

**Course No:** BY613

**Course Title:** Metagenomics, and Next Generation Sequencing Technologies

**Credit:** 3-0-0-3

**Prerequisites:** BY606 or consent from the faculty

**Students for which course is offered:** B.Tech/M.Tech./PhD

**Elective or Compulsory:** Elective

**Semester:** Even/Odd

**Course Outline:**

This course will cover Metagenomics and Metatranscriptomics of prokaryotes, eukaryotes, and viruses. Some introduction to Genomics and Transcriptomics will also be given. The next-generation sequencing technologies will be covered with specific emphasis on different types of data produced and tools and resources used to analyze the data.

**Unit 1: Next-generation sequencing technologies (22 Lectures)**

Introduction to different sequencing technologies including Capillary based (Sanger), pyrosequencing (454), Illumina, Solid, and others. Differences in data generated by these methods such as read length, throughput, read qualities, etc. Tools and resources that are available to analyze the generated data from different sequencing methods. Types of sequencing data that can be produced from different sequencing methods, such as genomic, metagenomic, amplicon, exome, transcriptome, targeted sequencing, CHIP-seq, 16S, etc.

**Unit 2: Metagenomics (20 Lectures)**

Topics are Metagenomics-specific issues like calling taxa, functional annotation, metagenome assembly and comparative metagenomics. This course will help participants answering questions like:

- For what type of questions can metagenomics help?
- What are possible approaches of metagenomics?
- How to monitor and predict environmental conditions and change?
- Biological insights, phylogenetic diversity.
- Examining genes/operons for enzyme and natural products.

Many hurdles arise in the analysis and assembly of environmental genomics records, among which short sequence reads, high species complexity in samples and the availability of specialized software for microbial genomics analysis.

Among the many topics in metagenomics addressed in this course are: experimental approaches; sequencing technologies; platforms and platform specific issues; methodologies; Sample preparation; QC-reports & quality controls; mapping sequence reads; taxonomic annotation; functional annotation & function determination; unknown gene prediction; comparative metagenomics; amplicon sequencing; shotgun metatranscriptomics; calling taxa; metagenome assembly; evaluation; visualization and reporting of results; tools & algorithms; 16S profiling; databases; mapability; k-mer profiling; cross assembly; QIIME; MG-RAST; iPath.

### **References:**

1. A Bioinformatician's Guide to Metagenomics. Victor Kunin et al. MICROBIOLOGY AND MOLECULAR BIOLOGY REVIEWS, Dec. 2008, p. 557–578.
2. Next-generation sequencing data interpretation: enhancing reproducibility and accessibility. *Anton Nekrutenko & James Taylor Nature Reviews Genetics* September 2012 Volume 13 No 9 667.

Other Latest research articles will be advised related to the topic being taught from time to time.