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**Abstract**

Embedding inquiry driven research in undergraduate courses allows integration of core concepts and competencies necessary to developing scientific thinking and lab skills. These are critical skills for undergraduates to be successful in science careers and for admission into graduate school. However, there are only a handful of examples of collaborative CUREs in Biology where students have an opportunity to connect with a network of researchers outside of their own institution, and none in the field of parasitology. In Spring 2021, we piloted a mini-CURE where student groups from University of Mary Washington and Georgia State University collaboratively completed research projects as part of a research-intensive course on Molecular Parasitology. The benefits of this approach were immediately obvious as students interacted across institutions, learned from each other’s disciplinary expertise, and informed their own research with data collected by their collaborators. It provided enrichment to the course by adding networking opportunities as well as cross-disciplinary knowledge sharing. We present here our CURE model as a way for other educators to design and implement similar cross-institutional interdisciplinary CUREs that can be modified to align with their research expertise.

**Keywords**: CURE, Graphical Abstract, Bioinformatics, Molecular parasitology, interdisciplinary, cross-institutional

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# INTRODUCTION

The benefits of Course-based Undergraduate Research (CURE) are numerous and well documented. For students at Primarily Undergraduate Institutions (PUI), these provide high-impact research experiences that can culminate in retention in STEM careers and motivation to pursue graduate level education. They provide opportunities for students to make discoveries, collaborate, engage in meaningful research and develop a sense of ownership of their lab work. For faculty, especially at PUI, these provide tractable models of modern, collaborative science and move toward the complex, interdisciplinary nature of scientific investigation as an effective platform for integrating the goals of research and education. A wide variety of successful CUREs have been developed with different research themes, however only a handful of CUREs currently prioritize on the benefits of collaborative research across institutions. Two collaborative CUREs that are widely reported and highly successful are the malate dehydrogenase CURE (Bell et al. 2020) and the HHMI SEA- PHAGES CURE (Staub et al. 2016). Our CURE, Experiential Collaborative Parasite Research across institutions (ECoPaR) provided students an opportunity to engage in a cross-institutional, cross- disciplinary research experience and effectively contribute to ongoing Kinetoplastid research. This collaboration was between students and faculty of University of Mary Washington, Georgia State University and Albright University.

# Secondary heading

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# *Tertiary heading*

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**STUDENT OUTLINE**

**Objectives**

Use bioinformatics tools

Evaluate DNA sequence variations in specific genes

Describe molecular basis for inherited diseases

**Introduction**

As first demonstrated in a classic paper by Linus Pauling and co-workers (1949), mutations in hemoglobin lead to changes in protein structure, which in turn lead to a molecular explanation for the development of an important human disease, sickle-cell anemia. Since this classic study, many other papers have described examples of mutations that lead to changes in protein structures, and which in turn lead to the development of diseases (Steward et al. 2003). Over the next few weeks, you will have the opportunity to gain, using various bioinformatics tools, a structural perspective on the molecular basis of genetically-inherited diseases. As you saw in your introductory genetics course, human genetically-inherited diseases are caused by DNA sequence variations. Although disease-causing DNA sequence variations can occur in both non-coding and coding regions of the genome, the majority of characterized mutations occur in the coding region of genes. Since they can be found in the coding region of genes, these mutations often affect the structure and function of proteins. For this laboratory exercise, we will focus on genetically-inheritable diseases that are caused by this type of mutation. More specifically, we will focus on genetically-inheritable diseases that result from a missense mutation. Recall that a missense mutation is a change in the nucleotide sequence of a gene, where one or more nucleotides is or are replaced by another. This mutation results in a new codon, which causes a different amino acid to be inserted into the growing polypeptide chain during translation. For this laboratory exercise, you will be asked to work with your laboratory partner. You and your laboratory partner will be guided in the use of various bioinformatics tools to study the effects of disease-causing mutations on protein structure and function. We will specifically focus on different levels of protein structure and how they are intimately related to one another in the formation of the final, fully-folded protein. At the end of this exercise, you and your laboratory partner will be asked to orally present your results to the other members of your laboratory session via a 10-minute Power Point presentation.

**Methods and Data Collection**

Part A: Selecting Your Topic

The first part of this project involves selecting your topic. There are eleven topics from which to select, and only one pair per laboratory section can work on each topic. So, topic selection is first come, first served. All eleven available topics are listed in Appendix A. Also included in Appendix A are the protein structure coordinates for the wild-type protein and a file with a “.pse” file name extension. You will need this file for your work with the protein visualization software PyMOL. Appendix A also contains one seed reference for each disease, to help you get started in locating background information on your topic as well as structural information and the disease-causing mutation.

Part B: Studying the Protein Structure and Physiochemical Properties

To help you complete your project, you will be guided through all of the steps using the K-Ras protein, which has been implicated in lung cancer. To make it easier for you, screenshots using the K-Ras example have been inserted in the text below.

Data Analysis

Insert text as appropriate.

**Discussion**

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**MATERIALS**

A computer with Internet access and the PyMOL program (educational version freely available for download from http://pymol.org/educational/) is required for each pair students. LCD projector and computer are required for student presentations.

Often, this section will consist of a list of materials, equipment and supplies required conduct your laboratory study with a typical class of 20-30 students. Provide vendor information and current costs as appropriate.

**NOTES FOR THE INSTRUCTOR**

One of the major challenges that we faced in implementing an inquiry-based exercise in a large class of over 500 students was to organize the exercise in a way that maximized the inquiry experience of each student without placing excessive demands on the limited time and resources of a small team of graduate teaching assistants, librarians and instructors.

Several design elements of the exercise were specifically chosen to meet this significant challenge. First, an introductory computer-based workshop session is conducted during a regularly scheduled, weekly laboratory section of the introductory biochemistry course. The relatively small groups of students in individual laboratory sections (approximately 22 students in each of 24 laboratory sections) facilitated the interactive nature of the computer- based exercises by providing opportunities for one-on-one interactions with teaching assistants and librarians, as well as peer-to-peer learning. Following this introductory session, students are given six weeks to complete the remaining self-guided exercises and to prepare their Power Point presentation, before the final student presentations.

One of the most difficult challenges facing this project was to devise a way to evaluate how students performed in the inquiry-based exercises. Since the oral presentation was designed to be the culmination of the student-initiated inquiry-based learning process, the overall performance of the students in this exercise was evaluated by marking the quality of the oral presentations for each pair of students. To standardize the evaluation of students in a large number of separate laboratory sessions, we developed a detailed marking rubric that provided specific guidance to the graduate teaching assistants regarding the grading of the final student presentations (Appendix A).

The marking rubric was carefully designed to emphasize the importance of creativity and inquiry, as opposed to a nonselective listing of information. Students were informed well in advance of their presentations that they would be marked for their creativity and the quality of their presentation, as well as for the scientific accuracy and completeness of information. As a result, students needed to master basic concepts and apply them in a meaningful way to prepare a successful presentation.

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**About the Authors**

Author's name has been an Instructor at the University of Calgary since 2006, where she teaches large courses in genetics and biochemistry, primarily at the second-year level.

**APPENDIX A**

# Mission, Review Process & Disclaimer

The Association for Biology Laboratory Education (ABLE) was founded in 1979 to promote information exchange among university and college educators actively concerned with teaching biology in a laboratory setting. The focus of ABLE is to improve the undergraduate biology laboratory experience by promoting the development and dissemination of interesting, innovative, and reliable laboratory exercises. For more information about ABLE, please visit <https://www.ableweb.org/.>

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