Building KiMoSin:
Design Requirements for Kinetic Interfaces in Protein Education

by

Ashlie Brown

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ABSTRACT

Design guidelines for tools to enhance protein education are developed and applied to a prototype tool. A literature search and personal experience suggest kinetic, tangible models fill the current gaps in protein education. Thirty-six personal interviews with biology instructors and students set a mandate for three design guidelines for appropriate kinetic, tangible tools. The guidelines – simplicity, accuracy, and intuition – form a simple mantra to guide protein education tool design. The guidelines are then used to develop the prototype of an educational model of kinesin, a simple and vital motor protein. Application of these guidelines should result in design that provides students an interactive medium to discover the world of proteins. The prototyped kinesin model, nicknamed KiMoSin, shows promise of fulfilling that goal.

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INTRODUCTION

Shortly after their discovery, proteins were named after the Greek word *protas* meaning "of primary importance(1)." As protein study advances, this name proves increasingly accurate. Proteins mediate every process in the human body, from translating genetic information to digesting nutrients (2). Our understanding of the human body starts with the study of proteins. Yet, the future doctors and researchers of the world are often introduced to proteins by a few paragraphs in a junior high school biology textbook. In a world of great technological achievement, there remains ample room for improvement in a student's first encounter with biology's prime mover and shaker: the protein.

TANGIBLE EDUCATIONAL TOOLS

Educators have long accepted the idea that students learn best in an interactive environment(3). The Tangible Media Group (TMG) and the Future of Learning Group, both at the Massachusetts Institute of Technology (MIT) Media Lab, have amassed a large collection of educational prototypes and studies emphasizing the importance of interactive hands-on learning (4)(5). The introduction of advanced tangible educational tools in biological curriculum, which relies heavily on invisible spatial relationships, promises great improvement in biology education. Simply giving students a crude physical representation of proteins could greatly enhance their understanding of biology(6).

A BRIEF HISTORY OF PROTEIN MODELING

Physical representations of proteins were first attempted in the 1950s with crude ball-and-stick mockups(7). Researchers and engineers have been working on protein representation ever since. With the growing popularity of computers, digital representations have been the primary protein models. Crystallography techniques allowed computers to compile structural data files for any protein that could be isolated. Online databases of these files are free and open to the public, as a result of many universities' commitment to the spread of knowledge. Open source molecular viewers like RasMol and Pymol offer researchers and students a free, high accuracy look at their proteins of interest. The biggest recent break-through in physical representations has been the ability to 3D-print from molecular viewing programs.

3D-PRINTED TANGIBLE MODELS

The Python-based Molecular Viewer (PMV) developed at the Scripps research institute was the first molecular viewing program to output 3D-printable files. The Molecular Graphics Lab (MGL), also at Scripps, has used PMV to produce a wide variety of tangible protein models(8). The first models were one-piece, rigid representations of specific proteins. These tangible models provided incredible insight into well-known structures, simply by bringing structural information into the physical world(9). Soon, articulated models introduced flexibility into the proteins by

breaking the protein into multiple, interconnecting units. Many of the articulated models were further enhanced by the addition of magnets simulating bonds between molecules. These connections and the overall flexibility of the model provided scientists with unique tool for studying protein interactions. Finally, articulated models were then paired with digital information in an augmented reality environment. Special augmented reality (AR) markers on the model are used to superimpose additional structure onto the tangible models. This feature enables scientists to virtually change the amino acids in the structure quickly and cheaply. The MGL tangible models, and others following them, have proven incredibly valuable to protein study(9).

A New Approach in Protein Education

The success of MGL's tangible protein models in the laboratory suggests that tangible protein models can also succeed in the classroom. A new environment requires a new approach, however, and the role and form of educational protein models must be considered carefully.

The following pages develop the design requirements for tangible educational tools for biology. Personal interviews with thirty-six biology professors and students emphasize the opportunity for improvement in protein education. That opportunity is explored with multiple conceptual prototypes exploring potential shapes, subjects, scale, level of automation, and more. The prototypes are reviewed and revised until one model – a partially-automated, kinetic model of kinesin – is chosen. A final prototype is constructed according to determined design requirements.

Interviews: The Mandate for a New Tool

Thirty-six personal interviews were the first step in developing the design requirements for a tangible tool in protein education. Interviewees included professors, lab instructors, researchers and students. The interviews included a number of topics:

- Educational background and philosophy – Understanding the educational perspectives and experiences of the interviewees enhanced the value of their feedback through context.
- Critique of existing biology curriculum – An open discussion of the failures and successes of the current educational tools and methods reveals the relative importance of tangible models.
- Suggestions for new tools – Motivated by their own learning/teaching styles, interviewees provided ideas and clarification for the type of tool needed.
- Review of current conceptual prototype – Most interviewees were presented with a conceptual model at the end of the interview and asked to give feedback and suggestions for the next model.

