

## THE NEXTBIO PROJECT: A STUDENT COLLABORATORY FOR BIOLOGY CYBERLEARNING

The NextBio project is submitted as a research and development project in response to the NSF Directorate DR-K12 solicitation challenge #2, “How can all students be assured the opportunity to learn significant STEM content?” This project aims to address diverse populations of biology teachers and students at the high school level. The NextBio project responds to the need for students to understand the experimental basis behind biology concepts, and to the exponential increases occurring in biology knowledge today. NextBio will study the feasibility of engaging students in an environment where they can learn firsthand how science knowledge develops in the rapidly changing biology fields of bioinformatics and DNA science by performing collaborative, simulated experiments to solve open-ended problems.

Through learning modules and extended scenarios involving populations of mythical dragons, students will manipulate models and simulations to learn about the core biological concepts behind key experimental methods of bioinformatics and DNA science, and to learn about the methods themselves. Students will apply these methods to study quandaries and maladies within the dragon population, collaborating to share knowledge and results as they combine the results from multiple experimental methods. By publishing short summaries of results and debating others’ findings and methods, students will learn important biology knowledge by participating in scientific investigation. The NextBio project will research students’ learning about biology concepts, their integration of biology knowledge, their skill at scientific argumentation and their knowledge of the process of science. The NextBio project will also study the conditions that enable teachers to implement this cyberlearning environment effectively into the classroom.

**Intellectual Merit.** The NextBio project will advance understanding of how students learn biology concepts and how they learn about and practice the process of science itself. The project will contribute important research findings about how to apply transformative cyberlearning models to core biology learning and how these new models can be effectively implemented in the classroom. The NextBio project represents a convergence of over fifteen years of work from the Concord Consortium and partners and leverages the work and infrastructure from numerous previously funded NSF cyberlearning projects. Project partners include the Concord Consortium, the Maine Mathematics and Science Alliance, the Jackson Laboratory, BSCS and TERC. This group brings a strong core of biology scientific research, biology curriculum research and development, professional development, evaluation experience, and cyberlearning development.

**Broader Impacts.** The work done by students in this virtual collaborative laboratory environment will represent a significant step forward for biology curriculum and cyberlearning. By researching a virtual laboratory that emphasizes the experimental basis of biology through conceptual biology content, NextBio will contribute to understanding of the use of virtual laboratories and knowledge about conceptual biology learning. By studying the integration of core biology concepts and contemporary experimental procedures, NextBio will set a stage for learning about increasingly vital complex biology concepts. By forging advanced means for encouraging student experimentation, collaboration and argumentation, NextBio will enhance student learning about the process of science while creating and testing structures for researching this learning. The NextBio project will disseminate its work broadly via conferences and the web, where it will be freely available. An open implementation phase of the project will support nationwide participation in the program.

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## THE NEED

Science derives fundamentally from empirical observation and experimentation, and understanding this experimental nature is a vital element of learning science. Science curricula and pedagogy in many areas have long embraced this perspective [1, 2]. Yet biology curricula nationwide continue to reward students for memorizing vocabulary and huge amounts of information instead of emphasizing conceptual understanding and encouraging fluency with the scientific process. Decades of recommendations have failed to increase the role of experimentation or change the way biology ideas are presented in textbooks [3, 4].

**We must help students understand biology as an active, experiment-driven science.** This lack of emphasis on the experimental nature of biology is both lamentable and dangerous. Recipe-like laboratory methods can keep students from understanding the nature of science, and can go so far as to deter them from pursuing careers in science, technology, engineering and mathematics (STEM) fields altogether [5-7]. Concerns as large as the nation's security and economic stability hinge on increasing the numbers of well prepared students entering these careers [8-10]. In this era of accelerating scientific discovery, even those not pursuing science careers require firm knowledge of the nature of science simply to make informed judgments about important civic matters or make personal medical decisions.

**The nature of biology is changing rapidly, and learning must reflect this change.** Biological sciences involving genetics and biological data have grown explosively in size and complexity over the past two decades. The amount of public sequence DNA data available has doubled every 14 months for twenty years running [11]. A technique announced in January, 2009 promises to make DNA sequencing 30,000 times faster, sequencing an entire human genome in less than 30 minutes for under \$1000 [12]. Despite these clear signs, biology education has not kept pace. A recent survey of hearing parents with deaf children revealed that 98% of the parents had a fundamental misunderstanding of the concept of inheritance [13]. Biology textbooks are routinely more than 1000 pages long, but most devote only a few pages to discussing the science of bioinformatics. In a biology increasingly defined by a deluge of data, students must learn more about this increasingly prominent content and build the skills necessary for "computational thinking" [14, 15].

**Biology learning should include sharing and debating experimental evidence.** While biology has shifted to accommodate the exponential increase in information, the study of biology has become not only more computer-intensive but also increasingly interdisciplinary and collaborative [16-18]. The laboratory experiences students do have in introductory biology fall far short of answering the need for these skills. As phrased so cogently by Vincent Lunetta, "To many students, a 'lab' means manipulating equipment, but not manipulating ideas" [19]. Instead, students must participate in the processes of science. Engagement with scientific argumentation helps students understand both science content and the process through which scientists learn about the world [20, 21].

## PROJECT GOALS AND OBJECTIVES

### The Role of Technology

The explosive growth of bioinformatics and DNA science has had repercussions throughout biology. Results from this work have found their way into textbooks and curricula, but the explanations of how they were obtained have generally not. We plan to develop computer-based activities that allow students to answer the question “How do we know?” for results from bioinformatics and DNA science. To do this, we will give students highly contextualized challenges related to genetics that can be solved using simulated tools and methods of these disciplines.

