EPiC Series in Education Science
Volume 3, 2020, Pages 188–199
Proceedings of the MIT LINC 2019 Conference

Choosing Your Own Adventure: Engaging the New Learning Society through Integrative Curriculum Design

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Abstract

In our increasingly data-driven society, it is critical for high school students to learn to integrate computational thinking with other disciplines in solving real world problems. To address this need for the life sciences in particular, we have developed the Bio-CS Bridge, a modular computational system coupled with curriculum integrating biology and computer science. Our transdisciplinary team comprises university and high school faculty and students with expertise in biology, computer science, and education. Our approach engages students and teachers in scientific practices using biological data that they can collect themselves, and computational tools that they help to design and implement, to address the real-world problem of pollinator decline. Our modular approach to high school curriculum design provides teachers with the educational flexibility to address national and statewide biology and computer science standards for a wide range of learner types. We are using a teacher-leader model to disseminate the Bio-CS Bridge, whose components will be freely available online.

1. Introduction to the need: integrating biological practices and computing approaches to teach students how to address real-world problems

Over the past decade, many leading scientific organizations have published reports emphasizing the need for fundamental change in the teaching of biology in order to better prepare students to solve complex real-world problems [1,2]. Perhaps the most influential of these was a report from the American Association for the Advancement

C. Urrea (ed.), LINC 2019 (EPiC Series in Education Science, vol. 3), pp. 188–199

of Science, ‘Vision and Change in Undergraduate Biology Education: A Call to Action’ [1]. The report emphasized the need for students to learn scientific practices, including the process and interdisciplinary nature of scientific discovery, communication and collaboration, quantitative data interpretation, and experience with modeling, simulation, and systems approaches to biology. The report stressed that computing and computational thinking are now integral to biological inquiry.

Many of these recommendations have received widespread support at the K-12 level. Research has shown that students are more engaged when they are involved in solving real-world problems they perceive to be important [3]. The curriculum becomes more relevant when there are connections between subjects rather than when they are taught in isolation [4]. In particular, if we want all STEM students to understand and utilize computational knowledge, approaches, and methodologies from computer science, it is critical to integrate or ‘bridge’ these across STEM curricula rather than teaching them in isolation in elective computer science classes [5].

The National Research Council (NRC) Framework for K-12 Science Education [6] reflects these ideas drawn from the scientific community. The vision for K-12 science and engineering education is that students

“…actively engage in scientific and engineering practices and apply crosscutting concepts to deepen their understanding of the core ideas in these fields. The learning experiences provided for students should engage them with fundamental questions about the world and with how scientists have investigated and found answers to those questions. Throughout grades K-12, students should have the opportunity to carry out scientific investigations and engineering design projects related to the disciplinary core ideas.”

The scientific and engineering practices referred to in the Framework include developing and using models, analyzing and interpreting data, mathematical and computational thinking, constructing explanations and designing solutions, and engaging in argument from evidence. The Massachusetts science standards, which teachers use in developing curricula, are an adaptation of the Next Generation Science Standards (NGSS) based on the NRC Framework; thus, many standards require integration of scientific practices, computing, and computational thinking [7]. However, it is difficult for educators to design and implement curricula that integrates scientific practices with computing and computational thinking, because they often have little understanding of the terminology, key concepts, tools and approaches that each side has to offer. We propose that fostering interactions among biology (Bio) and computer science (CS) educators and students is critical for developing highly effective Bio-CS integrated curricula, which will in turn provide students with an interdisciplinary approach to solving complex real-world problems.

1.1 Our approach: transdisciplinary modular curriculum design

To create effective Bio-CS curricula, we have assembled a team comprised of university faculty and high school teachers with expertise in Biology, Computer Science, and Education, as well as graduate, undergraduate and high school students. Biology and Computer Science members of the team are providing a conceptual framework that fully integrates biological concepts with computational tools, which is then translated by Education members into a standards-based, modular curriculum. Teachers can then select curriculum modules best suited for the range of learner types in their classroom, or 'choose their own adventure'. For example, biology teachers can select modules containing computational tools that will enable students to model natural phenomena and test hypotheses, while computer science teachers can select modules containing biological questions to guide the design of such tools. We use our own research work on pollinator decline and biodiversity conservation as a motivating biological problem.

