

GENI and GENI-ACT Projects Provide Authentic Undergraduate Research Experiences in Genome Analysis

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Extended Abstract

The Genomics Education National Initiative (GENI; <http://www.geni-science.org/>) project has partnered with the Microbial Genome Annotation Network (MGAN; <http://mgan-network.org/index.html>) to create an online toolkit that consolidates publically available bioinformatics tools into a single platform for the purpose of providing an authentic research experience in microbial genome annotation to undergraduates and high school students. Previously known as the DOE Joint Genome Institute's IMG-ACT (Ditty *et al.*, 2010), the GENI Annotation Collaboration Toolkit (GENI-ACT; <http://www.geni-act.org/>) builds on the capabilities of the previous toolkit by: 1) expanding to include access to all sequenced genomes in GenBank; 2) allowing for public dissemination of student work; and 3) allowing for multi-instructor collaborations. As a follow-up to gene annotation studies, the GENI project provides detailed instructions for subsequent functional genomics studies, which is the wet-lab complement to the bioinformatics analysis. MGAN provides training workshops for the GENI-ACT platform. This poster describes the GENI and GENI-ACT projects, faculty resources to obtain training in the bioinformatics platform, and faculty development opportunities that will help instructors develop a personal research program.

Defining Gene/Genome Annotation and Functional Genomics

Gene annotation is the process of using computer technology to predict a biological function for a gene or region of a chromosome. There are many different bioinformatics tools currently available, which makes choosing among them a daunting task for a novice annotator. Functional genomics is the process of performing wet-lab experimentation to confirm the function predictions. GENI and GENI-ACT make it easier to implement an authentic research experience in genome analysis by providing training and faculty resources.

Three Steps to an Authentic Research Experience in Genome Analysis Using GENI-ACT and GENI.

In *Step 1*, the instructor or students identify a microbe whose genome has been sequenced, but for which little published work is available. A good starting point is with the databases called Integrated Microbial Genomes (IMG; <http://img.jgi.doe.gov/>) or National Center for Biotechnology Information (NCBI; <http://www.ncbi.nlm.nih.gov/>). Many genomes identified in IMG as belonging to the Genome Encyclopedia of Bacteria and Archaea (GEBA; <http://jgi.doe.gov/our-science/science-programs/microbial-genomics/phylogenetic-diversity/>) project are relatively unstudied. In *Step 2*, either the instructor or the student chooses an annotation approach. A few of the annotation questions that one might ask using GENI-ACT are these:

- An initial automated gene call is made following sequencing. Is the automated gene call accurate?
- Have the genes in a particular region of a chromosome been accurately called?
- Does an organism-of-interest possess the genes for a particular pathway, process or cellular structure?
- What is a predicted function of a gene identified as coding for a “hypothetical” protein?
- Does a particular gene in a genome-of-interest show evidence of horizontal gene transfer?

A myriad of other questions can be asked that utilize some or all of the bioinformatics tools associated with GENI-ACT. In *Step 3*, students collect experimental evidence to support the function prediction. For example, the GENI project provides faculty with most of the biologicals needed for the complementation assay. In this protocol, a mutant *E. coli* strain lacking only the *E. coli* gene that is predicted to have the same function as the gene-of-interest is transformed with the expression plasmid containing the gene from the organism-of-interest. Using auxotrophy as the assay for the function of the missing gene, students evaluate the ability of the gene-of-interest to restore function to a wild type phenotype. Several recent publications demonstrate the feasibility of using the GENI-ACT platform as the cornerstone of an authentic research project (Beagley, 2013; Ditty *et al.*, 2013; Reed *et al.*, 2013; Shapiro *et al.*, 2013). Additional examples of single and multi-institution genome analysis projects can be found at the MGAN website, which includes samples of student work and a detailed protocol for identifying suitable project questions.

Hurdles in Implementing a Genome Analysis Project

The biggest hurdle in starting a genome analysis project is finding faculty development opportunities. Get training in the use of the GENI-ACT platform through MGAN, which provides regional training workshops for 10 or more participants. Workshops are free of charge, and workshop facilitators will come to your region within the US. Travel awards, funded by an NSF RCN-UBE award (DBI 0954829), are available on a competitive basis to attend workshops outside of your home region. Contact Lori Scott at loriscott@augustana.edu for more information on MGAN workshops and travel awards. Contact Brad Goodner at GoodnerBW@hiram.edu for information about an upcoming functional genomics workshop in the summer of 2015 at Hiram College, OH. Contact Katie Houmiel at houmik@spu.edu for instructional resources associated with GENI.

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