It is important to emphasize what we are **not** doing. The proposed materials will **not** be a substitute for current laboratory investigations. The project will **not** simulate laboratory techniques that can and should be part of every biology course. Instead, it will introduce bioinformatics and DNA science as experimental fields that students can explore using software provided by the project. The computer-based investigations will have many of the properties of an excellent experimental laboratory activity because students will be able to choose tools, manipulate variables, collect and analyze data, debate findings, write reports, and share their conclusions. All these activities will be on-computer, which is appropriate for these information-rich disciplines.

Technology can help engage students in the process of science [22] especially in biology, where biological processes may occur slowly, essential concepts occur at scales far too small to visualize in the classroom, and many important experiments are too expensive or dangerous to attempt in the secondary classroom. Technology-based models and simulations can be used when real labs are not feasible. This promise has led NSF to explicitly encourage the development of virtual laboratories [15, 23]. Over fifteen years of research and development at the Concord Consortium have proven cyberlearning’s potential to help students understand cross-cutting science concepts and gain complex interdisciplinary skills (see Prior Work section).

### The Project Goal

The NextBio project will *determine the feasibility of engaging students in experimental bioinformatics and DNA science* by developing and studying computer-based materials that could be used in high school biology courses and widely disseminated.

Project collaborators will develop cyberlearning modules and an integrated virtual laboratory environment for use in this research. The materials will explicitly support conceptual biology learning and foster open-ended, collaborative problem solving. Rich biological models will undergird all aspects of the environment, and the experimental methods of modern DNA science and bioinformatics will be applied to these models in an environment fostering student exploration. The NextBio modules and laboratory will relate core concepts in pre-college genetics to important experimental methods in current use in biological research: activities and investigations will simulate these methods accurately and appropriately. NextBio activities and investigations will provide motivation and context by using model genetics of various real and mythical organisms popularized for over a decade by the Concord Consortium’s genetics modeling software. The project will emphasize the importance of in-depth and ongoing professional development in the use of its curriculum elements, and will study its adoption and implementation within existing curricula.

The project will investigate whether the proposed materials convey a deeper understanding of the experimental basis of modern genetics and what aspects of the materials influence the findings.

## Project Objectives

The project will have several specific sub-goals and objectives:

**Design core curriculum modules involving experimental methods.** We will create two kinds of cyberlearning curriculum modules: one set of modules suitable for introductory biology courses and a corresponding set of extended “bridge” modules. Each introductory module will last two to three days, link to core biology concepts, and connect to an experimental method from current research practice. Corresponding extended “bridge” modules will engage students more deeply in the biology concepts and specifics of particular experimental methods of focus.

**Create an interlinked biology virtual laboratory.** The integrated virtual laboratory will represent the culminating learning level of the NextBio project, in which students apply their biology knowledge and various experimental methods to open-ended scenarios. These scenarios will require students to extend their work with specific experimental methods, to collaborate with others or to link results from several different methods in order to solve a problem or dilemma.

**Assemble a rich underlying genetic model.** Each of the organisms used in the project software simulations will operate according to a robust genetic underpinning. Scientists from the Jackson Laboratory will extend and design the genomes for dragons (and their accompanying model organisms dubbed “drakes”) according to current research findings. They will embed model features such as genetic diseases, protein-coding and non-coding regions, and gene networks into the organism genomes, and will incorporate sequences from the DNA of actual organisms.

**Foster student collaboration through engaging narratives.** The modules and virtual laboratory will incorporate a set of engaging narrative scenarios carefully designed to reflect experimental issues encountered by scientists and medical researchers. In the modules and virtual laboratory, the scenarios will present open-ended problems at a variety of difficulty levels. Solutions to some narratives will require independent student work with one experimental method, while others will require distributed work across multiple students or involve several experimental means.

**Embed formative performance assessment into the cyberlearning core.** Embedded performance assessment elements, derived from extensive prior NSF-funded projects at the Concord Consortium, will log student actions with selected simulations and curriculum elements and create formative and summative reports for use by teachers and researchers.

**Provide supportive, ongoing teacher professional development.** All teachers involved in the project will receive extended professional development both in person and online, and the project will closely monitor professional development activity and classroom curriculum implementation as part of its research design. Professional development and content training will assist participating teachers in obtaining the necessary technological pedagogical content knowledge base to support their effective use of project materials in the classroom.

**Research the project assumptions.** The research plan is designed to determine the feasibility of engaging students in experimental bioinformatics using the project materials and to inform future NextBio materials. The project will study its impact on content and process knowledge and student interest in science using a quasi-experimental design. The research study will have three phases, involving three teachers in initial piloting and at least 25 teachers in both introductory and advanced high school biology classes from diverse schools in its final phase.

**Disseminate.** A Web site will feature all project research, materials, reports, and contributed materials. Staff will widely disseminate program information to reach interested high school teachers and college faculty nationwide through talks, workshops, publications, and newsletter articles.

## PRIOR WORK

The NextBio project builds on and incorporates work from numerous NSF-funded projects. It is a direct outgrowth of the Concord Consortium's long-term research study of the educational potential of scripted, manipulable computer models that pose problems to students and log their actions.

**GENIQUEST** (DRL-0733264, \$295,788, 9/15/07-8/31/09, Mokros, PI)-The partnership among NextBio members leverages staff, content and findings from GENIQUEST, a project that supports students in seeking out gene locations through the bioinformatics technique of Quantitative Trait Loci (QTL) analysis.

