

Center for Global Health and Diseases

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Nord Grant Proposal - Introduce Whole Genome Sequencing and Bioinformatic Analyses to Undergraduate Students

Purpose – The goal is to introduce undergraduate students to laboratory technology used in whole genome sequencing and downstream bioinformatic analyses.

Background and Rationale - Over the past two years, the scientists assembled in this proposal have been discussing the importance of introducing whole genome sequencing and bioinformatic analyses to the CWRU undergraduate curriculum in the Biology Department, and the need to develop the capacity to enable this. Our motivation to submit this proposal stems from technology advances that have led to significant reductions in costs to generate sequence data. Confidence that we will be able to complete whole genome sequencing of targeted organisms (below) and make significant progress on bioinformatics training and data analysis comes from two years of experience gained in a pilot project with Christopher Cullis, PhD, Chair of Biology, sequencing the flax genome. In addition to Dr. Cullis, the project team includes David Serre, PhD, and Ricky Chan, PhD (Cleveland Clinic Genomic Medicine Institute); Michael Benard, PhD. and Mr. Kyle Logue (CWRU Biology Department); and Pete Zimmerman, PhD (CWRU Center for Global Health & Diseases, and Biology Department).

Initially, the proposed course work can be carried out in the context of an existing Biology Department course (BIOL 301, Biotechnology Laboratory: Genes and Genetic Engineering, 3 Units). Currently BIOL 301 offers laboratory training in recombinant DNA techniques. Students isolate and characterize DNA, construct recombinant DNA molecules, and reintroduce them into eukaryotic cells (yeast, plant, animal) to assess their viability and function. Prerequisites for this course include BIOL 214 and 214L, the first of three Biology major requirements that introduce biological molecules (focus on DNA and RNA), cell cycles, gene expression, genetics, population genetics, evolution, biological diversity and ecology.

A variation of BIOL 301, and ultimately one or more new courses, would offer laboratory training in recombinant DNA techniques that lead to the complete sequencing of an organism's whole genome and/or transcriptome (expressed gene sequences) and an introduction to basic skills in bioinformatics. This opportunity to study all the genes and potentially analyze how they are expressed offers a comprehensive glimpse at an organism's biology, far beyond the conventional undergraduate lab experience. Further, as it is estimated that the global bioinformatics market is poised to reach \$9.1 billion by 2018 (sustained compound annual growth rate over 20%), the Bureau of Labor and Statistics anticipates growth in the field to stem from research and development in biotechnology, specifically in the areas of gene identification and sequencing. Therefore, to prepare our undergraduate students for

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career opportunities in this growing and innovative sector of the job market it is crucial that we develop training capacity that will provide access into this expanding field.

Needs Assessment Undergraduate Instruction – Presently, there are no courses in the undergraduate curriculum that teach bioinformatics or enable students to gain the necessary proficiencies to perform meaningful bioinformatic analyses. This creates new problems for traditional Biology Departments, as existing faculty members are not prepared to instruct courses that will teach the basic skills and concepts needed to support these academic research and biotechnology communities.

To address these needs, we have developed the working group (above) to develop whole genome sequencing capacity and bioinformatics (Serre, Chan & Logue). We have also identified a number of model and not-so-model organisms already used by CWRU Biology Department faculty that provide interesting and meaningful whole genome sequencing opportunities. They include the cockroach (*Blaberus discoidalis*) used by Roy Ritzman, PhD and the sea slug (*Aplysia californica*) used by Hillel Chiel, PhD in their neurophysiology and locomotion studies; the Wood frogs (*Rana sylvatica*) used by Michael Benard, PhD and the invasive garlic mustard (*Alliaria petiolata*) studied by Jean Burns, PhD in their ecology and evolution studies.

None of these organisms have attracted attention of genome sequencing projects to date, but genome sequencing has significant potential to contribute to dozens of undergraduate research projects aligned with each of the faculty member's laboratories. As a result, we believe that juxtaposing an undergraduate course with Biology Department labs and faculty research will also create new relationships between the classroom and the academic research laboratories. Therefore as this initiative evolves, we will be interested to observe how this project influences the traditional relationships between the classroom and laboratory. Traditionally, the lab provides new insights and opportunity to classroom, in the proposed project, the classroom potentially generates preliminary data for new and interesting opportunities for the laboratories.

Sincerely,

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