

Computational Core for Plant Metabolomics

A brief report of Seminar cum Workshop: “Towards Collaborative Metabolomics” CCPM 5 held on April 21, 2015

To announce and familiarize the potential users with the features of the new release of CCPM version 3.4 (<http://metabolomics.iiit.ac.in>), we organized a one-day seminar-cum-workshop on April 21, 2015. Invitations with the detailed program and link to registration and workshop portal were sent to DBT experts and DBT plant metabolomics network partners across the country. The participants were given an option to attend the seminars and workshop physically at JNU/IIIT-H or online through skype. A total of 55 researchers participated in the workshop. Out of these, ten were online participants, 29 participants joined at III-H and 16 at SC&IS, JNU.

The agenda included presentations by five experts in the morning session followed by demonstration and hand-on training to familiarize the users with functionalities of new version. The seminars were physically organized at SC&IS, JNU and streamed online through skype for participants at IIIT-H. The morning session comprised of five presentations from renowned speakers with diverse backgrounds who shared their expertise on transcriptomics, metabolomics, metabolic networks and graph databases.

Dr. Alok Bhattacharya inaugurated the workshop and elaborated the expectations from CCPM. After an intensive discussion, a need for a meeting between PIs, DBT experts and project team was identified in near future to facilitate successful completion of the objectives of the project.

The first speaker of the seminar session, Dr. Sanjay Kapoor (University of Delhi, South Campus) presented his excellent work on “Transcriptomics-led insights into regulation of starch biosynthesis in cereals” and elaborated how integration of omics technologies helped them decipher the mechanism of starch biosynthesis in rice seeds. Dr. Arun Sharma (University of Delhi, South Campus), who is also one of the PIs in the project presented his work on “Genetic manipulation for improving tomato fruit quality” with a brief summary of their work plan using metabolomics. One of the students from Prof. Ashwani Pareek (SLS, JNU), who is also PIs on the project, presented their ongoing work on understanding the mechanism of salt tolerance in rice using transcriptomic, proteomic and metabolomics. Their work highlighted the need for integrating the data from various omics fields to derive better biological conclusions. Dr. Anirban Banerjee (IISER-Kolkata) shared his work on “Phylogeny of metabolic Networks” which induced extensive discussion among participants. The last talk of the session was delivered by Prof. Subhasis Mukhopadhyay (Calcutta University) on “Graph Database Approach: What it can offer to the biologists”, where he introduced the participants with the new realm of graph databases. All the presentations were streamed through Skype for online participants.

After lunch, an online demonstration and hands on training of CCPM v3.4 was organized at both JNU and IIIT-H. The participants got an opportunity to register with CCPM and test the functionalities and features of new GUI. The hands-on-training was followed by interaction with the team members at both JNU and IIIT-H through skype. Uploaded literature data was used by the participants for trying out the different features of the portal. Details of how to use these features were explained using the tutorial. During this interaction session, participants clarified their doubts and gave their feedback on CCPM v 3.4. Based on their feedback, an action needed report was prepared. This is being intensively reviewed internally and necessary action is being taken to address the concerns and incorporate the new features in

CCPM. These include exploring converters for uploading raw data from different vendor machines into CCPM, providing scores in metabolite identification to help biologist prioritize the top hits, making high quality images available for download which can be used for publication purposes and integration of pathway analysis tools with the CCPM.