Although GENIQUEST has just completed its piloting phase, preliminary results demonstrate increased student understanding of concepts such as genetic recombination and inbred strains, and comments from student interviews indicate that the software can help students learn about the advanced topic of QTL analysis (Fig. 1). To support student learning of genetics, the GENIQUEST project centers on the same dragons and related organisms that will make up the NextBio storylines, and students—especially females—have universally commented on the compelling effects of these characters and the narrative storylines employed. These results are in keeping with many past studies involving students in studying genetics through these models—while the use of artificial creatures might seem to generate student misconceptions, for example, numerous previous projects and studies have shown this not to occur [24-30].

**Modeling Across the Curriculum (MAC)** REC-0115699, \$7,024,406, 10/1/01-9/30/06, PI-Paul Horwitz.) MAC developed dozens of structured activities for physics, biology, and chemistry, including the BioLogica model at the heart of this project [31, 32]. BioLogica consists of several linked, manipulable models that interact at different levels of description. Organisms within species can interbreed and inherit traits via a model of transmission genetics that includes polygenicity, mutations, and recombinant events such as genetic recombination during meiosis. A “pedigree tool” enables students to study inheritance patterns, and a chromosome and DNA tools enable them to explore the consequences of genotypic changes. A cellular level serves to tie the others together by

*Figure 1.*

**Student quotes after using pilot software from the GENIQUEST project:**

*“I definitely...have a better understanding now how once you have a QTL and once you have a vertical confidence interval, how to take that information and bring it back to what you are looking for in going through all those genes...”*

*“Now I actually get what the x and y axis represent on QTL graphs.”*

*“Definitely [using a gene mapping database] makes a lot more sense...rather than reading every bit of information...you just need to find what you're looking for.”*

**On the motivating effects of the dragons used in the simulations:**

*“Breeding [the dragons] was really interesting...”*

*“It was neat just to figure out all the weird dragons.”*

*“I wanted to experiment and try different things.”*

*“The dragons were more interesting than just a bunch of squiggles.”*

enabling students to observe and interact with the complementary processes of meiosis and fertilization.

The MAC project defined scaffolded, open-ended tasks and created over a dozen activities using BioLogica, ranging from simple challenges such as giving a dragon wings by changing its genes to quite complex ones, such as breeding studies to ascertain the dominance or recessiveness of a trait. By analyzing students' manipulations and choice of affordances, we could infer the depth of their conceptual understanding and modeling and inquiry skills [33]. We particularly examined the systematicity of the students' performance, *i.e.*, how purposeful they were in using a model in an unfamiliar situation. Systematicity has been found to be a reliable measure of students' strategic learning and knowledge acquisition strategies [34] and bears on their skill at estimation and metacognition [35]. Our results show that performance on even a single inquiry task was a significant predictor of future learning success [33, 36, 37].

**BioLogica**, and its preceding project, **Genscope**, have produced a successful, manipulable model for teaching genetics at multiple levels. An important finding is that *BioLogica* is motivating for disaffected students in lower performing schools where attendance is marginal and dropout rates extremely high [27]. More details, software and activities are at <http://pedagogica.concord.org>.

**Molecular Workbench: Reasoning with Atomic-Scale Models** (12/1/99 – 8/31/04. \$1,364,944. REC-9980620. Berenfeld, PI). **Molecular Logic: Bringing the Power of Molecular Models to High School Biology** (2/03 – 6/06. \$1,416,623. ESI-0242701. Berenfeld, PI.) **The Molecular Rover project** (REC-0537224. \$299,815. 10/1/05 – 9/30/07. Tinker, PI, Xie, Co-PI.) **Science of Atoms and Molecules (SAM)** (NSF DRL-0628181 \$1,139,836. 10/06 – 5/09. Berenfeld, PI, Tinker, Co-PI). **Electron Technologies: Modeling Pico Worlds for New Careers** (NSF DUE-0802532. \$898,516. 5/08 – 5/11. Berenfeld, PI, Xie, Co-PI)

These projects each expanded and involved research on materials using the Molecular Workbench (MW) platform and its associated authoring and delivery system. The open-source, free learning environment of Molecular Workbench (MW) allows students to experiment with atomic-scale systems to intuitively understand the physical origins of a very wide range of phenomena including reaction pathways, protein conformation, and the shape and function of biomolecules as well as physical science concepts and electron-related properties and interactions.

**The Center for Technology Enhanced Learning of Science.** (ESI-0334199, 2003-2009, \$10M, PIs Tinker, Linn, Slotta) TELS, a Center for Teaching and Learning, defines the state of the art for the effective use of information technologies in STEM learning. It has developed a theory-based approach to support student learning via guided inquiry of dynamic visualizations. TELS research has resulted in 40 new fellows, nine postdocs, 104 active TELS teachers in 42 diverse schools nationwide, and 106 published papers with 32 more in press.<sup>1</sup> To support its research, TELS partners have developed SAIL, the Scalable Architecture for Interactive Learning, which includes facilities for launching client-side learning materials like MW and tracking student use of materials. SAIL includes methods for persistence—allowing students to pause and continue activities later, possibly on another computer—and provides an instructor's portal with student progress reports and control of student assignments, polls and student computers.

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<sup>1</sup> See <http://www.telscenter.org/>. For a brief introduction to SAIL see: <http://tels.concord.org/SAIL.overview5.pdf>.

TELS Center funding is nearing its end, but its work continues under a series of grants to the three main partners: the University of California, Berkeley, the Concord Consortium, and the University of Toronto. SAIL is being used in other projects at the partner institutions and other research groups worldwide.

## PROJECT OVERVIEW

### The Collaborators

NextBio is a collaborative project between the Concord Consortium (CC), the Maine Mathematics and Science Alliance (MMSA), the Jackson Laboratory, BSCS and TERC. CC will be the lead organization, developing project software and curriculum. The proposed curriculum and models build on GENIQUEST, a related ongoing DR-K12 project at CC, MMSA, and the Jackson Laboratory. BSCS will conduct the project's independent research, and TERC will serve as project evaluator, monitoring teacher professional development and classroom implementation.

