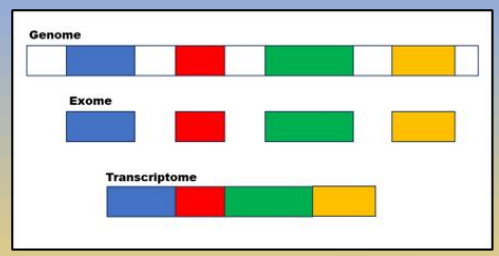
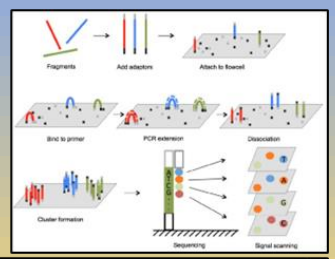
Hands-on workshop
on
Exome sequencing and Data analysis

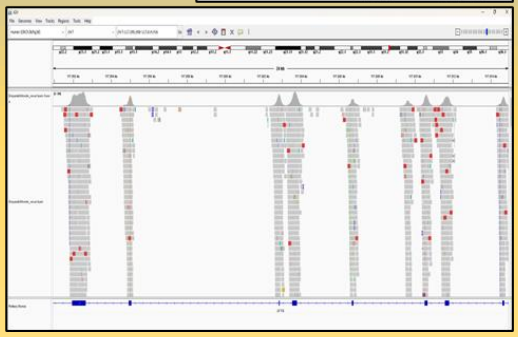
29th April – 3rd May 2024

Centre for DNA Fingerprinting and Diagnostics, Hyderabad

Single Nucleotide variants (SNVs) are genomic rearrangements that lead to genetic disorders. The SNVs in a small gene are easy to identify by Sanger sequencing. However, the SNVs in the large genes and novel variants can be best identified by Exome sequencing. The Sequencing by Synthesis chemistry helps in the generation of short reads in greater depth which can identify all types of SNVs very easily.







This workshop aims to introduce the technology and hands-on experience for the diagnosis of Single nucleotide Variants and Transcriptome analysis by using Short-read sequencing

HANDS-ON TRAINING IN

Pre-Sequencing

- **Exome Library Preparation**

Sequencing

- **Sequencing by NextSeq 2000**

Post-Sequencing

- **NGS Analysis Pipeline**
- **Exome Data analyses from vcf files**
- **Transcriptome analysis**
- **IGV visualization**
- **Case-based discussions**

WHO CAN APPLY?

Young Scientists, Medical professionals, and Students with minimum qualification of MSc/ PhD/ MBBS

Last date for application:
15th March 2024

Selection process: 30 participants would be selected based on screening of applications and writeup

CONTACT INFORMATION:

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