Here, we introduce our Bio-CS Bridge conceptual framework and computational system, and describe components of our modular curriculum developed thus far, as well as our plans for assessing and disseminating the Bio-CS Bridge System.

1.2 The motivating biological problem: pollinator ecology and conservation

Over the past decade, pollinators have experienced unprecedented worldwide declines in species abundance and geographic distribution for unknown reasons [8]. These declines pose a significant threat to agricultural productivity, biodiversity, and ecosystem health due to the important role that pollinators play in the reproduction of crop and wild plants [9]. Pollinator decline therefore represents a complex real-world global biological problem. Although the cause of pollinator decline is currently unknown, human-introduced environmental stressors such as pesticides, habitat destruction, disease, exotic species, and climate change are hypothesized to be significant contributing factors [10]. However, we presently lack knowledge of wild pollinator ecology needed to identify which of these factors are actually driving population decline.

In order to design effective pollinator conservation strategies for threatened species, and therefore prevent a global ecological catastrophe, it is imperative that we collect, analyze and interpret data on native pollinator-plant interactions in the wild. Our Bio-CS Bridge will foster the development of these important skills in teachers and students through the use of a computational system and agent-based simulations designed specifically for the study of bumblebees, an important pollinator group in North America with wild populations of many species in rapid decline. Through the Bio-CS bridging process, students will also acquire the skills to apply and integrate a computational approach to address other scientific problems that they will encounter throughout their lives.

2. Methods: Our ecologically-inspired modular computational system

Next generation science learning standards place particular emphasis on the scientific practices of collecting, analyzing, and interpreting data, and developing and using models and computational approaches. To facilitate the implementation of these key features of the scientific inquiry into the classroom, we have created a computational system comprised of several interconnected components (Figure 1). Our system can be used to gather and visualize data on bumblebee-flower interactions and to model this ecological system to study pollinator decline. The system also has the flexibility to serve a larger role, as a model to teach students how to integrate biological approaches and computational thinking to solve any complex scientific problem.

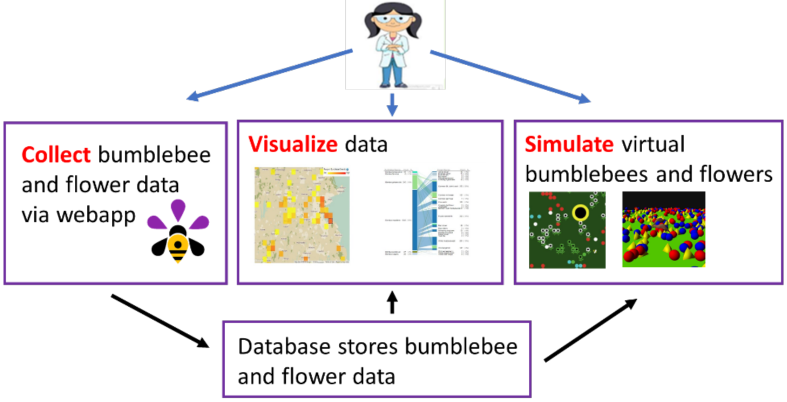
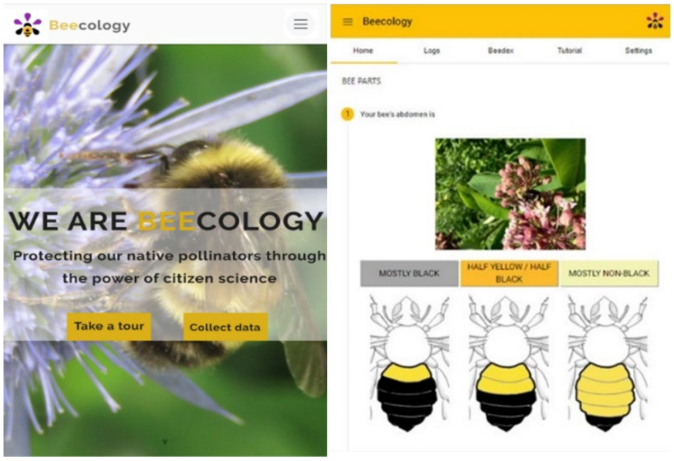


Figure 1. Overview of the Bio-CS Bridge Computational System.