The two sides of education – instructors and students – were well represented, with some interviewees currently in both roles. All agreed, no matter their position, that there is significant opportunity for improvement in protein educational tools.

STUDENTS

The interviewed students unanimously agreed, one by one, that they arrived at college unprepared to tackle advanced protein concepts. Several students (~40%) were uncomfortable applying protein knowledge even after taking several courses in the Massachusetts Institute of Technology Biology Department curriculum, because they never fully understood the basic protein concepts. One student summed up her difficulty, saying, "Proteins are a three dimensional concept and textbooks and chalkboards have two dimensions. We're missing a third of the input information(10)." Another student pointed out that "proteins move due to forces that we can't see or experience, so it's hard to visualize that movement(11)." The student interviews collectively suggested the need for educational tools with distinct characteristics:

- Tangible Interface – Protein shape and spatial interaction determine function, and are complicated three dimensional concepts. Being able to hold the model and manipulate it in physical space adds a spatial understanding lacking in current tools.
- Kinetic Automation – The movement of a protein is difficult to visualize but crucial to understanding function. Automated models offer kinetic information in an intuitive form.

INSTRUCTORS

The response from interviewed instructors was widely enthusiastic and very specific. The instructors supported the students' claim that tangible, kinetic models are needed, but named cost as the number one obstacle to incorporating tangible models in the classroom. For a tool to be useful, it must provide enough value in student learning to justify the investment. There are few tools available that meet that criterion. The instructors collectively outlined the qualities of an effective educational tool:

- Appropriate Focus – A model that offers too much information will only overload and confuse students. A model that offers too little will not add to the student's experience.
- Durability – Passing models out in lecture often results in damage. A robust model that withstands student wear will improve the experience of more students.
- Integrated with common curriculum – A model must fit into a typical protein lesson plan to provide strong ties to course material. A stand-alone example will not draw connections between major concepts.

One instructor interviewee recalled a useful model in her recent research:

It was just a piece of wire bent in the approximate shape of our protein of interest. [Our collaborator] brought it in to lab and we were amazed by what we could observe in such a crude model. After studying this protein for years with state-of-the-art digital modeling software, we gained several insights from a couple of minutes holding a bent piece of wire(6).

This quote illustrates the extent of information stored in simple tangible models and their inherent usefulness to the human learner.

The qualitative results of the compiled student and instructor interviews contributed significantly to the development of the design requirements.

DESIGN REQUIREMENTS: THE FRAMEWORK FOR CONCEPTS

Based heavily on the extensive series of personal interviews, three main design requirements were determined: simplicity, accuracy, and intuition.

SIMPLICITY

To effectively communicate concepts, a learning tool must be simple. When a tool becomes too complex, the emphasis of interaction moves from the intended educational goal to the unintended task of understanding the tool itself [10, 3]. The science of biology is endlessly detailed, so an important task will be to choose the details of interest and to keep the focus solely on those intended details.

ACCURACY

Biological concepts are characteristically complex and multi-faceted. Those concepts must be simplified to make an effective learning tool, but it is important to maintain accuracy in the process. Simplification of an idea may inadvertently create false conceptual ideas [2]. The main concepts of biology rest upon the smaller details, so while they must be neglected for simplicity, the tool must implicitly represent them accurately. Continuous user evaluation is critical for avoiding this problem.

INTUITION

In any subject, the material is easier to learn when presented in an intuitive way. The complexity of most biology concepts can completely block learning altogether if not presented intuitively. Coupling intended biological expectations with innate expectations about the physical world gives students a strong sense of major concepts [8, 9, 11]. The details behind this intuition can then be supplemented with biological logic and background to provide a thorough understanding. The challenge lies in mapping the forces acting on the model (e.g. gravity) to the forces that act on the protein in nature (e.g. thermodynamics).

CONCEPTUAL PROTOTYPES: EXPLORING THE POSSIBILITIES

The three design requirements – simplicity, accuracy, and intuition – are applied to every major design decision of the model: subject, scale, form, and level of automation. At each step, the requirements are further clarified.

SCALE

The scope of protein study can be as big as the proper diet for complex organism and as small as the movement of one amino acid with respect to another. From that broad range, the proper scale for a tangible model must be determined. Three scale concepts were examined: an amino-acid-based protein building set, a single protein model, and an interactive exploration of protein interaction.

