

THE UNDERSTANDING AND ANALYSIS OF GENOMES

Since the completion of the Human Genome project in April 2003, the genomes of many different organisms have been sequenced. Prokaryotes are organisms that have smaller genomes that lack introns, making the analysis of their genomes simpler than in eukaryotes. Marine bacteria is a group of prokaryotic organisms not very well known up to now, but recent studies of their genome have shown indications of the importance of these organisms in our environment. In this module we will use genomes of several marine bacteria to teach students how genomes are analyzed.

In this module students will:

- a) be introduced to a genome project
- b) get an overview of how genomes are sequenced
- c) learn about Bioinformatics
- d) be able to perform gene annotation
- e) connect and review learned material

This module is covered in five days; each day will consist of a different activity.

Day 1

1. Students will be introduced to the Human Genome Project using a 5 minute video from the National Human Genome Research Institute “Exploring our molecular selves” www.genome.gov/25520211
2. Student will follow the essential steps in sequencing a genome presented in “How to sequence a genome” (NHGRI) www.genome.gov/25019885, following the guidelines in “How to Sequence a Genome” [handout](#)

3. Students will read the information presented in the link “Bioinformatics” www.genome.gov/25019999 and will answer the questions on the reading guide [handout](#)

Day 2

1. Students will construct a graphic organizer using the words in the glossary of the Bioinformatics link from www.genome.gov/25019999 to show their understanding of Bioinformatics.
2. Students will use glossary words to play the “genetic mind reader review” (see www.genome.gov/10506354).

Day 3

1. Using the Campbell CD, students will review the three steps of cellular respiration in detail.
2. Students will make a list of enzymes found in three major metabolic pathways: Glycolysis, Citrate Cycle, and Oxidative Phosphorylation. A class list will be generated.
3. In small groups, students will choose an enzyme from one of these pathways and research it using the KEGG web site (www.genome.jp/kegg/; Kyoto Encyclopedia of Genes and Genomes)
4. Students will become familiar with the KEGG website [KEGG.doc](#)
5. Students will learn how to use BLAST [handout](#)

Day 4

1. Students will access the genomes of seven species of bacteria using the Roseobase web site (www.roseobase.org/blast/APBio.html).

2. Students will work in groups that will be assigned a bioinformatics project for different species of marine bacteria. Students will perform gene annotation for the enzymes present in the glycolysis, citrate cycle, and oxidative phosphorylation pathways for their species of bacteria.
3. A class table will be generated based on the following data collected by the student groups for each enzyme in the three pathways: E.C. # - Name of Enzyme – Name of Organism – E value. Students will compare data to a reference table ([pathway.xls](#)).

The final class table will be used as the assessment for this module. The data collected by the students will show that the students know how to use bioinformatics tools and the interpretation of their data will show their understanding of the process.

Day 5

At the end of this module associations will be made with other biological topics ([handout](#)).