Cold Spring Harbor Laboratory
DNA Learning Center

High School Field Trips

The DNA Learning Center (DNALC) is a unique educational resource—the nation's first facility dedicated to improving DNA science education. In our modern teaching laboratories, DNALC staff stresses an interactive approach linking the process of discovery to learning. Students perform key techniques used by genetic engineers. Laboratory protocols were developed by Cold Spring Harbor Laboratory's DNA Literacy Program and have been performed by thousands of teachers and students.

The following laboratory experiences will be offered for 2024-2025. The **DNA Fingerprint** lab is an introductory lab appropriate for classes that want to work with DNA but have little or no experience in molecular biology. **DNA Restriction Analysis** and **Bacterial Transformation** are required by the Educational Testing Service as part of the Advanced Placement Biology Curriculum, and provide students of many levels with an extensive hands-on laboratory experience. The **Detecting a Jumping Gene**, **Human Mitochondrial Sequencing,** and **Forensic DNA Profiling** labs allow students to view their own DNA.

DNA Fingerprint

(Lab time: 2 hours)

Human DNA is more alike than different, so how do we find the differences? Restriction enzymes are proteins that recognize specific DNA sequences and can be used to determine whether a particular DNA sequence is present. In this lab, DNA from "evidence" and "suspects" will be compared using restriction enzyme digest and agarose gel electrophoresis. DNA analysis will then be combined with crime scene data to draw conclusions about each suspect.

DNA Restriction Analysis

(Lab time: 3½ hours)

The DNA restriction analysis experiment demonstrates that DNA can be precisely manipulated with enzymes that recognize and cut specific target sequences. In this lab, restriction enzymes—the scissors of molecular biology—are used to digest DNA from the bacteriophage lambda. After cutting, the DNA fragments are visualized by agarose gel electrophoresis, allowing students to identify a "mystery" enzyme through comparison with controls.

Bacterial Transformation

(Lab time: 2½ hours)

The bacterial transformation experiment illustrates the direct link between an organism's genetic complement (genotype) and its observable characteristics (phenotype). Two genes, for antibiotic resistance and luminescence, are introduced into the bacterium *E. coli*. Following overnight incubation, transformed bacteria are compared to non-transformed bacteria for their ability to grow in the presence of ampicillin and glow when exposed to ultraviolet light.

Detecting a Jumping Gene (formerly Human DNA Fingerprinting)

(Lab time: 4 hours, guardian consent required*)

This lab examines a region of DNA from chromosome 16 that can contain a short nucleotide sequence called Alu within a noncoding region of the chromosome. *Alu* insertions are segments of DNA that "jump" around in the genome. Students will prepare a sample of their own DNA from cells obtained by saline mouthwash, use PCR to amplify the targeted locus, and agarose gel electrophoresis to determine the presence or absence of this *Alu*, which jumped into the chromosome tens of thousands of years ago. Back at school, class data can be used as part of an exploration of allele frequencies and population genetics and to identify classmates who are related.

Human Mitochondrial Sequencing

(Lab time: 4 hours, guardian consent required*)

Comparison of the control region within the human mitochondrial genome reveals that people have distinct patterns of single nucleotide polymorphisms (SNPs). These sequence differences, in turn, are the basis for far-ranging investigations on human DNA diversity and the evolution of hominids. In this lab, students prepare a sample of their own DNA from cells obtained by saline mouthwash, use PCR to amplify a section of their own mitochondrial DNA and agarose gel electrophoresis to confirm the result. DNA is then sent for sequencing, and results are uploaded to the DNALC's *BioServers* website. Back at school, students can perform bioinformatic analysis of their own DNA sequences to explore the theories behind how modern humans evolved and how related they are to their classmates and people from around the world.

Forensic DNA Profiling

(Lab time: 4 hours, guardian consent required*)

This lab examines a highly variable tandem repeat polymorphism on chromosome 1 called D1S80, similar to what the FBI uses to create a genetic profile. Students will prepare a sample of their own DNA from cells obtained by saline mouthwash. After amplification by PCR, the improved size resolution of a DNA chip allows students to identify their genotype, something impossible with traditional agarose gel electrophoresis. This is an advanced lab, appropriate for classes with some background in molecular biology and genetics.

*Participation in this lab requires a signed consent form (provided by the DNALC) from the parent/guardian of students under 18 years of age

Cold Spring Harbor Laboratory
DNA Learning Center

Bioinformatics: *Using* Alu *Insertions to Study Population Genetics*

(Lab time: 2 hours, Grade 10+)

Students will learn about *Alu* insertions—segments of DNA that "jump" around in the genome—and use real population data to study variation in alleles, calculate allele frequencies, and examine Hardy-Weinberg equilibrium in populations. Computer simulations will be used to model genetic drift.

Bioinformatics: *Tracing Human Evolution*

(Lab time: 2 hours, Grade 10+)

Students will analyze mitochondrial sequence data to test models of human evolution. Were Neanderthals direct ancestors of modern humans? Did we all arise from a single founding population in Africa? Students will be guided through *BioServers* and DNA Subway to help answer these questions and more!

