Analysis of Co-designed Biology Units Integrated with Computational Thinking Activities

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Abstract: To support student learning of Computational Thinking (CT) in disciplinary contexts, it is important that teachers have agency and ownership in the design process of creating curricula. We conducted a 4-week-long summer institute for teachers to co-design CT-integrated high school science units. Our approach to CT integration into Science and Mathematics contexts is based on a *taxonomy-of-practices* of CT in Science and Mathematics professional contexts. The co-design teams in our summer institute used a version of this taxonomy to create CT-integrated lessons. In this paper, we analyze two co-designed biology units to characterize CT integration in these lessons using the new taxonomy. The results illustrate various types of activities and questions developed as a way to promote student engagement in CT practices in the disciplinary context. Findings yield implications for CT integration in disciplinary contexts as well as co-design of CT-integrated units based on a *taxonomy-of-practices*.

Keywords: computational thinking, practices, taxonomy, co-design, science education

Introduction

As computing becomes ubiquitous in science, technology, engineering, and mathematics (STEM) fields and society, researchers and educators have argued that it is crucial to build foundational Computational Thinking (CT) and literacy skills in K-12 settings (Wing, 2006; Grover & Pea, 2013; Wilensky et al., 2014). In our work, we integrate computational thinking (CT) into mathematics and core science courses because: (1) Unlike elective computer science courses offered in high school, the integration of CT into science courses ensures all students engage in CT and build computational literacy, addressing issues of underrepresentation and self-selection in computing fields (Wilensky et al., 2014); (2) The integration of CT into science and mathematics can support deeper learning of the science content (e.g., Levy & Wilensky, 2009); (3) With such integration, students can learn authentic disciplinary practices recommended by the Next Generation Science Standards (NGSS) (NGSS Lead States, 2013; Dabholkar et al., 2020).

Inviting teachers to be design partners of new units has increased teacher ownership of curricular changes and supported appropriate pedagogical shifts (Kyza & Georgiou, 2014). In order to design CT-integrated curricular units, we partnered with high school science and mathematics teachers. We conducted a 4-week-long summer institute to co-design units with newly designed computational tools and pedagogical activities to support learning. Our co-design approach foregrounded teachers' views on how the curriculum aligns with learning objectives, teaching strategies, and expectations for student learning (Severance et al., 2016). In this paper, we analyze two co-designed biology units to characterize CT integration in a disciplinary context.

Theoretical framework

Prior work defined a taxonomy of CT practices in the context of science and math that includes modeling and simulation, data, problem solving, and systems thinking practices (Weintrop et al., 2016). Our team has used this *taxonomy-of-practices* to design and co-design CT-integrated science and math units over the past several years, resulting in several important outcomes for student learning (e.g., Arastoopour Irgens et al., 2020) and teacher learning and attitudes (Peel et al., 2020; Wu et al., 2020). Based on our experiences, a new version of the *taxonomy-of-practices* (ToP 2.0) is currently in development that represents a wider set of CT practices that we feel the original taxonomy did not include or did not give enough attention to (Peel et al., 2021). An initial beta version of the new taxonomy was piloted in this project. There are six practice categories in the CT-ToP2.0-beta: *computational modeling and simulation, computational data, computational visualization, algorithms, computational problem-solving,* and *programming*. The CT-ToP2.0-beta was used as a framework to integrate in science and mathematics curricular units. This paper uses the CT-ToP2.0-beta to frame our analysis of two co-designed biology units. The following research question guided the analysis: *How were CT practices integrated into co-designed biology units?*

Research and co-design context

Our team worked with 11 teachers in summer 2020 during a 4-week summer institute. Due to COVID-19 regulations, the summer institute was held remotely. Teachers learned about CT integration and pedagogy by engaging as learners in the first week of the summer institute. The following three weeks were used to co-design new CT-integrated science and math units. Each teacher, or pair of teachers, partnered with a member of the research team to co-design CT-integrated units and computational tools to support student engagement in CT practices and learning of science/math content. Teachers read a Google Slides presentation that introduced them to the CT practices. They were then asked to read a document with descriptions and curricular examples of each practice category.