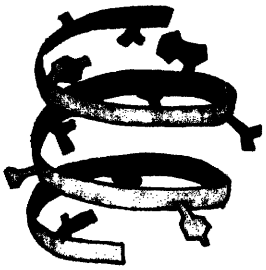

Figure 1. Amino Acid Constructive Assembly System

AMINO ACID CONSTRUCTIVE ASSEMBLY SYSTEM

An amino acid constructive assembly (AACA) system (Figure 1) would allow students to connect a series of amino acid pieces together and then fold them manually. Amino acids are the smallest and most basic level of protein structure, so any kind of structure can be made. The folding would be guided by mechanical and digital restraints built into every piece. Once folded, it is easy to understand the flexibility inherent in proteins and conformation changes that must occur before interacting with other proteins.

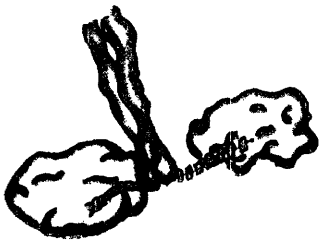

Figure 2. Kinetic Model of a Single Protein

KINETIC MODEL OF A SINGLE PROTEIN

A kinetic model of a single protein (KiMoSin) can demonstrate many simple protein concepts: function, conformation, energy use, etc. The model would demonstrate the movements and functions of a single protein and one interacting partner protein. Student interaction with the protein would be at the functional level: maneuvering pieces into place or adding needed energy.

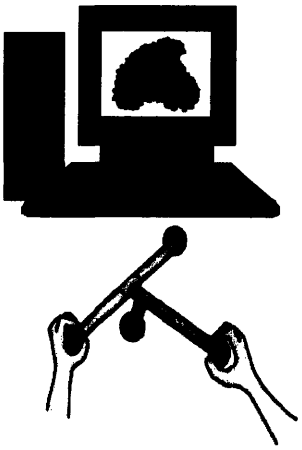

Figure 3. Haptic Augmented Reality

HAPTIC AUGMENTED REALITY

The haptic augmented reality (HapAR) environment (Fig2) starts with a crude constructive assembly system. Each piece will contain mechanical and digital properties and the pieces fit together in a rough approximation of any protein. The model connects to a computer and a protein-viewing program. As the researcher twists and bends the model, the computer sends information about resistance to bending and bond strength to the model. With each new conformation, the researcher can feel the relative ease with which a protein can be molded and explore potential interactions between proteins based on conformation changes.

APPLICATION OF DESIGN REQUIREMENTS

To determine the appropriate scale, the three design requirements are considered.

1. *Simplicity* – The AACA system and the HapAR environment are considerably complex. Both models depend on highly accurate and very quick calculation of the molecular forces governing the placement of each amino acid with respect to its neighbor. KiMoSin avoids the amino acid interaction calculations in favor of modeling a well-studied protein. The crucial amino acid and protein-protein interactions are known and well described and the model can focus on those points, thereby providing simplicity. BEST CONCEPT: **KiMoSin**
2. *Accuracy* – The complexity of the molecular forces between amino acids provides a significant challenge to model accuracy. If the calculations are not fast enough or if a small error propagates, the entire model can convey false information. KiMoSin is the only concept that avoids this potential source of error. Additionally, modeling a well-known behavior of a single protein reduces the probability of error from other sources. BEST CONCEPT: **KiMoSin**
3. *Intuition* – In this category only, the three concepts have rather equal pros and cons. Humans are accustomed to manipulating objects with their hands, giving all three concepts an intuitive feel. AACA and HapAR both provide a hands-on opportunity to cause a protein conformational change. The conformational change in KiMoSin is preprogrammed, which means the user assists rather than causes change but instead allows them to see the effects of that change. The entire importance of conformational change is connected to the effect it has on a protein's function, so KiMoSin sacrifices a small amount of user interaction for a large payoff. The conformational change effect follows logically from the observed cause and KiMoSin ultimately provides a more intuitive insight into the importance of conformational change. BEST CONCEPT: **KiMoSin**

Careful consideration of the three design requirements emphasized the superiority of the KiMoSin concept. Interviewees unaware of the determined design requirements strongly preferred KiMoSin over the other concepts, supporting the usefulness of the requirement approach.

SUBJECT

The next step in developing the kinetic model of a single protein is to choose the single protein. A multitude of proteins were considered and eliminated one by one, until three options remained: kinesin, myosin, and helicase. All three proteins were considered for their well-defined motion and prevalence in every cell.

