

Pick any two individuals at random and their genomes (DNA sequences) are estimated to differ by approximately 1%. Such sequence variations are known as polymorphisms, which are useful to study evolutionary relationships, mechanisms of disease, and identity testing. Interestingly, many known polymorphisms reside in regions of the human genome that do not encode for proteins. Students in the bioinformatics/genome science camp will examine and analyze an example of a human polymorphism both in the laboratory and through computation.

Students will do the following in camp:

Extract and isolate DNA from your own cells

Use PCR to amplify a specific region of your genome

Use gel electrophoresis to visualize and analyze the PCR products

Use restriction enzyme digestion to analyze DNA

Use the Basic Local Alignment Search Tool (BLAST) to identify sequences in databases

Use CLUSTAL W algorithm to perform multiple sequence alignments

Use Map Viewer tool to visualize genes on chromosomes