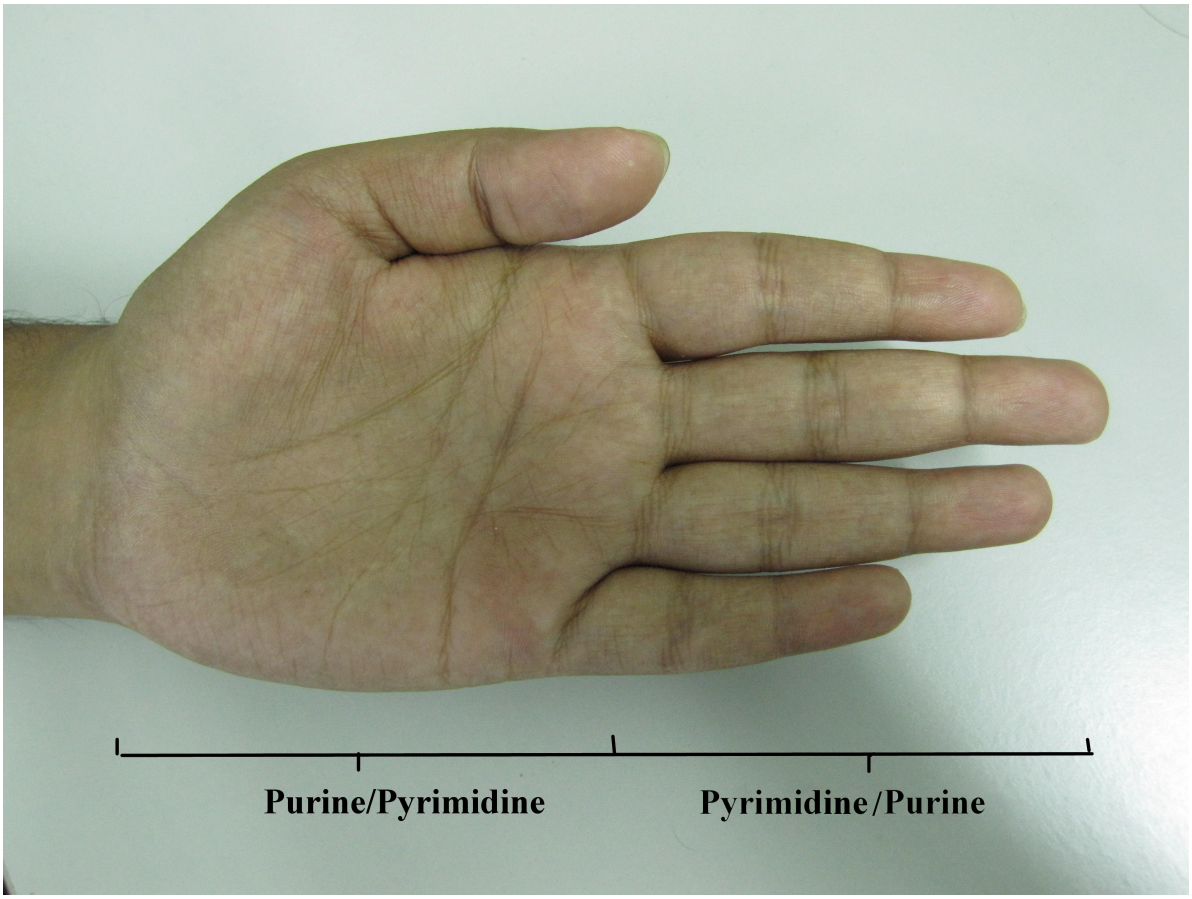


Figure 2.3: 'Palm gesture' with palm representing one N base and straightened fingers representing the complementary N base

respectively to the 'observer viewpoint' and 'character viewpoint' gestures/actions discussed by Goldin-Meadow and Beilock (Goldin-Meadow & Beilock, 2010). Here the actions are of course, not actually carried out, but mentally simulated.

2.8 Preparing the background (Days 1, 2, and 3)

Day 1 explored students' understanding of the concept of DNA as the genetic material. We probed their familiarity with the terms like 'genetic material', 'gene', 'heredity' etc. Students were asked about cells, the location of genetic material and DNA as genetic material. Almost all the students had problem in understanding the relationship between the gene and DNA, for example, whether gene is inside the DNA or DNA is inside the gene. A discussion

on the Hershey and Chase experiment, which proved that DNA is the genetic material, showed that all the students were unclear about the structure and function of a virus, or bacterium, and they were unable to recall anything about radioactivity. Each day from Day 2 till Day 6 began with students' diagrammatic representations of the DNA ladder and the double helix as some approximation of the two familiar textbook diagrams (Figure 2.2a) and 2.2b)). Day 2 focused on recapitulating elementary background related to the chemistry of the DNA molecule where, despite many confusions revealed along the way, students were re-introduced to the idea of nitrogenous bases (purines and pyrimidines) and the electronegative nitrogen atom in them which can interact with a positively charged hydrogen atom of another nitrogenous base to form a hydrogen bond. On Day 3 students explored different pairing possibilities between the bases using cutout models of the N-bases. They eventually used the cutouts to form the A-T double bond and G-C triple bonds, to demonstrate that the base pairs were planar and of identical lengths.

2.9 Introduction to the nucleoside (Day 4)

At the start of Day 4, students were introduced to the 'palm gesture' (Figure 2.3), asked to imagine its correspondence with the planar base pairs, and to use the gesture against the M1 and/or M2 model. All students began with an incorrect gesture, i.e., they showed the base pairs in the plane of the straightened parallel backbones. This was the first episode of the microgenetic study to which we will turn in the coming sections. Day 4 then continued with questions and tasks which required re-visiting of the concepts like chemical bonds and the valencies of atoms depicted in the cutouts of the nitrogenous bases and the sugar molecule. Students were shown the M4 model of the sugar phosphate backbone and were asked to depict base pair orientation against it through the 'palm gesture' as well as through the cutouts of the bases. The day also involved instructions regarding heterocyclic atoms, functional groups and IUPAC numbering conventions for bases and sugar. This line of

discussion was significant to help students understand the structure of the nucleotide unit and the antiparallel nature of the two strands.

Sharada and Aakriti needed to build their background on atomic structure and bonds (hence they were introduced to M4 only on Day 5). The purpose of Days 2, 3 and 4 was to familiarize the students with the planar structures formed through the bonding of the purines and pyrimidines and the chemistry involved in the formation of individual DNA units along with introducing gesture and analogy as tools to visualize the orientation of the nitrogenous base pairs. Student interactions on Days 5 and 6 then dealt largely with the 3-Dimensionality of the DNA structure, which was analyzed microgenetically.

2.10 Data analysis (Microgenetic study)

The video data from Day 4 to Day 6 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) (Figure 2.4). 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.

The un-shaded events in Tables 2.3 - 2.7 indicate that the straight ladder structure is under discussion. Models M1-M4 are always straight ladder structures. If model M5 is being used, or if the gesture is being made in air (i.e., without support of one of the backbone models),

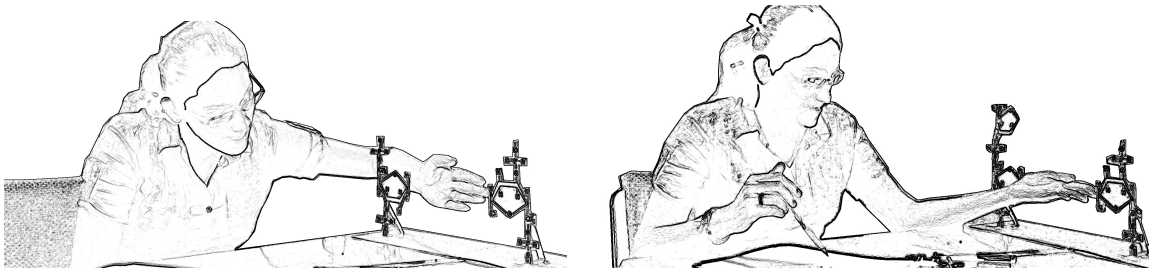


Figure 2.4: Palm gesture used with M4 model a) Incorrect (-) gesture and b) Correct (+) gesture

a) Anuja

Day	Day 4											Day 5							Day 6					
[1]Start time	7.5 min		37.1 min								55.5 min	74.09 min		122.3 min	125.6 min		134.4 min		164.2 min					
Episode No. (Duration)	**I** (0.3 min)		**II** (5.6 min)								**III**	**IV** (0.4 min)		**V**	**VI** (1.1 min)		**VII** (3.0 min)		**VIII** (2.2 min)					
[2]Event +							M3	M2	M4	M4 (c)	M4 (c)	Air z	Air z	M5 x	M5	M5	M5 z	M5 z			M4	M4 (c)		M4 (c)
[3]Event -	M1	M1	M4	M1	M2	M2													M4 (c)	M4			M4 (c)	

M5 ladder construction (Start time - 75.0 min)
M5 helix formation (Start time - 119.3 min)

Table 2.3: Sequence of correct (+) and incorrect (-) events for Anuja

b) Sharada

Day	Day 4		Day 5										Day 6
[1]Start time	4.4 min		56.1 min						110.2 min			121.2 min	134.1 min
Episode No. (Duration)	**I** (1.6 min)		**II** (1.1 min)						**III** (1.0 min)			**IV**	**V**
[2]Event +								Air		M4	M4 (c)	M4 (c)	M4 (c)	M5 z
[3]Event -	M1	M2	Air	Air z	Air z	Air z	Air		M4 (c)					

M5 ladder construction (Start time - 58.1 min) **M5 helix formation (Start time – 130 min)**

Table 2.4: Sequence of correct (+) and incorrect (-) events for Sharada

then the ladder structure under discussion could be straight (un-shaded event) or helical (shaded event).

2.11 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'. Notice that the first event on Day 4 for every student is a '-' event,

c) Nitin

Day	Day 4								Day 5																
[1]Start time	8.2 min		55.3 min	65.4 min					76.5 min	115.4 min						122.1 min	125.2 min							
Episode No. (Duration)	**I** (0.8 min)		**II**	**III** (3.6 min)					**IV**	**V** (3.5 min)						**VI**	**VII** (1.1 min)							
[2]Event +							Air	M4 (c)	Air				M1	M4	M5				M4		M4		M4 (c)	
[3]Event -	M1	M2	M4	M4	M4	Air				M4 (c)	M4	M1				M4 (c)	M4 (c)	M4		M4 (c)		M4 (c)		

M5 ladder construction (Start time - 77.2 min)

Nitin Contd.

Day	Day 5 Contd.				Day 6						
[1]Start time	129.1 min			132.2 min	158.3 min			172.5 min			
Episode No. (Duration)	**VIII** (0.5 min)			**IX**	**X** (0.3 min)				**XI** (2.1 min)		
[2]Event +			M4 (c)	M4 (c)	M5		Air	Air z	M5 0	M5 z	Air z
[3]Event -	M4 (c)	M4 (c)				Air					

M5 helix formation (Start time – 133.1 min)

Table 2.5: Sequence of correct (+) and incorrect (-) events for Nitin

d) Sandhya

Day	Day 4																Day 5
[1]Start time	4.4 min		36.2 min		42.6 min		46.6 min				52.4 min	57.3 min					71.1 min
Episode No. (Duration)	**I** (0.8 min)		**II** (2.3 min)		**III** (0.3 min)		**IV** (2.2 min)				**V**	**VI** (2.0 min)					**VII**
[2]Event +					M4		M4 (c)	M4 (c)		M4 (c)	M4 (c)	M4 (c)	M4 (c)	M4 (c)		M4 (c)	Air
[3]Event -	M1	M2	M4	M4		M4 (c)			M4 (c)						M4 (c)		

M5 ladder construction (Start time – 71.2 min)
M5 helix formation (Start time – 106.5 min)

Sandhya Contd.

Day	Day 5 Contd.														Day 6					
[1]Start time	121.3 min														151.4 min					156.4 min
Episode No. (Duration)	**VIII** (4.3 min)														**IX** (3.0 min)					**X**
[2]Event +					M1	M5		M5	M1	M2			Air	M5 x		M5 y	Air	Air y	Air z	Air z
[3]Event -	M5	Air	M3	M1			M5				Air 0	Air 0			M5 y					

Table 2.6: Sequence of correct (+) and incorrect (-) events for Sandhya

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 Figure 1 b) which is common in textbooks.

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

e) Aakriti

Day	Day 4		Day 5															Day 6							
[1]**Start time**	6.2 min		62.2 min					101.2 min									109.3 min	144.1 min	159.5 min	166.1 min			179.1 min	182.4 min
Episode No. (Duration)	**I** (1.2 min)		**II** (2.7 min)					**III** (3.6 min)									**IV** (1.2 min)	**V** (0.1min)	**VI**	**VII** (2.7 min)			**VIII**	**IX**
[2]**Event +**				M1	M1	M1	M1		M1		M4		M4 (c)	M4 (c)	M4 (c)	M4 (c)	M4 (c)	M5	Air	M5	Air z	Air z	Air z	Air z
[3]**Event -**	M1	M2	M1					M4		M4		M4 (c)												

M5 ladder construction (Start time – 71.2 min) **M5 helix formation (Start time – 117.3 min)**

[1]Start Time : The start time denotes the beginning of the episode with Day 4 starting at t=0
[2]Event + : Palm gesture or cutout orientation (c) perpendicular to DNA axis (correct)
[3]Event - : Palm gesture or cutout orientation (c) parallel to DNA axis (incorrect)
M4 (c) indicates that the cutouts of the N-bases were being used to show orientation. In all other cases, the palm gesture was being used.
The shaded events depict palm gesture in reference to the helical model, in M5 or in Air.
0: none of the base pairs twisting; x: Only two base pairs twisting; y: Partial or non-uniform twisting; z: uniform twisting

Table 2.7: Sequence of correct (+) and incorrect (-) events for Aakriti

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, Table 3 shows that 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 (described later) and positive encouraging feedback (a broad shared smile, and 'good!' or 'very good!') from the interviewer. The type of model being used during the episode was one factor which may have determined their response.

With Anuja the first '+ve' transition happened with the use of M3, that is, when she picked up the parallel pencils (representing the backbone) lying on the table and held them to stand vertically (Episode II). Anuja sustained the correct orientation through Day 4 and even Day 5, when she worked with M5, the clothespin model. But on Day 6, when Anuja returned to the M4 (cutout) model, she reverted to a series of incorrect and correct orientations (Episode

VIII).

With Sharada and Nitin the first "+ve" transition happened as they were doing the palm gesture in the air. But both of them underwent a "-ve" transition when they had to place the base pair cutouts against the M4 model. With Sharada, use of the palm gesture (Episode III) helped to correct her orientation, and she maintained the correct orientation through till the end of Day 6. Nitin however went through 6 "-ve" and 6 "+ve" transitions between Day 5 and Day 6.

In Sandhya, the first "+ve" transition happened on Day 4, using the palm gesture with M4. However, when in the next episode, four minutes later, Sandhya had to place the base pair cutouts against the M4 model, she reverted to the incorrect orientation. Over a total period of 16.7 minutes on the same Day (Episodes III VI) as she was using the M4 (c) base cutouts, Sandhya showed a series of 3 "-ve" and 3 "+ve" transitions. In Episodes VIII and IX too, as she worked with the straight and then helical M5 model, Sandhya showed 4 "-ve" and 4 "+ve" transitions.

Aakriti's '-' events of Day 4 continued on Day 5 with the M1 model. Her first "+ve" transition occurred in Episode II when she was using the palm gesture with M1. But, she too was stumped when, in Episode III, she was asked to depict the base pair orientation using the 'palm gesture' against M4, the cutout model. In a remarkable sequence of flip-flops, when she was asked to go back to M1 she recalled the correct orientation and then also corrected her gesture in M4, but, just as quickly, when she picked up the cutouts of the N-bases, she first oriented them in the wrong way (Table 3(e), Episode III). At this point it was the ladder analogy which helped her correct herself (see 'Context of the "+ve" transitions').

Aakriti, who was otherwise very shaky on her chemistry and biology concepts, was the only one who achieved a stable correct response on Day 5, which continued into Day 6. Sharada, Nitin and Sandhya achieved a stable response on Day 6. Anuja however was fluctuating in her response till the end of Day 6.

2.12 Students' difficulties with the helical structure

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 36°) 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.

In Tables 2.3 - 2.7 the shaded events indicate that students were showing the base pair orientation in the helical structure. A '+' or '-' event indicates that the base pair is shown perpendicular (correct) or parallel (incorrect) to the axis of the helix. The twisting of the base pairs is shown by a 0, x, y or z in the shaded boxes, with 0 for no twisting of the bases, x for relative twisting of two base pairs only, y for non-uniform or partial twisting of some base pairs and z for uniform or continuous twisting of all base pairs such that the first pair is aligned with the eleventh one (correct response).

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 Anuja and Sharada 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. Anuja and Sharada indicated a continuous twisting in air with the base pairs perpendicular to the DNA axis (Anuja, Episode IV) or parallel to the axis (Sharada, Episode II).

The construction of the M5 model is indicated by two arrows below the Tables, a hollow arrow for the straight ladder and a shaded one for the twisted ladder. The straight ladder construction involved attaching the clothespins (bases) to the plastic tubing (backbone) and pairing the A-T and G-C bases. With some help 3 of the students (except Nitin and Aakriti) placed the bases equidistant along the backbone. However when it came to twisting the ladder something unexpected happened. Anuja and Sandhya crossed the two backbones and, instead of making a helix, pressed the backbones and the bases flat on to the table. Nitin did the same, even before he was asked to form the helix. The shape that these three students formed looked uncannily like the diagram (Figure 2.1b) in their textbook. In this configuration the distance between the two backbones decreased and went to zero at the crossing, hence it was no longer possible for the students to fit any base pairs in the narrowed space. They dealt with this problem by moving the base pairs away from the point of crossing, leaving a gap there. All these three students had earlier asserted that the distance between any two base pairs was 3.4 Å, but after forming their helix they said there would a gap at the "point" of the helix. Anuja even suggested that when the DNA replicates an incision is made at this "point"!

Sharada and Aakriti made a reasonable M5 helix, but Sharada spoke (in Episode V) about the turning in the molecule, the place where it rotates and the two units of the helix. Aakriti too spoke in Episode V about a point of the helix. Even after the construction of the M5 helix (shaded 17 arrow in Tables 2.3 - 2.7) it was not immediately obvious to the students that each base pair was turned by the same angle with respect to its adjacent base pair. This was a classic case of observation being shaped by preconceptions!

All the students remembered that there were 10 (Nitin thought 8) base pairs in one helical turn, and there was a 36° angle involved somewhere, but none guessed that 36° was the constant angle between the base pairs. Even as she handled the M5 helical model, Anuja still thought that only the two base pairs at the "center" were turning (Episode V). This was in contradiction to to the correct gestures in air that she had shown in Episode IV. Notwithstanding their problems with the M5 model, all except Nitin had some idea of a helical shape as in a telephone cord, spiral-bound note-book or a spiral staircase. Nitin however was misled by the Marathi term 'sarpil' for helix, meaning 'snake-like', which he illustrated with a wavy 2-D shape made from stiff wire. When shown a wire wound around a pencil he said in Marathi, "It is like a snake wound around a tree."

Next there was a pedagogical intervention to remind the students about "10 base pairs in a helical turn", "one turn is 360°" and "$10 \times 36° = 360°$". In all the students this led to an 'Aha!' moment, i.e., sudden realization or acceptance of the fact of uniform turning of the base pairs, indicated verbally or through a convincing facial expression. The intervention took place in or after the final gesture episode for all the students, except with Anuja, for whom the intervention happened in Episode VII. We cannot tell about the stability of this learning, since it happened at the very end of the sessions. The 'Aha!' moments were more prominent in the contexts of the "+ve" transitions (parallel to perpendicular orientation of the base pairs) which are analyzed next.

2.13 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 were usually the result of an interjection or a hint by the interviewer.

Of the 19 "-ve" transitions for all the students, 12 took place when the students used the cutouts with the M4 model. Here they had to simultaneously grapple with the chemical bonding between the bases and sugar, and the orientation of the base pairs with respect to the backbones. They had to recall that the bases were to be bonded with the Carbon atom at the 'first (prime)' position of the sugar molecule, and that it was the Nitrogen atom at the first and the ninth position of a purine and a pyrimidine respectively which bonded with the sugar. With Sandhya several negative transitions happened while using the M5 model where she had the twin task to consider the perpendicular orientation of the bases to the backbone or axis, as well as the angular turn of N-base pairs.

The "+ve" transitions were more interesting, since they represented a learning episode. Hence we asked, what were the types of intervention that led to "+ve" transitions? Table 2.8 summarizes the number of "+ve" transitions for each student and the context of each transition. The first "+ve" transition for each student occurred after they were given the ladder analogy: "Have you seen a ladder?" Initially, for Anuja, Nitin and Sandhya, 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. Anuja, Sharada, Sandhya and Aakriti spontaneously laughed out aloud. Sharada asked incredulously, "The real ladder?!" She then proceeded to correct her orientation without further instructions for mental simulation. Nitin was generally more reserved in his expression but he too gave a hint of a smile with vigorous shaking of head, showing he had realized something.