All the components of our system have been developed using modular design to enable students to easily understand the source code and learn best software development practices, as well to adapt, modify and/or extend the source code to apply it to other scientific problems. Two websites provide central locations for students and teachers to find and interact with the computational system (beecology.wpi.edu) as well as acquire educational resources related to our Bio-CS curriculum (biocsbridge.wpi.edu).

2.1 Gathering field data via the webapp

Our webapp enables users to upload pictures or videos that they have taken of a bumblebee-plant species interaction in the wild (Figure 2). The webapp implements a bee identification algorithm analogous to a dichotomous key that guides users through the process of identifying which out of eleven species historically present in New England the bee belongs to and whether it is a worker or male (sex). This identification process is based on species- and sex-specific coloration patterns of the abdomen, thorax and head of the bee. Once the bumblebee has been identified, the webapp asks the user to input information on the plant species that the bee was visiting (flower color, shape and tube length) as well as the behavior of the bee (nectar versus pollen foraging). Bee-plant information is then stored locally and transferred to our central database together with date and location information. For biology teachers, the webapp is a computational tool that allows students to gather and store critically needed biological data.



Protecting our native pollinators through the power of citizen science

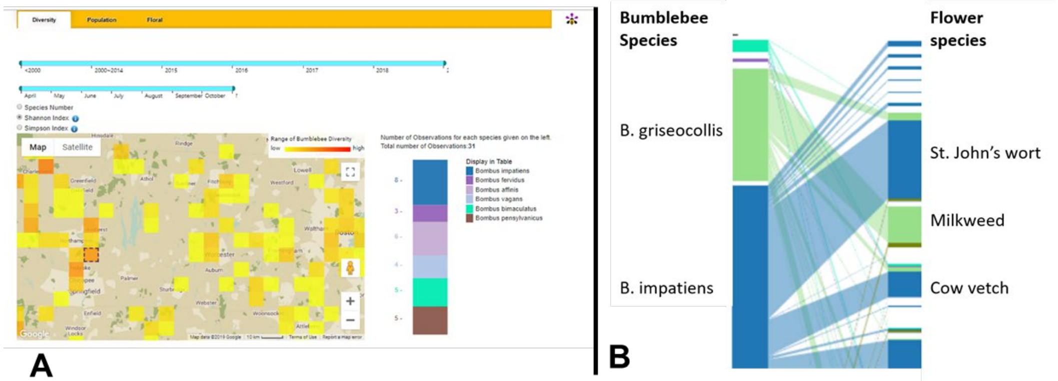
Your bee's abdomen is

Figure 2. Our webapp enables data collection of bumblebee-flower species interactions

For computer science teachers, the webapp represents the solution to a biologically-based design problem (crowdsourcing the collection and storage of data). We implemented the webapp using the Angular platform [11] so that the webapp can run on a wide range of devices (mobile phones, tablets, laptops and desktop computers) and operating systems (Android, iOS, Windows, Mac OS). We used a modular design for our webapp in order to facilitate the development of curricula for high school computer science classes while demonstrating good programming practices to students. Students are also able to practice implementing individual modules of the webapp, at different levels of complexity as appropriate for the course level. The modularity of the webapp enables it to be easily extensible, as students can implement new modules that add functionality to the webapp. Furthermore, students can use the modules from this app and modify them as needed to construct a webapp for a different biological or scientific problem.

