

A COLLOQUIUM BY: Dr. Thiruvarangan Ramaraj



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Advanced sequencing technologies & computational genomics to investigate biological systems

Due to the significant lowering of cost and the incredible upturn in data-production capacity, next generation sequencing and other whole genome mapping technologies have revolutionized biological research by increasing our genome-wide knowledge of various organisms and its systems. Some of the key applications include DNA sequencing, establishing reference genomes and transcriptomes for many model organisms, gene regulation analysis, quantitative and qualitative sequencing-based transcriptome analysis, SNP discovery and small and large scale structural variation analysis, DNA – protein interaction analysis (ChIP-Seq), sequencing based methylation analysis, small RNA discovery and analysis, exploring long non-coding RNAs, 16S/18S/ITS gene sequencing for identification, classification and quantification of microbial communities in complex environmental and human gut samples, meta-genomics and meta-transcriptomics. This talk will focus on, (i) how next generation technologies and bioinformatics approaches have been used for standard and novel sequencing applications and (ii) case studies from ongoing research work tackling computational challenges for different sequencing applications.