LEARNING BIOLOGICAL EVOLUTION
THROUGH COMPUTATIONAL THINKING

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ABSTRACT

Computational thinking is a contemporary mathematical and engineering concept that has been introduced to US science classrooms due to its emphasis within the *Next Generation Science Standards* (NGSS Lead States, 2013), yet it stands with no clear definition nor explicit methods for inclusion. Because biological evolution, an essential theory within biology, spans across temporal and organizational scales (Aho, 2012), computational thinking may facilitate evolution learning (Wilensky & Reisman, 2006), specifically by overcoming misconceptions, reinforcing the nature of science (NOS), and allowing student embodiment (as students become emerged in their models, i.e., personification; Weinthrop et. al. 2016). The complex nature of both teaching computational thinking and biological evolution lends toward the need for a learning progression that identifies the instructional context, computational product and computational process and spans from simple to complex (as modified from Berland & McNeill, 2010). I developed and present an appropriate learning progression that outlines biological evolution learning coupled with computational thinking. The defined components of computational thinking (input, integration, output and feedback) are coupled with biology student roles. Two major themes of biological evolution, unity and diversity have each been paired with both computational thinking and specific corresponding NGSS standards at levels of increasing complexity. To investigate the effectiveness of the learning progression, I developed and conducted a quasi-experimental research design study.

I designed two learning experiences (interventions) which merged computation and biological evolution content based on AP biology laboratory lessons (College Board,
I also developed two instruments for use in the study, one to assess computational knowledge and the other to assess biological evolution knowledge across scales. I measured knowledge gains in both biological evolution and computational thinking quantitatively and explored participant use of biological levels of organization and computational complexity through qualitative analysis of participant artifacts. The quantitative and qualitative results of the study support the argument to include computational thinking into biological evolution knowledge instruction. Knowledge gains differed between the two interventions indicating that one intervention was significantly more successful in learning both biological evolution and computational thinking. Students who made biological level connections across scales (spanning from the micro to the macro levels) also had significantly greater gains in biological knowledge. Considering the results collectively, computational thinking deserves a much greater emphasis within biology classrooms. There are virtually no previous studies which relate computation and evolution across scales and the present study paved the way for questions of importance, support, benefits and overall student achievement in relation to the advancement of science in education.
This work is dedicated to my Grandma Carol, in remembrance of her beautiful spirit.  
I am grateful for her unconditional love and support throughout my life. Although she was not physically with us during my research journey, she continued to be a constant positive light, illuminating what I so often could not see in myself. She genuinely encouraged me to pursue my passions and to advocate for what I believe in. She was always excited to hear about my life experiences, no matter how trivial. I can only hope to instill this feeling in others in the ways that she did for me. I have grown so much and continue to because of you. Thank You for your love and acceptance as it still encourages me today.
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# TABLE OF CONTENTS

<table>
<thead>
<tr>
<th>Chapter</th>
<th>Title</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>ABSTRACT</td>
<td>iii</td>
</tr>
<tr>
<td></td>
<td>DEDICATION</td>
<td>v</td>
</tr>
<tr>
<td></td>
<td>ACKNOWLEDGEMENTS</td>
<td>vi</td>
</tr>
<tr>
<td></td>
<td>LIST OF TABLES</td>
<td>xiii</td>
</tr>
<tr>
<td></td>
<td>LIST OF FIGURES</td>
<td>xiv</td>
</tr>
<tr>
<td>1.</td>
<td>INTRODUCTION</td>
<td>1</td>
</tr>
<tr>
<td></td>
<td>Problem</td>
<td>1</td>
</tr>
<tr>
<td></td>
<td>Purpose</td>
<td>6</td>
</tr>
<tr>
<td></td>
<td>Research Questions</td>
<td>8</td>
</tr>
<tr>
<td></td>
<td>Significance</td>
<td>10</td>
</tr>
<tr>
<td></td>
<td>Definition of Terms</td>
<td>14</td>
</tr>
<tr>
<td></td>
<td>Organization of Dissertation</td>
<td>20</td>
</tr>
<tr>
<td>2.</td>
<td>LITERATURE REVIEW</td>
<td>22</td>
</tr>
<tr>
<td></td>
<td>Background</td>
<td>22</td>
</tr>
<tr>
<td></td>
<td>Theoretical Framework</td>
<td>29</td>
</tr>
<tr>
<td></td>
<td>Learning About Biological Evolution</td>
<td>29</td>
</tr>
<tr>
<td></td>
<td>Misconceptions About Evolution and Conceptual Change</td>
<td>31</td>
</tr>
<tr>
<td></td>
<td>Social and Emotional Aspects of Evolution Learning</td>
<td>35</td>
</tr>
</tbody>
</table>
3. METHODOLOGY ........................................................................................................88

Setting and Participants..............................................................................................87

Setting .......................................................................................................................87

The Pine Bay School District .....................................................................................87

The East High School .................................................................................................87

The West High School .................................................................................................88

AP Students within the Pine Bay District .................................................................89

Participants ...............................................................................................................92

Class Format ..............................................................................................................91

Experimental Design .................................................................................................91

Study Materials .........................................................................................................96

Data Collection Instruments .....................................................................................96

  Biological Evolution Content Knowledge

  Instrument (BECKI) ...............................................................................................96

  Computational Thinking Content Knowledge

  Survey (CTCKS) ....................................................................................................99

Interventions ............................................................................................................103

  Intervention 1: Hardy-Weinberg Activity .............................................................104

  Intervention 2: Phylogenetic Tree Activity ..........................................................106

Pilot Study .................................................................................................................107

Procedures ...............................................................................................................111

  Week One ..............................................................................................................113

  Week Two .............................................................................................................114
Week Three .................................................................................................................. 115
Week Four .................................................................................................................... 117
Data Analysis ................................................................................................................ 117
Preliminary Analysis ..................................................................................................... 117
Analyses for Research Questions ................................................................................. 118
  Research Question 1 .................................................................................................... 118
  Research Question 2 .................................................................................................... 118
  Research Question 3 .................................................................................................... 120
4. RESULTS AND ANALYSES ..................................................................................... 122
  Participants .................................................................................................................. 123
  Analyses of Research Question 1 and 2: Pre to Post Instruction Changes ............ 125
    Preliminary Data Analysis ......................................................................................... 126
    Data Outliers ............................................................................................................ 126
    Reliability of Instrument Scores .............................................................................. 128
      BECKI Reliability ................................................................................................. 128
      CTCKS Reliability ................................................................................................. 129
    Bivariate Correlations ............................................................................................ 130
    Group Differences Pre- to Post-Instruction ............................................................ 132
      Means and Standard Deviations ........................................................................... 132
      Assumptions Testing ............................................................................................. 133
      Potential Classroom Effects .................................................................................. 135
      Multivariate Effect ............................................................................................... 139
Follow-up Univariate Analysis on Significant Interaction

Effects......................................................................................................................142

Simple Effects-Analyses .......................................................................................143

Pairwise Comparisons ..........................................................................................144

Knowledge Growth Summary ..............................................................................148

RQ 1 Summary of Biological Evolution Knowledge

Growth ......................................................................................................................149

RQ 2 Summary of Computational Knowledge

Growth ......................................................................................................................150

Analyses of Research Question 3: Results of Qualitative Analyses .....................150

RQ 3a: Conceptual and Relational Analysis of Written

Explanations.............................................................................................................150

Defining Biological Levels of Organization.........................................................151

Means and Standard Deviations.........................................................................156

Bivariate Correlations ..........................................................................................157

Means and Standard Deviations: Comparing

Interventions ...........................................................................................................159

Exploring the Scope of Biological Levels ............................................................160

Scope of Biological Levels: Comparing Interventions .......................................163

Relational Analysis .................................................................................................166

Means and Standard Deviations of BLCs ..............................................................166

Three Types of BLCs ...............................................................................................167

Relational Analysis: Comparing Intervention Groups .........................................169
RQ 3a: Conceptual and Relational Analysis Summary ..........171

RQ 3b: Analysis of Computational Complexity .........................174

Means, Standard Deviations & Frequencies of Complexity .....177

Computational Complexity Comparing Interventions .............179

Computational Complexity Summary ..................................180

Results Summary ..................................................................181

5. DISCUSSION ....................................................................185

Summary of the Findings ......................................................185

Quantitative Analysis Findings: RQ 1 & RQ 2 .......................187

Qualitative Analysis Findings: Biological Levels of Organization

(RQ 3a) ............................................................................188

Qualitative Analysis Findings: Computational Complexity (RQ 3b) .....191

Combined Discussion of Findings .......................................192

Limitations of the Study ......................................................196

Experimental Design .........................................................196

Ethics ..............................................................................200

Nature of LBECT-LP ...........................................................201

Cost ..............................................................................202

Implications for Instruction ................................................204

Scaffolding and Complexity of the LBECT-LP ......................204

Implications for Use within NGSS .......................................206

Implications for Future Research .......................................207

Concluding Thoughts ......................................................213
REFERENCES .......................................................................................................................... 217

APPENDICES

A. INSTRUMENT: BIOLOGICAL EVOLUTION CONTENT KNOWLEDGE
   INVENTORY (BECKI) ............................................................................................................ 235

B. INSTRUMENT: COMPUTATIONAL THINKING CONTENT
   KNOWLEDGE SURVEY (CTCKS) ..................................................................................... 241

C. INTERVENTION PRESENTATION EXAMPLES ................................................................. 245

D. HARDY-WEINBERG ASSIGNMENT (INTERVENTION 1) ............................................... 251

E. PHYLOGENETIC TREE ASSIGNMENT (INTERVENTION 2) ......................................... 262

F. EXAMPLES OF STUDENT WORK FROM PILOT STUDY ............................................. 267

G. EXAMPLES OF STUDENT WORK FROM DISSERTATION STUDY ............................. 271

H. TEMPLE IRB APPROVAL (RESULT: EXEMPTION) ..................................................... 278

I. SITE APPROVAL LETTER ............................................................................................... 279
# LIST OF TABLES

<table>
<thead>
<tr>
<th>Table</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>1. Computational Science Components and Associated Domains and Student Skills</td>
<td>48</td>
</tr>
<tr>
<td>2. Levels of Biological Organization and Applicable Computational Representations</td>
<td>57</td>
</tr>
<tr>
<td>3. Learning Biological Evolution Through Computational Thinking: Learning Progression</td>
<td>66</td>
</tr>
<tr>
<td>4. Components of Computational Thinking and Student Roles</td>
<td>69</td>
</tr>
<tr>
<td>5. Breakdown of Computational Thinking Survey Construct Items</td>
<td>102</td>
</tr>
<tr>
<td>6. Means and Standard Deviations for Pilot Study</td>
<td>109</td>
</tr>
<tr>
<td>7. Bivariate Correlations for the Pilot Study Variables</td>
<td>110</td>
</tr>
<tr>
<td>8. Study Timeline</td>
<td>113</td>
</tr>
<tr>
<td>9. Intervention and Testing Plan at Prospective Schools</td>
<td>116</td>
</tr>
<tr>
<td>10. Bivariate Correlations for the Dissertation Study Variables</td>
<td>130</td>
</tr>
<tr>
<td>11. Mean Scores for Dissertation Study Variables</td>
<td>133</td>
</tr>
<tr>
<td>12. Intra-class Correlation Coefficient (ICC) Values for the Study Variables Clustered by Class</td>
<td>137</td>
</tr>
<tr>
<td>13. Intra-class Correlation Coefficient (ICC) Values for the Study Variables Clustered by Teacher</td>
<td>139</td>
</tr>
<tr>
<td>14. Biological Levels Identified from Participant Artifacts</td>
<td>153</td>
</tr>
<tr>
<td>15. Conceptual Analysis: Means, Standard Deviations, Minimum and Maximum of Biological Words and Levels Identified</td>
<td>157</td>
</tr>
<tr>
<td>16. Kendall’s tau-b Correlations for the Biological Levels Within Participant Artifacts</td>
<td>158</td>
</tr>
<tr>
<td>17. Means and Standard Deviations for Biological Words and Levels Identified Between Intervention</td>
<td>160</td>
</tr>
</tbody>
</table>
18. Conceptual Analysis: Biological Level Totals Including Attempted (SD) Percent, Accurate Percent (SD), Overall Percent Correct and Kendall’s W Rank………………………………………………………………………..161

19. Percents and SD of Biological Levels Comparing Interventions………………………………………………………………………………….164

20. Relational Analysis: Summary of Total Biological Connection Attempts Means and Standard Deviations………………………………………..161


22. Scoring Rubric for Computational Component Complexity within Participant Artifacts………………………………………………………………..175

23. Comparing Intervention Groups: Summary of Total Biological Connections Means and Standard Deviations …………………………………………..177

24. Scores, Frequencies and Percentages of Computational Complexities ……….178

25. Means of Computational Complexity Comparing Interventions………………………..179
# LIST OF FIGURES

<table>
<thead>
<tr>
<th>Figure</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>1. Student understanding of evolution via unity at increasing complexity according to the learning progression.</td>
<td>73</td>
</tr>
<tr>
<td>2. Computational thinking associated with unity as part of the computational thinking about learning evolution learning progression.</td>
<td>74</td>
</tr>
<tr>
<td>3. Student understanding of evolution via diversity at increasing complexity according to the learning progression.</td>
<td>75</td>
</tr>
<tr>
<td>4. Computational thinking associated with diversity as part of the computational thinking about learning evolution learning progression.</td>
<td>76</td>
</tr>
<tr>
<td>5. Evolution knowledge scores over time for the two intervention groups, with bars showing standard errors.</td>
<td>140</td>
</tr>
<tr>
<td>6. Computational knowledge scores over time for the two intervention groups, with bars showing standard errors.</td>
<td>141</td>
</tr>
<tr>
<td>7. Biological level frequency attempted by students and frequency of correct instances.</td>
<td>163</td>
</tr>
<tr>
<td>8. Biological level attempt frequency between intervention 1 and 2.</td>
<td>165</td>
</tr>
</tbody>
</table>
CHAPTER 1

INTRODUCTION

Problem

Computational thinking is a contemporary mathematical and engineering concept emphasized within the Next Generation Science Standards (NGSS Lead States, 2013). The NGSS are the national K-12 classroom expectations for science students. Although the NGSS provide educators the flexibility to design engaging learning experiences for students, computational thinking has no clear definition nor explicit methods for inclusion in science learning (Wing, 2006). Presenting classroom activities which integrate computational thinking blended with scientific content has been a challenge for science educators due to a lack of theoretical grounding (Weinthrop et al., 2016).

Modern science, particularly biology, is becoming increasingly computational in nature (e.g., bioinformatics, data analytics, genomics, ecosystem modeling, etc.). To serve science students in a world where technological change is exponential, computation should be infused into curricular materials using theory that blends computational, scientific, and educational perspectives (Sengupta, Kinnebrew, Basu, Biswas, & Clark, 2013). The NGSS also emphasizes the development of subject specific skills alongside nature of science (NOS) practices, both of which may be facilitated through computational thinking (Wing, 2006). Throughout this dissertation I emphasize biological evolution as the [scientific] domain content and claim computational thinking is necessary to learn the construct.

Along with an inconsistent definition of computational thinking for educators, there is a gap in research exploring effective methods of implementation and benefits (of
computation) for science students (Wilensky, 2014). I use the term “computational thinking” to describe students’ cognitive processes associated with computational science in the way one would use “scientific thinking” to describe cognitive processes associated with science. I define computational science—modified from Wing (2006)—as the intersection of three major constructs: scientific content (e.g., biology), mathematics (e.g., algorithms) and computer science (e.g., writing code). I have defined the components of computational thinking as input, integration, output, and feedback (as modified from Weinthrop et al., 2016). Combinations of these components should be incorporated into all science classrooms however, unique problems arise in life science classrooms (Navlakha & Barr-Joseph, 2011).

Defining and understanding the relationship between variables within scientific systems is common practice in science learning. It is more often that basic algorithms and equations are introduced in physical science curricula (i.e., physics and chemistry) as compared to life science courses (Gobert, 2000). Activities that occur in physical science classrooms present mathematics practices more plainly to students, lending to more straightforward infusion of computational thinking in these areas. Foundational topics of biology are rarely presented to students in arithmetical format, but rather as a series of worded phrases, rules or conditions which students often memorize (Gross, 2004). For example, mathematical equations are typically presented within the physical sciences to represent Newton’s laws as a foundational concept. Most often educational research associated with computational thinking (regardless of the domain) is through the context of interface friendly tasks (i.e., most code is hidden, complex visual representations, including click and drag items) or video game development (Grover, 2011). There are
advantages to using interface friendly tools in biology classrooms (such as population simulations) however, these are generally not the instruments used by practicing biologists. I alleviate these issues by presenting a logical sequence of increasing complexity through the development of a unique learning progression, which uses computational thinking to explore biological evolution (Guo, Wagh, Brady, Levy, Horn & Wilensky, 2016). For example, I present these user, face-friendly tasks as simple and emphasize that students should transition toward more complex types of computation while studying biological evolution over time.

As scientists (e.g., biologists) solve problems, it requires thinking about their data (input), the relationship of the variables (integration), the results (output), and re-modeling their original assessment (feedback). Computational thinking in the way I have defined it (within the context of education) fully encompasses this scientific process through use of the computational components. For example (under the context of input), scientists think about how and where they might obtain their data (e.g., database, simulation, the environment), where they might store it, or how they might format it. Under the context of integration, scientists might think about the relationship between their variables and the appropriate tools they have to address this relationship (e.g., interface friendly tool, hard coding). I argue that these types of NOS processes are what science students should be doing in classrooms (Gallagher, Coon, Donley, Scott, & Goldberg, 2011; NGSS Lead States, 2013).

Biological evolution, the foundational phenomena in biology, can explain the unity and diversity of life, while simultaneously providing explanations for all other biological processes (Campbell et al., 2000). Students can learn about biological
evolution through various formats including cases that would naturally align with computational thinking. However, computational thinking is rarely incorporated into biology classrooms (Navlakha & Barr-Joseph, 2011), especially in accordance with the foundational concept of biological evolution (Speth, Long, Pennock, & Ebert-May, 2009).

Biological evolution spans across temporal and organizational scales, requiring students to reason through abstractions (Guo et al., 2016). Computational thinking can facilitate deeper evolution learning because abstractions can be made more concrete, potentially alleviating misconceptions, reinforcing the nature of science (Sengupta et al., 2013), and allowing student embodiment (Wilensky & Reisman, 2006). My learning progression identifies the instructional context, computational product and computational process and spans from simple to complex (as modified from Berland and McNeill’s [2010] learning progression). For example, the simple level within my progression may include user face friendly premade models (computational process) with heavy teacher scaffolding (instructional context), whereas a complex level would involve student driven projects (instructional context) and hard coding for students (computational process).

Currently, there is no theoretical framework merging computational thinking and biological evolution (Sengupta, Kinnebrew, Basu, Biswas & Clark, 2013).

Students experience computational technologies at an early age (both in school and at home); however, they are not versed in how to maximize their efficiency (Grover & Pea, 2013). Activities such as computer coding are becoming more popular for students, but it is also important that the content is implemented in ways that would be most beneficial to all students (Wilensky, 2014). Merging computational skills and core
content (as opposed to presenting it alone) would encourage and prepare students to partake in activities which are most comparable to practicing scientists. It would also provide structure for students to better understand or conduct relevant scientific research (Guo, et al., 2016).

Specific software programs are more common in certain fields than others, areas which lend as suitable for student exploration within domain specific classrooms. For example, individuals who work within scientific fields frequently use certain types of software to solve relevant scientific problems and perform research (Wang & Zhu, 2008). With the increase in biotechnology careers, it is important that students are prepared to understand the related computational processes (Speth et al., 2009). Even understanding the movement and relationships between the individual units or boxes in Microsoft Excel (or Google sheets) requires an introductory form of computational thinking. Use of such programs are relevant to student lives and is useful in various domains (Quin, 2009).

There is a definite urgency to incorporate computational thinking practices into scientific curriculums according to the NGSS, however, incorporation strategies are currently vague, and definitions for computational thinking as applied in classrooms are still unclear. Therefore, the relevant problems regarding computational thinking are: (1) there is that there is no consistent definition for science educators (Selby & Woollard, 2013); (2) researchers and educators are unsure of most effective methods of implementation in science classrooms (Wilensky, 2014); (3) and if and how computational thinking is beneficial to science students (Speth et al., 2009). There is little exploration of these problems especially in the context of the life sciences (including the foundational concept of evolution).
Purpose

The long-term goal of the dissertation research is to provide an avenue for life science educators to implement computational thinking within their classrooms. Although the dissertation research hones in on integrating computational thinking with biological evolution, the results of the research and scope of the learning progression may expand to other content areas. The literature review provides a consistent definition of computational thinking and merges it with scientific content and associated NGSS standards across grade levels. I developed a learning progression using ideas from two previously published learning progressions, the first from Plummer and Krajcik (2010) and the second by Berland and McNeill (2010), with the concepts from my learning progression naturally emerge from the ideas presented in the literature review. For example, Plummer and Krajcik (2010) developed a learning progression which uses spatial thinking to understand celestial motion and I modified their framework to using computational thinking to understand biological evolution. The aim of my learning progression is to assist educators in developing course work which blends computational thinking with learning biological evolution. Describing the important aspects of computation as well as how to scaffold these aspects through biology learning will be helpful for teachers to better serve their students.

I have developed and presented this theoretical framework and associated learning progression to embed computational thinking within learning about biological evolution because it is an essential concept within biology (found in Chapter 2). In the learning progression I developed components of computational thinking and coupled them with biology student roles. The learning progression also pairs two themes of biological
evolution, unity and diversity (Campbell et al., 2000) with the three computational thinking components (instructional context, computational process and computational product). I developed computational components through the modification of argumentation components from the learning progression developed by Berland and McNeill (2010). I have paired each of the computational components and applicable NGSS standards at the corresponding increasing levels of computational complexity. In order to test the effectiveness and applicability of the learning progression, I designed a quasi-experimental design research study.

Not only is implementation of the learning progression appropriate from an expansive educational researcher’s perspective (i.e., broad aspects of computation and evolution) but it also may provide insight on more specific research studies. For example, it may be used to assess and hone in on specific skills, lessons and objectives. Skills, standards and assessments already practiced in biology classrooms may be modified to incorporate these computational thinking skills. For example, lab experiments may also be performed computationally so that students may physically view one or two generations of a population during a lab activity, but then use computational thinking to generate, display and observe the same phenomenon for hundreds of generations through the use of computational tools. Instructors may facilitate, computational thinking by promoting activities at the allele level through to the population level. Public data bases may be used to find and compare protein sequences for students to generate phylogenetic trees, as these are activities already encouraged (computationally) by the AP biology curriculum (College Board, 2019). If instructors scaffold these ideas with proper computational thinking contexts, researchers may then be
able to identify the degree to which computation contributes to student learning. The learning progression encourages students to produce a range of computational products based on inquiry, communication and skill level. These trends displayed in the learning progression naturally align with current educational trends promoting inquiry labs and appropriate differentiation for students.

Research Questions

The learning progression developed from the theoretical framework found in the literature review naturally lends itself to three major research questions as presented below:

1. How does instruction promoting integration of biological evolution concepts and computational processes (input, integration, output, and feedback) compare to instruction focused only on biological evolution concepts, specifically in changing students’ knowledge of biological evolution?

2. How does instruction promoting integration of biological evolution concepts and computational processes (input, integration, output, and feedback) change students’ knowledge of computational processes (i.e., input, integration, output, and feedback)?

3. In what ways do students’ computational products (artifacts) constructed during instruction promoting biological evolution concepts and computational processes (i.e., input, integration, output, and feedback) display:
   a. Student understanding of different levels of biological organization (i.e., from molecular to ecosystem scales); and
b. Different levels of complexity in computational thinking (i.e., simple, developing, and complex)?

The research questions and associated research methods were aimed at exploring student learning of biological evolution and computational thinking through testing knowledge of both of these constructs over time. The interventions, data collection, and analyses methods are described in Chapter 3. In order to identify if and how computational thinking encourages biological evolution learning, I developed two interventions that incorporate computational thinking and biological evolution, both of which were presented to students in this dissertation study. Student computational knowledge and biological evolution knowledge were measured as dependent variables. I developed two instruments to measure student knowledge of computational processes (input, integration, output, and feedback) as well as biological evolution knowledge (which spans scales), each of which have been validated in various ways.

These instruments were used to identify if student knowledge of biological evolution or computation increased as compared to evolution lessons which did not involve computation. Results from the dissertation study indicated there was a significant interaction between computational knowledge growth and evolution knowledge growth for one of the two computational interventions. Exploring student understanding of biological organization and different levels of complexity in computational thinking (simple, developing and complex) was performed in the dissertation study through analysis of student artifacts. My results from the study shed light on if (and to what degree) and how merging computational thinking would be beneficial to science (specifically biology) students.
If educators continue to implement aspects of the learning progression in their teaching, it will provide an avenue for researchers to explore the working relationship between computational thinking and evolution learning. Researchers may better understand the influence of computational thinking on overall biological science understanding. The learning progression and associated dissertation research is robust in that the results may be used at the elementary level or the graduate level, and provides contexts of student assessment for educators and researchers alike, especially when coupled with the relevant teaching standards (I have aligned specific NGSS standards to the learning progression in Chapter 2). Avenues in which the research was performed and analyzed is described in the sections below. Teaching methods which promote biological evolution and computational processes were used and compared to traditional teaching methods. Two instruments have been developed and are also described in the sections below.

Significance

There is a discernible gap in science education research describing the relationship between computational practices and evolution learning. All previous research studies have used pre-programmed simulations during student learning about evolution which represent models and visualizations rather than the essential components of computational thinking (Guo et al., 2016). Most computational research in education combines core content with the development of video games to promote student interest, or fails to incorporate subject specific core content all together (Leutenegger & Edgington, 2007). There is little or no investigation of computation coupled with exploration of evolution across various levels of biological organization, a component
which is essential for evolution learning (Wilensky & Reisman, 2006). I hypothesized that using computation would strengthen student knowledge and NOS processes, contributing to biology understanding (Gallagher, Coon, Donley, Scott, & Goldberg, 2011). The results from the dissertation study support this claim, specifically in learning biological evolution across scales. Students may become more comfortable developing new computational tools and thought processes or apply these skills to other disciplines. It is still unknown how computational processes explored through this proposed type of learning progression may relate to overall student achievement or collaborative learning outcomes. There are no assessment tools that measure computational skills as applied across disciplines (Werner, Denner, Campe, & Kawamoto, 2012). Future research may include the examination of how computational processes will help students to better understand evolution and in turn how this might strengthen their knowledge within the collective domain of biology (Guo et al., 2016).

The dissertation research suggests that greater organization of conceptual perspectives on computation, in combination with life science pedagogies and learning could result in deeper understanding of biological evolution. However, the learning outcomes for deeper conceptual understanding and knowledge transfer for topics associated with evolution are still unknown, especially how these topics relate to overall biology understanding (Jacobson, 2006). Researchers and curriculum developers have not yet clearly defined the computational instructional practices, computational process, and computational products that would facilitate teaching and learning, especially within domain specific contexts (Gallagher et al., 2011). In the dissertation study I defined and applied these constructs and developed both quantitative and qualitative (i.e., rubric)
assessment methods. Better suited assessments which combine computation and content (such as biology) are relevant issues for both teachers (application) and researchers.

Within the dissertation study it was important to address student understanding of the interaction between biological levels of organization within the context of evolution through the computational thinking process. Wilensky and Reisman (2006) conducted a study using computation as an avenue for students to explore evolution however the computation was heavily interface friendly and acted only as a model to reinforce the idea of evolution at one scale. There was evidence for student embodiment (as students became emerged in their models) during the study however students lacked understanding of evolution between organizational units (or levels) in biology. It is evident that certain computational practices encourage evolution learning, and this idea prompted the research questions. Although the AP curriculum for example stresses that evolution is important in biology learning and emphasizes computation to do so, it does not identify how and to what degree the activities specifically contribute to learning of biological evolution and biology as a whole (Román-González, Moreno-León, & Robles, 2017). Many of the associated resources are difficult for teachers to understand and become outdated quickly.

The three research questions were broad enough to allow exploration of specific components presented in the theoretical framework and learning progression models (i.e., emergent phenomena). Examples of emergent phenomena include: the identification of which components of organizational scales of biology students better understood through computation or to what degree computational complexity contributed to evolution learning. Results indicated students who made biological level connections from the
micro level through the macro level made the most gains in biological evolution knowledge. Directions for answering future questions did arise through the research process (i.e., which biological levels to further explore). The research questions were student centered but may eventually develop into questions about educator or district practices. These questions as well as others may be explored in the future through the results of the three overarching research questions.

The NGSS representation of computational thinking represents mathematical and modeling skills that should be developed through grade levels. I describe and have defined computational thinking differently in the theoretical framework below (Chapter 2). The development of an assessment for computational skills alone or the assessment of computation alongside and integrated within content knowledge is necessary in order to monitor student progress. These assessments are essential for continued research, however the type of information that this assessment would measure is still unknown partially due to the lack of a consistent definition for computational thinking (Wing, 2006), especially as it is presented alongside various content within classrooms. Research is also required to pair testable components of biological systems with how a student’s thinking about biology may have changed. Therefore, not only would a student’s understanding of biology be affected by computation, but the student might think differently, and more like a scientist with advanced skills using the available computational tools contributing to NOS specific skills and overall science achievement.

Not exposing our young science student learners to computational thinking at an early age is a major disservice to them and may hinder their future within STEM fields. Computational methods incorporated into biology classes to learn biological evolution is
controversial; however, it has the potential to alleviate misconceptions, reinforce the nature of science, and encourage student embodiment. Researchers, educators, and curriculum designers could use the learning progression to facilitate learning that embeds computational thinking within the context of biological evolution. The learning progression may also promote students’ use of thought processes that may encourage higher order science understanding and promote curricular relationships across disciplinary domains. As educators implement such strategies, the learning progression may provide a robust resource and alternative ways to promote student engagement in authentic scientific practices. This might allow students to develop deeper understanding of scientific content (Plummer & Krajcik, 2010). The results from the dissertation study support and encourage specific aspects of the learning progression, therefore it encourages educators to implement computation into their courses. The learning progression, and dissertation which promotes learning using the learning progression, provide specific content (unity and diversity) and standards-based computational strategies for biology teachers. The learning progression promotes holistic type learning and structure for biology teachers to implement lessons which are new, cross curricular and engaging.

Definition of Terms

This section presents the terms and definitions used throughout my literature review, learning progression, and in my dissertation study. There may be various definitions for these terms within science and education alike, however the listed definition is the context for which they are used in my research.
• **Computational Thinking** - Computational thinking is the thought process involved in formulating problems (e.g., algorithms) so that their solutions (e.g., representations; Denning, 2017) may be presented through most effective computational steps (Aho, 2012). Defining computational thinking as such does not confine such reasoning strictly to computer science, but also has components from mathematics and implications across fields including but not limited to biology, physics and chemistry. Computational thinking parallels computational science just as scientific thinking parallels science content and sits at the intersection of the following three components: a scientific discipline, computational construct and mathematical concept.

• **Computational Science** - Computational thinking in science involves the intersection of computer science, mathematics, and a specific science discipline. Computer science relates specifically to information sciences and associated technologies. Applied mathematics includes but is not limited to numerical models and statistics. Science disciplines involve knowledge and epistemic stances of a particular community of research and practice (e.g., biology, physics, or chemistry) (Wing, 2006).

• **Biological Evolution** - Biological evolution is the explanation for the mechanisms which drive populations and in turn species of living organisms to change over time through the forces of natural selection (Campbell et al., 2000). It is a fundamental aspect of biology at all physical and temporal scales, as stated in various ways by many famous
biologists such as Dobzansky (1973), who claims that nothing in biology makes sense except in the light of evolution.

• **Natural Selection** - Natural selection is the concept that inheritable traits which help an organism survive and reproduce within its environment become more common in a population over time. This can be observed at various scales, including allele frequencies or number of individuals within populations (Campbell et al., 2000).

• **Unity** – [Biological] unity focuses on similarities (such as common ancestry or comparing similar DNA strands) and uses this as a lens to explore biological evidence. (i.e., the “how is life so similar component” of: “how is life so similar yet also so different?”). Although it can be seen at any biological level, it is easier seen in the smaller levels of biological organization.

• **Diversity** - The [biological] diversity component focuses on the diversifying of organisms (through a phylogenetic approach for example) or looking at things from a larger environmental aspect. This is easier seen in the larger levels of biological organization. (i.e., “the how is life so different” component of “How is life so similar yet also so different?”).

• **Embodiment** – As students undergo unique experiences that allow for immersion with content (such as their constructed models), it is known as embodiment. In biology learning, embodiment occurs as students imagine and develop new ideas about how certain biological agents interact within
their own constructed systems (Wilensky & Reisman, 2006). It is often achieved through the necessary components of computational thinking.

- **Learning Progression** - Researchers have described learning progressions (LPs) in various ways. However, Berland and McNeill (2010) describe three components of LPs: (1) how understanding develops, (2) increasing levels of complexity and (3) using pathways. I combined this framework with Plummer and Krajcik’s (2010) framework in which construct maps are also defined to show the progression of learning more clearly to develop our LP called learning biological evolution through computational thinking (LBECT-LP).

- **Computational Process** – Actual act of student development of and with the computational components (input, integration, output and feedback) which is displayed in various ways within the classroom by students. This concept was modified from Plummer and Krajcik’s (2010) framework (from spatial thinking to computational thinking) to include computation. This process allows for growth in computational thinking knowledge and skills. Depending on sophistication of computational process displayed by students, it spans from simple to complex. The computational knowledge variable is based on these components.

- **Input** – A form of information used in a computational process. It takes a variety of forms, and may come from a database or be generated. It may be stored in spread sheets, sound files, fingerprints, pictures etc. Examples include numbers representing population changes, DNA
sequences, weather data or frequencies of alleles in a population. This information is interpreted by learners and used within computational integration.

- **Integration** - The representation of how the input is related to the output. This includes the code written with algorithms that apply scientific principles. This maybe within a program or its own script all together. It may be written by a student or hidden behind an interface as written by an external user. For example, this is the specific equation, such as the Hardy Weinberg population equation which relates allele frequencies (input) to individuals within a population (output). Another example is the code written that identifies how many DNA mutations/differences there are in concurrent sequences between species. The corresponding output would be the interpretation and identification of how the species are evolutionarily related.

- **Output** – The information, documents or display that the integration (i.e., program or script) generates or produces. This may be in the form of another data set, graph or file etc. depending on what is needed. It is important to note that within a computational science context, it should be checked and compared to what we know about the scientific phenomenon in order to verify accuracy and robustness (this is sometimes referred to in the literature as debugging).

- **Feedback** – The aspect of the phenomenon where the output re informs the input. The output can regulate the input or change it by having the
program adjust based on itself. These are often in the form of negative or positive feedback loops within biological systems. Due to the fact that they are essential in understanding and representing biological phenomena I assign an entire computational process component to feedback. Not all programs require feedback but in a population model for example over many generations, the output of one generation (offspring) would be the input or starting data for the new or upcoming generation.

- **Computational Product** – The actual product (i.e., artifact or description of the computational process) developed by the student which is a combination of the computational process and instructional context and ranges from simple to complex.

- **Instructional Context** – The role played by the teacher or educational system to facilitate computational thinking in the classroom. This aspect also ranges from simple to complex. Generally greater teacher support and supplements occur at the simple level, with less assistance provided at the complex level.

- **AP - Advanced Placement (AP)** are high school courses which are offered to students in certain districts as developed by the College Board. These courses include a worldwide test at the end of the year in which the resulting student score from 1-5 dictates if the student will receive college credit for the course. Generally, there are requirements and prerequisites to enroll in an advanced placement course. The courses are considered
high stakes, sometimes have a weighted impact on GPA and are more rigorous than other courses offered at high schools.

Organization of Dissertation

In this Chapter, I presented the problem which warrants the development of a learning progression. The learning progression and supporting literature review has been outlined in Chapter 2. I have also provided a context for the problem being studied. This context and problem naturally lend themselves to the research questions generated by the literature and gaps within the literature. I present the methodology from the associated dissertation study to support the learning progression in Chapter 3. In Chapter 4, I outline the results from the dissertation study and draw conclusions in Chapter 5. Chapter 1 concluded with a definition of terms to clarify any preconceived ideas or for the instances that the terms have multiple meanings.

Chapter 2 presents an overview of the previous relevant literature from areas of research concerning computational thinking and biological evolution learning as it applies to the NGSS. It then provides a theoretical framework and learning progression merging computational thinking and biological evolution.

Chapter 3 explains the methodology for my dissertation study. Chapter 3 includes a discussion of the sample students, my development of two interventions and the two instruments that I used to measure the variables of interest (biological evolution knowledge and computational knowledge). Chapter 3 concludes the with a description of the analyses for each research question and potential implications of the dissertation study.
Chapter 4 presents the results from the data obtained during the dissertation study. The results are presented alongside the three research questions. The quantitative analysis relates to student knowledge growth of biological evolution as well as computational thinking through the use of computational teaching methods. The qualitative results present context, analysis and results of the exploration of student artifacts. These quantitative analyses investigate student understanding of biological levels and the complexity of computation used by students. Chapter 4 concludes with a summary of the findings.

Chapter 5 further explores the summary of the findings and presents limitations of the study. In this Chapter I also present practical (education) implications as well as research implications. I conclude with directions for future research and summarizing statements regarding the study’s contribution to science education.
CHAPTER 2

LITERATURE REVIEW

Background

Standard life science courses facilitate student exploration of the natural living world (across grade levels) by encouraging unique thought processes and learning experiences as encouraged by the Next Generation Science Standards (NGSS Lead States, 2013). Biology courses (a standard life science course) are developed, revised and scaffolded by ever changing curriculums, and are heavily influenced by the NGSS (the national K-12 classroom expectations for science students; NGSS Lead States, 2013). Presenting classroom activities which integrate computational thinking (a contemporary mathematical and engineering concept emphasized within the NGSS) blended with scientific content has been a challenge for science educators due to a lack of theoretical grounding (Weinthrop et al., 2016). In this dissertation I argue that incorporating computational thinking into life science classrooms can provide an avenue to address both content (i.e., biological evolution) and nature of science (NOS) concepts. I make this argument through the lens of the NGSS (and present its global relevance) in order to provide a practical learning progression for educators across grades. Biological evolution was selected as the domain content I focus on throughout the article because it is an essential and overarching theme in biology.

Our understanding of biological evolution (the explanation for the mechanisms, which drive populations, and in turn species of living organisms to change over time through the forces of natural selection; Campbell et al., 2000) informs every aspect of modern biology (McCain & Kampourakis, 2016). Many famous biologists agree with
Dobzansky’s (1973) claim that: “Nothing in biology makes sense except in the light of evolution”. As students master foundational evolutionary ideas (i.e., natural selection, the concept that inheritable traits which help an organism survive and reproduce within its environment become more common in a population over time; Campbell et al., 2000) it fosters thought processes associated with both “the how” and “the why” of life’s changes over various time and organizational scales. Once students and scientists alike develop a working understanding of evolution, they can hypothesize about biological topics to a greater extent (e.g., how species are related, inherent human behaviors, various aspects of molecular genetics, and ecosystem dynamics; Griffith & Brem, 2004).

Various learning tools, practices, and interventions have been applied to student learning of biological evolution to facilitate understanding of this critical concept (i.e., the Concord Consortium [2018] list eleven current, and three former research projects associated with students’ learning about biological evolution). There are also a variety of instructor and student apprehensions, frustrations, and obstructions in teaching and learning evolution (Sinatra et al., 2003). Unique instructional methods that focus on teaching students how to construct knowledge (and think) like scientists promotes critical evaluation of information (i.e., construction of valid explanations about phenomena [such as biological evolution] in alignment with NOS). I define this type of thinking as “scientific thinking” (the ability to generate, test and evaluate claims, data and theories; Levinson, 2010), as it paves the foundation for scientific literacy (Schmaltz, Jansen, & Wenckowski, 2017).

In order to achieve scientific literacy (encouraging science learning as praxis by allowing students to identify solutions which transform practical relevant scientific
problems; Levinson, 2010; Aikenhead, 2007) by graduation, the National Research Council (2012) recommends that computational thinking should be integrated into life science courses and biology classrooms through the K-12 curriculum. In order to be effective, computation should be infused into curricular materials using theory that blends computational, scientific and educational perspectives (Sengupta, Kinnebrew, Basu, Biswas, & Clark, 2013). This is especially important (in serving students) because modern science, particularly biology, is becoming increasingly computational in nature (i.e., bioinformatics, data analytics, genomics, ecosystem modeling etc.) and technological change (in general) is exponential. Along with the fact that using computational thinking is inherently cross-curricular, it allows for students to identify and solve technological problems which have and will continue to arise within democratic societies (Shen, 1975).

Although the NGSS encourages computational thinking and provides educators the flexibility to design engaging learning experiences for students (i.e., emphasizing the development of subject specific skills alongside NOS practices as facilitated through computational thinking), computational thinking has no clear definition nor explicit methods for inclusion in science learning (Wing, 2006). Computational thinking parallels computational science just as scientific thinking parallels science content and sits at the intersection of the following three components: a scientific discipline (i.e., biology), computational construct and mathematical concept (Denning, 2017). It is the thought process involved in formulating problems (e.g., algorithms) so that their solutions
(e.g., representations) may be presented through most effective computational steps (Aho, 2012). This definition of computational thinking is vague for typical educators.

In order to best serve students in biology classrooms I present a learning progression that integrates computational thinking (i.e., a common practice employed by biologists) alongside evolutionary concepts as aligned with standards from the NGSS. Because evolution spans across several temporal and organizational scales, computational thinking is essential for biologists (and students) to better understand the full domain (Guo et al., 2016). Some have even speculated that understanding computational thinking can only be done through an evolutionary lens since both biological life and computer code emerge through and are guided by evolutionary progressions (Toffoli, 2004).

For example, students may need to explore the properties of individual agents such as cells that make up tissues and eventually organs and organ systems within organisms. As students assign properties to cells using computational tools (i.e., coding), the emergent properties of organisms become more evident to students (because different levels of biological organization may display different ontological properties; Chi, Roscoe, Slotta, Roy, & Chase, 2012). This level of understanding may occur through computation as students envision themselves within models they develop using these thought processes (i.e., embodiment, which also aligns with the NOS). In this way, emergent properties of biological evolution parallel emergent computation (and the tools required in learning emergent computation resemble those used by scientists in the field).

In order to supplement the previous example I present the three aspects of computation (from my learning progression) within the context of a classroom setting: (1)
the computational context (as provided by instructor), (2) computational product (as produced by student) and (3) the computational process (actual act of student development of and with the computational components). The student’s computational process as facilitated by the instructor includes the student reasoning and implementation of four computational components: input, integration, output and feedback (as modified from Weinthrop et al., 2016). This process may allow students to predict phenomena at a variety of biological levels, resulting in a higher level of cognitive engagement, and thereby deepening students’ understanding of evolution. In parallel, as scientists solve problems (in conjunction with our computational components), it requires thinking about their data (input), the relationship of the variables (integration), the results (output) and re-modeling their original assessment (feedback). Computational thinking in the way I have defined it (within the context of education) fully encompasses this scientific process through use of the computational components (further aligning it with NOS practices).

As previously stated, educational theory and perspectives must also be considered for proper development of my learning progression. As students work actively through using computational thinking in cooperation with their classmates, information is brought from a social context toward the individual student as supported by Vygotsky’s social constructivist theory (1962). This idea that learning is both an active and social process parallels the framework within the NGSS (Basawapatna, Repenning, Koh, & Nickerson, 2013). The NGSS also emphasizes that students transform and rationalize new information based on their prior knowledge and internalized mental schema, which is synonymous with Piaget’s learning assimilation theory (1976). This combination of social and cognitive constructivist philosophies outline an active process of shared and
individual knowledge construction that promotes deep learning (Fisher, Giakoumis, & Dorner, 2016); computational thinking reinforces both of these theoretical learning concepts (Wing, 2006; Guo et al., 2016).