With Aakriti the first and the second "+ve" transitions came by suggesting to her the ladder analogy and going from the M4 to the M1 model. Her third and fourth transitions, which came in the space of one minute and twenty one seconds (Episode III), brought the spontaneous 'Aha!' moment accompanied by wholehearted laughter. All through the rest of

Name of the student	No. of '+' ve transitions	Context of the transitions
Anuja	3	1. [1]**Ladder analogy with mental simulation**; 2. reminder about gesture against M1; 3. reminder about orientation.
Sharada	2	1. **Ladder analogy**; 2. palm gesture.
Nitin	7	1. **Ladder analogy with mental simulation**; 2. palm gesture; 3. palm gesture; 4. reminder of earlier orientation; 5. reminder of earlier orientation; 6. ladder analogy with mental simulation; 7. ladder analogy with mental simulation.
Sandhya	8	1. **Ladder analogy with mental simulation**; 2. **ladder analogy**; 3. reminder about base positioning; 4. reminder about earlier gesture; 5. palm gesture; 6. ladder analogy with mental simulation; 7. ladder analogy; 8. reminder about the base placement.
Aakriti	4	1. Ladder analogy; 2. ladder analogy; 3. **ladder analogy with mental simulation**; 4. **ladder analogy**.
Total	**24**	Ladder analogy (6), ladder analogy with mental simulation (7), palm gesture (4), reminder (7)

Table 2.8: Summary of Number of "+ve" Transitions and their Contexts
*All contexts which had direct bearing on the 'Aha!' moment of the student are given in bold font.

Day 5 and Day 6 she maintained the correct orientation.

Out of the total of 24 "+ve" transitions for the five students, 13 transitions came about when the interviewer gave the ladder analogy, by itself or accompanied by instruction to mentally simulate walking up the ladder. Sandhya and Aakriti had a second 'Aha!' moment with just the ladder analogy, after the instruction to simulate had been given in a previous episode or event. Possibly mental simulation recurred in those events, 19 spontaneously, without being cued explicitly by the interviewer.

After the initial 'Aha!' moment seven of the subsequent "+ve" transitions occurred simply with a reminder to the students about their previous gesture or orientation. Four of them occurred when the students spontaneously corrected their gesture. Of these self-corrections two occurred while gesturing with the M1 model. The other two occurred with the M4 model, when the students were asked to use the palm gesture. Thus, after the 'Aha!' moment a

simple reminder or use of the palm gesture was sufficient to bring about a "+ve" transition.

2.14 Visualizing the 3-D structure of DNA

The results of this study were striking and surprising to us. We anticipated that biology students might have some problem in visualizing the precise 3-D structure of the DNA molecule. 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 to follow from the common diagrams for example, Figure 1 b). 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 (J. D. Watson & Crick, 1953) original paper mentions it.

What surprised us then 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 bondings, 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 criss-crossing backbones with base pairs between them, forcibly flattening them to lie flat on the table! The DNA helix is an icon of modern scientific culture. Undergraduate science students in urban India are exposed to this image not only in their classrooms but also in the media. All the students in our sample had attended tutorial classes in which

they had been exposed to clear and more detailed diagrams than available in their regular textbooks. In informal conversation they told us that in the (1-3 day) interval between two sessions they had looked up their study materials and also videos and illustrations of DNA structure on the internet. Despite this considerable exposure they had not realized the essential 3-Dimensionality of DNA structure.

It seems to us that the idea of a helical ladder structure is not a difficult one to convey, if it is done early enough, before the students' minds get cluttered with details of the molecular model. The dimensional details including the equidistant placing of the base pairs (3.4 Å), 10 base pairs per helical turn, and 36° angles between the base pairs, could also be taught, before the molecular model is built up on this basic structure.

2.15 Palm gesture as an instructional tool and a diagnostic tool

The palm gesture could be a basic, simple tool to convey the orientation of the base pairs in the ladder structure. We used the gesture as a means to connect the multiple models (M1-M5) of the DNA backbone. The gesture is powerful and flexible enough that it is not tied to any specific orientation of the backbone. Models M1 and M2 were laid flat on the table, M3 and M4 standing up, and M5 could be rotated in any direction. Gestures in air could be done in any direction, which students sometimes did. The palm gesture served to abstract out the idea of base pair orientation, independent of the particular model that was being used. It was for us as a diagnostic tool to begin with, but as the interaction proceeded, it also became an instructional tool.

2.16 Use of analogy for visualization

The ladder analogy was crucial in correcting the students' base pair orientation. The planarity of the base pairs arises due to the hydrogen bonds between them, while their perpendicularity to the DNA backbone comes from N-glycosidic bond between the base and the sugar molecule. The helical ladder structure of DNA is formed due to the tendency of the bases to avoid contact with water and stack one above the other, an arrangement that is further stabilized by Van der Waals forces and polar interactions between the adjacent bases.

The ladder structure, thus, has functional implications, though students may learn about these only at a later stage. Structure-function linkages in biology help students make sense of what they learn, and are thought to play a role in mental visualization (Mathai & Ramadas, 2009). Yet in the absence of knowledge about functional features, the ladder analogy helped students find a beautiful and pleasing consistency between what they knew and what they had to learn.

In the framework of Goldin-Meadow and Beilock (Goldin-Meadow & 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 then 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, gesture could be used to link 2-D representations with multiple 3-D models of DNA structure, and mental simulation involving changing 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

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.

Constructivist models of learning suggest that learners learn by building upon their unique cognitive and conceptual resources (Taber, 2011) (Von Glasersfeld, 1989) (Novak, 1993) (council et al., 1996). Learners actively create and modify their understanding, by assimilating new information into existing knowledge structures, or by modifying their knowl-

edge structures to accommodate new information (Flavell, 1963) (Ausubel, 1963). In this view, analysis of existing knowledge structures, and the process by which they are modified, is key to assessing and improving learning.

However, in the most frequently administered assessment instruments, viz. multiple choice questions, fill-in-the-blanks, knowledge is measured by testing memory of isolated chunks of information (Mintzes & Quinn, 2007), rather than the hierarchical network of connections suggested by constructivist education research. While more sophisticated assessment instruments such as clinical interviews exist, they are labor-intensive and difficult to scale up, and hence have limited applicability. Thus, there is currently a mismatch between pedagogical interventions that seek to improve student learning, and the assessment techniques to probe the extent of their learning (Schwartz, Lindgren, & Lewis, 2009).

While the space of pedagogical interventions have grown, with many approaches that build on different aspects of learners' existing knowledge structures, e.g. in problem/discovery/inquiry/project based learning curricula, innovation in assessment methods has been slow, particularly in developing methods that help in capturing students' existing knowledge networks, and the process by which these are modified to create new knowledge networks. From a psychological standpoint, most popular assessment tools are purely recall-based instruments, and these would be adequate tests of understanding only if the architecture of knowledge resembled a series of filing cabinets populated by reams of unconnected propositions. In such a view of knowledge, every question has a correct or incorrect answer, and the error rate in retrieval of propositions from these filing cabinets is a useful proxy for judging competence. But such methods cease to be useful if the architecture of knowledge is visualized as interconnected webs of concepts, with linkages synergistically reinforcing understanding, as research both in cognitive psychology and education increasingly suggests (Ortony, 1977) (A. Clark, 1997) (Barsalou, 1999) (Prinz, 2002).

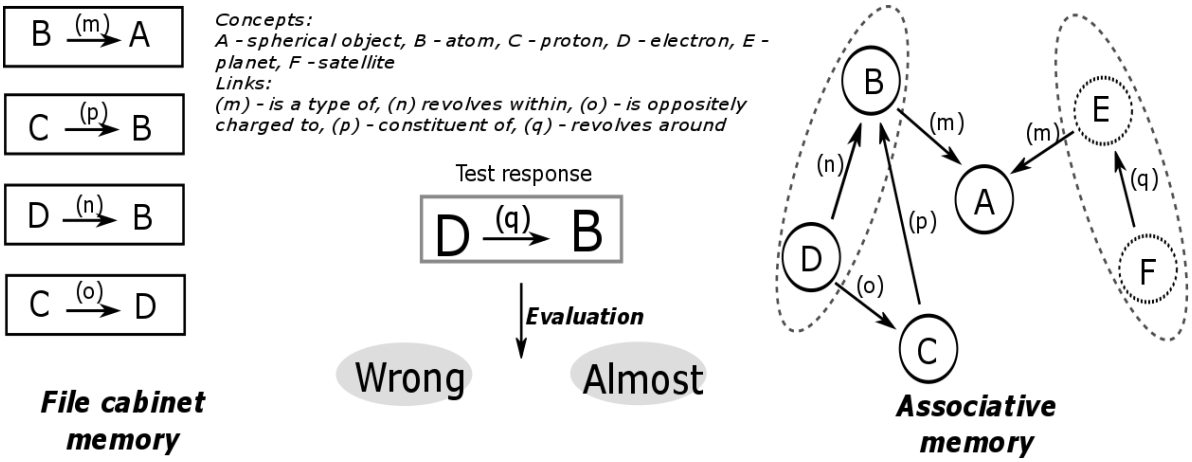


Figure 3.1: Illustrating how assumptions about students' cognitive architectures can influence an instructor's evaluation of the source of their errors. Adopting a network view of conceptual linkages makes it feasible to probe for inappropriate analogies, generalizations and categorizations that frequently cause conceptual misunderstanding in learners.

Consider, for instance, the stylized example in Figure 3.1 student responds to a question asking her to describe the relationship between atoms and electrons by saying that electrons revolve around atoms. A fill in-the-blank scoring system would mark this as an error and move on. A sensitive educator, on the other hand, might probe deeper into the source of the error, and might uncover that it came about because the student used a planetary system metaphor to visualize the atom while learning. In this case, the student has intuited an important symmetry between two systems of incommensurate scales, but this intuition has translated into mistakes during assessment. If we tell this student, "You're wrong", she may get the answer to the question correct the next time in her middle school exam. At the same time, by breaking the intuitive link between planetary systems and atomic orbitals that she has serendipitously formed by naive analogy, we may reduce the delight she may have experienced in finding inverse square laws governing forces in both systems in high school. While coarse assessment instruments are useful for competitive testing and merit assignment, they have limited value in moving students from such nebulous stages of understanding to clarity.

More detailed assessment instruments like clinical interviews, which probe knowledge at deeper levels and provide insights into the learning process (and obstructions therein) of students, these are effort-intensive for instructors, and due to their subjective, interpersonal nature, are difficult to scale and standardize across students and instructors. It is this methodological gap in education research that we try fill in this paper, by developing an assessment instrument that acknowledges the interconnected nature of conceptual understanding, but still remains sufficiently objective and scalable to be standardized across student-instructor sets.

To design an assessment instrument that seeks to uncover obscure stages of learning, we are best served by developing one based on subject matter that strongly resists traditional instruction. Multiple authors have commented on the difficulty that biology learners experience in reconciling large arrays of facts (Dauer, Momsen, Speth, Makohon-Moore, & Long, 2013), often linked via multiple levels of understanding (viz., macro/micro/symbolic). Within the larger biology literature, it has been specifically found that learners find structure-function linkages in elementary genetics very difficult (Lewis & Wood-Robinson, 2000) (Marbach-Ad & Stavy, 2000) (Marbach-Ad, 2001) (Lewis & Kattmann, 2004).

Specializing still further, within genetics as a whole, learning about the structure of the DNA molecule presents a unique set of difficulties. The relation between genes, chromosomes and DNA, as well as the functions of DNA (replication, transcription and translation) has been identified as difficult areas to learn (Lewis & Kattmann, 2004) (G. Venville & Donovan, 2007) (Rotbain et al., 2005). In other research, for instance, it was found that biology undergraduates interpreted the 3-D structure of the DNA molecule as 2-D structure, the way they had seen it in textbooks (Srivastava & Ramadas, 2013). These difficulties may be ascribed to the perceptual inaccessibility of genetics concepts, as well as to the complex organization of genetics knowledge, which requires multiple levels of understanding (Marbach-Ad & Stavy, 2000) (Duncan & Reiser, 2007). Learning about DNA, thus, satisfies

the broad criteria for a test case for our instrument, as well as an area that would benefit greatly from its use, if successful.

In response to the difficulties identified above, educators have used diverse external representations, such as physical models, animations, or drawing-based activities (viz., (Rotbain et al., 2006) (Tsui & Treagust, 2003) (Rotbain et al., 2005) as pedagogical aids. Active engagement in the process of learning is also encouraged. In the context of 3-dimensional literacy, physical models are considered to bolster the transition of learners from abstract to concrete knowledge (Malacinski & Zell, 1996; Roberts et al., 2005). However, supporting our critique of the difference that exists in the sophistication between teaching and testing methods, assessment in such studies has relied largely on questionnaires, surveys or interviews (e.g., (Bahar et al., 1999) (Marbach-Ad & Stavy, 2000) (Lewis & Kattmann, 2004) (G. Venville & Donovan, 2007) (Rotbain et al., 2005)). Since we are interested in understanding the process by which existing knowledge is extended to develop new knowledge, we sought to develop a tool that would reveal this process.

Our new assessment instrument is built on top of existing one - concept-mapping - a widely popular tool for eliciting learners mental models (Novak, 1998) (Shavelson, Ruiz-Primo, & Wiley, 2005) (Ifenthaler, 2010). Concept-mapping is a graphical format that lets instructors or learners arrange concepts in physical space. The maps use arrows to represent direct relationships, and physical proximity as a proxy for general conceptual relatedness. Rather than simply evaluate the final maps that students generate, we designed objective measures of competence that can be measured during the process of map construction. This development allowed a finer-grained view of students' understanding, even identifying individual concepts within the subject-area that any one student might be having difficulty with. As proof of concept, we administered this instrument to a small sample of biology undergraduate students, who were asked to build concept maps reflecting their understanding

of DNA structure, and found interesting individual differences across both students and concepts. More holistically, the pattern of observations seen in this study led us to develop quantitative variables that measure a more granular level of understanding than traditional assessment instruments, while remaining scalable and objective.

3.1 Concept maps

Concept-mapping was first proposed as a way of coding interviewers' judgments about the conceptual linkages that students were discussing in clinical interviews (Novak & Gowin, 1984). This graphical format provided a compact and standardized representation of students conceptual understanding, particularly the relationships between concepts, than clinical interviews.

From their origin as tools for retrospectively coding clinical interviews, concept maps have emerged as pedagogical tools in their own right (Kinchin, 2001). The central argument in favor of using concept-mapping as a teaching/learning tool is that, unlike more linear methods of teaching and testing (lectures/multiple choice questions etc.), concept-mapping forces students to directly engage with the interconnected nature of relationships between concepts, which requires moving away from rote learning (Novak & Cañas, 2008). Unlike diagrams and writing, concept maps make explicit not just 'what' a student knows about a particular concept, but also 'how' that conceptual knowledge is organized in the student's mind (Kinchin et al., 2000).

Therefore, assessments based on concept-mapping hold the promise of striking a balance between the objectivity and scalability of evaluation that traditional assessment methods provide, and sensitivity to students' existing knowledge structure that more interactive but intensive methods like clinical interviews do.

Figure 3.2: A sample concept map created by one of the builders; shows concept cards connected by arrows, with linking phrases specified on top of pin-up labels.

Concept-mapping tasks generally involve writing key terms (concepts) and arranging them in meaningful patterns, connecting concepts by drawing lines, and labeling the nature of the relationship between two concepts (Novak & Gowin, 1984) (Novak, 2004). This process is usually done using pencil and paper, where participants generate the concepts, lines and linking phrases. Changes are cumbersome in the pencil-paper mode, but software implementations allow changes to be made more easily. In the work reported here, we modified the concept-mapping technique by using movable elements for concepts (cards), arrows (paper-cuts) and labels (pin-up labels) (see Figure 3.2). This was because we wanted a more flexible task, where participants could sort and cluster cards, and easily organize and re-organize the network. Drawing is less flexible (Martin & Schwartz, 2005) and could lock participants into connections, and thus prevent (and also make invisible to researchers) further search processes and re-visits to the connections. We predicted that the freely manipulable elements would lead to multiple physical organizations and re-organizations, which would provide insights into the dynamic nature of the internal representation of the concept, as well as the way concepts are accessed and re-organized during map construction.

3.2 What can the process of concept-mapping tell us?

The physical act of concept-mapping naturally promotes self-directed recognition, rehearsal, and hence re-consolidation of concepts in long-term memory. By virtue of its physical implementation, concept-mapping allows participants to explore both modes of declarative memory - recognition and recall (Mandler, 1980). The former has a much larger capacity, is easier to train, and is more prone to error. For any particular connection between two concepts, a student could simply recall what connects them. Or, she might only recognize that the two concepts 'go together' somehow when juxtaposed, typically after comparing several combination possibilities. What makes concept map-building a good method for process analysis is this exploration of knowledge, and the fact that this entire spectrum of understanding can be observably expressed in physical space- all the connections that students contemplate are manifest in the physical moves they make with concept cards. Thus, information, not just about which propositions students can recall entirely, but which ones they vaguely recognize and explore, is available in this elicitation format.

Historically, educational research using concept maps has focused on assessing finished versions of students maps (Novak & Cañas, 2008). We suggest that such outcome-based assessments throw away information about recognition-reliant understanding and exploration of knowledge, information that a systematic process analysis would make available.

However, process analyses are notoriously effort-intensive, difficult to standardize across instructors and difficult to compare across students (Langley, 1999); since our purpose is to design a practical assessment instrument, we focus on one specific element of the process that is unambiguous to observe (and hence to automate), standardizable across instructors and comparable across students. Specifically, we show in this paper that the number of 'moves' made using each concept during map-building is a useful variable, measuring the effort required to recall concept linkages connected to the corresponding map element.

If a student can explicitly recall propositions connecting some map element with the concept card they want to use next, they will simply join the two and move on to the next card. In contrast, if the concept on a card is completely unfamiliar to a student, they will likely not even try to put it on the map. In addition to these extreme perfect knowledge-no knowledge cases, physical concept-mapping also lets us observe behavior characteristic of vague understanding, where the student is unsure about the specific connection, but has rough intuitions about which map elements the card in their hand might go better with. It is such behavior, characteristic of vague understanding, which we try to characterize and quantify in this paper.

Clearly, the repertoire of such behavior is very large, and not easy to coherently describe, let alone measure. We simplify our proposal by focusing on characterizing the influence of a single process component- the number of times a student has to manipulate a concept during concept map-building. We show that this (clearly observable) variable correlates well with the perceived effort of processing the corresponding concept within the constraints of our task- which we take as an indicator of more generalized difficulty in processing it in other contexts also.

The central contribution of this paper is, thus, our use of this idea to map different levels of subject-area competence to the bivariate interplay between move count and accuracy in handling individual concepts. Building upon this primary contribution, we introduce a series of quantitative and graphical representations of subject-specific competence that allow educators to develop a fuller picture of students' conceptual understanding, identifying points where they find the process of connecting concepts difficult, so that interventions may subsequently be targeted specifically to these points.

3.3 Methods

Sample

Twelve biology undergraduate students (5 male, 7 female) from two different colleges in the city responded to a general call for a biology concept-mapping study. Consent and permission to videotape the sessions were obtained from all participants. All students had prior exposure to the basic structure of the DNA molecule during high school (Grade 12). A few revisited the concept during their undergraduate classes. All of them were previously exposed to concept-mapping sessions as part of another project. These sessions (7) were conducted twice a week, and required students to build concept maps related to biological structure and processes, viz. cellular structure and function of organelles. The instructors in these sessions largely followed Novak's concept map-building elements (Novak & Gowin, 1984) and participants were introduced to Cmap (a software tool) to build digital maps on computers.

Material

We used physically manipulable elements in the task and, hence, the task was introduced by the researcher (first author) to individual students by giving a short power-point presentation on concept-mapping through the example of a representative concept map on 'animal cell' (DiCarlo, 2006). After the introduction, students were asked to build concept map focusing on the structure of the DNA molecule making use of the physical elements, viz., printed cardboard concept cards, chart-paper arrows, pin-up labels, and styrofoam sheets(s). The cardboard concept cards stood for the concepts, where each of 37 concepts (selected by the authors based on their prominence in exposition of DNA in standard textbooks) was type-written on a cardboard card. A list of the concept cards used is presented in **Table 1 (Appendix B)**. The chart-paper unidirectional arrows were to be used to represent the link between two concept cards. The pin-up labels were to be used for writing linking phrases

indicating the specific relation between two concepts. The styrofoam sheet(s) stood for the working sheet(s) on which the concept map was to be built. Students were also provided with push-pins to pin arrows (link) between concept cards (concepts) on the working sheet(s).

Instructions

While other researchers have emphasized the importance of structural elements such as hierarchy, cross-linkages, modularity etc. for well-constructed concept maps, we chose to give students no such special instructions, letting them build any structure they preferred for their maps, even though the example chosen for the introduction ('animal cell') was hierarchical and had cross-linkages. While this deviates from the canonical Novak formulation, and as Ruiz-Primo & Shavelson (Ruiz-Primo & Shavelson, 1996) suggest- if concepts are inherently hierarchically learned, the concept maps that students generate will naturally be hierarchical. Therefore, we did not impose any restrictions on the structure. After the introduction, students were simply asked to build the concept map with the provided materials, using as many of the provided concept cards as possible. There was no time limit for the task; students took between 43 to 98 minutes to complete it in individual sessions. Time taken by individual students to complete the task is given in **Table 4 (Appendix B)**. Further, students were not probed verbally for explanations during the task, and questions about the procedure, but not about the content, were answered.

