COMPUTATIONAL BIOLOGY WEBINAR @ IMSc

EFFICIENT MAPPING OF MICROBIAL METABOLIC SYSTEMS BY INTEGRATING GENOMICS WITH 13C FLUXOMICS

DR. SHYAM K. MASAKAPALLI
IIT MANDI

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13C fluxomics integrated with other -omics provide Genotype to Phenotype predictive framework and unprecedented insights into the cellular systems. This talk will mainly focus on strategies we adopt in efficient integration of comparative genomics and 13C tracer studies to decode the metabolic phenotypes of microbial metabolic systems. First, the standardized workflow leading to efficient metabolic mapping and flux maps of bacterial systems will be introduced. Secondly, our latest work on deciphering metabolic phenotypes of a phytopathogen *Ralstonia solanacearum* using parallel 13C tracer feeding and metabolic modelling will be presented. The study highlights how the metabolic models and flux maps have relevance to agriculture and industrial bioprocessing. Finally, the bottlenecks and potential opportunities in deciphering Plant-microbial metabolic cross talk using stable isotopes will be discussed.

GOOGLE MEET LINK:

meet.google.com/peq-gykw-rzp