Genes and ConSEQUENCES: Using Genetic Databases

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Overview

In the fast-paced world of genetic research, scientists around the world are generating a tremendous amount of DNA sequence data. During the Human Genome Project, a public database was created to store, analyze, and search the sequence data. This database, housed at the National Center for Biotechnology Information (NCBI), constantly grows and changes as new chunks of data are added. In this lab, students will interpret a section of DNA sequence and access a component of NCBI known as the BLAST program, to compare their sequence to gene segments contained in the database. Students will then explore their gene matches on another NCBI database called Genes and Disease. Students will determine the location of the gene and the role of that gene in disease. Throughout this process, concepts related to the central dogma of molecular biology will be reinforced.

Note: This kit is not designed to serve as a tool for comprehensive instruction in database use but to provide students with an overview of the types of resources available for scientists in the field of genetics, and to give students real-world examples of the complexity of genetic interactions.

Objectives

Students will

- use specific examples to explain the major components of the central dogma.
- define *bioinformatics*.
- use a sequence of DNA to generate an mRNA strand and a polypeptide chain.
- decipher an electropherogram.
- explore the use of the NCBI database as a source of biological information.
- perform an NCBI database search with a given sequence of DNA in order to identify the gene name, chromosome number, location on a chromosome, and possible disorders associated with variant forms of the gene.
- relate changes (mutations) in DNA to disease processes.
- understand the significance of the Human Genome Project and describe how knowledge gained during the project impacts both the present and the future of genomics and medicine.

Content Standards

To view the national and local standards met by this kit, visit **www.carolina.com/correlations**.

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Time Requirements

Preparation . . . . . .15 minutes

Day 1: Gene Book . . . . . .45–60 minutes

Introduction to DNA sequencing and bioinformatics

- Have students read the background information in their handout and answer the pre-lab questions.

Creating the GeneBook

- Have students construct GeneBooks, using the template provided. Additional directions are included in the Procedure section of the Teacher's Guide.

Central Dogma meets bioinformatics

- Direct students to use electropherograms to decode the sequence of nucleotides for "My Sequence." From this sequence, generate the "My Complement," "My Transcript," and "My Sequence of Amino Acids."
- Review major concepts of the central dogma.

Patient Analysis

- Direct students to use the Case Study Cards to generate a "My Patient's Sequence," "My Patient's Transcript," and "My Patient's Amino Acid Sequence."

Day 2: NCBI . . . . . .45–60 minutes

Bioinformatic research on patient

- Discuss the Human Genome Project and how the data from the project is organized into databases.
- Students use computers to perform BLAST searches and additional research in NBCI databases to complete the information for their study guide.
- Lead a summary discussion of the kinds of information in biological databases and the uses of such information. Answer the Post-lab Questions.

Optional Teaching Pathways

This lesson is designed for use in a variety of classroom settings. The teacher protocol is written as a culminating activity for a central dogma unit and is designed for two 60-minute periods. To accommodate alternative schedules, timing for each section is included. If the class is scheduled on a block format (90-minute segments), the following modifications may be made:

- Distribute and discuss Background information and questions during class time.
- Transcribe and translate patient sequences during class time.
- Move discussion of genes and alleles, NCBI, the Human Genome Project, and Bioinformatics to Day 1.
- Have students conduct independent online research on their assigned genetic disorder.