2.2 Testing hypotheses/analyzing data via visualization tools

Our webapp (see section 2.1) was developed to allow teachers and students from across the state to collect and submit field data to our central database, where it is integrated and combined with data from citizen scientists, research labs, and museum archives. However, the development of biology curricula focused on the analysis and interpretation of data requires that this wealth of information be easily accessed by users and displayed in a way that is scientifically meaningful. For example, to test for potential effects of agricultural intensification on bumblebee diversity, users need a way to display and visually compare historical and current data on species abundance. To facilitate this process, we have developed a web-based visualization tool that enables a wide range of ecological information from our database to be viewed and manipulated by users (Figure 3).



Number of Observations for each species given on the left.
Total number of Observations:31

Figure 3. Our web-based visualization tool. A, Bumblebee biodiversity across Massachusetts. B, Bipartite graph showing bumblebee-flower relationships.

Elements of this tool include:

1) Diversity: Users view a map of Massachusetts showing the composition of bumblebee communities at different locations (Figure 3, panel A). Sliders enable users to view species compositions at specific time intervals (ranges of years or months within a year). After selecting specific time and location information, users are presented with a stacked bar graph showing the actual number of different species.

2) Population: Users view information on bumblebee species: Location (display of species abundances on a map of Massachusetts), Season (display of species abundance from May-October on a line graph), and Summary (display of observation frequency at specific year-month combinations on a heat graph).

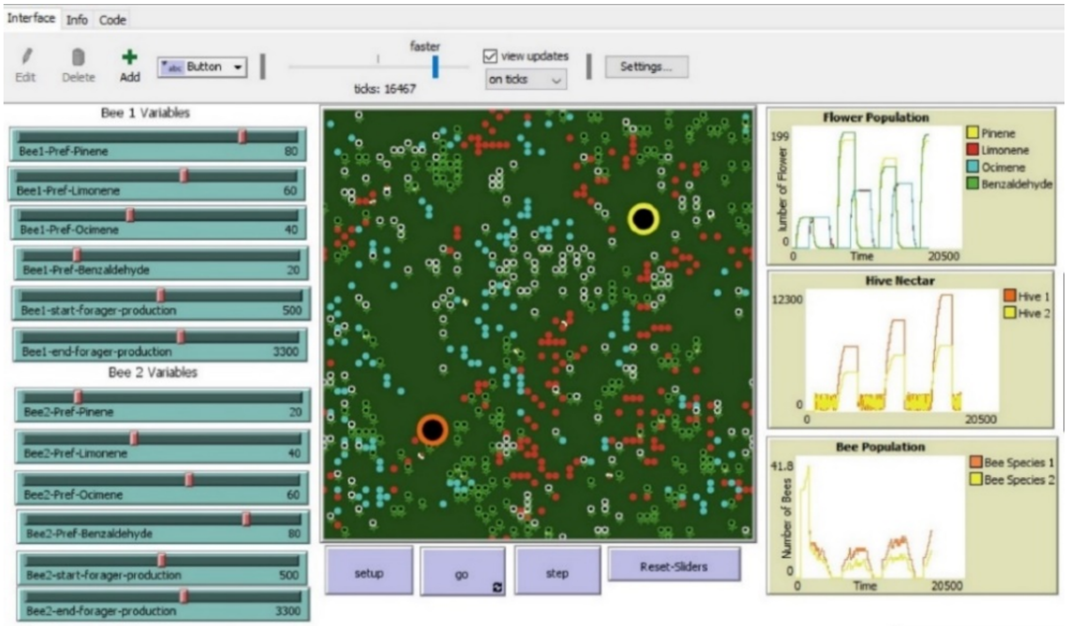
3) Floral: Users view bumblebee-plant species interactions on a bipartite graph (Figure 3, panel B). Filters allow users to view interactions based on specific behavioral traits (pollen versus nectar foraging, tongue length, and gender) and floral traits (color and tube length). In this way, students can explore questions about the structure and diversity of bumblebee pollination systems such as 'Do threatened species have more specialized floral needs than common species?' and 'Do male and female bumblebees differ in their floral preferences?'.