3.4 Data sources and research design

All sessions were videotaped, and the final concept-map was photographed. As the students were seated on the floor, they made use of both the floor as well as the working sheet (styrofoam) to organize their conceptual structure. The first author of this paper, along with an assistant, transcribed all videos, recording each relevant move made by students across the duration of the exercise. The video transcripts of the concept-map building sessions

were the major data source for analysis. Transcripts of all students' map-building process are made available through a web-link in **Appendix B**.

The study's analytical framework is informed by microgenetic research protocols, which require dense data collection and intensive observation of subjects to infer possible causes for changes in competence (Siegler, 2006). Our study shares Siegler's methodological approach of using high density of observations, followed by minute data analysis. However, unlike the microgenetic approach, our emphasis is not to detect change in competence, but use overt changes in behavior to develop an index of the current degree of competence. Thus, our focus is to identify useful aggregate measures of process, unlike in microgenetic studies, wherein aggregate measurements are considered suspect because they miss out on the critical small periods of time where competence actually changes.

3.5 Data Analysis

We performed a novel two-phased analysis on the data to - **a)** obtain map-level performance data using outcome-based scoring methods (structural analysis), and **b)** obtain concept-level performance data using novel procedural analysis methods.

The first gave us the macro-view, which provided us with quantitative elements to identify patterns and compare concept maps, while the second gave us a detailed micro-view of how each concept was understood by the participants.

Structural analysis

Scoring 'accuracy' at map-level.

The Novak scoring scheme is generally considered to be the most comprehensive method for quantitatively assessing the quality of concept maps, but is primarily directed towards

evaluating hierarchical maps and so is not directly applicable to our set-up. A more general method for scoring maps that need not be hierarchical can be adapted from the research of McClure & Bell (McClure & Bell, 1990), 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 generated a balanced estimate of map accuracy 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. Specifically, it is a relative measure of the number of times we see two concepts meaningfully connected by a linking phrase in a map. The relationship between the two concepts is captured by a proposition, which can be accurate or inaccurate. As is standard, we define a proposition as occurrences of concept-linking phrase-concept sequences. As illustrated in Figure 3.3, each participant's accuracy in capturing the propositional relationship between two concepts was scored, using a range from 0 to 1. Every correct proposition earned a score of '1' and every incorrect proposition, a score of '0'. If a concept, A, was linked by a single linking phrase L to more than one concept, B, C, D, and E, then the score of '1' was equally divided among all the four propositions, i.e., 0.25 for A-L-B, 0.25 for A-L-C, 0.25 for A-L-D, and 0.25 for A-L-E. These scores were submitted to an inter-rater reliability test. Three graduate students, with a background in biology, independently scored the propositions. The inter-rater reliability was quite high

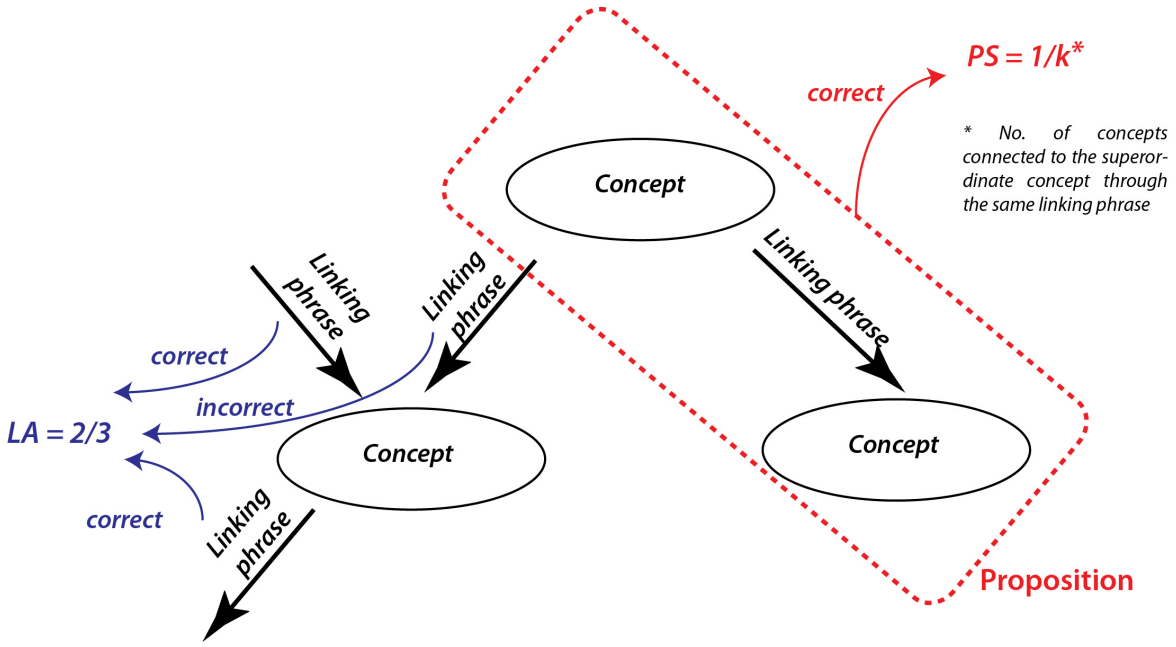


Figure 3.3: This diagram illustrates the calculations underlying our two different measures of accuracy. Map-level propositional accuracy is obtained by summing proposition scores computed for all propositions in the map. Proposition scores are binary (0 & 1), except when a parent concept links to multiple 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.

(Cohen's $\kappa = 0.94$), in line with reliability measures of similar scoring schemes seen in the literature (Novak & Gowin, 1984) (Lomask, Baron, Greig, & Harrison, 1992).

The total number of true propositions expected in a map given a concept set, needed to compute recall, is a harder quantity to estimate. One way of arriving at it would be to ask experts to construct criterion maps and use the average number of propositions in them. However, since our design allows students to write their own linking phrases, scoring such criterion maps would prove difficult since there would be several cases where the set of linking phrases that an expert uses will differ from those that the students would use. Given this constraint, we approximate recall as the number of concept cards used to the total number of concept cards available.

To appreciate that this is a reasonable approximation, note that we can directly measure an unnormalized variant of the true recall in the form of the number of valid propositions made by a student; the unobservable quantity of number of possibly valid propositions remains constant across all students. For our approximation to be reasonable, all that is needed is for the number of valid propositions a student makes to be directly proportional to the number of concept cards she has used. In our sample, this condition holds with a strong quantitative correlation seen ($\rho = 0.68$). Thus, the recall approximation is quantitatively reasonable, and is much simpler to calculate than having to build a criterion map for every concept set tested to determine the number of possibly valid propositions.

We finally combine precision and recall scores obtained from students concept maps to compute the F measure as,

$$F = \frac{2 \times \text{precision} \times \text{recall}}{\text{precision} + \text{recall}}, \tag{3.1}$$

where, precision is the ratio of number of valid propositions made to the total number of propositions made, recall is the ratio of number of concept cards used to the total number of concept cards available, and k is a parameter that modifies the F-measure to privilege either precision or recall. For our calculations in this paper, we restrict ourselves to using k = 1, which weights them both equally, but the flexibility added by this parameter has considerable pedagogical potential, making it possible for instructors to weight their assessment of students' competence along the dimensions of breadth and precision of knowledge separately.

The F-measure calculation gives us a scalar measure of the accuracy of the completed concept map for each student **(see Table 2, Appendix B)**. As we discuss above, the subjective elements of this computation, assigning validity to students propositions, are statistically reliable across multiple judges ($\kappa = 0.94$). All other elements are observable, leading us to believe that this scoring method is a reliable indicator of final map quality.

While the F-measure does not score structural elements of the concept maps, both the structural complexity of concept maps and their overall accuracy provide convergent evidence of the map-builder's competence, so in principle should be correlated. To verify this in our case, we further calculated the structural complexity index (SCI) (Arneson, 2005) of each of our subjects' complete concept maps. SCI is a purely structural measure of map complexity that takes proposition count, number of branches, number of chains and the average chain length, but not propositional accuracy, into account. In spite of its epistemic indifference to propositional accuracy, we find that SCI is positively correlated with the F-measure scores for our sample (= 0.57), showing that the F-measure is measuring the underlying competence of subjects quite well, even though it does not undertake structural scoring. SCI scores for all subjects are given in **Table 3 (Appendix B).**

Procedural analysis

While the outcome-based map scoring provides a useful method to analyze learners overall competence, it doesnt take into account the dynamic patterns and cognitive conflicts which give rise to the final organized map. Naturally, capturing the procedural patterns and scoring them objectively is a practical challenge. The solution we propose is to get down at the level of concepts and analyze builders actions with each concept. Specifically, we attempt to compute two measures on a per concept basis: **(i)** a measure of effort for the use of the concept, and **(ii)** a measure of concept-specific accuracy.

Number of moves as measure of effort.

The term 'move' is operationalized as any action of the map-builder which leads to changes in the position of a concept-card, viz., picking, dropping, placing, and shifting. Given a particular set of concepts, an omniscient participant would require a very small number of moves to complete her concept map- she would place each card on the map surface only once, in its correct spot. Such a performance would justifiably be considered maximally efficient;

optimum accuracy with minimum effort. Extending this intuition further, shifting or picking up already placed cards, etc. can be construed rationally as markers of inefficiency. Thus, counting the number of moves a student takes up to make up their mind about where a concept card belongs can be used as a measure of how effortful it is for them to handle this concept in the task; thus, we interpret number of moves made with a concept as a measure of its perceived effort. For our analysis, the numbers of moves were documented from the video transcripts, where all moves made were coded by the first author during the transcription process.

One might argue that the time spent on the task could also be used as a measure of effort. The problem with using such a measure is that tracking time spent on a particular concept is difficult in concept-mapping, wherein builders switch their focus between different concepts multiple times. The overall time taken to build the map could indeed be used as a map-level measure of confidence, and in fact time taken is weakly inversely correlated with the F-measure in our sample ($\rho = 0.23$), as one would expect of a reasonable measure of effort- participants who can do the task more accurately are likely to find it less effortful also **(Table 4, Appendix B)**. However, since we are interested in concept-level effort measurements, using time measurements is unrealistic- we would have to track time spent on each concept as the participant switches to and away from it multiple times during map construction. As a realistic approximation, we use move counts.

Scoring 'accuracy' at concept level.

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 7 illustrates how link accuracy differs from standard propositional accuracy used in previous scoring schemes, including our own outcome-based scoring scheme described above.

Having defined measures of concept-specific effort and accuracy, we are now in a position to address the key research questions of our study- can we characterize map-builders facility in using individual concepts, and is this facility related to these two indices of 'effort' and 'accuracy'?

3.6 Results

The primary goal of our research design was to connect the map building processes of students to their final outcomes. We did this by using a novel quantification of concept-level effort and accuracy to assess students overall facility in using individual concepts, while building concept maps in this subject area. The results we report here use only 10 of the 12 students in our original sample. One student created her own concepts and added them to the map, and another student used ambiguous linking lines. We could not find a way to equitably compare their performance to the rest of the sample; hence these were not included in the analysis.

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

Figure 3.4 plots the normalized number of moves (X-axis) against the normalized accuracy (Y-axis) associated with each concept averaged across all students in our study. The point of origin at the X-Y axis intersection indicates the mean value for both the normalized number of moves and the normalized accuracy. Any positive plot value on the X-axis, thus, suggests that the number of moves made is higher than the mean, and vice-versa; also, any positive plot value on the Y-axis suggests that the concept accuracy is higher than the mean, and vice-versa. This visualization strategy gives us a plethora of information about students relative 'fluency' in using each of these concepts during map-building, where fluency is defined as

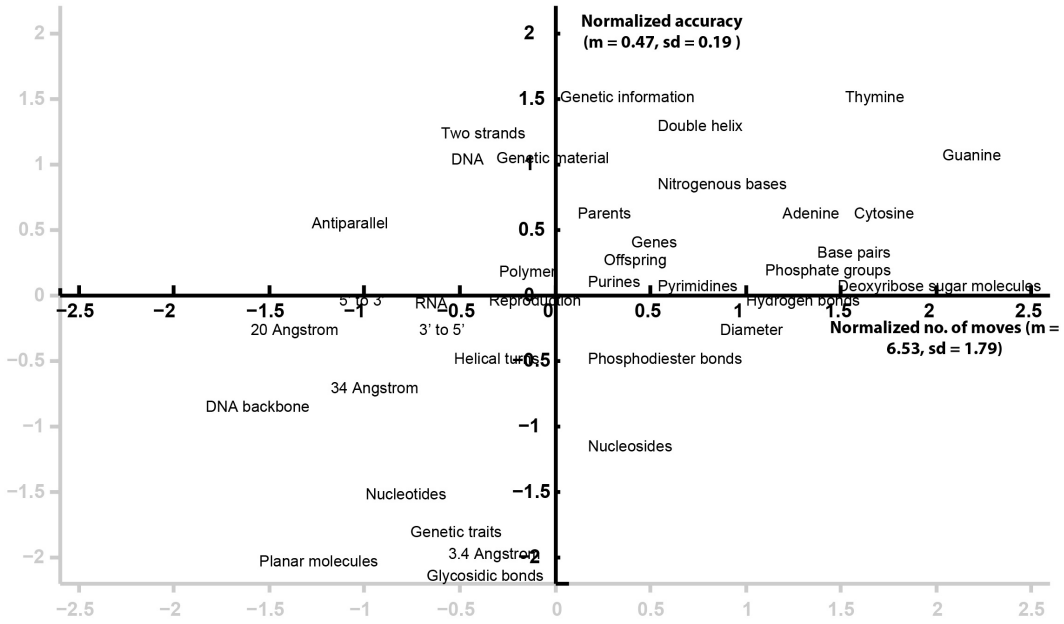


Figure 3.4: Plotting normalized move count (X-axis) against normalized accuracy (Y-axis) averaged across all 10 subjects for each concept used in the map building exercise. This plot visualizes the overall fluency with which students can use individual concepts (fluency decreases clockwise from quadrant II)

the ability to use the concept both accurately (high accuracy) and efficiently (fewer moves).

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 concepts that clearly relate functionally to DNA e.g. anti-parallel, parents, offspring etc., but are less fluent in handling concepts associated with the biochemistry of DNA (e.g. planar molecules, phosphodiester bonds, glycosidic bonds etc.). The lack of cross-disciplinary education opportunities at the high school and college levels in the country could be one reason for this finding.

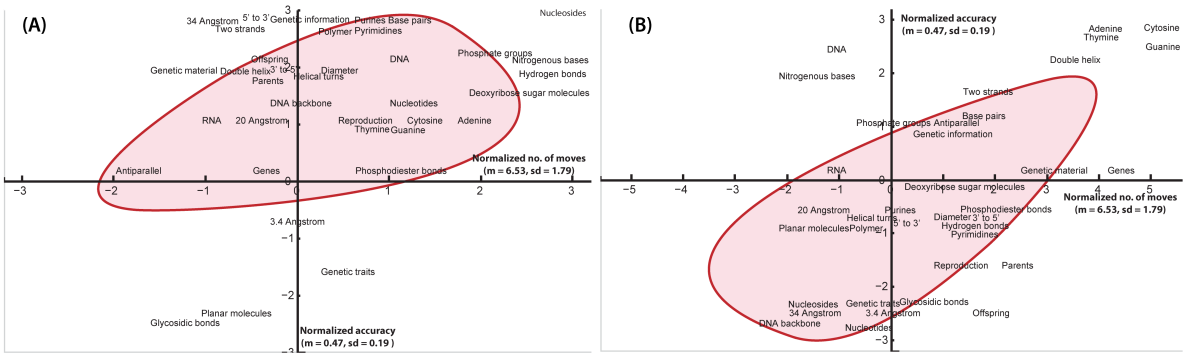


Figure 3.5: This figure illustrates concept-specific accuracy against move count for (A) the best three performers of the task, and (B) the worst three performers of the task. We drew contours for respective plots on the basis of number of concepts falling in each quadrant. The area occupied the contour curve is drawn proportional to the number of concepts lying in the quadrant.

Understanding contours: an alternative holistic measure of concept-map building performance.

What is the relationship between outcome-based 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 8 contains useful information about the level of subject-area understanding. Rather than try to shoehorn this information into a number, it is 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 outcome-based map-scoring, reveals stark differences (Figure 3.5).

In general, the contour for better performers (Figure 9A) 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

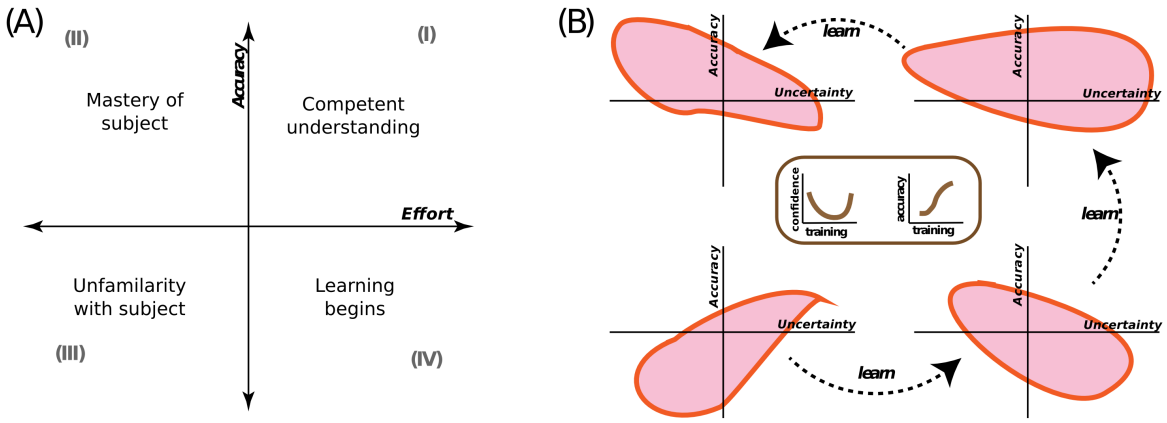


Figure 3.6: (A) An illustration of the learning zones defined through our analyses. (B) Insight from prior literature on the individual relationships between learning, accuracy and effort (see inset) suggest that subjects will follow a progression through the quadrants III → IV→ I→ II as they progressively understand the concept space better.

performers (Figure 9B) predominantly covers quadrants III and IV, showing that they either know they don't know much 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.

Based on our results, an intuitive interpretation of the four quadrants in Figure 3.4 emerges, as shown in Figure 3.6. Understanding contours for experts will span quadrant (II) reflecting high accuracy obtained with low effort. Learners with a relatively good grip on the concepts will demonstrate relatively high accuracy alongside high effort measurements, whereas weaker students will be seen to exert great effort but obtain low accuracy scores. Novices completely unfamiliar with the concepts will neither exert effort, nor arrive at accurate propositions.

Since all the student participants in our study sample engaged with the task we set them, with varying degrees of success, we have a large representation of quadrant I and IV- heavy understanding contours in our data.

3.7 Validation study

By our account, if we gave experts the same task, we would expect their understanding contours to be dominated by quadrant II. To verify this simple prediction based on our learning progression, we conducted a small follow-up study wherein we asked three subject matter experts - in increasing order of expertise, a graduate student, an assistant professor and a senior professor in biology- to perform the concept-mapping task using the same set of physical materials as our student sample. We predicted that these experts would therefore complete the concept maps correctly using much fewer moves than our student sample. Our predictions were borne out - while we did not transcribe these subjects' videos in the same manner as for our original sample, the difference in move count density could be easily seen directly in the videos **(web-link in Appendix B)**. For instance, the senior professor rarely moved a concept card more than once in his map-building session. The other two participants followed the same pattern of sparse movements, though not to such a radical degree. Based on direct counting of moves from the video data, we estimated an average of 3-4 moves per concept card for our three subjects, compared with the 7.8 average for our original sample, and with very few errors in their completed maps. While statistical testing is inappropriate given the small size of our expert sample, the difference in move counts is sufficiently large for us to be confident that experts used fewer moves. This level of performance, if mapped onto our coordinate system, would yield understanding contours dominated by quadrant II, as predicted.

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 3.6a. Our proposal is supported indirectly by empirical studies of skill acquisition, which find a U-shaped relationship between training magnitude and perceived competence (Csikszentmihalyi, Abuhamdeh, & Nakamura, 2005) and a sigmoid relationship between training magnitude and accuracy in multiple learning tasks (Gallistel, Fairhurst, & Balsam, 2004). Only a learning progression

that traverses the quadrants in the order III $\rightarrow$ IV $\rightarrow$ I $\rightarrow$ II proposed in Figure 3.6a is compatible with both these observations.

This methodological contribution has straightforward practical applications. Designing understanding contours (see Figure 3.6b) from procedural statistics yields a compact and intuitive visualization of a students holistic understanding of a subject area. Also, tracking understanding contours longitudinally would allow educators to track the progression of a student's understanding quantitatively. 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 curriculum/pedagogy design.

3.8 General Discussion

To summarize, we have built upon the existing methodology of concept-mapping to develop an assessment tool that permits identifying individual problem areas and stages in students' understanding of complex and interconnected concepts, viz., biological concepts. In particular, this method allows an instructor to quantify how well a student has understood the relationship between a concept and its neighbors. We do this by introducing a new way of measuring conceptual confidence, a metric for evaluating learning that complements response accuracy by taking the amount of effort needed to generate a response into account. This metric provides insights into difficulties in the process of learning, and holds promise for revealing the locations within students' mental network of conceptual understanding where misunderstandings, uncertainty, vagueness and incomplete information reside. Such knowledge would permit instructors to better personalize remedial instruction, crystallizing the constructivist principle of using students' existing knowledge structure in a replicable, testable and scalable manner. Such remediation is expected to be particularly helpful in higher biology education, where complex and interconnected concepts such as DNA structure and function are usually only partially understood by students.

