DAY 1 (11th January 2019)

9:00 am - 8:00 pm

Hands on Cancer Bioinformatics for NGS Data Analysis: a Primer for Clinicians

Despite wider acceptance of comprehensive profiling of cancer patient using next-generation sequencing for clinical application, the hurdle of genomic analysis for clinical utilization remains one of the major blockage for the clinicians. This one-day workshop is primarily aimed to introdue key applications of cancer genomics, along with the analytical methods used in identification of clinically relevant mutations and disease sub-type specific gene expression patterns. Further, participants will be also introduced to a complementary application of NGS datasets for the discovery of pathogens.

In particular, the participants would be introduce <u>ClinOme</u> – an easy to use clinical cancer genomics analysis and reporting tool for identification of therapeutically relevant genomics alterations and pathogenic infections. ClinOme integrates standard line of treatment recommendation and clinical annotations from various sources and provides a comprehensive genetic diagnosis report from next generation sequencing data. This easy to use graphical user interface widens the utility of ClinOme for biologists and clinicians without computational expertise.

This one-day cancer informatics hands-on workshop would emphasize on the following:

1. Whole transcrptome analysis to identify molecular sub-classes of different tumor types

- Quantification of transcripts from RNA-seq data using alignment and/or quasi-alignment based methods
- Processing, normalization of gene/ transcript counts and its use to identify differentially expressed genes
- Clustering of samples for identification of disease sub-type classes from expression datasets

2. Clinome: an automated computational tool to identify clinically relevant therapeutic alterations

- Generation of variants from the whole genome, exome and targeted sequencing data (primary, secondary, tertiary analysis of DNA sequencing data)
- Filtration and annotation of variants with germline variant databases, like TMC-SNPdb, ExAC and dbSNP
- Clinically relevant variant calling and automated clinical report generation

3. Discovery and tumor association of pathogens associated with cancer using NGS datasets

- Computational subtraction methods and HPV identification using HPVDetector
- Cancer associated pathogen discovery using Cancer Pathogen Detector
- Application of pathogen discovery to complement traditional genomic analysis

The 20 selected participants would require bringing their own laptop. The minimum recommended specifications are as follows: 1024x768 screen resolution, 1.5GHz CPU, 2GB RAM, 10GB free disk space, and a recent version of Windows, Mac OS X or Linux operating systems. Participants with prior rior computational skill will be preferred.

DAY 1 (12th January 2019

08.30 - 09.15 AM	Registration	
Session Coordinators		
09.30 - 9.45 AM	Welcome by Director, ACTREC/ Introduction to MPAI by President, MPAI	
Session Coordinator		
09.45 - 10.30 AM	Plenary presentation on "Changing Landscape of Cancer Incidence in India"	
10:30 - 11.00 AM	Tea/Coffee Break/Poster installation	
11:00 - 1.00 PM	Parall	el Sessions
	Session IA (Basic Cancer Biology)	Session IB (Solid tumor)
Session Coordinators		
	Industry presentation	Industry presentation
1:00 - 02.00 PM	Lunch Break with Poster Presentation	
Session Coordinators		
02.00–3:00 PM	Panel Discussion: Molec	cualr diagnostics in oncology
03:00-04.00PM	Proffered papers/ oral presentation by young investigators (5 talks)	
04:00-04.30PM	Tea/Coffee Break with Poster Presentation	
04:30 -06.30PM	Session IIA (Genetic Disorder/ Hereditary Dieseases)	Session IIB (Haemato Oncology)
Session Coordinators		
	Industry presentation	Industry presentation
6:30-7:15	MPAI general body meeting	
07:00-08:00 PM	Cultural programme	
07.00 00.00 11.1		1

DAY 2 (13th January 2019)

Session Coordinator		
08.30 - 09.30AM	Proffered papers/ oral presentation by young investigators (5 talks)	
Session Coordinator		
09.30 - 10.15 AM	Plenary lecture on "Infectious diseases"	
10:15- 11:00 AM	Plenary lecture on "Diagnosis and Treatment of Cancer using Genomics"	
11.00 - 11.30 AM	Tea/Coffee Break with Poster Presentation	
11.30 - 01.30 PM	Parallel Sessions	
	Session IIIA (Molecular diagnosis in Clinical Oncology)	Session IIIB (Infectious Diseases)
Session Coordinator		
	Industry presentation	Industry presentation
01.30 - 02.30 PM	Lunch Break with Poster Presentation	
02.30 -3:30 PM	Hereditary Cancer clinic live show enactment by Rajiv Sarin and group	
03.30 - 05.30 PM	Parallel Sessions	
	Session IVA (Translational Cancer Research)	Session IVB (Advances in Genetic Diagnosis using NGS & Microarray)
Session Coordinator		
	Industry procentation	Industry procentation
05:30-06.00PM	Industry presentation Valedictory F	Industry presentation
05.50-00.001 M	Valedictory Function	