Bioinformatics: *Barcoding & Phylogenetics*

(Lab time: 2 hours, Grade 11+)

Phylogenetics is the practice of determining the evolutionary relatedness of groups of organisms. Much of this work is done utilizing DNA data. In this lab activity, students will learn about different methods of building phylogenetic trees and practice building them using both morphological and genetic data. Students will use sample data on the bioinformatics platform *DNA Subway* to compare species and build phylogenetic trees.

Standard and Bioinformatics Lab Reservation Details

- Forensic DNA Profiling, Human Mitochondrial Sequencing, Detecting a Jumping Gene are restricted to students in 10th, 11th, or 12th grade.
- Using *Alu* Insertions and Tracing Human Evolution labs are restricted to students in 10th grade and up, and Barcoding & Phylogenetics is restricted to 11th or 12th grade.
- The group rate is **$600** for classes up to 24 students, **$750** for classes of 25–32 students.
- Unless other arrangements have been made in advance, all labs begin promptly at 9:30 AM.
- Download laboratory protocol PDFs, teacher prep, and standards alignments at https://dnalc.cshl.edu/programs/fieldtrips/hsschool.html

To make a reservation go to:

https://dnalc.cshl.edu/programs/fieldtrips/field-trip-reservations.html

Cold Spring Harbor Laboratory
DNA Learning Center

Advanced Inquiry Labs

Advanced Inquiry labs are for AP, advanced elective, or research classes looking for a wet-lab experience that includes extended analysis of data. While performing open-ended experiments to detect DNA variations in themselves and other organisms, students have time to explore the use of online bioinformatics tools to analyze DNA. Labs include use of Basic Local Alignment Search Tool (BLAST), DNA sequence alignments, construction of phylogenetic trees, and population simulations.

Detecting Genetically Modified Foods (Lab time: 6 hours)

Genes that encode herbicide resistance, insect resistance, drought tolerance, frost tolerance, and other traits have been added to many commercial plants—including most of the corn and soybeans grown in the United States. In this laboratory, students isolate DNA from plant tissue and processed food products. Then, polymerase chain reaction (PCR) and gel electrophoresis are used to identify a promoter that drives the expression of most plant transgenes. During the lab, bioinformatics tools allow students to predict the outcome of the experiment and discover genes and functions transferred into GM plants.

*Using a SNP to Predict Bitter Tasting Ability ** (Lab time: 6 hours)

The ability to taste the bitter compound PTC (phenylthiocarbamide) is often used to illustrate Mendelian inheritance. Three SNPs (single nucleotide polymorphisms) in the gene encoding the PTC taste receptor strongly affect tasting ability. In this experiment, students extract DNA from cheek cells and use PCR to amplify a short region of the gene. After a diagnostic restriction digest, student genotypes are scored on an agarose gel, allowing them to predict their phenotypes. Students then test their tasting ability and compare genotypes and phenotypes, allowing them to discover that PTC tasting is genetically more complex than the model. This experiment is a close analog to how precision or personalized medicine uses genotypes to predict drug response.

Using DNA Barcodes to Identify and Classify Living Things (Lab time: 6 hours)

Just as unique universal product codes (UPC) identify products, unique "DNA barcodes" use specific DNA sequences to identify living things. In this laboratory, students use DNA barcoding to identify plants, fungi, or animals—or products containing them. DNA is extracted from samples, the barcode region is amplified by PCR, and the PCR product is sequenced. *DNA Subway*, our bioinformatics website, is used to search a DNA database for close matches to sample sequences and to construct phylogenetic trees that show evolutionary relatedness. Students have the option of bringing in their own samples to test, providing the opportunity for mini-projects to sample local environments or to test food products.

Using an Alu *Insertion Polymorphism to Study Human Populations ** (Lab time: 6 hours)
(extension of *Detecting a Jumping Gene*)

The DNA from any two people varies at many sites. These polymorphic sequences that make each person's DNA unique are used in the study of human evolution. This experiment examines a polymorphism that is caused by the insertion of an *Alu* transposon, the most common DNA sequence in the human genome. DNA is extracted from student cheek cells, and PCR is used to amplify the region containing the *Alu* insertion site. Students score their genotypes on an agarose gel, and the compiled class results are used as a case study in human population genetics. On the *BioServers* Internet site, students use tools to test Hardy-Weinberg equilibrium, explore the geographic distribution of the insertion in world populations, and simulate the inheritance of a new *Alu* insertion.

*Participation in this lab requires a signed consent form (provided by the DNALC) from the parent/guardian of students under 18 years of age.

Advanced Inquiry Reservation Details

- 8:30 a.m.–2:30 p.m. (6 hours)
- The group rate is **$800** for classes up to 24 students, **$950** for classes of 25–32 students.

To make a reservation go to: https://dnalc.cshl.edu/programs/fieldtrips/field-trip-reservations.html