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Persistence in the SEA of bioinformatics with phage genome annotations

Michèle Barmoy[1]

[1]Allegany College of Maryland, Science Department, 12401 Willowbrook Road, SE, Cumberland, MD, 21502, USA

Abstract

SEA-PHAGES (Science Education Alliance – Phage Hunters Advancing Genomics and Evolutionary Science) is a two-semester CURE (Course-Based Undergraduate Research Experience) that begins with simple digging in the soil to find new viruses, but progresses through a variety of microbiology techniques and eventually to complex genome annotation and bioinformatic analyses. The first semester is the discovery phase of SEA-PHAGES, ending with the extraction and characterization of phage DNA. The second semester is the bioinformatics semester. That will be the focus of this poster. Bioinformatics uses computers to understand biological data. It is a field that is rapidly becoming a critical component in all areas of biology and medicine – from ecologists who study populations and migration patterns to epidemiologists who study emergent diseases and assess threats to public health. At the most basic level, the field of bioinformatics is about recognizing patterns. We use bioinformatics in the SEA-PHAGES semester to find patterns in the sequence of nucleotides in a phage's genome, so we can predict where genes are located and better understand phage genetics. Students work in groups of two or three, each backchecking the other. Later, students work in larger groups, again checking each other. Students use their genome to manipulate genomic tools (DNA Master, GeneMark, Glimmer, BLAST, Phamerator, HHpred, Starterator, PECAAN) and practice calling genes and functions. Students then investigate the types of genes they come across and produce a quality genome annotation. The final project in the course consists of a poster presentation. Sample student posters are included in the poster.

Keywords: gene annotations, SEA PHAGES

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Correspondence to: **Michèle Barmoy, mbarmoy@allegany.edu**

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