**Supporting student collaboration and argumentation** – Prior work from CC and other project partners has shown success at helping students learn complex topics through cyberlearning. In order to understand the experimental nature of biology, students must also join in the process of argumentation that makes up science investigation and discovery. NextBio will extend and connect student learning, allowing students to share elements of their work across teams, classrooms or the entire NextBio user community. Learning scenarios will require students to seek assistance from others, post quandaries they encounter for other students to ponder, or divide the elements of a larger problem among themselves and their classmates. As students uncover details of larger problems, they will create miniature “papers” about their findings, reference the work of others and submit them to a central area for review and publishing to other students. This direct practice in the process of science encourages student understanding of the nature of science and furthers student motivation [38, 39]. Additionally, this is precisely the type of collaboration enabled by information technology that is burgeoning in biology today [40].

In narrative threads running through and across modules, scenarios will engage students as investigators using the tools and methods of bioinformatics and DNA science to solve problems within the dragon population. To understand the multiple levels and interlocking nature of the NextBio **overarching scenarios**, it is perhaps easiest to examine one in some detail.

**Overarching scenario example: *The Shadow of Pale*** – In a scenario called *The Shadow of Pale*, students find themselves at the center of a historical mystery concerning two royal families of dragons and a curious genetic disease. As a young prince and princess from the two different families fall in love and hope to marry, the dragon population is conflicted: this disease has appeared in both royal families in the past. In order to solve this dilemma, students must use the NextBio models and experimental methods to determine the genetic basis for the disease and determine whether the two can marry without fear of passing this disease on to their royal child.

Students encounter this scenario gradually and can enter it from a variety of directions. Students first discover the dragons' problems through an **introductory module** in which they learn about basic genetics concepts by studying the inheritance of the disease the dragons call *Pale*. Since dragon lifespans are over 500 years long, students learn about genetically similar model organisms called “drakes” that exhibit a similar disease and can be bred easily. Students conduct drake breeding experiments, reinforcing Mendelian genetics content and isolating a specific recessive gene as the cause of the disease.

But when students collaborate to share and interbreed their pairs of “reliable carrier” dragons from these individual experiments, the mystery deepens. Dragons that have consistently passed the disease on in individual experiments within groups have consistently healthy offspring when bred across experiment groups. What can be causing this strange behavior?

Figure 2 <b>Introductory module topic</b> (Underlying national standards in italics)	<b>Associated experimental techniques / Bridge module</b>
DNA composition* ( <i>NSES C2-1; BSL 5B/H3</i> )	Genetic database use, Oligonucleotide synthesis
DNA replication and translation* ( <i>NSES C2-1; BSL 5B/H2, M2c</i> )	DNA hybridization*, PCR amplification*, DNA sequencing*
Meiosis and genetic recombination* ( <i>NSES [5-8] C2-4; BSL 5B/H2, H4a</i> )	Linkage mapping/QTL analysis*
Protein structure and function* ( <i>NSES C1-3; BSL 5C/H4a</i> )	X-ray crystallography*
Genetic variation* ( <i>NSES C2-2; BSL 5B/H2</i> )	SNP profiling
Genetic expression ( <i>NSES C1-6; BSL 5C/H4b; BSL 5B/H6a,b</i> )	Microarray analysis
Mutations and their effects and non-effects* ( <i>NSES C2-3; BSL 5B/H4, H5</i> )	Mutagenesis*
(NSES: [41]; BSL: [42]) *Indicates existing base activity or resource from prior NSF projects	
<b>Additional proposed overarching scenarios</b> ( <i>See definition and explanation below.</i> )	
<p><b>Genetic screening</b> - In this scenario, students uncover a genetic disease that is more prevalent among certain sub-populations of dragons. Students use DNA sequencing to create single-nucleotide polymorphism (SNP) profiles of the populations that permit genetic screening.</p> <p><b>Biopharmacology</b> - Students learn that a certain drug is effective in some dragon sub-populations, but ineffective or dangerous in others. Isolating diseased and non-diseased individuals, students design an expression microchip of cells that overexpress genes involved in the disease. By applying drugs to these chips, students evaluate the abilities of candidate drugs to suppress this gene expression more effectively across populations.</p> <p><b>Protein identity and gene determination</b> - Students learn that a certain protein is associated with a genetic condition, but that its encoding sequence is only partially known. Using the known amino acid sequence from one end of the protein, students generate a complementary probe sequence and isolate the mRNA encoding the protein. Students amplify the corresponding DNA via PCR and sequence the gene. As an extension, students use a protein database to compare sequences and attempt to determine the disease-causing mutation.</p> <p><b>Protein structure and function</b> - Students identify and sequence the gene responsible for a genetic disorder in the dragons. Through a database search, they uncover a protein matching the non-diseased sequence. Via x-ray crystallography, students can compare the two versions of the protein to identify its modified structure as the cause of the disease.</p>	

Searching for the solution—that the disease is passed on by any matched pair of gene mutations among multiple possibilities along a biological pathway—brings students into the next level of the NextBio curriculum. Depending upon student interests, academic levels and biology curriculum, students can explore the problem along any of a variety of paths. Students can complete related NextBio **bridge modules** to learn the biological basis of experimental methods such as DNA sequencing or Quantitative Trait Loci (QTL) analysis. After successfully completing a bridge module, students qualify as “certified” in the corresponding method and can apply it to locate or describe the Pale gene further. Other classes or groups will conduct systematic breeding



experiments to isolate various disease strains. Students involved in more advanced study can learn and apply methods, such as microarray experiments, or connect results from several methods.

