

Next Gen Science: Origami of life with Bioinformatics

Venue: Seattle Pacific University

Pick any two individuals at random, 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