2.3 Simulating ecological systems using agent-based models

Computational modeling, simulation, and systems thinking are key scientific practices that students and teachers typically have little experience using. Agent-based models are intuitive to biologists, and allow a gentle and engaging introduction to computational thinking and approaches. In our 'SimBeecology' models, the basic agents are bumblebees and flowers, which are each programmed to follow rules based on known or hypothesized biology. Each individual agent can have its own attributes, such as memory (bee) or nectar level (flower), and as is true in real bumblebee pollination systems, local interactions among agents are key to the behavior of the system as a whole. Students can use these models to test hypotheses by choosing particular starting conditions, running the model, generating data, and then analyzing and comparing predictions. The models are modular, and can also be modified to allow students to address questions of interest to them. We have developed models using both the block-based StarLogo Nova [12] and text-based NetLogo [13] platforms. Because these platforms are high level languages, students can also learn to design and implement their own simulations.

Our Netlogo 'Blooms' model allows students to use some of the data in the Beecology database to make predictions about what might occur if a stable ecological system were subjected to a stress, such as climate change or an invasive species (Figure 4). Students can set conditions in the simulation to mirror the preferences of two simulated bumblebee species for four flower species, and choose appropriate floral bloom times and bumblebee phenology (life cycle timing) based on data in the database. By running the simulation for multiple 'years' under various conditions, students can assess the long term effects of human-induced changes on floral and bumblebee populations, and the influence of exotic species on ecosystem function and biodiversity.

Building their own simulations can be even more valuable to students than simply using existing ones, because it forces them to translate what they know about a biological system into behavioral rules that can be encoded into a program [14]. Because all models are simplifications of a system, students must reflect on what they expect will be the most important system components to include in a model, in order to capture the essential features of the system. The ultimate goal is to engage students in the 'simulation cycle': build a simple model; generate predictions by running the model; compare the predictions to actual data; and modify the model to better match the data [15]. Through engaging in this process, students generate a deep understanding of the biological system they are modeling. They learn that modeling is an ongoing process that seeks to build increasingly better and more useful representations of biological systems.



Bee 1 Variables

Bee1-Pref-Pinene 80

Bee1-Pref-Limonene 60

Bee1-Pref-Ocimene 40

Bee1-Pref-Benzaldehyde 20

Bee1-start-forager-production 500

Bee1-end-forager-production 3300

Bee 2 Variables

Bee2-Pref-Pinene 20

Bee2-Pref-Limonene 40

Bee2-Pref-Ocimene 60

Bee2-Pref-Benzaldehyde 80

Bee2-start-forager-production 500

Bee2-end-forager-production 3300

Figure 4. 'Blooms' agent-based model allows students to make predictions about the consequences of ecological stresses. Interface at center shows bees moving from flower to flower gathering nectar. Orange and yellow doughnuts represent bumblebee hives; colored dots represent seeds; colored flowers represent flowers in bloom. Sliders at left allow students to set bee preferences for floral species; additional sliders allow setting floral bloom times (not shown). Graphs at right display data on bee and flower populations, as well as nectar gathered; data can be downloaded for analysis. Model generated using the Netlogo platform [13].

3. Results: Initial curriculum design, implementation, assessment, and dissemination

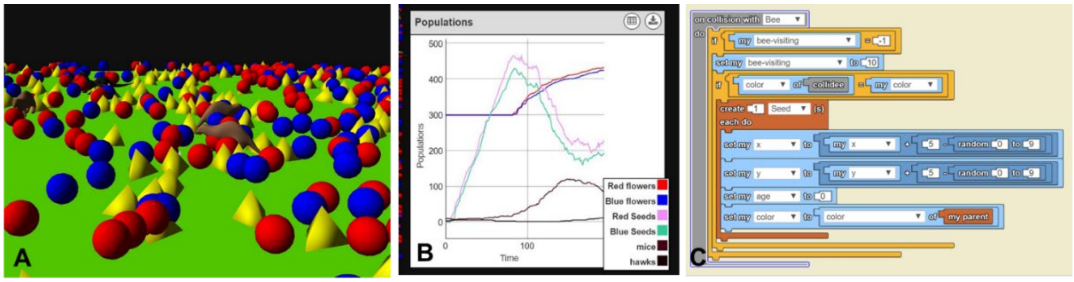
Curriculum using the Bio-CS Bridge System has been developed by our biology and computer science high school faculty team members following their participation in the initial Bio-CS Bridge Summer Institute (July 2018). These teacher-leaders, who are two teams of biology and computer science teachers from two local high schools, piloted the curriculum during the academic year 2018 – 2019. We have created a modular format for each curricular unit, linking each set of lessons to biology and computer science standards. We have developed detailed tutorials to introduce software tools to both teachers and students with varying levels of expertise. This will enable teachers to select Bio-CS modules most appropriate for their students. Following a teacher-leader model, our initial teacher teams (the teacher-leaders) trained nine teacher integrators on the curriculum in the Bio-CS Bridge Summer Institute (July 2019). Both the teacher-leaders and the teacher-integrators will implement the curriculum in their classrooms during academic year 2019-2020. We will evaluate the effectiveness of the curriculum through assessments addressing student content and practice metrics, as well as teacher knowledge and leadership metrics [16]. Both our computational system and the curriculum itself will be freely available online on our website.