Although the majority of this dissertation explores concepts through the perspective of the NGSS (the U.S. science standards), I have ensured international relevance (of the NGSS) to support our arguments. Science standards and expectations across the globe parallel the NGSS by focusing on active learning and social classroom environments (Moore, Tank, Glancy, & Kersten, 2015). These environments promote approaches and methods which encourage students to ask questions, evaluate evidence, and justify the validity of their own ideas, as well as the ideas of others (National Research Council, 2010). The International Society for Technology Education (ISTE) declared global standards are quite similar to the NGSS in emphasizing computational thinking (and related concepts) as well as embedding computation across disciplines (Grover & Pea, 2013). The NGSS have ensured global relevance by adding research-derived benchmarks that compare the NGSS to international tests (i.e., one of these benchmark studies, qualitatively analyzed standards and standardized tests from ten countries including Canada, Chinese Taipei, England, Finland, Hong Kong, Hungary, Ireland, Japan, Singapore and South Korea; Moore et al., 2015). Studies indicate that cross cutting concepts (such as computational thinking) were common to all science courses across countries and considerable attention was also given specifically to the
NOS, as well as the nature of technology and engineering practices (National Research Council, 2012).

Thus far, I have emphasized the importance and difficulty of biological evolution learning (and instruction), defined computational thinking and made an argument that it is crucial for learning biological evolution as supported by my learning progression (especially within the context of the NGSS). I have identified the importance (and global relevance) of computational thinking within the NGSS as supported by educational theory (i.e., through the lens of Piaget and Vygotsky’s learning theory). The remainder of the review is divided into four sections, the theoretical framework, the learning progression, previous studies considering computation and evolution, and the emergent research questions.

In the first section I begin the theoretical framework by presenting relevant challenges of biological evolution education (conceptual change, misconceptions, social and emotional implications, and its relationship to the NOS and NGSS). I then address distinct characteristics of computational thinking and illustrate its relationship to the NGSS and biology learning. The purpose of the framework is to lay theoretical grounding for my learning progression. In the second section, I discuss a proposed learning progression for biological evolution as supported by computational thinking. The proposed learning progression describes a transition from simple to complex and includes instructional contexts, computational process and computational products that would be displayed and practiced by students within classrooms. Two major themes of biological evolution have been identified as unity and diversity and have each been paired with computational thinking processes and specific NGSS standards. The third
section concludes the review by highlighting gaps in our current understanding of how learning about biological evolution may be facilitated by computational thinking. Addressing these research gaps has the potential to direct future researchers and educators toward fully fleshing out a more robust and effective learning progression through development of specific student tasks, assignments and assessment tools. After considering these limitations (of the learning progression) I suggest that practitioners use it to incorporate computation into lessons they already teach as a practical starting point.

Theoretical Framework

*Learning About Biological Evolution*

Computation may promote embodied experiences within biology and encourage the development of skills that seek truth over societal worldviews (Wilensky & Reisman, 2006). As individuals become scientifically literate, they tend to use their scientific knowledge to shape their worldview holistically (Stocum, 2015). As this type of thinking becomes the norm, it may cause societal shifts in scientific thinking. For example, evolutionary biologists are frequently called upon to bridge gaps between various disciplines such as biology and medicine or biology and psychology because evolutionary concepts provide interdisciplinary explanations (Antolin et al., 2012). This is especially important at a time when students have access to a variety of competing information. Increased scientific literacy allows students to better navigate scientific constructs (including and) much different from evolution, such as the belief in and understanding of climate change (Stocum, 2015). The cognition patterns required for learning biological evolution may be translated to other scientifically relevant phenomena for students (Beggrow & Sbeglia, 2019).
Having knowledge of biological evolution is required by citizens of a democracy to make informed long term environmental decisions, to cultivate sustainable agriculture, to stay ahead of pathogenic diseases, to battle genetic conditions, and to make sense of human emotion among many other phenomena. Evolutionary principles lay the foundations for student understanding of modern medicine, sustainable conservation and human psychology (Sinatra et al., 2003). Learning evolution urges students to think like scientists, recognize biological processes, better grasp the dynamics of nature and the limits of science. Identifying how and why scientific inquiries and questions are important within the holistic domain of biology requires a genuine and authentic understanding of biological evolution (Alters, 2002).

Understanding biological evolution also allows students to better appreciate biology as a discipline as it can be observed at and between all levels of biological organization (Campbell et al., 2000). The two major themes of biological observations in scientific study that have stimulated students and scientists at various levels of complexity are the exploration of the unity and diversity of life. In other words, how is there such a diversity of life on Earth and among all this diversity, how can the various similarities among organisms be explained? We know that organisms are related to each other but understanding exactly how and why may answer these two questions at various levels of biological organization and temporal scales (College Board, 2009).

Teaching biology without (ensuring) proper student understanding of evolution does not allow for students to bridge this overall order and coherence that fosters a comprehensive scientific understanding of life. Defining and understanding the relationship between variables within scientific systems is common practice in science.

30
learning. It is not always easy to compare the fundamental concepts in the physical sciences to biology but this is only because of the compounding interplay of variables that are involved in biological systems (Guo et al., 2016). I propose that computation may bridge the gap between biological evolution learning, variable relationships and mathematics the way it naturally occurs in other classrooms (i.e., physical science classrooms; Gross, 2004).

Teaching biology without proper student understanding of evolution does not allow students to bridge this overall order and coherence that fosters a comprehensive scientific understanding of life. In physics for example, teachers use mathematical equations representing Newton’s laws as a foundation to help students learn the physical sciences. However, the foundation of biology is rarely presented in this arithmetical format, but rather as a series of worded phrases, rules or conditions which students often memorize (Gross, 2004). When defining scientific systems, it is more often that basic algorithms and equations are introduced in physical science curricula (i.e., physics and chemistry) as compared to life science courses (Gross, 2004). Computation may bridge the gap between biological evolution learning, variable relationships and mathematics.

*Misconceptions About Evolution and Conceptual Change*

Conceptual change about biological evolution may be facilitated by computational thinking because students become more deeply engaged around the topic in a manner similar to practicing biologists (Dole & Sinatra, 1994). This may be emphasized specifically by reasoning about individual biological elements at multiple levels of organization within biological systems (as prompted by computational thinking; Toffoli, 2004). Biology students may have ideas about the nature of biological evolution,
but these ideas may be unsophisticated and/or incorrect. For example, Coley, Arenson, Xu, and Tanner (2017) reported that students’ naive intuitions about biology persist from middle school to the university level, revealing little influence of high school biology on students’ learning. Specifically, students persist in thinking about evolution in ways that are (a) teleological (i.e., causal reasoning in which a goal, purpose, function, or outcome of an event is taken as the cause of that event; Keil, 2006), (b) essentialist (i.e., some unobservable essential property, such as an “underlying reality” or “true nature” conveys category identity and causes observable similarities among category members; Gelman, 2003), and (c) anthropocentric (i.e., attribute human characteristics to non-human or inanimate objects; Gee, 2013). As such, evolution is a difficult concept for students to learn and may require conceptual change (Sinatra, 2003).

Conceptual change has been of strong interest in science education for many decades and must occur in order for most students to learn and understand evolution due to common misconceptions such as humans evolved from modern day apes or the impossibility that complex life forms arose from very simple ones (Sinatra, Brem & Evans, 2008). A relatively early theoretical position on conceptual change was established by Posner, Strike, Hewson, and Gertzog (1982), which later became known as the Conceptual Change Model (CCM; Pintrich, Marx, & Boyle, 1993). The CCM model incorporates Piaget’s knowledge assimilation theory (1976), which states that when students encounter a new idea it must “fit into” what they know.

The CCM assumes that students have their own ideas on concepts (e.g., naive theories about biology and biological evolution) that are inconsistent with scientific understanding. These naive theories must be modified through the most effective
instructional practices for students to fully understand a scientifically accurate perception. Students are then responsible for reflecting on their conceptions in order to resolve the misconceptions they may have. Conceptual change requires four conditions. Students must be (1) dissatisfied with their current conception and realize that their way of thinking does not answer all of the scientific questions that they may pose. (2) Students must find the new concept intelligible. Not only must students engage in and understand the topic but they must be able to explain it to their classmates. (3) Students must find the concept plausible. The concept must encourage students to solve relevant problems and answer the questions they are currently asking (i.e., the new concept must make more sense [to them] than their previous conceptions). (4) The new concept must be beneficial in that it must open new avenues of inquiry and expand to topics that hold student interest (Zirbel, 2004). Some biology curricula, such as the modeling-based labs in AP Biology (College Board, 2012), use the CCM as a learning framework.

Success in conceptual change requires appropriate teacher facilitation and sufficient cognitive activation experienced by students, both of which are heavily dependent on student’s activities and interactions within a classroom (Duit, 2010). As students become involved with computation they undergo unique learning experiences that allow for immersion within their computational models, this phenomenon is known as embodiment (which can facilitate transformative experiences; Wilensky, 2006). In biology learning, embodiment occurs as students imagine and develop new ideas about how certain biological agents interact within their own constructed systems (Wilensky, 2006). Students understand, imagine and personify what it is like to be a biological entity (such as a cell) in order to properly develop the appropriate computational processes (i.e.,
setting up parameters for cells). This type of learning contributes to conceptual change because embodiment makes evolution more plausible (believing it to be truthful), intelligible (knowing what it means) and fruitful (useful) as students become immersed (Vosniadou, Vamvakoussi, & Skopeliti, 2008) within their computational processes (i.e., models).

Students must grasp specific concepts at various biological levels in order to understand evolution. Frequently these steps of understanding occur in a specific order, and these steps are naturally built into the NGSS. In order for natural selection (the driving force of evolution) understanding to occur students must understand the concepts of variation and the fitness of organisms, variance of individuals within a population, reproduction over time and the concept of inheritance and heredity (Campbell et al., 2000). The typical steps in understanding natural selection for students occur in (1) the initial student understanding of spontaneous mutation variation, (2) the requirement of the change in the environment, (3) individuals with suitable characteristics survive, (4) characteristics are inherited and finally (5) over many generations the frequency of these traits may change in population (Brumby, 1979).

Even many advanced biology students believe the common misconception that a change in the environment induces mutation which adapt individuals to changed conditions, and these are the acquired characters are passed on (i.e., Lamarck’s Theory of Inheritance of Acquired Characteristics which was deemed incorrect through Darwin’s research; Catley, Lehrer, & Reiser, 2009). In reality mutation is spontaneous (and most often random) and only sometimes results from explicit environmental change (i.e., radiation which is frequently detrimental). Additional common misconceptions include
the distortion of the time scales of evolution or the belief that adaptation is a process that drives toward a positive end (Brumby, 1979). Students may represent these concepts computationally in order to combat these misconceptions through proper development of their input, interpretation and output which are based on real biological facts and principles (i.e., representing randomness). This becomes especially helpful to students as they start to develop ways in which their model outputs can re-inform the next set of input based on phenomena that occur in nature (Chandrasekharan & Nersessian, 2015).

Instructional practices associated with evolution should reinforce the ideas that many processes in the natural and physical world are open ended and dynamic. Because evolution is an emergent process, it is not neatly bounded, and it is ongoing without a clear start or end, ontological shifts in student thinking may be required for students to comprehensively understand evolutionary theory (i.e., the misconception that evolution is a direct process as compared to the accepted perception that evolution is an emergent process; Chi et al., 2012). Interestingly, such an ontological shift toward evolution as an emergent process may be facilitated by computational thinking because (the student process of) computation itself is an emergent process (Berland & Wilensky, 2015).

Social and Emotional Aspects of Evolution Learning

Unique ideas and thought processes that are just outside of students’ comfort zones, while still maintaining a low level of frustration, are optimal for developing a manageable environment to confront and consider conceptions counter to [students’] naive theories (Vygotsky, 1978). It is important to consider that learning about evolution affects students emotionally, culturally, and personally (Sinatra, Southerland, McConaughy, & Demastes, 2003). Maintaining comfortable emotions and sustaining
motivation are imperative in learning about evolution (Broughton, Sinatra, & Nussbaum, 2013). Using computational thinking in classrooms has the potential to promote positive experiences (Ioannidou, Bennett, Repenning, Koh, & Basawapatna, 2011) in learning biological evolution.

Cognitive dissonance may occur for students learning biological evolution if those close to them do not accept the notion or if evolution conflicts with religious beliefs. For example, some students hold a belief that as people accept the theory of evolution they become increasingly racist and selfish or that there is an inverse relationship between acceptance of evolution and personal spirituality (Griffith & Brem, 2004). Some biology students worry that the acceptance of evolution will diminish their sense of purpose and self-determination as they confront the idea that they may only be a mass of evolving neurons with no divine direction (Sinatra et al., 2003; Campbell et al., 2000). Not only do students have this worry, but it is also a major concern of biology teachers which leads to apprehension toward the subject matter (Griffith & Brem, 2004).

There is a possibility that evolution learning fosters frustration because associated concepts are complex and or abstract (Mead, Hejmadi, & Hurst, 2018). Educators who have more knowledge in biology (and of NOS practices), and have been exposed to scientific experiences (i.e., research projects) are less likely to have misconceptions and accept the theory (Nehm, Kim, & Sheppard, 2009). Therefore, not only is it important for students and educators to maintain comfortable emotions while learning the subject matter, but also that they have scientific aptitude (Mead et al., 2018).

In order for students to let go of old theories and accept new ones (i.e., about biological evolution), the new idea needs must be interconnected with other ideas they
already have about the world (Piaget, 1976). It is also beneficial for learning if their peers show an interest or belief in these new ideas (Dole & Sinatra, 1994). Fostering positive dialogue about differences in cultural or religious beliefs coupled with emphasizing the nature of science may be one of the most effective instructional methods for teaching evolution, especially when it is controversial for students (Pobiner, Beardsley, Bertka & Watson, 2018).

Computational thinking incorporates many of these aspects (positive emotions, motivation, personal relevance, and productive social context) and may provide a student learning experience that promotes deep understanding of biological evolution through embodiment (Wilensky & Reisman, 2006). Interestingly, standards of effective computational tools support positive learning experiences (including embodiment) because these standards encourage: (1) a low threshold, (2) a high ceiling, (3) proper scaffolds, (4) the enablement of transfer, (5) the support of equity and (6) systemic and sustainable experiences (Ioannidou, Bennett, Repenning, Koh, & Basawapatna, 2011).

Evolution and Teaching the Nature of Science (NOS)

On one hand, misunderstandings of the NOS may contribute greatly to resistance in learning evolutionary theory, but on the other hand, deeper understanding of the NOS could help students to better understand and accept the scientific validity of evolution (Nelson, Scharmann, Beard & Flammer, 2019). The NOS definition explored here (a systemic gathering of scientific information) demonstrates the interplay between science, intellectual and cultural traditions, which in turn can illuminate contemporary issues (AAAS, 1990). Biology instruction requires unique solutions and specific implementations tailored to address these misconceptions while developing student
understanding of the NOS. For example, students may need to engage in evaluating the connections between lines of evidence and alternative explanations that are both scientific (i.e., the theory of biological evolution) and non-scientific (e.g., intelligent design) as suggested by Heddy and Nadelson (2013). Such an evaluation may be facilitated through computational thinking (considering student use of and engagement with computational input, output, integration and feedback) and could help to reconstruct common misconceptions about biological evolution, such as teleologicalism, essentialism, and anthropocentrism (Sinatra, Brem, & Evans, 2008). It is reasonable to hypothesize that computation should strengthen student knowledge and NOS processes contributing to biology understanding, but it is unclear to what degree and in what ways (Gallagher, Coon, Donley, Scott, & Goldberg, 2011).

Language of evolution is another challenge for students because some terms such as design, need, theory and adaptation have everyday meanings, but are highly specific when learning about evolution. This language may contribute to misconceptions and are also linked to student understanding of the NOS (Sinatra et al., 2008). For example, evolution may be mistaken as a fact (i.e., due to misuse of the word theory) and not as an observable process that can be seen at all levels of biological organization, from the micro to the macro biological levels. These concepts are not limited to biology learning, but more broadly associated with the NOS. Evolution is (an example of) a specific topic where confusion between everyday language and scientific language may contribute to students’ misunderstanding. Therefore, computational thinking (i.e., using computation as a tool) may clear some of this confusion because students actively use NOS vocabulary as they construct knowledge.
NOS instruction also involves teaching about methodological principles of scientific knowledge, the nature of scientific understanding as well as the limits of scientific knowledge. As students better understand scientific practices and modes of thinking, emotional demands may diminish for those who view evolution as contrary to their religious beliefs (Sinatra et al., 2008). Furthermore, engaging in scientific practices may foster open mindedness and the idea that science involves the process of knowledge construction; it is not an intrinsic source for answers nor a contradiction to religious beliefs. Dole and Sinatra (1994) claimed that high levels of engagement required by complex activities such as inquiry, personal reflection and justifying reasoning, encourages students to compare their beliefs to the content of evolution. This willingness to think deeply about complex problems may allow for questioning of personal beliefs (Sinatra et al., 2003). Thus, higher engagement with NOS and scientific inquiry via computational thinking may be help students to practice methods facilitating their acceptance of the theory.

NGSS has chosen to embed the NOS within their three dimensions (a) scientific practices, (b) disciplinary core ideas and (c) crosscutting concepts (Lederman & Lederman, 2014). The NGSS’s three-dimensional framework posits that as students engage in scientific practices, they will develop deep understanding of both scientific concepts and the NOS (NGSS Lead States, 2013). The NGSS framework claimed that integrating scientific practices and content “will require substantial redesign of current and future curricula in order to provide increasingly sophisticated [science learning] experiences across grades” (p. 247). In the case of biological evolution, increasingly sophisticated learning experiences (such as computational thinking) could be used to
reconstruct naive theories that may contradict scientific understanding in a way that productively engages students. For example, because emergent properties associated with evolution provide difficulty for students (Chi et. al, 2012), the learning tasks associated with biological evolution in classrooms should allow for exploration of these emergent properties while also exploring the relationship between evidence and explanations. Computational thinking is a novel way to engage students and would mimic how scientists gather and evaluate reliable evidence and construct valid explanations (Lederman & Lederman, 2014).

NGSS: Biological Evolution as Unity and Diversity

In the United States, educational stakeholders formulated the Next Generation Science Standards (NGSS Lead States, 2013) based on the science education framework released the year prior (National Research Council, 2012). The NGSS integrates scientific practices, disciplinary core idea, and crosscutting concepts to form performance expectations (aka learning standards). Many of these performance expectations grant flexibility for educators and include both computational thinking as a scientific practice and biological evolution as a disciplinary core idea. The NGSS threads in specific scientific practices in which evolutionary biologists engage, such as computational thinking, both of which can be used to explore life’s unity and diversity.

There are a variety of NGSS standards that are emphasized by using examples such as the integration of biological unity and diversity with computational thinking across grade levels (NGSS Lead States, 2013). Educators already incorporate these standards into their classrooms using little (or very simple forms of) computation (based on the ways I have defined computation in this dissertation). At the elementary level (as
per the NGSS), students are expected to develop appropriate NOS processes and simple biological principles that set them up for more advanced biological evolution principles in middle school (as per the NGSS). For example, by third grade students should recognize life cycles and commonalities between life forms. In middle school, students are expected to analyze and interpret data for patterns in the fossil record that document existence, diversity, extinction and the change of life forms through Earth’s history (as per NGSS Performance Expectation [PE] MS-LS4-1). This student exploration takes place under the assumption that natural laws operate in the past the same way they do today (students are expected to apply these thought processes to historical evidence). Students should also be able to construct explanations based on evidence that describes the genetic variation of traits in a population. This includes those traits that increase an individual’s probability of surviving and reproducing in a specific environment (as per NGSS PE MS-LS4-4). At the middle school level students are also expected to gather and synthesize information about technologies that influence the way humans alter inheritance of desired traits in organisms (i.e., artificial selection or genetic engineering). Students should also be able to use mathematical representations to support explanations of how natural selection may lead to increases or decreases in specific traits over time (as per NGSS PE MS-LS4-6).

At the high school level, the NGSS (2013) prompts students to display and communicate appropriate information regarding common ancestry and that biological evolution is supported by many lines of evidence (as per NGSS PE HS-LS4-1). Students are expected to construct an explanation based on evidence that the process of evolution results from 4 factors: (1) the potential for a species to increase in number, (2)
heritable genetic variation of individuals in a species due to mutation and sexual reproduction, (3) the competition for limited resources and (4) the proliferation of those organisms that are better able to survive and reproduce in their environment (as per NGSS PE HS-LS4-2). Statistics and probability should be used to support student explanations that organisms with advantageous heritable traits tend to increase in an environment as compared to organisms without the trait (as per NGSS PE HS-LS4-3). Students should be able to construct an explanation based on evidence for how natural selection leads to adaptation of populations (as per NGSS PE HS-LS4-4). Students should also be able to evaluate evidence supporting the claims that changes in environmental conditions may result in: (1) an increase in number of individuals of some species and (2) the emergence of new species over time and (3) the extinction of other species (as per NGSS PE HS-LS4-5). These biological evolution areas from the NGSS can be naturally explored using the NOS. Frequently topics among these standards are presented in a disjointed manner and are not reconnected for students between grades or within holistic contexts in a way that (I claim) computational thinking would resolve.

*Computational Thinking*

Thoughts on computational thinking have progressed over time in terms of its definition, its necessity, its role in education and its relationship to various scientific disciplines. Depending on the domain (i.e., content area), specific reasoning topics or modes of thinking related to computational thinking have continued to emerge. This is especially due to exponential growth in technology which has in turn has contributed to theory (i.e., game theory and theoretical bioinformatics; Holyoak & Morrison, 2012). Computational thinking for example has been associated with the rising field of computer
science since the 1940s. Perlis, Simon and Newell (1967) wondered if computational thinking would span across fields by the mid 1960’s through integration within different domains; interestingly, this is one of the goals of the NGSS. For the purposes of our learning progression in terms of initial implication, it is suggested that educators consider current lessons they have and identify ways to incorporate computation. I suspect this assimilation process may become more complex over time as practitioners become more familiar with the constructs.

Certainly, this integration has not been fully realized and the question of how and why computational thinking spans across domains is still relevant. For example, should computation associated with weather (i.e., atmospheric computation) be integrated within the context of meteorology or should computational thinking be taught as domain general process? Some think of computational thinking solely within the specific context of designing models and developing the skills that are required for developing and designing software packages that are implemented by electronic machines (e.g., computers). Specifically, in the realm of education, it is thought that computational thinking will allow students to become better problem solvers in a digital world and across different disciplines (Denning, 2017).

Newel, Perlis and Simon (1962) argued that computer science was a legitimate area of study because of the complex thought process required by humans (Denning & Freeman, 2009). Thinking associated with computational analysis yields important empirical and theoretical results (Holyoak & Morrison 2012). Although there is overlap between computer science and computational science, there are distinct differences. Computer science is specifically focused on engineering, theory, experimentation, design,
and associated practices that are associated with computer technology. Although computational thinking may involve computers, the direct focus is using computation to explore scientific (and other) disciplinary problems (in other words, computation is at a trifold intersection of a domain [science], computational aspect and mathematical construct; Aho, 2012). Marr (1974) suggested that complex systems, such as computers and the human mind, have different levels of analysis: computational, algorithmic, and representational, with the computational level preceding the algorithmic level, which in turn precedes the representational level. Marr stressed the importance of the computational thinking as foundational. Aho (2012) similarly claimed that computational models are abstractions that are at the heart of computational thinking.

Today’s teachers struggle with what computational thinking is, how it is assessed and if it is appropriate for everyone to learn (Denning, 2017). The relevant problems regarding computational thinking are: (1) that there is that there is no consistent definition of for science educators (Selby & Woollard, 2013) (2) that researchers and educators are unsure of most effective methods of implementation in science classrooms (Wilensky, 2014) (3) and exactly if and how it is beneficial to science students (Speth et al., 2009). Defining computational thinking as such does not confine such reasoning strictly to computer science, but has implications across fields including biology, physics and chemistry.

*Computational Thinking Within the Learning and Teaching Process*

Vygotsky (1978) claims that knowledge is constructed through the interactions with others and with tools (e.g., the multiplicity of technologies that surround us, including digital artifacts of the media world and specialized processes of the digital
New technology is immersive in nature in that it supports, disrupts, and reorganizes human thinking and leaves humans to act and be acted upon based on actor-network theory (Latour, 2005). Therefore, key elements of computational thinking can allow us to think-with and in the learning and the teaching processes (Gadanidis, 2016).

With the exponential increase in technology, ethical concerns over fields such as bioinformatics, simulations (abstractions), and artificial intelligence (AI) are of interest to psychologists, mathematicians, computer scientists, biologists, cognitive scientists, and engineers. Moor’s computer ethics and bioethics have not yet been considered together, however the rise of bioinformatics alone warrants research in terms of the future of health care and other socioeconomic implications (Hongladarom, 2006). Artificial intelligence already has a platform in formal education, as AI can act as a tutor, facilitate open online courses, and is responsible for many online searches. Here I define AI as the study associated with developing computers and software capable of intelligent behavior. Agency and associated features of self-regulation and self-learning are key aspects of AI and synonymously student agency is emphasized in computational thinking education environments. Today’s students should explore the use, development, limits, future projections, and ethical concerns of AI.

Science education, artificial intelligence, and computational thinking each have three key elements which include agency, modeling, and abstraction (Gadanidis, 2016) all of which are important contexts for classroom incorporation. Our trajectory of engagement with abstraction seems to intensify as a society, especially as digital code writes war machinery (e.g., weaponized drones), stock market transactions, robotics, and
AI (Tamatea, 2019). Abstraction may play a particularly important role in AI development, as the programmer “tells” the computer how to recognize certain features and set parameters based on certain elements and variables. Abstraction is also the key element of computational thinking because concepts are generally symbolic and represented by code. Although Piaget claims that young children may not be capable of abstract thinking (Gadanidis, 2016), abstraction may allow students to better manage complexity by reducing complex information and details. In other words, exposing students to computational thinking at younger ages may allow for more effective learning later on (Gadanidis, 2016).

In many computational thinking practices, students must assimilate knowledge into what they already know about computational processes per Piaget’s knowledge assimilation theory (1976). Proper scaffolding of computational processes may facilitate a higher ceiling for students to abstract, automate, and dynamically model concepts, for both computational and content knowledge. For example, as students change computer code, they may simultaneously change parameters within their models. This allows students to manipulate and model information related to the content (e.g., students can “play” with concepts and bring them to life; Gadanidis, 2016). In such a learning scenario, computational thinking includes: (1) formulating problems for use with a computer to facilitate the solution, (2) logically organizing and analyzing data, (3) representing data through abstractions, (4) automating solutions through algorithmic processes, (5) identifying analyzing and implementing possible solutions as the most efficient and effective combination of steps and resources, and (6) generalizing and transferring this process to a variety of problem areas (Ioannidou, Bennett, Repenning,
Koh, & Basawapatna, 2011). I have modified (i.e., merged) and emphasized these (computational) components in my learning progression.

Peel, Sadler and Friedrichsen (2019) conducted a study in which natural selection was learned through computational thinking using an “unplugged” design method, meaning students used hand-written “computational” explanations. Such thinking might be considered simple, as defined by my proposed learning progression because computational tools were not considered. Students performed all components without technology. It was identified that abstractions associated with natural selection can be “extracted” from the computer, while still allowing students to emphasize the scientific process. This unplugged version was performed because students did not require access to a computer, nor did they need previous knowledge of coding. The results of the study indicated knowledge transfer of natural selection across contexts, and it reduced student misconception on the topic, and that “re-plugging” and incorporating additional computational components might result in greater knowledge gains.

Distinct Characteristics of Computational Thinking

The definition and application of computational thinking as a distinct mode of reasoning varies throughout the literature. For example, some have differentiated computational thinking from scientific thinking. Dunbar and Klahr (2012) defined scientific thinking as both reasoning about science content (e.g., force and motion, photosynthesis, and atoms and molecules) and reasoning like scientists (e.g., via induction, deduction, experimentation, and theory building; Dunbar & Klahr, 2012; Holyoak & Morrison, 2012). In this regard, scientific thinking does not necessarily involve computational thinking (i.e., where computational thinking is “thought processes
involved in formulating problems so that solutions can be represented as computational steps and algorithms;” Aho, 2012, p. 832).

Scientific thinking in itself does not necessarily involve computational thinking. Computation is the descriptive word, computational tasks are the actual acts performed by students and or scientists (or the like), and computational technologies are the (usually computer) programs that allow for students to perform computational thinking. Therefore, many aspects of scientific thought, such creativity and critique, fall outside of the idea of computational thinking as reasoning about problems through programmed steps and algorithms (Grover & Pea, 2013).

Computational thinking parallels computational science just as scientific thinking parallels science content. As shown in Table 1, computational thinking in the context of science learning is at the intersection of computer science, mathematics, and a specific science discipline. Computer science relates specifically to information sciences and associated technologies. Applied mathematics includes numerical models and statistics. Science disciplines involve knowledge and epistemic stances of a particular community of research and practice (e.g., biology, physics, or chemistry). When scientists use computational thinking, they apply computation, including information technologies, programmed steps, and algorithms to conduct observations, collect data, generate lines of evidence, and construct valid explanations about phenomena (Barr & Stephenson, 2011).
Table 1

*Computational Science Components and Associated Domains and Student Skills*

<table>
<thead>
<tr>
<th>Fields and Examples</th>
<th>Information Science</th>
<th>Mathematics</th>
<th>Scientific Discipline</th>
</tr>
</thead>
<tbody>
<tr>
<td>Data science, data structures, information technology</td>
<td>statistics, algorithms, graphs, variables</td>
<td>biology*, chemistry, physics, marine science, medicine, physiology</td>
<td></td>
</tr>
</tbody>
</table>

| Student Learned Skills | Data structures, refinement, appropriate programs to use, computer languages, computer theory, development of data | Relationship of input and output, applied mathematics, appropriate representations, modeling | content from discipline, questions posed from discipline, applied theory from discipline, appropriate selection of context from discipline |

*Note: *indicates my domain content area of interest

In terms of a science learning progression, computational thinking would involve students’ understanding and application of input, integration, output and feedback based on sets of questions and problems within specific scientific domains. Applied mathematical practices, such as algorithms and statistics, would also be crucial to developing and understanding concepts within domains at appropriate ability levels. Therefore, computational thinking would involve the knowledge and application of appropriate tools that merge the mathematical aspects and computational tools to ultimately display, revise and become immersed within (scientific) content specific models. Merging these educational aspects for the purpose of gaining knowledge is the type of higher-level learning that is expected of professionals within the field of biology; I propose this is also beneficial for biology students.
Computation must involve an input, integration, output and method of re-information of the input if appropriate to the construct. Student understanding of the most efficient practices and specific programs associated with their scientific practices is a key component in learning through computation. A student may model a scientific phenomenon using these aspects of computation however these aspects are distinct from modeling. Computation allows students’ models to be dynamic, changing and emergent. Computation may be in the form of a model, but not all computation are forms of models.

**NGSS Computational Thinking: Practice 5**

Because the NGSS has incorporated computational thinking into its core practices, Weinthrop (2016) provided four categories including data practices, modeling and simulation practices, computational problem solving practices, and systems thinking practices as essential components of computational integration for science curriculums. This type of thinking should be woven throughout math and science practices due to increased demand of technology education and the interdisciplinary benefits that may be associated with domain emphasis (Wing, 2006). Thus far, there are no examples of disciplinary content paralleled with computation which may be of use in classrooms (in the way I have defined computational components as a progression with increasing complexity).

The NGSS states that computation is a fundamental tool for science, engineering and mathematics learning in order to represent physical variables, recognize, express and apply their relationships across levels. According to (the progression of standards laid out by) the NGSS, in primary school computational thinking builds on prior experience and allows students to understand that mathematics may be used to describe the natural
world. At this level, students are counting and using patterns to describe the world while also designing simple graphs and alternate solutions to a problem. At the elementary level students are using computation and mathematics to analyze data and compare alternative design solutions. Students are also expected to organize data sets to understand patterns and relationships. Computation may be used to describe, measure, estimate or graph scientific questions or problems while incorporating simple algorithms.

At the middle school level students move to larger sets of data and use this data to support explanations and arguments. Students should be using digital tools to identify trends and support scientific conclusions. Students may be able to create algorithms to solve or design solutions. At the high school level students should be revamping various types of functions and computational tools for statistical analysis to model data. Simple simulations are created and used based on mathematical models or assumptions. Students should be revising or designing models that represent scientific processes or systems. Students should be comparing their models to the real world and what is known about their phenomenon (NGSS Lead States, 2013). The NGSS expects a gradual and achievable sequence of objectives (as listed above) through a series of events as students navigate through mathematical and computational thinking; however, the description of application as provided by the NGSS is vague.

The success of the integration of computational tasks in chemistry and physics courses has been explored (Gobert, 2000) however research gaps exist in how these tasks facilitate student understanding, learning and conceptual change in specific topics within these courses. A major unifying factor in biology is evolution at various scales, and distinguishes the field from the physical sciences. Rapid improvements and availability in
technology has increased the demand within the fields of bioinformatics and computational biology, however computational tasks are rarely integrated into life science courses and especially not in terms of a logical progression (Guo et al., 2016).

**Computational Thinking to Support Biology Evolution Learning**

The proposed framework compliments the idea that computational thinking supports learning biological evolution ultimately developing more advanced life science students who can reason and think like scientists. One of the best ways to represent the rudimentary concepts, intricacies and complex systems of biological evolution is through computation due to its robustness and disguised simplicity (Toffoli, 2004). In short, computational process has the ability to stand unaffected although input variables may change. This implies that the computational output may be very different from the input although the code is relatively straight forward for users. For example, a simple population growth rate formula consisting of a few variables may be used to re-inform itself through proper implementation of coding and biological principles to develop a vast display simulating multiple generations of associated evolutionary changes. Another example are the changes within representative strings of letters, including A’s, T’s, G’s and C’s, corresponding to the nucleotide sequences (adenine, thymine, guanine and cytosine) found within the genome of an organism.

These sequences may become computationally modified through a very simple “random” function via simulated generations to display a quantitative analysis of natural genetic mutations found in nature. The math behind the random function is hidden, as it takes a value \(x\) as defined by the user (i.e., students) and multiplies this \(x\) value by ‘rand\(x\)’ to provide a totally random output value which differs for each iteration. In
turn, these sequences may further be translated into the respective proteins and or altered and potentially displayed as defective proteins based on the random mutations that would occur in nature. Students could use simple compare functions to read through A, T, G, C nucleotide sequences of various organisms in order to develop broad yet accurate evolutionary relationships in the form of phylogenetic trees. Educators could use scaffolding and appropriate differentiation with the assistance of the LBECT-LP to determine appropriate classroom practices based on the biological examples above. For example, if students initially lack coding skills, they can perform the activity using Excel or Google Sheets versus software such as the R stats package (a free coding program). Each of the previous examples directly represents the phenomena of biological evolution computationally (Quin, 2009).

There is an important relationship between scientific knowledge, the learning of science and pedagogy (Driver, 1994). Adapting these NOS practices to classrooms provide benefits of authenticity for science learning and this includes techniques, attitudes and social interactions. Vygotsky’s Social Constructivist theory (1962) states that knowledge is co-constructed and it is imperative that individuals learn from each other in a way that increased social engagement. Although technology is important for classrooms and integration has been difficult to incorporate in practice, it allows students to become active learners (while using skills that are interactive contemporary and relevant; Edelson, 1997).

Some complex systems are integrated into the life science curriculum such as evolution, equilibrium, and homeostasis, but the overall theme that conjoins these ideas has not been developed. There are methods (i.e., agent-based modeling, information
flows, system environment interaction, developmental trajectories, self-organization etc.)
which allow for both domain based qualitative reasoning and quantitative modeling. The
gaps in the curriculum (due to inherent lack of computational implementation) does not
allow students to cognitively bridge between separate curricular elements and prevents a
conceptual framework of coherence. Complex system perspectives that may be explored
through computational modeling and network analysis provide new methods and insights
for learning science research. This research may potentially extend theory in the learning
sciences through computational modeling of systems for learners and educators.
Computation has the ability to enhance learning science research involving micro and
macro levels of cognitive learning (Jacobson & Wilensky, 2006).

The study of complex systems in association with computational technologies
allow researchers to study aspects of the real world where structure and order may coexist
at many different scales of time, space and organization. These ideas are being integrated
into other professions such as engineering, medicine, finance, law etc. and are not limited
to the sciences (further presenting the argument that this type of learning is important for
all students). The biological perspective involves interdependence and coevolution with
emergent patterns formed by self-organization and this understanding is fundamental to
biology but is not frequently practiced by students (Jacobsen & Wilensky, 2006).

Although modeling is not the only aspect of computation, integrating this practice
as well as other computational components has been very difficult in classrooms (Lehrer
et al., 2006). Students can start practicing computational thinking in the years prior to
kindergarten because modeling, an aspect of computational thinking is a complex form of
epistemology that must be developed early on in student careers (in order for them to
properly inquire about natural systems later on in their education). Models that work best for students are the type in which they can see the direct relationship between the natural world and the model such as a compost pile and they tend to find these types most relatable and easiest to understand (Krajcik, 2012); therefore, students can use computation to supplement these types of models. Professional scientists use models and computational thinking at all levels whilst solving problems so when the idea translates to the classroom, it should result in a variety of representations and models that can be used to build layers of description and potentially display different aspects of represented phenomena (Toffoli, 2004). Computational representations at different levels should relate to each other in ways that students can understand so their ideas should circulate and interlock resulting in a system that enhances student understanding of the natural world (Lehrer et al., 2006).

Students at all levels have difficulty working at the intersection of mathematics, computer science and a scientific discipline; these aspects are what prevent students from performing genuine research in the ways scientists do. When life science students conduct genuine research (usually through working on a portion of a mentor’s larger research project during a graduate and rarely during an undergraduate research experience) it is usually the first time they are faced with the task of developing their own questions while concurrently developing mechanisms using computation (i.e., coupling input with statistics) to answer those questions (Ryder et al., 1999). Inquiry based research projects and other activities that develop the foundation for students to start developing these basic scientific skills has started at the middle and high school levels and is becoming increasingly used by teachers and is reinforced through the NGSS
(NGSS Lead States, 2013). Learning and doing cannot really be separated when talking about scientific practices. This implies that students should learn to do something until it becomes second nature while using appropriate knowledge and tools to meet learning objectives (Bybee, 2011).

The Relationship between Biological Evolution, Levels of Organization and Computation

As students work with computational programs they learn to better set up problems and relate their working knowledge with tools that they have available. They may better lay out their problem at hand and intuitively select programs that may maximize input or have the right capacity for a working statistical analysis. Students may select which programs work well together to select the most appropriate display output for the intended audience (Chandrasekharan & Nersessian, 2015). The only way students may understand the best practices is by working with these specific programs, and eventually learning these new tools becomes easier. Students will start to think about content knowledge and data as sharing a relationship that is more intimate and interrelated since output may be looped back and used as new input within their systems (Jacobsen & Wilensky, 2006). Students may develop examples at all biological levels from computational scratch which would also enforce or challenge their working content knowledge in biology. The various levels of biological organization, relevant examples and computational aspects are displayed in Table 2.
<table>
<thead>
<tr>
<th>Level of Biological Organization</th>
<th>Broad Examples</th>
<th>Applicable Examples:</th>
</tr>
</thead>
<tbody>
<tr>
<td>Biosphere</td>
<td>Earth</td>
<td>- Ecosystem interactions</td>
</tr>
<tr>
<td></td>
<td></td>
<td>- Global nutrient and energy flow</td>
</tr>
<tr>
<td>Ecosystem</td>
<td>Estuary, open ocean, deciduous forest, tundra</td>
<td>- Environmental influence on biota at various levels</td>
</tr>
<tr>
<td></td>
<td></td>
<td>- Ecosystem modeling (nutrients &amp; energy)</td>
</tr>
<tr>
<td>Community</td>
<td>Grassland community, coral community, pond community, gastrointestinal microbiota</td>
<td>- Community structure and changes</td>
</tr>
<tr>
<td></td>
<td></td>
<td>- Interspecies interactions: i.e., competition</td>
</tr>
<tr>
<td></td>
<td></td>
<td>- Communal influence on organisms</td>
</tr>
<tr>
<td>Population</td>
<td>Honeybee population, osprey population, seagrass population</td>
<td>- Variation</td>
</tr>
<tr>
<td></td>
<td></td>
<td>- Interspecies interactions: i.e., competition</td>
</tr>
<tr>
<td></td>
<td></td>
<td>- Growth, decline &amp; carrying capacity</td>
</tr>
<tr>
<td></td>
<td></td>
<td>- Genetic (allele) changes within populations</td>
</tr>
<tr>
<td>Organism</td>
<td>Pitch pine tree, horseshoe crab, blue jay, diatom</td>
<td>- Competition</td>
</tr>
<tr>
<td></td>
<td></td>
<td>- Reproduction</td>
</tr>
<tr>
<td></td>
<td></td>
<td>- Energy conservation due to processes associated with homeostasis</td>
</tr>
<tr>
<td>Tissues and organs</td>
<td>Muscle tissue, heart, osteons (bone tissue)</td>
<td>- Similarities and differences within and among organisms hold evolutionary explanations (Vestigial structures, homologous structures etc.)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>- Exploring explanations for variations within populations and between species based on environment</td>
</tr>
<tr>
<td>Organelles and Cells</td>
<td>Nucleus, mitochondria, chloroplast, flagella, neurons, osteocytes</td>
<td>- Cell interactions within and between organisms operating under evolutionary principles</td>
</tr>
<tr>
<td></td>
<td></td>
<td>- Organelle structure operating under energy conservation principles</td>
</tr>
<tr>
<td></td>
<td></td>
<td>- Cell Structure operates under energy conservation</td>
</tr>
<tr>
<td></td>
<td></td>
<td>- Cellular evolutionary differences and similarities between organisms</td>
</tr>
<tr>
<td>Atoms, Molecules and macromolecules</td>
<td>Na+, Cl+, H2O, CO2, Protein, lipids, DNA, RNA, Carbohydrates (sugars)</td>
<td>- Diffusion, transport and molecule interaction working under energy conservation principles and availability within environment.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>- Similarities and differences between organisms</td>
</tr>
<tr>
<td></td>
<td></td>
<td>- Production, inhibition, blockage and development of systems using specific compounds based on environmental pressures</td>
</tr>
<tr>
<td></td>
<td></td>
<td>- Variation at this level (gene or protein)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>- Mutations occur at this level</td>
</tr>
</tbody>
</table>

Note: Examples of levels of biological organization and evolutionary (including: unity and diversity) principles associated that can be explored computationally in learning progression. Some of the levels (explored separately later in the dissertation) have been grouped together.
Evolutionary thinking is required as early as in middle school in order for students to properly model these biological systems later on in their educational careers. Leher (2006) claims building blocks of understanding of evolution include variability, change and ecosystems. Variability distinguishes between directed and random variation and students must understand the relationship between the change in organisms, populations and ecosystems and discover ways of describing interactions between organisms. Understanding involves coordinating change at all levels of biological organization and relating this to how it works in ecosystems. Leher claims that modeling and associated thinking processes allows students to think more deeply about evolutionary questions. Ideally by the time students reach high school, they have worked through the process required for complex evolutionary thinking through the process of various activities (such as modeling) as displayed in my proposed learning progression.