Although exceptional students may discover answers to overarching scenarios on their own, students quickly realize that they can achieve their aims more quickly by working together. Individual students' experimental results are published in a reviewed "journal" visible to all. These results may range from information such as a specific gene sequence to rich artifacts such as a dragon with an unusual disease. Once published, these results and artifacts can be used by other students within a group defined by the teacher—this group may be as small as an individual classroom or as large as the entire NextBio user community.

In this way, students have access to overarching scenarios at varying levels of difficulty, with multiple routes toward various "solutions." Students will discuss their progress online, using experimental results as evidence to corroborate or refute findings. Some will become "experts" in a particular experimental method, fielding requests and running experiments for other students. Along the way, students will encounter many opportunities to succeed at completing sub-goals, and will also contend with imposed constraints of cost or time.

This example demonstrates the core elements of all NextBio scenarios. It conveys biology's experimental nature, introduces contemporary DNA science content and elicits both scientific argumentation and collaboration. Fidelity to the underlying scientific model is paramount: The disease Pale is modeled after the genetic disease Hermansky-Pudlak syndrome [43] and will be designed directly into the dragon and drake genomes by scientists from the Jackson Laboratory. Figure 2 outlines additional planned modules and scenarios. These will involve new experimental methods or combine methods in different ways. As indicated by asterisks in the figure, many modules will make direct use of already-developed resources from previous NSF-sponsored projects. Overarching scenarios such as those indicated will be drawn from scenarios and conditions of actual scientific practice and integrated into the mythical dragon narratives. A subset of these will be chosen for full development based upon piloting and field test results. Scenarios will be rooted in core biology concepts, developed following a "backward-design" process [44], and calculated to address both introductory and advanced learners. Robust design strategies [45] will ensure effective use in a wide range of classrooms.

**Standards and Learning Progressions** – We will pattern the models and learning for project research after learning progressions research in genetics [46, 47], and inform them further with well thought-out expectations for literacy at the undergraduate level, *e.g.*, [48].

**Embedded formative assessment and reporting capabilities** – The NextBio project will also employ features under active development via NSF funding at the Concord Consortium (DRL-0733299, DRL-0822833, DUE-0603389). Advanced logging capabilities will enable the NextBio project to monitor ongoing student progress within activities in great detail. Systems will report the results of student and group actions to classroom teachers in real time. These capabilities can be included with any or all of the project elements, enabling teachers to keep close tabs on student learning and adjust instruction accordingly.

## CURRICULAR COHERENCE AND FOUNDATIONAL PREPARATION

Upon publication 15 years ago, national standards did not explicitly include NextBio's topics of DNA science and bioinformatics, though they noted their importance. Scholars have since noted

the growing need to include these topics [49, 50]. NextBio directly aligns with the diverse needs of high school biology classrooms and curricula and helps bridge this gap. As Figure 2 shows, introductory modules directly support traditional curricular content and sequences, while bridge modules advance student knowledge about the introductory modules' experimental methods. Overarching scenarios combine techniques from the individual modules and fully engage the process of science. Teachers can select any or all individual modules that fit their given curriculum, textbook or class constraints, and advanced classes can use the introductory modules as study or review, moving more directly to the extended learning and overarching scenarios.

## WORK PLAN AND TIMELINE

The NextBio project will be a five-year project aimed at the “Design, Develop and Test” phase of the Cycle of Innovation (see Program Solicitation- NSF 08-609, p.4). The project will take place in three phases, a development and pilot phase, an initial field-testing phase and an extended field-testing and open implementation phase.

**Development and pilot phase – (project year 1):** Curriculum and software developers at the Concord Consortium will plan and create project introductory and bridge modules. Scientists at the Jackson Laboratory will design the project organisms' model genomes and identifying realistic scenarios disorders to embed within them. Three active teachers from Lexington High School and Randolph High School near the Concord Consortium will assist curriculum development and pilot curriculum throughout the year. MMSA will create pilot professional development workshop and work with teachers to create “voices from the field” reflections.

**Initial field-testing phase – (project years 2-3):** The original three teachers will pilot advanced modules and virtual laboratory scenarios. An additional seven teachers will begin to field test already-piloted and improved modules. Developers will use teacher and student feedback to modify both pilot and field-test software, and will test and revise embedded assessments. MMSA will implement a five-day summer workshop for pilot and field-test teachers.

**Extended field-testing and open implementation – (project years 4-5):** Fifteen new teachers will be added for the final phase of field-testing, for a total of 25 teachers. These teachers will implement the finalized materials over the last two years in both introductory and second-year biology classes. Open enrollment through a public Web site will enable public informal enrollment, with surveys and embedded assessment providing the project additional teacher and student data. MMSA will hold a final version of professional development workshops, write and test deliverables and disseminate the project through online discussions and distribution of deliverables.

## PROFESSIONAL DEVELOPMENT

To be incorporated into biology courses effectively, the new materials must directly address teachers' concerns about the rationale for the curriculum, how the content can be integrated into existing courses, what students will take away and how they will be prepared for the future, and how to “manage” a curriculum that involves cyberlearning tools as a basis for experimentation and inquiry. The focus of professional development will be on implementing the NextBio project into courses in a meaningful and sustained manner.

The professional development will focus on the following:

**Addressing alignment of the NextBio project** with national and state standards, the demands of college level biology, and the revised AP Biology curriculum scheduled to be in place by 2011.