There are several other ancillary benefits for adopting such an assessment instrument. For instance, using it would allow an instructor to judge students' understanding in a holistic way, and not just based on propositional accuracy which can be gamed using rote learning and teach-to-test tactics (Sommer, 1990). And, hence, we did not look if the concept maps were 'excellent' or 'good' (Cañas, Novak, & Reiska, 2015) but we looked into the process if it could give us an objective measure to quantify understanding. Our two-dimensional measurement of conceptual competence provides an empirical window into the heretofore under-studied progression from solid competence to mastery, which is of particular interest in professional education settings, e.g. in medical school. The novel representation of 'understanding contours' provides a succinct quantitative summary of insights from the process analysis of concept-mapping, one that is easy to track and report. Thus, we believe the methods, the analysis framework, and the novel representations we report here, with further refinement, could contribute significantly to how students' understanding is assessed. While the results we report here are specific to biological concepts, this approach should prove useful for assessing any area of knowledge where students find it difficult to learn complex concepts that are interconnected at multiple levels.

It is also pertinent to note that, while we have restricted ourselves to interpreting the number of moves required per concept as a measure of effort, it is also likely to correlate to some degree with students' underlying confidence about the concept. Concepts that are clearly understood will require few exploratory moves to get right during map-building, whereas concepts that students do not yet clearly understand will be moved around more often, as they probe the penumbral recesses of their understanding to see whether some particular exploratory pattern of card placements triggers a recognition cue.

This interpretation is supported by recent work showing an inverse correlation between confidence and response times (Lasry, Watkins, Mazur, & Ibrahim, 2013) and the understanding of concept maps as a method of externalizing the process by which people arrive

at internal conceptual associations (Novak & Cañas, 2008). While response time is difficult to measure in a concept-mapping study, wherein students switch between a large number of associations over and over again, the number of times a particular concept card is moved is an excellent alternative. Current models of the decision-making process (e.g., (Busemeyer & Townsend, 1993) (S. D. Brown & Heathcote, 2008)) suggest that greater response times are caused by greater pre-response internal deliberations in subjects. In physical concept-mapping, these deliberations are, to a significant degree, externalized, permitting us to just count them directly instead of approximating them via chronometry.

Concerning limitations of this study, we first address two possible criticisms we consider unfounded, and then describe what we believe are the true limitations of our current work. Superficially, it might appear as if our empirical study suffers from a small sample size (n = 10). To a very large extent, the intensive nature of our analysis limits the size of possible studies of this nature in terms of number of subjects studied. At the same time, it is important to realize that the true subjects of procedural analysis, which was the main thrust of this study, are concepts, not people. Our goal in this study was to develop methods that could identify patterns (such as difficulty/complexity) within sets of concepts, not within people. Therefore, while the generalizabilty of our results may not be as clear cut as we would have ideally liked, they are complementary to the concept-level analysis we present, which does not suffer from this flaw.

Another possible criticism is the absence of pre-test scores and/or alternative evaluations of student knowledge of DNA. To the extent that alternative measures of DNA knowledge were available, they all loaded strongly on the accuracy element of our scoring, for which outcome-based concept map scores are already known to have reliable correlates in the existing assessment literature (McClure, Sonak, & Suen, 1999) (Francisco, Nakhleh, Nurrenbern, & Miller, 2002). Multiple studies comparing concept-mapping performance with regular test scores have been conducted previously in the literature (Ruiz-Primo & Shavelson, 1996),

suggesting moderate to strong correlations. Therefore, alternative valuations of DNA knowledge were considered unnecessary for this study. Existing assessments of non-accuracy components of knowledge, e.g. efficiency/confidence, are scarce in the literature. However, as we describe above, Lasry et al., (Lasry et al., 2013) have shown that conceptual confidence varies inversely with question response times. Since concept maps are simply externalizing the internal deliberations that typically cause greater response times, greater deliberation (as measured by move counts) should correlate inversely with conceptual confidence, which is precisely what our methodology assumes.

This study had three major lacunae. One, our study is not longitudinal. Since we report the possibility of tracking students' understanding contours, it would ideally have been more compelling to present data showing how such contours evolve in individual students as they progress through their college career, for instance. Longitudinal studies using concept maps have, in fact, been recently reported in the literature. For example, Dauer et al., (Dauer et al., 2013)report patterns of change observed over a semester of instruction, in which students iteratively constructed concept maps representing their 'gene to evolution', GtE mental models. They measure change in terms of overall architecture of students' models and the quality of language used to describe relationships. Similarly, Speth et al., (Speth et al., 2014) have used student-generated conceptual models to assess understanding of the origin of variation using multiple cycles of instruction, assessment and feedback. At semester's end, a substantial proportion of students significantly improved their representation of how variation arise. Unfortunately, logistical difficulties prohibit our undertaking such a project ourselves. However, conducting a longitudinal study tracking change in understanding contours over time is a potent avenue for future work in this project.

Second, counting external moves instead of measuring response times ignores the role of invisible mental calculations and simulated moves by participants. In particular, our effort scoring rubric would likely unfairly penalize students who externalize their thinking process.

It is therefore necessary to clarify that we do not assign deep ontological commitments to our interpretation of the effort variable- it is simply measuring the externalized portion of students' cognitive effort. In the same way that we can only judge students' understanding by the answers they give to the questions that were asked on a test, not on the answers they might have given to questions they were never asked, epistemic limitations enforce our use of a limited proxy for a student's overall effort during such a task. Alternative process measurements like response time are inapplicable in non-linear tasks like concept-mapping, unless we can find a way to establish how much time a participant is spending thinking about a particular concept at multiple time-points during map construction. At the same time, while mental simulations are possible, they are not likely to be particularly helpful in provoking vague recognition cues in our particular task. Thus, while imperfect, move counting appears to be a reasonable measure of effort for concept-mapping.

Finally, since our ultimate goal is to design an assessment tool that is practical, it could be argued that the analysis is too labor-intensive to effectively apply in classroom settings. This is almost certainly true if the protocol were to be implemented with the same exactitude as in the research study. However, we find post hoc that a simple modification to the design can make the analytic load tractable. For example, instead of using just one card per concept as we did, teachers could provide students with multiple copies of cards for each concept, with the injunction that anytime they decided to move a particular concept, they had to use a new copy, discarding the old one. This would produce an automatic count of the number of moves students make at the end of the exercise, approximating the true count to the extent that students follow the teachers instructions not to reuse cards. The rest of the analysis is straightforward and not labor-intensive. In resource-rich settings, software to track physical manipulations on touch-screen surfaces could easily be developed to support analytics of the form we propose in this study. For resource-poor settings, a simplified way of using concept-mapping for assessment in a frugal manner is described in the next chapter, based

on a reanalysis of the data from this study.

Note also that, with the increasing proliferation of online courses (MOOCs), student engagement with concepts could be measured with even more generality than our specific confidence-level counts. Problem areas in such a generalized analysis might correspond to concepts with which students appear to have engaged frequently (as measured during their online activity), but on which their test scores don't appear to be improving. In such settings, understanding contours could be evaluated using purely data that is collected already as a matter of course. Thus, while the current physical operationalization of our task design is effort-intensive, we believe its basic insights can be integrated into scalable practical applications.

Chapter 4

Using element placement order in assessment

As we discuss towards the end of the last chapter, one of the problems with using concept maps as assessment tools is that the actual assessment tends to be labor-intensive. Instructors have to score individual propositions in maps, keep track of additional process indicators as we discuss, and put the statistics together to devise useful quantiative measurements of a student's understanding. To address this concern, we present a much simpler, though necessarily rough indicator of student understanding. Reanalyzing the concept-mapping process of the eighteen volunteers from the study reported above, we discovered that the order in which students place the physical concept map elements on the mapping surface is, in fact, a predictor of the quantitative summary of merit of the final map. This observation naturally suggests that instructors are well-advised to pay attention to the order of element placement in concept-mapping, in order to be able to intervene and encourage students in real-time. We report our analysis and empirical results to this effect in this chapter.

Video-recording of the map-building process formed the major data source for this analysis. The video-data was subjected to a time-sequence analysis where it was broken into a series of snapshots taken every minute, for every participant. For each snapshot, the number of cards

(C), arrows (A) and phrases (P) on the working-sheet were recorded. We also photographed the built map to compute 'F-measure' to assess participant's comprehension.

4.1 Potential strategies

We hypothesized that students would subscribe to one of four possible placement strategies (described below) for aligning the map elements to construct the concept map. But we were not sure if students would remain consistent with the use of individual strategies and not switch.

We predicted that a map-builder with perfect knowledge of the correct relationships between all concepts to be placed on the mapping surface will likely treat these relationships as the focal points of the construction process, thereby placing card-arrow-phrase combinations on the mapping surface together. In contrast, a map-builder with very vague knowledge of relationships will be more likely to treat the concept cards themselves as the focal points of the construction process, and place them all on the surface first.

In general, assuming the logical temporal flow of placement must involve cards before arrows before phrases, there are four possible strategies of map element placement, as illustrated in Figure 4.1, differing only in which sets of map elements are placed on the mapping surface first. We denote these, using dashes to represent time delays, as:

a) C-AP: Most cards placed first on the workspace, followed by arrow and linking phrase placement, typically assigning a linking phrase to each arrow as soon as it is placed.

b) CA-P: Cards and arrows placed on the workspace together, and linking phrases were added later.

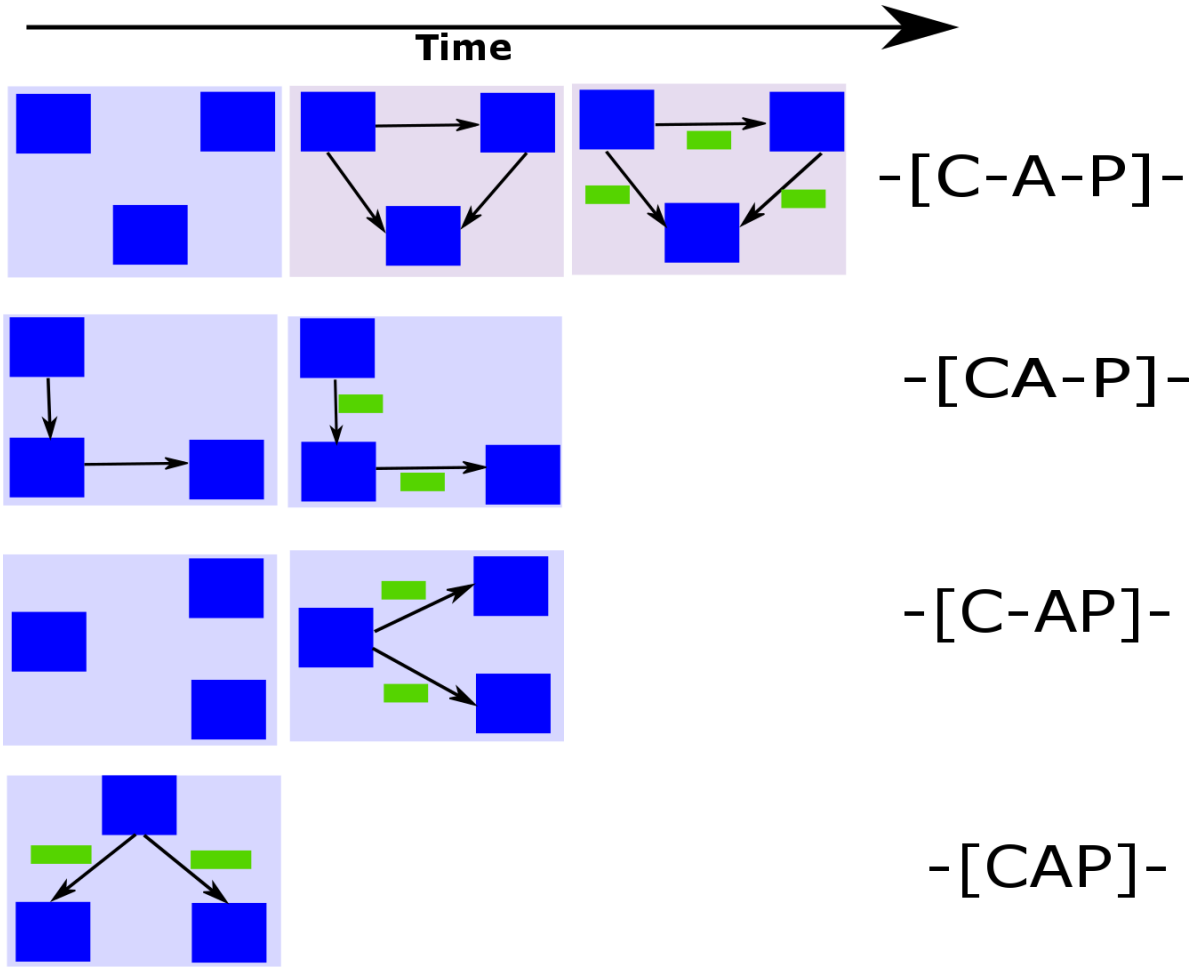


Figure 4.1: Possible concept map element (cards, arrows and phrases) placement strategies.

c) CAP: Map elements placed together in systematic propositional order.

d) C-A-P: First all cards, then all arrows, then all linking phrases.

As we describe above, at least some of these strategies appear intuitively correlated with varying degrees of subjective confidence about domain area knowledge. We expect, a priori, for instance, that students that follow the -[CAP]- strategy are more confident in their ability to construct maps than students following the -[C-A-P]- strategy. If this confidence is driven by metacognitive assessment of the navigability of internal mental maps, then such

subjective confidence should lead to objective better concept maps. If this is true, then visually observing the order of placement of concept cards could give instructors a quick, holistic sense of students knowledge levels.

4.2 Results

Strategy use was systematic and unmixed throughout map building

One of our pre-analysis concerns was the possibility that experiment participants may switch between strategies over the course of the map-building process, which averaged about 50 minutes for our students. We had preliminarily assumed that our analysis would have to tease apart the influence of different strategies probabilistically as a function of their dominance in any one participants map-building process.

Fortunately and remarkably, we discovered post-analysis that none of our 18 participants ever switched to a different strategy once they had settled on one. Figure 4.2 shows representative plots of card, arrow and phrase counts observed on the mapping surface (y-axis) at different points in time (x-axis) for one student each per strategy. Systematic use of these four different strategies is immediately evident visually.

CA-P strategy associated with lower map quality

The map quality of all 18 participants was plotted (y-axis) as a function of their map building strategy (x-axis). Figure 4.3 shows the plot. A ceiling effect is likely present for concept map is quite a lenient format for eliciting valid propositions from students. Nonetheless, a clear performance difference is seen.

Specifically, the data suggests that lower map quality is uniquely characterized by adoption of the CA-P building strategy. A one-way ANOVA test excluding the CA-P cohort shows

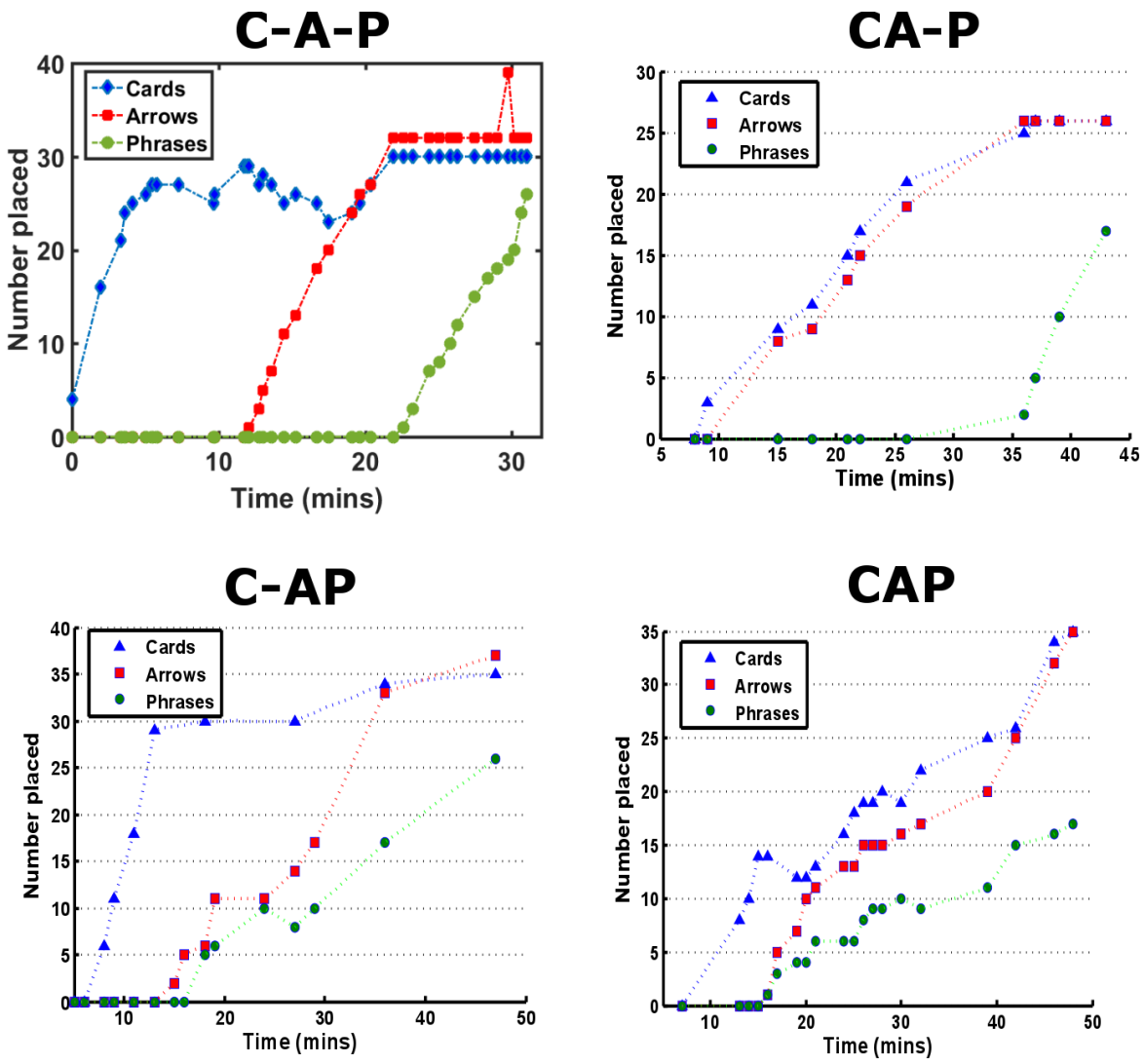


Figure 4.2: Participants selected a building strategy at the beginning of map building and used it exclusively throughout.

insignificant differences in the mean F-measure for the remaining population (F2 = 1.17, p = 0.35); a one-way ANOVA including this cohort shows extremely significant difference (F3 = 7.75, p = 0.0027), substantiating the statistical significance of the discrepancy.

4.3 Discussion

Complementing previous proposals for using concept maps as assessment instruments (Cañas et al., 2015), we have sought to identify a low-effort characteristic of the concept-mapping

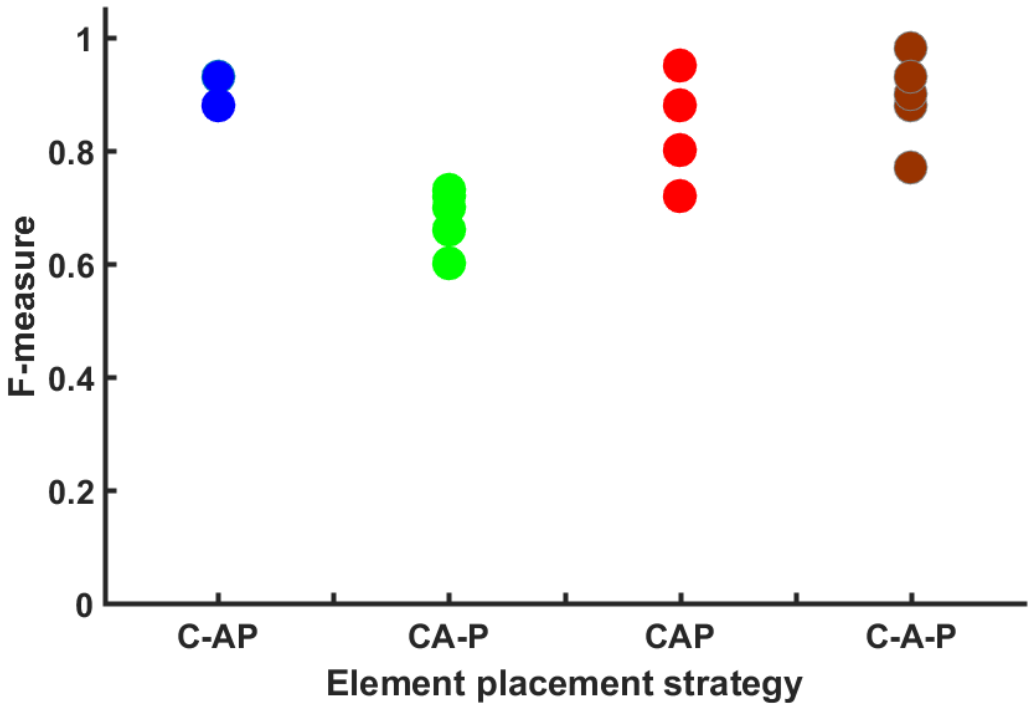


Figure 4.3: Map quality as a function of map building strategy use.

process, so that these may be used as efficient assessment tool not just in resource-intensive First World environments, but also in the large classrooms of the developing world. Based on recently identified symmetries between how people navigate their internal cognitive maps and external spatial environments (Hills, Todd, & Goldstone, 2008), we hypothesized that differences in the level of detail and precision in the internal maps, if available to introspection, might become apparent in the order in which people place elements on the map. To this end, we conducted this study using physically manipulable elements for constructing concept maps, yielding the results reported in this study.