Forrest (1990) claimed that emergent computation requires the explicit and the emergent levels of a system to be developed and displayed through computation and information that is not present at lower levels will exist at the level of collective activities. There must be a collection of agents, interactions between agents and these agents must follow instructions which have directions at the macroscopic level, which parallels most biological systems. If the phenomenon being observed is also computation itself, there may be feedback between the levels. This idea is stressed in computational learning and as a principle in biology, especially in terms of evolution. Three themes of this phenomena are self-organization, collective phenomena and cooperative behavior (Forrest, 1990). The sum of the parts within a system is greater than individual parts, a common theme in biology as well as computation.
Biological functions are a result of mechanisms that occur at various scales and biological levels of organization (Campbell et al., 2000) as seen in Table 2. Modeling and simulations are computational tools that are necessary for description, prediction and understanding these mechanisms in a quantitative and integrative way. Dada (2012) claimed that understanding biological functions should be aided by computational thinking and encompass and span various spatial and temporal scales. Understanding systems in biology is not possible without using computational technology and looking at various levels of biology. These scales range from molecules, genes and proteins through to cells, tissues, organs, organisms and the interactions with other organisms and the environment (Guo et al., 2016). Time scales may range from microsecond to hundreds of thousands of years. In order to understand behavior of a system it requires various interactions that occur on these diverse scales. Exploration of these items occur now at the educational and professional level but the need is growing exponentially in the field of biology especially for research. Researchers may explore a top down or bottom up approach and approaches may be discrete or continuous. There are general computer languages and platforms that researchers may use, or explicit programs tailored for specific content based computational tasks. Regardless of the approach, in order to explore systems within biology, all levels must be explored and integrated through computation (Dada, 2010).

Of the few documented interventions which combine evolution learning with computational thinking there are none which span between the organizational levels of biology. Guo (2016) conducted a study involving high school students in which agent based software was used to simulate frog population changes over time. Although the
students did make knowledge gains in evolution, additional instruction and computational tools that would allow students to make better connections between micro and macro levels of biology were required (Guo et al., 2016). Students have trouble understanding the connections between these levels; the process of evolution, which operates at and between these scales, presents a promising opportunity for student exploration of these level connections. At any given time, topics in biology may be taught at a single level (molecular, cellular, anatomic, organismic, or ecological level) and ideas often become isolated from one another.

Parker et al. (2012) identified that because the explanations of phenomena apparent at one [biological] scale often lie at a different scale, biological level connections between the micro and macro levels contributes significantly to biology evolution learning. “Slippage between levels” is sometimes used to describe the disconnects (or student inability) to make micro to macro scale connections (Brown & Schwartz, 2009).

Cross level understandings may be explored through embodied experiences while using computational thinking. For example, as students better understand behavior of molecules, it allows them to get a better grasp on cellular processes, or as students develop an understanding of agent (i.e., organism behaviors), it may allow them to better explain ecosystem processes. These types of relationships would not only emphasize each topic, but should allow students to better understand biology as a whole (Wilensky, 2006). It is of benefit for all students to have the ability to think like scientists and use tools that promote scientific inquiry (Wilensky & Reisman, 2006). Even more so, computational thinking is not limited to science; computational skills and specific
software programs are increasingly used by professionals across disciplines and within associated careers.

*Computational Thinking Becomes a Working Tool for Students*

Computational thinking and learning is encouraged for student access in STEM careers because it becomes a working tool in problem solving that may also be applied in other domains. Computational experiences are becoming increasingly available to students due to reduced prices of technology and due to easier access to data and improved methods of data streaming during experiments (Jacobson & Wilensky, 2006). Realistic ways of doing science in the field involve both direct observations and computational modeling practices. It is becoming increasingly difficult for students to distinguish models and simulations from observations. Simulation translates everything including algorithms into digital information and uses computation to construct any object, even if it is an abstraction (Lenhard, 2010). This is due to the fact that many models have controlled sensors or external devices which stream and interpret live data. Practicing scientists have opportunities to use these technologies and there is a need to understand how students and teachers may best learn to utilize them in practice.

These complex system informatics and representation tools allow student development in thinking about, interpreting and representing data through relevant complex systems, concepts and principles such as those associated with evolution. Designing learning environments and selecting appropriate tools that make organizing conceptual framework explicit to the student is also important for instructors (Jacobson & Wilensky, 2006). It is important to develop students who can distinguish between data,
merge ideas and tools associated with computation which concurrently allow them to thrive within their content areas (Kong & Abelson, 2019).

This emphasis of student awareness with respect to computation and abstraction is a specific example and extension of Baudrillard’s (1981) book that described simulacra and simulation, as well as the relations between reality, symbols, and society. This book was one of the inspirations for the famous science fiction movie associated with computer science and programming, The Matrix (Wachowski et al., 1999), where (most of) the characters unknowingly start their lives immersed in a computational abstraction of reality (Tamatea, 2019). Baudrillard’s (1981) concern was that individuals within a society would not be able to understand or know the difference between truth, reality and simulation, in other words that the abstraction would be indistinguishable from reality. Copies of copies of copies of original information would be the entity that reaches individuals and that the hyper real rather than the real would inform discussions. For example, an individual may have never been to France however they know it exists due to news stories, pictures, maps and personal accounts. What they know of the country is not based on personal observations but is informed solely by societal constructs and abstractions. This idea may be similar to the “realness” of a scientific concept, such as the idea of a cell and how students may or may not understand and explore it. One of the criticisms of The Matrix film is that the select few main characters know when they are in the simulated world and when they are in the real world. The characters in the film use programming as a tool to better navigate and understand the simulation, and this idea is synonymous with technology infiltrating the sciences and science learning. Baudrillard (1981) states that abstraction will eventually be the only means through which we access
the real as we (as a society), already tend to prefer the map of France (abstraction) over the territory (which is real; Tamatea, 2019). Learning coding seems to be one effective way in which we can engage with the abstractions.

Students should be able to make distinctions between what they experience and what is constructed in science and simulations; without building these tools (i.e., through computational thinking) students may have difficulty distinguishing what is scientifically valid. Computational thinking practices would allow students to get a better understanding of the development of scientific simulations and representations (even though they might not fully understand them). Pioneer science, hypothetical experiments, in situ experiments, and computational models should be distinguishable for students. In today’s world, understanding information science and respective abstractions as it relates to science such as biology is extremely important because of the radical changes information science has already made (and will likely continue to make) in our society (Tamatea, 2019).

A Learning Progression for Computational Thinking in Evolution

Learning progressions (LPs) vary across the educational literature; however, Berland (2010) describes three explicit components of LPs. The initial component, (1) is described as a developmental progression for how understanding develops, the second component (2) as a progression in increasing levels of complexity of the disciplinary knowledge and practices, and the third component (3) is described as using pathways to support student learning. Analysis of disciplinary knowledge is essential for identifying the big ideas in science such as biological evolution, which is the primary focus of learning progressions. My specific LP, called learning biological evolution through
computational thinking (LBECT), is modified from Berland’s (2010) framework, which was grounded in both science studies of disciplinary practice and research on student learning. LBECT-LP focuses on merging dominant ideas in biological evolution and computational thinking practices. My goal is to assist practitioners in increasing computational thinking in classrooms, therefore the LBECT-LP is flexible. Educators must consider where they themselves, their students, and their districts are realistically situated in terms of practical application (i.e., when considering how to incorporate the LBECT-LP).

*Instructional Context, Computational Product and Computational Process*

The LBECT-LP has three dimensions as displayed in Table 3: (a) instructional context (i.e., educator role) (b) computational process (i.e., student activities), and (c) computational product (i.e., student artifacts). These three dimensions can be either simple, developing or complex depending upon the level and progression of the student. Each of the three components of the learning progression may be evaluated per student as they show evidence from the simple, developing or complex categories. The LBECT-LP includes various components, including student engagement by considering multiple student perspectives, constructive group interaction, and complex thought processes to process multiple pieces of information (i.e., computational process). These components continually align with learning biological evolution through computation across grade levels. Students have some idea of what biological evolution is however their elementary viewpoints or misconceptions may contribute to their multiple perspectives. Viewing evolution at various time scales and levels of organization provides various alternate perspectives. Computation activities may also be highly interactive and involve multiple
smaller pieces of evidence to construct the larger idea if properly scaffolded (i.e., instructional context).
<table>
<thead>
<tr>
<th>Instructional Context</th>
<th>Simple</th>
<th>→</th>
<th>Complex</th>
</tr>
</thead>
<tbody>
<tr>
<td>- Question closely defined with limited set of answers</td>
<td>- Data set large</td>
<td>- Question has multiple potential answers</td>
<td></td>
</tr>
<tr>
<td>- Data set is small</td>
<td>- Moderate scaffolds</td>
<td>- Students define or develop data set</td>
<td></td>
</tr>
<tr>
<td>- Detailed scaffolds</td>
<td>- Platforms with some coding</td>
<td>- Data set includes appropriate and inappropriate data</td>
<td></td>
</tr>
<tr>
<td>- Simple platforms (interfaces)</td>
<td>- Data set limited to appropriate data</td>
<td>- No scaffolds</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Computational Product</th>
<th>Simple</th>
<th>→</th>
<th>Complex</th>
</tr>
</thead>
<tbody>
<tr>
<td>- Idea is computationally represented, may be inappropriate</td>
<td>- Idea is computationally represented appropriately</td>
<td>- Idea is computationally represented in various forms</td>
<td></td>
</tr>
<tr>
<td>- Not most appropriate design or output representation</td>
<td>- More than one design was considered for output representation</td>
<td>- Most appropriate design or computational representation understood</td>
<td></td>
</tr>
<tr>
<td>- Student unable to produce written component describing computational process</td>
<td>- Student able to produce some written component describing computational process</td>
<td>- Student able to produce various types of open-ended written component describing computational process</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Computational Process</th>
<th>Simple</th>
<th>→</th>
<th>Complex</th>
</tr>
</thead>
<tbody>
<tr>
<td>- Weak development of input and little use of data modification and data synthesis</td>
<td>- Development of input and proper use of data modification and adequate data synthesis</td>
<td>- Student able to describe input and proper use of data modification and adequate data synthesis</td>
<td></td>
</tr>
<tr>
<td>- Weak development of mathematical/statistical component</td>
<td>- Development of mathematical/statistical component</td>
<td>- Student uses combinations of mathematical/statistical components</td>
<td></td>
</tr>
<tr>
<td>- Student unable to make connection between domain idea and computational aspect</td>
<td>- Student able to make connection between domain idea and computational aspect</td>
<td>- Student develops new connections between domain idea and computational aspect</td>
<td></td>
</tr>
<tr>
<td>- Model unable to reinform itself</td>
<td>- Model able to reform itself</td>
<td>- Model able to reform itself and other models and various output methods</td>
<td></td>
</tr>
<tr>
<td>- Student unable to produce written component describing computational process</td>
<td>- Student able to produce written component describing computational process</td>
<td>- Student able to develop new computational processes and ideas associated with domain</td>
<td></td>
</tr>
</tbody>
</table>

Table 3

Learning Biological Evolution Through Computational Thinking: Learning Progression
Table 3 specifically represents these components through students’ classroom behaviors (i.e., computational process) that promote learning about biological evolution. For example, the data used in the computational process in the LBECT-LP may be provided by the teacher or developed by the student through the computational process, depending on the level of the student (i.e., instructional context). Students may produce various complex outputs which they then will have to reasonably evaluate. Students will learn to make arguments that support their claims through the computational process. These claims will involve decision making regarding the data, computational reasoning, and the principles of evolution as their understanding improves within their domain area. Instructors can develop differentiated activities, rubrics, and assignments based on these three dimensions (i.e., instructional context). The NGSS standards can be appropriately assigned by the teacher depending on grade level using the LP.

As students progress from simple toward complex, initial questions provided through instruction will be closely defined with limited sets of answers and data sets will be provided, again as represented in Table 3. As students progress toward more complex understanding and thinking, the questions become multifaceted and students display understanding of multiple plausible answers. Eventually little scaffolding is required, and students must determine which data is appropriate and determine how to select their data using computational reasoning. The simple computational product is not necessarily represented efficiently or appropriately, and students have difficulty describing their computational process. As student abilities increase in complexity, their representations take various forms and become appropriate for the design at hand. There are various
types of representations and students can describe and justify their computational ideas as related to their content area. In terms of simple computational processes, students may have a weak development of input and have little data modification ability. There is a weak or provided mathematical component and basic understanding of the relationship between domain science and computation is evident. As students move toward a complex computational process, they are able to describe and justify input, manipulate proper modification or synthesize their own data. Students eventually develop and justify their mathematical representations and integrations. Students are also able to revise their thought processes and communicate the connections between the domain science and their computation. At the highest levels of complexity students may develop new computational tools (i.e., computational products) or representations or challenge domain specific content and ideas (Wilensky & Reisman, 2006).

Input, integration, output and feedback are integral components of the various aspects of computation as displayed in Table 4. The development of computational process and product through instruction as shown in Table 3, will encourage students to think more specifically about their computation. As students integrate content knowledge into their computational processes and products, they will not only be developing their content knowledge and computational skills, but they will also be improving their scientific communication skills.
### Table 4

**Components of Computational Thinking and Student Roles**

<table>
<thead>
<tr>
<th>Computational Thinking Component</th>
<th>Input</th>
<th>Integration</th>
<th>Output</th>
<th>Feedback</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Scientific Knowledge</strong></td>
<td>Student decides the variables to include based on scientific knowledge and practices.</td>
<td>Student decides which aspects of working science knowledge are important and which applied science concepts are important.</td>
<td>Students decide if and or how output applies to their problem or phenomena.</td>
<td>Does this knowledge support or contradict working science knowledge?</td>
</tr>
<tr>
<td></td>
<td>Student decides which aspects of working science knowledge are important and which applied science concepts are important.</td>
<td>Student identifies the strengths and weaknesses of each program based on their scientific problem</td>
<td>Students compare output to working knowledge and body of science knowledge.</td>
<td>Student decides how to re assess personal working knowledge.</td>
</tr>
<tr>
<td></td>
<td>Students decide if and or how output applies to their problem or phenomena.</td>
<td>Students decide how to re assess personal working knowledge.</td>
<td>What other types of questions might it solve?</td>
<td>Did I discover anything new that may contribute to science?</td>
</tr>
<tr>
<td><strong>Computational Knowledge</strong></td>
<td>Students select how aspects are represented or modified in the program?</td>
<td>Students decide which formulas will be used.</td>
<td>Students ensure robustness.</td>
<td>What other modifications or variables may make it more accurate?</td>
</tr>
<tr>
<td></td>
<td>Students decide which variables will interact</td>
<td>Students decide which program they will use and develop working knowledge as to why.</td>
<td>Students compare types of output.</td>
<td>What modifications may make it more robust?</td>
</tr>
<tr>
<td></td>
<td>Students decide which program they will use and develop working knowledge as to why.</td>
<td>Students decide which program they will use and develop working knowledge as to why.</td>
<td>Students decide which program they will use and develop working knowledge as to why.</td>
<td>Is the computational process efficient?</td>
</tr>
<tr>
<td><strong>Communication</strong></td>
<td>Students decide complexity and type of interface. Will it be for working problem solving only or communicated?</td>
<td>Is any pseudo code required?</td>
<td>Students decide the most appropriate format for output (graph, visual, numbers, sound, website, package, file etc.) based on audience.</td>
<td>How can this tool be used and applied to other disciplines?</td>
</tr>
<tr>
<td></td>
<td>Who needs to read or use the program?</td>
<td>Students decide which formulas will be used.</td>
<td>Students ensure robustness.</td>
<td>How may I modify to make it easier for others to use?</td>
</tr>
<tr>
<td></td>
<td>Students decide which variables will interact</td>
<td>Students decide which program they will use and develop working knowledge as to why.</td>
<td>Students compare types of output.</td>
<td>How can I make this a standalone package so that others can use it to solve the same types of problems?</td>
</tr>
</tbody>
</table>

*Note.* Student role may be in the form of question, action or artifact. Feedback is student deciding how to revamp model or how output might affect input.
The LBECT-LP facilitates students’ development of scientific knowledge, computational knowledge and communication skills as they experience the computational process and developing computational products. Specific computational components of input, integration, output and feedback examples are directly related to specific scientific, computational and communication skills as displayed by specific student roles in Table 4. For example, as students decide what information is important and relevant to their scientific discipline to solve problems related to the scientific phenomena at hand, they are contributing to their working knowledge associated with the scientific discipline. As students decide what equations to use and how they are related within their scientific field, they are further building upon their scientific knowledge. As they decide which information is important to display as output, they are evaluating which components of their scientific system is relevant. As students decide how to reintegrate information to inform their system, they are further engaging in making associations between working scientific knowledge within their content area.

As students are contributing to their scientific knowledge through these aspects of computation, they are also developing their computational knowledge as displayed in Table 4. As students decide which scientific input to use, they are better understanding how to define variables, a crucial component in computation. While students write their programs in computer code using relevant scientific information, they learn additional logical computational skills such as loops and if-then statements. When students display their output, they are learning which tools are available to visualize various representations and decide which is most relevant, another essential component of
computation and communication. As students re-inform their models, they are practicing revision, while ensuring their models are valid and robust, additional critical components of computation.

Various aspects of communication are a critical component of the learning process but also as a component of the computational and scientific learning aspect as displayed in Table 4. As students input their information and integrate their code, pseudocode may be used. Pseudocode is text written into computer code that is not processed by the computer, and only used as notes or a means to communicate with others reading their code. As students decide which information to display in their pseudocode, it dictates how many others may use their written script. When students decide how their code and packages run, it dictates how user friendly it is for others and essentially who can viably use their work.

As students progress from simple toward complex in the learning progression they will develop advancing understanding of scientific knowledge and computational knowledge. As additional scaffolding is provided through instruction, they will continually progress from simple toward complex understanding tracks within different scientific units or topics to get a holistic understanding of their phenomenon and eventually their domain. Students will start with simple scientific information as well as simple types of computation. The most developed types of scientific understanding occur as students start to make connections within and between their scientific domains as well as when students design and conduct their own research through asking their own questions in the context of gaps in scientific knowledge. The most advanced types of computational knowledge include efficient means of writing raw computer code and
developing packages and software in various computer languages. Although these are the most complex aspects of the learning progression, simple computation may involve programs with user friendly interfaces (e.g., MS Excel, Scratch, or App Inventor).

Construct Maps: Biological Unity and Biological Diversity

To break down the LBECT-LP further, I developed four construct maps representing student learning of biological evolution through computational thinking. Shown in Figures 1 through 4, these maps represent two fundamentally important ideas for learning about biological evolution: unity (Figures 1 and 2) and diversity (Figures 3 and 4). These construct maps have been developed (by me) by adapting Plummer’s (2010) LP for lunar motion and spatial reasoning. These maps reveal a structured process toward a more complete student understanding of evolution. Based on Plummer (2012), the LP shown in each map is dependent upon the instructional design that supports student progress toward understanding. The LP presents cognitive challenges as presented by the lower levels of understanding evolution as students progress to deeper levels of understanding (Plummer, 2010). This idea of progression is well accompanied and supported by computational thinking and integrates embodiment, which can further enhance learning.
<table>
<thead>
<tr>
<th>Level 5</th>
<th>Accurately explains evolution through the unity of life. Apparent similarities between organisms is described through the evolutionary process using multiple lines of evidence.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Level 4</td>
<td>Construct applications to support explanations as to how a trait may change over time leading to longer term changes in biological systems based on the idea that life shares a common ancestor</td>
</tr>
<tr>
<td>Level 3</td>
<td>Constructs explanations based on evidence that the process of evolution results from 4 factors: the potential for a species to increase in number, the heritable genetic variation of individuals in a species due to mutation, competition for limited resources and the proliferation of those organisms that are better suited for their environment</td>
</tr>
<tr>
<td>Level 2</td>
<td>Constructs evidence that changes in environmental conditions result in: increases in some individuals of a species, emergence of new species over time and the extinction of others</td>
</tr>
<tr>
<td>Level 1</td>
<td>Constructs explanations based on evidence for how natural selection leads to evolution of populations from a common ancestor</td>
</tr>
</tbody>
</table>

*Figure 1. Student understanding of evolution via unity at increasing complexity*
Goal: Increasingly engaged in computation as a multistep process of manipulating computational information. Students should be relating biological concepts associated with unity at various temporal and organizational scales to describe the evolutionary process using computational tools.

Considers how evolution works at different time scales and levels of biological organization. The common relationship between organisms at these levels can be described through methods of computational thinking.

Common ancestor-based frame of reference: increasing sophistication in understanding the interactions that take place in biological systems over time based on the idea of a common ancestor.

Constructing explanations that connect life across time scales and organizational levels. Increasingly sophisticated use of embodiment allows students to understand and distinguish how fundamental units in biology will interact at the various levels and time scales. Students can relate these ideas back to common ancestry.

Figure 2. Computational thinking associated with unity progress. Students should be increasingly engaged in computation as a multi-step process of manipulating evolutionary information and embodiment. Students will be exploring and producing evidence for the unity of life as explained by the evolutionary process through computation.
<table>
<thead>
<tr>
<th>Level 5</th>
<th>Accurately explains evolution through the diversity of life. Apparent differences between organisms is described through the evolutionary process using multiple lines of evidence.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Level 4</td>
<td>Construct applications to support explanations as to how a trait may change over time leading to longer term changes in biological systems</td>
</tr>
<tr>
<td>Level 3</td>
<td>Constructs explanations based on evidence that the process of evolution results from 4 factors: the potential for a species to increase in number, the heritable genetic variation of individuals in a species due to mutation, competition for limited resources and the proliferation of those organisms that are better suited for their environment</td>
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</tr>
<tr>
<td>Level 1</td>
<td>Constructs explanations based on evidence for how natural selection leads to evolution of populations</td>
</tr>
</tbody>
</table>

*Figure 3. Student understanding of evolution via diversity at increasing complexity*
Goal: Increasingly engaged in computation as a multistep process of manipulating computational information. Students should be relating biological concepts associated with diversity at various temporal and organizational scales to describe the evolutionary process using computational tools.

Consider how evolution works at different time scales and levels of biological organization. The relationship between the diversity of organisms at these levels can be described through methods of computational thinking.

Constructing explanations that connect life across time scales and organizational levels. Increasingly sophisticated use of embodiment allows students to understand and distinguish how fundamental units in biology will interact at the various levels and time scales.

Biological ‘unit’ based frame of reference: increasing sophistication in understanding the interactions that take place in biological systems over time.

Figure 4. Computational thinking associated with diversity progress. Students should be increasingly engaged in computation as a multi-step process of manipulating evolutionary information. Students will be exploring and producing evidence for the diversity of life as explained by the evolutionary process through computation.

Each construct map has the scientific explanation for separate biological phenomenon as the top anchor. These construct maps can be staked or aligned to create a full learning progression toward a core idea, biological evolution. For each of the two topics (unity and diversity) there are three integrated elements of the LP: the model of cognition, instructional design, and assessment (Plummer & Krajcik, 2010). As students gain scientific knowledge through learning the NOS and applying computational thinking, emerging ideas, capacities for computation, alternative representations, and
causal reasoning are shown. Students should be engaged in higher ways of knowing, learning and thinking about ideas, evidence and claims associated with evolution. As the LPs start earlier in a student’s education the communication, thought processes and computational abilities will become more advanced in association with biology (Duschl, 2011).

Conceptual change about evolution would be facilitated by computational reasoning because computational thinking will increase students’ cognitive engagement (Dole & Sinatra, 1998). Of the various factors that allow conceptual change associated with evolution, embodiment, is key. Embodiment is achieved through the necessary components of computational thinking as students put themselves within computational models to think how the model agents and components of the model would interact (Wilensky & Reisman, 2006). For example, in the Dole and Sinatra (1998) conceptual change framework, embodiment could promote a higher degree of cognitive engagement through greater elaborative connections and more metacognitive reflection.

Computational thinking and its facilitated embodiment relate to the importance of how evolution spans across temporal and organizational levels of biology while it also parallels emergent computation through learning.

Pathways to really understand evolution become evident through the learning progression which includes instructional context, computational product and computational process as paralleled by appropriate construct maps displaying the process of unity and diversity of life as explained by biological evolution. Each construct has different component of evolution at top of anchor can be stacked or aligned to focus on that single idea (Wilson, 2009). The bottom anchor is the evidence and learning progress
of students. These two models as displayed by Figures 1 through 4 have been modeled from Plummer’s (2010) progression, changing astronomy learning through spatial thinking to biological evolution learning through computational thinking.

Two major ideas unity and diversity are displayed as construct maps in Figures 1 through 4. The understanding of evolution through unity and diversity each represent a different map and each have levels 1-5 which correlate with NGSS standards. The corresponding tables (Table 2 & 4) displays how computation will be used to support the learning progression of evolution. The major difference between unity and diversity learning would be, unity focuses on common ancestry and uses this as a lens to explore evidence and generate computational processes whereas the diversity component focuses on the diversifying of organisms through more of a phylogenetic approach or looking at things from a larger environmental aspect. Aspects of both unity and diversity can view all levels of organization and a variety of time scales however unity would naturally align with smaller levels and diversity at larger levels. This can and should be done computationally for both unity and diversity, using computation as a bridge between physical and temporal scales.

Considering Previous Studies through the Lens of The Learning Progression

Because computational reasoning involves inquiry, students have the ability to see changes in real time through the constructive nature of computation and building computational models. Learning about specific controversial topics such as evolution may lead to conceptual change if common obstacles between conceptual change and evolution are overcome through computational thinking, contributing to student understanding of biology and a more advanced understanding of the NOS.
Computational learning requires appropriate scaffolding however the best practices, facilitation and student interactions that enhance computational thinking in students in order to induce conceptual change are still unknown. Previous research studies have primarily used user-friendly programs such as Netlogo or Scratch. Educational research associated with computation have used specific interventional tasks and it may warrant interaction between various communities (i.e., computer science or scientific community). For example, Wing (2006) has stressed the importance of the computer science community in educational research regarding computation.

Agent Based Computational Biology Study

In their NetLogo study, Wilensky and Reisman (2006) found that students were able to develop explanatory models of various phenomena and made sense of problems on their own through this computational process. The students tended to go back and forth between new hypotheses and researching existing solutions. Talia, a particular student who partook in the study, modeled a predator - prey relationship across generations. Frequently, biologists use a mathematical model to simulate this equation. Talia was able to display understanding of what was occurring in the model while simultaneously describing the predator prey Lotka - Volterra model discreetly. Talia developed the idea that many of the components in the model are random which is very difficult for students to understand on their own without using a computational tool. As her models did not match what would occur in nature, she continued to change her parameters until the output matched what would make sense in nature or what would make sense to her working knowledge. She wanted to set parameters around her model that would mimic nature but through this process she came to various conclusions about
why her observations resulted in ways they did. As she set out to correct her model, she underwent the process of debugging and sought out literature that was associated with her phenomenon. She found that her model fit the Lotka-Voltera model and also realized that modeling in a lab is different from nature, and there are different assumptions and parameters that must be added at each level of organization. In many cases such as Talia’s students start to think differently about biological rules and phenomenon.

Paul, another student who took part in the NetLogo study used the program to study the pattern of flashes displayed by a specific species of firefly. In nature there are rules and patterns that alter the flashing patterns of these insects. Paul wanted to understand this behavior by modeling the rules in NetLogo. Paul made initial assumptions such as the fact that all fireflies follow the same rules or that the fireflies’ mechanism becomes synchronized upon coming into contact with other fireflies. He began with a simple model but was left to think about other additional rules as to why the fireflies would synchronize with each other. He related these rules to ideas associated with environmental conditions as he ‘thought like a firefly’. He had to think about the type of information each firefly would receive as an input. He proceeded to research the literature in order to develop better modeling practices. As his model developed more questions presented themselves. He thought about how he could change his model to fit other species and why there were outliers in his program. As his research continued, he developed a decision-making process and unique tools that merged identifying relevant content knowledge with computational thinking. Paul actually developed new knowledge from his model that contributed directly to the field and this information would have been nearly impossible to discover through field work alone.
The Role of Instruction in Improving Computational Thinking in Learning Biological Evolution

The Advanced Placement (AP) Biology Curriculum as developed by College Board stresses aspects of computation and modeling reflected by the NGSS. The curriculum also promotes the importance of understanding evolution, reflecting evolutionary evidence and relevance within every section. AP biology courses are thought to be the most complex life science course offered at the high school level and should prepare students for the scientific thinking required of college students.

In the AP biology curriculum there are labs which require computational thinking in order to display and work through evolutionary content. Students essentially develop methods to display a series of generations within a population or use a free database and associated computational tool (https://www.ncbi.nlm.nih.gov/) in order to develop phylogenetic trees. As students model their simulated populations based on code, modifications and proper display methods they eventually work to generate proper working explanations which involve multiple levels of organization as well as a proper understanding of time to explain evolution. These explanations merge working biological principles with computational principles and the models may become more advanced as students develop their skills and content knowledge. The tools provided by the College Board frequently become outdated (as current biological websites frequently change) and both of the examples from the AP biology curriculum are difficult for teachers (and students) to follow. Because these are lessons that students within AP biology should already be receiving, I have modified them to emphasize computational
aspects within my dissertation study. I elaborate on these lessons in Chapter 3 and Chapter 4 as they became my interventions used in this dissertation study.

The type of learning that supports, develops and enforces computational thinking is not currently supported by many scientific disciplines in classrooms and it is especially not supported by the teaching of biological evolution. There are a variety of reasons why computational thinking is not supported in biology classrooms including teacher preparation and their comfort with the technology and concepts. This frequently drives the discussion on whether students should learn programming separately within a stand-alone course or incorporate computation within their other domain courses. The stand-alone course would be taught by a programming or computer science teacher, likely with limited content specific applications and, students would not be required to take the course, limiting the population of students who would be exposed to computation.

The nature of math and physics courses makes computational thinking more applicable because there are less variables within systems associated with these domains. It is easier for students and instructors to directly relate mathematical equations and concepts to these fields. However, in biology there are systems with very complex webs and interactions of variables between levels of organization. In terms of programming, this would include more if and then statements within code however the simplicity and complexity of evolution may be displayed with applied computational thinking at the appropriate level of the user (as displayed in the LBECT-LP). This may pose greater benefit to the student because simple computation to display evolutionary principles may develop into more complex ones. In many computational marine labs for example the interactions between organisms that are modeled are assumed however the overall model
still works well and displays what we know is occurring in nature. As more knowledge is gained, the model becomes more specific and complex, and the unknowns become replaced with knowns as the models are developed.

Research Questions

The three research questions for the dissertation study focused on gains in computational and evolution knowledge as well as exploration of the complexity of these gains. The research questions are:

1. How does instruction promoting integration of biological evolution concepts and computational processes (input, integration, output, and feedback) compare to instruction focused only on biological evolution concepts, specifically in changing students’ knowledge of biological evolution?

2. How does instruction promoting integration of biological evolution concepts and computational processes (input, integration, output, and feedback) change students’ knowledge of computational processes (i.e., input, integration, output, and feedback)?

3. In what ways do students’ computational products (artifacts) constructed during instruction promoting biological evolution concepts and computational processes (i.e., input, integration, output, and feedback) display:
   a. Student understanding of different levels of biological organization (i.e., from molecular to ecosystem scales); and
   b. Different levels of complexity in computational thinking (i.e., simple, developing, and complex)?
The two interventions both of which merge computational processes (input, integration, output and feedback) and biological evolution were implemented during biology instruction. Traditional teaching methods pertaining to biological evolution were compared to teaching methods which concurrently promote computational processes. I developed two instruments (as described in Chapter 3), one to measure student knowledge of biological evolution (RQ 1) and the second to measure student knowledge of computational processes (RQ 2). These two instruments provided measures of student biological evolution knowledge and computational processes knowledge before the interventions, after the first intervention as well as after the second intervention. Due to separate classes being exposed to traditional teaching methods and teaching methods involving the two interventions at separate times, the traditional teaching methods were compared to the teaching methods which promoted computational processes. This comparison was done through comparing student knowledge of biological evolution (RQ 1) and student knowledge of computational processes (RQ 2) using the two developed knowledge measures for the separate classes.

The instrument which measures student knowledge of biological evolution contained 18 multiple choice items. These items have been selected and modified from a combination of standardized tests and practice materials pertaining to biological evolution. This biological evolution knowledge instrument was given as a pre-test, after the first intervention and after the second intervention.

I have also developed a knowledge survey on computational processes which includes the components of input, integration, output and feedback to measure knowledge of computational processes. There are no previously developed instruments which
measure the specific computational processes as proposed in the learning progression.

The knowledge of computational processes survey was given before the interventions as a pretest, after the first intervention and after the second intervention.

I qualitatively analyzed student artifacts obtained from instruction during these interventions. The analysis included a qualitative content analysis on the student artifacts coding for inductive themes pertaining to RQ 3a, student understanding of different biological levels of organization and for item RQ 3b, the complexity of computational thinking. The levels of biological organization ranged from the molecular to ecosystem scales as displayed by student artifacts. Different levels of complexity in computational thinking were measured as simple, developing and complex as defined in the learning progression. I further explore and expand upon the methodology of the dissertation study in Chapter 3.
CHAPTER 3

METHODOLOGY

The purpose of this dissertation study was to explore the relationship between computational thinking and science learning. More specifically, whether or not computational thinking practices had an impact on student learning about biological evolution. I further examined the complexity of computational thinking through the constructs of computational processes: input, integration, output and feedback as exhibited by students. I also explored if students made connections between levels of complexity in biological evolution, from the micro scale through the macro scale.

In this chapter, I describe and justify the experimental design, the methods of data collection and organization, as well as the analyses that I used in this study. I begin by presenting the setting, participants, and an explanation of the research design and sampling technique that I used. I describe the two interventions that were presented to students and the timeframe and order that students received these interventions. I then describe how each of the two instruments were created and validated, and how they were administered in my dissertation study. I used these methods so that groups were compared appropriately, and the needs of the cooperating teachers were considered. In conclusion, I present an explanation of the analysis methods that I used for each of the two research questions, my theorized expected outcomes, and future implications. The appendices provide examples of the computational knowledge and evolution knowledge instruments and interventions that I used in the dissertation study. The appendices also include student examples from a pilot study that was used to inform the dissertation
study. Additional documentation of permissions for the dissertation study include
waiving of Temple’s IRB and district permission, which are also found in the appendices.

Setting and Participants

Setting

The Pine Bay School District

I performed the dissertation study in the Pine Bay School District (I am using a
pseudonym for the name of the district to protect anonymity, as well as pseudonyms for
the two high schools in the district, which I call the East School and the West School).
This district is located near the coast in the mid-Atlantic region of the United States. The
Pine Bay District is home to ten total schools within one township, educating
approximately 9,000 students at a time. The district is comprised of six elementary
schools two middle schools and two high schools. I conducted my research at two large
public high schools which collectively comprise the secondary schools within the one
large school district. The two high schools are the focus of the study, with the East High
School opening in 1964 and the West High School opening in 2006. Although many of
the programs and curriculums between the schools are the same, the number of students,
the school culture and the social demographic of students at each school varies slightly.

The East High School

There are 1,558 students who attend the East High School and are evenly spread
among the 9th through 12th grade levels. Eighty four percent of the school identifies as
White, 7% as Hispanic, 6% as Black and 3% as Asian. Multiple races and American
Indian/Alaskan Native comprise less than .1% of the school. Forty six percent of the
students identify as female while 54% identify as male. Ten percent of students are
enrolled in the free lunch program while 4% are enrolled in the reduced price lunch program with a total of 14% of students who are economically disadvantaged. According to the state-required tests (PARCC & SASC [pseudonym]) a majority of students fall within the 30th percentile for college and career readiness. There is a 14:1 ratio of staff to students. The graduation rate at the East High School is 94%, with a mathematics proficiency of 23% and a reading proficiency of 28%. Because the focus of the study is on students enrolled in AP biology at both the East and West high schools, the following information is presented regarding AP course statistics for the East High School. The national percentile on college-level exams (AP exams) is 83% at the East High School. The proportion of 12th grade students who took an advanced placement course is 43% and those who score over a three on the exam is 30%. Exam takers in 12th grade who scored over a 3 on the exam is 60% with an 59% overall exam pass rate (greater than 3) for the school.

The West High School

The West High School is also part of the Pine Bay School District and services grades 9 through 12 with a population of 1,285. The building is significantly newer and there is a staff to student ratio of 13:1. Seventy seven percent of the population identify as White, 13% as Hispanic, 7% as Black, 3% as Asian and 1% as multiracial. Forty nine percent of students identify as female and 54% identify as male. Twenty two percent of students are involved in the free lunch program while 7% receive reduced price lunch with a total of 29% economically disadvantaged. The overall percentile for college and career readiness at the West High School is 30.5%. The national percentile on college level exams (AP exams) is 75%. The proportion of the 12th grade class who took an
exam is 35% and those who scored over a 3 on the exam is 23%. Those students who are in 12th grade who scored a 3 or over on an AP exam is 68%. The exam pass rate (greater than a 3) overall at the West High School is 54%. The mathematics proficiency is 13% and the reading proficiency is 37%. The graduation rate is 94%. Neither high school is entitled to Title I funding. These statistics were obtained through the US News & World report for the 2016-2017 school year (this was the most recent data available).

*AP Students within the Pine Bay District*

Advanced Placement (AP) courses are academically rigorous and have been developed by the College Board. Within the Pine Bay District, many AP courses are reserved for 11th and 12th grade students who have met specific academic requirements. In the event a student does not meet the requirements, they may advocate to enroll in the class under specific circumstances after obtaining permissions. There is one teacher responsible for the AP biology courses at the West School and one teacher at the East High School. Each teacher has one AP course open to those students who opt to take the class and one for those who are in the STEM program. 9th grade STEM students are required to take AP Biology within the district. Therefore, all those who are in the STEM program and enrolled in AP Biology are in 9th grade and travel together throughout the school day while the other AP class is reserved for students who meet academic requirements and have an interest in the course. All students enrolled in the course are expected to take the AP test in May. Those students who score a three or above may receive some form of college credit depending on their prospective school and chosen major. The local community college has also offered college credit for students enrolled in the class regardless of the AP test score. If students and parents decide to obtain and
pay for the credits early during the school year and if they pass the course they will obtain community college credits. Although both AP teachers follow the same curriculum, they are entitled to academic freedom within their classrooms.

Participants

The participants involved in my dissertation study were those enrolled in AP biology for the 2019-20 academic school year within the Pine Bay School District. This includes two AP biology classes at the East School and two classes at the West school. One class at each high school consists of “traditional” AP students, upperclassmen who meet the AP biology academic requirements and decide to take the course. The other class is reserved for those 9th grade students enrolled in the STEM program. Students enrolled in the traditional AP courses have generally taken a Biology course before whereas the STEM students are new to secondary biology. STEM students were selected in the 8th grade after passing a science specific test and have parents or guardians who have advocated that they become enrolled into the unique STEM program. These students are enrolled in the same rigorous science and math courses throughout high school and have a choice of electives. In order to stay enrolled in STEM students must maintain an above average GPA and continue to meet dynamic STEM program expectations.

For the dissertation study, I used all AP biology students within the district. Consent and assent was waived due to exemption from Temple’s IRB. I was exempt from IRB because interventions and classroom activities were modified versions of topics which were already present in the curriculum. These students are split between two AP biology teachers respectively. The STEM class enrollment size tends to be similar
between the East and West schools, however there tends to be more students interested in taking AP biology (and AP courses in general) at the East School as compared to the West School. I collected student specific data through Genesis, which is a web-based student information system database where all district and individual student information is stored. The information I needed was limited to gender and ethnicity data.

Class Format

Students at the East and West High Schools attend AP biology once daily. Each class meeting is approximately one hour and twenty minutes. The instruction is varied to also include laboratory experiences some of which are outlined in the AP lab manual (College Board, 2019). Teachers at both high schools have attended AP training and are devoted to providing rigorous instruction. Biology was a tested science for the past six years in the state. Recently the testing switched toward a comprehensive science test, part of the SASC which is given to 11th graders. The science portion of this test also assesses sciences practices. Passing each section (language, math, science) is required for graduation.

Experimental Design

In this section, I describe the overall experimental design, the study materials, both of the data collection instruments and provide a description of both interventions. I then describe a pilot study which was used to inform the dissertation study followed by the procedures and data analysis used for the dissertation study.

The dissertation research was a quasi-experimental within group and between group combination design study. Students were tested and compared over time (within group) as well as compared to other groups or classes that had received different
interventions (between group). Because groups of students were nested within classes, it was important to consider distinct initial differences between the groups ensuring that the groups are truly random to start. The research design fits the parameters of a quasi-experimental design because if the groups were not truly random to start (although statistical methods indicated they were), the independent variable (computational intervention vs traditional teaching method) would have been manipulated before the dependent variables were measured (computational and evolutionary knowledge). After data collection, I identified if there were major differences among pretest variables within classes. This was done to indicate if the data should be normalized, treated as different initial groups or if the data should have been summed prior to analysis (Cook & Campbell, 1979).

The dissertation research was a modified pretest-posttest design study. The pretest was given to all groups and the posttest 1 was given was to both groups although only one group received the computational intervention. After this initial posttest, the group which did not receive the intervention received a different computational intervention (intervention 2) and the initial group who did receive the intervention (intervention 1) received traditional education. A second posttest was administered to all groups. The pretest, posttest intervention 1 and posttest intervention 2 were compared between both groups over time. The groups of classes are dependent upon the time the class was exposed to the computational intervention (either first or second). This type of design which merges nonequivalent groups with a pretest posttest design is considered better than either of the nonequivalent groups or the pretest posttest design alone because it combines aspects of nonequivalent groups with the pretest posttest design (Cook &
Campbell, 1979). The dependent variables (or computational and evolutionary knowledge) were tested and compared between the groups (classes) for the pretest, posttest intervention 1 and posttest intervention 2, potentially indicating if there was more of an increase in knowledge associated with the computational teaching interventions. The pretest, posttest intervention 1 and posttest intervention 2 contain the same items in the same order, the only difference was the time that the students took the tests. This study is also considered an action research study (as described in the sampling methods section). The design of the study used mixed methods because both quantitative methods as well as qualitative methods were used. Quantitative methods were used to identify differences in the resulting knowledge between groups and how much difference exists between them and qualitative methods were used to explore complexity of computational and biological evolutionary knowledge while also potentially providing further insight (Palinkas et al., 2015).

For my dissertation, I analyzed data collected from all students who were present on the testing days. Because some students were absent periodically, combined with the fact that the classes of students have distinct nested differences, the sample was not considered random. As a full time high school teacher, part time college professor and graduate student, accessibility of my sample was a priority when choosing a site to consider for the study. Due to the circumstances, the samples for the dissertation study and the pilot test may be considered convenience samples (they were easily accessible by me the researcher). According to Etikan, Musa, and Alkassim (2016), convenience samples are sometimes not representative of the whole; they include biases of the researcher and produce limited results.
These limitations of convenience samples are not applicable for this dissertation study because specific criteria were met for students to be included, indicating that it is more likely a purposive sample rather than a convenience sample (Etikan, Musa & Alkassim, 2016). In order to be included in the study students must be enrolled in AP biology within the Pine Bay School District, therefore students purposefully enrolled in the course. Purposeful sampling includes accurately representing a specific larger group. In this case, the sample of students of the Pine Bay District represented in the study are accurate representations of students who would enroll in the course across similar districts, assuming AP and life science students are the larger group. It is also helpful during purposive sampling to set up comparisons among different types of cases. The students of the Pine Bay District are nested within classes, teachers and schools and can be compared if necessary for future study.

The dissertation study may be considered a variation of action research. Criticisms of action research include researcher bias, or lack of scientific rigor while conducting research due to the fact that the researcher may be closely involved with the community in which they study. Greenwood and Levine (1998) defined action research as instances when the researcher intervening encourages the community with whom the researcher is conducting research. The researcher does this to investigate their own social condition to recognize the constraints operating on it with the goal of improving it. In many cases the action researcher has special knowledge about the social condition and documents progress and results with the hope of changing and improving the system (Greenwood & Levine, 1998). I as a teacher integrate computation into student learning but recognize the fact that most educators do not. This would be an instance when I the
researcher have the intent to better understand computational thinking integration with long term goals of changing the district for the betterment of students due to my background in computational science.

In order to perform sound action research, researchers must be scientifically rigorous, not impose their agendas and share learned information back with their community. It is important that the researcher practices good data collection, research methods and analysis. The researcher must specifically ensure reliability and validity. In order to ensure the action research study is rigorous the researcher must ensure it is suitable for the underlying critical research paradigm and particular situation at hand. I have made this justification through my extensive literature review relating computation and biology.