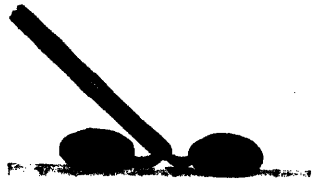

Figure 4. Kinesin walking along a microtubule

KINESIN

Kinesin is a simple motor protein responsible for transportation along the microtubules in the cell cytoskeleton. The protein consists of two parts that "walk" along the microtubule in a hand-over-hand motion.

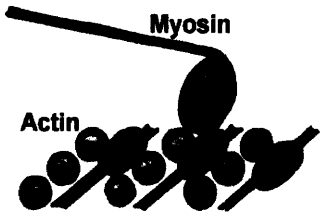

Figure 5. Myosin ratchets along an actin helix

MYOSIN

Myosin is another simple motor protein interacts with the structural protein actin to produce contractions in a cell and and cell motility. Myosin also consists of two parts but moves along actin due to a ratcheting motion.

Figure 6. Helicase (19)

HELICASE

Helicase is the protein responsible for "unzipping" DNA before replication. The functional helicase protein consists of six identical parts, all acting at individual time points.

APPLICATION OF DESIGN REQUIREMENTS

The three design requirements are applied to determine the appropriate protein.

1. *Simplicity* – A simple comparison of components gives the dimers (kinesin, myosin) an advantage over the hexamer (helicase). In addition to sheer number, the motion of helicase is a time-lapse system with several kinds of movement. Kinesin and myosin each rely on one type of motion; kinesin "walks" and myosin ratchets. However, the microtubule construct is static when interacting with kinesin, while the actin filaments are changing simultaneously with myosin. Focusing on one mechanism in one protein gives kinesin the simple advantage. BEST CONCEPT: **Kinesin**
2. *Accuracy* – As with the scale decision, simplicity and accuracy are closely linked. Helicase again proves a poor choice due to the difficulty in modeling the complex hexamer accurately. Another problem with accuracy is a lack of consensus on the protein mechanisms. This is still a large problem for helicase, but also affects kinesin. Several details of the kinesin mechanism remain controversial due to conflicting studies. Myosin has been studied more thoroughly than the other two and boasts a vast resource of literature describing its behavior. Any significant controversy that might have surrounded myosin has long been settled. BEST CHOICE: **Myosin**
3. *Intuition* – Again, the subject and scale decisions parallel, as no subject choice has a clear advantage on the others in terms of mechanism. Function, however, is another story. For someone new to biology, the concept of a kinesin transporter carrying cargo down a microtubule "road" is much more intuitive than the idea of myosin and actin moving with relation to each other to contract the cell or kinesin preparing DNA for replication. BEST CHOICE: **Kinesin**

The design requirement analysis suggests that kinesin is the best subject choice, but the accuracy concern is worrisome. Though the detailed kinesin mechanism is still the subject of some controversy, the simple mechanics of kinesin motion are accepted knowledge. The model will be as simple as possible, allowing

the neglect of the more controversial details. In the final prototype, the controversy does prove to be a major problem, showing the foresight of these requirements.

FORM

With the scale and subject chosen, the physical form of the model is the next consideration. Two conceptual choices are readily available: a crystallography-based 3D print or a simplified abstract form. The two choices represent extremes of a spectrum that is polarized by ease of manufacturing; a form in the middle of the spectrum would take considerably more work than either extreme.

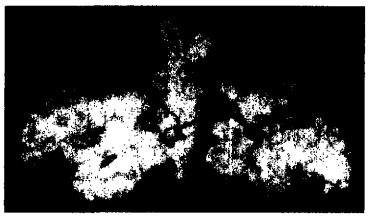

Figure 7. 3D-printed kinesin structure

CRYSTALLOGRAPHY 3D PRINT

Crystallography files are the most accurate protein representation available, relying on experimental data and heavy computation. The files are readily available from online structural databases and easily printed with a line of code inserted into a structural viewing program.

Figure 8. Abstract form of kinesin

SIMPLIFIED ABSTRACT FORM

This form could be any artistic model of the protein's structure. In this case, it is a carefully sculpted clay model used as the mold for hollow plastic forms.