**Integrating NextBio with biology curricula** in use by the field test teachers so that it will not be seen as an “add on.” Teachers need concrete strategies for determining how to integrate the new

program into existing curricula. The professional development will address this question: *How does NextBio make the curriculum deeper and more cohesive?*

**Introducing new content.** Because much of the content will be unfamiliar, professional development will provide opportunities to understand the underlying processes, how these link to familiar content, and how to translate this content for students (pedagogical content knowledge).

**Using the new cyberlearning tools to promote student inquiry and experimentation.** One focus of the work will be on the collaborative use of the tools, so that students are able to share and discuss their methods and emerging findings.

The professional development program for teachers will use proven models, including a modified version of Curriculum Topic Study (CTS) [51], a process that will help teachers decide what biological content is “core” and how to bring out the elements of the experimental techniques that reinforce these core concepts. Professional development in formative assessment will enable teachers to examine evolving student learning during NextBio work. Research has shown that as teachers use formative assessment, they learn new content themselves and better recognize the challenges students face in understanding new material and processes [52]. In brief written “voices from the field” pieces, teachers will share implementation strategies and challenges, enabling project staff and field test teachers to quickly identify and address emerging pedagogical and pragmatic issues. These pieces will also provide a foundation for the final phases of teacher professional development and a vehicle for project dissemination.

The professional development deliverables will include: 1) a self-study guide for new NextBio teachers teaching introductory or advanced biology courses, containing tools to help teachers to align modules with existing curriculum; 2) an accompanying manual and on-line discussion component centering on “voices from the field,” and 3) a “tools for biology experimentation” document addressing the need for students to learn about inquiry in biology, as well as how to use the platform to promote meaningful individual and collaborative inquiry in the classroom.

## RESEARCH PLAN

The NextBio research plan is designed to determine the feasibility of engaging students in experimental bioinformatics using the project materials. This research will also inform future design and implementation of the NextBio resources, materials, and technologies.

The study will employ a quasi-experimental design, with a comparison population comprised of teachers and students in schools matched for socio-economic and race/ethnicity variables. Researchers will examine the ability of the NextBio resources to provide equitable opportunities to learn, disaggregating data by the potentially moderating variables of student socio-economic status, race/ethnicity and gender wherever possible.

The study will concentrate on two research questions:

**Question 1: What are the impacts of the NextBio materials on student learning outcomes, and how do these impacts compare to those from typical materials?**

The study will address this question by comparing student posttest scores from a group of teachers using the NextBio approach with those from a second group of teachers using their usual biology materials using the measures described below.

**Content Knowledge.** Researchers will examine differences in student learning between the two groups using three student learning outcomes: 1) Facts and vocabulary in relevant standards as measured using multiple-choice items developed from existing genetics instruments and test

banks (e.g., [53]); 2) Understanding and reasoning about the experimental basis of knowledge in genetics, bioinformatics and DNA science; and 3) Integration of student knowledge concerning genetics, bioinformatics and DNA science. The latter two outcomes will be measured using two-level questions consisting of a multiple-choice part and an open-ended explanation.

**Process Knowledge.** A second set of measures will focus on more general student understandings and skills that are critical across science. These will include understanding of the processes of scientific inquiry; ability to construct and critique scientific arguments (argumentation); and learning in subsequent science classes. Researchers will base measurement of these understandings and skills on currently available approaches (e.g., [54, 55]).

**Interest in Science.** A measure of students' attitudes toward science will be used that includes students' interest in pursuing a second biology course in high school and career aspirations in related fields. Researchers will develop survey instruments to measure these constructs based on currently available instruments, (e.g., [56] and [57]).

## **Question 2: What factors mediate the effects of the NextBio materials, and what can support their effective use?**

The study will address mediating factors using qualitative data from classroom observations, teacher surveys, and clinical interviews, and using quantitative measures of teachers' pedagogical content knowledge. The study will also use data from the project evaluation.

**Professional Development.** Researchers will collect data on the extent of use of the professional development using the online PD delivery system, items on teacher surveys, and questions in teacher interviews.

**Content Knowledge.** A test of teacher's content knowledge related to genetics, DNA science and bioinformatics will help determine teacher content knowledge in content used in the NextBio materials. Since much of this is outside of the scope of the normal curricula, the study will also survey teachers on barriers and supports to gaining this knowledge.

**Fidelity of Implementation.** Researchers will develop a rubric for measuring the level of fidelity and use scored classroom observations. The rubric will build upon previous work by BSCS on assessing fidelity in two NSF funded projects. Electronic logs, teacher survey items, and interview questions will provide additional sources of fidelity data.

## **Data Collection and Analysis**

The NextBio materials will include electronic recording of student responses to assessment items, computer scoring of multiple-choice items, and logging of student actions. The logging will give quantitative data on how often the materials are used, for how long, whether in school or at home, and how systematic students are in exploring models. These functions will simplify data collection and help with the fidelity study.

The open-ended parts of items in Question 1 will be scored twice using different rubrics. One will use a rubric developed in learning progressions research, which scores student responses along a continuum from informal ideas about science to accounts in which students trace matter, energy and/or information across scales (e.g. [58, 59]). The second scoring will use Knowledge Integration rubrics, [60] which measure students' ability to evaluate, organize and make accurate connections among ideas and can access higher-level reasoning.

Student pretest scores will be a covariate in the analyses and researchers will examine the moderating effects of race/ethnicity, gender and socio-economic status. Although the second research question examines the mediating role that multiple teacher variables play on the effectiveness of NextBio materials, the study will examine both questions mainly within the same HLM analyses.