The research must also be negotiated with the research group rather than imposed. In order to ensure this, I spoke personally with the appropriate teachers and supervisors to ensure that being a part of this research was something that they might want to try with their students. Both AP biology teachers were open to me trying the interventions with their students informing me that they also would like to learn alternative ways to approach these evolutionary concepts and claimed it might be beneficial to their students. My science supervisor and superintendent were open to the idea of implementing my interventions, providing me permission upon giving them each a detailed description of the interventions (Appendix H).

Action research must also be inclusive, involving, and informative to those supplying the data. It also must be practical and likely to result in practical new knowledge and systematic and be sustained rather than impulsive (Melrose, 2001). I as
the researcher suspected that implementation would result in new knowledge. I supported this claim through my experience as a teacher combined with the theoretical support from my literature review. I presented my results (at a public invited talk) to the research committee at the community college where I performed the pilot study. I plan on discussing results with the district and conducted research rigorously and systematically. The methods which I used to do so have been outlined in the sections below.

Study Materials

Data Collection Instruments

I created two data collection instruments for the dissertation study. The first instrument measured biological evolution content knowledge (BECKI). The second instrument measured computational thinking knowledge (CTCKS). A description of the structure and development of each of the two items are found in the following two sections. Validation of the surveys is described and discussed later on in the pilot study section.

Biological Evolution Content Knowledge Instrument (BECKI). The BECKI (as seen in appendix A) contains 18 multiple choice questions which I obtained and modified from five previously published assessments. No biological evolution content knowledge test exists that assesses biological evolution from the micro through to the macro scales of evolution. The previous tests were too narrow or too broad in that they focused on one aspect of biological evolution, one biological scale, or on biology as a whole. Students are required to understand evolution at all biological scales and the connection between them, therefore I selected questions which are representative of the micro through the macro scales of evolution. Concurrently, the questions also represent assessment of the
understanding of both unity and diversity of life. These original tests include the Biological Concept Inventory (Klymkowsky & Garvin-Doxas, 2008), the Measure of Understanding Macroevolution (Nadelson & Southerland, 2010), the Basic Tree Thinking Assessment (Baum et al., 2005), Concept Inventory of Natural Selection (Anderson, Fisher & Norman, 2002), and the Concept Assessment of Natural Selection (Kalinowski et al., 2016).

BECKI items 1, 2, 3, and 14, are modified versions from the Biological Concept Inventory (Garvin-Doxas & Klymkowsky, 2008) which include both a range of micro scale through macro scale evolutionary questions. The Measure of Understanding Macroevolution as developed by Nadelson and Southerland (2010) focuses on biological macroscales. BECKI items from this measure include 4, 8, 9. All of these items had been re-worded for simplicity and readability. The Basic Tree Thinking Assessment developed by Baum et al. (2005) was used to develop questions 10, 11, 12 and 13 on the BECKI measure. All four of the items from the Basic Tree Thinking Assessment contain phylogenetic tree images in which students must interpret. I modified all of these items to ensure that students had an idea of the exact type of organism that was being represented on the tree which was a suggestion from a non-expert. The Concept Inventory of Natural Selection developed by Anderson, Fisher and Norman (2002) was used to develop questions 15-18 which refers to a small passage, these questions generally represented macro scale evolutionary concepts. The Concept Assessment of Natural Selection developed by Kalinowski et al. (2016) also contained a series of passages with associated questions. These passages were modified to develop questions 6 and 7 in the BECKI which represent both micro and macro scales of evolution. I
developed question 5 as another item directly related to micro scales of evolution in order to contribute to content validity. These are multiple choice questions and were scored as either a 0 (incorrect) or 1 (correct). The percent of the total correct was taken as the score (out of 18 questions).

A few non experts reviewed the BECKI to provide feedback on the instruments’ face validity. Face validity refers to the assessments presentation and weather the items seem reasonable to test takers (Oluwatayo, 2012). For example, it might also become apparent at this point if one of the answer choices was obviously correct. Face validity is a desirable feature of tests and it may be achieved by having non experts in the field of study rate the instrument for its intended use. Although face validity cannot be used alone in determining validity in the procedure of research, it should be presented to display the research is meaningful and robust. I had eight high school teachers and one college professor review and comment on the test items. I also considered information and comments from the ten student test takers in the pilot study (see details on the pilot study below). Their comments contributed to my evaluation of face validity. In considering their comments, I made some slight changes to item wording to improve clarity and precision.

Biology experts also reviewed the BECKI to help in my evaluation of content validity. Content validity is a concept which indicates if the instrument shows evidence and comprehensive coverage of the domain of and concepts that it claims to cover (Oluwatayo, 2012). Not only does this form of validity ensure that the elements of the main issue are covered but that the elements chosen for the research study are addressed in depth and breath. These judgements should be made by experts in the respective fields.
from the content which the instrument claims to measure. I had three biology experts review the BECKI. Based on their feedback, I made an adjustment to one item to increase its accuracy and clarity (i.e., stating explicitly that a trout is a fish). Although the BECKI test measures overall biological evolution content knowledge, future study might involve quantitatively analysis of the individual questions representing the micro and macro scales in combination with qualitative analysis of student artifacts in order to get a better understanding of student knowledge of biological scales.

*Computational Thinking Content Knowledge Survey (CTCKS).* I developed the CTCKS using the four components of computational thinking: input, integration, output and feedback (see Chapter 2 for details on these four components). There have been no previously published assessments which have selected those four constructs of computational thinking as testable components. The only computational thinking test surveys that have already been published focus on: abstractions, logical thinking, algorithms and debugging or considers personal connections and attitudes toward computation itself (Werner et al., 2012). Data practices, modeling and simulation practices, computational problem solving and system thinking practices were used by Weinthrop (2015) in order to define computational thinking. Weinthrop’s taxonomy included various facets such as (but not limited to): “persistence in working through challenging problems”, “ability to deal with open-ended problems”, “representing ideas in computationally meaningful ways” and “breaking down large problems into smaller problems”. These ideas are not necessarily specific to computational thinking (Weinthrop et al., 2015). In order to merge Weinthrop’s components and the computational thinking practices from my literature review, I have defined them from a
science systems context. Data practices according to Weinthrop involves creating data, analyzing data, manipulating data or collecting data, and this would best align with my context of input. Weinthrop identifies programming, choosing effective computational tools, trouble shooting and debugging and creating computational abstractions with computational problem solving practices, and this best aligns with my construct of integration. Modeling and simulation practices include assessing computational models, designing computational models and using computational models to understand a concept and this naturally aligns with my concept of output. Systems thinking includes understanding the relationships within a system, thinking in levels and investigating a complex system as a whole, and this naturally aligns with my concept of feedback. I define the computational processes that students consider in the classroom as input, integration output and feedback and relate it directly to the scientific systems that the students are representing, therefore I was directly concerned with these four components. The components also naturally align with NOS processes (as described in Chapter 2).

The entire CTCKS is shown in Appendix B. Questions 1 through 4 assess input, questions 5 through 8 involve integration, questions 9 through 12 test output, and questions 13 through 16 assess feedback. For example, to measure the input component, item 2 reads, “Data may be generated or modified by using a computer program” This item specifically assesses students understanding that information input as data may simulate a natural scientific phenomenon by using a computer program and that it may also be modified (i.e., averaged, interpolated, concatenated etc.) by a program. Likewise, to measure the integration component item 5 says “Precise rules can be used to relate
variables,” to assess if students understand that algorithms are precise rules that relate input to output. To measure the output component, item 11 says, “Output data may aid in the generation of new scientific knowledge” to evaluate if students understand that in some cases output or interpreted results may challenge or provide better support for known scientific ideas. Finally, as an example of a feedback item, question 14 reads, “System output allows adjustment of performance to meet a desired response in feedback” to assess if students recognize that when feedback is used, it allows a program to regulate itself.

The CTCKS contains 16 questions. The participants rated each item on a 5-point Likert scale gauging the level of agreement that they thought a biologist would indicate for each statement, ranging from 1 = strongly disagree to 5 = strongly agree, for example, “Certain computer programs and mathematical processes are more efficient than others” (see Appendix B for full survey). Using a scale measuring the level of agreement with biologists allows me to gauge understanding of the scientific explanation (within the context of computational thinking), not acceptance of or attitudes toward scientific explanations. The design and scale of the CTCKS has been modified from Lombardi, Sinatra, and Nussbaum (2013). Table 5 depicts an overview of the CTCKS items as they pertain to input, integration, output and feedback as well as which items were negatively-worded.

Seven of the CTCKS items are negatively-worded to gauge internal consistency. Negatively-worded items ensure that participants are paying attention to what is being asked of them. If students answer all 5 or all 1 or there is a patterned response, it may indicate that there is participant disengagement (Furr & Bacharach, 2008). Negative
coding ensures that the correct answer is a random series of both 5 (strongly agree) and 1 (strongly disagree), rather than a series of only 5’s as the correct answer.

Table 5

*Breakdown of Computational Thinking Survey Construct Items*

<table>
<thead>
<tr>
<th>Construct</th>
<th>Items</th>
<th>Negatively-Worded Items</th>
</tr>
</thead>
<tbody>
<tr>
<td>Input</td>
<td>1-4</td>
<td>1,4</td>
</tr>
<tr>
<td>Integration</td>
<td>5-8</td>
<td>6,8</td>
</tr>
<tr>
<td>Output</td>
<td>10-12</td>
<td>10,12</td>
</tr>
<tr>
<td>Feedback</td>
<td>13-16</td>
<td>16</td>
</tr>
</tbody>
</table>

*Note.* This table shows the breakdown of items for Computational Thinking Knowledge Survey with each of the four constructs (input, integration, output and feedback) and which are negatively worded.

Two high school teachers and one college professor reviewed the CTCKS for face validity. In considering their comments, I made some changes to item wording mainly focusing on making them more concise. Two computational experts also reviewed the CTCKS to help in my evaluation of content validity.

Although the CTCKS measures overall computational thinking knowledge, the individual questions may provide insight on input, integration, output and feedback understanding as it relates to learning scientific systems. Qualitative analysis of student artifacts may be coupled with the CTCKS to get a better understanding of student knowledge in future studies. It is beneficial that the items are measured on a Likert scale, so that it provides more of a gradient as to how and which items students understand.
Simple to complex forms of each of these computational constructs were identified through analysis of these computational artifacts.

**Interventions**

The interventions were lessons which have been modified from the AP Biology Lab Manual (College Board, 2019). These interventions were inspired by my experience as an AP biology teacher. At AP trainings and discussing these labs with other AP teachers, it became evident that they are difficult not only for the teachers to follow but also for the students to interact with. Teachers frequently skip them or provide a lesson on what the students were supposed to understand from the lab. It is evident to me that these labs are incorporating computational ideas with biology without explicitly stating so. This biology incorporation coupled with the computation based activities are not clear to all instructors and the provided examples are outdated (i.e., functions in excel and websites described are no longer in use). For both interventions I developed a PowerPoint and activities which I used to describe computation and its relationship with biology. Example images from the PowerPoints can be found in Appendix C and assignments for both interventions can be found in Appendices D and E respectively. These assignments involved approximately ten questions about biological and computational content students encountered within the lessons. Some questions prompted students to discuss specific biological components within the activities (i.e. “What is the function of your selected protein?”) and other questions asked specifically about the computational components as they were represented within the activities (i.e. “What is the input represented within your model?”). I collected the assignments as artifacts to address RQ 3a and RQ 3b. During the interventions I described the 4
components of computational processes: input, integration, output and feedback and coupled them with biological examples. I then described a specific aspect of evolution (depending on the intervention) and provided a working example that I developed and described the computational elements within my examples. I passed out an assignment to students and allowed them to work together to complete the computational task. I then had them turn in an assignment that prompted them to ask and answer computational and biological questions. Students were to describe the input, integration, output and feedback of their work and also provide screenshot examples. Although students were allowed to work together, they were instructed to each turn in their own assignment.

**Intervention 1: Hardy-Weinberg Activity**

During the first intervention the students listened to my lecture on evolution and allele frequency coupled with computation and received a copy of my examples (virtually) along with an assignment sheet. Students learned about the Hardy-Weinberg law of genetic equilibrium and studied the relationship between evolution and the change in allele frequency by using a computational model to demonstrate what can happen over many generations. Generally, students saw that the H-W formula displayed a population in evolutionary equilibrium, or showed a population not evolving. These numbers of alleles were compared to populations in the nature. Students then observed if they were undergoing evolution or not. In the case they were undergoing evolution, questions may have been asked why (i.e., environmental changes, adaptations, human impacts etc.). Students worked with computer programs such as Microsoft Excel or Google Sheets in order to develop a spreadsheet which mimicked two successive generations. Students designed their computational products so that there was a single input value that the rest
of the model ran on. The integration was the student’s depiction of the H-W equation and the output was the new allele frequencies and respective graphs for each generation. The generations output informed the next generation, and students should have recognized this as the feedback. The final generation required students to make a modification based on an environmental change. In this case, the students were forced to really think about how the input should have been modified, and students manipulated the H-W equation to display the appropriate output. For example, none of the homozygous recessive individuals may survive (students multiply that aspect of the output by zero), or the heterozygotes have double a chance of surviving (students multiply that aspect of the output by two) based on a hypothetical environmental change that the student imagined and described. For example: Hypothetical homozygous recessive sea otter individuals have long hair, and because the hypothetical local environment experienced an average five-degree temperature increase due to a new nuclear power plant, it might result in a 50% loss in the homozygous recessive otter individuals. Students were expected to model how that 50% loss should affect future generations evolutionarily using the appropriate equation and modifications.

What students did not complete during class was assigned as homework. The actual assignment can be found in Appendix D. After the completion of this assignment students should have been able to calculate the frequencies of alleles and genotypes in the gene pool of a population using the H-W formula (for successive generations) and discuss natural selection and other causes of microevolution as deviations from H-W equilibrium. They should have an understood how using a data set can reflect the genetic makeup of a population over time and how computational methods can be used to
investigate the cause and effects of these changes. Students should have also identified that evolution is an ongoing process and that it works between biological scales.

*Intervention 2: Phylogenetic Tree Activity*

During intervention two, I had a lecture and discussion on computation as it related to evolution which was very similar to intervention 1. Then the students listened to my lecture on evolution coupled with the structure and development of proteins within a computational context. I described and showed them how to navigate the NCBI (National Center for Biotechnology Information) website (including BLAST which is a basic local alignment search tool) (Geer et al., 2010). Students compared DNA and protein sequences to understand evolutionary relationships using computational tools. Students also used these tools to develop phylogenetic trees. Students created phylogenetic trees (or cladograms) that depict evolutionary relationships. They also received a copy of my protein sequence examples and an assignment sheet which allowed them to explore available databases. This information was exported, manipulated and input into the online BLAST tool (Geer et al., 2010). This tool utilized a code (students could not see) which aligned the entered sequences based on how alike they were. The program also provided a statistical analysis output of the sequences as well as a phylogenetic tree. Students picked their own protein to research and then used this protein to observe which organisms were most closely related and speculated on why. The input was the file or the (DNA or protein) sequences that students imported into the online BLAST tool. The integration was the program looking for alignment of sequences and identified the amount of similarity between the sequences. The output was the
statistical analysis or phylogenetic tree. Feedback was not utilized in this example (although students were prompted to speculate instances of useful feedback).

After this activity, students should have been able to analyze biological data with sophisticated bioinformatics tools. Students should also be able to use phylogenetic trees and computational tools to ask questions and apply the concepts to what they know or do not know about computation or evolution. If students did not complete the activity during class, it was completed as homework. The assignment sheet can be found in appendix E.

Pilot Study

I performed a pilot study at a local community college in the process of validating my data collection instruments and in informing my interventions for the dissertations study. Participants (N = 11) were enrolled in an introductory biology course that I taught (Biology 2). Most of the students were white (80%) and female (70%). I conducted the pilot study when teaching the evolution part of the course. In the pilot study, I administered the BECKI and CTCKS prior to evolution instruction. Then I conducted the first intervention and had the students complete the two instruments after this lesson. Finally, I conducted the second intervention and had the students complete the two instruments a third time immediately after finishing this second intervention.

Results from the pilot study showed uneven reliability in the BECKI, with Cronbach’s alpha values equal to .133, .645, and .757 respectively at pretest, posttest intervention 1, and posttest intervention 2. Reliability values were “unacceptable” at pretest, “questionable” at posttest intervention 1, and “acceptable” at posttest intervention 2 (Cortina, 1993). Although some of these values were below the acceptable threshold, I
opted to keep all of the items in the subsequent analyses and for the dissertation because the low Cronbach alpha values were likely due to a small sample size in the pilot and it may have also been swayed by large numbers of guesses at pretest.

Cronbach’s alpha values for the CTCKS surveys were .637, -1.39, and .308 for the pretest, posttest intervention 1, and posttest intervention 2, respectively (negative value likely due to small sample size, as this value was checked extensively for coding errors). The pretest Cronbach alpha value was questionable. The posttest intervention 1 and posttest intervention 2 Cronbach alpha values were unacceptable. These low values were probably due to small sample sizes (Hays, 1981). However, I also kept all 16 items from the CTCKS in the dissertation study. Because experts in the field had claimed that the instrument had content validity, instead of reconstructing the test, I modified the interventions to explicitly use computational vocabulary when describing scientific systems. Students were exposed to computational terms for the first time during the interventions, which may have contributed to the computational consistency results of the pilot. Table 6 shows the means and standard deviations of the biology evolution knowledge scores (i.e., the total percent correct of all the BECKI items) and the computational knowledge scores (i.e., the average of all the CTCKS items, which were all on a 1 to 5 Likert-type scale) from the pilot study.
Table 6
*Means and Standard Deviations for Pilot Study*

<table>
<thead>
<tr>
<th>Variables</th>
<th>Means</th>
<th>Standard Deviations</th>
</tr>
</thead>
<tbody>
<tr>
<td>Evolution Knowledge Pretest</td>
<td>47.5</td>
<td>9.21</td>
</tr>
<tr>
<td>Evolution Knowledge Posttest 1</td>
<td>58.9</td>
<td>15.8</td>
</tr>
<tr>
<td>Evolution Knowledge Posttest 2</td>
<td>60.5</td>
<td>18.9</td>
</tr>
<tr>
<td>Computational Knowledge Pretest</td>
<td>3.73</td>
<td>.362</td>
</tr>
<tr>
<td>Computational Knowledge Posttest 1</td>
<td>3.74</td>
<td>.148</td>
</tr>
<tr>
<td>Computational Knowledge Posttest 2</td>
<td>3.72</td>
<td>.311</td>
</tr>
</tbody>
</table>

*Note.* Evolution knowledge scores (from BECKI) are represented as percents, while computational knowledge scores (from CTCKS) are raw averages (with 5 as a maximum score).

Table 7 shows associations between biology and computational knowledge variables the pretest, posttest intervention 1, and posttest intervention 2. There was a strong correlation between the pretest computational knowledge scores and the posttest 2 computational knowledge scores with a Pearson correlation value of .652. There was a strong correlation between the posttest intervention 1 computational scores and the posttest intervention 2 computational scores with a Pearson correlation value of .716.
There is a strong correlation between the posttest 1 and posttest 2 evolution scores with a Pearson value of .714.

**Table 7**

<table>
<thead>
<tr>
<th>Variable</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
<th>6</th>
</tr>
</thead>
<tbody>
<tr>
<td>1. Pretest Computational Average</td>
<td>−</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2. Pretest Evolution Percent</td>
<td>.135</td>
<td>−</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>3. Post1 Evolution Percent</td>
<td>.544</td>
<td>-.001</td>
<td>−</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>4. Post1 Evolution Percent</td>
<td>.081</td>
<td>.660</td>
<td>-.235</td>
<td>−</td>
<td></td>
<td></td>
</tr>
<tr>
<td>5. Post2 Computational Average</td>
<td>.652*</td>
<td>.110</td>
<td>.716*</td>
<td>-.182</td>
<td>−</td>
<td></td>
</tr>
<tr>
<td>6. Post2 Evolution Percent</td>
<td>.402</td>
<td>.383</td>
<td>-.014</td>
<td>.714*</td>
<td>.001</td>
<td>−</td>
</tr>
</tbody>
</table>

*p ≤ .05

*Note. Evolution tests were calculated as percents while computational scores were averages.

I conducted a within-subjects repeated measures multivariate analysis of variance (MANOVA) to gauge changes in both biological and computational knowledge scores over time. There was not a significant increase in the combined knowledge scores over time, Wilks’ λ = 0.56, $F(4,5) = 1.58, p = .311$. However, follow up univariate tests indicated that there was a significant increase in biology knowledge scores over time, $F(2,16) = 4.29, p = .032, \eta^2 = .349$, with large effect size; but no significant difference in computational scores over time, $F(2,16) = .026, p = .974$. 
Because the computational test was validated in multiple ways (face validity and content validity), the lack of student knowledge gains in computation influenced me to modify the interventions to better expose the students to computational vocabulary. In looking at the student artifacts (assignments) from the pilot, I decided to make the computational vocabulary more explicit during the dissertation study intervention, as many students did not use the vocabulary properly in their assignments. I was also able to identify that student testing time for the BECKI is approximately 12 minutes and the testing time for CTCKS is approximately 10 minutes (this informed structure of my dissertation study).

Procedures

The length of the full administration of both instruments was approximately four weeks. This included instruction and discussions with teachers, pretest, intervention 1 and posttest 1 followed by intervention 2 and posttest 2. These estimates were based on timing from the pilot test and on discussions I had with the two teachers I worked with within the Pine Bay district. Both pretests, the BECKI and CTCKS were combined and given before the evolution unit to all four classes which participated. This included 16 computational knowledge items and 18 evolutionary knowledge items. The pretest, posttest intervention 1 and posttest intervention 2 contained identical items, the only difference was when students took the tests.

The timeframe of the dissertation study is outlined in Table 8, and it was modified from the pilot to include two teachers each with two classes, rather than one teacher (me) providing the interventions to all students. I informally discussed plans with both of the AP biology teachers within the district, and both of which were open to trying the
interventions and having their classes be involved in the study. Interventions and associated student assignments associated with these interventions examples can be seen in appendices C, D, E and F. Temple’s IRB claimed that there was no IRB approval required for the pilot study because all of the student participants were older than 18 and materials were part of the curriculum. Upon undergoing the IRB process for the dissertation study, the Temple IRB department also claimed that there was no IRB required (Appendix G). I obtained permission from the science supervisor within the Pine Bay district who oversees the science departments at both the East and West High Schools. I also obtained official permission from the Superintendent at the Pine Bay district to conduct the dissertation study (see Appendix H). The interventions were also part of the AP biology curriculum within the Pine Bay District and were modified by me to include exclusive, distinct and obtainable components of computational thinking.
Table 8

Study Timeline

<table>
<thead>
<tr>
<th>Week One</th>
<th>Data Collection</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>• Teacher and Researcher met to discuss and confirm procedures of the study</td>
</tr>
<tr>
<td></td>
<td>• Student participants completed pretest</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Week Two</th>
<th>Data Collection (Intervention 1)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>• Intervention 1 presented to all classes</td>
</tr>
<tr>
<td></td>
<td>• Student participants completed posttest 1</td>
</tr>
<tr>
<td></td>
<td>• Student submitted assignment (artifacts) from intervention 1</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Week Three</th>
<th>Data Collection (Intervention 2)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>• Intervention 2 presented to all classes</td>
</tr>
<tr>
<td></td>
<td>• Student participants completed posttest 2</td>
</tr>
<tr>
<td></td>
<td>• Student participants submitted assignment (artifacts) from intervention 2</td>
</tr>
<tr>
<td></td>
<td>• I collected any remaining student assignments (artifacts)</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Week Four</th>
<th>Organization and Analysis</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>• I assigned students and teachers random, but organized identification numbers</td>
</tr>
<tr>
<td></td>
<td>• I translated all student responses into spreadsheet and imported to SPSS</td>
</tr>
</tbody>
</table>

Week One

I met with each teacher to finalize the timing and dates for the dissertation study. Directly prior to the evolution unit, I had the two teachers present the students with the pretests. Each teacher provided their students both the BECKI and the CTCKS just prior to starting the units as an exit ticket activity. I worked with one teacher from the West High School and one teacher from the East High School. I inquired about additional
information regarding students or accommodations needed with the individual teachers. These meetings were no longer than one hour.

Week Two

All students participated in the study due to the fact that the interventions were variations of the normal curriculum. I collected surveys and assignments for data analysis from the students and organized and entered data into a statistical program. The interventions began during week two. Absent students made up assignments (artifacts) and took interventions when appropriate, as long as the time frames or teacher effort required was within reason and would not affect the outcome of the study.

I worked with two teachers, one at the East High School (Teacher 2) and one at the West High School (Teacher 1). Each teacher had two classes of AP biology which makes a total of four classes that underwent the study (Table 9 depicts a detailed description of these four classes and the timing of the interventions). I had teacher 1 teach the first evolution lesson using normal instruction for class 1, and students were given the posttest 1. During this same day, I taught Class 2 using the computational intervention 1 which consists of the Hardy Weinberg Activity. During these activities, I had exposed students to computational vocabulary and evolutionary examples. Then I had students complete a computational activity to develop a spreadsheet which applies the Hardy-Weinberg formula and allowed them to observe allele frequencies and population changes over time. Class 2 also took intervention posttest 1 at the completion of this intervention.

During this same time period (i.e. Week Two), Teacher 2 at the East High School taught their class (Class 3) the normal evolution lesson while I provided the same
computational intervention to students of Teacher 2’s second class (class 4). At this time collection of the post 1 surveys and artifacts was done by teacher 1 and 2 with the help of myself, the researcher.

**Week Three**

During week 3, I provided computational instruction to Class 1 in the form of computational intervention 2, the BLAST activity. In this activity students were initially provided computationally relevant biology examples and exposed to computational vocabulary. Students then used an online database to identify the DNA sequence of a protein and developed a phylogenetic tree from obtaining DNA sequences from the database. I provided relevant computational examples and used the computational vocabulary and computational tools. Teacher 1 taught Class 2 using a normal evolution lesson where the same biological components are taught in a traditional manner. At this time (conclusion of lessons) posttest intervention 2 was provided to both Class 1 and Class 2.

During this same time period I traveled to the East High school in order to provide computational intervention 2 to Class 3 while Teacher 2 provided a normal evolution lesson with Class 4. At this time, artifacts from the second intervention were collected and posttest intervention 2 was provided to Class 3 and 4. The class labels, timing, tests and associated teachers, and interventions are listed below in Table 7. Although teachers were present for the computational interventions, they were not expected to help students with answers, only to help the class run under normal procedures. Myself, Teacher 1, and Teacher 2, helped to direct students if they had trouble understanding the Likert scale for the CTCKS, but they were told to do their best to complete the BECKI in answering the multiple choice questions. After I collected the
surveys for each of the tests (or had the teachers collect the tests and artifacts) I ensured they were placed in correct color coded folders, organized, and coded properly. An organized outline of the classes is presented in Table 9.

Table 9

Intervention and Testing Plan at Prospective Schools

<table>
<thead>
<tr>
<th>Class</th>
<th>Location &amp; Teacher</th>
<th>Test Time 1</th>
<th>Classroom Activity (Intervention), Teacher Time 1</th>
<th>Test Time 2</th>
<th>Classroom Activity (Intervention), Teacher Time 2</th>
<th>Test Time 3</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Normal Evolution Lesson1 with Normal Teacher</td>
<td></td>
<td>Intervention 2 (BLAST activity) with</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Computational Teacher</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Week</td>
<td>Class Location &amp; Teacher</td>
<td>Test Time 1</td>
<td>Classroom Activity (Intervention), Teacher Time 1</td>
<td>Test Time 2</td>
<td>Classroom Activity (Intervention), Teacher Time 2</td>
<td>Test Time 3</td>
</tr>
<tr>
<td>-------</td>
<td>-------------------</td>
<td>------------</td>
<td>-----------------------------------------------</td>
<td>------------</td>
<td>-----------------------------------------------</td>
<td>------------</td>
</tr>
<tr>
<td>1</td>
<td>West School, Teacher 1</td>
<td>1</td>
<td>Pretest (BECKI &amp; CTCKS)</td>
<td>2</td>
<td>Posttest 1 (BECKI &amp; CTCKS)</td>
<td>3</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Intervention 1 (Hardy Weinberg Activity) with Computational Teacher</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>West School, Teacher 1</td>
<td>Pretest (BECKI &amp; CTCKS)</td>
<td>Intervention 1 (Hardy Weinberg Activity) with Computational Teacher</td>
<td>Posttest 1 (BECKI &amp; CTCKS)</td>
<td>Normal Evolution Lesson 2 with Normal Teacher</td>
<td>Posttest 2 (BECKI &amp; CTCKS)</td>
</tr>
<tr>
<td>3</td>
<td>East School, Teacher 2</td>
<td>Pretest (BECKI &amp; CTCKS)</td>
<td>Normal Evolution Lesson1 with Normal Teacher</td>
<td>Posttest 1 (BECKI &amp; CTCKS)</td>
<td>Intervention 2 (BLAST activity) with Computational Teacher</td>
<td>Posttest 2 (BECKI &amp; CTCKS)</td>
</tr>
<tr>
<td>4</td>
<td>East School, Teacher 2</td>
<td>Pretest (BECKI &amp; CTCKS)</td>
<td>Intervention 1 (Hardy Weinberg Activity) with Computational Teacher</td>
<td>Posttest 1 (BECKI &amp; CTCKS)</td>
<td>Normal Evolution Lesson 2 with Normal Teacher</td>
<td>Posttest 2 (BECKI &amp; CTCKS)</td>
</tr>
</tbody>
</table>

Note. Computational Intervention 1 is Hardy Weinberg Activity and Computational Intervention 2 is the BLAST activity. The normal teacher is referring to the teacher the students normally have class with while computational teacher is referring to me.
Week Four

Data collection was completed during week four and organized at this time. I organized the completed BECKI and CTCKS instruments from the pretest, posttest intervention 1 and posttest intervention 2 time periods. Because the test items were identical, I ensured students included the date and I used the header section to print pre, p1 or p2 on the bottom right corner of the instruments in small print. I graded the completed surveys and generated raw scores for both the BECKI and CTCKS for each student and each time period. Each student was assigned a random identification number prior to recording the data in a spreadsheet.

All raw survey responses were translated to the spreadsheet; I converted the alphabetical ratings to number ratings. For the BECKI I used 0 and 1 to indicate if the answers were correct for the 18 items. For the CTCKS the ratings were translated from A-E to 1-5, with 5 being the highest score for each item. I then reversed negatively worded items so that the highest appropriate score receives a 5 for each of the 16 items, this was done by taking the raw score and subtracting by 6 to ensure that the negative coding was reversed. Once this was completed for each of the tests, I uploaded the data to SPSS version 25 for statistical analysis.

Data Analysis

Preliminary Analyses

Data analysis included quantitative and qualitative techniques. After completion of data collection and entry, the data were uploaded into the statistical program SPSS version 25.0. I determined Cronbach’s alpha for the pretest, posttest intervention 1 and posttest intervention 2 trials in order to determine reliability for both instruments. I also
calculated the student scores, means and standard deviations for the different time intervals. Skewedness and kurtosis for each test at the different time intervals was also calculated. ICC scores were also calculated to ensure the tested differences were not due to inherent classroom or teacher effects. The descriptive analysis was done prior to the analysis as is pertinent to the research questions.

*Analyses for Research Questions*

*Research Question 1*

How does instruction promoting integration of biological evolution concepts and computational processes (input, integration, output, and feedback) compare to instruction focused only on biological evolution concepts, specifically in changing students’ knowledge of biological evolution?

Research question 1 and 2 were addressed using scores from the BECKI and CTCKS. Analysis was performed simultaneously for both research questions, considering combined knowledge scores (both evolution and computation) as well as separately for biological evolution scores (RQ 1) and computational knowledge scores (RQ 2). These analyses are described in the next section.

*Research Question 2*

How does instruction promoting integration of biological evolution concepts and computational processes (input, integration, output, and feedback) change students’ knowledge of computational processes (i.e., input, integration, output, and feedback)?

Traditional teaching methods pertaining to biological evolution was compared to teaching methods which concurrently promote computational processes to answer RQ 1 and RQ 2. The BECKI instrument was developed to measure student knowledge of
biological evolution. The CTCKS instrument measured student knowledge of computational processes. These two instruments provided measures of student biological evolution knowledge and computational processes knowledge before the interventions, after the first intervention as well as after the second intervention. Due to separate classes being exposed to traditional teaching methods and teaching methods involving the two interventions at separate times, the traditional teaching methods were compared to the teaching methods which promote computational processes. This comparison was done through comparing student knowledge of biological evolution and student knowledge of computational processes using the two developed knowledge measures for the separate classes at separate times.

I ran ordinary least squares analysis. This allowed me to identify that my data was linear and normal. The data fit a normal distribution, therefore it aligned with the assumptions made by ordinary least squares analyses. I ran a correlation to identify relationships between the testing times. I then ran a repeated measures analysis and a multivariate analysis of variance MANOVA to examine both research questions 1 and 2, for computational knowledge as well as evolution knowledge. I conducted a repeated measures analysis comparing both the biological evolution content knowledge over time (3 times) as well as the computational knowledge over time (3 times). I compared variables using the between subjects measure since some of the students had been treated and some untreated at different times. I also compared estimated marginal means to compare the main effects. This took the alpha of .05 and divided it by 3 due to the 3 intervals of time.
In the MANOVA the time (1-3) was the between subjects variable and the student scores (evolution or computation) were the dependent variables. The estimate of effect sizes from this test indicated the robustness. The Pearson correlations calculated determined the effect size and if there was a relationship between any of the variables. I then qualitatively analyzed student artifacts through exploratory sequential design (complementary design). This allows qualitative methods to help better explain the quantitative results (Creswell, 2013) through the exploration of research questions 3a and 3b.

Research Question 3

In what ways do students’ computational products (artifacts) constructed during instruction promoting biological evolution concepts and computational processes (i.e., input, integration, output, and feedback) display:

a. Student understanding of different levels of biological organization (i.e., from molecular to ecosystem scales); and

b. Different levels of complexity in computational thinking (i.e., simple, developing, and complex)?

Two interventions both of which merge computational processes (input, integration, output and feedback) and biological evolution were implemented during biology instruction. I qualitatively analyzed student artifacts obtained from instruction during these interventions to answer research question 3a and 3b. The analysis included a qualitative content analysis (including component and relational analysis) on the student artifacts coding for inductive themes related to, student understanding of different biological levels of organization. A rubric was created (found in Chapter 4) based on the
learning progression (from Chapter 2) to code and explore complexity of computational thinking. The levels of biological organization ranged from the molecular to ecosystem scales as displayed by student artifacts (biological scales can be observed in Table 2). Different levels of complexity in computational thinking were identified as simple, developing and complex as defined in the learning progression (computational complexity and computational components can be seen in Table 3 and Table 4 respectively). Because BECKI items were also designed with micro to macro scales, it identified if individual students were making knowledge gains at larger, smaller, or between scales depending on which items they got correct. This is applicable for future study. These patterns were observed through coding student artifacts using the respective coding schemes and rubrics presented in Chapter 4.

The computational product as part of the learning progression seen in Table 3 outlines specific components that can be seen at the simple, developing and complex levels of computation as displayed by students. The assignments which were analyzed as artifacts also have distinct questions which hone in on specific biological and computational scaled questions prompting student responses that provided insight on student gains. For example, students are explicitly asked: “What the input, integration and output is for the biological system they are exploring” as seen in the assignments found in Appendix D and E.
CHAPTER 4
RESULTS AND ANALYSES

This chapter discusses the quantitative and qualitative analyses used to address this study’s three research questions. Research question 1 reads: How does instruction promoting integration of biological evolution concepts and computational processes (input, integration, output, and feedback) compare to instruction focused only on biological evolution concepts, specifically in changing students’ knowledge of biological evolution? My hypothesis for research question 1 was the following:

- H1: Explicit instruction promoting computational thinking to teach evolution will result in increased knowledge of biological evolution

Research question 2 asked: How does instruction promoting integration of biological evolution concepts and computational processes (input, integration, output, and feedback) change students’ knowledge of computational processes (i.e., input, integration, output, and feedback)? My hypothesis for research question 2 was the following:

- H2: Explicit instruction promoting computational thinking to teach evolution will result in increased knowledge of computational processes

Research question 3 asked: In what ways do students’ computational products (artifacts) constructed during instruction promoting biological evolution concepts and computational processes (i.e., input, integration, output, and feedback) display:

a. Student understanding of different levels of biological organization (i.e., from molecular to ecosystem scales); and
b. Different levels of complexity in computational thinking (i.e., simple, developing, and complex)? My hypotheses for research question 3 were the following:

- **H3a:** Artifacts will reveal discernible relationships between computational intervention exposure and unique aspects of biological levels of organization. Students with stronger biological and or computational knowledge (as derived from the quantitative analysis in RQ 1 & 2) will use more biological levels, make more biological level connections and make larger biological connections (i.e., connections that span a larger range) within their artifacts.

- **H3b:** Artifacts will reveal discernible relationships between computational intervention exposure and level of complexity in terms of understanding of computational thinking (simple, developing or complex). Students with stronger computational or biological knowledge (as derived from the quantitative analysis in RQ 1 & 2) will display higher levels of computational complexity within their artifacts.

Prior to describing the results and analyses for these three research questions (RQs), I initially describe the study participants.

**Participants**

Sixty-four high school students ranging from grades 9 to 12 participated in the study. The participants were enrolled in AP biology within one of two high schools within the Pine Bay School District, located near the shore in the Mid Atlantic Region. The Pine Bay School District as well as the East High School and the West High School
are pseudonyms I use throughout the dissertation to protect anonymity. All 64 students enrolled in AP biology within the district were invited to participate in the study, approximately 80% ($N = 51$) fully participated in computational and evolution knowledge testing (RQ 1 & 2). I included data from students that fully completed the surveys to perform all calculations for descriptive statistics, correlations and analyses of variances (ANOVAs). If students failed to answer a few (i.e. 5 items left blank or less) questions from the surveys, I was still able to calculate averages for the pretests and each of the two posttests (posttest 1 and posttest 2).

Additionally, 61% ($N = 39$) of students completed and turned in their written work, which was considered artifacts from the study and used to explore RQ 3. Assessment (BECKI & CTCKS) accuracy and quality of collected artifacts did not affect student grades. I modified two lessons (intervention 1 and intervention 2) from the preexisting AP biology curriculum by infusing computational thinking into instructional activities therefore consent and assent were not required according to Temples IRB (Appendix I).

Fifty percent of the participants were from East High School ($n = 32$) and 50% were from West High School ($n = 32$) and generally the participants reflected the demographics of their respective schools (as described in Chapter 3). In total about 42% of the “full” participants were male ($n = 27$). At the West High School 77% of the population identify as white, 13% as Hispanic, 7% as Black, 3% as Asian and 1% as multiracial. Fourteen percent of the students are economically disadvantaged. At the East High School 84% of the students identify as white, 7% as Hispanic, 6% as Black and 3% as Asian. Multiple races and American Indian/Alaskan Native comprise less than 0.1%
of the school and 10\% of students are economically disadvantaged. A more extensive
description of participants can be found in Chapter 2.

The participants were enrolled in one of four AP biology classes taught by two
different teachers. I randomly assigned participants to the treatment and comparison
groups at the class level. Two classes received the first intervention, one class normally
taught by Teacher 1 and one class normally taught by Teacher 2 and the second two
classes received the second intervention, one class normally taught by Teacher 1 and one
class normally taught by Teacher 2. The total number of students in Teacher 1’s first
class was 12 (n = 12), there were 20 students (n = 20) in their second class. The total
number of students in Teacher 2’s first class was 11 (n = 11), there were and 21 students
(n = 21) in their second class.

Analyses of Research Questions 1 and 2: Pre to Post-Instruction Changes

Of the three research questions that motivated this dissertation study, research
questions one and two related to the participants’ changes in two types of knowledge
from pre to post instruction (biological evolution knowledge [RQ 1] as well as
computational knowledge [RQ 2]). I measured changes that occurred in these knowledge
constructs by comparing test results at three different times. Testing time 1 (which I refer
to as the pretest), testing time 2 (which I refer to as posttest 1) and testing time 3 (which I
refer to as posttest 2). The test participants received at each time was identical and
included both the BECKI & CTCKS to measure biological evolution knowledge and
computational knowledge respectively (development of these instruments is described in
Chapter 3).
It is important to note throughout these analyses that participants in intervention group 1 received the pretest, then they received the computational intervention lesson 1 taught by me. The participants turned in their artifacts and took posttest 1 directly after. Participants then received a traditional biological evolution lesson from their teacher followed by posttest 2. Participants in intervention group 2, received the pretest, a traditional biology lesson on evolution (taught by their teacher) followed by posttest 1. Participants then received a different computational intervention (intervention 2) taught by me. Following this lesson, participants turned in their artifacts and took posttest 2. A detailed sequence for both groups of participants (intervention 1 and intervention 2) is outlined in Chapter 3 (Table 9). In order to address RQ 3, I collected participant artifacts the day after they participated in the computational biological evolution lessons taught by me.

This section details the preliminary data analyses. I then discuss analyses I used to determine group differences (intervention 1 and intervention 2) over time. Finally, I demonstrate how these differences relate to the nature of the instructional activities and not to the individual effects from the classrooms. Data was recorded and manipulated in excel before being uploaded to SPSS in order to perform the following statistical analyses.

**Preliminary Data Analysis**

*Data Outliers*

I used Mahalanobis distance to calculate multivariate outliers. This multidimensional measure represents the distance of a particular case from the center of all variables and other cases within a data set. It is used in a classification process where
there are several groups and the purpose of the study is exploring the affinities between the groups, especially in a hierarchical scheme (McLachlan, 1999). The multivariate Mahalanobis distance values ranged from 1.31 to 2.90 and there were no cases that were particularly separated from the others. Mahalanobis distances at \( p < .001 \) are evaluated using \( \chi^2 \) with the degrees of freedom equal to the number of variables. There were two dependent variables measured at pre and post 1 and post 2 instruction yielding a \( df = 6 \) and a critical \( \chi^2(6) = 3.39 \). Therefore, none of these cases were outliers.

I used \( z \)-score to calculate univariate outliers. There were two univariate outliers (\( z \)-values > 3), one for a participant’s pre computational test score (\( z \)-value = 3.59) and one for another participant’s computational post 2 test score (\( z \)-value = 3.29). I opted not to remove the data, as there were the only two cases, they were separate cases and it did not have significant impact on multivariate outliers (Iglewicz & Hoaglin, 1993). These cases may be due to random variation or to something scientifically interesting and I did not want to reduce the sample size. I discuss this later on in the chapter as a potential limitation.

**Reliability of Instrument Scores**

The theoretical development of the LBECT-LP as described in Chapter 2 informed the notion that using computational thinking to teach biological evolution would increase student knowledge of biological evolution as well as computational thinking knowledge. There are no published tests that measured computational thinking knowledge nor biological evolution knowledge in the ways they I defined in the learning progression. I developed both the BECKI (measure of biological evolution knowledge) and the CTCKS (measure of computational thinking knowledge). These tests were
validated using content and face validity. I also calculated Cronbach alpha values for all measures to ascertain reliability (I described this process in detail within Chapter 3).

**BECKI Reliability.** I attained content and face validity for the BECKI with the assistance of professional biologists and teachers as described above. All questions had been published in various instruments and then slightly modified for readability. I selected the questions to include concepts regarding all scales of biological evolution. The resulting Cronbach alpha values calculated during the dissertation study to determine internal consistency for the BECKI were .474, .547 and .623 for the pretest, first posttest and second posttest respectively. The pretest value of .474 was unacceptable, the first posttest with a value of .547 was poor and the second posttest of .623 was questionable.