3.1 Case study: Using agent-based modelling to demonstrate the effects of pollinator decline on ecosystem function and biodiversity

To illustrate how our curriculum works to bridge the fields of biology and computer science in the classroom, we provide a summary of the bumblebee-inspired ecological web curricular module that has been used by our teacher-leaders in both introductory biology and computer science classes (9th grade students). In the biology classroom, students use our existing simulation to test hypotheses, while in the computer science classroom, the model is used as a basis from which students design and implement their own extensions. In both classrooms, teachers can choose supporting material as needed, including bumblebee background slides and exercises, as well as tutorials to introduce students to programming using StarLogo. Our modular curriculum is designed to encourage the melting of artificial borders between biology and computer science. Biology teachers who want their students to actually build simulations can guide them to do so; and computer science teachers who want their students to better understand the biological system they are modeling have the resources to help them.

High school biology and computer science standards addressed by the ecological web module include:
Biology Standard: HS-LS2-2. Use mathematical representations to support explanations that biotic and abiotic factors affect biodiversity, including genetic diversity within a population and species diversity within an ecosystem. [7]
Computer Science Standard: Modeling and Simulation [9-12.CT.e]. Create models and simulations to help formulate, test, and refine hypotheses. [17]

The ecological web module introduces bumblebee pollinators as 'keystone species' that are necessary to support flower pollination and reproduction, as well as supporting higher trophic levels in the food web through the cascading products of pollination events (food, shelter, nest sites). The agents in the simulation that supports the module include bumblebees, flowers, seeds, mice, and hawks (Figure 5). The simulation is simple but engaging, and utilizes both the 2-D and 3-D functionality of StarLogo Nova [12]. This block-based platform is appealing to beginning programmers; commands can be dragged out of 'drawers' rather than needing to be memorized, and syntax errors are impossible to make, since the blocks of code 'click' together (Figure 5, panel C). Despite its simplicity, StarLogo Nova allows the introduction of many fundamental computational principles, including modularity of design, and can produce surprisingly powerful simulations.



```
on collision with Bee
do
  if my bee-visiting = -1
    set my bee-visiting to 10
    if color of collidee = my color
      create 1 Seed (s)
      each do
        set my x to my x + 5 - random 0 to 9
        set my y to my y + 5 - random 0 to 9
        set my age to 0
        set my color to color of my parent
```

Figure 5. Bumblebees as keystone species: modeling an ecological web.

A, StarLogo 3-D view of the simulation. Yellow pyramids represent bumblebees; red and yellow spheres represent flowers in bloom; brown animals represent mice. Seeds and hawks not shown. B, StarLogo graph showing population changes over time as the model runs. Note that seed populations (pink and green lines) fall as mice populations (brown lines) 'eat' the seeds. Flower populations (red and blue lines) increase as seeds that are not eaten become flowers. C, StarLogo block-based code [12].