APPLICATION OF DESIGN REQUIREMENTS

The two form choices are compared using the design requirements

1. *Simplicity* – The 3D print includes a large amount of unnecessary structural information, while the simplified abstract form can include a custom amount of information tailored to the model's specific needs. BEST CHOICE: **Abstract Form**
2. *Accuracy* – Contrary to initial expectations, the 3D print is in fact highly inaccurate for a kinetic model purpose. This problem rises from the method of compiling crystallography files. The crystallography experiment produces structural data for the protein in a very specific conformation based on experiment conditions. The model is now "stuck" in one conformation by design. The abstract form model, however, allows the conformation of the protein to change by design. The minute, and ultimately unimportant, details of the proteins are more accurate with a 3D print, but the overall structure and function is more accurately described by an abstract form model. BEST CHOICE: **Abstract Form**
3. *Intuition* – The human mind expects things that look like one object to act like a single object; things that look like a group of many objects are expected to act as many objects. The abstract form looks like a single object, conveying the proper expectations. The 3D print appears to be a conglomeration of thousands of tiny balls, giving the expectations associated with thousands of pieces grouped together. Additionally, the streamlined shape of the abstract form removes all unnecessary visual information, giving the user a clear view of the important details only. BEST CHOICE: **Abstract Form**

This comparison is yet another example of the usefulness of the three design requirements. When presented with both a 3D print and an abstract form, professionals spoke in awe of the 3D print but picked up the abstract form to illustrate points. Students eyed the 3D print with suspicion or confusion and were captivated by the color and form of the abstract form.

LEVEL OF AUTOMATION

The final design decision is the balance between user interaction and model automation. Three levels of automation were considered: fully automated, partially automated and fully manual.

FULLY AUTOMATED

The automated model would run completely by itself. This model would serve as more of a demonstration than an interactive tool, much like a movie.

PARTIALLY AUTOMATED

The partially automated model would respond to user action with an action of its own. The user would have to trigger certain steps in a sequence, while others happened immediately. This model is the most interactive, as both the user and the model are acting.

FULLY MANUAL

The fully manual model would require complete user control and action. This model would function much like a physical puzzle, as the user tries to fit the pieces together.

APPLICATION OF DESIGN REQUIREMENTS

The level of automation is considered through evaluating the design requirements for each choice.

1. *Simplicity* – Though it would be the least simple to construct, the simplest choice to use would be the fully automated model and its no effort approach. BEST CHOICE: **Fully Automated**
2. *Accuracy* – Proteins function through a complicated system of action and reaction. The protein must receive a signal of some sort to function, and it in turn gives a signal of its own. The model that most accurately represents this cause and effect relationship is the partially automated model. The fully automated model indicates that the protein is completely autonomous, which is wholly untrue, and the fully manual model indicates that proteins are passive molecules, another fallacy. BEST CHOICE: **Partially Automated**
3. *Intuition* – A good tool will work with a student's current intuition to build more intuition. The fully automated model does not require any intuition at all, but it also does little to cultivate it. The fully manual model requires a large amount of intuition, unreasonable for introductory biology students, and may prove more frustrating than helpful. The partially automated model requires some intuition, but also offers clues to the next step. Successfully completing the sequence will leave the student with more intuition than before because the model guides students to the proper sequence. BEST CHOICE: **Partially Automated**

Despite the user simplicity of the fully automated model, the clear choice is the partially automated model. The fully automated model sacrifices everything for simplicity, including the interactive portion of the tool.

FINAL CONCEPT

With the assistance of the three design guidelines, many possibilities have been narrowed down to one final concept: a partially-automated kinetic model of kinesin in abstract form. The lessons from the conceptual models are carried over into the building of the final prototype.

KIMOSIN KINESIN: BUILDING THE FINAL PROTOTYPE

Several conceptual prototypes and the three design requirements – simplicity, accuracy, and intuition – served as the basis of the final model concept. The final concept is a partially-automated kinetic model of kinesin in abstract form. The designed final prototype is shown in Figure 9 Building the final concept has gone through three stages: form, mechanical, and fully functional.