CT-STEM website and Biology units

The curricular units developed in the summer institute are hosted on a website that facilitates curricular design and use in classrooms (https://ct-stem.northwestern.edu). Each curricular unit consists of several lessons, and each lesson has multiple pages containing questions that prompt student engagement. Lesson pages can include embedded computational tools (Figure 1). For example, Figure 1A shows a computational model embedded in the lesson titled: *How do the instructions to make proteins work?* The students are asked to explore the model and note the observations they find interesting. The follow-up questions on the subsequent pages provide scaffolding to support student learning of specific biological aspects regarding the process of DNA replication and transcription.

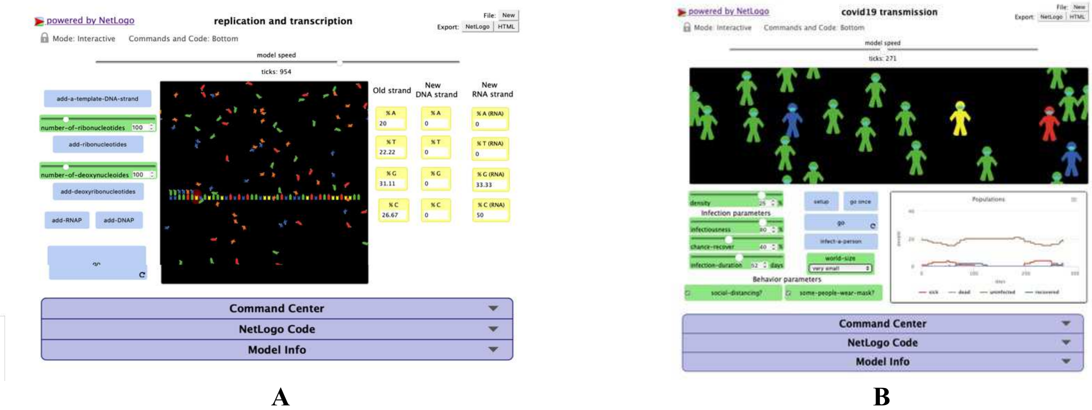

Figure 1. A screenshot of embedded computational models in lessons in CT-STEM website

The two co-designed biology units that we analyze in this paper were about the Central Dogma and Covid-19 transmission. The Central Dogma unit, of the lead-co-designer teacher Ms. Kate (pseudonym), has computational activities that engage students in learning about Central Dogma. The second biology unit about Covid-19 transmission, of the lead-co-designer teacher Ms. Sara (pseudonym), is designed for student to use computational models for learning about transmission of COVID-19, focusing on the infectiousness of the virus and behavior of people.

Methods

We created a codebook to code questions in the lessons for taxonomy 2.0-beta categories. It contains the explanations and examples of each code. We coded 272 questions from 16 lessons in the two biology units. If a question prompted students to engage in multiple categories of practices, it was coded positive for all the categories. Author 1, 2, and 3 were involved in coding. Cohen's *Kappa* was used to determine interrater reliability. *Kappa* > 0.75 was considered as a cut-off. To characterize the units in terms of CT practice integration, we calculated percentage integration for each of the practices. To further characterize the how the practices were integrated in the lessons, we calculated the extent of integration (density) and presence of different types of CT practices (variety) for each page. We calculated Density and Variety scores using the following formulas: Density = total number of practice codes / total number of questions; Variety = practice categories coded / total number of practice categories.

Analysis and findings

In this section, we first present analysis of the units in terms of integration of CT practices. Then we discuss a page that has high density and variety of CT practices as an illustrative example of CT integration.

CT practices integration

Computational modeling and simulation practices were most prominently integrated in the lessons (Figure 2). *Computational visualization practices* and *Computational data practices* have more than 10% integration. Though this claim needs to be substantiated on the basis of student responses to the questions, we expect that minimum of 10% integration is needed for each category to provide adequate exposure. We used density and variety scores to identify high CT integration pages, one of which is discussed below to illustrate integration of the CT practices.

