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An Authentic Undergraduate Research Experience that Combines Genome Annotation and Functional Genomics

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Expanded Abstract

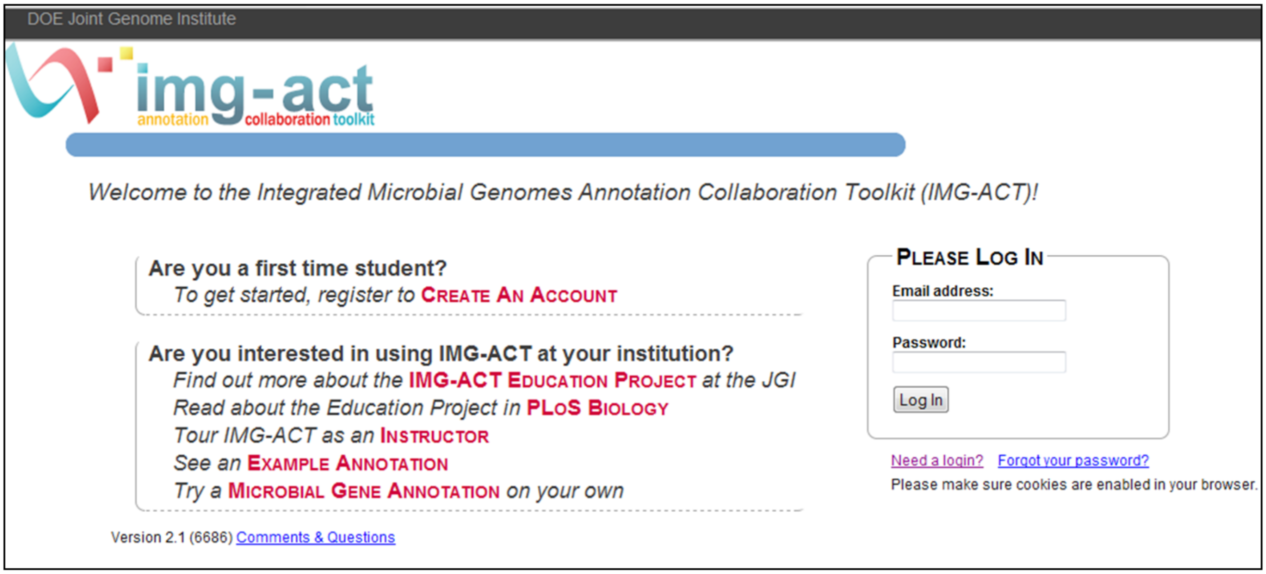
Genome analysis is on the forefront of genetic research. It has implications for advances in basic research, medicine, agriculture, justice, environmental science and archaeology. One strategy to study genomes is called genome annotation, which is subdivided into three stages: 1) using computer technology (*a.k.a.* bioinformatics) to predict functional elements within an organism's genome; 2) using computer technology to predict the biological function of those elements; and 3) providing evidence from benchtop research to support the functional predictions (a.k.a. functional genomics). The frustrations for undergraduate educators who wish to incorporate genome annotation and functional genomics into their courses and research are: 1) choosing from the myriad of different online bioinformatics tools available; 2) becoming proficient in the applicable technologies; and 3) giving students the opportunity to hone their developing genome annotation skills in a real-world setting where their results matter.

To address these issues, the Joint Genome Institute (JGI) of the U.S. Department of Energy, working with undergraduate teaching faculty from across the country, developed the Interpret-a-Genome Education program and its companion Integrated Microbial Genomes Annotation Collaboration Toolkit (IMG-ACT) (Ditty *et al*., 2010). As a participant of the Interpret-a-Genome program, faculty members interpret one or more prokaryotic genomes available through the Integrated Microbial Genomes database (IMG). The available genomes include the first 56 genomes completed as part of the JGI Genomic Encyclopedia of Bacteria & Archaea (GEBA) project (Wu *et al*., 2009; **www.jgi.doe.gov/education/genomeannotation.html**). All bacterial genomes are full of novelties. However, the GEBA organisms are relatively unusual and from under-studied branches of the tree of life, so there is a greater likelihood of exciting discoveries and interesting variations on classical pathways.

IMG-ACT is a course management and bioinformatics analysis platform that allows interpretation and deeper annotation of user-selected genomes within diverse course and curriculum settings. Prospective users of the IMG-ACT can tour the IMG-ACT website as an instructor, see a sample annotation and try an annotation from the IMG-ACT login page (Fig. 1). Using IMG-ACT, faculty members can assign genes to individual students or groups of students for analysis using one or more of nine annotation modules (*e.g.*, predicted cellular localization of encoded protein) and monitor student progress. Figure 2 illustrates the diversity of courses within which gene annotation using IMG-ACT could be integrated. For example, in introductory biology courses students will work with bioinformatics programs that use the concepts of the central dogma, gene structure and function, protein localization, and evolution; students in biochemistry courses can annotate fundamental metabolic pathways; in microbiology, pathways, structures, and systems characteristics of the organism's lifestyle will be traced; and in numerous courses, novel genes and pathways can be discovered by examining clusters of hypothetical proteins in a comparative genomics context (that will include phylogenetic profiling and ecological considerations).