We found that map-builders do not combine multiple element placement strategies, participants in our study converged to the strategy they would use till the end at the very beginning of their session, suggesting that any strategic consideration of strategy use was pre-meditated and not a function of manifest task difficulties.

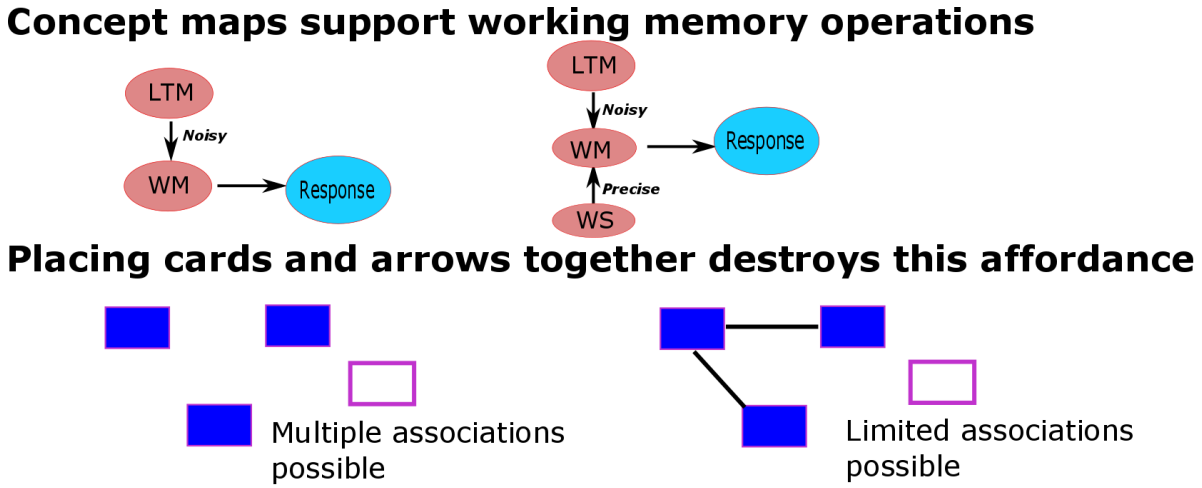


Figure 4.4: Possible explanation for the pattern of results seen in our concept-mapping study. LTM: Long term memory, WM: Working memory, WS: Working space

We also found a pattern of results rather different from our preliminary intuitions about which strategies would correspond to better maps. Whereas wed assumed that map-builders following strategies that placed all cards on the surface first would do badly, this did not in fact happen for the C-A-P strategy. Rather, the strategy that stood out as resulting in poor quality maps is CA-P, wherein participants placed cards and arrows on the map together first, and then wrote in linking phrases at the end.

We conjecture an alternative hypothesis to explain the specific deficits seen in the CA-P strategy. As we argued at the outset, it is unsurprising to find that participants following the CAP strategy end up making high quality maps, since this corresponds to a construction mode where the fundamental units of construction are the conceptual relationships, and its use suggests that these relationships are clearly accessible to the map-builder in their internal mental navigation.

The use of other strategies indicates less facile access to internal representations of conceptual relationships. However, note that concept maps are a paradigmatic example of a physically distributed learning artifact (Martin & Schwartz, 2005). Whereas a student may not immediately remember the conceptual relationship between concepts A and B, seeing them together in physical proximity can support delayed retrieval of the conceptual link-

age from LTM (long term memory). As illustrated in the top panels of Figure 4.4, on this account, the spatial affordances of concept maps support map construction by serving as a disembodied working memory container, complementing the information content of noisy memory engrams from the map-builders memory.

Crucially, C-AP & C-A-P are relatively flexible strategies that can exploit this affordance of the working surface via conceptual reorganization. In both cases, map-builders arrive at an intermediate stage of construction where most of the concept cards are on the surface, while arrows and phrases arent. This specific arrangement of cards is substantially amenable to reorganization and associative linkage. On the other hand, a builder following the CA-P strategy will see, at any intermediate stage of construction, a working surface where cards are already linked to other cards via arrows. The CA-P strategy fails to utilize the physical distributed cognitive abilities of the concept-mapping task. Thus, map-builders using it fail to construct satisfactory maps.

So, we believe that the reason our prior intuition for strategy-quality correspondence was not entirely corroborated is that the concept-mapping tasks supportive affordances masked this effect for map builders who placed only cards on the working surface. This factor was also complemented by lenience in our judgment criteria we asked only that individual linking phrases be valid, not necessarily optimal descriptors. Thus, the bar for creating high quality maps, by our quantification, was set somewhat low, which naturally led to a ceiling effect.

Notwithstanding these limitations, the performance deficit for the CA-P strategy was clearly evident. In conjunction with the systematic use of one of these four strategies by all our participants, these results suggest that studying the impact of element placement order on map quality is a feasible project. The low-cost and immediacy of this measurement renders it an attractive assessment option for low-resource settings as exist in the educational environment of developing countries.

At the same time, order of placement can serve as a useful marker of student confidence and/or subject matter comprehension in resource-intensive settings also. Concept-mapping software that tracks map-building on desktop and touchscreen surfaces is readily available. Particularly in large classrooms, MOOCs and other classroom models where instructor attention is a scarce resource, element order placement can serve as a signaling mechanism for attracting the instructors attention to students struggling with the material.

Chapter 5

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.

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.

Figure 5.1: Photographs depicting nucleotide base pairs (left) built by model builders from component atoms and (right) given as starting element to model dissectors

5.1 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.

5.2 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 (See Appendix C).

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. 5.1). 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.

5.3 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. 5.2). 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.

5.4 Model dissection works better

While the overall sample showed improvement in test scores, this increase was larger for the dissector group, as illustrated in Figure 5.3. The difference between the performance of the

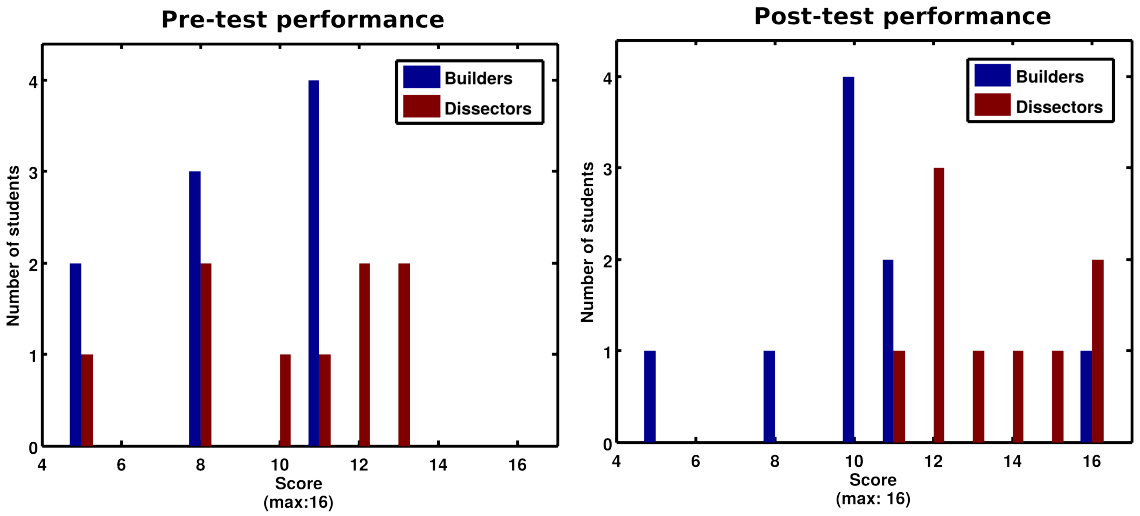


Figure 5.2: Comparing pre- vs post-test performance for both our cohorts as measured by the number of questions (out of 16) each student got correct. While both groups showed improvement on the post-test, the 'dissector' group showed greater improvements than the 'builder' group, with nearly all students in the dissector group scoring above 75 % on the post-test.

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.

5.5 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.

5.6 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

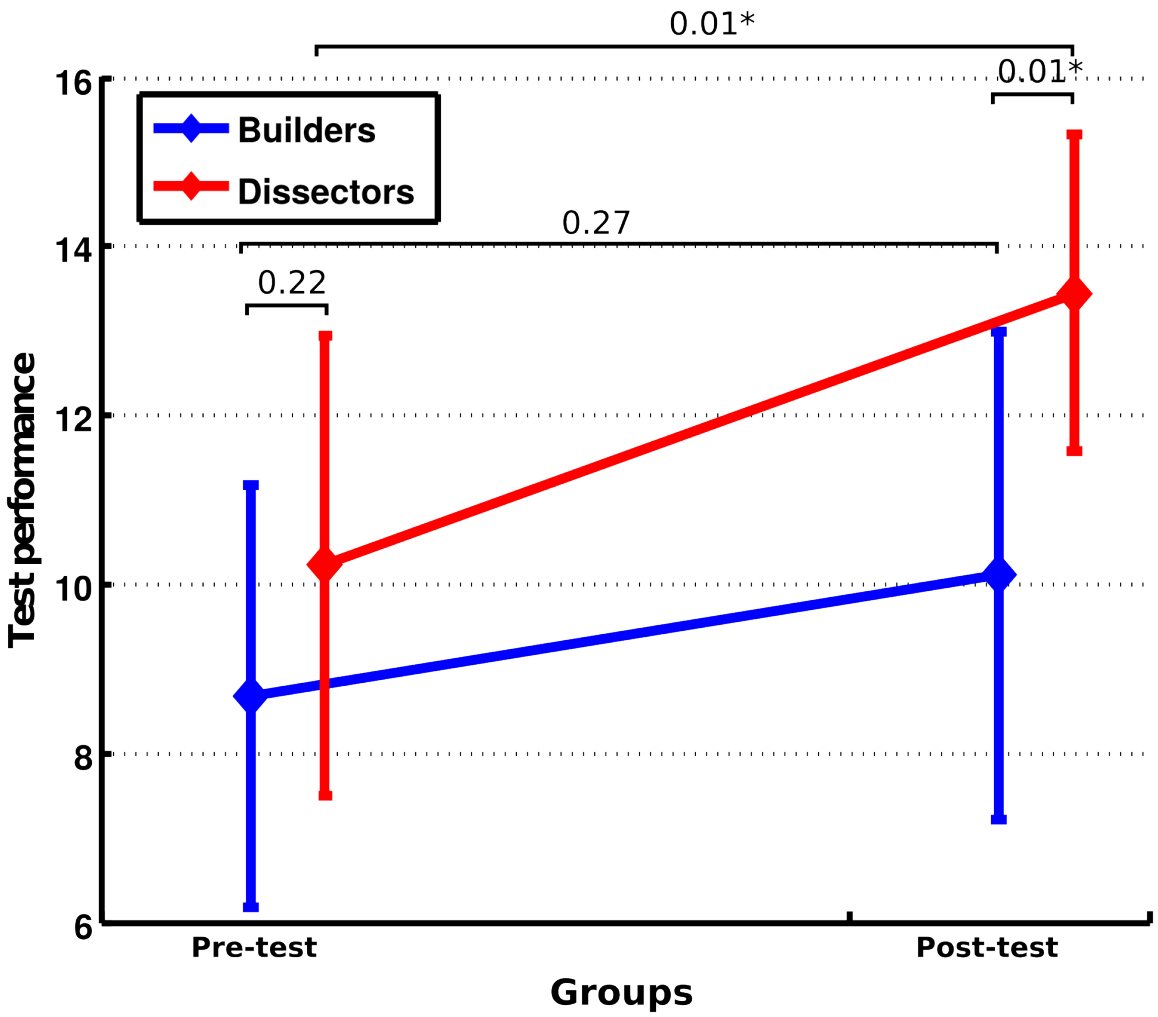


Figure 5.3: Illustrating performance improvement in pre- vs post-tests of knowledge about DNA structure. All results are sample averages. Error bars represent +/- 1 SD. p-values are derived from two sample T-tests in all cases.

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 6

Difficulties within and across 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.

6.1 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:

- construct a concept map using preset concepts related to DNA structure
- dissect a symbolic 3-D model or,
- 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 (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

- properties of representation,
- demands of the task &,
- 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 (K. J. Schönborn & 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, Dickerson, Boone, & Libarkin, 2004) (Reiss & Tunnicliffe, 2001) (Gobert, 2000) (Gobert & Clement, 1999) (K. J. Schönborn & Anderson, 2009).

6.2 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.

6.3 Analysis & Findings

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.

Tracking internal representations: Diagrams

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:

1. **Spatial**: Here, elements are located (symbolically or in molecular details) within the diagram without being labeled as a term.

2. **Verbal**: Here, elements are not located within the diagram but are verbally mentioned and/or elaborated upon the sidelines of the diagram.

3. **Spatial-Verbal**: Here, 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.

Participant	Verbal-Spatial Scores		Diagrammatic pattern in D1-D2
	D1	D2	
Concept-mapper 1	0.67	0.83	H -- H
Concept-mapper 2	0.86	0.83	H -- H
Concept-mapper 3	0.3	0.8	L -- L
Concept-mapper 4	0.8	0.83	H -- L
Concept-mapper 5	0.57	0.89	H -- L
Symbolic-modeler 1	0.38	0.5	H -- L
Symbolic-modeler 2	0.82	0.89	H -- L
Symbolic-modeler 3	0.5	0.7	L -- L
Symbolic-modeler 4	0.5	0.5	H -- H
Symbolic-modeler 5	0.17	0.33	H -- L
Molecular-modeler 1	0.89	0.86	H -- L
Molecular-modeler 2	0.22	0.86	H -- H
Molecular-modeler 3	0.25	0.88	H -- L
Molecular-modeler 4	0.78	0.75	H -- L
Molecular-modeler 5	0.29	0.5	H -- L

Table 6.1: Table showing shift in verbal-spatial scores and in the corresponding diagrammatic pattern.

Almost every participant improved

As shown in Table 6.1, 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.

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 (Figure 6.1). More striking, though, was the finding that

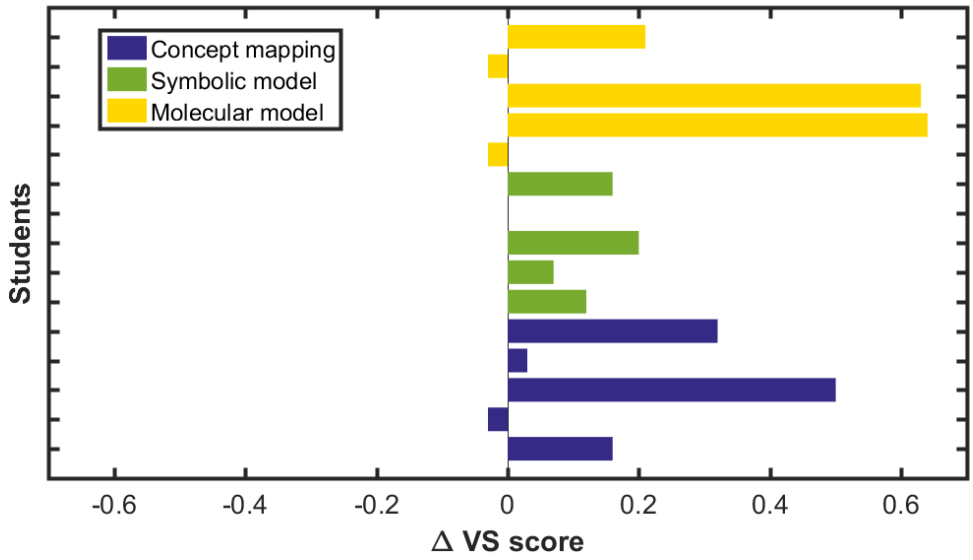


Figure 6.1: Almost every participant improved on the verbal-spatial scores post interaction with the respective external representation.

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.

Diagram structures converged

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.

Tracking overt behavior: ER interactions

1. Concept-map

Table 6.2 summarizes the task performance for participants who were assigned to build concept maps.

Map-builder	Total propositions	Valid propositions	F-measure
Concept-mapper 1	24	13.5	0.70
Concept-mapper 2	20	15	0.77
Concept-mapper 3	28	22	0.88
Concept-mapper 4	24	19	0.88
Concept-mapper 5	28	22	0.88

Table 6.2: Task performance for concept-map builders.

2. Symbolic-model dissection

Table 6.3 summarizes the task performance for participants who were assigned to dissect symbolic models.

Dissector	Concept to be dissected				
	Nucleotide	**Nucleoside**	**Deoxyribose sugar molecule**	**4 nitrogenous bases**	**Phosphate group**
Symbolic-modeler 1	X	√	X	√	-
Symbolic-modeler 2	√	√	√	√	√
Symbolic-modeler 3	X	√	√	√	-
Symbolic-modeler 4	X*	X	X	√!	-
Symbolic-modeler 5	X	X	-	√	-

Table 6.3: Task performance for symbolic-model dissectors.

3. Molecular-model dissection

Table 6.4 summarizes the task performance for participants who were assigned to dissect molecular models.

As Tables 6.2, 6.3 & 6.4 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.

Dissector	Concept to be dissected				
	Nucleotide	**Nucleoside**	**Deoxyribose sugar molecule**	**4 nitrogenous bases**	**Phosphate group**
Molecular-modeler 1	√	√	√	X	√
Molecular-modeler 2	X	X	√	X	√
Molecular-modeler 3	√	√	√	X	√
Molecular-modeler 4	√	√	√	X	√
Molecular-modeler 5	X	X	√	X	√

Table 6.4: Task performance for molecular-model dissectors.

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.

6.4 Critiquing the external representation

As part of the clinical interview (see Appendix D), all participants were asked to critique their respective external representations. Based on their experience of working with the representation for the duration of their respective tasks, they chose to answer questions regarding advantages, disadvantages and the ways of improving the ER. Tables 6.5, 6.6 & 6.7 give information to this end.

ER	Interactor	Advantages of the ER	Disadvantages of the ER	Suggestion for improvement
Concept-map	Concept-mapper 1	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	-
	Concept-mapper 2	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.	-
	Concept-mapper 3	(Makes it) easy to understand	Time consuming; not easy to make	Should be used in conjunction with diagram.
	Concept-mapper 4	I liked it and I enjoyed it; I'll likely remember it forever	-	-
	Concept-mapper 5	(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.

Table 6.5: Concept-map builders critique the representation.

ER	Interactor	Advantages of the ER	Disadvantages of the ER	Suggestion for improvement
Symbolic-model	Symbolic-modeler 1	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
	Symbolic-modeler 2	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.
	Symbolic-modeler 3	Makes it easy to visualize and, hence, to represent & understand; easy to make	Insufficient to explain concepts like formation of phosphodiester bond, or the 5'- 3' running strands.	Will represent the bonds and also name the elements
	Symbolic-modeler 4	Easy model; not time-taking; easy to explain others	-	I'll use spring to show (helical) turns; also make it a little bigger
	Symbolic-modeler 5	Clarifies nucleotide, nucleoside & N bases	You cannot know it completely (sugar & phosphate group)	-

Table 6.6: Symbolic-model dissectors critique the representation.

The clinical interview on critiquing the representation presents an interesting insight about learners point of view. The disadvantages and the suggestions for improvement prominently

ER	Interactor	Advantages of the ER	Disadvantages of the ER	Suggestion for improvement
Molecular-model	Molecular-modeler 1	This is a luxury (3-D model)	So many balls can mess up with your thoughts	-
	Molecular-modeler 2	An interesting model; clarifies concepts	Confusing at times	-
	Molecular-modeler 3	Big (prominent) Po4 group & N bases; looks very nice	It has balls; you need to remember the color of the ball first and then recognize.	Will wrap paper around these balls and name carbon, nitrogen etc.; also show bonds through strips
	Molecular-modeler 4	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.
	Molecular-modeler 5	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)

Table 6.7: Molecular-model dissectors critique the representation.

reflected their own points of difficulties that they faced while completing the task.

6.5 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.

Figure 6.2: A molecular modeler struggles to identify the limits of the nitrogenous base while dissecting the given base pair

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 (see Figure 6.2).