The Cronbach alpha scores for the pilot (N = 9) were .133, .645, and .757 respectively. I did not modify the BECKI instrument between the pilot and the dissertation study. Although the pilot study involved a small number of participants, these students were enrolled in a second semester biology course at a local community college, therefore they likely had more evolution background knowledge. The pilot study participants also experienced both interventions (where as dissertation study participants only experienced one). The participants in the dissertation study had very limited understanding of biological evolution prior to instruction and this may have caused them to respond randomly. I would gather that as participants became more familiar with biological evolution throughout the study, it caused the reliability to increase. Cronbach alpha values may have been poor due to small sample size. Content and face validity were considered in multiple ways (Gliem & Gliem, 2003) therefore I kept all items from the BECKI for the dissertation study analyses.
CTCKS Reliability. I attained content and face validity for the CTCKS as described above. Each of the sixteen questions were developed to assess the computational components: input, integration, output and feedback based on the LBECT-LP. The Cronbach alpha values calculated during the dissertation study to determine internal consistency for the CTCKS were .514, .594 and .446 for the pretest, first posttest and second posttest respectively. Based on threshold values the pretest and posttest 1 were poor whereas the second posttest was considered unacceptable however the values I obtained from the dissertation study were a general improvement from the Cronbach alpha values from the pilot study (α = .637, -1.39 [error likely due to very small sample size], and .308; N = 9).

It is likely that participants part of the dissertation study (as well as the pilot) had very limited prior knowledge on these constructs which may have led to the low internal constancy. Student participants were exposed to computational terms for the first time during the interventions, which may have contributed to the poor computational consistency results of both the dissertation study and the pilot. For the dissertation study I kept all 16 items from the CTCKS. Because experts in the field had claimed the instrument had content validity, instead of re constructing the test between the pilot and the dissertation I modified the interventions to explicitly use computational vocabulary when describing scientific systems. I also spent more time distinctly describing the computational components along with examples during both interventions in the dissertation study. The potential implications (and ways to improve) of the unacceptable, poor and questionable values of the BECKI and CTCKS is discussed in Chapter 5.
Bivariate Correlations

Pearson bivariate correlations for computational knowledge and evolution knowledge scores at all testing times (1, 2 and 3) for the dissertation study are displayed in Table 10. Effect size ($r$) determines the strength of the correlations, or how strong the relationship is between the variables ($-1 \leq r \leq 1$). If the effect size range is less than the absolute value of .3 it is “small”, if it is between .3 and .5 there is a “medium” effect size and if it is larger than .5 the effect size is considered “large” (Ferguson, 2009). All of the following values have been provided so that $p \leq .05$. All of the correlations described below are positive, meaning the correlated items tended to increase together.

Table 10:

<table>
<thead>
<tr>
<th>Variable</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
<th>6</th>
</tr>
</thead>
<tbody>
<tr>
<td>1. Pretest Computational Average</td>
<td>−</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2. Pretest Evolution Percent</td>
<td>.300*</td>
<td>−</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>3. Post1 Computation Percent</td>
<td>.420*</td>
<td>.343*</td>
<td>−</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>4. Post1 Evolution Percent</td>
<td>.248</td>
<td>.467*</td>
<td>.491*</td>
<td>−</td>
<td></td>
<td></td>
</tr>
<tr>
<td>5. Post2 Computational Average</td>
<td>.313*</td>
<td>.297*</td>
<td>.620*</td>
<td>.382*</td>
<td>−</td>
<td></td>
</tr>
<tr>
<td>6. Post2 Evolution Percent</td>
<td>.440*</td>
<td>.588*</td>
<td>.447*</td>
<td>.623*</td>
<td>.333*</td>
<td>−</td>
</tr>
</tbody>
</table>

*Note. Evolution tests were calculated as percents while computational scores were averages
*p $\leq .05$
There were small positive correlations between the computational pretest scores and the evolution pretest scores \((r = .300)\). The computational pretest scores had a medium positive correlation with the computational posttest 1 scores \((r = .420)\), and the computational pretest scores were also positively correlated with computational posttest 2 scores \((r = .313)\). There was a medium positive correlation between the computational pretest scores and the evolution posttest 2 scores \((r = .440)\).

There was a medium correlation between the pretest evolution knowledge scores and the posttest 1 computational knowledge scores \((r = .343)\). The pretest evolution knowledge scores had a small positive correlation with the post 2 computational knowledge scores \((r = .297)\). There was a medium correlation between the pre evolution test scores and the posttest 1 evolution test scores \((r = .467)\). There was also a strong correlation between the pretest evolution knowledge scores and posttest 2 evolution knowledge test scores \((r = .588)\). There was a medium correlation between pre evolution test scores and the posttest 1 computational test scores \((r = .343)\) as well as between the pre evolution test scores and the posttest 2 computation test scores \((r = .297)\).

There was a medium correlation between the posttest 1 computational scores and the posttest 1 evolution test scores \((r = .491)\). There was a strong correlation between the posttest 1 computational test scores and the posttest 2 computational scores \((r = .620)\). There was a medium correlation between the posttest 1 computational scores and the posttest 2 evolution test scores \((r = .447)\).

There was a medium correlation between the posttest 1 evolution test scores and the posttest 2 computational test scores \((r = .382)\). There was a strong correlation between the posttest 1 evolution test scores and the posttest 2 evolution scores \((r = .623)\).
The posttest 2 computational scores had a medium correlation with posttest 2 evolution test scores \((r = .333)\). No bivariate correlations exceeded a value of .7 which reduced the possibility of multicollinearity, or that the variables were redundant measures of each other (Brandler & Roman, 2007).

These correlations address part of research questions 1, and 2: exploring the relationship between learning biological evolution through computational thinking and (1) biological evolution knowledge scores and (2) computational knowledge scores. These correlations address which variables (computational knowledge and biological evolution knowledge) displayed some relationship or association at the various testing times.

*Group Differences Pre- to Post-instruction*

*Means and Standard Deviations*

I calculated mean scores and standard deviations for the knowledge instruments (BECKI and CTCKS) at each of the three testing times. I also calculated variable score means and standard deviations for each intervention group. These scores contained a valid sample size of 51 \((N = 51)\). The raw CTCKS score range is between 1 and 5, with 5 being the desired score. The closer participants scored to a 5 on each item, the “higher” their knowledge was on the computational thinking instrument. I addressed all negative coding for the CTCKS before import into SPSS. I calculated BECKI mean scores based on percent correct out of the 18 multiple choice items.

All means \((M)\) and standard deviations \((SD)\) are listed in Table 11 below. The table shows the total means and standard deviations for both knowledge variables (computational and evolutionary) at each of the three testing times. Means and standard
deviations for groups of participants undergoing intervention 1 ($n = 21$) and intervention 2 ($n = 38$) are also listed.

*Table 11*

**Mean Scores for Dissertation Study Variables**

<table>
<thead>
<tr>
<th>Variables</th>
<th>Combined</th>
<th>Intervention 1</th>
<th>Intervention 2</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>$M$</td>
<td>$SD$</td>
<td>$M$</td>
</tr>
<tr>
<td>Evolution Knowledge Pretest</td>
<td>36.5</td>
<td>13.2</td>
<td>39.9</td>
</tr>
<tr>
<td>Evolution Knowledge Posttest 1</td>
<td>43.3</td>
<td>15.3</td>
<td>53.6</td>
</tr>
<tr>
<td>Evolution Knowledge Posttest 2</td>
<td>40.3</td>
<td>16.1</td>
<td>47.2</td>
</tr>
<tr>
<td>Computational Knowledge Pretest</td>
<td>3.39</td>
<td>.348</td>
<td>3.36</td>
</tr>
<tr>
<td>Computational Knowledge Posttest 1</td>
<td>3.52</td>
<td>.392</td>
<td>3.71</td>
</tr>
<tr>
<td>Computational Knowledge Posttest 2</td>
<td>3.46</td>
<td>.339</td>
<td>3.56</td>
</tr>
</tbody>
</table>

*Note.* ($N_{Total} = 51$), ($n_{Intervention 1} = 21$) & ($n_{Intervention 2} = 38$)

**Assumptions Testing**

To address research questions one and two I performed a repeated measures multivariate analysis of variance (MANOVA) to assess changes pre to post instruction between two separate interventions, resulting in a total of 3 testing times (one pre and two post instruction tests). This analysis included group (treatment or intervention) as the between subjects variable and time (pretest, posttest 1, and posttest 2) as the within-
subjects variable. Biological knowledge and computational knowledge are the dependent variables assessed by the BECKI and CTCKS. Normality of the data is assumed in MANOVA designs, therefore I examined outliers (as discussed above) as well as skewness and kurtosis values.

It is important to identify that data is in fact normally distributed in order to appropriately run MANOVA tests. Skewness is the measure of asymmetry of distribution of a variable, the skewness value of data with a perfectly normal distribution is zero. Positive or negative skewness is indicated by a positive or negative value. If the skewed value is greater than the absolute value of 2, it suggests that the data is not normally distributed and is an indicator that ordinary least squares tests cannot be used and a non-normative tests may be used to properly assess data (Kim, 2013). In the data sets used to evaluate RQs 1 and 2, all skewed values were < 2.

Kurtosis is the measure of the peaked-ness of a distribution and all values should be < 7 when assuming normality of the data (Kim, 2013). All of the kurtosis values in the data sets used to address RQ 1 & 2 were < 7 therefore ordinary least squares (normal distribution) is assumed. All skewedness statistics values were ≤ 0.634 and skewed standard error values were ≤ 0.311. All kurtosis statistic values were ≤ 2.40 and kurtosis standard error values were ≤ 0.613 so the normality assumption was held.

I also examined the basic MANOVA assumptions of linearity and homogeneity of the variance-covariance matrices. Scatterplots for pair combinations of the dependent variables did not reveal concern regarding linearity. Similarly, scatterplots of standardized residuals for each of the dependent variables revealed no concerns regarding linearity. This analysis also met the assumption of homogeneity of the variance-
covariance matrices based on Box’s $M$ test, with $F(21, 3930) = 1.22, p = .220$. A $p$-value greater than .001 indicates homogeneity with the relatively conservative Box’s $M$ test.

**Potential Classroom Effects**

Individual participants were nested in one of four classrooms and between one of two teachers. This grouping could create possible statistical dependencies among student participants within these classrooms or between two the teachers. For example, there may be dynamics that existed for the participants in one classroom more than another classroom. Intra-class correlations (ICC) is a measure of reliability and is representative of how similar individuals are within a group (such as within a classroom) as compared to individuals between groups (or between classrooms; Koo & Li, 2016). These groups or assemblages can become problematic if the effects within these assemblages are not the effects being tested.

I calculated ICC values to ascertain levels of statistical independence among the observations for each of the dependent variables (computational knowledge and evolution knowledge). The ICC is a measure between 0 and 1, with a high value indicating that participants within a particular assemblage (classroom) have a strong within group dependency, therefore I obtained ICC measures for each of the dependent variables for classes (4 groups) and for teacher (2 groups). ICC can also be used to discern phenomena for groups that would only be possible within the specific group (i.e., unique collaboration within a particular classroom).

ICC can be determined by calculating the proportion of variance for those within a particular group (Bliese, 2000). The following formula can be used to calculate the ICC using a one-way analysis of variance (ANOVA):
\[
\text{ICC} = \frac{MS_B - MS_W}{MS_B + (m - 1) MS_W}
\]

\(MS_B\) represents the mean sum of squares between groups and \(MS_W\) is the mean sum of squares within groups and \(m\) is the group size. Mean group size can be used for \(m\) when groups are unequal (Bliese, 2000). In order to determine whether potential group effects are significant (using \(p\)-value) Fisher’s \(r\) – to – \(z\) transformation may be used (The Pearson bivariate correlation \([r]\) is replaced with the calculated ICC value to determine whether potential group effects are significant; Konishi, 1985). ICC values and mean cluster size were used to determine the test statistic (\(z\)) and respective \(p\)-values.

Table 12 shows the ICC values that I calculated for all dependent variables with a one-way ANOVA (with class as the independent variable). The ICC values ranged from .00984 (computational knowledge posttest 2) to .205 (evolution knowledge posttest1) with all \(p\)-values greater than .05. A multi-level model must be used if the ICC is significant, otherwise a standard regression may be used without concern because there is no evidence of group effect (i.e., classroom effect) in the data (Bliese, 2000).

Evolution knowledge scores at time 2 had an ICC value of .205, which is considered poor, but only slightly above the threshold of .200 (Bliese, 2000). This could be due to uneven class (sample) sizes and or low reliability of the BECKI testing instrument. The potential classroom effect for evolution scores at time 2 may be indicative of substantially high or low scores at this testing time. Because the value is slightly above the threshold it is only of minor concern and will be considered later on in the analysis.

Because all dependent variables had no significant ICC values and were less than .205 it is not likely that the participants in a particular class had a significantly greater
similarity than the overall similarities in the treatment (intervention) groups (explored in subsequent analyses). This indicates a potential difference between the treatment and comparison groups are a result of the instructional activities and not due to classroom effects. This further indicates the OLS assumptions required for the following statistical analyses (such as the repeated measures MANOVA) have been met and ensures true independence in observations.

\textit{Table 12}

\textit{Intra-class Correlation Coefficient (ICC) Values For The Study Variables Clustered by Class, with } N_{\text{Class}} = 4 \text{ and } m \text{ (Mean Cluster Size) } = 15

<table>
<thead>
<tr>
<th>Variable</th>
<th>$MS_B$</th>
<th>$MS_W$</th>
<th>ICC</th>
<th>$z$</th>
<th>$p$-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Evolution Knowledge Pretest</td>
<td>49.2</td>
<td>180</td>
<td>.051</td>
<td>1.17</td>
<td>.879</td>
</tr>
<tr>
<td>Evolution Knowledge Posttest 1</td>
<td>949</td>
<td>195</td>
<td>.205</td>
<td>0.192</td>
<td>.576</td>
</tr>
<tr>
<td>Evolution Knowledge Posttest 2</td>
<td>439</td>
<td>251</td>
<td>.048</td>
<td>0.192</td>
<td>.576</td>
</tr>
<tr>
<td>Computational Knowledge Pretest</td>
<td>0.056</td>
<td>0.125</td>
<td>.038</td>
<td>0.891</td>
<td>.814</td>
</tr>
<tr>
<td>Computational Knowledge Posttest 1</td>
<td>0.388</td>
<td>0.141</td>
<td>.105</td>
<td>0.064</td>
<td>.526</td>
</tr>
<tr>
<td>Computational Knowledge Post Test 2</td>
<td>0.131</td>
<td>0.114</td>
<td>.009</td>
<td>0.426</td>
<td>.665</td>
</tr>
</tbody>
</table>

Table 13 shows the ICC values that I calculated for all dependent variables with associated one-way ANOVA using teacher as the independent variable. I also calculated
z- and p-values. The ICC values ranged from .00350 (evolution knowledge pretest 2) to .0349 (computational knowledge posttest 1) with all p-values greater than .637. Because all dependent variables had no significant ICC values and were greater than .200, the participants who had a particular teacher did not have a significantly greater similarity than the overall similarities in the treatment (intervention) groups (which is explored in subsequent analyses). This indicates a potential difference between the treatment and comparison groups are a result of the instructional activities and not due to teacher or school effects. Participants who had the same teachers also differed between school (East vs. West High Schools) therefore the ICC values calculated to determine teacher effects could also explain school effects.
Table 13:

*Intra-class Correlation Coefficient (ICC) Values For The Study Variables Clustered By Teacher, with $N_{\text{Teacher}} = 2$ and $m$ (Mean Cluster Size) = 29.5*

<table>
<thead>
<tr>
<th>Variables</th>
<th>$MS_B$</th>
<th>$MS_W$</th>
<th>ICC</th>
<th>$z$</th>
<th>$p$-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Evolution Knowledge Pretest</td>
<td>35.9</td>
<td>10000</td>
<td>.00349</td>
<td>0.461</td>
<td>.678</td>
</tr>
<tr>
<td>Evolution Knowledge Posttest 1</td>
<td>1.01</td>
<td>13600</td>
<td>.0351</td>
<td>0.720</td>
<td>.764</td>
</tr>
<tr>
<td>Evolution Knowledge Posttest 2</td>
<td>172</td>
<td>15200</td>
<td>.0347</td>
<td>0.804</td>
<td>.789</td>
</tr>
<tr>
<td>Computational Knowledge Pretest</td>
<td>0.0330</td>
<td>6.70</td>
<td>.0349</td>
<td>0.670</td>
<td>.749</td>
</tr>
<tr>
<td>Computational Knowledge Posttest 1</td>
<td>0.163</td>
<td>8.77</td>
<td>.0344</td>
<td>0.537</td>
<td>.704</td>
</tr>
<tr>
<td>Computational Knowledge Post Test 2</td>
<td>0.144</td>
<td>6.65</td>
<td>.0343</td>
<td>0.351</td>
<td>.637</td>
</tr>
</tbody>
</table>

**Multivariate Effect**

The repeated measures MANOVA revealed a statistically significant interaction between group (intervention) and time for the combined scores of computation and evolution knowledge, with $F(4, 194) = 4.79, p < .001$. There was a medium to large effect size of $\eta^2 = .090$. Effect sizes (standard for analysis of variance) are derived using $\eta^2$ and are classified as: “very small” = $\eta^2 < .01$, “small to medium” = $.01 \leq \eta^2 < .06$, “medium to large” = $.06 \leq \eta^2 < .14$, and “large” = $\eta^2 \geq .14$ (Moore, McCabe, & Craig, 2012).
I used the multivariate analysis of variance to explore additional interactions of combined knowledge scores. The MANOVA revealed a significant interaction between combined knowledge scores (computation and evolution) and group (intervention), $F(2, 48) = 4.30, p = .019$. There was a large effect size $\eta^2 = .152$. There was a significant interaction between combined knowledge scores and time with, $F(4, 194) = 5.73, p < .001$. There was a medium to large effect size of $\eta^2 = .106$.

\[\text{Figure 5. Evolution knowledge scores (represented as percent correct) over time for the two intervention groups, with bars showing ± 1 standard error.}\]
Follow-up univariate analyses on significant interaction effects

Follow-up univariate analyses of variance indicated that the interaction between time and group (intervention) was significant for evolution knowledge, $F(2, 405) = 4.72$, $p = .018$, $\eta^2 = .0791$ (medium to large effect size). There was also a statistically significant interaction between time and group for computational knowledge, $F(2, 0.391) = 5.71$, $p = .005$, $\eta^2 = .104$ (medium to large effect size). These two analyses were run concurrently, so to account for family-wise error, I used Bonferroni adjusted critical value ($\alpha = .025$) as a conservative gauge of significance (i.e., significance was gauged at the values $\leq .025$; Rupert, 2012).

I used the univariate tests to explore additional interactions of the computation and evolution knowledge constructs. Evolution knowledge scores had a significant interaction with time, $F(2, 693) = 7.20$, $p < .001$, $\eta^2 = .128$ (medium to large effect size). Computational knowledge also had a significant interaction with time, $F(2, 0.328) = 4.79$, $p = .018$, $\eta^2 = .0791$ (medium to large effect size).
There was a significant interaction between evolution knowledge and intervention group with a large effect size, $F(1, 357) = 8.74, p = .005, \eta^2 = .151$. There was no significant interaction for computational knowledge and intervention group ($p = .142$).

**Simple Effects Analyses**

For the two variables that showed a significant interaction (computational and evolution knowledge) in the follow-up univariate tests, I conducted an additional simple effects analysis. I performed this analysis to determine the exact nature of the group differences (intervention) at pre-instruction (time 1), after the first lesson (posttest 1, time 2) and after the second lesson (posttest 2, time 3). There were no significant differences pre instruction between the intervention groups for evolution nor computational knowledge, with all $p$-values $\geq .262$.

When considering the interactions at post instructional times, time 2 had a significant interaction with combined knowledge scores, $F(2, 48) = 9.42, p < .001, \eta^2 = .282$. There was a large effect size at time 2 and an overall increase in both knowledge constructs at this time, however there was no significance for combined knowledge scores at time 3 ($p = .089$). Evolution knowledge scores were significantly greater at time 2 with, $F(1, 49) = 17.8, p < .001, \eta^2 = .266$ (large effect size). There was also significantly greater computational knowledge scores at time 2 with, $F(1, 0.933) = 7.09, p < .010, \eta^2 = .126$ (medium to large effect size). Only the first intervention group had a significant interaction with time and combined knowledge scores with, $F(4, 46) = 7.41, p < .001, \eta^2 = .392$. There was no significance for the second intervention group ($p = .896$).
Pairwise Comparisons

The following results of the Bonferroni post hoc tests (pairwise comparisons) allowed me to explore the particular relationships between the two knowledge constructs, time and intervention groups for the variables that showed significant interactions. Significance was gauged at $p \leq .025$ to account for familywise error. Considering the measure of evolution knowledge, participants in intervention group 1 scored a significantly higher at time 2 ($M = 53.5, SD = 3.19$) as compared to time 1 ($M = 39.8, SD = 3.29$). There was no significant gain in evolution knowledge between time 1 and 3 for the first intervention group ($p = .032$). Considering the second intervention group, there were no significant differences in evolution knowledge between the testing times (all $p$-values $\geq .353$).

It is important to note (as stated in univariate analysis above) that there was no statistical significance between intervention group and computational knowledge scores as determined from the previously run univariate tests. However, Bonferroni post-hoc tests have the potential to identify group differences even if the univariate tests fail to determine significance due to more focus and statistical power (Ruxton & Beauchamp, 2008). Bonferroni post-hoc results indicated that for the first intervention group there was a statistically significant gain in computational knowledge between time 1 ($M = 3.36, SD = 0.508$) and time 2 ($M = 3.71, SD = 0.353$; directly after their intervention lesson) but not between time 2 and time 3 ($p = .050$). For the second computational intervention group, there were no significant gains in computational knowledge between testing times (all $p$-values $\geq .658$).
At time 2, participants in intervention group 1 had greater computational knowledge scores ($M = 3.71, SD = 0.353$) as compared to intervention group 2 ($M = 3.42, SD = 0.383$). Participants in intervention group 1 also had significantly greater evolution knowledge scores at time 2 ($M = 53.5, SD = 3.19$) as compared to participants who were part of intervention group 2 ($M = 37.1, SD = 2.26$). There was no significant difference between the intervention groups at time 3 when considering computational knowledge scores ($p = .116$) nor when considering the evolution knowledge scores ($p = .042$).

However, Levine’s test (an ANOVA) showed that the variances for the evolution posttest 2 scores (taken at time 3) were not equal, with $F(1, 49) = 5.19, p = .024$. See Table 11 for all means and standard deviations, as well as graphical displays of means and standard errors in figures 5 and 6.

**Knowledge Growth Summary**

I am interested in identifying if instruction using computational thinking to learn biological evolution has an effect on evolution knowledge (RQ 1) and computational knowledge (RQ 2) and used two different computational interventions and three testing times in my experimental design, where testing times 2 and 3 were post instructional. The interaction between time and intervention was significant for combined knowledge scores and for both evolution knowledge, with $F(2, 405) = 4.72, p = .018, \eta^2 = .079$ (medium to large effect size), and computational knowledge, with $F(2, 0.391) 5.71, p = .005, \eta^2 = .104$ (medium to large effect size). However, only the first intervention produced statistically significant gains in evolution knowledge at post instructional testing time 2 ($p$-values for intervention 2 were $\geq .896$). Computational knowledge gains were only statistically significant at time 2 for participants within the first intervention group.
One potential reason for the lack of interaction between interventions groups and knowledge scores (at time 3 for example) may be the poor reliability of ICC scores of evolution knowledge at time 2. Low reliability for this score could mean that there was a greater difference between classes due to some other untested variable that occurred in a particular classroom at that testing time. The potential tested differences between the intervention groups would be more difficult to identify if this was the case.

Another reason for the lack of interaction may be due to the poor to questionable instrument validity of the BECKI and the CTCKS mentioned above. (Cronbach’s $\alpha = .474, .547$ and $\alpha = .623$ for the BECKI and Cronbach’s $\alpha = .514, .594$ and $\alpha = .446$ for the CTCKS at respective testing times). Some educational researchers consider 0.7 to be the cutoff threshold for reliable instrumentation because lower reliability tends to weaken results due to higher signal to noise ratios (Lombardi, Bailey Bickel, & Burrell, 2018). In other words, lower reliability diminishes differences in distribution samples and this attenuation would be most pronounced at the ends of the sample distribution. In this dissertation study, the lower reliability would dampen pre to post instruction differences, and it is very unlikely that lower reliability instruments would result in Type II experimental error (Lombardi, Bailey, Bickel, & Burrell, 2018).

Sometimes low reliability of instruments may not be indicative of actual knowledge scores. Therefore, questions within the tests may not actually be measuring computational knowledge or evolution knowledge in the way I have defined them. In this case, it is more likely that true knowledge scores are more difficult to ascertain. This is because there is less of a chance of identifying statistical differences (due to low reliability within the instruments) although the differences identified are true. In other
words, if the instruments had greater reliability there may have been stronger statistical
differences identified. Future study with larger sample sizes may provide an avenue to
identify faulty items (questions) within these instruments using statistical means. Because
particular questions were selected (BECKI) or developed (CTCKS) to represent certain
biological or computational constructs, the qualitative analyses (part of research question
3) was used to provide evidence for which constructs supported student learning. I
discuss these limitations further in Chapter 5.

The quantitative results indicated that computational intervention 1 \((n = 21)\) was
more successful in student participants learning biological evolution as compared to
computational teaching intervention 2 \((n = 38)\). I discuss the rationalization and study
limitations of the uneven intervention groups in Chapter 5. Participants as part of
intervention 1 received the computational lesson between the pretest and testing time 2
and received a traditional evolution lesson (by their normal teacher) between testing time
2 and 3. Participants in intervention 2 had their computational lesson between testing
time 2 and 3. Biological instruction during the non-computational lessons could have
contributed to posttest biological evolution knowledge scores. Therefore, results of
testing time 2 for intervention group 1 and testing time 3 for intervention group 2 scores
would have been most indicative of biological evolution growth as related to
computational knowledge instruction. The significant evolution knowledge growth of
intervention group 1 at time 2 may have been a result of the computational instruction;
however, this growth was not sustained at testing time 3 (retention of knowledge may be
of interest in future study).
The success of intervention 1 may have been related to the nature of the specific instructional activities, particular biological components, and biological (organizational level) connections that were emphasized in this intervention. There was a shared computational component of the lesson (i.e., description and biological examples related to input, output, integration and feedback) which was the same for both intervention groups. The increase in biological evolution knowledge associated with computational intervention 1 might have been due to better alignment with instrument questions as compared to the traditional biological evolution teaching (and or the activities in computational intervention 2).

The activities in intervention 1 entailed more computational complexity in terms of instructional context (see Table 3 for instructional context) as compared to intervention 2. For example, the platform (google sheets) provided more computational activity (i.e., more coding and less scaffolding) for the participants as compared to the interface friendly BLAST program presented in intervention 2. Instruction related to intervention 1 also emphasized a wider range of biological organization (particularly, the molecular biological level [alleles] through to the ecological biological level [population and environment]). Intervention 2 specifically emphasized the molecular level (DNA and protein) through to the species level, which was a smaller range of biological organization. Additionally, the instrument questions may have been better aligned with the nature of the lesson within intervention 1. At face value this is particularly interesting because there were multiple phylogenetic tree questions on the BECKI which were better aligned with intervention 2. Therefore modifying the instruments or the particular interventions may result in stronger significant interactions in a follow up study to this
dissertation. Further discussion of the nature of the intervention differences is presented in Chapter 5.

*RQ 1 Summary of Biological Evolution Knowledge Growth.* Research question 1 focuses on quantitative components of biological evolution knowledge growth. Biological evolution knowledge is often assessed using specific constructs such as tree thinking or natural selection (i.e., Phylogenetic Tree Thinking Assessment developed in 2005 by Baum or the Conceptual Inventory of Natural Selection [CINS] developed in 2002 by Anderson). In this dissertation, I wanted to assess biological evolution at and between various scales (which I argue is also emphasized through computational thinking) I modified and combined constructs from 5 previously published assessments into the BECKI to measure biological evolution knowledge at various scales in this study.

As I mentioned above participants undergoing intervention 1 experienced a significant increase in evolution knowledge, specifically at time 2 (which was directly after their computational lesson intervention). Because BECKI questions ranged from molecular scales to ecosystem scales, identifying which questions (and associated biological levels) participants made greater gains in may differ between interventions at different times. Exploring participant answers of the specific BECKI questions may be appropriate for a follow up study to this dissertation. This study is unique not only because it indicates students might develop a better understanding of biological evolution through computational thinking, it specifically explores the understanding at and between biological scales (as biological evolution also occurs at and between all scales). Research question 3a (qualitative components) provides further insight on student use of biological scales.
**RQ 2 Summary of Computational Knowledge Growth.** Research question 2 focuses on quantitative components of computational knowledge growth. The CTCKS instrument items were developed to focus on the four computational components. I would have expected computational knowledge growth might have some relationship with the specific interventions and or with biological evolution knowledge growth.

As I mentioned above participants undergoing intervention 1 experienced a significant increase in computational knowledge, specifically at time 2 (which was directly after their computational lesson intervention). Participants in intervention 1 also experienced a small non-significant decrease in computational knowledge between time 2 and 3 indicating that knowledge was not retained. Computational knowledge retention may be explored in future study.

Computational knowledge growth results are particularly interesting because participants within both intervention groups received a similar computational lecture component. The difference between the intervention groups was primarily the biological activities, both of which infused computation. Therefore, the nature of computation within intervention activities may be unique (particularly as they related to the biological aspects). In other words, the intervention activities (computation coupled with biological evolution aspects) may have contributed to student learning computation more so than the direct instruction on computation alone.

Because CTCKS questions focused particularly on input, output, integration or output, identifying which questions participants made greater gains in might be an appropriate follow up study to this dissertation. It is also important to note that the interventions were the first time that the majority of student participants had been
exposed to the computational constructs as defined in the LP. I ascertained this information through assumption and by verbally asking the participants about prior computational component exposure during the interventional instruction. Research question 3b (qualitative components) provides further insight on the complexity of student knowledge of the computational components (as defined in the BELCT-LP).

Analyses of Research Question 3: Results of Qualitative Analyses

Research question 3 asks about the association between the participants artifacts produced during the computational interventions and:

a) Student understanding of the levels of biological organization and
b) The complexity of computational thinking.

RQ 3 drives a complimentary design mixed methods study because I used the qualitative results to enhance and or elaborate the results from the qualitative analysis (Greene, Caracelli, & Graham, 1989). In this section, I present the development and results of my coding analysis. I then discuss the results of the biological level scoring and associations that emerged from the coding analysis (RQ 3a). I then discuss the development of the computational complexity rubric. I used the rubric to score computational complexity for the participants written artifacts based on the LBECT-LP. I present and discuss the associated computational complexity results (RQ 3b).

RQ 3a: Conceptual and Relational Analysis of Written Explanations

Content analysis has two major forms, conceptual analysis and relational analysis both of which I used to answer RQ 3a. In conceptual analysis, a concept is chosen and the analysis involves quantifying its presence (Kalinowski, Leonard, & Taper, 2016). Conceptual analysis is particularly important in science education research because it
allows various terms (used by student participants) to represent a larger construct (identified by researcher). This allows the researcher to develop an appropriate concept definition (i.e., the concept of “cell”) with specific borderlines for rich results (i.e., neurons and eosinophils are two very different terms for the construct of “cell”). Explicit terms representing biological organization are the items that I selected within the participant data to answer RQ 3i and range from level 1 (L1) through L14. These levels were selected prior to coding participant artifacts. Participant identifiers of these biological levels varied greatly due to the nature of the intervention questions.

Relational analysis is a specific form of content analysis which explores explicit relationships identified (by participants) within texts. It provides higher levels of statistical rigor as compared to other qualitative methods used in educational research because it allows researchers to make specific inferences from participant artifacts (Robinson, 2011). Artifacts were coded using relational analysis to explicitly identify if participants made connections between biological levels, which is more meaningful than identifying if the two levels occurred together through statistical means (i.e., a bivariate correlations). I performed a relational analysis to identify and better understand the nature of relationships participants made between these biological levels.

*Defining Biological Levels of Organization*

To address RQ 3a, I specifically examined the participant artifacts that were generated from questions in intervention 1 (see Appendix D) and intervention 2 (see Appendix E). The questions were designed to be answered during and directly after the interventions. Questions were specific to the intervention and there was one shared computational question between the interventions. Most questions within the
interventions prompted students to identify and describe computational and biological components in an open-ended form (for example: “Identify what you observed in your populations” or “How does BLAST [computational tool] actually compare these [molecular] sequences?”). Activities within the interventions themselves allowed participants to pick from a database of DNA sequences or proteins (Intervention 2), or to imagine a hypothetical group of organisms and environments (Intervention 1). Due to participant choice to work with infinite biological scenarios (i.e., pick a protein of interest), I had to examine participants answers in detail to identify which biological levels were present based on participant use of key biological words. I read through the participant artifacts multiple times until no new biological words (and associated biological levels emerged).

Biological words within participant artifacts were used to classify the presence of biological levels (atom through biosphere; based on Table 2 from the LBECT-LP). Biological levels and associated participant examples and concept definitions are displayed in Table 14. I derived concept definitions for the biological levels from Biology in Focus, a textbook written by Campbell, Mitchell and Reese (2000) which is accepted by AP biology curriculums and many college level biology courses.
### Table 14

**Biological Levels Identified from Participant Artifacts**

<table>
<thead>
<tr>
<th>Level</th>
<th>Biological Level</th>
<th>Participant Examples</th>
<th>Concept definition</th>
</tr>
</thead>
<tbody>
<tr>
<td>14</td>
<td>Biosphere</td>
<td>No participants recognized this level</td>
<td>The earth and interactions of its regions</td>
</tr>
<tr>
<td>13</td>
<td>Ecosystem</td>
<td>The habitat, the environment</td>
<td>Community of organisms and their physical environment</td>
</tr>
<tr>
<td>12</td>
<td>Community</td>
<td>Biotic factors, all living organisms</td>
<td>Interacting group of species in common location</td>
</tr>
<tr>
<td>11</td>
<td>Species</td>
<td><em>Mus musculus</em>, all dogs</td>
<td>Group of organisms that can produce viable offspring</td>
</tr>
<tr>
<td>10</td>
<td>Population</td>
<td>Bird population, the next generation</td>
<td>Organisms of a species in a particular location within a given time</td>
</tr>
<tr>
<td>9</td>
<td>Organism</td>
<td>The fish, the organism</td>
<td>Discrete and complete individual living thing</td>
</tr>
<tr>
<td>8</td>
<td>Organ System</td>
<td>Central nervous system, the bones</td>
<td>Group of organs working together to perform function</td>
</tr>
<tr>
<td>7</td>
<td>Organ</td>
<td>Heart, skin</td>
<td>Group of tissues which perform a specific function</td>
</tr>
<tr>
<td>6</td>
<td>Tissue</td>
<td>Blood, muscle tissue</td>
<td>Similar cells which carry out a specific function</td>
</tr>
<tr>
<td>5</td>
<td>Cell</td>
<td>Red blood cell, nerve cell</td>
<td>Smallest structural and functional unit of an organism</td>
</tr>
<tr>
<td>4</td>
<td>Organelle</td>
<td>Ribosome, mitochondria</td>
<td>Specialized structures within a cell which perform a function</td>
</tr>
<tr>
<td>3</td>
<td>Macromolecule</td>
<td>Protein, DNA</td>
<td>Large complex molecule</td>
</tr>
<tr>
<td>2</td>
<td>Molecule</td>
<td>Glucose, gene sequence</td>
<td>Two or more atoms covalently bonded</td>
</tr>
<tr>
<td>1</td>
<td>Atom</td>
<td>Oxygen, hydrogen ion</td>
<td>Smallest unit of matter that contains its properties</td>
</tr>
</tbody>
</table>

*Note.* Concept definitions modified from Campbell et al., 2000

I classified this as a conceptual analysis because I counted biological words if they “fit” one of the 14 concepts listed in Table 14. For example if a participant wrote “neuron” (a type of nerve cell), that was counted as a biological word, classified and quantified as one attempt at the cellular level (L5). If a participant wrote “the environment”, I classified it at the ecosystem level and it would count as one attempt at the L13 level. I defined these concepts based on important biological properties.
associated with each level. For example, molecules (L2) comprise macromolecules (L3) or environments are comprised of the interaction of the living and non-living components of an ecosystem (L13). I recognize that some of my defined levels may be imperfect in terms of classification. For example, technically the way oxygen is found in nature (within air for example) it is a molecule (O₂), but when broken apart and used in the body it may be become (or act as) an individual atom. However, oxygen in the way participants use it, one atom vs two, is not the focus here. In the instances that participants used it, oxygen’s overall behavior in biological systems better aligns with the atom level; therefore, I classified oxygen at the atom level (L1). Usage was not always explicit within the artifact and in those (few) cases I did not quantify the construct.

There is also some inconsistency among scientific fields between how many bonded atoms comprise a molecule versus a macromolecule (i.e., a macromolecule is a large molecule). Biology courses spend time on this differentiation, the typical macromolecules presented to biology students are: proteins, nucleic acids (DNA or RNA), carbohydrates and lipids, therefore I defined molecules of this size at the macromolecule level. Some of the macromolecules participants identified were “proteins” and “DNA”. If portions of these macromolecules were referenced (monomers), I classified them at the molecule level (“amino acid” or “nucleotide”). These words came from the individual conditions participants developed during instructional activities.

Other levels that were important to distinguish were organism (L9), population (L10) and species (L11). Organisms are individual living beings. Populations are groups of organisms, usually living in the same region, and are composed of multiple
generations. Species are all of the organisms that have the ability to viably reproduce (which is determined by DNA similarity) and are assigned specific scientific names. All three of these definitions are blurry, even to those within the scientific community. For example, *Canis lupus* (wolf) and *Canis familiaris* (dog) are distinctly different species due to the fact they normally would not be able to interbreed given where they typically reside, however they do have the ability to produce viable offspring and are sometimes referred to as *Canis lupus familiaris*. I classified biological levels based on the ways participants used them.

I counted and classified all of the biological words within each participant’s artifact that would distinctly represent an organizational level. If participants referenced a specific protein such as “keratin” it was classified at the macromolecule level (L3) and if the participant referenced the world “protein” again in a different context it was counted as another word at the L3 level. It was possible for participants to identify multiple biological words at each biological level. If participants used the word “keratin” more than once however, this second instance was not counted again. If it was not clear that the participant identified the level (i.e., there was no context given or example was too vague) it was not counted. I quantified the total number of “biological words identified” as well as the “biological levels attempted” which were identified for each participant from their digitally submitted artifact.

I also identified “levels correctly identified” by excluding incorrect attempts in which the participant used the inappropriate context with the biological word. In theory each biological word represented a biological level, however not all representations were accurate. For example if a participant used the word “organism” but used it in the
context of a species, I counted it as an incorrectly identified instance at the organismal level (L9). It is also important to note that not all participants turned in an artifact and not all participants completed all questions for the interventions. If students did not answer all questions within artifacts but there was enough meaningful information present within answered portions for scoring (greater than 80% of questions responded to) they were scored. This on average may have reduced the reported averages of biological levels and biological level connections. There were a total of 39 participants who turned in artifacts \( (N = 39) \). I counted the number of biological words and biological levels attempted within each artifact as well as the levels correctly identified and uploaded data into SPSS for analysis. The artifacts were not scored by a second biology expert due to time constraints (and discussed later as a potential limitation of the study).

**Means and Standard Deviations**

Research question 3a specifically asks about what ways artifacts developed during computational interventions display different levels of biological organization. The means were calculated to represent average values per participant artifact (each participant turned in one artifact). The average number of biological words per participant was 5.75 \( (SD = 2.38) \) with a minimum of zero and maximum of 12. The average biological levels attempted per participant was 4.28 \( (SD=1.64) \) with a minimum of 0 and maximum of 8 levels. The average of correctly identified levels per participant (excludes incorrectly identified biological levels) was 3.38 \( (SD=1.53) \) with a maximum of 7 correctly identified levels (and minimum of 0). The means and standard deviations
(per participant) for biological words identified, biological levels attempted, and levels correctly identified are listed in Table 15.

Table 15

Conceptual Analysis: Means, Standard Deviations, Minimum and Maximum of Biological Words and Biological Levels Identified

<table>
<thead>
<tr>
<th>Category</th>
<th>M</th>
<th>SD</th>
<th>Minimum</th>
<th>Maximum</th>
</tr>
</thead>
<tbody>
<tr>
<td>Biological Words Identified</td>
<td>5.95</td>
<td>2.38</td>
<td>0</td>
<td>12</td>
</tr>
<tr>
<td>Biological Levels Attempted</td>
<td>4.28</td>
<td>1.64</td>
<td>0</td>
<td>8</td>
</tr>
<tr>
<td>Levels Correctly Identified</td>
<td>3.38</td>
<td>1.53</td>
<td>0</td>
<td>7</td>
</tr>
</tbody>
</table>

Note. (N = 39)

Bivariate Correlations

A Kendall’s tau-b correlation was used to identify the strength and associations for all biological levels within each artifact. I used this correlation because the data were not normally distributed excluding the possibility of using the Pearson correlation. Kendall’s tau-b correlations are used to rank similarity of the orderings of the data and are relatively robust against outliers (as compared to Spearman correlations; Schober, Boer, & Schwarte, 2018). Effect size ($\tau_b$) determines the strength of the correlations or how strong the relationship is between the variables. Positive effect sizes indicate the biological levels that participants tended to use together, whereas negative effect sizes indicate levels that participants tended to avoid using together. Effect sizes less than .3 are considered “small”, effect sizes between .3 and .5 are considered “medium” and effect sizes greater than .5 are considered “large” (Schober, Boer, & Schwarte, 2018).
All of the Kendall’s tau-b correlation effect size ($\tau_b$) values can be found in Table 16. All values have been provided so that $p \leq .05$.

**Table 16**

*Kendall’s tau-b Correlations for the Biological Levels Within Participant Artifacts (N=39)*

<table>
<thead>
<tr>
<th>Level</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
<th>6</th>
<th>7</th>
<th>8</th>
<th>9</th>
<th>10</th>
<th>11</th>
<th>12</th>
<th>13</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
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<td>-</td>
<td>-</td>
</tr>
<tr>
<td>2</td>
<td>.130</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>3</td>
<td>.320*</td>
<td>.110</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
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<td>-.220</td>
<td>.241</td>
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<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>5</td>
<td>-.890</td>
<td>-.141</td>
<td>.217</td>
<td>.016</td>
<td>-</td>
<td>-</td>
<td>-</td>
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<td>.431*</td>
<td>.368</td>
<td>-.313</td>
<td>-.00511</td>
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</tr>
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</table>

*Note. Biological levels represented 1 = atom, 2 = molecule, 3 = macromolecule, 4 = organelle, 5 = cell, 6 = tissue, 7 = organ, 8 = organ system, 9 = organism, 10 = population, 11 = species, 12 = community, 13 = ecosystem, 14 = biosphere (L14 was not identified by participants). All significance listed at *$p \leq .05$.

Biological level 1 had a medium positive correlations with L3 ($\tau_b = .320$), and with L6 ($\tau_b = .376$). Biological level 2 had medium positive correlations with L10 ($\tau_b = .330$). Biological L3 had strong negative correlations with L10 ($\tau_b = -.543$), and L13 ($\tau_b = -.585$). L6 had a medium to strong positive correlation with L7 ($\tau = .507$). L8 had a medium positive correlation with L12 ($\tau_b = .480$). L10 had small to medium negative correlations with L11 ($\tau_b = -.385$), and L12 ($\tau_b = -.330$). These correlations partially answer RQ 3a through indicating which variables participants tended to identify within the same artifact (positive) or which variables participants tended to avoid using together (negative). These correlations are indicative solely of biological level identification, not
to be confused with biological connections intentionally and explicitly made by participants, which I explored in following sections through relational analysis.