The module begins with a brief introduction to pollinator-plant interactions ('Bumblebees 101'). The class then brainstorms the key features of the biology they have just learned that would need to be represented in any model of the system. Students discuss how to translate these features into behavioral rules that agents in the model would need to carry out. For example, bees should collect nectar and pollen from flowers, and flowers should make seeds only if pollinated by pollen from their own species. Following a self-guiding tutorial, students next run and observe our existing simulation. Using what they have just learned, they determine that each agent type is functioning appropriately in the model (bees forage on and pollinate flowers; flowers produce seeds only if correctly pollinated; mice eat seeds; hawks each mice). Students then run *in silico* experiments using the simulation; they collect the numbers of each species that are present in the simulation after it has run for a standard length of time, starting with default numbers of bees, flowers, mice, and hawks. Students are instructed to run the simulation through multiple experiments using the same initial conditions. They learn that just as in real-world experiments, there is variability in the output from each simulation run, so multiple experiments are required to compare different conditions.

Most students notice that with the default values given, there are usually no hawks remaining at the end of the simulation, even though there are plenty of mice. Why is this? If they have watched the simulation carefully, they will realize that the hawks die off early, because there are not enough mice to support them initially. Students are asked to come up with a hypothesis to test using the simulation, and many of them want to create a situation that will support more hawks in the system. Should they begin the experiment with more hawks? More mice? More bees? More flowers? In the process of making predictions and generating data to test their hypothesis, they discover (often to their surprise) that the number of bumblebees in the system – the keystone species -- is critical to the number of hawks that can survive.

Although students may understand superficially how food webs work before working with the simulation, by the end of the lesson, they have more deeply understood the biology. They have thought about how to design a simulation, and they have seen how useful the model is in representing the biology and allowing them to do *in silico* experiments and make predictions. In addition, they have done some data collection and analysis and observed the importance of replication and reproducibility. In classrooms where teachers want students to construct their own models, they now have a basis on which to build.

3.2 Next steps: Implementation and Assessment

We recruited nine Massachusetts high school teachers (four biology, five computer science) to our Summer Institute in July, 2019. Three sets of teachers are biology/computer science teams from three high schools, while the remaining four are individual teachers from different schools. The Summer Institute was led by our teacher-leaders and served to introduce teacher integrators to our Bridge computational tools and curriculum. Teacher integrators will implement at least two of the Bridge curricular modules in at least two of their classes in academic year 2019-2020 and will participate in follow-up meetings during the year, as well as a weeklong workshop in the summer of 2020 to evaluate and finalize the curriculum.

Evaluations of student attitudes towards STEM and computer science were developed by our external evaluator based on existing, validated surveys [18]. Initial assessments of scientific and computational content and practices for each curricular module were developed by our teacher-leaders. These assessment and evaluation instruments will will be administered by all teachers to their classes in academic year 2019-2020. Evaluations of teacher belief in their ability to use an integrated modular curriculum to embed computational thinking in biology was measured with a pre/post administration of an adapted version of an existing instrument [19] during the Institute and showed a large gain in confidence for most teachers. The quality, focus, and transferability of the developed modular curriculum itself will be assessed using the *STEM Education Quality Framework* developed by the Dayton Regional STEM Center as an observational tool [20].

4. Conclusions

To address the need for integrated curricula to prepare students to solve complex biological problems using computational thinking, we have developed and implemented the Bio-CS Bridge. The integrated Bridge curriculum addresses standards from the Massachusetts Curriculum Frameworks and ensures that rigorous, inquiry-based science is introduced to high school students. The modularity of both the system and the curriculum will allow it to be adapted to address other biological problems, and address many levels of biology and computer science classroom implementation, from introductory to advanced classrooms. Our ongoing teacher-led Bio-CS Summer Institutes combined with freely available online access of the software system and curriculum will ensure its dissemination to many school systems.

5. Acknowledgements

This paper is based upon work supported by the National Science Foundation under Grant No. 1742446. Any opinions, findings, and conclusions or recommendations expressed in this paper are those of the authors and do not necessarily reflect the views of the National Science Foundation. We gratefully acknowledge the curricular work of our teacher-leaders: Ronald Cochran, Jennifer Field, Jennifer Hardy, and Johanna vanderSpek.

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