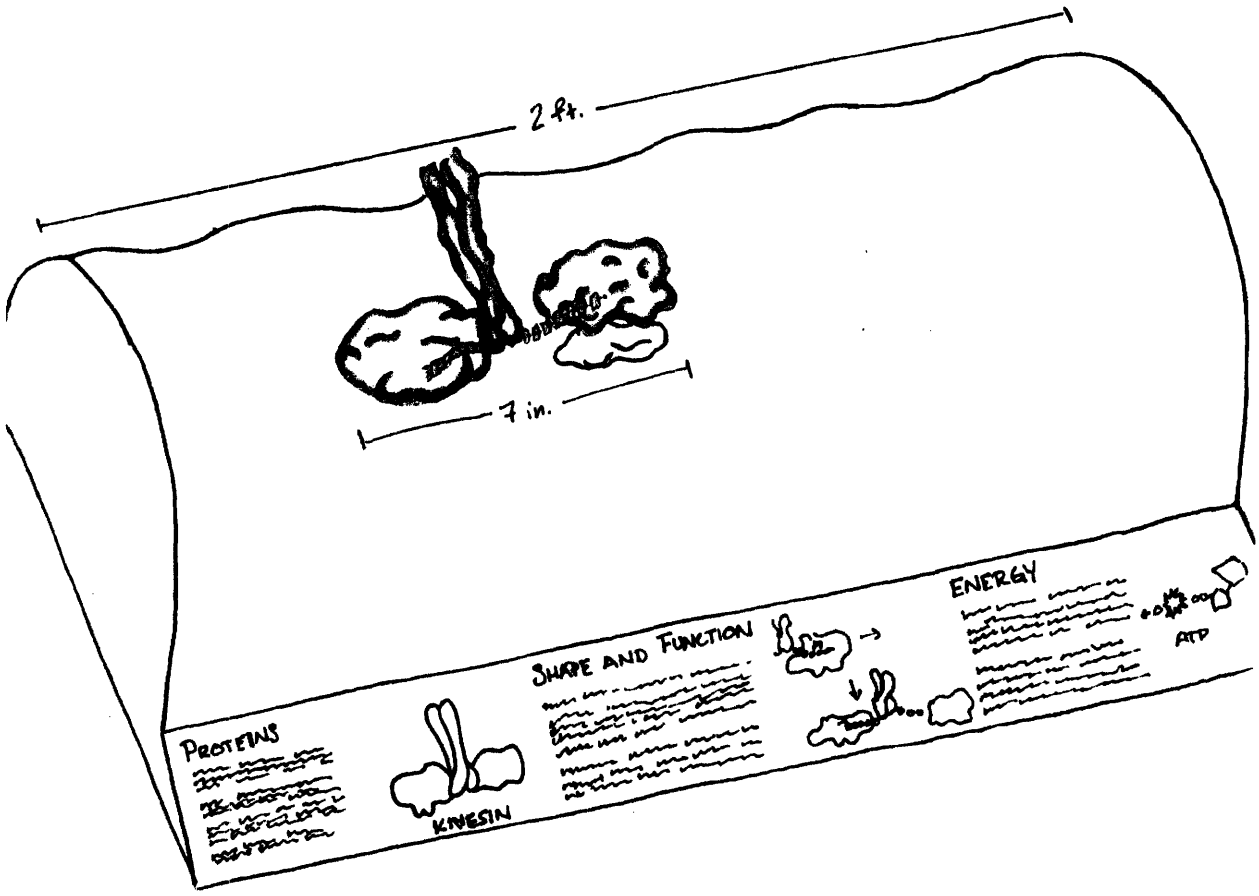

Figure 9. Conceptual Sketch of KiMoSin final form. The kinesin model and microtubule base are shown in their relative sizes and final form.

FORM PROTOTYPE

The form prototype is the first stage in final prototyping. In this stage, the size and overall appearance of the model is explored and determined. The form has no functional parts, but provides the general framework to build function upon in the mechanical and fully functional prototypes.

The kinesin monomer has four domains: head, neck, stalk, and tail. The tail domain is the farthest form the microtubule and binds to the cargo. The head is the globular domain that binds to the microtubule to power kinesin's movement. The stalk binds two monomers together into a kinesin dimer and connects the tails/cargo to the two heads walking down the microtubule. The last domain, the neck, is the smallest and connects the head to the stalk. Conformational changes in the neck are the driving force in kinesin motility.

The neck region must be extremely flexible to support kinesin movement. The blue portion of the prototype in Figure 10 corresponds to the neck region of kinesin. A series of small parts connected by a string simulates the flexibility needed in the neck. The rest of the model is rigid, as the head, stalk, and tail domains do not change conformation as drastically as the neck and can therefore be considered solid bodies.

The form prototype has a smooth and organic look and feel. The organic shape of the model is meant to remind users that the model is of a natural protein and to deemphasize the engineering and mechanics in the model. The smooth component of the design is important for keeping user focus on intended details instead of unnecessary physical information. The two components fit nicely to form an aesthetically pleasing shape that is pleasant to hold.