As a complementary example, the phosphate group (PO4) 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 PO4 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

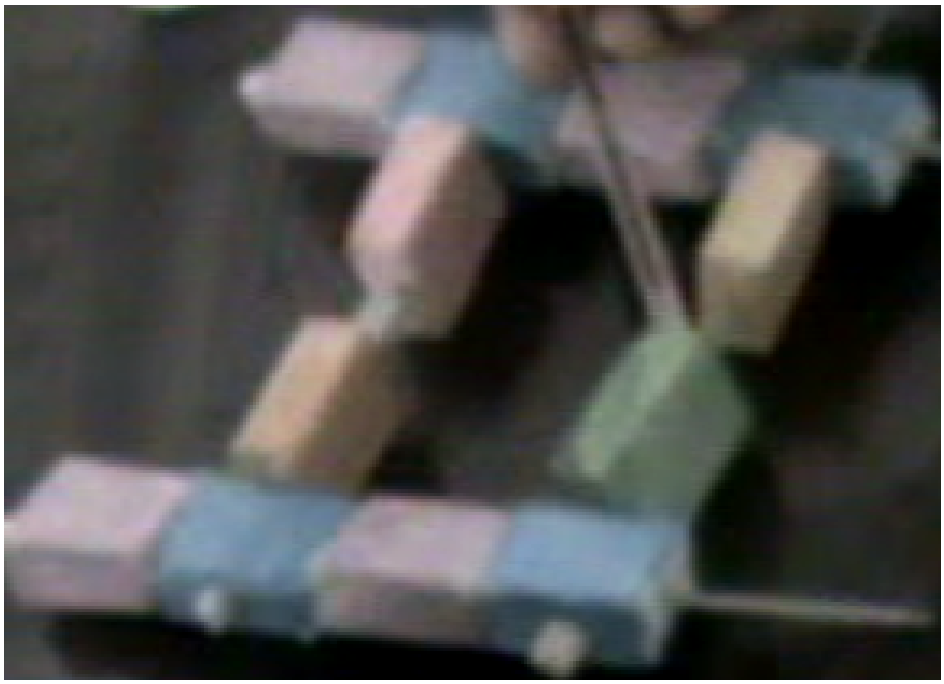


Figure 6.3: A symbolic modeler incorrectly points to denote the position of deoxyribose sugar molecule.

the structure. Is the base directly attached with the sugar molecule or to the phosphate group?

In Figure 6.3, 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 7

A database of DNA instruction aids

A major motivation behind this dissertation project was an awareness of 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, weve 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 several structural representations of DNA to create the database.

7.1 Sources

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

7.2 Basis of organization

This database is under construction and is based upon categorizing different representations, used worldwide, which have been employed or referred to in the context of learning about the structure of the Deoxyribonucleic Acid (DNA) molecule. All representations may be linked to each other through various degrees of exposition of the structural components. The structural components we consider for this purpose include the 'nitrogenous bases' (Adenine, Thymine, Guanine and Cytosine) which form the 'base pairs' (A-T; G-C) through 'hydrogen bonds' (two hydrogen bonds between A & T; three hydrogen bonds between G & C), and are attached through 'glycosidic bonds' to 'deoxyribose sugar molecules', which are then connected through 'phosphodiester bonds' to 'phosphate groups'. Since there is a huge repertoire of such representations, and, thus, different ways in which these structural elements may be depicted in the representation, one of our first tasks was to categorize these into different groups of representations. Each group includes multiple other representations which share a common structural appearance. Specifically, these groups are-

1. Molecular: In such representations, each and every atom of the component molecule is represented. However, representations may or may not show the hydrogen atoms. It may also show bond angles and bond orientations. In a space filling model, all the atoms may not be clearly distinguishable since it gives the top view of the molecule. A 'completely molecular' representation would depict the atomic details of different components of DNA structure.

2. Symbolic: These representations are characterized by including specific markers for

individual structural components. These could include specific- a) shapes and/or b) colors for different components. Symbolic models could be further characterized into- i) Skeletal representation: where, different components are charaterized by distinct physical outlines, and ii) Letter representations: where, different components are identified using the initial letter of the name of the component. For instance, 'S' for sugar molecule or 'P' for Phosphate group.

3. Helical: These representaions focus on the 3-D helical nature of the DNA structure with no molecular (details about constituent atoms), skeletal (physical outline of constituent components), symbolic (different symbols for constituent components) or letter (different letters used to depict different components). Different components may or may not be labeled.

However, there are no clear-cut boundaries for such categorization and there are substantial number of representations which show huge overlaps across the above categories. Our database highlights this overlap, while describing their structural presentation (see Appendix E).

Further, this database exploits the idea of 'model-dissection' (Srivastava, 2016), where physical models are dissected upon to identify different structural components of the representation. 'Dissection' activity is a physical manipulation exercise where students/learners can be asked to dissect out following components from the given category of model: **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).

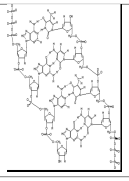
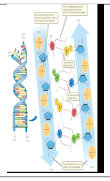
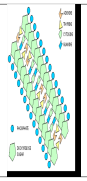
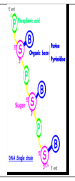
Structural elements to be 'dissected' or 'demarcated'		External representation				
						
Nucleotide		√	√	√	√	X
Nucleoside		√	√	√	√	X
Deoxyribose sugar		√	√	√	√	X
4 N bases		√	√	X	√	X
Phosphate group		√	√	√	√	X
Bonds	**Hydrogen**	√	√	X	X	X
	Glycosidic	√	√	√	X	X
	Phospho-diester	√	√	√	X	X

Table 7.1: Sample organization of 5 external representations of DNA structure on the basis of identification & 'demarcation' of the five elements.

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.

7.3 Database organization

The homepage of the database shows number of representations and each of them represents a category based on its structural focus, viz., molecular, symbolic or helical. However, these representations are organized in an order where the lower levels include representations which can be completely dissected/demarcated to identify the above components. As we move up, the representations show decrease amenability to dissection/demarcation.

Further, each representation is clickable and a click leads to the page where the categorical label of its group is described and a description of its amenability to dissection is given.

In Table 7.1, one can easily demarcate the five elements in the first two representations and, hence, these two will lie in the lower rung of the organization scheme, 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 in the upper rung of the organization scheme. However, the actual database is not in the form of a table.

7.4 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 upper hierarchy (viz., helical representations) first and then move lower 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, across the three categories of molecular, symbolic or helical representations.

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 8

Discussion & Implications

The goal of this dissertation was to understand how external representations influence the process of learning and how we can tap this knowledge to develop effective and efficient pedagogical tools. Pragmatically, this aim translated into assessing students' difficulties specific to the ER used and to remediate the difficulties, again using the same ER. To capture the process of interaction, we made learners manipulate different ERs in the context of specific problem-solving tasks. We, then, made dense observations of this process followed by intensive analysis of the data. The density of our observations gave us rich information about students' conceptual and representational difficulties and it also gave us information about the ways in which we could improve the efficiency of existing tools used for capturing these difficulties.

At the heart of our investigation lay the two-way interaction between external and internal representations of conceptual knowledge. Using gestures, concept maps, physical models and diagrams, we sought to render this interaction transparent at specific points during students' trajectory of understanding the structure of DNA. By repeatedly measuring this interaction for the same conceptual area across different external representations, we obtained consilient lines of evidence about this classically unobservable process. We describe below these lines of evidence, as well as the general picture of the two-way interaction that emerged from their

synthesis.

In the first study (Chapter 2), we explored students' understanding about the structure of DNA molecule in general, and their understanding about the orientation of nitrogenous base-pair in particular. As discussed in the first chapter, we were aware that the concept of spatial orientation would be tough as it was both 'abstract' and 'complex', and, hence, one of our first aims was to help students anchor their intuitive understanding using relevant ERs. Even though we used a series of ERs, which were different versions of the backbone of the DNA molecule, these only helped us identify students' difficulties. However, the task of helping them to mentally visualize the correct orientation of the base-pair remained. We also used the well-referenced, famous biology analogy for DNA structure, which compares it to a 'ladder'. This prompted us to introduce a novel, simple, yet powerful *'palm gesture'*. The 'palm gesture' depicted a base pair and it was initially used as a diagnostic tool to reveal students' mental conception of the base-pair orientation. We, then, used this gesture in concord with the 'ladder analogy' to help students focus on the rungs of this ladder which were actually composed of the base-pairs. So, the question - 'how do you step on a ladder?' - triggered them to correct their 'palm gesture'. Here, they were trying to connect how steps in a ladder correspond to the base pair orientation in the DNA structure.

Via this study, we identified that the 'palm gesture' fulfilled twin cognitive roles - a) It concretized the abstract concept of base-pair orientation by drawing upon the strength of ladder analogy, and b) it anchored students' intuitive reasoning grounded in their common experience of climbing up a physical ladder to climbing up the abstract ladder of the DNA structure. Given the striking difficulty students had in visualizing the 3D structure of the DNA backbone given 2D diagrams, this gesture provides a valuable scaffold to ease the transition.

Having diagnosed and remedied important visualization difficulties in understanding DNA structure, we shifted our emphasis to understanding language-related ones. Using concept-mapping (Chapter 3 & 4), we investigated how general facility in linguistically associating different concepts related to DNA might be measured in objective and standardizable ways. To ensure that we could track not just the final concept map but also the process that led up to it, we used a concept map task which required students to physically manipulate different elements to build a conceptual map of DNA structure. We made dense observations of this process of individual student's interaction with the concept map elements, which was followed by intensive analysis of their 'moves' and 'accuracy'. A striking interaction between accuracy and move counts across participants was found, supporting a tentative identification of move count with mental facility in using concepts.

Building on this analysis, we developed a novel assessment instrument - *'understanding contours'* - to holistically track a student's journey from inception to familiarity to expertise to mastery of concepts within a subject area. Complementing this somewhat intensive measure of students' linguistic competence surrounding DNA, we also discovered a much more frugal predictor for it - the order in which students place concept map elements on the mapping surface. These two novel indicators of holistic map quality promise to be useful pedagogical tools across subject areas and study domains.

Then, having studied both visualization and linguistic difficulties surrounding DNA structure, we sought to identify purely conceptual difficulties in students' understanding, using 3D models of DNA for the purpose. The use of such highly realistic models removed both visualization and linguistic difficulties from the palette of possible problems students might have had. When the model is a close visual match to the actual DNA molecule, there remains no need to visualize; when the mode of answering questions can involve simple deictic gestures, the role of language and jargon is also side-stepped. As such, difficulties encountered in studying DNA structure using physical models were likely to be mostly conceptual

in nature.

Here again, as with our engagement with concept-mapping, we were able to contribute a new method to the existing literature as part of our investigation. Specifically, we wanted to reduce the instructor's level of engagement with students without compromising on the flexibility of possible configurations students could potentially end up with no supervision. To do so, we thought we'd experiment with having students dissect pre-built models rather than build them from components, as is traditionally done. We were able to show, using a controlled experiment, that *'model dissection'* is even more effective in teaching students about DNA structure than traditional model building, while requiring less effort on the part of the instructor. The difficulties students faced in working with the 3D model, while highly specific to DNA structure, also showed more generally that demarcation is a major problem in working with models.

Finally, we ran a study to comparatively analyze how students' mental representations of DNA changed as a function of the identity of the intervention aid they were taught with. Three cohorts of students were taught using, respectively a physical concept map, a symbolic model and a molecular model of DNA structure. Pre- and post-assessments were made using diagrams and clinical interviews. Whereas we had previously evaluated each external representation's affordances and their interaction with students' mental models individually, the comparative analysis we were able to conduct now accentuated the contrasts between these ERs in very discriminative ways. Concept maps improved the quantity of students' verbal output, but at some cost of precision. Symbolic models were dominated by molecular models in improving students' verbal-spatial precision in understanding DNA structure. The findings from this study gave us both a highly specific repertoire of typical difficulties *caused* by ERs for teaching DNA and a very general blueprint for how to go about finding similar difficulties in other subject areas.

8.1 Implications for the pedagogical community

Our specific contributions to biology education emerged as particularized answers to the general questions of - a) how to assess students' conceptual difficulties using specific ERs, and b) how to remediate them using specific ERs? More broadly, our contributions to the field can be categorized into the following themes:

1. By reporting on the range of conceptual difficulties that students face while learning about the DNA structure (Chapters 2, 3 & 6), 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.

2. 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 5 & 6) , 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.

3. 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.

4. 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 can 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.

8.2 Limitations

In the limited time span of this dissertation, we tried to meaningfully engage with students' conceptual, language-related and visualization-related difficulties. However, our efforts were met with certain limitations, which we discuss in this section.

In the first study, we acknowledge that we were quite fortunate to have hit upon the design of 'palm gesture' and were able to leverage it over the pre-established 'ladder analogy'. Since the process of interaction with any representation is constrained by its 'affordances', or the set of possible actions that can be performed on it, we were fortunate to be able to work with the most prominent affordance of the 'ladder analogy', i.e.,'given a ladder, we can climb it up'. And, incidentally, this affordance had a strong coonect with students' prior experience with a ladder and so they exactly knew *'how'* to place one's foot over the step of a ladder that would enable them to climb up the ladder.

Thus, our specific intervention of designing the palm-gesture was hugely constrained by the affordance of the analogy and it was a thread of fortune that enabled us to succesfully connect intuitve reasoning, prior experience of students with their ability to mentally visualize the base-pair orientation. And, hence, what plays behind the success of this novel and accurately-placed gesture intervention, is also a huge limitation for the usability of this gesture. It is higly contextual and we realize that it has extremely limited scope to be generalized to the understanding of other conceptual areas.

In the second study, we recognize the labor-intensive nature of our concept map assessment tool and this plays as a major limitation to the usability of this work. Even though the novel process analyses, including the design of 'understanding contours' presents an opportunity to be applied in various other contexts, both to characterize students' difficulties and to identify their knowledge zone within the learning trajectory (refer to the four quadrants of learning described in Chapter 3), the work is based upon identifying the number of valid moves made throughout the process of map-building. This tracking of moves appers to be quite cumbersome to be executed as part of a regular class. However, there are ways that we have discussed under the section on limitations in Chapter 3, which could be used to ease the process of tracking the moves. Still, we acknowledge the temporal limitation of this dissertation and that this work requires another phase of research work to make it usable

for pedagogical consumption.

In the third study where we propose 'model-dissection' as a significantly better pedagogical tool than 'model-building', the limitation is restricted to the conduct of the study. Ideally, we would have liked to conduct it within the natural setting of a classroom, rather than as part of an experimental setting, where students did not know each other but still collaborated together to solve the problem at hand. This, we realize is also a way forward for future research work.

In the last study, we compared the three representations of concept-map, symbolic-model and molecular-model using a fourth representation - 'diagram'. A major limitation of this study concerns accessibility and use of the models. A molecular model is time-consuming to make and quite expensive to procure. On the other hand, a symboli-model is not expensive and easy to make but requires serious thought on behalf of the instructor to think about what affordances of the representation does she want her students to focus upon. However, we realize that this could be an interesting classroom activity to be employed in the class.

In sum, we acknowledge that the tools we have designed and the methodological improvements we have suggested could be made more efficient over a period of time, and, thus, has implications for future research work.

8.3 Research implications and future directions

Through a series of studies, we have showed how simple pedagogical tools can be used to both characterize difficulties and also to remediate them, when the affordance of the working ER is carefully exploited. In addition to emphasizing mindful working with the affordances of representation, this work also advocates the use of physical manipulation of external representations to decipher the trajectory of learning. We 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 (Martin & 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. This, in turn, 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 future research efforts.

Particularly, further research can focus on designing multiple physical gestures which could be grounded in learners' experience and could successfully connect their intuitive reasoning with affordances of ERs. We have shown that this possible in the case of understanding nitrogenous base-pair orientation and we believe that this has paved way for such studies to be done in other cocneptual areas as well.

We also believe that future research work can also improve methods for calculation of moves, possibly leveraging touchscreens etc. to significantly enhance the pedagogical value of the concept-mapping assessment tool.

Also, even though we focused on a specific biological concept - DNA structure several generalizable conclusions have emerged, which can be used as foundations for future research work. Primarily, the process of learning was observed to be punctuated by episodes of conceptual difficulties triggered by interaction with specific affordance(s) of 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 learners 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 (Limón, 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 nave 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 may engage with the additional complexity generated by students misconceptions about the structure-function mapping.

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Appendices

Appendix A

SI for Chapter 2

A.1 Clinical interview questionnaires

The questionnaires were designed to be used as a guiding principle for the clinical interview so that it could be conducted in a structured manner, without much deviation. This was crucial because the answers of the student led to the formulation of the next question and the time for the interview was limited.

There were six different themes for the 6-days' interview and these questions were designed based on the theme for the day. The pattern of the questions mostly followed the standard textbook folled by the students.

A.2 Day 1 - Theme - 'DNA as genetic material'

(Used for the interview on Nov 9, 2010)

Introduction

1. This is a clinical interview-cum-teaching session.

2. There will be six such sessions over a period of six days.

3. Each session will be divided into a few parts.

4. Each part will have questions which will be simple in nature.

5. During the session, if you find that you have learned something new, do let us know. Do let us know even when you know these things already.

6. Periodically (at the end of each part), we will stop and review the points. Let us know what new things you learned at the end of each part and also at the end of each session.

Abbreviations

Q : Question (marked as S (structure), F (function), S-F (structure-function) & TR (transformational reasoning))

CR : Correct response

ER : Expected response

I : Direct Instruction, i.e. text statement(s) or information to be given to students

D : Diagrams

Part I: Introduction of terms - genetic material, gene, heredity, inheritance, variation and genetic trait.

Q. What is the first term that comes to your mind when we talk about 'genetic material'?(S)

ER: Gene.

Q. What do you mean by the term ‘genetic material’?(F)

CR: This material must be able to 1. replicate, 2. store information, 3. express information hence, 4. pass on characteristics from generation to generation, and 5. allow variation by mutation (which is necessary for evolution to act) .

ER: 1. and 4. are sufficient at this point.

Q. Do you know what is a ’gene’?

CR: A gene is a basic unit of heredity in living organisms. It is a segment of DNA which is involved in coding of the amino acid sequence of a polypeptide chain. An allele is an alternate form of a gene, located at a specific location on a chromosome; each individual organism has two alleles for each trait, which may be the same (homozygous) or different (heterozygous).

ER: One which is passed on from parents to offspring(s).

Q. What is ’heredity’?

CR: Heredity refers to the biological similarity of offspring and parents.

Q. Do you know the meaning of ’inheritance’?

CR: Inheritance refers to the receiving of an 1. allele, 2. gene, 3. phenotype, 4. characteristic, etc. from one’s parents by genetic transmission.

ER: 2. and 4. are sufficient at this point.

Q. Do you know the meaning of ‘variation’?

CR: Variation refers to the differences among parents and their offspring or among individuals in a population.

Q. What is a ’genetic trait’?

CR: A genetic trait is a physical characteristic brought about by the expression of a gene or many genes. Examples of traits are height, eye color, and the ability to roll one's tongue. Variations in these characteristics are dependent upon the particular alleles an individual has for the genes determining the trait.

Part II: Location of the genetic material; DNA as genetic material.

Q. Do all living things have genetic material?

CR: Yes. Plants and animals have their genetic material within the nucleus of their cells. Since bacterial cells do not have a nucleus, their genetic material floats around in the cytoplasm, the 'nucleoid'. Viruses simply consist of genetic material surrounded by a protein coating. (Note on exclusion: Prions are infectious proteins. Several prions have been identified in fungi where they behave as non-Mendelian cytoplasmic genetic elements. Most of these prions propagate as self-perpetuating amyloid aggregates thus providing an example of structural heredity. We leave aside the fungi case and just mention that genetic material is present in the cytoplasm.)

Q. Can you draw a sketch of the following to show the location of the genetic material?

a) a plant and an animal cell

b) a bacterium and

c) a virus

Q. Can you compare the sizes of the above cells?

CR: A virus is smaller than a bacterium and the bacterium is smaller than an animal or a plant cell.

Q. Can you differentiate between an eukaryotic cell and a prokaryotic cell?

CR: The term eukaryotic is derived from two Greek words: 'eu' meaning 'true' and 'karyon'

meaning 'the nucleus'. An eukaryotic cell contains a nuclear envelope around the nucleus and contains other organelles which have double membranes around them. The term prokaryotic is derived from two Greek words: 'pro' meaning before, prior to, or primitive and 'karyon' meaning 'the nucleus'. A prokaryotic cell lacks nuclear membrane around the nucleus and also other double membranous organelles.

D: Diagram of plant cell (Diagram no.1), animal cell (Diagram no.2), virus (Diagram no.3) and bacterial cell (Diagram no.4) showing the location of the genetic material.

Q. Is virus a living organism?

CR: It is non-living as long as it is not attached to a living organism. It needs a living organism to replicate its genetic material and to reproduce.

Q. Can a virus replicate its genetic material?

CR: Yes, but not on its own. It needs another living cell to replicate its genetic material as it lacks replicating machinery.

Q. How do you think can a virus replicate and transfer its genetic material to its offspring(s)?

CR: It needs a living host like a bacterial cell, where it can inject its genetic material and control the replicating machinery of the host cell such that many copies of the viral genome are made and released by the bacterial cell after the genome getting covered by the protein capsule.

Part III: The Hershey and Chase experiment.

Q. Have you come across the term 'bacteriophage'? Do you know how does it replicates?

CR: The word 'bacterio' refers to a bacterium and the word 'phage' means 'to devour' or 'to

engulf'. A bacteriophage is a virus which utilizes a bacterial host cell to replicate its genetic material. It replicates by attaching itself to the bacterial cell with the help of its tail fibers and injecting its genetic material within the bacterial cell and using the host cell machinery to copy its genetic material and producing copies of itself.

Q. Can you draw a diagram of the T2 bacteriophage?

Q. Can you label the diagram of the T2 bacteriophage to show its important structures?

Q. Can you point out what is the function of the different components (DNA, Protein and Tail fibers)?
CR: DNA-genetic material, Protein- capsule (coat), Tail fiber- attachment to the bacterial cell.