Means and Standard Deviations: Comparing Interventions

The quantitative analysis indicated that interventions resulted in different gains in computational and evolution knowledge. RQ 3 was designed to better explain the quantitative results therefore the intervention groups were also compared separately. There were 17 participants who turned in artifacts within intervention group 1 \((n = 17)\) and 22 participants who turned in artifacts within intervention group 2 \((n = 22)\). Means, standard deviations, minimum, and maximum identifications for each of these constructs are listed in Table 17 for each intervention group. I ran a Kruskal-Wallace test, a rank-based nonparametric test to identify significant differences between intervention groups for biological word and biological level (correct and attempt) means. The Kruskal-Wallace test did not identify any statistical significance between the intervention groups \((p \geq .076)\). Although there is less statistical power in the Kruskal-Wallis test as compared to a typical ANOVA or \(t\)-test, it was used because the data did not meet the assumptions for normality (Martin, Bateson, & Bateson, 1993).
Table 17

Means and Standard Deviations for Biological Words and Levels Identified Between Intervention

<table>
<thead>
<tr>
<th>Category</th>
<th>Intervention</th>
<th>M</th>
<th>SD</th>
<th>Min</th>
<th>Max</th>
</tr>
</thead>
<tbody>
<tr>
<td>Biological Words Identified</td>
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<td>2.20</td>
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<tr>
<td></td>
<td>2</td>
<td>6.45</td>
<td>2.44</td>
<td>2</td>
<td>12</td>
</tr>
<tr>
<td>Biological Levels Attempted</td>
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<td>3.65</td>
<td>1.73</td>
<td>0</td>
<td>6</td>
</tr>
<tr>
<td></td>
<td>2</td>
<td>4.77</td>
<td>1.41</td>
<td>2</td>
<td>8</td>
</tr>
<tr>
<td>Levels Correctly Identified</td>
<td>1</td>
<td>3.00</td>
<td>1.50</td>
<td>1</td>
<td>7</td>
</tr>
<tr>
<td></td>
<td>2</td>
<td>3.68</td>
<td>1.52</td>
<td>0</td>
<td>7</td>
</tr>
</tbody>
</table>

Note. \((N_{\text{Total}} = 39), (n_{\text{Intervention 1}} = 17) \& (n_{\text{Intervention 2}} = 22)\), No statistical significance between interventions

Exploring the Scope of Biological Levels

I calculated the proportion of participants who attempted each level as well as the proportion of participants who accurately identified each level. I represent these proportions as percentages throughout the rest of the dissertation for readability (“percent attempted” and “percent correct”). The levels which participants attempted the most frequently were L2 (molecule; 89.7%) L3 (macromolecule; 59.0%), and L11 (species; 56.4%). In other words, 89.7% of participants identified L2, 59.0% of participants identified L3 and 56.4% of participants identified L11. The levels attempted least frequently were L12 (community; 10.3%), L6 (tissue; 10.3%), L8 (organ system; 2.60%), and L14 (biosphere; 0%).

I also calculated the percent correct (for each biological level) from the difference between the attempted percent and the accurate percent which represents the mean for overall participant accuracy. For example, 30.8% of participants attempted L7, and 23.1% identified it accurately resulting in 90.3% correct for L7. Percent correct reveals
the biological levels participants had difficulty representing most often within their artifacts (and this is not necessarily representative of the levels that were used most often). Biological levels in which less than 70% of participants identified correctly were L12 (50.0%), L11 (32.1%), L8 (0%) and L4 (57.2%). Whereas students most often correctly identified L1 (100%), L2 (100%) and L7 (90.3%). Table 18 displays the percentage of participants who attempted each level (along with accompanying SDs), the percentage of participants who correctly attempted each level (and SDs) as well as the percentage correct for each level (representing overall participant accuracy). Table 18 also includes Kendall’s W rank which are values used to generate Kendall’s coefficient of concordance (W).

Table 18

<table>
<thead>
<tr>
<th>Level</th>
<th>Attempted (%)</th>
<th>Accurate (%)</th>
<th>(%) Correct</th>
<th>Kendall’s W Rank</th>
</tr>
</thead>
<tbody>
<tr>
<td>14</td>
<td>0</td>
<td>0</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>13</td>
<td>25.6</td>
<td>20.5</td>
<td>80.7</td>
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<td>12</td>
<td>10.3</td>
<td>5.10</td>
<td>50.0</td>
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<td>11</td>
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<td>17.9</td>
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<td>10</td>
<td>48.7</td>
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<td>9</td>
<td>43.6</td>
<td>35.9</td>
<td>81.8</td>
<td>7.69</td>
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<tr>
<td>8</td>
<td>2.60</td>
<td>0</td>
<td>0</td>
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</tr>
<tr>
<td>7</td>
<td>30.8</td>
<td>28.2</td>
<td>90.3</td>
<td>6.86</td>
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<td>10.3</td>
<td>7.70</td>
<td>80.0</td>
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<td>23.1</td>
<td>74.2</td>
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<td>7.70</td>
<td>57.2</td>
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<td>3</td>
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<td>51.3</td>
<td>86.4</td>
<td>8.69</td>
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<td>89.7</td>
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<td>12.8</td>
<td>12.8</td>
<td>100</td>
<td>5.69</td>
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</tbody>
</table>

*Note.* *Kendall’s W = .295, χ²(12, N = 39) = 138, p < .001.
Kendall’s coefficient of concordance ($W$) was used to determine ordinal associations between the biological levels which were identified by the participants. $W$ summarizes the concordance among all lists and ranges from 0 (perfect disagreement) to 1 (perfect agreement). The following formula can be used to calculate $W$.

$$W = \frac{12S}{m^2 (n^3 - n)}$$

$S$ represents the sum of squared deviations, $m$ represents the number of participants and $n$ represents the total number of objects (biological levels in this case). The resulting $W$ of .295 was low. This low $W$ value indicates that there is little agreement in the frequency of the biological levels used among the participants (Legendre, 2010).

In other words, there was a large variation of biological levels used among the participants. A chi-square test of independence was used to show significance of $W$ with, $\chi^2(12, N = 39) = 138, p < .001$.

Figure 7 is a visual display of the percentage of attempts of biological levels in decreasing biological size order along with the correctly identified percents at corresponding biological levels. This figure explicitly displays which levels were identified most by participants and which they may have had trouble correctly identifying.
Figure 7. Biological level percentages attempted by participants and percentage of correct instances, with bars showing ± 1 standard error. Biological levels represented 1 = atom, 2 = molecule, 3 = macromolecule, 4 = organelle, 5 = cell, 6 = tissue, 7 = organ, 8 = organ system, 9 = organism, 10 = population, 11 = species, 12 = community, 13 = ecosystem, 14 = biosphere.

Scope of Biological Levels: Comparing Interventions

A Kruskal-Wallace test is a rank-based nonparametric test that can be used to determine if there are statistically significant differences between groups of independent variables. I used this test to compare biological level attempts between intervention groups because the data did not meet normality assumptions (excluding the possibility of running a paired t-test or standard ANOVA test). The Kruskal-Wallace test showed that there were significant differences between intervention groups for the identification of 5 biological levels (L1, L3, L10, L11 and L13).

Table 19 depicts the percentage of participants who attempted each level (percentage attempted) and the percentage of participants who accurately represented each level (accurate percentage) with respective standard deviations for each of the intervention groups. Percent correct is also listed for each level which represents the overall accuracy at each level (calculated from the difference between the correct
attempts and the total attempts). These values were provided with the accuracy of two significant digits, the maximum level of accuracy ascertained from proportion data in SPSS outputs. Significance was gauged at \( p \leq .025 \) to account for familywise error.

Table 19

Percents and SD of Biological Levels Comparing Interventions

<table>
<thead>
<tr>
<th>Biological Level</th>
<th>Intervention Attempted %</th>
<th>SD</th>
<th>Accurate %</th>
<th>SD</th>
<th>% Correct</th>
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<tbody>
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<tr>
<td></td>
<td>2</td>
<td>23</td>
<td>4.29</td>
<td>23</td>
<td>4.29</td>
</tr>
</tbody>
</table>

Note. \( N_{Total} = 39 \), \( n_{Intervention\ 1} = 17 \) & \( n_{Intervention\ 2} = 22 \)

*Significant at \( p \leq .025 \)

There was a significant difference between intervention groups for L3 with, \( H(1) = 34.2, p < .001 \) where participants within intervention group 2 identified L3 more frequently (100%) as compared to intervention group 1 (6%). There was a significant
difference between intervention groups for, L10 with, $H(1) = 13.3, p < .001$ where participants within intervention group 1 identified L10 more frequently (82%) as compared to intervention group 2 (23%). There was a significant difference between intervention groups for, L11 with, $H(1) = 17.9, p < .001$ where participants within intervention group 2 identified L11 more frequently (86%) as compared to participants within intervention group 1 (18%). There was a significant difference between intervention groups for, L13 with, $H(1) = 11.5, p < .001$ where participants within intervention group 1 identified L13 more frequently (53%) as compared to intervention 2 (5%). Significant differences between intervention groups 1 and 2 were also found at the same biological levels for correct attempts ($p \leq .038$). A visual representation of the average percent identified of each biological level (differentiating intervention) is depicted in Figure 8.

*Figure 8.* Biological level attempt percentage between intervention 1 and 2, with bars showing ±1 standard error. Biological levels represented 1 = atom, 2 = molecule, 3 = macromolecule, 4 = organelle, 5 = cell, 6 = tissue, 7 = organ, 8 = organ system, 9 = organism, 10 = population, 11 = species, 12 = community, 13 = ecosystem, 14 = biosphere.
Relational Analysis

In order to answer research question 3a more robustly, I wanted to determine how participants understood the relationship between the biological levels. I did this by identifying how many explicit connections were made between the identified biological levels. For example if participants claimed that “allele frequencies” (molecule level, L3) influenced “generations” (population level, L10) I counted it as a connection attempt with 7 levels in-between. I read through the artifacts until no new biological level connections (BLC) emerged. I counted explicit connections that participants made, the number of levels in-between and if the connections were “accurate”. These connections were prompted by various questions (not explicitly asked about).

Means and Standard Deviations of BLCs

I calculated the means and standard deviations of BLCs. There was an average of 2.56 “BLC attempts” per participant (SD = 1.25), while “the average levels between attempts” was 5.59 (SD = 2.22). Because participants made multiple BLC attempts, the minimum number between levels “levels between min” (M = 3.46, SD = 3.11) as well as the maximum number between levels “levels between max” (M= 7.87, SD = 2.28) was also identified for each participant. The means and standard deviations of the BLC constructs are displayed in Table 20.

Although there was an average of 2.56 connection attempts per participant (M = 2.56, SD = 1.25), the accurate connection average was 1.64 connections per participant (M = 1.64, SD = 1.01), resulting in 61.6% of participants who made accurate BLCs. The average levels between BLC attempts was 5.59 (M = 5.59, SD = 2.22) as compared to 3.46 (M = 3.46, SD = 3.11), for the BLCs that were accurate. This indicates that accurate
BLCs on average were smaller (in biological scale) than those for participants which attempted more levels in-between.

Table 20

Relational Analysis: Summary of Total Biological Connections Means and Standard Deviations

<table>
<thead>
<tr>
<th>BLC Construct</th>
<th>M</th>
<th>SD</th>
</tr>
</thead>
<tbody>
<tr>
<td>BLC Attempts</td>
<td>2.56</td>
<td>1.25</td>
</tr>
<tr>
<td>Accurate Connections</td>
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</tr>
<tr>
<td>Levels Between Min</td>
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<td>3.11</td>
</tr>
<tr>
<td>Levels Between Max</td>
<td>7.87</td>
<td>2.28</td>
</tr>
<tr>
<td>Average Levels Between Attempt</td>
<td>5.59</td>
<td>2.22</td>
</tr>
<tr>
<td>Average Between Accurate Attempts</td>
<td>3.98</td>
<td>3.08</td>
</tr>
<tr>
<td>Micro Level Connections (L1-L9)</td>
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<td>.986</td>
</tr>
<tr>
<td>Macro Level Connections (L9-L13)</td>
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<td>.384</td>
</tr>
<tr>
<td>Micro to Macro Connections (L1-L9)</td>
<td>.44</td>
<td>.598</td>
</tr>
</tbody>
</table>

Note. (N = 39)

Three types of BLCs. I selected Level 9 as a pertinent distinction between “micro” and “macro” levels within this study. Level 9 (organism level) was selected because students use vastly different methods to study levels below L9 as compared to levels above L9 (i.e., microscopes vs ecosystem models). Facets of biology that are smaller than L9 include cellular biology or anatomy. Facets of biology that are larger than L9 include ecology or population dynamics. Fewer biological studies (and corresponding biology units within classrooms) tend to bridge these levels. Biological unity (micro) and diversity (macro) are frequently associated with smaller or larger biological levels, although they may be seen at and between all scales. Both unity and diversity contribute to the understanding of biological evolution. I suspected that students require connections between this level to fully grasp evolution at all scales.
I further quantified and classified the types of BLCs that participants made into one of 3 groups. It is important to note that I only counted instances of these three types of connections if they were accurate within the participant artifacts. The first type of connection were connections which were made below L9 (connections between L1 through L9, which I refer to as “micro levels connections”) such as a connection between macromolecule (L3) and cell (L5). Eleven participants (28.2%) identified 1 micro level connection, 10 participants (25.6%) identified 2 micro level connections, 3 participants (7.7%) identified 3 micro level connections and 15 participants (38.5%) did not identify this type of connection. Twenty-four students of the total thirty-nine (N = 39) correctly made at least 1 micro level connection with an average of 1.03 micro level connection per participant (M = 1.03, SD = .986).

The second type of connection were the connections above L9 (connections between L9 through L14, which I refer to as the “macro level connections”). An example of a macro level connection would be between populations (L10) and ecosystems (L12). Two students made 1 micro connection (5.1%), 1 student made 2 micro connections (2.6%) and 36 students (92.3%) did not make any micro connections. Three students correctly made at least one macro level connection with an average of 0.10 micro level connection per participant (M = 0.10, SD = .384).

The third type of connection were the connections that were made directly through level 9 such as connections between molecule (L2) and population (L10) (“micro through macro level connections”). Thirteen students (33.3%) made 1 micro through macro level connection, 2 students (5.1%) made 2 micro through macro connections and 24 students (61.5%) did not make any micro through macro level connections. Fifteen
students made at least one accurate micro through macro level connection with an average of 0.44 micro through macro level connections per participant \( M = 0.44, SD = .598 \). The means and standard deviations for these counts are also displayed in Table 20.

**Relational Analysis: Comparing Intervention Groups**

I calculated the percent of correctly made BLC attempts between intervention groups (from the difference between BLC attempts and BLC accurate attempts). For intervention 1, 41.8% of participants correctly made BLCs and 27.0% of participants correctly made BLCs in intervention 2. I ran a Kruskal-Wallace test in order to compare additional BLC constructs between intervention groups. This test was used to identify statistical significance between the groups because the data did not meet normality assumptions. Significance was gauged at \( p \leq .025 \) to account for familywise error.

The average BLC attempts was significantly different between intervention group with, \( H(1) = 10.3, p < .001 \). Participants significantly made more connection attempts in intervention 2 \( (M = 3.14, SD = 1.08) \) as compared to intervention 1 \( (M = 1.82, SD = 1.07) \). The average minimum levels between attempts was significantly different between intervention groups with, \( H(1) = 8.69, p = .003 \). Participants within intervention group 1 significantly had more levels between their minimum attempts \( (M = 5.24, SD = 3.41) \) as compared to participants within intervention 2 \( (M = 2.09, SD = 2.04) \). There was no significant different between the intervention groups for the average maximum biological levels between connections \( (p = .672) \).

The average number of individual biological levels between connections was significantly different between intervention groups, with \( H(1) = 19.23, p = .002 \). Participants a part of intervention 2 had made BLCs which were significantly closer
together \( (M = 4.74, SD = 1.41) \) as compared to intervention 1 \( (M = 6.69, SD = 2.53) \). In other words, participants in intervention 1 had more individual biological levels between their BLC attempts on average. There was a significant difference for the amount of correct connections between interventions with, \( H(1) = 6.31, p = .012 \). Participants in intervention 2 \( (M = 2.00, SD = 0.870) \) significantly had more correct BLCs as compared to participants in group 1 \( (M = 1.18, SD = 1.01) \). Means, standard and deviations are listed in Table 21 for the intervention groups.

When considering the three types of connections, there was a significant difference for micro level connections \( (L1-L9) \) between intervention, with \( H(1) = 24.1, p = .01 \). Participants in intervention group 2 made more micro level connections \( (M = 1.68, SD = 0.780) \) as compared to participants within intervention group 1 \( (M = 0.18, SD = 0.393) \). There was also a significant difference in the average number of participants making connections between the micro through macro levels between intervention groups with \( H(1) = 24.1, p = .01 \). Participants part of intervention 1 \( (M = 0.76, SD = 0.664) \) significantly made more connections through biological L9 as compared to participants part of intervention group 2 \( (M = 0.18, SD =0.395) \). There was no significant difference for connections at the macro level \( (p = .391) \) between the interventions groups.

Significance was gauged at \( p \leq .025 \) to account for familywise error. All of the BLC means and standard deviations between the intervention groups are listed in Table 21.
Table 21

Relational Analysis Comparing Intervention Groups: Summary of Total Biological Connections Means and Standard Deviations

<table>
<thead>
<tr>
<th>Category</th>
<th>Intervention</th>
<th>M</th>
<th>SD</th>
</tr>
</thead>
<tbody>
<tr>
<td>Connection Attempts*</td>
<td>1</td>
<td>1.82</td>
<td>1.07</td>
</tr>
<tr>
<td></td>
<td>2</td>
<td>3.14</td>
<td>1.08</td>
</tr>
<tr>
<td>Levels Between Connections Min*</td>
<td>1</td>
<td>5.24</td>
<td>3.41</td>
</tr>
<tr>
<td></td>
<td>2</td>
<td>2.09</td>
<td>2.04</td>
</tr>
<tr>
<td>Levels Between Connections Max</td>
<td>1</td>
<td>7.76</td>
<td>2.88</td>
</tr>
<tr>
<td></td>
<td>2</td>
<td>7.95</td>
<td>1.75</td>
</tr>
<tr>
<td>Levels Between Average Attempt*</td>
<td>1</td>
<td>6.69</td>
<td>2.53</td>
</tr>
<tr>
<td></td>
<td>2</td>
<td>4.74</td>
<td>1.51</td>
</tr>
<tr>
<td>Correct Connections*</td>
<td>1</td>
<td>1.18</td>
<td>1.01</td>
</tr>
<tr>
<td></td>
<td>2</td>
<td>2.00</td>
<td>.870</td>
</tr>
<tr>
<td>Correct Average Between Connections</td>
<td>1</td>
<td>4.98</td>
<td>3.70</td>
</tr>
<tr>
<td></td>
<td>2</td>
<td>3.21</td>
<td>2.10</td>
</tr>
<tr>
<td>Correct Micro Level Connections*</td>
<td>1</td>
<td>.180</td>
<td>.393</td>
</tr>
<tr>
<td></td>
<td>2</td>
<td>1.68</td>
<td>.780</td>
</tr>
<tr>
<td>Correct Macro Level Connections</td>
<td>1</td>
<td>.180</td>
<td>.529</td>
</tr>
<tr>
<td></td>
<td>2</td>
<td>.050</td>
<td>.213</td>
</tr>
<tr>
<td>Correct Micro Through Macro Level Connections*</td>
<td>1</td>
<td>.760</td>
<td>.664</td>
</tr>
<tr>
<td></td>
<td>2</td>
<td>.180</td>
<td>.395</td>
</tr>
</tbody>
</table>

Note. Note. (N<sub>Total</sub> = 39), (n<sub>Intervention 1</sub> = 17) & (n<sub>Intervention 2</sub> = 22)

*Significant at p ≤ .025

RQ 3a: Conceptual and Relational Analysis Summary

The total biological levels identified by participants ranged from L1 to L13 with a majority of participants identifying levels at the micro (L2 & L3) scales and the macro scales (L10, L11 & L13); however, there was a decrease in the frequency of levels in-between (middle scales). It is also important to note levels which participants most frequently identified incorrectly: L8, L11 and L12. For example, 56% of participants identified L11 but less than 40% of participants who recognized it identified it correctly. Participants hypothesized about organisms at L11, because usually organisms here were a component of phylogenetic trees (output, intervention 2), or they were depicted in the
hypothetical populations (integration, intervention 1). Participants had difficulty identifying species (all organisms which have the ability to viably reproduce) and identifying that individual organisms were part of populations (organisms within a local area). Although individual organisms are important to distinguish within biological systems, participants frequently referred to them incorrectly. Biological levels 1, 2 and 3 had greater than 80% accuracy in correct participant identification of these levels. In most cases, participants used resources directly to define these levels (i.e., to search and find the function of a specific protein). Student participants also spend the beginning of the year learning about these microscales, which may have contributed to accuracy at these levels.

Participant identification of Levels 1 and 3 (micro scales) as well as 10, 11 and 13 (macro scales) differed on average based on intervention group. There were significantly more level identifications focused at levels 1, 3 and 11 for intervention group 2 on average, and at levels 10 and 13 for intervention group 1 on average. Because participants a part of intervention 2 frequently identified L11 incorrectly, it may have had an impact on biological knowledge scores. Although participants in intervention 1 identified levels 10 and 13 more frequently, they did not identify L2 and L3, the smallest scales, as frequently.

Participants in intervention 1 had more growth in evolution knowledge as compared to intervention 2 (interpreted from the quantitative analysis); however, according to the relational analysis participants in intervention 2 significantly made more connection attempts, more correct connections, smaller numbers of biological levels between attempts, and had more micro level connections (between L1-L9). Participants a
part of intervention 1 made more connections through micro and macro levels (between L9) and larger BLCs on average. This presents evidence that making larger connections and connections between the micro and macro levels contributes significantly to biological evolution learning. This may be because in biological systems the explanations of mechanisms of phenomena (such as biological evolution) apparent at one scale often lie at a different scale (Parker et al. 2012).

This problem of student inability to make micro to macro scale connections is sometimes referred to as “slippage between levels” (or disconnects between levels) and is also associated with fragmented and compartmentalized knowledge (Brown & Schwartz, 2009). This problem has not received much attention in the literature on evolution education (Jördens, Asshoff, Kullmann, & Hammann, 2016). Fluidity between these levels allows students to reason across them and contribute to biological literacy (Brown & Schwartz, 2009).

This finding is particularly interesting because it emphasizes one of the 5 chief strategies that encourage thinking across levels in biology (Parker et al. 2012). Thinking across levels in biology consists of: (1) distinguishing different levels of organization, (2) interrelating concepts at the same level of organization (horizontal coherence) (3) interrelating concepts at different levels of organization (vertical coherence), (4) thinking back and forth between levels (yo-yo thinking) and (5) meta-reflection about the question which levels have been transcended (Jördens, Asshoff, Kullmann, & Hammann, 2016). This finding presents the importance of point 3 (vertical coherence) and 4 (yo-yo thinking) in biological evolution learning, which may have been supported by computational thinking within intervention 2. More emergent phenomena occur for
students as their BLC distances increase, and these phenomena may have become more apparent for participants in intervention 2. Previous studies have considered the importance of macro and micro level connections (Jördens, Asshoff, Kullmann, & Hammann, 2016); however, there is a gap in research explicitly identifying multiple levels within the micro and macro level ranges and connection distances in the ways that I have.

*RQ 3b: Analysis of Computational Complexity*

Research question 3b seeks to answer the question of how student artifacts display computational complexity. I determined computational complexity within student artifacts for the computational components of input, integration, output and feedback. I only coded and quantified complexity from artifacts if student participants explicitly stated the computational components. Each intervention had at least one question which explicitly stated to identify each of the computational components within their activity. Accuracy and complexity definitions that I used to code artifacts are outlined in Table 22. I scored complexity for all of the computational components (input, integration, output and feedback) as either “simple”, “developing” or “complex” based on participant description (as classified according to the LBECT-LP). Participants scored no points for absence of the component or a 1 within the simple category, developing category or complex category for each component (if it was mentioned).
Table 22

**Scoring Rubric for Computational Component Complexity within Participant Artifacts**

<table>
<thead>
<tr>
<th>Component</th>
<th>No points</th>
<th>Simple</th>
<th>Developing</th>
<th>Complex</th>
</tr>
</thead>
<tbody>
<tr>
<td>Input</td>
<td>Absence of the word input</td>
<td>Participants describe input as provided by the instructor</td>
<td>Participants uniquely decide on the input data for their computational component, recognize what it is and identify correctly in writing</td>
<td>Participant able to find and modify input data on their own</td>
</tr>
<tr>
<td>Integration</td>
<td>Absence of the word integration</td>
<td>Participants describe integration as a formula or program</td>
<td>Participants accurately describe which variables are interacting within the integration</td>
<td>Participants describe which variables are interacting and how they are doing so explicitly within their computational representation</td>
</tr>
<tr>
<td>Output</td>
<td>Absence of the word output</td>
<td>Participants describe as a graph or model</td>
<td>Participants correctly identify their output and make the connection between the visual output and the integration</td>
<td>Participants have multiple representations of output</td>
</tr>
<tr>
<td>Feedback</td>
<td>Absence of the word feedback</td>
<td>Participant recognition that the model reinforms itself</td>
<td>Participant describes how output reinforms model</td>
<td>Participant description of how output reinforms model and provides alternate ways</td>
</tr>
<tr>
<td>Model</td>
<td>No Model (0 points)</td>
<td>Model Present (1 point)</td>
<td>Working and distinctly different from instructor examples</td>
<td>Participants use alternate computational tools to generate models. (No examples provided for participants at complex level)</td>
</tr>
</tbody>
</table>

**Model Complexity**

| Model Present | No Model | Present and similar to instructor examples | Working and distinctly different from instructor examples | Participants use alternate computational tools to generate models. (No examples provided for participants at complex level) |

*Note.* Classified according to the LBECT-LP found in Chapter 2

For example, if a participant described input as “The FASTA sequence” the participant scored a 1 in the input category because this is how I (the instructor) described the input during the lesson. If participants explicitly identified their FASTA sequence accurately and identified what it represented biologically they scored a 1 in the developing category for input (i.e., “The input was the coded amino acid sequence of keratin from a common mouse which I found from the NCBI database”). If participants used an alternate database to find DNA or amino acid sequences on their own and
described this as their input, they would have received a 1 in the complex category for input. If participants failed to mention input, they received zero points in the input category. I used this same process to categorize complexity for integration, output and feedback for each participant based on the parameters in Table 22.

Along with complexity, I also identified if participant models were present within their artifacts and how complex the models were (under the parameters of integration within the LBECT-LP). Instructions indicated that participants should either supply links or screenshots of their working computational models which they developed during the interventions, however not all participants followed these directions. Simple models for example varied very little from the provided examples. Developing models showed participants manipulating their models based on computational instructions. Model level ranged from 0 (absent) through simple or developing as also shown in Table 22.

According to the complex category from the learning progression, participants would need to display multiple unique and accurate models with little teacher scaffolding to score in the complex category (none of which did so).

Most participants who mentioned the computational components scored within the simple or developing categories. After receiving one computational lesson, the learning progression predicts there would be very few instances of complex computational components as defined by participants. This level of coding was determined from the learning progression (Chapter 2). Teachers can use the learning progression similar to the way that I did to develop rubrics for specific lessons and select the applicable components to include based on classroom instructional activities. I expand further on educational applications in Chapter 5.
Means, Standard Deviations & Frequencies of Computational Complexity

Table 23 displays the means and standard deviations for each of the computational complexity categories that was summed for all participants (participant scores within each category ranges from 0-4). It also includes the percentage of participants who included models and the level of their models as based on the rubric in Table 22.

Table 23

Means and Standard Deviations of Computational Complexity Displayed by Participant Artifacts

<table>
<thead>
<tr>
<th>Category</th>
<th>M</th>
<th>SD</th>
</tr>
</thead>
<tbody>
<tr>
<td>Simple</td>
<td>.920</td>
<td>1.22</td>
</tr>
<tr>
<td>Developing</td>
<td>1.31</td>
<td>1.20</td>
</tr>
<tr>
<td>Complex</td>
<td>.030</td>
<td>.160</td>
</tr>
<tr>
<td>Model Level</td>
<td>1.23</td>
<td>.842</td>
</tr>
<tr>
<td>Model Present</td>
<td>%</td>
<td>SD</td>
</tr>
<tr>
<td>Model Present</td>
<td>74.0</td>
<td>44.2</td>
</tr>
</tbody>
</table>

Note. (N = 39)

Participants had four opportunities to score within the simple category (0 to 4 comes from a combination of complexity scores of the computation components [input, integration, output and feedback]). For example, a participant may have scored in the simple category for input, the developing category for integration and output, then failed to mention feedback (Participant score: simple = 1, developing = 2, complex = 0).

Approximately 74% of participants included a model and model complexity average was between simple and developing ($M = 1.23$, $SD = 0.842$; 0 for model absent, 1 for simple model present, and 2 for developing model present). On average participants’ complexity of the computational components (input, integration, output and feedback) were not broken down further due to limited data (resulting in inconsequential results) and due to
the fact that complexity of the separate components was not explicitly addressed in RQ 3.

Explicit complexity of the separate computational components could be explored in a follow up to the dissertation study.

Participant scores for each of the complexity categories ranged from 0 (all components absent) through to 4 for each of the computational components (input, integration, output and feedback). Each of those four points could be distributed in each of the complexity categories. Participant frequency for computational complexity is shown in Table 24 below. For example, 20 participants scored 0 points within the simple category (51.3%), 10 students scored 1 point within the simple category (25.6%), 3 participants scored a 2 in the simple category (7.7%) and 2 participants scored all 4 of their possible points within the simple category (based on the combination of their computational components).

*Table 24:*

*Scores, Frequencies and Percentages of Computational Complexities*

<table>
<thead>
<tr>
<th>Computational Complexity</th>
<th>Score</th>
<th>f</th>
<th>% of Participants</th>
</tr>
</thead>
<tbody>
<tr>
<td>Simple</td>
<td>0</td>
<td>20</td>
<td>51.3</td>
</tr>
<tr>
<td></td>
<td>1</td>
<td>10</td>
<td>25.6</td>
</tr>
<tr>
<td></td>
<td>2</td>
<td>3</td>
<td>7.7</td>
</tr>
<tr>
<td></td>
<td>3</td>
<td>4</td>
<td>10.3</td>
</tr>
<tr>
<td></td>
<td>4</td>
<td>2</td>
<td>5.1</td>
</tr>
<tr>
<td>Developing</td>
<td>0</td>
<td>15</td>
<td>38.5</td>
</tr>
<tr>
<td></td>
<td>1</td>
<td>5</td>
<td>12.8</td>
</tr>
<tr>
<td></td>
<td>2</td>
<td>11</td>
<td>28.2</td>
</tr>
<tr>
<td></td>
<td>3</td>
<td>8</td>
<td>20.5</td>
</tr>
<tr>
<td></td>
<td>4</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Complex</td>
<td>0</td>
<td>38</td>
<td>97.4</td>
</tr>
<tr>
<td></td>
<td>1</td>
<td>1</td>
<td>2.6</td>
</tr>
<tr>
<td></td>
<td>2</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td>3</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td>4</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>

*Note.* Frequency based on a combination of participant computational components, \(N = 39\)
Computational Complexity Comparing Interventions

It is important to note there were major differences in the instructions of these interventions. There was technically no feedback within intervention 2 for participants to identify (although participants were prompted to hypothetically recognize it, none of them did). I ran a Kruskal-Wallis Test (data was not normally distributed) and results indicated there was a statistical difference between intervention group for the developing category with $H(1) = 4.89, p = .027$. Participants in intervention 2 ($M = 1.68, SD = 1.21$) scored significantly higher in the developing category as compared participants in intervention 1 ($M = 0.82, SD = 1.02$). There was also a significant difference in intervention groups for the model present category with, $H(1) = 10.1, p < .001$. All participants had a model present for intervention 1 (100%) and a little over half of the participants included their models in intervention 2 (55%). The means and standard deviations comparing interventions for computational complexity are shown in Table 25.

Table 25

Means of Computational Complexity Comparing Interventions

<table>
<thead>
<tr>
<th>Category</th>
<th>Intervention</th>
<th>$M$</th>
<th>$SD$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Simple</td>
<td>1</td>
<td>1.41</td>
<td></td>
</tr>
<tr>
<td></td>
<td>2</td>
<td>.86</td>
<td>1.08</td>
</tr>
<tr>
<td>Developing*</td>
<td>1</td>
<td>.82</td>
<td>1.02</td>
</tr>
<tr>
<td></td>
<td>2</td>
<td>1.68</td>
<td>1.21</td>
</tr>
<tr>
<td>Complex</td>
<td>1</td>
<td>0</td>
<td></td>
</tr>
<tr>
<td></td>
<td>2</td>
<td>.050</td>
<td>0.045</td>
</tr>
<tr>
<td>Model Level</td>
<td>1</td>
<td>1.47</td>
<td>0.514</td>
</tr>
<tr>
<td></td>
<td>2</td>
<td>1.05</td>
<td>0.999</td>
</tr>
<tr>
<td>Model Present*</td>
<td>1</td>
<td>100</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td>2</td>
<td>55</td>
<td>5.10</td>
</tr>
</tbody>
</table>

*indicates significance at $p < .05$ between interventions
Computational Complexity Summary

Computational complexity ranged from simple, developing and complex. Most participants exhibited simple and developing complexity among the computational components mentioned in their artifacts. It is important to note that participants explicitly wrote their answers identifying the computational components and their answers were scored based on accuracy as displayed in Table 21. On average more participants exhibited scores in the developing category ($M=1.31$, $SD=1.20$) as compared to the simple category ($M=0.93$, $SD=1.22$) and the difference was significant between intervention groups.

When comparing intervention groups 1 and 2, participants in intervention 2 significantly had more participants score in the developing category ($M=1.68$, $SD=1.21$) as compared to the simple category ($M=.82$, $SD=1.02$). Significantly more participants within intervention group 1 (100%) had their models present within their artifacts as compared to intervention group 2 (55%). These differences may be attributed to the specific activities and components emphasized within the interventions coupled with participant’s ability to learn from them. Quantitative results (RQ 1 & 2) indicate participants in intervention 1 produced greater knowledge growth in both knowledge constructs, however qualitative results regarding computational complexity indicate model presence was the only construct that significantly measured higher for this group. It was interesting to note from RQ 2 analysis that overall computational knowledge growth was not considerable (only at time 2), and this could be because it was the participants first time interacting with computational constructs. Additionally, all tested groups were exposed to computational learning. There was a shared aspect of the
computational lessons and as well as unique computational aspects between the interventions. A follow up to the dissertation study might compare a group of student participants who had not been exposed to computational learning interventions at all.

Results Summary

The results showed evidence of participant biological evolution knowledge and computational knowledge growth through interventions that emphasized computational thinking. In order to address RQ 1 (changes in biological evolution knowledge) and RQ 2 (changes in computational knowledge), univariate analysis of variance indicated both evolution knowledge change over time and computational knowledge over time was significant with medium to large effect sizes. The interventions both involved teaching biological evolution through computational means; however, they involved distinctly different activities that may have emphasized different biological aspects of biological knowledge and complexity of computational processes (explored in through RQ 3). There was a significant relationship between intervention and evolution knowledge, but not for computational knowledge. There was also a statistically significant difference in the measure of evolution knowledge considering the interaction of time and intervention with a small effect size. To further explore the knowledge changes, the effects of the interventions were explored separately.

Only the first intervention group produced statistically significant gains in evolution knowledge at time 2 (the first post instructional testing time of 2). Computational knowledge gains were also only statistically significant at time 2 for participants within the first intervention. When considering the post instructional testing times (time 2 and time 3), only time 2 was significant overall. This aligns with the idea
that intervention 1 was more successful for participant learning both knowledge constructs. Knowledge gains (evolution and computation) were significant at testing time 2 because the participants within the first intervention received the computational intervention between the pretest (time 1) and posttest 1 (time 2). There was no significant knowledge gains (or retention) between time 2 and 3 for evolution knowledge or computational knowledge for either of the intervention groups.

The Cronbach alpha scores for both the BECKI and CTCKS measuring biological evolution and computational knowledge ranged from poor to questionable which could have some effect on the reliability of the analyses. It is also important to note there were 2 instances of outliers considering all test data points ($N = 102$) and an ICC score that may have indicated potential classroom effects for computational knowledge at time 2. These shortcomings were minimal considering the significance and effect sizes of the overall results.

When considering the participant artifacts produced during the study (RQ 3a) participants identified a range of biological levels with the most frequency occurring at lower biological scales (L2 and L3) and higher scales (L10, L11 and L13) with less incidence of scales in-between. When considering the 5 chief strategies that encourage thinking across levels in biology (Parker et al. 2012) this presents a deficiency of the first strategy, identifying the levels of organization. Sometimes micro and macro scales are presented alongside certain properties within biology classrooms, however the scales in-between may not be presented as often. Certain levels were easier for participants to identify correctly (L1 and L2) where as other levels (L11, L10 and L8) were more difficult for participants to identify correctly. These findings present the levels that may
need more attention within biology classrooms. There were also statistically different levels identified between the interventions. Participants in intervention 1 identified L11 and 13 more frequently where-as participants in intervention 2 more frequently identified L2, L3 and L10. These differences were likely due to the nature of the interventions.

The BLC counted within the artifacts revealed differences between the interventions. Although biological evolution growth for participants in intervention 2 was not significant, on average these participants made more connection attempts, had smaller numbers of biological levels between attempts, and had more micro level attempts (between L1-L9). Participants a part of intervention 1 made more connections through micro and macro levels (between L9) which might be related to biological evolution knowledge growth as indicated from the quantitative analysis.

Computational complexity was explored to support RQ 3b. On average more participants scored in the developing category as compared to the simple category based on the developed rubric (but not significantly). When comparing interventions, significantly more participants part of intervention 2 scored in the developing category and significantly more participants turned in representations of their computational models in intervention 1. Intervention group 1 produced more complex models on average although there was no statistically significant difference for model complexity between the interventions. For most participants it was the first time that participants had interacted with computational components, especially in the way they were defined in the LP.

The results indicate that there was biological and evolution knowledge growth, which indicates support for the LBECT-LP however there was variation between the
effectiveness of the interventions. Biological levels (RQ 3a), BLCs (RQ 3a) and computational complexity (RQ 3b) displayed by participant artifacts also differed between the intervention groups. These differences may have attributed to specific biological and evolution knowledge gains. I will discuss implications of these findings in the next chapter. Specifically, how these results provide support for computational thinking in teaching biological evolution and how they support the LBECT-LP. I will also discuss implications for instruction and potential avenues for further study.
CHAPTER 5
DISCUSSION

This chapter discusses the results of the dissertation study within the context of the LBECT-LP, specifically by considering the role of computational thinking to learn biological evolution. This chapter also discusses the implications of the learning progression (and its support from the study) on instruction and future research. Prior to discussing these implications, I briefly summarize the study’s findings from the perspective of the three research questions and associated hypotheses as well as the study’s limitations.

Summary of the Findings

Researchers have hypothesized that using computational thinking to learn scientific concepts may contribute to student learning outcomes (Aho, 2012). These outcomes include but are not limited to concepts associated with NOS processes, individualized learning (i.e., learning assimilation theory), social learning (i.e., social constructivist theory) and conceptual change (Sinatra, Brem & Evans, 2008). The LBECT-LP (learning progression I developed in Chapter 2) merges educational, scientific, and computational theory and perspectives and serves as a framework for the dissertation study. Research questions 1 and 2 asked about knowledge growth in biological evolution (RQ 1) and computational thinking (RQ 2) based on instruction that promotes biological evolution concepts using computational thinking.

Because evolution spans across biological scales, I hypothesized that students must also make connections at and between biological levels (RQ 3a) to better understand evolutionary concepts (Winthrop et al., 2016). Not only did I define and
assess the construct of computational thinking knowledge (RQ 2), I also assessed computational complexity as displayed by participant artifacts (RQ 3b). Overall, the results support the use of the LBECT-LP that focuses on biological evolution learning using computational thinking.

I developed the assessment instruments and computational lessons (interventions 1 and 2) using the LBECT-LP framework. Knowledge constructs were assessed quantitatively using the BECKI instrument (biological evolution; RQ 1) and CTCKS instrument (computational thinking; RQ 2) at three time points (two of which were post instructional). The first intervention was presented to group 1 between testing times 1 and 2 and the second intervention group received a different computational lesson between testing time 2 and 3. When not undergoing the intervention lessons, the participants received traditional evolution lessons from their respective teachers. The results of the analyses showed evidence of biological evolution knowledge (H1) and computational knowledge growth (H2) with the use of (one of the two) interventions that emphasized computational thinking.

The interventions prompted participants to work with a range of biological levels and computational thinking components (input, integration, output and feedback). Artifacts were collected during the study to answer RQ 3a (presence and relationship of biological levels of organization) and RQ 3b (computational complexity). It is important to note that although both interventions involved teaching biological evolution through computational means, they included distinctly different activities. Results indicated there were distinct differences in the presence and relationship of biological levels of organization (H3a) as well as computational complexity (H3b) between the
computational intervention groups. The study is outlined in Table 9 and Appendices (A through G) include screenshots of intervention activities, instruments, and participant samples.

**Quantitative Analysis Findings: RQ 1 & RQ 2**

The results of the quantitative analysis indicated there was a significant interaction between intervention group and time for combined knowledge scores (evolution and computation knowledge). There was also a significant interaction for intervention group and time for both evolution knowledge and for computational knowledge constructs. The first intervention group produced statistically significant gains in evolution knowledge and computational knowledge at post instructional testing time 2. This supports the idea that certain components of intervention 1 might have attributed to the significant knowledge gains.

When considering intervention group 1, knowledge gains (both evolution and computation) were only significant at testing time 2. This is meaningful because the participants received the computational intervention between the pretest (time 1) and posttest 1 (time 2). These findings partially support both my hypotheses, regarding biological evolution knowledge growth (H1) and regarding computational knowledge growth (H2). This is only partial support of the hypotheses because knowledge gains were only significant for intervention group 1, which further indicates it was successful for student learning both knowledge constructs whereas intervention 2 was not.

Although there was a raw increase in both computational and evolution knowledge between testing time 1 and 3 (the span of the study), these gains were not significant for either intervention group, nor for combined group scores. For intervention
group 1 there was a non-significant decrease in biological evolution knowledge scores and computational knowledge scores between time 2 and 3 potentially indicating that the non-computational evolution lesson was less effective for evolution learning as compared to the computational lesson. Participants did not receive any additional computational knowledge instruction after their initial intervention (between time 1 and 2 for intervention group 1). These findings also motivate future study in computational and or evolution knowledge retention.

Knowledge gains were not significant for intervention group 2 between times 2 and 3 indicating that intervention 2 was not as successful as intervention 1 (as this is when participants received the computational intervention). It is interesting to note that there was very little change in computational knowledge and evolution knowledge for intervention 2 during this time. Knowledge gains were also not significant for the testing times following any of the lessons that used traditional teaching throughout the study (i.e., between time 1 and 2 for intervention 2). There were no comparison groups who received only traditional biology evolution lessons from their teachers due to the quasi-experimental design of the study, which partially limits true differences in knowledge gains (explicitly due to computation). I discuss further in the Limitations section.

**Qualitative Analysis Findings: Biological Levels of Organization (RQ 3a)**

I used the qualitative analysis to support the quantitative findings. Before performing the dissertation study, I suspected that the interventions may have emphasized different biological levels of organization (RQ 3a) or prompted different degrees of computational complexity (RQ 3b). The quantitative results indicated there were differences in effectiveness between the intervention groups for evolution and
computational learning. I suspected this effectiveness may have a relationship with the participants’ use of biological levels of organization, biological level connections and or computational complexity.

I used student artifacts to answer both components of RQ 3. There was a range of biological levels identified by participants overall (L1-L13) however there were more frequent instances of levels occurring at the micro scales (L2 molecule and L3 macromolecule) and macro scales (L10 population, L11 community and L13 ecosystem) with less incidence in mid-level scales. There was variance overall in the identified biological levels between individual participants as well as statistically significant differences between the interventions. There were 4 biological levels identified at significantly different frequencies between intervention groups (L2 molecule, L10 population, L11 species, and L13 ecosystem). For example, intervention group 1 identified L10 population and L13 ecosystem more frequently. The only macro scale level that intervention group 2 identified significantly more frequently was level 11 species, it is important to note that this level was often incorrectly identified. Additionally, there were certain levels (L11 species, L10 population, L8 organ system and L7 organ) which participants had difficulty identifying correctly. This supports my hypothesis (H3a) that there would be a discernible emergent relationship between student [participant] understanding of biological levels of organization in response to computational intervention exposure. It also supports that the group with greater knowledge gains (intervention group 2) more frequently identified scales at the macro level. Participants within intervention group 1 identified more macro scale levels and
showed a greater ability to identify them accurately. These differences may have attributed to the significant knowledge gains present for intervention group 1.