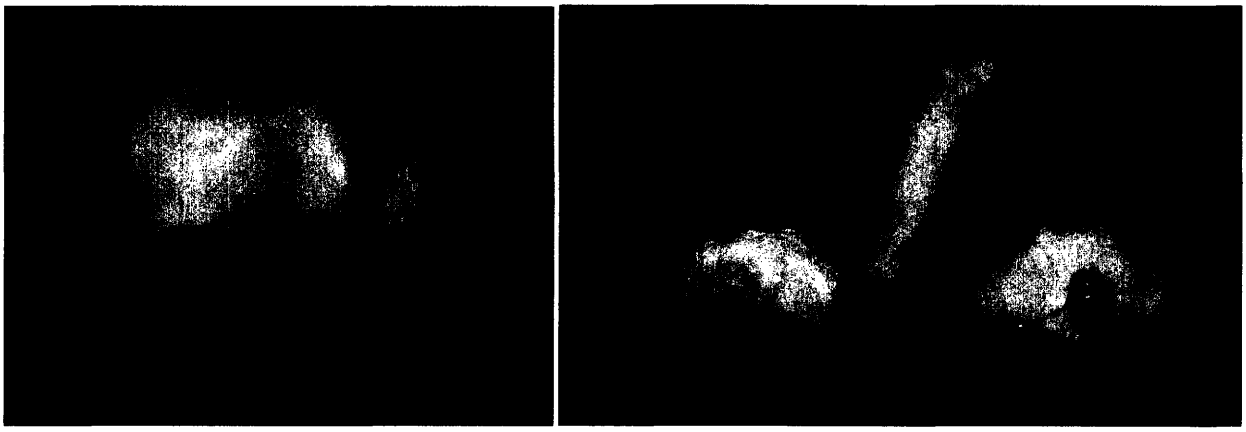

Figure 10. Form Prototype. Two views of the form prototype for kinesin model. Blue pieces are part of the neck section.

The form prototype is made of hollow plastic shells molded from clay sculptures of the protein. The light weight of the plastic model eliminates unnecessary load on the components added in the mechanical prototyping stage. Additionally, the hollow interior provides ample space for motors and mechanisms.

MECHANICAL PROTOTYPE

The mechanical prototype incorporates functional components into the form prototype. The physical mechanisms of the system are tested and developed in this stage, ending in a final mechanical prototype that is ready for the addition of electronic control.

This prototype does not use custom built electronics, but rather makes use of a 3D constructive assembly system, Topobo, that features kinetic memory to provide movement. Topobo was developed in the MIT Media Lab Tangible Media Group to facilitate learning about dynamic structures (12). Topobo motors remember and play back physical input with the press of a button, making them a convenient system for quickly testing the dynamics of a model.

The critical dynamic problem is modeling the conformation change in the neck. In nature, a combination of ATP interaction and microtubule binding provide the energy and force needed to change the structure of the neck automatically. When the neck is not activated, it is extremely limp and flexible. When ATP and microtubule binding activate the neck, it snaps quickly into a rigid shape that propels the stalk forward. In a mechanical model, ATP and microtubule interaction must be replaced with motors.

Figure 11 shows the final prototype mechanism. A motor is placed in the stalk domain and connected to the heads through flexible neck tubes. The neck tubes are attached firmly to the head and motor at each end. An inflexible string passes through the neck tube and is connected to the motor and the head, but not the neck. The neck tube and string are free to move independently of each other. The string of each head is tied to the motor at the same point and the motor rotates back and forth. When the motor is turned towards one head, the string connected to the near head is slack. The string connecting the other head is pulled taught, putting the neck tube in compression. The neck tubes are notched to curl into a specific conformation when under compression. The right side of Figure 11 shows this mechanism clearly. The motor is turned toward the viewer's right. The string connecting the right side head is therefore slack and the right sight neck tube is limp. The left side string is taught and the left neck tube is compressed tightly into the designed conformation.