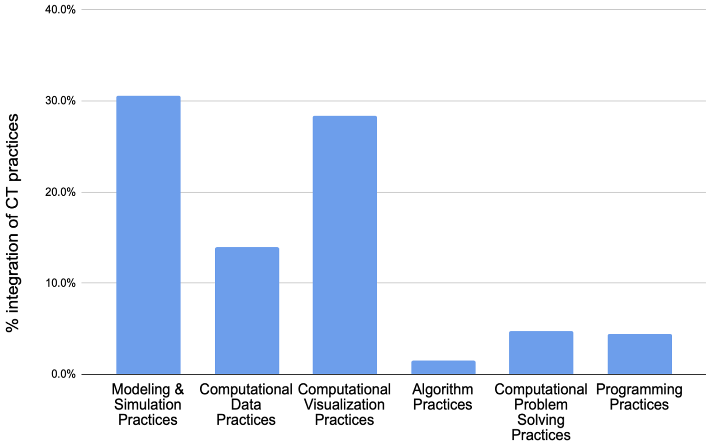

Figure 2. Percentage integration of CT practices in the biology units

An illustrative example of CT integration

We used density and variety metrics to identify pages that have high CT integration. We present qualitative analysis of CT integration in Page 3, 4 and 5 of lesson 5, of the Central Dogma unit (density score > 1 and variety score => 0.5) to illustrate how CT-ToP2.0 -beta practices were integrated. Lesson 5 was designed for students to understand the underlying biological processes that result in differences in hair color. In this lesson, students use a computational model built in NetLogo (Wilensky, 1999) (See Figure 1A). It is a test tube model of DNA replication and transcription. In this model, students can add appropriate 'ingredients' computationally and observe the outcomes. After students were asked to explore the model and make observations, to understand the processes and the functions of various macromolecules (e.g., DNA polymerase). Kate and her team designed these questions for students to use a *computational visualization* of a manipulable process in a scaffolded manner to engage in *computational modeling and simulation*. The model shows percentages of bases on the old DNA strand and the new strand. The questions ask students to make qualitative observations and collect qualitative data regarding the process of DNA replications. On the next page, students are asked to more systematically engage in *computational data practices* by performing trials and collecting data to identify a pattern regarding DNA replication (Chargaff's law).

On page 6, students are asked *to make RNA based on a DNA template.* This requires students to think about how to use a computational tool by providing appropriate inputs to generate a desired output. This requires them to engage in *computational problem solving practices*. This page has a model that has an intentionally placed bug. After students engage in *computational problem solving*, they are asked to identify a bug in the model. They are asked to engage in *programming practices* by modifying the program to fix the bug.

Discussion and implications

Integration of CT practices in disciplinary contexts serves two reciprocal purposes: (1) CT practices can have pedagogical value for learning the disciplinary content; (2) Disciplinary contexts can provide rich ways to engage in CT practices. Different levels of engagement in CT practices in disciplinary contexts can be thought of as a spectrum of sophistication. In disciplinary contexts less sophisticated practices, such as changing model parameters and observing the effects, are of pedagogical value whereas the disciplinary context provides ways for engaging in more sophisticated practices, such as understanding algorithmic logic in a model and modifying it. The example activities discussed in the results section demonstrate the co-design team's intentions of engaging students across the full range of sophistication to support the learning of key disciplinary ideas regarding DNA replication and RNA synthesis and then using the context to engage students in understanding programming and debugging.

The co-design approach for CT integration into these units was predominantly based on co-designing computational models and then using those models to engage in other CT activities. It is possible that the practices more prominently present in the lessons are due to the nature of the computational tool, NetLogo (Wilensky, 1999), that was used for CT integration. NetLogo is a highly effective modeling platform that allows easy creation of computational visualization of phenomena, performing multiple experimental trials and collecting data. In addition, the NetLogo code can be easily accessed, read and manipulated to debug and extend computational models. These affordances of the NetLogo environment open possibilities for integration of the full range of CT practices at all levels of sophistication. However, we anticipate that such wholistic intertwining of CT practices with a model-centered CT integration approach would require more intentionality in the co-design process. Even though new practices such as algorithm and programming practices were not present in high density, the addition of these practices in the taxonomy possibly resulted in the design of activities about understanding and modifying the code and writing algorithms for understanding computational aspects of biological processes. Our other work has demonstrated that sophistication and variety in CT integration can increase through the co-design experience of teachers over a couple of years (Peel et al., 2020). We anticipate more variety and sophistication in future units designed by these teachers.

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