Q. Do you know about Hershey and Chase?
ER/ CR: Yes.

Q. What did they do? What was the outcome of their work?
CR: They did an experiment which proved that the DNA is the genetic material and not the protein.

Q. Do you know how did they go about doing the experiment?
I: Students are shown the DNA questionnaire-1, in case they cannot recall the experiment.
CR: They took two sets of T2 bacteriophage viruses. They labeled one set with radioactive Phosphorus-32 and the other set with radioactive Sulphur-35. These viruses were then made to infect bacterial cells (E.coli). These bacterial cells were then centrifuged using a high speed blender which caused the viral coats to be separated from the bacterial cells. The

bacterial cells infected with radioactively labeled P-32 showed radioactivity but the other set didn't and this proved that DNA is the genetic material and not protein since Phosphorus is a component of DNA and not protein, and Sulphur is a component of protein and not DNA.

Q. Can you name the different atoms which constitute the protein and the DNA molecule?
CR: Protein- Carbon, Nitrogen, Hydrogen, Oxygen and Sulphur (present in the amino acids: Cysteine and Methionine)
DNA- Carbon, Nitrogen, Oxygen, Hydrogen and Phosphorus.

I: Hershey and Chase did some experiments with the T2 bacteriophage, which is actually a virus.

Q. Do you know why Hershey and Chase used P-32 as the radioactive label for one set of the viruses?
CR: P is a component of DNA and not of protein and hence, bacterial cells showing radioactivity after being infected with viruses labeled with P-32 would prove that DNA is the genetic material.

Q. Do you remember what you have learnt about radioactivity (in Physics)?
CR: Radioactivity is the spontaneous disintegration of atomic nuclei. During this process the nucleus emits certain radiations like the alpha, beta and gamma rays.

Q. Can you differentiate between radioactive Sulphur (S-35 isotope) from the usual Sulphur, or radioactive Phosphorus (P-32 isotope) from the usual Phosphorus?
CR: There is no visible difference but the radioactive isotope will emit certain radiations which can be detected through specific detectors.

Q. Do you have any idea what is meant by labeling a virus with radioactive P or S? How could it be done?
CR: Labeling refers to incorporation of the radioactive elements in the viral components. It could be done by growing the virus (using a bacteriophage in this case) in a medium containing radioactive Phosphorus or Sulphur.

Q. What do you think that Hershey and Chase expected to be the outcome of just labeling viruses with radioactive P-32 and why?
CR: DNA would be labeled radioactively and in case they were the genetic material, the bacterial cells infected by the P-32 labeled viruses would show the radioactivity, and not the cells infected by the S-35 labeled viruses.

Q. Will the viruses that have been labeled with radioactive P-32 show radioactivity?
CR: Yes.

Q. Do you think that the bacterial cells which are infected by P-32 radioactively labeled viruses will show radioactivity?
CR: Yes.

Q. Will the viruses that have been labeled with radioactive S-35 show radioactivity?
CR: Yes.

Q. Do you think that the bacterial cells which are infected by S-35 radioactively labeled viruses will show radioactivity?
CR: No.

Q. If suppose the genetic material of the T2 phage was contained in its capsule and not

on its inside and the protein was found on the inside of this capsule (in its interior, core). These viruses were then made to infect certain bacterial cells.(TR)

a) How do you think will such a phage replicate?

b) According to you which portion of the T2 phage would have been injected in the bacterial cells?

c) Which component of the virus do you think would have been stayed on the outside of the bacterial cell (core or the capsule)?

d) If after the viral infection, the bacterial cells were centrifuged by using a high speed blender, what do you think would happen? (critical)

CR:

a) The phage will attach itself with the help of tail fibers to the bacterial surface and then inject its capsule within the bacterial cell, leaving the core on the surface.

b) Capsule

c) Core

d) The protein core would have been separated from the bacterial cells.

Q. Consider the actual structure of the T2 phage. If suppose the genetic material of a T2 phage was protein and not DNA and then these viruses were grown on a medium that contained radioactive 'Phosphorous' & few others on medium that contained radioactive 'Sulphur'. Now, when these viruses are made to infect bacteria. What would have been the genetic material if:

a) Bacterial cells infected by viruses grown in radioactive 'Sulphur' showed radioactivity?(S-F)

b) Bacterial cells infected by viruses grown in radioactive 'Phosphorous' showed radioactivity?(S-F)

c) What do you think would have been the result of this experiment out of the above (a & b) options?

CR: a) protein

b) DNA

c) Those bacterial cells would have shown the radioactivity which were infected with viruses grown in radioactively labeled Sulphur medium (a).

*The following was part of our plan but we couldn't do this part due to time constraints.

Q.12. Unequivocal proof that DNA is the genetic material came from the experiments of Alfred Hershey and Martha Chase (1952). They grew some viruses on a medium that contained radioactive 'Phosphorous' (P; component of DNA & not Protein) & few others on medium that contained radioactive 'Sulphur' (S; component of Protein & not DNA). These viruses were then made to infect bacteria. What is the genetic material if:

a) Bacterial cells infected by viruses grown in radioactive 'Sulphur' showed radioactivity?(S-F)

b) Bacterial cells infected by viruses grown in radioactive 'Phosphorous' showed radioactivity?(S-F)

c) What do you think would have been the result of this experiment out of the above (a & b) options? What does it tell us about the function of the genetic material?(S-F)

References

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

2. National Council of Educational Research and Training (2006). Molecular basis of inheritance. In Textbook for class XII 'Biology', Chapter 6 (pp. 95-125). New Delhi: NCERT.

A.3 Day 2 - Theme - 'DNA structure and the Chemistry pre-requisites'

(Used for the interview on Nov 10, 2010)

A.4 Abbreviations

Q : Question (marked as S, F, S-F & TR) CR : Correct response

ER : Expected response

I : Direct Instruction, i.e. text statement(s) or information to be given to students

D : Diagrams

T : Task given to students

Part I: Structure of DNA-Stage 1

Q. What is the structure of a DNA?

ER/ CR: Double helix/ twisted ladder.

Q. Do you know what are the different components of the DNA molecule?

CR: Bases, deoxyribose sugar and phosphate group.

T. Draw a diagram of an untwisted DNA (ladder) and label its components.

T. Draw the usual structure of DNA showing position of the nitrogenous bases.

Q. Which component forms the rungs of the ladder?

I/CR: Each rung of the DNA ladder is made up of two nitrogen bases. The bases are joined by a hydrogen bonding.

Part II: Electronic configurations, valency, electronegativity & covalent bonding.

Q. What is the atomic number of H, O and N?

CR: 1, 8 & 7.

Q. How many electrons are present in each of the above elements?

CR: 1, 8 & 7.

Q. What are the valencies of the above atoms?

CR: 1, 2 & 3.

I: Valency is the number of electrons required or lost by an atom so as to complete its octet or duplet.

T. Draw the electronic configuration of the above elements.

D. Electronic configurations of Hydrogen, Nitrogen and Oxygen (Diagram no. 1, Diagram no. 2 and Diagram no. 3)

Q. What is electronegativity?

CR: It is the chemical property of an element which measures the tendency of an atom to attract electrons which participate in chemical bonding. It tends to decrease down a group and increase across a period in the periodic table.

Q. What makes an element electronegative?

CR: This characteristic feature of the element is dependent on its atomic number. With

increase in the size of the atom (across a period) the tendency to accept electron to complete the octet in the valence shell increases. It increases with increase in the oxidation state of the element as with increasing loss of electrons from the valence shell increases the net positive charge on the nucleus giving it the tendency to attract electrons.

Q. What is a covalent bond? Give examples.

CR: A covalent bond is a chemical bond which is formed by the sharing of electrons between two atoms, where each atom contributes one electron to the bond. For e.g. water, methane etc.

Part III: Hydrogen bonding

Q. What is a hydrogen bond? How are hydrogen bonds formed?

CR: A hydrogen bond is a weak bond formed by the interaction between a more electronegative atom and the hydrogen atom. It is weaker than a covalent bond.

Q. Where do you find hydrogen bonds?

CR: Water, ammonia, proteins etc.

T: Show diagrammatically the formation of a Hydrogen bond.

D: Hydrogen bonding in water and ammonia (Diagram no. 4).

Part IV: Nitrogenous bases

Q. What are bases? Can you give an example of a base?

ER: Those which combine with an acid to form salt and water.

CR: acceptors of hydronium ions, oxides and hydroxides of metals, electron pair donors or donors of hydroxide anions.

Q. What do you mean by nitrogen bases?(S-F)

ER: Bases containing nitrogen atoms.

CR: Nitrogen-containing molecule having the chemical properties of a base. It is an organic compound that owes its property as a base to the lone pair of electrons of a Nitrogen atom.

Q. What do you think is the significance of the N atoms in the nitrogenous bases?(S-F)

CR: A Nitrogen atom is an electronegative atom which facilitates its interaction with a Hydrogen atom to form a Hydrogen bond.

I: Purines and Pyrimidines are types of nitrogenous bases.

Part V: Purines and Pyrimidines

Q. The nitrogenous bases are classified as either the purines or the pyrimidines. Do you know about the basic structure of these two molecules?

CR: Purines are 9-atom containing dicyclic aromatic ring whereas the pyrimidines are 6 atom containing mono-cyclic aromatic ring.

D: Basic structure of a purine and a pyrimidine ring (Diagram no. 5).

Q. Do you know what are the different Purine and Pyrimidine bases in the DNA molecule?

CR: AG-Purine and CT-Pyrimidine

Q. Do you know what is the usual base-pairing rule in the DNA molecule?

CR: AT (two Hydrogen bond) and GC (three Hydrogen bond).

T: Given skeletal structure of a) Adenine and Thymine bases and b) Guanine and Cy-

tosine bases, specifying the position of Oxygen, Nitrogen and Hydrogen atoms, show the formation of Hydrogen bonds at appropriate places.

References

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

2. National Council of Educational Research and Training (2006). Molecular basis of inheritance. In Textbook for class XII 'Biology', Chapter 6 (pp. 95-125). New Delhi: NCERT.

3. Malacinski, George M. & Freifelder, D. (1998). Essentials of Molecular Biology. Boston: Jones and Bartlett.

A.5 Day 3 - Theme - 'DNA structure and Hydrogen bonds'

(Used for the interview on Nov 11, 2010)

Abbreviations

Q: Question (marked as S, F, S-F & TR)

CR: Correct response

ER: Expected response

I: Direct Instruction, i.e. text statement(s) or information to be given to students

D: Diagrams

T: Tasks

Base (pair) representation through paper cutouts (c)

Part I: Structure of DNA-Stage 2

Q. Draw a straightened ladder structure of the DNA molecule.

Q. Do you think that the two strands of the DNA ladder get separated?

CR: Yes, during replication (transcription) etc.

Q. Show how the two strands of the DNA molecule get separated and copy themselves.

Part II: Purine, Pyrimidine and Hydrogen bonds

Q. Draw the skeletal structure of purine and pyrimidine.

D: Basic structure of a purine and a pyrimidine ring.

Q. Do you know what are the different Purine and Pyrimidine bases in the DNA molecule?
CR: AG-Purine and CT-Pyrimidine

T: Given paper cutouts (c) of Adenine, Thymine, Cytosine and Guanine bases, specifying the position of Oxygen, Nitrogen and Hydrogen atoms, try different possible ways of getting them hydrogen bonded. See if the pairing works. Say why or why not they work.

References

1. Maharashtra State Board of Secondary and Higher Secondary Education (2009). Biotechnology. In Standard XII 'Biology', Chapter 2 (pp. 13-33). Pune: MSBSHSE.
2. National Council of Educational Research and Training (2006). Molecular basis of inheritance. In Textbook for class XII 'Biology', Chapter 6 (pp. 95-125). New Delhi: NCERT.
3. Malacinski, George M. & Freifelder, D. (1998). Essentials of Molecular Biology. Boston: Jones and Bartlett.

A.6 Day 4 - Theme - 'Visualisation of DNA structure and function'- Introduction to the multiple representations

(Used for the interview on Nov 16, 2010)

Abbreviations

Q: Question (marked as S, F, S-F & TR)

CR: Correct response

ER: Expected response

I: Direct Instruction, i.e. text statement(s) or information to be given to students

D: Diagrams

T: Tasks

Backbone representation (M1-M4)

Base (pair) representation through cutouts (c) or palm gesture (pg)

Part I: Structure of DNA-Stage 3

Q. Draw the ladder structure of the DNA molecule.

Q. Show the different components of the DNA structure.

Q. Draw a diagram of a twisted DNA (ladder) and label its components.

T: If suppose that the palm of your hand depicts the purine and pyrimidine molecule (pg), can you show the DNA structure making use of your palm supposing that the edges of the given sheet (M1) are the back bone of the DNA molecule?

* Student are also asked to depict palm gesture (pg) against M2 (two pencils laid on the table) and M3 (two pencils held to stand erect on table) model.

Part-II: Numbering of bases

*Paper cutouts of N-bases presented to student.

Q. Can you identify the different atoms in this pyrimidine ring (c)?

Q. Is there any atom at the corners of the ring (c)?

Q. Check if the valencies of all the atoms are satisfied.

Q. Do you know what is a heterocyclic atom?

CR: In a closed ring structure, the atom which is other than the carbon atom is termed a heterocyclic atom.

Q. Can you identify the heterocyclic atom in this ring (c)?

Q. Do you know what is a functional group?

CR: An atom or group of atoms, such as an amino group, that replaces hydrogen in an organic compound and that defines the structure of a family of compounds and determines the chemical properties of the family.

Q. Can you identify the functional group (s) in this ring (c)?

I: The nomenclature and numbering of the atoms of compounds are done according to IUPAC (International Union of Pure and Applied Chemistry) conventions. According to this

convention, as applied to the numbering of atoms in a heterocyclic ring, the 'hetero' atom is assigned position 1 and the substituents are then counted around the ring in a manner so as to give the lowest possible numbers to the 'hetero' atoms [1].

T: Can you number a pyrimidine ring according to the IUPAC conventions?

I: The numbering of the purine ring system is anomalous. It doesn't follow the usual IUPAC convention. Purine numbering is shown.

Part-III: Structure of sugar molecule in DNA and directionality

Q. Can you name the sugar molecule which is a constituent of the DNA structure?
CR: Deoxyribose sugar.

Q. Can you draw a skeletal diagram of the deoxyribose sugar?

D: Diagram of a deoxyribose sugar (Diagram no. 1).

Q. What are the different atoms in this sugar molecule?

I: The carbon atoms in the sugar are also numbered. To differentiate between the carbon atoms of the purine and pyrimdine rings, the carbon atoms are depicted by prime positions.

Q. Can you number the atoms of the sugar molecule?

I: Numbering of the sugar molecule is shown.

I: Shown M4 (cardboard cutout of a sugar molecule attached with two Phosphate molecules

(2 sets) standing on a base) model.

Q. What is attached above and below the sugar molecule?

Q. In reference to your diagram of the DNA molecule in part-I, identify which part of the DNA molecule is shown in the model (M4)?

Q. Identify the sugar molecule and the phosphate groups.

Q. How many phosphate groups are attached to a sugar molecule?

I: The part that you are observing forms the backbone of the DNA molecule. Both are continuous strands which are further extended on either side (not shown).

T: Place your palms (pg) and try to depict the position of the bases in the DNA ladder diagram that you made.

T: Place your palms (pg) and try to depict the position of the bases in the M4 model.

Q. What do you think will be placed above the phosphate groups?

T: Place your palms (pg) and try to depict the position of the next pair of bases.

Q. Is there any difference between the two sugar molecules that you are observing?
CR/ ER: Yes. The sugar is inverted in one case.

Q. Does it tell you something about the structure of DNA?

CR: The two strands run antiparallel.

Q. To which carbon atoms are the Phosphorus groups attached?

Q. Which is the 3' end and which is the 5' end?

Q. Why are the two strands called antiparallel?

CR: They run in different directions (5' to 3' and 3' to 5').

TR: If suppose the two sugar molecules were aligned in the same direction, what do you think would have been the effect on the DNA structure?

ER: DNA strands would have been parallel.

Part-IV: Specificity of Base pairing

Q. In this pyrimidine molecule (c), which of the H atoms have slight positive charge?

Q. Which part of the pyrimidine will get attached to the OH of the sugar molecule?

I: The Nitrogen atom at the 9th position of a purine gets bonded with the Carbon at the 1' position of the sugar and the Nitrogen atom at the 1st position of a pyrimidine gets bonded with the Carbon at the 1' position of the sugar [1].

T: Try to attach a pyrimidine (say Thymine) (c) with the given deoxyribose sugar molecule.

Q. Are you facing any problem with the bonding?

Q. Do you know what is a condensation reaction?

CR: Condensation is a chemical process by which 2 molecules are joined together to make a larger, more complex molecule, with the loss of water. It is the basis for the synthesis of all the important biological macromolecules (carbohydrates, proteins, lipids, nucleic acids) from their simpler sub-units.

I: A nitrogenous base undergoes a condensation reaction to get bonded with the sugar molecule.

D: Condensation reaction.

Q. Do you know what kind of bond is present between the sugar and the base?

CR: Covalent bond–N-glycosidic bond (which depicts a nitrogen-sugar bond).

I: The bases are at right angle to the sugar molecule.

TR: What are the possible ways of forming the nitrogen-sugar bond?

Q. What do you think is the most appropriate plane for the bases to bond with the sugar molecule? Why?

Q. Can you now attach the nitrogenous base (Thymine) at appropriate position?

T: Now try to attach any other base to the second sugar molecule and position them such that you are able to form hydrogen bonds with the initially attached nitrogenous base.

Q. What are the problems that you are facing with the pairing?

CR: Steric hindrance or distance constraint and inability to form bonds.

Q. Are you now able to form different hydrogen bonds at different positions from the standard position?

Q. How many sets of bases did you find which were able to get hydrogen bonded with each other? Also specify the number of hydrogen bonds that was formed in each set.

Q. Can you write down the specific atoms along with their positions in the two rings which participated in hydrogen bond formation?

I: This is the standard Watson and Crick pairing which you explored now.

References

1. Bansal, Raj K. (2010). 'Heterocyclic Chemistry'. New Delhi: New Age International Publishers.

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

3. Malacinski, George M. & Freifelder, D. (1998). Essentials of Molecular Biology. Boston: Jones and Bartlett Publishers.

4. National Council of Educational Research and Training (2006). Molecular basis of inheritance. In Textbook for class XII 'Biology', Chapter 6 (pp. 95-125). New Delhi: NCERT.

A.7 Day 5 - Theme - 'Visualisation of DNA structure and function'- 3-D structure of the DNA molecule

(Used for the interview on Nov 18, 2010)

Abbreviations

Q: Question (marked as S, F, S-F & TR)

CR: Correct response

ER: Expected response

I: Direct Instruction, i.e. text statement(s) or information to be given to students

D: Diagrams

T: Tasks

Backbone representation (M1-M5)

Base (pair) representation through cutouts (c) or palm gesture (pg)

Part I: Structure of DNA-Stage 4

Q. Draw the ladder structure of the DNA molecule.

Q. Show the different components of the DNA structure.

Q. How will you make a helical structure out of this ladder?

Q. Suppose the ladder is twisted to form a helix, how will the base pairs be oriented? Show the base pair orientation making use of the palm gesture (pg).

T: Use the given clothespin and the plastic pipe to build the DNA structure (M5).

Q. Describe the different parts of the 'clothespin model'(M5).

(Students are given enough time before proceeding).

Q. What does the plastic tube depict?

CR: Plastic tube depicts the phosphate sugar backbone.

Q. How is it different from the real phosphate sugar backbone?

CR: It is short and neither gives the molecular detail nor is antiparallel.

Q. What do the clothespin represent?

CR:The clothespins of four different colors represents the four bases (ATGC).

Q. Specify the different colors of the clothespin which correspond to the ATGC nitrogenous bases.

Q. How is it different from the real base pairs?

CR: Only specific pairs bond.

Q. Why are the clothespin interlocked?

CR: To depict hydrogen bonding.

Q. How is this hydrogen bond different from the actual hydrogen bond?

CR: This represents a physical bond but actually its a chemical bond which is formed by weak interaction of slightly negative and slightly positive charges.

Q. How are the bases different from the actual DNA bases?

CR: All bases shown here are of the same sizes but the Purine rings are bigger than the

Pyrimidine rings in the actual case. Base pairs are flat; there are millions of them; only specific bases form Hydrogen bond.

Q. How are the bases oriented in the clothespin model that you have made?

T: Try to form helix out of this ladder structure.

Q. What is the distance between each nitrogenous base pair?

Q. Is the distance between the successive nitrogenous base pairs constant throughout the helix?

Q. Can you show one helical turn? How many bases constitute one helical turn?

Q. Are the two backbones physically crossing each other?

*The following was part of our plan but we couldn't do this part due to time constraints.

Part II: Handedness of the Helix

I: Helices can be either right-handed or left-handed. With the line of sight along the helix's axis, if a clockwise screwing motion moves the helix away from the observer, then it is called a right -handed helix; if towards the observer then it is a left-handed helix. Handedness (or chirality) is a property of the helix, not of the perspective: a right-handed helix cannot be turned or flipped to look like a left-handed one unless it is viewed in a mirror, and vice versa.

References

1. Venville, Grady G. (2008). Effective Biology Analogies. In Harrison, Allan G. & Coll, Richard K. (Eds.) (2008). Using Analogies in Middle and Secondary Science Classrooms: The FAR guide- An Interesting Way to Teach With Analogies. USA: Corwin press.