Through their genome annotations, students will experience first-hand the process of scientific inquiry and reinforce basic biological concepts such as gene structure, protein structure and function, gene homology, sequence similarity, protein localization, genome organization, gene regulation, and evolution of genes and genomes. Students will also learn how various bioinformatics tools are connected to basic aspects of gene and protein structure/function as well as how to interpret a wide range of quantitative information (Fig. 3).

To help faculty across the U.S. and abroad get acquainted with using IMG-ACT in a course setting, a group of early adopters worked with JGI to develop a professional development program called the Microbial Genome Annotation Network (MGAN at **http://mgan.jgi-psf.org/**). MGAN is supported by a NSF Research Collaboration Network grant and can help instructors in one of two ways. One, travel grants are available to support the travel of an individual faculty member to attend the IMG-ACT training session held annually at JGI headquarters in Walnut



DOE Joint Genome Institute

img-act annotation collaboration toolkit

Welcome to the Integrated Microbial Genomes Annotation Collaboration Toolkit (IMG-ACT)!

Are you a first time student?
To get started, register to **CREATE AN ACCOUNT**

Are you interested in using IMG-ACT at your institution?
Find out more about the **IMG-ACT EDUCATION PROJECT** *at the JGI*
Read about the Education Project in **PLOS BIOLOGY**
Tour IMG-ACT as an **INSTRUCTOR**
See an **EXAMPLE ANNOTATION**
Try a **MICROBIAL GENE ANNOTATION** *on your own*

PLEASE LOG IN
Email address:
Password:
Log In

Need a login? Forgot your password?
Please make sure cookies are enabled in your browser.

Version 2.1 (6686) Comments & Questions

Figure 1. From the IMG-ACT login page, educators can learn more about this resource and the annotation process. This page is available at the IMG-ACT login page **http://img-act.jgi-psf.org/user/login**.

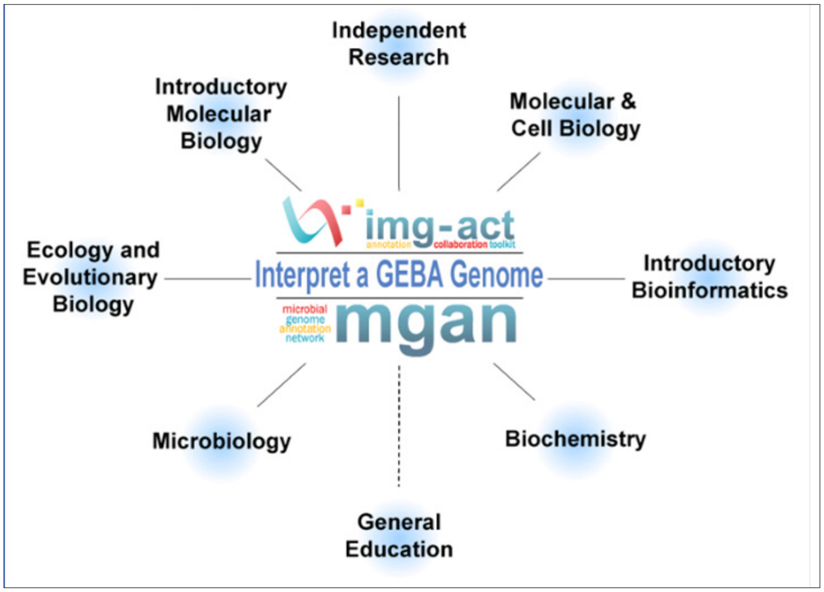


Figure 2. The Interpret-a-Genome project can be incorporated into diverse courses and across the curriculum.

Creek, CA. Two, a group of at least 10 faculty members at nearby institutions can request a regional training workshop; grant funds will support the travel of MGAN trainers to conduct an IMG-ACT workshop over a weekend. Additional information about training options can be found at the DOE/JGI's Interpret-a-Genome website (**www.jgi.doe.gov/education/genomeannotation.html**) or the MGAN website (**http://mgan.jgi-psf.org/**).

In this mini workshop, participants: 1) used a sampling of the bioinformatics tools within IMG-ACT to annotate a putative gene from the *Meiothermus ruber* genome, which is the adopted organism of the *Meiothermus ruber* Genome Annotation Project; 2) received information about the JGI-sponsored IMG-ACT training workshop and the opportunity to apply for travel grants from the NSF-funded Microbial Genome Annotation Network; and 3) received information about the resources available through the Genomics Education National Initiative (GENI) as one option for the functional genomics component of gene annotation (**http://geni-science.org/**). All the resources provided at this workshop can be found at the website created for this workshop (**https://sites.google.com/a/augustana.edu/able2011/**).

Literature Cited

Ditty, J., C.A. Kvaal, B. Goodner, S.K. Freyermuth, C. Bailey, R.A. Britton, S.G. Gordon, S. Heinhorst, K. Reed, Z. Xu, E.R. Sanders-Lorenz, S. Axen, E. Kim, M. Johns, K. Scott, & C.A. Kerfeld. 2010. Incorporating genomics and bioinformatics across the life sciences curriculum. *Public Library of Science (PLOS) Biology* 8(8): e1000448.