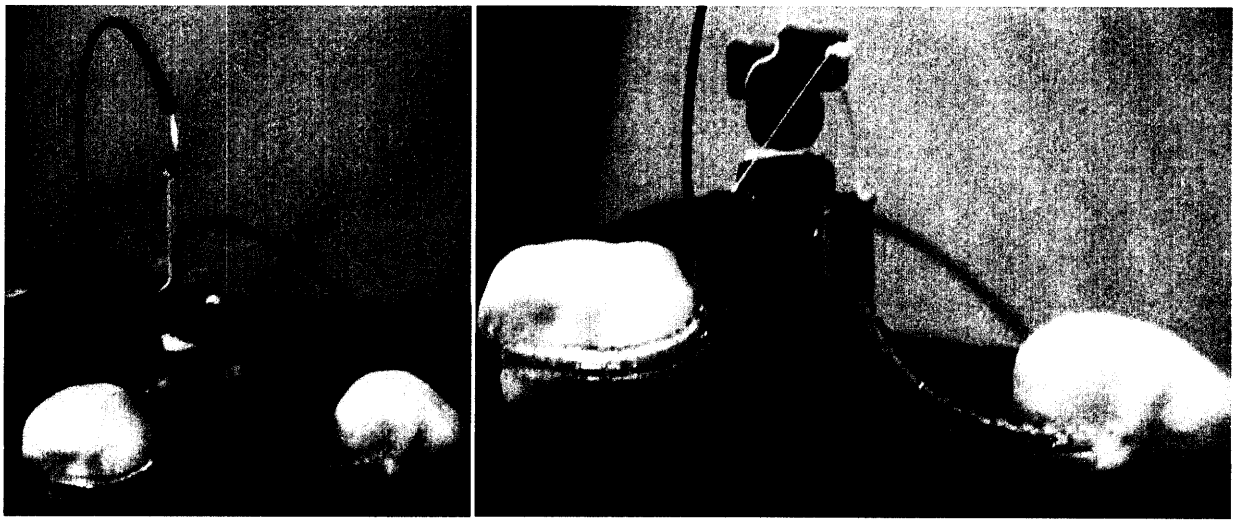

Figure 11. Mechanical Prototype. Two views of the mechanical prototype for the kinesin model.

The weight of the Topobo motor is too much to allow free movement, so the weight is counteracted by suspending the motor in air and thereby greatly reducing the effect of gravity in the load on the motor.

The mechanical prototype must be controlled with a custom built electronic control system. This component of the model is added in the last stage of prototyping a fully functional model.

FULLY FUNCTIONAL PROTOTYPE

The fully functional prototype will incorporate the electronic system of control into the mechanical prototype. The electronic system consists of electromagnets for kinesin-microtubule binding, a stock of charged capacitors representing ATP interactions, and a small motor to tighten the kinesin neck hinges. At the thesis due date, the electronic control model is not complete but will be incorporated by the end of the term.

CONCLUSIONS AND RECOMMENDATIONS

Protein education is a field with significant opportunity for improvement with educational tools. Careful consideration of personal interviews with thirty-six professors and students led to the development of three design requirements for protein educational tools: simplicity, accuracy, and intuition.

DESIGN REQUIREMENTS FOR KINETIC INTERFACES IN PROTEIN EDUCATION

Simplicity, accuracy, and intuition were the design requirements used to chose the final educational tool prototype. With the help of these three requirements, several concepts were narrowed down to the final choice: a partially-automated model of kinesin in abstract form. The final concept has been through several stages of prototyping and initial response to the progress has been very positive. The enthusiasm of the original interviewees for the current model supports the usefulness of the determined design requirements. If applied carefully and thoroughly, the three design requirements will lead future developers to successful educational tools for the study of proteins.

FUTURE WORK

After the fully functional prototype is completed, the next step is to test the model in the classroom. Four introductory protein lessons are conveyed by the model:

1. ATP carries energy in the body
2. ATP hydrolyzation causes protein conformation changes
3. Conformational changes are also dependent on interaction with other proteins
4. Conformational changes allow or cause the mechanisms necessary for protein function

A brief lesson plan is suggested in Appendix A for future study. A potential plan for testing is to contact students who have passed classes covering the four introductory lessons outlined above. Students should be presented with a short presentation and then allowed to interact with the model. A brief oral interview before and after the session will be sufficient to determine the effectiveness of the model. If understanding increases significantly after the use of the kinesin model, then there is a need for these tools in protein education and similar tools should be developed.

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APPENDIX A

KIMOSIN LESSON PLAN

A Closer Look at Protein Function
An activity highlighting the mechanisms of kinesin

Objectives:

- ATP carries energy in the body
- ATP hydrolyzation causes protein conformation changes
- Conformational changes are also dependent on interaction with other proteins
- Conformational changes allow or cause the mechanisms necessary for protein function

Background:
Before this activity, students should be familiar with the ATP cycle and general protein theory (i.e. amino acids, conformation change, function).

Additional materials:
http://www.scripps.edu/milligan/research/movies/kinesin_text.html
This movie shows the motion of kinesin, and can serve as a visual guide during the activity. Additionally, the supporting text for the movie is highly detailed and may be appropriate for advanced students.

Activity:
The model is an educational puzzle. Students must use their knowledge of ATP and proteins to maneuver through the steps necessary to cause a conformation change.

1. Kinesin binds loosely to the microtubule
   Matching magnets on kinesin and microtubule guide students to the appropriate placement and hold the two proteins in place
2. ATP is hydrolyzed by kinesin
   Adding the ATP piece connects the molecule to kinesin. Pulling out the third phosphate group causes kinesin to bind tightly to the microtubule and a conformation change occurs
3. Kinesin moves forward
   By moving the second head to the appropriate spot on the microtubule, the first head is unbound and the cycle continues

Follow-up:
The ideas presented in this activity should be extrapolated to all proteins, not just kinesin. Throughout the activity, general terms should be used instead of terms specific to kinesin (e.g. conformation change instead of the movement of the kinesin neck), because general terminology may ease the mental switch from kinesin function to a general view of protein function.