*Student Sheet : Students are given few questions which requires them to to go through certain exercises pertaining to their understanding of the handedness of the DNA helix.

Day-5: Student Sheet

T: Make a right handed double helix from the 'clothespin model' that you have made.

T: Make a left handed double helix from the 'clothespin model'.

T: Make a right and left handed double helix from the two given wires.

Q. Which of these two shows the usual DNA structure?

T: Draw two single helices, one right and the other left-handed.

T: Draw two double helices, one right and one left-handed.

Q. Can you convert a right handed helix to a left handed helix or vice versa?

T: Use a mirror to view the helix. What do you see?

A.8 Day 6 - Theme - 'Base pairing and Replication'

(Used for the interview on Nov 19, 2010)

Abbreviations

Q: Question (marked as S, F, S-F & TR)

CR: Correct response

ER: Expected response

I: Direct Instruction, i.e. text statement(s) or information to be given to students

D: Diagrams

T: Tasks

Backbone representation (M1-M5)

Base (pair) representation through cutouts (c) or palm gesture (pg)

Part I: Structure of DNA-Stage 5

Q. What is the shape of the DNA molecule?

CR: It is a double helix.

Q. Can you show the formation of helix in the given clothespin model (M5) of DNA?

Q. What is the distance between two nitrogenous base pairs after the formation of helix?

Q. How are the nitrogenous bases oriented after the helix formation?

Q. Show with the palm gesture how the base pair orientation will change after the formation of the helix.

Q. Is there a turn in the helix at a particular place in the DNA molecule?

Q. What is the distance covered by the DNA molecule in one helical turn?

Q. Can you show one helical turn in the 'clothespin model'?

I: One helical turn of the DNA molecule spans 360 and since there are ten base pairs in one helical turn, each base pair forms an angle of 36 with the adjacent nitrogenous base pairs.

Part II: DNA replication

T. How do you think can replication begin in this clothespin (M5) model ? Show it.

Q. What all do you know about replication?

T: Demonstrate replication with the unique (specific) base pairs using the tubing and the pins.

Q. Supposing instead of just two pairs (of nitrogen bases), there are different possible base pairs which are possible to fit easily into a double stranded molecule. Is there any problem with such a molecule?

T: Construct such a molecule from the tubing and pins that you have.

Q. Are you facing any problem?

T: Demonstrate replication with this molecule.

Hint 1. Can this molecule function as a genetic material?

Hint 2. How will this molecule replicate?

Q. What connection can you can draw between complementary base pairing and the replication process?

I/CR: Faithful copying of the genetic material is possible only when a unique base pairing exists.

References

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

2. National Council of Educational Research and Training (2006). Molecular basis of inheritance. In Textbook for class XII 'Biology', Chapter 6 (pp. 95-125). New Delhi: NCERT.

3. Malacinski, George M. & Freifelder, David. (1998). Essentials of Molecular Biology. Boston: Jones and Bartlett Publishers.

4. Venville, Grady G. (2008). Effective Biology Analogies. In Harrison, Allan G. & Coll, Richard K. (Eds.). Using Analogies in Middle and Secondary Science Classrooms: The FAR guide- An Interesting Way to Teach With Analogies. USA: Corwin press.

Appendix B

SI for Chapter 3/4

B.1 List of concept cards used in the study

Table B.1: List of concept cards used in study

3' to 5'	Genes	Antiparallel	Guanine	Purines
5' to 3'	Genetic information	Base pairs	Helical turns	Pyrimidines
3.4 Angstrom	Genetic material	Cytosine	Hydrogen bonds	Reproduction
34 Angstrom	Nucleotides	Deoxyribose sugar molecules	Nitrogen bases	Glycosidic bonds
20 Angstrom	Offspring	Diameter	Nucleosides	Two strands
Thymine	Parents	Genetic traits	Planar molecules	DNA backbone
Phosphate groups	Adenine	DNA	Double helix	Phosphodiester bonds
RNA	Polymer			

B.2 Quantitative performance metrics for all the map builders in the study

Table B.2: Quantitative performance for all the map-builders in the study

Subject	Precision	Coverage	F-measure	Placement strategy
Builder 1	0.86	1	0.93	C-AP
Builder 2	0.87	0.73	0.80	CAP
Builder 3	0.80	0.97	0.88	C-AP
Builder 4	0.94	0.95	0.95	CAP
Builder 5	0.58	1	0.73	CA-P
Builder 6	0.66	0.78	0.72	CAP
Builder 7	0.86	0.62	0.72	CAP
Builder 8	0.58	0.76	0.66	CA-P
Builder 9	0.75	0.70	0.72	CA-P
Builder 10*	0.86	0.54	0.6	CA-P
Builder 11	0.79	1	0.88	C-A-P
Builder 12	0.79	0.97	0.88	CAP
Builder 13	0.79	1	0.88	CAP
Builder 14	0.75	0.8	0.77	C-A-P
Builder 15	0.56	0.93	0.70	CA-P
Builder 16	1	0.97	0.98	C-A-P
Builder 17	0.81	1	0.9	C-A-P
Builder 18	0.86	1	0.93	C-A-P

$$\text{Precision} = \frac{\#\text{valid propositions}}{\#\text{ of propositions made}},$$
$$\text{Coverage} = \frac{\#\text{ of cards used}}{\#\text{ of cards available}},$$
$$\text{F-measure} = \frac{2 \times \text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}}.$$

B.3 Structural Complexity Index

Parameters	Map-builder									
	Supriya	**Kishore**	**Shreya**	**Urmika**	**Lalita**	**Bhanu**	**Yogesh**	**Divya**	**Akhil**	**Harsh**
Propositions (P)	36	26	36	33	41	30	23	27	25	19
Branches (B)	9	7	7	6	9	7	4	4	5	3
Chains (C)	16	17	30	19	23	25	9	15	12	10
Average chain length (Cavg)	72/16= 4.5	47/17= 2.8	306/30= 10.2	91/19= 4.75	116/23= 5.04	120/25= 4.8	39/9= 4.33	38/15= 2.54	32/12= 2.67	27/10= 2.7
SCI [(Cavg*P)+ (B*C)]	306	226	577	270	412	319	136	128	127	82

Where, P= number of propositions contained in the concept map; B= number of concepts that have more than one proposition originating from itself; C= the number of independent paths through the concept map; Cavg= the average number of propositions contained in the chain.

Table B.3: Structural Complexity Index for our participants

B.4 Time taken by each student to build concept maps in Chapter 3

Table B.4: Time on task for concept-map building (in minutes)

Map-builder	**Time taken (minutes)***
Builder 1	50
Builder 2	43
Builder 3	53
Builder 4	53
Builder 5	98
Builder 6	61
Builder 7	62
Builder 8	51
Builder 9	48
Builder 10	57

* Correlation with F measure is weakly negative, $\rho = 0.23$.

B.5 Other Supplementary Information for Chapter 3

1. Number of moves cross-tabulated across both students and concepts are available at http://www.hbcse.tifr.res.in/data/pdf/anveshna/number-of-moves

2. Transcripts of the video data for all the students and expert videos are available at https://www.dropbox.com/sh/pjxed9fqg27tk0h/AABzKhtlEjZOlgTHj0bRrCSIa?dl=0

Appendix C

SI for Chapter 5

C.1 Pre-test questionnaire (MCQs)

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

C.2 Post-test questionnaire (MCQs)

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

Appendix D

SI for Chapter 6

List of clinical interview questions, pre and post-exposure.

Phase I: Probe past exposure

1. How did you learn about the DNA structure? (What were your sources of learning about the DNA structure?)
2. Have you seen representations of DNA structure in the past?
3. What kind of representations have you seen? (Encourage drawings)
4. Which representation do you think was more clarifying? (Encourage drawing)
5. Do you think that your diagram is closer to that representation?
6. When was the last time when you learnt about the DNA structure?
7. Can you describe your diagram and tell me how is that similar or dissimilar to that representation?

Phase II: Probe conceptual understanding

Free probe

1. Do you know what is a polymer?

2. Can you give me examples of a polymer?

3. What do you think about DNA- is it a polymer or not?

4. If yes, what is its monomer?

5. What is DNA?

Location

1. Where do we find DNA?

2. Do you have it?

3. What does not contain DNA?

Structure

1. What is the DNA made up of? (What are the different components of the DNA molecule?)

2. What are bases?

3. What are the different kinds of bases?

4. How are the bases oriented? Can you show it using your palm?

5. What are the two strands of the DNA made up of?

6. Which components form it?

7. What does the 3' and 5' end signify?

8. Do you know the molecular structure of different components? If yes, please draw.

Phase III: Probe internal representation

1. What is the first thing that comes to your mind when you hear the word DNA?

2. What picture comes to your mind when you think about DNA? Can you draw that?

3. Is this picture similar to what you have drawn?

4. If yes, how? If no, what is different?

5. What does the DNA look like? Can you think about any other structure which is similar to the DNA?

Phase IV: Probe difficulties

1. Are there any parts of the DNA structure that you do not remember?

2. Do you find difficulty in understanding any part of the DNA structure? What are these?

Post-intervention

1. How did you find the task?

2. What difficulties you faced during the task?

3. Did you learn anything new?

4. Ask about changed representation, if any.

Critique the representation (concept map, skeletal model or molecular model)

1. What are the advantages and disadvantages of the representation used?

2. If you had to modify the given representation, what features would you add or subtract? Why?

3. What is interesting about this representation?

Appendix E

SI for Chapter 7

The database is a collection of multiple webpages and provides an interactive platform for visualizing different categories of structural representations. It also gives information about a particular representation's amenability with dissection/demarcation of its components. We present here screenshots of some pages of the website, including the home page and the methodology page, along with some examples of structural categories.

It is to be noted that this database is an ongoing project since there is no end to the different forms of representations that could be added to the set. And, therefore, the categories of representations are meant to act as a base on which further examples could be added. This, we believe, will facilitate the process of both teaching and learning, and it may be included as a classroom activity.

A database on the DNA (Deoxyribonucleic Acid) structure

The representation scheme you see below identifies categories of DNA representations based on their structural properties. This categorization responds to two different questions-

1. What class of representation these structures belong to?
2. Can the given representation be used as a model upon which 'dissection' could be performed? If yes, what structural elements of the DNA molecule can be dissected?

These representations may appear to be randomly scattered. However, these are placed in an order that moves across through 'molecular' to 'symbolic' to 'helical' representations. Pragmatically, it means that when instructors/learners wish to engage with detailed structures, they will have to explore the lower rungs of the following representation scheme and when they are interested to engage with models which give an overview of the DNA structure without molecular details, they will have to explore the upper rungs of the representation scheme. Since each of the following representations present a group of structural categorization, please *'click'* on individual diagrams to know more about its categorization.

This database includes information as to which structural components of the DNA structure may be 'dissected' or 'demarcated' clearly in the given representation. Since the lower rungs of this representation is rich in molecular representations, it is likely that these representations are more amenable to being dissected upon. Thus, when we move up in the scheme, the identification of constituent components via 'dissection decreases.

We hope this *database* of DNA representations will help both educators and students find the ones that best serve their purpose, and, further, they will enrich this database.

Click here to see how this database was made.

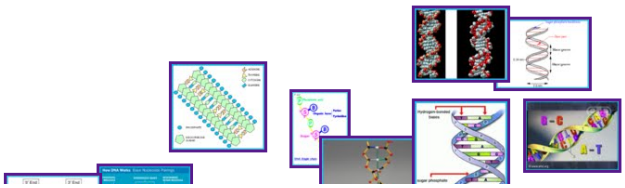
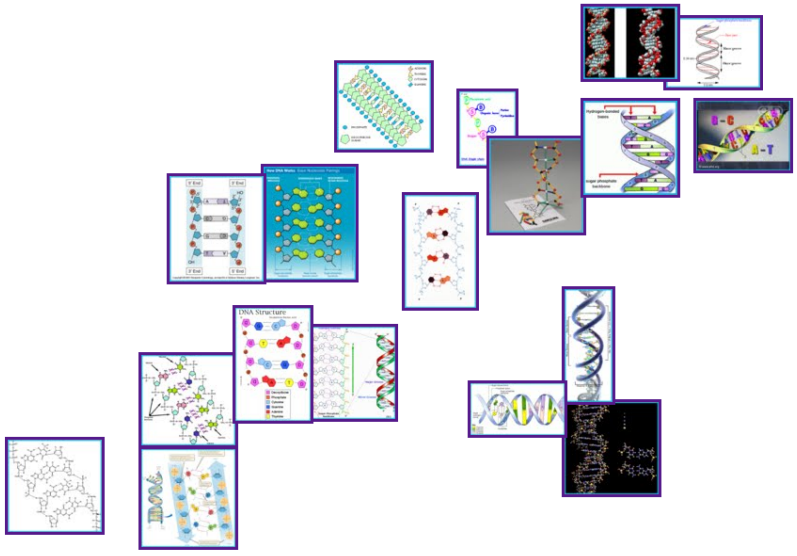


Figure E.1: Screenshot of the first half page page of the database home page on DNA structure

Click here to see how this database was made.



file:///home/cse/Dropbox/ProceduralAnalysis/Database/Webpage/completely-molecular-helical.html

Figure E.2: Screenshot of the second half page of the database home page on DNA structure

Figure E.3: Screenshot of the last part of the database home page on DNA structure

Methodology

< Home

Basis of organization:

This database is under construction and is based upon categorizing different representations, used worldwide, which have been employed or referred to in the context of learning about the structure of the Deoxyribonucleic Acid (DNA) molecule. All representations may be linked to each other through various degrees of exposition of the structural components. The structural components we consider for this purpose include the 'nitrogenous bases' (Adenine, Thymine, Guanine and Cytosine) which form the 'base pairs' (A-T; G-C) through 'hydrogen bonds' (two hydrogen bonds between A&T; three hydrogen bonds between G&C), and are attached through 'glycosidic bonds' to 'deoxyribose sugar molecules', which are then connected through 'phosphodiester bonds' to 'phosphate groups'. Since there is a huge repertoire of such representations, and, thus, different ways in which these structural elements may be depicted in the representation, one of our first tasks was to categorize these into different groups of representations. Each group includes multiple other representations which share a common structural appearance. Specifically, these groups are-

- a) Molecular: In such representations, each and every atom of the component molecule is represented. However, representations may or may not show the hydrogen atoms. It may also show bond angles and bond orientations. In a space filling model, all the atoms may not be clearly distinguishable since it gives the top view of the molecule. A 'completely molecular' representation would depict the atomic details of different components of DNA structure.
- b) Symbolic: These representations are characterized by including specific markers for individual structural components. These could include specific- a) shapes and/or b) colors for different components. Symbolic models could be further characterized into- i) Skeletal representation: where, different components are charaterized by distinct physical outlines, and ii) Letter representations: where, different components are identified using the initial letter of the name of the component. For instance, 'S' for sugar molecule or 'P' for Phosphate group.
- c) Helical: These representaions focus on the 3-D helical nature of the DNA structure with no molecular (details about constituent atoms), skeletal (physical outline of constituent components), symbolic (different symbols for constituent components) or letter (different letters used to depict different components). Different components may or may not be labeled.

Figure E.4: Screenshot of the first half page of the 'Methodology' page of the database on DNA structure

However, there are no clear-cut boundaries for such categorization and there are substantial number of representations which show huge overlaps across the above categories. Our database highlights this overlap, while describing their structural presentation.

Further, this database exploits the idea of 'model-dissection' (Srivastava, 2016), where physical models are dissected upon to identify different structural components of the representation. 'Dissection' activity is a physical manipulation exercise where students/learners can be asked to dissect out following components from the given category of model:

- 1. Nucleotide
- 2. Nucleoside
- 3. Deoxyribose sugar molecule
- 4. Nitrogenous bases
- 5. Phosphate group
- 6. Hydrogen bonds
- 7. Glycosidic bonds
- 8. Phosphodiester bonds

We realize that physical access to different representations may not be feasible every time and so, we introduce the concept of 'demarcation', where students/learners can be asked to demarcate the structural limits of the said component. Again, the above components could be considered for the task.

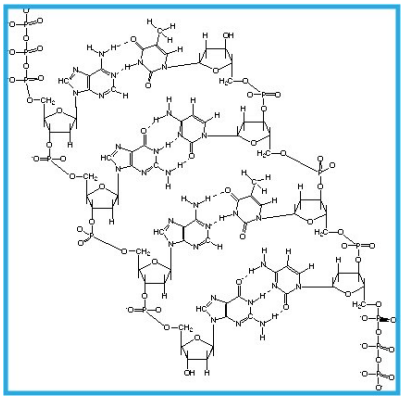
Reference:

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

Figure E.5: Screenshot of the second half page of the 'Methodology' page of the database on DNA structure

Completely Molecular Models

< Home



These models contain representations depicting each and every atom of the molecule. Representations may or may not show the hydrogen atoms. It also shows bond angles and bond orientations. In a space filling model, all the atoms may not be clearly distinguishable since, it gives the top view of the molecule. They are still classified as 'completely molecular' as it depicts all the atoms of the components.

Concepts that may be dissected/demarcated:

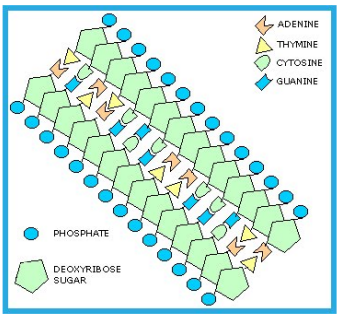
- Nucleotide: Yes
- Nucleoside: Yes
- Deoxyribose sugar molecule: Yes
- 4 Nitrogenous bases: Yes
- Phosphate group: Yes
- Hydrogen bonds: Yes
- Glycosidic bonds: Yes
- Phosphodiester bonds: Yes

Other examples:

Figure E.6: Screenshot of the 'Completely Molecular' category representation of the database on DNA structure

Symbolic Models

< Home



Representations involving different a) shapes and/or b) colors for different components. Since, all symbolic representations had skeletal representation of sugar molecule, they aren't categorized differently from symbolic ones.

Concepts that may be dissected/demarcated:

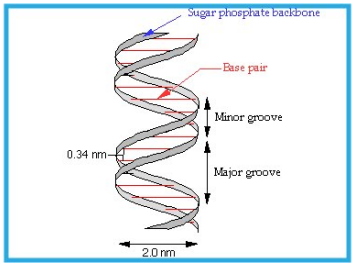
- Nucleotide: Yes
- Nucleoside: Yes
- Deoxyribose sugar molecule: Yes
- 4 Nitrogenous bases: Yes
- Phosphate group: Yes
- Hydrogen bonds: No
- Glycosidic bonds: No
- Phosphodiester bonds: No

Other examples:

Figure E.7: Screenshot of the 'Symbolic' category representation of the database on DNA structure

Helical models

< Home



Representations depicting 3-D helical structure of the DNA molecule with no atomic, skeletal, symbolic or letter details. Different components may or may not be labeled.

Concepts that may be dissected/demarcated:

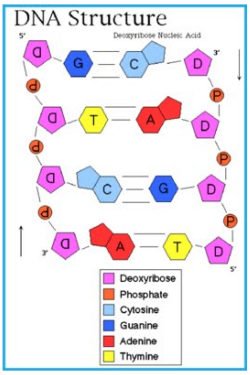
- Nucleotide: No
- Nucleoside: No
- Deoxyribose sugar molecule: No
- 4 Nitrogenous bases: No
- Phosphate group: No
- Hydrogen bonds: No
- Glycosidic bonds: No
- Phosphodiester bonds: No

Other examples:

Figure E.8: Screenshot of the 'Helical' category representation of the database on DNA structure

Skeletal, symbolic and letter-based models

< Home



The flat representation on the right shows different letters for different components: A, T, G, C for bases and P, D for phosphate group and deoxyribose sugar. It shows different colors for different components along with a circular shape for the phosphate group. It also shows skeletal structure of the bases and the sugar molecule.

Concepts that may be dissected/demarcated:

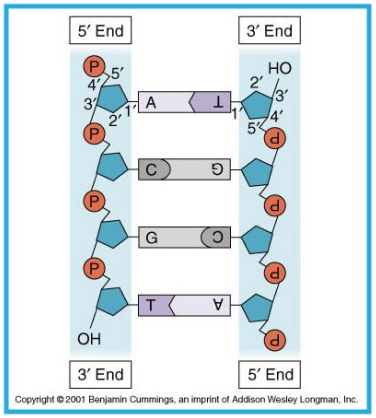
- Nucleotide: Yes
- Nucleoside: Yes
- Deoxyribose sugar molecule: Yes
- 4 Nitrogenous bases: Yes
- Phosphate group: Yes
- Hydrogen bonds: Yes
- Glycosidic bonds: Yes
- Phosphodiester bonds: Yes

Other examples:

Figure E.9: Screenshot of the 'Skeletal-symbolic-letter' category representation of the database on DNA structure

Symbolic letter-based models

< Home



The flat representation on the right shows different letter depictions for the bases and the phosphate group.
It also shows different colors and shapes for different components.

Concepts that may be dissected/demarcated:

- Nucleotide: Yes
- Nucleoside: Yes
- Deoxyribose sugar molecule: Yes
- 4 Nitrogenous bases: Yes
- Phosphate group: Yes
- Hydrogen bonds: No
- Glycosidic bonds: Yes
- Phosphodiester bonds: Yes

Other examples:

Figure E.10: Screenshot of the ‘Symbolic-letter’ category representation of the database on DNA structure