As this study looks primarily for the effects of a teacher-level treatment on student achievement, the effects data in this study are nested within teachers. Researchers will thus use Hierarchical Linear Modeling (HLM) [61] to estimate them accurately. Results from Optimal Design (OD) software [62] assisted in determining the number of teachers needed to participate in Years 4 and 5 of the study. OD allows researchers to determine the sample size needed to detect a meaningful effect by entering information related to several parameters (e.g. estimated effect sizes, intraclass correlations, and covariate correlations). Based on estimates of these parameters from previous studies and accepted standards, the OD software indicated that 17 teachers would be needed to detect student effects at  $d=0.33$ . To account for attrition and missing data, the project will recruit 25 teachers to participate in the study.

## EVALUATION

A team from TERC will conduct external project evaluation, documenting the development and research process throughout the project and evaluating teacher learning during the field test and open implementation stages. Ongoing evaluation updates and recommendations will keep partners informed about the many facets of project work, facilitate their communication, and enable them to modify work plans and timelines as needed. Formative findings about teacher learning will offer feedback for professional development and inform research so that more precise measures of student learning outcomes can be developed. Evaluators will summarize progress in annual evaluation reports submitted to the Advisory Board and the NSF.

**Documenting the development and research process.** The following questions will guide this segment of the evaluation: *1) To what extent and in what ways are partners collaborating during the design, field test, and implementation phases? What processes lead to coordinated efforts to forward the work and move toward project goals? How do teacher participants experience their interactions with project staff? 2) How do partners use evaluation and research data to revise the modules and/or professional development and to influence staff interaction and work plans?*

Early in the project, TERC will participate with partners to establish a timeline and benchmarks. Throughout the life of the project, TERC will observe key planning and decision-making project meetings. Evaluators will collect survey data from partners at several points each year to document work, accomplishments, and challenges, and annual interviews that allow for reflections about the development process will augment these data. In addition, TERC evaluators will collect survey data from participating teachers about interactions with project partners.

**Formative Evaluation of Professional Development.** The following questions will guide this aspect of the evaluation: *1) Based on teacher perceptions and levels of use, how accessible and informative are guides and tools for aligning modules and various professional development formats and experiences (e.g., on-line discussions, voices from the field, summer workshop, etc.)? 2) How does professional development impact teachers' knowledge of genetics and their ability to integrate modules, instruct with cyberlearning tools, and assess student learning?*

During the field test and implementation stages, evaluators will log teacher participation in professional development activities and observe a sample of all components to develop appropriate survey questions for teachers about perceived contributions of professional development. They will conduct focus groups with each cohort to probe survey responses and collect more nuanced information about the impact of training and resources on teacher confidence and use of modules with their students. Working with data collected by MMSA and BSCS, the evaluators will ana-

lyze teacher work and assessments, examining correlations among indicators in the evaluation dataset as well as pre-to-post changes on items. Associations and difference scores will offer important information on teacher growth and provide a first step in understanding how variation of an indicator might be related to other indicators.

## DISSEMINATION

The project will make the NextBio materials widely available through a project website and will recruit teachers for participation. The project curriculum will be available as open source, and we will widely publicize the availability of the curriculum modules and virtual laboratory. As mentioned, the project materials will be available and promoted through the final, open-adoption phase of the project. This open phase will be publicized at national teacher conferences and through general media exposure. The teachers participating in the open adoption segment of the project will be important disseminators themselves, and surveys of these teachers will determine the most promising avenues to which to target further project dissemination. We will present research results in reviewed papers and conferences, and present regular progress reports in *@Concord*, a free, semi-annual newsletter with hard-copy circulation of 10,000.

## PROJECT ADVISORS

The project will have an Advisory Board, consisting of the following individuals, will meet annually to review project progress, research findings, and the report of the Project Evaluator.

**Lynn Margulis** is a biology researcher and Professor in the Department of Geosciences at the University of Massachusetts Amherst, who pioneered the theory of the origin of eukaryotic organelles. She is a member of the National Academy of Science, and a recipient of the National Medal of Science and the London Linnean Society's semi-centennial Darwin-Wallace Award.

**Brad Williamson** has taught high school biology for nearly 30 years. He is a past president of the National Association of Biology Teachers and a co-author (with Neil Campbell and Robin Heyden) of the popular textbook "Biology: Exploring Life."

**Malcolm Campbell** is a professor of biology at Davidson College and author of the textbook *Discovering Proteomics, Genomics and Bioinformatics*. He is senior editor of CBE-Life Sciences Education and Director of the Genome Consortium for Active Teaching (GCAT).

**M. Patricia Morse** is a biology researcher and science educator at the University of Washington, a former NSF officer, and a past president of Sigma Xi and the American Society of Zoology. She headed a critical review of biology textbooks for the AIBS.

**Gary Churchill** leads the Churchill Lab, a cutting-edge bioinformatics research group at the Jackson Laboratory. His lab has generated over 75 refereed publications in the past four years.

**Chris Dede** is the Timothy E. Wirth Professor in Learning Technologies at Harvard's Graduate School of Education. His scholarship includes emerging technologies, policy, and leadership.

**Tim Erickson** is a national educational consultant, writer and teacher in Oakland, CA, and PI of Simulating the Nature of Science (DMI-0441550) and Big Time Science (OII-0620590).

## RATIONALE

Although the promise of a virtual laboratory may initially seem to pale next to its physical counterpart, simulations and virtual laboratories have demonstrated significant success in aiding student learning and building science process skills—at times demonstrating more effectiveness than physical labs [63]. The Concord Consortium has a long track record of success in develop-

ing effective cyberlearning curricula similar to the NextBio project components and will draw upon this extensive experience base for the project [24, 28, 30, 64-66].