Wu, D., P. Hugenholtz, K. Mavromatis, R. Pukall, E. Dalin, N.N. Ivanova, V. Kunin, L. Goodwin, M. Wu, B.J. Tindall, S.D. Hooper, A. Pati, A. Lykidis, S. Spring, I.J. Anderson, P. D'haeseleer, A. Zemla, M. Singer, A. Lapidus, M. Nolan, A. Copeland, C. Han, F. Chen, J-F. Cheng, S. Lucas, C. Kerfeld, E. Lang, S. Gronow, P. Chain, D. Bruce, E.M. Rubin, N.C. Kyrpides, H-P. Klenk, & J.A. Eisen, 2009. A phylogeny-driven genomic encyclopedia of bacteria and archaea. *Nature* 462:1056-60.

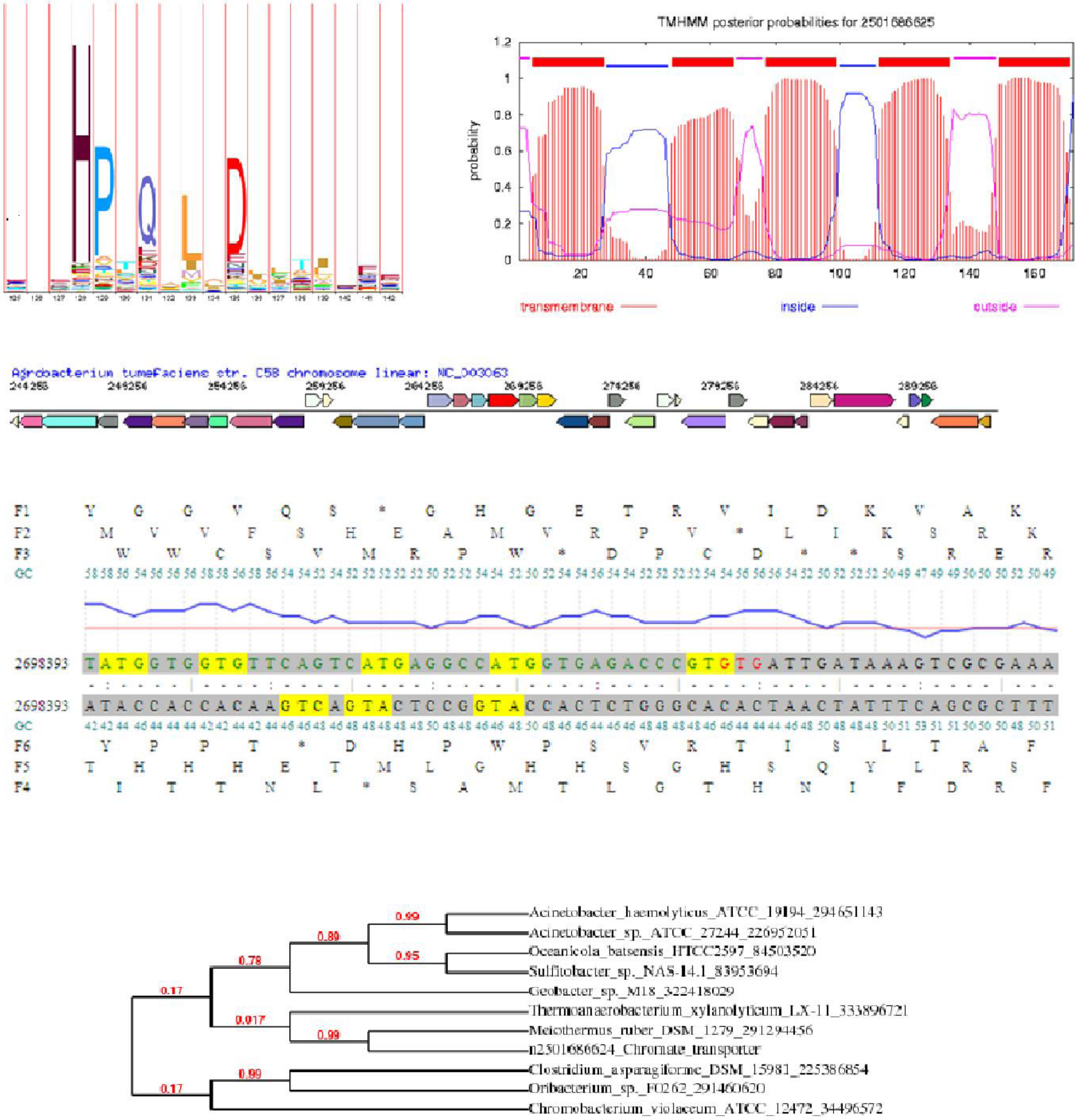


Figure 3 (Panels A-E). Using the IMG-ACT platform, students collect and then interpret data from bioinformatics programs such as BLAST, Pfam,/HMM logo (A), TMHHM (B), IMG 6-frame viewer (C), IMG gene neighborhood viewer (D), T-Coffee, and phylogeny.fr (E), to name a few.

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