LAST DATE FOR APPLICATIONS IS 31ˢᵗ JULY 2015
DBT Training workshop on "**Methodologies used in gene expression analysis**" at SP Pune University
Lectures (15): **One lecture daily from 9.30am to 11.00am**

Topic	No. of lectures
Gene expression- Central dogma of life. Regulators of transcription, post-transcriptional regulation. Brief introduction to translational and post-translational regulation.	2
Methods for studying gene expression 1: Northern blot, Reverse transcription, cDNA libraries, RT-PCR, cDNA AFLP, ESTs. Suppressive subtraction hybridization. cDNA and EST databases.	3
Methods for studying gene expression 2: Serial analysis of gene expression (SAGE), Super SAGE, massively parallel signature sequencing (MPSS).	2
Methods for studying gene expression 3: cDNA microarrays: construction, analysis, applications and limitations.	3
Methods for studying regulation of gene expression 4: Small RNA mediated regulation.	2
Methods for studying gene expression 5: Next generation sequencing (NGS) technologies for transcriptome sequencing and data analysis	3

Practicals (15): Would include wet lab experiments and hands on sessions on computers (for 5-6 h each day) **11.30am onwards on each working day**

Plant RNA extraction, Electrophoresis for checking quality and quantification of RNA. cDNA synthesis	2 days
Semi quantitative and quantitative RT-PCR for candidate genes. Identifying RNA / EST sequences from databases, primer design. Determination of fold-expression under contrasting conditions / development stages. cDNA AFLP	3 days
Introduction to microarray database: Gene Expression Omnibus (GEO), retrieval of the expression values for gene of interest, construction of gene expression heatmap using multiexperiment viewer software	2 days
Demonstration of ion torrent (NGS) sequencer and its application in transcriptome analysis	2 days
Determining target genes for miRNAs (psRNA target analysis server)	1 day
Use of Sequence Read Archive (SRA) from NCBI for gene expression analysis	2 days
Demonstration of handling NGS transcriptome data and its analysis for deducing candidate gene expression	3 days