

Bioinformatic Programming

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In the programming aspects, Python will be introduced and how it is important to learn today. How to use Python and its library Biopython to do the alignment of DNA sequences. How to use the library for comparing genes with N number of mismatches. There will be a hands-on session on HLA software, **Tulita** will be used in the training to show gene mapping in general and HLA typing in particular. I will talk about all the file format and how the aligned sequences are stored. How this information can be used to find the SNPs, insertions, and deletions. How to create consensus sequence and allele calling and Haplotype segregation. At the end of the session, I will also talk about how a non-biology person can contribute to genomics and how a biology person can become a programmer and work on many Bioinformatics problems.