Training Programme in NGS data analysis

CCMB proposes a training course in analysis of Next Generation Sequencing (NGS) Data to generate human resources that are employment-ready for the requirements of industries and academia. The program targets students and employees from government labs/ Institutes, Industries, Hospitals, and Universities with a view to train them to be able to establish a set-up for NGS data analysis at their respective institutes. Candidates currently not enrolled in a course or not associated with industry / academia are also encouraged to apply.

Duration	:	3 weeks
No. of seats	:	10-12 Nos
Education Qualifications	:	M.Sc., B.Tech., B.V.Sc., MBBS (minimum)
Age group	:	21-45 years (relaxation for SC/ST/OBC as per GOI Rules)
Date of Commencement	:	26th Feb – 16th March 2019
Venue of the Course	:	iHub; Annexe-II, CSIR-CCMB
Course Fee	:	Rs. 25,000/- (self/sponsored)
Residential/non-residential	:	Residential (accommodation provided)

Sponsorship: Established public/private sectors are welcome to sponsor candidates of their interest.

Training Curriculum:

Gene regulation and NGS analysis (Primer/Theory)

- DNA/RNA structure in biological processes
- Chromatin structure and epigenetics
- Introduction to NGS: Principles of NGS technology, Applications of NGS
- Data mining: Data warehouses / Repositories for large biological datasets, Sharing and uploading large data, Accessing information from biological databases, Genome builds, Sequence storage and retrieval and file formats

Primer on Linux (Hands-on)

- Working with the command line: File and folder navigation (cd, mkdir, rm, ls, mv); Basic file handling (cat, more, wc); File manipulation (cut, awk, sed, grep, sort)
- Basic R commands will be covered in the NGS analysis pipelines

NGS analysis pipelines (Theory/Hands-on)

- RNA-seq analysis: Quality control of datasets, Filtering, adapter removal, Spliced alignment to transcriptome, Post alignment QC, Transcript quantification, Differential gene expression analysis
- ChIP-seq analysis: Quality control of datasets, Filtering, adapter removal, Alignment to reference genome, Peak calling, Evaluation of peak quality, Peak annotation, Motif identification
- DNA methylation (whole genome bisuphite-seq) analysis: Quality control, Genome preparation, Alignment, Methylation calling, Statistical analyses, Identification of Differentially methylated regions (DMRs), Annotation
- De novo genome assembly: Typical workflow for assembly, evolutionary perspective (theory)

- Reporting and recording results: Data QC, Presenting NGS analysis results, Controlling for errors, Data analysis issues and pitfalls
- Perspectives from the NGS industry/data analysts

Downstream analysis and biological context (Hands-on)

- Gene Ontology (R pipelines and online tools) and Pathway analysis
- Data visualization: Genome browsers (UCSC, IGV)

- **Wet lab protocols (Primer/Demos):**
- Sequencing facility and sequencers
- Sample preparation workflow

Salient Features of the Training:

- 25% theory and 75% hands-on sessions as per the course curriculum.
- Tutorials (personal attention) along with course manual
- Lectures are assisted with multimedia aids
- Evaluation by assignments and exams
- A certificate will be issued to the successful candidates