The time is to develop this project. With the ongoing AP Biology redesign scheduled for 2011 [67] and the possibility of national funding for school modernization on the horizon, biology teaching is primed for a paradigm shift and a move toward cyberlearning. Current curriculum projects are already demonstrating that students can learn leading-edge bioinformatics content through experimental methods, and the NextBio project aims to continue and expand this trend [68-70]. As described below, the NextBio project itself builds on work and partnerships from a successful ongoing high school application of cyberlearning to advanced bioinformatics (GENIQUEST, DRL-0733264).

The NextBio project's length is also vital to its success. The three-phase plan relies on an iterative three-year design and development phase followed by a two-year implementation testing phase integral to the project's research plan. The project's comparison study baseline and measurement of students across multiple-year course sequences demand the full, five-year timeline.

## EXPERTISE

This project will demand a unique mix of cutting-edge biological knowledge, curriculum design, professional development and technology expertise, and the team of organizations and individuals assembled for the work represent these areas with consistent depth and experience.

**The Concord Consortium** – The Concord Consortium has fifteen years of experience designing interactive curriculum for cyberlearning and a wide body of research to attest to its effectiveness.

**Dr. Frieda Reichsman**, Principal Investigator, will be responsible for the curriculum design and overall project quality and accuracy. She holds a Ph.D. in Molecular & Cellular Biology from the University of Massachusetts at Amherst. She has taught biochemistry and co-developed the “MyDNA” undergraduate course there for non-scientists, which is currently in its seventh year. Dr. Reichsman has designed hundreds of interactive 3D animations of DNA and protein structures that appear internationally in classrooms, research journals, and leading textbooks.

**Chad Dorsey**, Co-PI, will assist with project direction and coordinate the subaward efforts. He holds an M.A. in Physics from the University of Oregon, has taught middle and high school in Germany, Oregon and Maine, has led professional development and educational technology projects at the Maine Mathematics and Science Alliance, and is currently president of the Concord Consortium. He is co-author of a best-selling NSTA Press book of formative assessment probes.

**Stephen Bannasch**, Director of Technology, will support project technology and assist in materials development and delivery. Stephen graduated in 1982 with a B.A. from Hampshire College where his thesis involved designing a microcomputer-based monitoring system to measure the performance of an experimental passive-solar home. He pioneered with Bob Tinker hardware and software innovations now used in schools worldwide.

**Daniel Damelin** will help design and deliver the curriculum, materials, and workshops. He has extensive experience with inquiry activities and professional development, taught high school chemistry for 16 Years. He is PI for the Rhode Island Information Technology Experiences for Students and Teachers (RI-ITEST) project (ESI-0737649). Dan has an MAT in chemistry, biology and general science from Tufts and a triple-major BA including computer science.

**Amy Pallant** will be the Project Manager, coordinating the project's curriculum development, research, and evaluation. She has been the Project Manager and senior science education researcher on the MW projects and contributes to several other research studies at the Concord Consortium.

Amy has an M.A. in Science Education from Harvard, and has developed curriculum at EDC for Insights in Biology: High School Curriculum and the Improving Urban Middle Schools Project.

**Dr. Qian Xie** will be the primary computational scientist on the project, responsible for adding functionality to MW. Dr. Xie holds a Ph.D. in Materials Physics from University of Science and Technology, Beijing, and post-doctoral experience at the Max Planck Institute in Dresden and at the University of Cyprus. He has extensive experience in modeling both physical and biochemical systems. His most recent academic work has been computing electron transfer in biological molecules using the quantum mechanical algorithms that will be added to MW.

**BSCS** – The staff at BSCS head up project’s research and evaluation arm with some of the strongest biology curriculum development and research experience in the nation. BSCS has a fifty-year history of supporting innovation in biology education and upholding the integrity of science. Along with award-winning textbook series, BSCS has produced several notable curriculum modules on bioinformatics and DNA science that inform the work of the NextBio project.

**Dr. Chris Wilson**, lead NextBio researcher, has a Ph.D. in Science Education from Michigan State University and extensive experience in educational research.

**Dr. April Gardner** holds a Ph.D. in Biology Education from Purdue University and is co-author of numerous widely distributed biology textbooks.

**Dr. Hee-Sun Lee**, research consultant, is an Assistant Professor of Education Research at Tufts. She will assist BSCS staff in the creation and scoring of Knowledge Integration assessments.

**The Jackson Laboratory** – The Jackson Laboratory represents the cutting edge of mouse genetics research worldwide, and Gary Churchill’s research group applies new statistical methods to the genetics of health and disease, investigating complex disease-related traits in the mouse, improving gene expression analysis and establishing relational networks among mouse traits.

**Randy Von Smith** from the Churchill lab will lead the design of the NextBio dragon and drake genomes and assist in creating accurate overarching curriculum scenarios. Randy has extensive experience with integrating cutting-edge biological methods into high school instruction and is a Co-PI on the related ongoing DR-K12 GENIQUEST project.

**The Maine Mathematics and Science Alliance (MMSA)** – MMSA has led high quality professional development in mathematics and science nationwide over its twelve years, and currently leads the DR-K12 GENIQUEST project, a direct progenitor of the NextBio project.

**Dr. Jan Mokros**, MMSA Executive Director, has many years of experience in education research and professional development and will oversee NextBio work at MMSA.

**Joyce Tugel**, an experienced science teacher and professional developer with nationwide presenting experience, will design and direct professional development for the NextBio project.

**TERC** – TERC is an education research and development organization reaching over 3.5 million students in the US and abroad each year. Their evaluation staff brings a wealth of experience to the NextBio project, including experience evaluating bioinformatics education projects.

**Karen Mutch-Jones** will direct the NextBio evaluation work, and **Jim Hammerman** will operate as co-evaluator. Both have extensive evaluation experience at TERC and elsewhere.



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