To further explore RQ 3a, I counted and classified biological level connections (BLCs) within the artifacts. There were discernable differences between intervention 1 and intervention 2 considering how many BLC attempts were made, the numbers of levels between attempts and the type of attempts that were made. This also supports my hypothesis (H3a) regarding the relationship between unique student [participant] understanding of biological levels of organization in response to the different computational interventions.

Participants part of intervention group 2 (the less effective intervention) made more connection attempts overall and more connection attempts at the micro scales. Participants in intervention 1 (the effective intervention) made more successful biological connections through level 9 (organism level) and their BLCs significantly spanned larger ranges. Because intervention group 1 made significant knowledge gains, this provides support that connection attempts through level 9 and larger BLCs on average (encompassing more scales) may have an impact on student learning biological evolution whereas the number of connection attempts for example did not. Larger BLCs might indicate that participants are making relationships more holistically (encompassing unity and diversity concepts; Jördens, Asshoff, Kullmann, & Hammann, 2016). Students making successful connections through level 9 are showing evidence of combining micro level concepts with macro level concepts. These connections may have been better supported through the computational aspects of intervention 1.
Qualitative Findings: Computational Complexity (RQ 3b)

I used the artifacts to explore computational complexity to support RQ 3b (based on the rubric I developed from the LBECT-LP shown in Table 22). There were discernible differences between the interventions when considering computational complexity within participant artifacts (computational products). Interestingly, significantly more participants in intervention 2 (less successful intervention) scored in the developing category (as compared to intervention group 1). Significantly more participants turned in representations of their computational models in intervention group 1.

In theory (based on LBECT-LP Chapter 2) the computational products are a combination of the instructional context and computational process experienced by participants. I would have suspected that increased computational complexity (exhibited by artifacts of intervention group 2) would have a relationship with computational knowledge gains or evolution knowledge gains. The results of the dissertation study did not support this relationship between increased complexity and knowledge gains. It is important to note that participant artifacts (computational product) were assessed to discern computational complexity. The LP indicates that computational product, computational process and instructional context should all be considered when assessing complexity (as derived from Berland and McNeill’s [2010] learning progression 2010). For the purposes of the dissertation study I made the assumption that computational products (artifacts) would accurately reflect a combination of complexity of the computational process and instructional context (this may have not been the case).
When considering the instructional context, the first computational intervention itself had more computational complexity as compared to the second intervention (google sheets, vs. BLAST program). In future studies, the instructional context, computational process and computational product may need to be considered simultaneously to truly assess success (and complexity) of computational instruction. These finding partially support my hypothesis (H3b) that there would be a discernible relationship between student level of complexity in terms of understanding of computational thinking (simple, developing or complex) in response to the different computational interventions. Although there was a relationship, it exhibited the inverse of my prediction.

**Collective Discussion of Findings**

My intention was to have intervention 1 and 2 be similar in terms of difficulty. In theory, students could have made connections between any of the biological levels regardless of their intervention group. Prior to the study I was unsure which biological levels would be identified (or emphasized) by participants or what types of connections would be made based on the intervention groups. I did suspect that there might be a difference between the intervention groups (RQ 3a). Both interventions started with a lecture and discussion on computation. I then lectured on pertinent biological evolution constructs that were specific to the intervention. I then described and modeled the activities and had students work on them for the remainder of the class period. In all four of the classes, students worked on their own computational models however there was also collaboration among the students. I did not scaffold the nature of the student interaction.
The nature of the activity within intervention 1 involved students developing a spreadsheet to model the H-W equilibrium equation. Students within this intervention scored significantly higher in both evolution and computational knowledge scores at testing time 2, meaning they successfully made knowledge gains on the tested constructs within the BECKI and CTCKS. Interestingly they made less connection attempts overall (as well as less successful connection attempts). Students within this intervention also successfully identified more BLC’s which spanned larger ranges. Although students identified a variety of biological levels, this intervention emphasized alleles and genes (L2) as well as populations (L10) and ecosystems (L11). Students may not have been as focused on the biological levels in-between (as compared to intervention group 2).

Students were performing “simple” coding within google sheets and the parameters of the activity were more open ended (inquiry driven) in terms of computational instruction (instructional context) as compared to intervention 2. Students frequently asked each other how they were developing their models by asking questions such as, “What is your input?” or “How are you changing your ecosystem?” Within their models’ students were prompted to construct allele frequency and hypothesize a population and potential environment change. Students were hypothesizing about these levels as they were writing parameters about them into their working “code”. The instructional context and computational process were relatively simple in terms of the learning progression. A developing instructional context would involve less scaffolding (by me) and a developing process would involve a different computational program. However, for the context of the study these (simple) computational aspects were most
appropriate (because students did not know how to code) especially considering the time frame.

Intervention 2 involved students identifying and selecting a protein and using a database to find the appropriate amino acid sequence. During the study Participants asked questions about the actual process of the activity and showed more confusion as to where they should plug in their sequences. For example, students asked and which “sequences they should select” (sequences were presented in various formats) and where they should “plug them in” because the selected sequences should have been entered into a program which developed a phylogenetic tree. Students did more hypothesizing about the computational processes rather than developing the code themselves. I suspected that this would have resulted in students scoring lower within the computational process category (as compared to intervention group 1 because they were doing less physical coding), however student hypothesizing (and asking each other questions) about these processes may have led to the higher score within the developing category of computation. Students may have also had the opportunity to spend more time thinking about the molecular scales by finding their sequence and thinking about the protein as well as the function of the protein in the body. Then students may have separately thought about evolutionary relationships resulting in smaller biological level connections. This activity may have been more successful overall if students had the opportunity to work actively for two days rather than one based on the complexity of the activity (even though the intervention was still relatively simple in terms of the learning progression because students were using premade computational interfaces). If the students worked
for more time, they may have been able to successfully make the smaller connections and then better bridge the gap by also relating these smaller connections to larger ones.

In a study by Kapur (2012) students exhibited productive failure during inquiry mathematical lessons. His results challenge the claim that there is little efficacy in having learners solve problems which target concepts which are novel to them in the absence of direct instruction. The thought is that students would lack adequate information, develop misconceptions or experience frustration and lack of motivation. Kapur identified that although students did not successfully “learn” the concepts through exploratory means during classroom activities they actually outperformed students on conceptual understanding and transfer as compared to students who learned “accurate” concepts through direct instruction. Kapur also claims (2008) that despite failing in their collaborative efforts (during class time for example) students outperformed their counterparts in well-structured near and far transfer measures suggesting a latent productivity in what initially seemed to be failure. Students within my dissertation study may have experienced productive failure (particularly because my measures were not well structured to test for this phenomenon). Although there was some direct instruction, ideas were novel (both computation and evolution) and students used inquiry (via computation) to explore the constructs. Students within computational intervention group 1 may have been more successful because the nature of the topic (H-W equilibrium) was not as complex. Participants within intervention group 2 may not have had enough time to successfully navigate the increased complexity of topics presented (along with the associated activities). Further research might include for a better structured design to test for productive failure, especially due to the fact that the computational intervention
spanned one class period. Ideally future research might include lengthening the time of
the activities (i.e. 2 class periods) or constructing proper scaffolding for student
collaboration.

For most participants it was the first time that they had interacted with
computational components, especially in the way they were defined in the LP.
Computational thinking was a novel concept for students, whereas biological evolution
and associated concepts were not. This novelty may have attributed to the differences in
computational knowledge scores as compared to biological evolution knowledge.
However, there was also no true control group by which computational complexity could
have been tested against (where participants experienced no computational intervention).
Participant computation scores from intervention 2 at time 2 as compared to time 3 would
have been indicative of this comparison; however, there was no significant difference in
these scores (there was a raw insignificant decrease in computational knowledge at this
time). Additional limitations of the study are presented in the next section.

Limitations of the Study

*Experimental Design*

Limitations are inherent within all forms of educational research and this study
was no exception (Fenwick, Edwards & Sawchuk, 2015). One limitation relates to the
degree to which the findings are generalizable based on the subset of participants. The
dissertation study sample is representative of advanced biology students in a
predominantly white middle class population. Researchers in general should take caution
when generalizing these results beyond this type of population. This raises the need for
future work on the relationships between computational thinking and evolution learning
with various other populations, ages and ability levels (i.e., including courses other than AP biology). Interestingly the LBECT-LP provides some structure for use with additional age and ability levels.

Another limitation lies within the nature of the quasi-experimental research design. I could not truly control the experimental situation through random selection of participants (Campbell & Stanley, 2015). Participants were already assigned to classes with teachers and depending on which class they were a part of, they underwent either intervention 1 or 2. Therefore, participants were randomly assigned at the class level. The number of participants within each class differed and the number of participants within intervention group 1 and intervention group 2 also differed. I was very limited in terms of availability (to teach the intervention groups) resulting in uneven numbers between the intervention groups. There were less participants within intervention group 1 \( (n = 22) \) as compared to group 2 \( (n = 38) \) although intervention group 1 produced significant knowledge gains.

The results did not indicate significant classroom or teacher effects allowing me to discern randomness. There was a much lower potential for unaccounted cofounding variables (contributing to internal validity) based on the analysis; however, it is impossible to control or account for unique aspects of classroom environments (Fenwick, Edwards & Sawchuk, 2015). Because there were differences between the interventions (and no significant differences between teacher or specific classroom) the computational instruction appears to be successful (specifically for intervention 1) in teaching biological evolution under various classroom conditions (although impossible to truly determine).
The lack of true experimental conditions might weaken the identified relationship between biological knowledge growth and computational interventions. However, in addition to results showing no significant classroom effects the study was based on a pre/post design (2 post instructional tests) and the results showed no significant differences between the interventions or between classes prior to instruction. The result also creates increased confidence levels that significant gains experienced by the groups were due to the instructional scaffold. The design was strategic in placement of the computational intervention (first or second) as compared to the traditional biology lesson in order to compare scored differences between the intervention groups. As mentioned previously, there was no true control group of participants (who did not experience computation in order to compare their tests or artifacts with) which might be a consideration in future studies.

The results indicated that there was a main effect for overall computational thinking knowledge and evolution knowledge due to the computational interventions however, these gains were only significant for the first intervention. The first intervention may have targeted unique aspects of evolution or computational thinking (as explored in RQ 3a & RQ 3b) which better aligned with the BECKI and CTCKS. The lack of computational knowledge or evolution knowledge (for intervention 2) may have been a result of the marginal reliability of the ICC or Cronbach alpha scores. The Cronbach alpha scores for the dissertation ranged from poor to acceptable for the BECKI and questionable to poor for the CTCKS. Overall the Cronbach alpha scores within the dissertation study for the CTCKS were an improvement from the pilot test however the scores were still relatively low. Low Cronbach alpha scores may have been due to the
fact that this was the first time students were exposed to computational vocabulary and concepts which led to more guessing (Cortina, 1993) and or the questions within the instrument may have been poorly correlated (i.e. not measuring the same construct). Low Cronbach alpha scores may be due to low numbers of questions or poor inter-relatedness between items or constructs (Tavakol & Dennick, 2011). Although the CTCKS measured computational knowledge, there were four specific computational constructs that were tested by the instrument (input, integration, output, and feedback). Further exploration of participant responses to these particular constructs might have led to a better understanding of the low Cronbach alpha scores (as there were no individual questions which would have greatly changed the Cronbach alpha scores upon their removal). These constructs might be considered separately in future study. The instruments underwent face and content validity which is why they were not changed drastically between the pilot and dissertation study (there was a minor change in the prompt between the pilot and dissertation as suggested by the dissertation committee to emphasize thinking like a scientist). I instead decided to emphasize computational vocabulary and introduce a short computational discussion during the interventions which might have led to the slight improvement between the pilot and dissertation study. Pairing CTCKS items to artifacts might also shed light on which constructs present particular difficulty to students. Further expansion of this computational discussion or exposing students to more than one computational intervention may contribute to improved Cronbach alpha scores within future study.

An alternative explanation is that the tests did not measure concepts addressed in the interventions (i.e., went beyond the instructional topics). For example, computational
complexity was based on the computational products (participant artifacts), which in theory is a combination of the instructional context and computational process. Addressing and assessing the instructional context and computational process along with the computational product (artifact) would provide more insight on computational complexity. However, these components of the LP were not addressed in the dissertation study.

**Ethics**

I played a major part in this research study due to the fact that I am a teacher in the district where I performed the study. Although there are benefits of action research (Greenwood and Levine [1998] defined action research as instances when the researcher intervening encourages the community with whom the researcher is conducting research; the researcher does this to investigate their own social condition to recognize the constraints operating on it with the goal of improving it, as discussed in Chapter 3), there are also drawbacks that may affect results of the study. For example, I previously had one of the student participants in class and they may have responded differently to my instruction as compared to other participants. Discussing research plans with my coworkers may have inflicted pressure on them as educators (i.e., teachers may have felt pressure to ensure I obtained good results). The novelty of me as the instructor (Schanzenbach, 2012) may have also had an impact on results (some of the student participants are registered to take my AP environmental course the following year).

It should be noted that I specifically developed the interventions and BECKI and CTCKS instrument, and therefore time and effort were invested in the research I was directly involved in (promoting subconscious bias). I am versed in computational
thinking therefore the applicability to other classrooms (with other instructors) may be
difficult to ascertain from this study. I could have trained the teachers on the
computational thinking lessons (and allowed them to teach) in order to address this
limitation, however due to the nature of the action research, it was most appropriate for
me to teach the interventions (i.e., lack of time, burden on other teachers).

Additionally, there were was no true group of individuals who did not experience
the computational intervention. Ethically, it is important to ensure fairness for student
participants (Schanzenbach, 2012). I ensured that student participants within all AP
Biology classes (in the district) had comparable learning experiences especially because
it is a high stakes course. It made the most sense to use AP students for various reasons.
These students may have benefit most within the district and as a general rule put fourth
more effort than students enrolled in lower level biology courses.

*Nature of LBECT-LP*

An additional limitation that should be considered is the nature of the defined
LBECT-LP. Ideally the structure of this LP spans across grade levels in terms of biology
standards and concepts students should recognize coupled with standards that include
computational thinking (at appropriate age levels). Participants were exposed to
computational thinking for the first time during this lesson, therefore the results support
the use of the LP. However, ideally (if a district used the LP for example throughout
grade levels) participants would have had prior established biological content knowledge
as well as computational skills before AP biology. Paradoxically, if participants had been
exposed to these skills prior to the dissertation study, they may have scored higher in
computational complexity (complex vs. simple) or in overall knowledge scores.
However, the study was designed so that the results would potentially support the use and potential expansion of the LP. I mention this because it is pertinent when considering implication or further study, as there is a clear disconnect between the defined LP and what students had been exposed to during the “single lesson” dissertation study.

Another limitation of the study and subsequent learning progression is teacher preparation and comfort with technology and computational concepts. I have provided structure for educators through the LBECT-LP while still maintaining flexibility so that they may modify their lessons (to include computation) as they see necessary. The computational instructional practices, process, and products are generally defined for instructors so that they may have flexibility in creating computational lessons. If I had trained teachers to teach the interventions, this may have provided more insight regarding limitations of the LP that I alone could not foresee (as someone experienced in computational thinking; Fenwick, Edwards & Sawchuk, 2015). This becomes an important consideration when contemplating future studies or applied implications of the LP.

Cost

Another limitation to consider in terms of application or future research is the deficit of funds (within schools and districts; Schanzenbach, 2012) for technology, hardware, software, and professional development required for teachers to become properly trained using computational tools. For example, some schools are limited in the number of computers that are available for students. Both teachers and administrators receive information (i.e., advertisements, professional development, yearly science catalogs) regarding potential educational software and hardware available to them.

202
Educators must also consider their budget while assessing these potential programs. Therefore, it makes the most sense that these programs might be utilized by a variety of disciplines. This becomes increasingly difficult when educators are not experienced with these programs (or the associated costs).

Most software that is user friendly and appealing to teachers are specific for performing one type of activity. Although the software itself may be advanced, it can be expensive and is actually counter intuitive to the LP. An electronic probe for example that measures and displays conductivity in a lab can only be used to measure and display conductivity in the way that it was written into the software. I consider these types of activities simple within the LP. As students use inexpensive or free programs such as R or C++ it would allow them to take the conductivity data (obtained from a probe for example) and imagine and write [code for] the ways it might be manipulated or displayed. These types of activities lend toward the developing levels of the LP. It may be difficult for educators to identify appropriate software and specifically recognize how they may use the software to scaffold lessons through the simple, developing and complex components of the LP.

Some districts might already have subscriptions to costly programs such as MATLAB (generally used in math or computer science courses); however, science educators may be unaware of the tools available to them (Gallagher, Coon, Donley, Scott, & Goldberg, 2011). There are some programs such as (R, Python or C++) which are free for users but take an extensive amount of time to learn (Wing, 2006). Because these programs are so robust, it requires instructors to become very knowledgeable and comfortable with them if they are to develop content-based activities with proper
scaffolds for students (Wing, 2006). Students would also need to download these programs at home if they are responsible for completing classwork outside the classroom. The payoff of learning these languages is great. Although it is a limitation (in terms of applicability) in the dissertation study, it lends toward the discussion of implications for instruction.

Implications for Instruction

Scaffolding and Complexity of the LBECT-LP

If teachers are open to using computational thinking in their classrooms (which may be a barrier within itself), in many cases (such as the previous probe example) they view it as a tool for one lesson and learn applications for those lesson specific concepts. Although there are aspects of computation within these activities, educators may not see computation as a robust tool that may be developed (and used itself) as a working [biological] instrument (Gallagher, Coon, Donley, Scott, & Goldberg, 2011). These technologies (preferably the less expensive programs) should also be presented to teachers with appropriate scaffolds to properly implement the LBECT-LP within their classrooms, across grades and ability levels. Educators should also see these programs as robust tools to design proper lessons for students.

Students are increasingly exposed to technologies at home and within classrooms at early ages yet they may not be taught to maximize efficiency of these technologies (Grover, 2011). Students may rely on interfaces without understanding how these technologies work computationally. For example, a student might know how to perform a Google search but may not understand the computational mechanism of the search. These searches involve selection and ranking of a plethora of valid and invalid
information found on the internet. This may result in students having the inability to
distinguish between legitimate search results or even the need to do so (partially due to
lack of understanding of the search mechanism, and partially due to understanding valid
content within search results). This is analogous to computational mechanisms and
[understanding valid] scientific content, which is why computation should be learned
alongside scientific content (such as biological evolution).

In the dissertation study, students used an interface friendly BLAST program
through NCBI, but the computational process was emphasized in the lesson, not only the
results. Students were prompted not only to use the computational tools but explain how
they were used (by means of biological aspects). Ideally, in a more computationally
complex version of this lesson (potentially presented at an appropriate ability level),
students would write programs which perform similar functions to the user-friendly
BLAST program. In the past, I have had AP biology students within my classes write
their own code in various programs (R and Python) for both of the intervention activities
used in the dissertation study. These students were more versed in coding, however their
communication with other students lent toward unique learning experiences for all within
the class. This increased complexity factor may have attributed to the success of
intervention 1 within the dissertation study.

It takes a great deal of time for students, teachers, and professionals in the field to
learn computer languages. The payoff for learning these languages is great because the
tools are then available for future use. The progressive component of [computer]
language learning is encompassed by the computational complexity aspect of the learning
progression. Computational processes and products are difficult to assess and teachers
may have difficulty in developing rubrics, but they may be made more concrete through use of the learning progression. Interpretation of assignment requirements may also be difficult or frustrating for students, especially initially (Wilensky, 2014).

Although the theoretical framework presented in Chapter 2 lends toward a full learning progression, very small components (i.e., simple computation from the LBECT-LP) can be used by districts initially before the entire learning progression may be able to be used fully and effectively due to limitations presented in the previous section. It is difficult for researchers to provide particular examples of interventions for educators because teachers have different training and teaching styles and many districts have limited resources. This is one of the reasons why I provided the computational instruction for the dissertation study.

**Implications for use within the NGSS**

Within the NGSS, the standards allow teachers freedom to develop classroom activities (NGSS Lead States, 2013), just as this LBECT-LP would allow freedom for teachers to develop their own interventions and written assessment methods to integrate computation. Because biological evolution is specific, other [scientific] topics taught computationally may have their own set of NGSS standards as well as learning objectives that would need to be aligned with different LPs. This would take extensive knowledge of a computational expert coupled with scientists and educational professionals (Wing, 2006). In order to alleviate this, computation should be taught during college courses (for prospective teachers) through genuine research experiences in their science or pedagogical courses. However, computational integration is not frequent in these courses and ironically part of my argument to push for computation earlier on in education.
Lack of computational knowledge and resources limits teachers, prospective teachers, and paradoxically even those within the scientific community.

The LBECT-LP provides specific content (unity and diversity), state standards and (computational) strategies for biology instructors or those in closely related fields. It promotes holistic type learning and structure for biology teachers to implement lessons which are new, cross curricular, and engaging. Not only would it hold potential for encouraging students to behave more like scientists, but it would also encourage this type of teaching from instructors. It may also inform teacher trainings, curriculum writers, science learning companies, technology companies, and computational biologists and or encourage their interaction. Because computational thinking is emphasized in the NGSS, it is applicable to other scientific fields. Computational thinking may also be used to reinforce NOS processes in other science disciplines (Gallagher, Coon, Donley, Scott, & Goldberg, 2011). Because these ideas are novel, I address them in the following future research section.

Implications for Future Research

An overwhelming gap in research stretches across computational thinking within educational settings, specifically for students enrolled in biology courses (Román-González, Moreno-León, & Robles, 2017). The most prominent research associated with computational thinking in education has been student development of video games or robotics (Grover, 2011). The student-guided construction of scientific information inherent within computational thinking promotes individualized learning and has unique social implications within classrooms (Ioannidou, Bennett, Repenning, Koh, &
Basawapatna, 2011). These educational environments may lead to internal generation of knowledge that contradicts what students currently believe [about evolution], a necessary component in conceptual change (Sinatra, Brem, & Evans, 2008). Facilitating computational learning requires appropriate scaffolding (as portrayed in the LBECT-LP). However, the best practices for helping students to think computationally to foster conceptual change in alignment with NOS processes are still unknown. This becomes especially important when considering differentiation to account for various ability levels found within classrooms.

Although there has been some model-based reasoning research conducted among science learners at higher educational levels, there is a gap in research about learning evolution through computation, with virtually no research at the K-12 levels (Wilensky et al., 2006). There has been some research and investigation on student learning of evolution and biological systems through agent based modeling; however, no studies have related computational thinking and reasoning to learning evolution across scales (Aho, 2012), nor have they defined computational thinking in the ways that I have.

My framework and learning progression explored in the dissertation study allows teachers to modify their current classroom activities in order to make their lessons and instructional units more computational. I provide this avenue by arranging and outlining ideas for instructional context (instruction), computational product (artifacts), and student roles within the learning progression. I also provided two example lessons for a biology classroom that were modified to be more computational from the AP lab manual. I described the complexity aspects of the progression (i.e., simple vs. complex student
roles) that can be applied for individual students or classes as a whole (promoting differentiation).

I recognize that this idea is novel, and therefore further testing of the LBECT-LP (or at least aspects of it) by the research community is warranted. Such research would include testing other lessons (i.e., interventions), instructional units, and modified (or new) assessments based on the LBECT-LP. This would allow researchers to better understand impacts on classroom practice, specific NOS processes, and overall effectiveness. The results from new interventions or assessments may be compared to groups of students who have not received computational interventions to better identify if and how computational thinking contributes to learning. Additional groups of students (ages, demographics or ability levels) should also be considered.

Further exploration of the specific biological levels or computational components is necessary, especially since there were distinct differences between the interventions within the dissertation study. For example, specific participant answers of the BECKI and CTCKS may be paired with specific biological levels, computational complexities, computational components, and or NGSS standards. The dissertation results indicated that biological scales (especially micro through macro scale connections) were important for biological learning. Although this was addressed through RQ 3, further exploration of specific biological levels (and BLCs) and their interaction (and emphasis) with computation lends for future research. Analogous to my assessment of biological levels, another scale to consider may be time (just as evolution occurs across biological scales, it also occurs over time). Improved assessments or additional interventions may be used to
further explore the specific relationship between biological evolution learning and computation.

Future research considering assessment as associated with computation is imperative. It is unclear how to assess computation alone, therefore assessment of other content knowledge such as biology while using computation as a learning tool may be better suited for students and teachers. Content knowledge, such as biological evolution, may be assessed based on specific skills that are developed by computation (Wilensky, 2016). The development of an assessment for computational skills alone (such as the CTCKS) or the assessment of computation alongside and integrated within content knowledge is necessary in order to monitor student progress and is essential for continued research. The most appropriate type of information that this assessment would measure is still unknown (i.e., computational knowledge and or biological evolution knowledge). There are also no assessment tools that measure computational skills as applied across disciplines (Werner, Denner, Campe, & Kawamoto, 2012). Within the dissertation study I presented input, integration, output, and feedback as constructs for assessment (as supported by the CTCKS). I have identified how these components relate directly to NOS processes and can be transferred to other scientific concepts and disciplines however incorporating these components into lessons (or across disciplines) may not be intuitive for instructors. It is crucial to test the CTCKS over time (or alongside other scientific content) to assess its effectiveness.

There is a definite urgency to incorporate computational thinking practices into scientific curriculums according to the NGSS, but the incorporation strategies are still vague (even within the LBECT-LP). The learning outcomes, pedagogies and tools for
deeper conceptual understanding and knowledge transfer for topics associated with evolution and computation are unknown, especially how these topics relate to overall biology understanding (Jacobson, 2006). The concepts of computational thinking, computational instructional practices, computational process, and computational products are not well defined for instructors. I provided structure for educators through the LBECT-LP while still maintaining flexibility so that they may modify their lessons as they see necessary. Finding a balance between flexibility and structure is another consideration for future study.

It is unknown how computational processes will help students to better understand evolution and in turn how this might strengthen their knowledge within the domain of biology as a whole. Using computation should strengthen student knowledge and NOS processes, but it is unclear in what ways. Students may become more comfortable developing new computational tools or applying these skills to other disciplines. It is also still unknown how computational processes explored through this type of learning progression may relate to overall student achievement or collaborative learning outcomes. It is also important to consider how the progression may apply to other scientific disciplines.

I initially presented the learning progression (Table 3 and Table 4) in a way that is content independent. As I developed the progression, I layered in domain specific components such as unity, diversity, and NGSS specific standards. I speculated that proper scaffolding would allow students to make connections across various levels of biological organization. With the assistance of the appropriate experts (i.e. chemists or chemistry educators), I suspect this learning progression can be modified and applied to
other domain areas (i.e. chemistry). These types of scales exist in chemistry just as they do in biology (i.e. atomic theory of matter through to property of materials). It is known that learning across scales is central in science, technology, engineering and mathematical learning. Relational reasoning (basic cognitive mechanism involved in the formation of conceptual categories and encompasses the ability to detect similarities and differences in patterns among objects, concepts and situations) has been presented to alleviate misunderstandings across scales however very few specific learning activities have been developed on the topic (Resnick, Davatzes, Newcombe and Shipley, 2016).

The act of computational thinking may encourage relational reasoning and activate unique cognitive processes that may be beneficial to other scientific domains which require engagement at various levels organizational or temporal scales simultaneously such as chemistry and physics. These ideas expand to include subfields of the major sciences such as biochemistry, physiology, marine science, or environmental science. Therefore, developing learning progressions for fundamental concepts within other scientific fields (in addition to biology) should be considered for future study.

Future study may also lend to the discussion of why computational thinking might be effective for learning across scales (i.e. biological levels). The act of learning about various biological scales frequently encourages the use of various tools (such as a microscope for the micro levels). Instead of focusing on these tools to explore the levels (and simultaneously removing interference), computational thinking may allow students to identify and focus on the similarities that are common to the levels or the forces and the phenomena that act between them. Wilensky and Jacobson (2006) used computational thinking to promote embodiment at one scale (i.e. thinking like a ‘wolf’ in
order to properly assign “wolf-like” parameters such as “eating sheep”) however; computational thinking may also facilitate this embodiment at various scales (i.e. biological levels). The cognitive processes associated with computational thinking may allow students to better holistically understand phenomenon (such as biological evolution) by using the same mode of thinking to assign parameters to genes while simultaneously observing emergent processes at other levels such as population dynamics. Students may similarly assign parameters to the resulting population dynamics (output) if necessary (in the form of feedback). These ideas relate to the concept that is presented in many biology texts (within various chapters), biological systems are much more than the sum of their parts (Campbell et al., 2000).

Computational thinking may provide students the tools and thought processes which allow them to account for all of the moving parts (i.e. biological levels) alongside the big picture (i.e. biological evolution across scales). Better understanding of the mechanism and benefits of this thought process may be considered for future study.

Concluding Thoughts

Improving science learning and promoting the field is currently of importance in the United States due to low test scores enrollment, low test scores, declining interest and inequality between various groups of student learners (McDonald, 2016). However, as the sciences have become more cross disciplinary, there have been few methods of implementation that are domain content heavy. The trends of coding and STEM in general are becoming more popular for students, but it is important that the content is implemented in ways that would be most beneficial to all students, which include merging these ideas with their core content subjects. Although my argument to
incorporate computational thinking is directly related to science courses, and specifically biology, the NGSS stresses the concept across various STEM fields. Not only should computational thinking be stressed in science courses but in all courses which emphasize STEM and the cross cutting concepts (NGSS Lead States, 2013). Students should envision computational thinking and its associated tools as processes they can use outside of computer science courses. As these technologies and associated processes gain popularity and become implemented, it is imperative that they are actually promoting student success within the STEM fields. Understanding the learning processes, hardships and benefits of these processes is essential for continued growth within STEM education to promote success among all types of students (McDonald, 2016).

There is a direct correlation in that the more formal science education a teacher has (i.e., post-baccalaureate graduate degrees), the more likely they are to teach evolution within their classrooms (Nehm, Kim & Sheppard, 2009). Along with teacher apprehension to teaching evolution, educators are also apprehensive to tools associated with computational thinking; this may be alleviated with the assistance of the LBECT-LP. Not exposing our young science student learners to computational thinking at an early age may hinder the future of STEM fields. Computational methods incorporated into biology classes to learn biological evolution is controversial, but it has the potential to alleviate misconceptions, reinforce the nature of science, and encourage student embodiment.

The learning progression I presented may be used by a variety of educational, science, and computational professionals. However, it is still important to consider the most appropriate application and integration. The LBECT-LP would encourage students
to practice thought processes that may encourage higher order science understanding and promote curricular relationships across disciplinary domains. As teachers implement these strategies, it would provide them with a new robust resource and alternative ways to promote learning similar to those working in science fields.

In many cases students encounter programming (a computational construct within the LP) as the means to an end to answer a scientific question. Often the first time this occurs for students, it is when students are doing independent research (sometimes as late as the graduate level of education). Students may feel overwhelmed when learning programming and associated computational thinking skills during this time (Wilensky, 2016). Independent thinking in which students develop tools or discover new knowledge should not be an experience reserved for graduate level students. Often lack of computational thinking skills is the reason students have difficulty in independent scientific thinking throughout their educational careers. In some cases, even professionals working in science fields hire specialists in computation (i.e., programmers or data analytics) to assist them within laboratory settings. These types of skills and associated scaffolds which I address within the LBECT-LP should be presented to students within the K-12 levels of education so that students can be versed in scientific content and computational constructs simultaneously (and early on in education).

Getting individuals to think like scientists early on in education is critical for democratic societies (Stocum, 2015). This is especially true with the rise in AI, bioinformatics, and threat of abstractions becoming indistinguishable from reality. A scientifically minded type of population may better understand and critically evaluate itself and its role in the natural world. Allowing students to develop creative and critical
viewpoints contributes to resisting anti scientific schools of thought (Longbottom, 1999). Using logic, creating variables and tools to simulate reality is inseparable from computational thinking; therefore, it is essential that we provide this opportunity for students in order provide them the best education possible within their biology courses.
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APPENDICES

APPENDIX A

INSTRUMENT: BIOLOGICAL EVOLUTION CONTENT KNOWLEDGE INVENTORY (BECKI)

Evolution Knowledge Test:

1. How can a catastrophic global event influence evolutionary change?
   a. Undesirable versions of the gene are removed.
   b. New genes are generated due to the event.
   c. *Only some species may survive the event.
   d. There are short term effects that disappear over time.

2. Natural selection produces evolutionary change by
   a. *Changing the frequency of various versions of genes.
   b. Reducing the number of new mutations in genetic material.
   c. Producing genes needed for new environments.
   d. Reducing the effects of detrimental versions of genes.

3. It is often the case that a structure (such as a functional eye) is lost during the course of evolution.
   This is because
   a. The structure itself (such as the functional eye) is no longer actively used.
   b. Mutations start to accumulate that disrupt its function.
   c. It interferes with other traits and functions in the organism.
   d. *The cost of maintaining it is not justified by the benefits it brings.

4. What might scientists infer about the eyes of ancient organisms in terms of evolution?
   a. Only animals living in the bright sunlight develop eyes because they need and use them.
   b. Eyes would bear no resemblance to eyes today, and would not be recognized.
   c. *The eyes of ancient organisms would have similar characteristics to eyes today.
   d. Only animals with bones would really be trying to develop useful functional eyes.

5. If there is a random mutation in the DNA of an organism, which is the next smallest biological unit in which it may be detected?
   a. *Protein
   b. Cell
   c. Organ
   d. Population

6. Thick blubber acts as insulation in cold waters, allowing animals to stay warm. Which of the following is the best description of the role cold water played in the evolution of thick blubber in some whales?
   a. It caused mutations that gave whales thicker and thicker blubber.
   b. *It helped determine which whales each generation survived and which did not.
   c. It directly influenced the growth and development of the whales.
   d. It made the whales work to stay warm and these efforts caused whales to change.

7. Some whales have thick skulls which assists in breaking ice in order for them to surface and breathe. What is the best way to describe the evolutionary changes that occurred among the whales while the species evolved thick skulls?
   a. The skull of each whale got a little thicker during its lifetime.
b. *Whales with thick skulls reproduced and became more common.
c. The population changed randomly each year.
d. Mutations increased the skull thickness of more and more whales each year.

Consider Figure 1 for questions 8 & 9:

8. Whales have been classified in a group (called ungulates, the even toed mammals) along with their closest relative the hippopotamus because:
   a. Whales and hippos are big, heavy, and have round bodies with large mouths.
   b. *Whales and hippos share a more recent common ancestor.
   c. Whales and hippos have similar diets and need to live in water.
   d. Whales and hippos display similar social and parenting behaviors.

9. The chart displayed in Figure 1 suggests that:
   a. The animals in this classification tree have four legs.
   b. Whales are not related to camels.
   c. Whales are more closely related to giraffes than to bison.
   d. *Whales are more closely related to deer than to pigs.
10. By reference to the tree above as shown in Figure 2, which of the following is an accurate statement of relationships?
   a. A green alga is more closely related to a red alga than to a moss
   b. A green alga is more closely related to a moss than to a red alga
   c. A green alga is equally related to a red alga and a moss
   d. A green alga is related to a red alga, but is not related to a moss

11. By reference to the tree above as shown in Figure 3, which of the following is an accurate statement of relationships?
   a. A crocodile is more closely related to a lizard than to a bird
   b. A crocodile is more closely related to a bird than to a lizard
   c. A crocodile is equally related to a lizard and a bird
   d. A crocodile is related to a lizard, but is not related to a bird
12. Which of the five marks in the tree above as shown in Figure 4 corresponds to the most recent common ancestor of a mushroom and a sponge?

a. a  
b. b  
c. c  
d. *d

13. If you were to add a trout to the phylogeny shown above in Figure 5 where would its lineage attach to the rest of the tree?

a. a  
b. b  
c. *c  
d. d

14. There exists a population in which there are three distinct versions of the gene A (a1, a2, and a3). Originally, each version was present in equal numbers of individuals. Which version of the gene an individual carries has no measurable effect on its reproductive success. As you follow the
population over a number of generations, you find that the frequency of a1 and a3 drop to 0%. What is the most likely explanation?

a. There was an increased rate of mutation in organisms that carry either a1 or a3.
b. Mutations have occurred in the population that changed a1 and a3 into a2.
c. Individuals carrying a1 or a3 were removed by natural selection.
d. *Random variations led to a failure to produce individuals carrying a1 or a3.

For questions 15 - 18 consider the following passage regarding Galapagos finches:

Scientists have long believed that the 14 species of finches on the Galapagos Islands evolved from a single species of finch that migrated to the islands one to five million years ago. Recent DNA analyses support the conclusion that all of the Galapagos finches evolved from the warbler finch. Different species live on different islands. One of the major changes in the finches is in their beak sizes and shapes, as shown in Figure 6

![Figure 6](image)

15. In the finch population, what are the primary changes that occur gradually over time?
   a. The traits of each individual finch within a population gradually change
   b. *The proportions of finches having different traits within a population change
   c. Successful behaviors learned by finches are passed onto offspring
   d. Mutations occur to meet the needs of the finches as the environment changes

16. What type of variation in finches is passed to the offspring?
   a. Any behaviors that were learned during a finch’s lifetime
   b. Only characteristics that were beneficial during a finch’s lifetime
   c. *All characteristics that are genetically determined
   d. Characteristics that were positively influenced by the environment

17. A female finch gives birth to a baby. What traits of the mother will the baby inherit?
   a. The mother’s traits that helped her survive and reproduce.
   b. The mother’s traits that changed because she used or did not use them.
   c. The mother’s traits that were changed by the environment during her lifetime.
   d. *The mother’s traits that were determined by genes.

18. Some finches evolved long beaks from ancestors that had short beaks. Think about the first finch to have a long beak. Why did this individual have such a long beak?
   a. The finch dug in trees with thick bark, and these efforts affected its beak.
   b. *The finch was lucky a genetic accident, giving it a long beak.
   c. The finch needed a long beak to scavenge in bark, so it developed.
   d. The finch needed a long beak to eat, so a mutation changed its DNA
Evolution Test Answers
1) C
2) A
3) D
4) C
5) A
6) B
7) B
8) B
9) D
10) B
11) B
12) D
13) C
14) D
15) B
16) C
17) D
18) B
Computational process knowledge survey (*italicized* text indicates negative worded items to be reverse coded; *italicized* text will be changed to normal text prior to administration. Bracketed items will also be removed prior to distribution):

Below are statements about computational processes which include: input, integration, output and feedback. Rate the degree to which you think that a scientist would agree with the following computational statements:

<table>
<thead>
<tr>
<th>Statement</th>
<th>Strongly disagree</th>
<th>Disagree</th>
<th>Neither agree nor disagree</th>
<th>Agree</th>
<th>Strongly agree</th>
</tr>
</thead>
<tbody>
<tr>
<td>1. Scientific data structure and formatting are automatically done by a computer. [input]</td>
<td><img src="#" alt="Select" /></td>
<td><img src="#" alt="Select" /></td>
<td><img src="#" alt="Select" /></td>
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<tr>
<td>2. Scientists may generate or modify data by using a computer program. [input]</td>
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<td><img src="#" alt="Select" /></td>
<td><img src="#" alt="Select" /></td>
<td><img src="#" alt="Select" /></td>
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</tr>
<tr>
<td>3. Variables defined by a scientist should represent components of a scientific phenomenon. [input]</td>
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<tr>
<td>4. The types of input data considered by scientists vary little in form and structure. [input]</td>
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<tr>
<td>5. Precise rules can be used to relate variables in science. [integration]</td>
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<tr>
<td>6. There are minimal alternative ways to relate scientific input to scientific output. [integration]</td>
<td><img src="#" alt="Select" /></td>
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<tr>
<td>7. Certain computer programs and mathematical processes used by scientists are more efficient than others. [integration]</td>
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<tr>
<td>8. Most computer programs have code visible to the scientist. [integration]</td>
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<tr>
<td>9. The representation of scientific output will vary in form depending on the audience. [output]</td>
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</tbody>
</table>
10. Output data is automatically checked and scientifically verified by a computer. [output]

<table>
<thead>
<tr>
<th></th>
<th>A</th>
<th>B</th>
<th>C</th>
<th>D</th>
<th>E</th>
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</thead>
</table>

11. Output data may aid in the generation of new scientific knowledge. [output]

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<thead>
<tr>
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<th>B</th>
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<th>D</th>
<th>E</th>
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</table>

12. One program will generate one type of scientific output. [output]

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<thead>
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<th></th>
<th>A</th>
<th>B</th>
<th>C</th>
<th>D</th>
<th>E</th>
</tr>
</thead>
</table>

13. Output data can be used to inform input data within a scientific computer program. [feedback]

<table>
<thead>
<tr>
<th></th>
<th>A</th>
<th>B</th>
<th>C</th>
<th>D</th>
<th>E</th>
</tr>
</thead>
</table>

14. System output allows adjustment of performance to meet a desired scientific response in feedback. [feedback]

<table>
<thead>
<tr>
<th></th>
<th>A</th>
<th>B</th>
<th>C</th>
<th>D</th>
<th>E</th>
</tr>
</thead>
</table>

15. Feedback can better allow a program to mimic a dynamic scientific system. [feedback]

<table>
<thead>
<tr>
<th></th>
<th>A</th>
<th>B</th>
<th>C</th>
<th>D</th>
<th>E</th>
</tr>
</thead>
</table>

16. There is little relationship between lines of feedback and complexity of a scientific computer program. [feedback]

<table>
<thead>
<tr>
<th></th>
<th>A</th>
<th>B</th>
<th>C</th>
<th>D</th>
<th>E</th>
</tr>
</thead>
</table>

242
Computational process knowledge survey
Answers with explanations
1. (A)
Explanation: Scientists need to ensure the input data is formatted properly in order for it to run in a program. This formatting includes items such as data structure and variable type.

2. (E)
Explanation: Data can be made to simulate a natural scientific phenomenon by using a computer program. It may also be modified (i.e., averaged, interpolated, concatenated etc.) by a program if using a data set etc.

3. (E)
Explanation: Scientists should have input variables represent the components of the real world phenomenon.

4. (A)
Explanation: There are many types, forms, representations and formats of input data.

5. (E)
Explanation: Algorithms for example are precise rules that relate input to output. Other examples include commands and Boolean statements.

6. (A)
Explanation: There are usually many ways in which variables can be related properly. Different algorithms or functions may be combined in various ways to produce the same desired result.

7. (E)
Explanation: Some programs are better suited for certain tasks than others. Some integration processes are more efficient than others. This becomes important when programs need to run most efficiently in terms of space and time.

8.(A)
Explanation: Many programs used (even by scientists) have code that is ‘hidden’ because interfaces overlay the raw code. This makes the program more efficient but also more ambiguous for the user. The BLAST computational tool for example will read and compare DNA sequences for the user although a similar program can be written from scratch in a program such as Python to perform the same function. Both BLAST and Python are computational tools available to scientists.

9. (E)
Explanation: The output of a program should differ depending on what the program is used for. The scientist must also consider the audience when designing an output.

10. (A)
Explanation: Scientists need to ensure that their data is valid and consistent with scientific knowledge. There are verification methods that may be written into code however in many instances scientists need to justify how reliable and robust their code is.

11. (E)
Explanation: Output or interpreted results may challenge or provide better support for known scientific ideas.

12. (A)
Explanation: Program to output ratio is not 1:1, one program or script can generate multiple types of output. This output may be but is not limited to the form of a data set, command, or graph or a combination of multiple forms.
13. (E)
Explanation: Output data can inform input data if directed by the user. I refer to this as feedback.

