

# **Analysis of RNA sequencing data in R**

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The RNA sequencing data obtained from the Next Generation Sequencing technologies is extensively used to obtain information on cellular transcriptome. Various types of possible analysis include the differential expression analysis, SNP studies, studies on different populations of RNA, alternate splicing of transcripts etc.

Analysis of this complex, large volume data involves sophisticated data storage and retrieval, innovative graphical representation and a wide range of statistical algorithms. The phenomenal growth of experimental methods and large data generation in this field was always matched by the development of suitable open source analysis tools. Large number of such tools are available as a part of the bioconductor package which is based on the opensource statistical package R.

In this session of the workshop, the basic elements of the RNA-seq data analysis will be explained followed by a hands on session on the analysis of a differential expression data from an RNA seq experiment using bioconductor packages in R. The participants will be able to learn the basic steps involved.