14. (E)
Explanation: When feedback is used, it allows a program to regulate itself. A common example of negative feedback is a thermostat. Applicable examples may be regulation within a population growth model or hormone secretions.

15. (E)
Explanation: Since nature is dynamic, negative feedback and positive feedback loops are commonly observed in the natural world.

16. (A)
Explanation: In many cases when a system becomes more dynamic there are more lines of feedback to regulate various aspects of the system.
APPENDIX C

INTERVENTION PRESENTATION EXAMPLES

Computational Components

- Input
- Integration (processing)
- Output
- Feedback

Where do we see this?

Can we think of biological examples?

https://www.recode.com/2019/3/18/18368938

Computational components described and video for discussion prompt

- Population changes
- Hormone regulation
- Environmental tipping points
- .....?

Computation as coupled with feedback loops and biological examples
Input Discussion Slide

### Table

<table>
<thead>
<tr>
<th>FiscalMonth</th>
<th>Value</th>
<th>Result</th>
</tr>
</thead>
<tbody>
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<td>100</td>
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<td>Jun</td>
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<td>Jul</td>
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<td>150</td>
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<tr>
<td>Aug</td>
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<td>-50</td>
</tr>
<tr>
<td>Sep</td>
<td>550</td>
<td>200</td>
</tr>
</tbody>
</table>

Integration Discussion Slide

Output Discussion Slide
What is Biological Evolution?
- change in the heritable characteristics of biological populations over successive generations

Evolution of populations
- Evolution (at this scale) = change in allele frequencies in a population
  - Hypothetical: what conditions would cause allele frequencies NOT to change?
- Non evolving populations: REMOVE all agents of evolutionary change
  - 1 very large population size (no genetic drift)
  - 2 no migration (no gene flow in our out)
  - 3 no mutation (no genetic change)
  - 4 random mating (no sexual selection)
  - 5 no natural selection (everyone is equally fit)

Description of how populations evolve (Intervention 1)
Relating how populations evolve through allele frequencies as related to the Hardy-Weinberg Equation (Intervention 1)

**H-W Theorem**

- **Counting Alleles**
  - Assume 2 alleles = B, b
  - Frequency of dominant allele (B) = p
  - Frequency of recessive allele (b) = q
    - Freq must add to 1 (100%) so
    - P + q = 1

Relating how populations evolve as related to the Hardy-Weinberg Equation by counting the individuals within a population (Intervention 1)

**Counting Individuals**

- Frequency of homozygous dominant: p*p = p^2
- Frequency of homozygous recessive: q*q = q^2
- Frequency of heterozygotes (p*q) + (p*q) = 2pq
- Frequencies of all individuals must add to 1 (100%) so: P^2 + 2pq + q^2 = 1
How might we display evolutionary relationships?
- Remember DNA → RNA → Protein
- What is a protein?
- What is a mutation?
- How do we identify evolutionary relationships?

Identifying if students know how we can display evolutionary relationships and assessing previous knowledge (Intervention 2)

Description of how to read phylogenetic trees & cladograms (Intervention 2)
Use NCBI

National Center for Biotechnology Information
- DNA, RNA, Protein comparison to make phylogenetic trees through BLAST
- Which would be most accurate?
- What is the: input, integration, output and feedback?

Description of our use of NCBI and BLAST tools (Intervention 2)
APPENDIX D

HARDY-WEINBERG EVOLUTION ACTIVITY ASSIGNMENT
(INTERVENTION 1)

The following worksheet will be provided to students during the H-W computational intervention

After your instructor’s discussion and lecture please review and complete the following activity. Be sure to turn in the required components as listed at the end.

Overview

In this activity you will:
1. learn about the Hardy-Weinberg law of genetic equilibrium
2. study the relationship between evolution and change in allele frequency by using a computational model to demonstrate what can happen over many generations

Before doing this activity you should understand:
1. how natural selection can alter allelic frequencies in a population
2. the Hardy-Weinberg equation and its use in determining the frequency of alleles in a population, and
3. the effects on allelic frequencies of selection against the homozygous recessive or other genotypes.

After this activity you should be able to:
1. calculate the frequencies of alleles and genotypes in the gene pool of a population using the Hardy-Weinberg formula, and
2. discuss natural selection and other causes of microevolution as deviations from the conditions required to maintain Hardy-Weinberg equilibrium,
3. use a data set that reflects a change in the genetic makeup of a population over time and apply computational methods and conceptual understandings to investigate the cause(s) and effect(s) of this change,
4. apply computational methods to data from a real or simulated population to predict what will happen to the population in the future,
5. evaluated data-based evidence that describes evolutionary changes in the genetic makeup of a population over time,
6. use data from computational models based on the Hardy-Weinberg equilibrium to analyze genetic drift and the effect of selection in the evolution of specific populations,
7. justify data from computational models based on the Hardy-Weinberg equilibrium to analyze genetic drift and the effect of selection in the evolution of specific populations,
8. describe a computational model that represents evolution within a population, and evaluate data sets that illustrate evolution as an ongoing process.

Background
In 1908 G.H. Hardy and W. Weinberg independently suggested a scheme whereby evolution could be viewed as changes in the frequency of alleles in a population of organisms. They argued that if a population met five conditions that there would be no changes in allele frequencies from generation to generation. Those five conditions are as follows:

1. The breeding population is large, reducing the effect of chance on changes in allele frequencies
2. Mating is random with respect to the gene in question. Individuals show no mating preference for a particular phenotype.
3. There is no mutation of the alleles.
4. No individuals enter or leave the population by migration (no immigration or emigration).
5. There is no selection. In other words, the alleles of the gene in question do not affect mating or survival, so every genotype has an equal chance of surviving and reproducing.

Hardy and Weinberg also described the distribution of alleles and genotypes within a population mathematically. The following variables are used, and each is expressed in decimal form:

\[
\begin{align*}
 p &= \text{frequency of the dominant allele} \\
 q &= \text{frequency of the recessive allele}
\end{align*}
\]

Note that \(p + q\) must always equal 1. The analysis does not work if there are more than 2 alleles of the gene being studied. (It can be done, but the math is much more complicated.)

In a population, \(p\) is also the likelihood of a dominant allele being passed on to an offspring, and \(q\) is the likelihood of a recessive allele being passed on. Thus, we end up with the following conclusions:

\[
\begin{align*}
 p^2 &= \text{frequency of homozygous dominant individuals in the population} \\
 2pq &= \text{frequency of heterozygous individuals in the population} \\
 q^2 &= \text{frequency of homozygous recessive individuals in the population}
\end{align*}
\]

Note that \(p^2 + 2pq + q^2\) should always equal 1.

How can this rule be applied to real populations? One cannot see the frequency of alleles in a population; one can only see phenotypes. Nonetheless, the rules can allow one to determine allele frequencies. The following steps allow one to determine the values of \(p\) and \(q\) in an observed population.
1. Determine the frequency of the recessive phenotype. The only way to have the recessive phenotype is to be homozygous recessive. Thus, the frequency of the recessive phenotype = \( q^2 \).
2. Taking the square root of the value determined in step 1 gives the value of \( q \).
3. Since \( q + p \) must = 1, the value of \( p \) can now be determined.
4. If desired, the values of \( 2pq \) and \( p^2 \) can also now be determined.

The Hardy-Weinberg equation describes an existing situation. If the five conditions are met, then no change will occur in either allele or genotype frequencies in the population. Of what value is such a rule? It provides a yardstick by which changes in allele frequency, and therefore evolution, can be measured. One can look at a population and ask: Is evolution occurring with respect to a particular gene locus? Since evolution is difficult if not impossible to observe in most natural populations, we will model the evolutionary process using a computational model. The purpose of this simulation is to provide an opportunity to test some of the basic tenets of evolutionary biology.

Evolution occurs in populations of organisms and involves variation in the population, heredity, and differential survival. One way to study evolution is to study how the frequency of alleles in a population changes from generation to generation. In other words, you can ask What are the inheritance patterns of alleles, not just from two parental organisms, but also in a population? You can then explore how allele frequencies change in populations and how these changes might predict what will happen to a population in the future.

Computational models are tools used to explore the complexity of biological systems that might otherwise be difficult or impossible to study. Several models can be applied to questions about evolution. In this investigation, you will use a program that models how a hypothetical gene pool changes from one generation to the next. This model will let you explore parameters that affect allele frequencies, such as selection, mutation, and migration.

In the second part of the investigation, you will generate your own questions regarding the evolution of allele frequencies in a population. Then you will be asked to explore possible answers to those questions by applying a computer model.

It is easy to understand how microscopes opened up an entire new world of biological understanding. For some, it is not as easy to see the value of mathematics to the study of biology, but, like the microscope, math and computers provide tools to explore the complexity of biology and biological systems — providing deeper insights and understanding of what makes living systems work.

This investigation also provides an opportunity for you to review concepts you might have studied previously, including natural selection as the major mechanism of evolution; the relationship among genotype, phenotype, and natural selection; and the fundamentals of classic Mendelian genetics combined with evolutionary principles.
**Procedure**

*Be sure to bring laptop with internet capabilities and google sheets*

**Part 1:**

Spreadsheets such as excel or Google sheets are valuable tools that allow us to ask What if? questions. They can repeatedly make a calculation based on the results of another calculation. They can also model the randomness of everyday events. Our goal is to computationally display how allele frequencies change through one life cycle of this imaginary population in the spreadsheet.

To explore how allele frequencies change in populations of organisms, you will first build a computer spreadsheet that computationally models the changes in a hypothetical gene pool from one generation to the next. You need a basic familiarity with spreadsheet operations to complete this lab successfully. You may have taken a course that introduced you to spreadsheets before. If so, that will be helpful, and you may want to try to design and build your model on your own after establishing some guidelines and assumptions. Otherwise, you may need more specific guidance from your teacher. Watch instructions from your teacher and use their example tools if necessary. The following steps are a guideline and you may deviate from the order in order to develop your final products and analysis.

Each part of the life cycle can be represented by a spreadsheet operation.

***Remember all parts of the spreadsheet should be reliant on changing ONE allele value***

1. **Set allele frequencies**
   a. assign a value to a cell, between 0 and 1 (This will be equal to p or frequency of allele A)
   b. The frequency of Allele B (or q) will be equal to 1 - the value of the frequency of allele A

2. **Use the random function (RAND) to generate a random number which will be compared to the allele frequency from step 1**

3. **Compare the random number to allele frequency and assign the appropriate allele.**
   (For example: =IF(RAND() <= D$2, "A","B")

4. **Repeat Steps 1–3 for the second allele from step 1b since this is based on the second allele.**
   a. Remember that each individual needs two gametes so this must be done twice

5. **Use the CONCATENATE function to combine the two alleles to form a zygote**
   a. For example: =CONCATENATE(E5,F5)

6. **Copy this procedure (Steps 2–5) for multiple offspring.**
   a. Make multiple rows below

More detailed directions:
The first step is to randomly draw gametes from the gene pool to form a number of zygotes that will make up the next generation. To begin this model, let’s define a couple of variables. Let \( p \) = the frequency of the A allele and let \( q \) = the frequency of the B allele. Bring up the spreadsheet on your computer. The examples here are based on Microsoft® Excel or google sheets, but almost any modern spreadsheet can work.

Somewhere in the upper left corner (in this case, cell D2), enter a value for the frequency of the A allele. This value should be between 0 and 1. Go ahead and type in labels in your other cells and, if you wish, shade the cells as well. This blue area will represent the gene pool for your model. (Highlight the area you wish to format with color, and right-click with your mouse in Excel to format.) This is a spreadsheet, so you can enter the value for the frequency of the B allele; however, when making a model it is best to have the spreadsheet do as many of the calculations as possible. All of the alleles in the gene pool are either A or B; therefore \( p + q = 1 \) and \( 1 - p = q \). In cell D3, enter the formula to calculate the value of \( q \).

In spreadsheet lingo it is 
\[=1-D2\]

Your spreadsheet now should look something like the figure below.

Let’s explore how one important spreadsheet function works before we incorporate it into our model. In a nearby empty cell, enter the function (we will remove it later). =Rand() Note that the parentheses have nothing between them. After hitting return, what do you find in the cell? If you are on a PC, try hitting the F9 key several times to force recalculation. On a Mac, enter cmd + or cmd =. What happens to the value in the cell?

The RAND function returns random numbers between 0 and 1 in decimal format. This is a powerful feature of spreadsheets. It allows us to enter a sense of randomness to our calculations if it is appropriate — and here it is when we are “randomly” choosing gametes from a gene pool. Go ahead and delete the RAND function in the cell. Let’s select two gametes from the gene pool. In cell E5, let’s generate a random number,
compare it to the value of p, and then place either an A gamete or a B gamete in the cell. We’ll need two functions to do this, the RAND function and the IF function. Check the help menu if necessary.

Note that the function entered in cell E5 is
=IF(RAND()<=D$2,“A”, “B”)

Be sure to include the $ in front of the 2 in the cell address D2. It will save time later when you build onto this spreadsheet. The formula in this cell basically says that if a random number between 0 and 1 is less than or equal to the value of p, then put an A gamete in this cell, or if it is not less than or equal to the value of p, put a B gamete in this cell. IF functions and RAND functions are very powerful tools when you try to build models for biology.

Now create the same formula in cell F5, making sure that it is formatted exactly like E5. When you have this completed, press the recalculate key to force a recalculation of your spreadsheet. If you have entered the functions correctly in the two cells, you should see changing values in the two cells. (This is part of the testing and retesting that you have to do while model building.) Your spreadsheet should look like the figure below.

Try recalculating 10–20 times. Are your results consistent with what you expect? Do both cells (E5 and F5) change to A or B in the ratios you’d expect from your p value? Try changing your p value to 0.8 or 0.9. Does the spreadsheet still work as expected? Try lower p values. If you don’t get approximately the expected numbers, check and recheck your formulas now, while it is early in the process.

You could stop here and just have the computer recalculate over and over — similar to tossing a coin. However, with just a few more steps, you can have a model that will create a small number or large number of gametes for the next generation, count the different genotypes of the zygotes, and graph the results.
Copy these two formulas in E5 and F5 down for about 16 rows to represent gametes that will form 16 offspring for the next generation, as in Figure 4. (To copy the formulas, click on the bottom right-hand corner of the cell and, with your finger pressed down on the mouse, drag the cell downward.)

We’ll put the zygotes in cell G5. The zygote is a combination of the two randomly selected gametes. In spreadsheet vernacular, you want to concatenate the values in the two cells. In cell G5 enter the function =CONCATENATE(E5,F5)
Copy this formula down as far down as you have gametes, as in the figure below.
Now, try different values for the starting frequency of allele A1 and run several simulations. Does your experimentation verify that any starting frequencies are in Hardy-Weinberg equilibrium? Explain how you know.

Now change the population size to 1000 and re-run this simulation (starting with allele A1 and A2 frequencies of 0.5 each). Run this simulation five times. Does the same thing happen each time? Why or why not? You will probably want to select the "Auto" button, which will allow you to compare the different simulations.

The next columns on the sheet, H, I, and J, are used for bookkeeping — that is, keeping track of the numbers of each zygote’s genotype. They are rather complex functions that use IF functions to help us count the different genotypes of the zygotes. The function in cell H5 is =IF(G5="AA",1,0) This basically means that if the value in cell G5 is AA, then put a 1 in this cell; if not, then put a 0. Enter the following very similar function in cell J5: =IF(G5="BB",1,0) Can you interpret this formula? What does it say in English? Your spreadsheet now should resemble the figure below.

Now let’s tackle the nested IF function. This is needed to test for either AB or BA. In cell I5, enter the nested function: =IF(G5="AB",1,(IF(G5="BA",1,0))) This example requires an extra set of parentheses, which is necessary to nest functions. This function basically says that if the value in cell G5 is exactly equal to AB, then put a 1; if not, then if the value in cell G5 is exactly BA, put a 1; if it is neither, then put a 0 in this cell. Copy these three formulas down for all the rows in which you have produced gametes.

Enter the labels for the columns you’ve been working on — gametes in cell E4, zygote in cell G5, AA in cell H4, AB in cell I4, and BB in cell J4, as shown in the figure below.
As before, try recalculating a number of times to make sure everything is working as expected. What is expected? If you aren’t sure yet, keep this question in mind as you complete the sheet. You could use a p value of 0.5, and then you’d see numbers similar to the ratios you would get from flipping two coins at once. Don’t go on until you are sure the spreadsheet is making correct calculations. Try out different values for p. Make sure that the number of zygotes adds up. Describe your thinking and procedure for checking the spreadsheet.

Now, copy the cells E5 through J5 down for as many zygotes as you’d like in the first generation. Use the SUM function to calculate the numbers of each genotype in the H, I, and J columns. Use the genotype frequencies to calculate new allele frequencies and to recalculate new p and q values. Make a bar graph of the genotypes using the chart tool. Your spreadsheet should resemble the figure below.

You now have a model with which you can explore how allele frequencies behave and change from generation to generation. Working with a partner, develop a plan to answer this general question: How do inheritance patterns or allele frequencies change in a population over one generation? As you work, think about the following more specific questions:
• What can you change in your model? If you change something, what does the change tell you about how alleles behave?
• Do alleles behave the same way if you make a particular variable more extreme? Less extreme?
• Do alleles behave the same way no matter what the population size is? To answer this question, you can insert rows of data somewhere between the first row of data and the last row and then copy the formulas down to fill in the space.

Try out different starting allele frequencies in the model. Look for and describe the patterns that you find as you try out different allele frequencies. Develop and use a pattern to select your values to test and organize your exploration. In particular, test your model with extreme values and intermediate values. Describe your observations and conclusions about the population inheritance patterns you discover.

Try adding additional generations to your model to look at how allele frequencies change in multiple generations. To do this, use your newly recalculated p and q values to seed the next generation. Once you’ve included the second generation, you should be able to copy additional generations so that your model looks something like the figure above, with each new generation determining the new p and q values for the next.

**Part 2**

You will be creating a Formula that Predicts the Genotypes of the Next Generation. Try to create a graph of p values over several generations, for different-sized populations. See if you can detect a pattern of how population size affects the inheritance pattern. Be sure to try out both large and small populations of offspring. This model relies on the RAND function to randomly select gametes from an infinite gene pool. Consider:
• What would happen if there were no randomness to this selection?
• What kind of pattern of genotypes would you expect in the next generation?

Here are two approaches to develop the formula. You might first try a graphical approach. Create a Punnet square, like the figure below and similar to what you might use to solve a Mendelian genetics problem. In this case, however, plot the values of p and q. Scale each side of the square based on the magnitude of the p or q values. Of course, you could also calculate the expected results for the next generation. Remember that p + q = 1 The probability of two A alleles combining in one organism in the next generation is p2. The probability of two B alleles combining is q2. The probability of a combination of AB is p * q, as is the probability of combination of BA alleles, for a total of 2pq.

For the next generation, the formula that predicts genotypes is (p + q)2 = 1, which works out to: p2 + 2pq + q2 Based on the calculations you made while testing your model, how would you answer the following questions?

• In the absence of random events (an infinitely large population), are the allele frequencies of the original population expected to change from generation to generation?
• How does this compare to a population that has random gamete selection but is small?
• What happens to allele frequencies in such a population? Is it predictable?

This mathematical model can predict allele frequencies from generation to generation. In fact, it is a null model. That is, in the absence of random events or other real-life factors that affect populations, the allele frequencies do not change from generation to generation. This is known as the Hardy-Weinberg equilibrium (H-W equilibrium). The H-W equilibrium is a valuable tool for population biologists because it serves as a baseline to measure changes in allele frequencies in a population. If a population is not in H-W equilibrium, then something else is happening that is making the allele frequencies change.

What factors can cause allele frequencies to change in a population? (Hint: There are many.) How could you model these factors using your spreadsheet?

What do you need to turn in?

1) Document that includes:
   a. Part 1
      i. General procedure and procedural information (be sure to define what you did, computational components, biological aspects)
      ii. Results (Be sure to identify what you observed in your populations and how it related to the H-W equation and evolution, be sure to include the micro through the macro scales and include time)
      iii. Conclusion (Overall what did you find, how does this display evolution, what computational processes did you use, what is the input, integration, output and feedback for this model)
   b. Part 2
      i. General procedure (what did you do to your model in part 1, provide the scenario)
      ii. Results (How did it change your model)
      iii. Conclusion (Overall what did you find from manipulating your population, how does this relate to evolution, what computational processes did you use, what is the input, integration, output and feedback for this model)

*Your document should include screen shots

2) Google or Excel spreadsheet
   a. Attach the computational model that you used during the activity

Adapted from the College Board AP Biology Student Lab Manual, 2001 edition and 2012 edition, as well as materials from Jon C. Herron (© 2003) and Amherst College
APPENDIX E

PHYLOGENETIC TREE EVOLUTION ACTIVITY ASSIGNMENT
(INTERVENTION 2)

The following worksheet will be provided to students during the phylogenetic tree computational intervention

After your instructor’s discussion and lecture please review and complete the following activity. Be sure to turn in the required components as listed at the end.

Overview

In this activity you will:
1. Compare DNA & protein sequences to understand evolutionary relationships using computational tools
2. Use computational tools to develop phylogenetic trees

After this activity you will be able to:
1. Create cladograms that depict evolutionary relationships
2. Analyze biological data with sophisticated bioinformatics tools
3. Use cladograms and computational tools to ask questions on your own
4. Apply concepts you know relating computation and evolution

Background

Between 1990-2003, scientists working on an international research project known as the Human Genome Project were able to identify and map the 20,000-25,000 genes that define a human being. The project also successfully mapped the genomes of other species, including the fruit fly, mouse, and Escherichia coli. The location and complete sequence of the genes in each of these species are available for anyone in the world to access via the Internet.

Why is this information important? Being able to identify the precise location and sequence of human genes will allow us to better understand genetic diseases. In addition, learning about the sequence of genes in other species helps us to understand evolutionary relationships among organisms. Many of our genes are identical or similar to those found in other species.

Suppose you identify a single gene that is responsible for a particular disease in fruit flies. Is that same gene found in humans? Does it cause a similar disease? It would take you nearly 10 years to read through the entire human genome to try to locate the same sequence of bases as that in fruit flies. This definitely isn't practical, so a sophisticated technological method is needed.

Bioinformatics is a field that combines statistics, mathematical modeling, and computer science to analyze biological data. Comparative genomics involves the use of computer programs that can line up multiple genomes and look for regions of similarity among them. Using bioinformatics methods, entire genomes can be quickly compared in order to detect genetic similarities and differences. Some of these sequence-similarity
tools are accessible to the public over the Internet. An extremely powerful bioinformatics tool is BLAST, which stands for Basic Local Alignment Search Tool. Using BLAST, you can input a gene sequence of interest and search entire genomic libraries for identical or similar sequences in a matter of seconds. BLAST is a set of programs designed to perform similarity searches on all available sequence data.

In this activity, you will use BLAST to compare several genes, and then use the information to construct a cladogram. A cladogram (also called a phylogenetic tree) is a visualization of the evolutionary relatedness of species. The figure below is a simple cladogram.

![Cladogram Image]

Note that the cladogram is treelike, with the endpoints of each branch representing a specific species. The closer two species are located to each other, the more recently they share a common ancestor. For example, Selaginella (spikemoss) and Isoetes (quillwort) share a more recent common ancestor than the common ancestor that is shared by all three organisms.

The figure below includes additional details, such as the evolution of particular physical structures called shared derived characters. Note that the placement of the derived characters corresponds to when (in a general, not a specific, sense) that character evolved; every species above the character label possesses that structure. For example, tigers and gorillas have hair, but lampreys, sharks, salamanders, and lizards do not have hair.
Historically, only physical structures were used to create cladograms; however, modern-day cladistics relies heavily on genetic evidence as well. Chimpanzees and humans share 95%+ of their DNA, which would place them closely together on a cladogram. Humans and fruit flies share approximately 60% of their DNA, which would place them farther apart on a cladogram.

Can you draw a cladogram that depicts the evolutionary relationship among humans, chimpanzees, fruit flies, and mosses?

Use the following data to construct a cladogram of the major plant groups:

<table>
<thead>
<tr>
<th>Organisms</th>
<th>Vascular Tissue</th>
<th>Flowers</th>
<th>Seeds</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mosses</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Pine trees</td>
<td>1</td>
<td>0</td>
<td>1</td>
</tr>
<tr>
<td>Flowering plants</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Ferns</td>
<td>1</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Total</td>
<td>3</td>
<td>1</td>
<td>2</td>
</tr>
</tbody>
</table>

Look at the following data and think about gene vs. protein similarity comparisons for the following organisms:

<table>
<thead>
<tr>
<th>Species</th>
<th>Gene Percentage Similarity</th>
<th>Protein Percentage Similarity</th>
</tr>
</thead>
<tbody>
<tr>
<td>Chimpanzee <em>(Pan troglodytes)</em></td>
<td>99.6%</td>
<td>100%</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>--------------------------</td>
<td>--------</td>
<td>--------</td>
</tr>
<tr>
<td>Dog (<em>Canis lupus familiaris</em>)</td>
<td>91.3%</td>
<td>95.2%</td>
</tr>
<tr>
<td>Fruit fly (<em>Drosophila melanogaster</em>)</td>
<td>72.4%</td>
<td>76.7%</td>
</tr>
<tr>
<td>Roundworm (<em>Caenorhabditis elegans</em>)</td>
<td>68.2%</td>
<td>74.3%</td>
</tr>
</tbody>
</table>

**Procedure**

1. Identify a protein that you would like to explore and do some research on that protein
2. Search that protein on NCBI:
3. Find FASTA sequences and copy into a doc
   a. Use the following example: [https://docs.google.com/document/d/1D9U154XPXnusn0IbewLCPwjLzkyAi-Zbok0bUT-vvgU/edit](https://docs.google.com/document/d/1D9U154XPXnusn0IbewLCPwjLzkyAi-Zbok0bUT-vvgU/edit)
4. Copy and paste into NCBI BLAST
5. Hit BLAST and let it run
6. Explore the results
   a. Click explore distance tree of results, taxonomy reports, etc
   b. Look up species (from scientific names)
   c. Draw conclusions about relationships

**Hints to consider:**
- The higher the score, the closer the alignment
- The lower the e value, the closer the alignment
- Sequences with e values less than le-04 (1 x 10^-4) can be considered related with an error rate of less than 0.01%.

**Analysis:**

For your protein consider:
1. What is the function of your protein
2. What species in the BLAST result has the most similar gene sequence to the gene of interest?
3. Where is that species located in your cladogram?
4. How similar is that gene sequence?
5. How does BLAST actually compare these sequences (general)?
6. What species has the next most similar gene sequence to the gene of interest?
7. How do the DNA relationships compare to morphology of what you would have thought about these relationships between these organisms?
8. How else could you explore these relationships?
9. What other questions might you ask about your protein or the relationships
10. What is the input, integration and output used by BLAST?

What do you need to turn in?

1) Document that includes:
   a. Answers to questions 1-10, some may be more applicable to your protein
      than others
   b. Screen shots of your exploration and phylogenetic trees

*Gets turned in as Lab 2 in Canvas Section of Lab
APPENDIX F

EXAMPLES OF STUDENT WORK FROM PILOT STUDY

The following have been obtained as examples from the pilot test

1. What is the function of your protein?
   a. Reflectin gives functionality to iridocytes and leucophores, which are reflective cells in the skin of cephalopods that give them the ability to readily change the color of their skin to blend in with their environment. This protein plays a large role in their survival and predation tactics under the conditions in which they live.

2. What species in the BLAST result has the most similar gene sequence to the gene of interest?
   a. Sepia officinalis has the most similar gene sequence to reflectin, with an e-value of 0.0, indicating that this species can be related to this gene with an error rate of 0.01%. The total score for this species is 546.

3. Where is that species located in your cladogram?
   a. This species is located in the bottom right corner of the cladogram.

5. How does BLAST actually compare these sequences (general)?
   a. BLAST compares these sequences by utilizing a system that automatically recognizes regions of the sequence that are identical or very closely similar; and then placing a numerical value on them (i.e. % identical; e-value, etc.). A comparison can be made based on these values; for example, species whose sequences are more similar to each other are more likely to have had a more recent common ancestor. At the same rate, BLAST also automatically recognizes regions of the sequence that are less similar to each other. As a rule of thumb:
      i. The higher the score, the closer the alignment
      ii. The lower the e value, the closer the alignment
      iii. Sequences with e values less than 1e-04 can be considered related with an error rate of less than 0.01%.

6. What species has the next most similar gene sequence to the gene of interest?
   a. Euprymna scolopes has the second most similar gene sequence to reflectin with an e-value of 9e-34 and 87.95% similarity rate to the reflectin sequence. This species has a total score of 452; and when compared to a total score of 546 in Sepia officinalis, it can be concluded that these two species are the closest in alignment.
9. What other questions might you ask about your protein or the relationships?
   a. Despite being in the same class, why don’t more cephalopod species have more similar sequences for this protein?
      i. Is it due to their environment, or other adaptations they may have developed over time as a result of their environment? Are these adaptations more or less successful than the development and use of the reflectin protein?
   b. Dating back further, does this protein exist in other classes besides cephalopods? Other phyla?

10. What is the input, integration and output used by BLAST?
    a. Input: Reflectin protein sequence
    b. Integration: BLAST computational system that compares similar sequences of other species that exist within the database.
    c. Output: Various species on the distance tree; % of how similar each sequence is to each other
To conduct this experiment, I took 10 samples of alleles for the tail length of lizards within a population over the course of 16 generations, changing the value of $p$ each time (starting at 1 and ending at 0). By changing this value, the value of $q$ automatically adjusted so that the sum of $p$ and $q$ would always equal 1. Using this input data, I was able to draw microevolution conclusions based on the output of percentages displayed by each phenotype. Likewise, I was able to draw macroevolution conclusions by using any output data to find a trend in the appearance of a given phenotype over time.

**Results:**

**Sample 1:**

**Input data:** $p=1.0; q=0$

\[ p^2 + 2pq + q^2 = 1 \]

- Homozygote dominant: 100%
- Heterozygote: 0%
- Homozygote recessive: 0%

**Sample 5:**

**Input data:** $p=0.6; q=0.4$

\[ p^2 + 2pq + q^2 \]

\[ (0.559016994) + (0.440983006) = 1 \]

- Homozygote dominant: 31.25%
- Heterozygote: 50%
- Homozygote recessive: 18.75%

- This data indicates that this population is not in Hardy-Weinberg equilibrium and will evolve to produce both heterozygotes (AB) and recessive homozygotes (BB), while remaining primarily dominant homozygotes (AA) for this trait.

- **Microevolution:** As the value of $p$ decreased, the likelihood of producing more heterozygotes and recessive homozygotes increased from generation to generation. This trend could be the result of: natural selection (dominant homozygotes having a higher chance of survival and in turn are more likely to pass their genes on); a mutation in alleles; the immigration of new individuals causing a change in mating preferences; or the emigration of existing individuals resulting in a smaller breeding population and limiting the number of available mates.

- **Feedback:** The input of all primarily dominant homozygotes will result in an output of primarily AA alleles with some AB and BB alleles and will feedback to primarily AA alleles.

- **Macrolevolution:** This population is expected to continue evolving on a grand scale and comprise itself of a mix between recessive homozygotes (BB) and heterozygotes (AB), while remaining primarily dominant homozygotes (AA) for this trait.
Sample 7:

**Input data:** \( p = 0.4; q = 0.6 \)

\[ \begin{align*} p^2 + 2pq + q^2 &= 1 \\ (0.433012702)^2 + (0.491025404) + (0.566972983) &= 1 \end{align*} \]

Homozygote dominant: 18.75%
Heterozygote: 43.75%
Homozygote recessive: 37.5%
APPENDIX G

EXAMPLES OF STUDENT WORK FROM DISSERTATION STUDY

Student A

H-W Activity

What do you need to turn in?

(Each section only needs to be a few sentences)

1) Document that includes:
   a. Part 1
      i. General procedure and procedural information (A summary, be sure to define what you did, computational components, biological aspects)
         • The general procedure is to open up the excel sheet and put in the input value for the frequency of allele A. The result of changing this value is a cascade effect in which the value for the frequency for allele B is changed and the random gametes and zygotes for the chart is produced.
            ii. Results (Be sure to identify what you observed in your populations and how it related to the H-W equation and evolution, be sure to include the micro through the macro scales and include time)
               • Within the populations, the larger the value for the frequency of allele A becomes, the smaller the frequency for allele B becomes. This also affects the chart of random zygotes because, for example, if the value of allele A’s frequency is 0, then there will only be B’s present for offspring. This relates to the H-W equation and evolution because what’s produced relates to the p and q above the equation. (Allele A is p and Allele B is q).
            iii. Conclusion (Overall what did you find, how does this display evolution, what computational processes did you use, what is the input, integration, output and feedback for this model)
               • Overall, I found that this displays evolution because the less of allele A present (the frequency), the more of allele B is present. In the environment, that would mean that the trait for allele A would die out eventually. I plugged in 0.6 for the frequency which resulted in more A alleles present for the chart or integration section. The output is considered the 0.4 frequency for allele B and the feedback is the p and q values towards the bottom of the section (which relate to the allele frequencies).
      b. Part 2
         i. General procedure (what did you do to your model in part 1, provide the scenario)
         • I plugged in 0.6 for the frequency of allele A which represented the long beak (and medium beak) trait. This resulted in a 0.4 frequency for allele B.
            ii. Results (How did it change your model)
         • This changed my model by having for A alleles present in the chart and making the graph make this representation too.
iii. Conclusion (Overall what did you find from manipulating your population, how does this relate to evolution, what computational processes did you use, what is the input, integration, output and feedback for this model)

- I found that by manipulating the population, there was a cascading effect in how the other allele was presented and expressed. This relates to population because if I were to make allele A frequency equal 0, then there would be no birds with long beaks left.

*Your document should include screen shots

2) Google or Excel spreadsheet
   a. Attach the computational model that you used during the activity

Examples: https://docs.google.com/spreadsheets/d/1mmcTq4I61bqNZpTuh27URcVeuNFj5y4xVlxFdEW4_YU/edit#gid=0

**Student B:**

H-W Activity

What do you need to turn in?

(Each section only needs to be a few sentences)

1) Document that includes:
   a. Part 1
      i. General procedure and procedural information (A summary, be sure to define what you did, computational components, biological aspects) Open up the google spreadsheet. Enter the frequencies of alleles A and B to determine the individual sums of the genotypes and the total sum of the genotypes altogether. This will also automatically display the frequency of the ‘normal’ population and the second generation along with the graph will be displayed if you scroll ever further to the left of the sheet. The genotype names can be changed, and here it displays as long, short, and medium beaks. The frequencies of each individual constant in the hardy weinburg equation are displayed for G1 and G2 along with the percentages of homozygote dominant, heterozygote, and homozygote recessive in the bottom above enviromental change. Under envirommental change displays the genotype frequency of the ‘modified’ population.

      ii. Results (Be sure to identify what you observed in your populations and how it related to the H-W equation and evolution, be sure to
include the micro through the macro scales and include time) In
the populations of the birds with different lengths of beaks, I
observed that the AA alleles for long beaks are most common in
the first generation, and in the second generation AA has 7
genotypes and AB has 8 genotypes most likely due to the
interbreeding of heterozygous parents.

iii. Conclusion (Overall what did you find, how does this display
evolution, what computational processes did you use, what is the
input, integration, output and feedback for this model) Through
this display of evolution I learned the exact genotypes and values
of the constants in the hardy weinburg equation. The inputs are
gametes and their frequencies, and the outputs are genotype
counts/ frequencies/percentages in two generations, and the graphs
which show the frequency of the normal and modified populations.

b. Part 2
i. General procedure (what did you do to your model in part 1,
provide the scenario)
ii. Results (How did it change your model)
iii. Conclusion (Overall what did you find from manipulating your
population, how does this relate to evolution, what computational
processes did you use, what is the input, integration, output and
feedback for this model)

*Your document should include screen shots

2) Google or Excel spreadsheet
   a. Attach the computational model that you used during the activity

Examples:
https://docs.google.com/spreadsheets/d/18pSvxDhn8fUVDSXKqlcwwTd12N_3R7gNw3sR7d0Hgds/edit#gid=0

Student C:

H-W Activity

What do you need to turn in?

(Each section only needs to be a few sentences)

1) Document that includes:
   a. Part 1
      i. General procedure and procedural information (A summary, be
sure to define what you did, computational components, biological
aspects)

I increased the frequency of allele A from 0.5 to 0.8. This made allele B decrease to 0.2.
ii. Results (Be sure to identify what you observed in your populations and how it related to the H-W equation and evolution, be sure to include the micro through the macro scales and include time)

For my model I wanted to cut the short beaked population in half so I divided by 2. In the original model 3 AA, 8 AB, and 1 BB. After cutting the population in half the amount of birds changed to 11 AA, 5 AB, and 0 BB. Unsure about time.

iii. Conclusion (Overall what did you find, how does this display evolution, what computational processes did you use, what is the input, integration, output and feedback for this model)

I found that if the short beaked birds are cut in half, it wipes the whole population of short beaked birds. The birds will all be long beaked and a smaller percentage will carry the recessive gene. The input is the allele frequency, the output is the birds with each type of beak, the integration is the formula, and the feedback is how the genes carry on by generation.

b. Part 2

i. General procedure (what did you do to your model in part 1, provide the scenario)

Changing the frequency in generation 1 made the frequencies change in generation 2. Frequency A doubled and frequency B increased by 5 times.

ii. Results (How did it change your model)

The results show that the short beak population drastically decreases. In generation 2 there were 1 AA, 12 AB, and 3 BB. With the decrease results change to 14 AA, and 1 AB and BB.

iii. Conclusion (Overall what did you find from manipulating your population, how does this relate to evolution, what computational processes did you use, what is the input, integration, output and feedback for this model)

When cutting the population of short beaks in half it lessens the amount of short beaks in further generations and the recessive gene as well.

*Your document should include screen shots

2) Google or Excel spreadsheet

a. Attach the computational model that you used during the activity

https://docs.google.com/spreadsheets/d/1ZapHXIrOVYHo2E_wW1ttxcALSydP8dMXD-ltFTylzY/edit#

Examples:
https://docs.google.com/spreadsheets/d/18pSyxDhn8fUVDSXKqlcwwTd12N_3R7gNw3sR7d0Hgds/edit#gid=0

**Student Samples Activity 2:**
Student D:
Phylogenetic Tree Activity (BLAST):

Analysis:

For your protein consider:

1. What is the function of your protein
   The protein I chose was p53, which is a tumor suppressor that regulates the cell cycle. It is very important in fighting and preventing cancer.

2. What species in the BLAST result has the most similar gene sequence to the gene of interest?
   Gorilla Gorilla Gorilla (gorilla).

3. Where is that species located in your cladogram?
   Next to homo sapiens

4. How similar is that gene sequence?
   The gene sequence is 100% similar

5. How does BLAST actually compare these sequences (general explanation)?
   BLAST takes the sequence of one specific strand of DNA and compares it with other sequences in the database.

6. What species has the next most similar gene sequence to the gene of interest?
   Papio anubis (baboon).

7. How do the DNA relationships compare to morphology of what you would have thought about these relationships between these organisms?
   These DNA relationships prove my thoughts about the relationships between these organisms. Most of the organisms that showed up were primates, such as baboons, orangutans, and gorillas. This experiment and analysis proved that these primates are closely related to humans, which I had already assumed.

8. How else could you explore these relationships?
   These relationships can be explored further through karyotyping. Similarities and differences of genes and genetic sequences can be investigated further.

9. What other questions might you ask about your protein or the relationships
   The major question I have is, “how effective is p53 in the organism with most closely related DNA?” For example, it is clear that humans and gorillas have almost identical p53 present. But is the gorilla p53 as effective in preventing cancer, like it is in humans?

10. What is the input, integration and output used by BLAST?
    The input is the FASTA sequence, the integration is the system that BLAST uses to compare genetic sequences to others in the database, and the output is the data provided in the form of the phylogenetic tree, as well as the list that shows all sequences displayed on the tree.

What do you need to turn in?

1) Document that includes:
   a. Answers to questions 1-10, some may be more applicable to your protein than others
b. Screen shots of your exploration and phylogenetic trees

**Student E:**

Phylogenetic Tree Activity (BLAST):

Analysis:

For your protein consider:

1. What is the function of your protein
   - The tau protein regulates the important functional processes in neurons of the CNS and the peripheral nervous system.
2. What species in the BLAST result has the most similar gene sequence to the gene of interest?
   - West Indian Manatee
3. Where is that species located in your cladogram?
   - It is on the 2nd leaf count
4. How similar is that gene sequence?
   - The gene sequences are very similar
5. How does BLAST actually compare these sequences (general explanation)?
   - It lines up the sequences of the animals and it compares which chromosomes are the same and which are different.
6. What species has the next most similar gene sequence to the gene of interest?
   - Aardvark
7. How do the DNA relationships compare to morphology of what you would have thought about these relationships between these organisms?
   - I did not think that the two organisms would have been so similar but seeing that so many of their chromosomes matched up was shocking.
8. How else could you explore these relationships?
   - You could explore the relations by
9. What other questions might you ask about your protein or the relationships?
   - If the tau protein isn’t working properly, how could that have affected the peripheral nervous system?
10. What is the input, integration and output used by BLAST?
    - The input is the information that is being put into the website for analysis, integration is when the analysis is occurring, and output is the results that come from the integration.

**What do you need to turn in?**

1) Document that includes:
   a. Answers to questions 1-10, some may be more applicable to your protein than others
   b. Screen shots of your exploration and phylogenetic trees
APPENDIX H

TEMPLE IRB APPROVAL (RESULT: EXEMPTION)

Not Human Subject Research Determination

Date: 07-Nov-2019

Protocol Number: 26250

PI: NEWTON, KRISTIE

Sponsor: NO EXTERNAL SPONSOR

Project Title: Student Learning Biological Evolution Through Computational Thinking Study

On 07-Nov-2019, the IRB reviewed the protocol 26250: Student Learning Biological Evolution Through Computational Thinking Study.

The proposed activity is not research involving human subjects as defined by DHHS or FDA regulations. Consequently, Temple IRB review and approval is not applicable. You are welcome to pursue this activity, obtaining any applicable administrative or departmental (non-IRB) approvals.

This determination applies only to the activities described in this IRB submission and does not apply should any changes be made. Changes could affect this determination, therefore please contact the IRB for guidance.

DHHS Definitions:
Research - a systematic investigation, including research development, testing and evaluation, designed to develop or contribute to generalizable knowledge.

Human subject - a living individual about whom an investigator (whether professional or student) conducting research:
1. Obtains information or biopspecimens through intervention or interaction with the individual, and uses, studies, or analyzes the information or biopspecimens; or
2. Obtains, uses, studies, analyzes, or generates identifiable private information or identifiable biopspecimens.

FDA Definitions:
Research - any experiment that involves a test article and one or more human subjects, and that either: a) must meet the requirements for prior submission to the Food and Drug Administration; or b) the results of which are intended to be later submitted to, or held for inspection by, the FDA as part of an application for a research or marketing permit.

Human subject - an individual who is or becomes a participant in research, either as a recipient of the test article or as a control. A subject may be either a healthy individual or a patient.

For additional information, please see HRP-001 Policy - Definitions and HRP-421 Worksheet - Human Research on the IRB Forms & Standard Operating Procedures page.

Please contact the IRB at (215) 707-3390 if you have any questions.
APPENDIX I

SITE APPROVAL

JACKSON SCHOOL DISTRICT
151 Don Connor Boulevard
Jackson, NJ 08527
(732) 833-4601
FAX (732) 833-4791
Dr. Stephen Genco, Superintendent

October 7, 2019

Attn: Institutional Review Board
Temple University
Philadelphia, PA 19122

Re: Student Learning of Biological Evolution Through Computational Thinking Processes (Dana Christensen)

Dear Review Board,

This letter serves to give permission to Dana Christensen to complete their research project, “Student Learning of Biological Evolution Through Computational Thinking Processes” during Fall 2019 at our facility. The research project has been described to me to my satisfaction.

Sincerely,

[Signature]
Jackson Township School District
Dr. Stephen Genco
Superintendent