Using integrative *omics* to disentangle plant gene regulatory networks involved in plant-endophyte interactions

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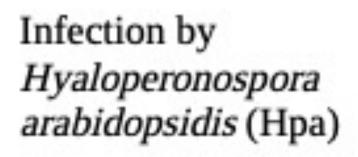
Abstract

Plant endophytes that are known to enhance plant's tolerance against (a)biotic stress have a largely unexplored functional potential. Unravelling the dynamics of interaction between the plant and endophytes provides enormous opportunities to address key societal problems of the 21st century, in particular the increased global demands for crops that are more resilient to (a)biotic stress and less dependent on fertilizers and pesticides. Hence, a critical step in developing new microbiome-assisted approaches to improve plant growth and health is to unravel the regulatory networks in plant-endophyte interactions. To this end, our project investigates the dynamics and architecture of plant gene regulatory networks and aims to decipher plant biosynthetic pathways by integrative omics strategies. Whole transcriptome and metabolomes from plant roots and root exudates will be investigated to connect genes and their expression patterns to metabolites that play a crucial role in the plant-endophyte interactions. With the proposed work, we aim to deepen the mechanistic understanding of plant-microbe interactions.

Objectives

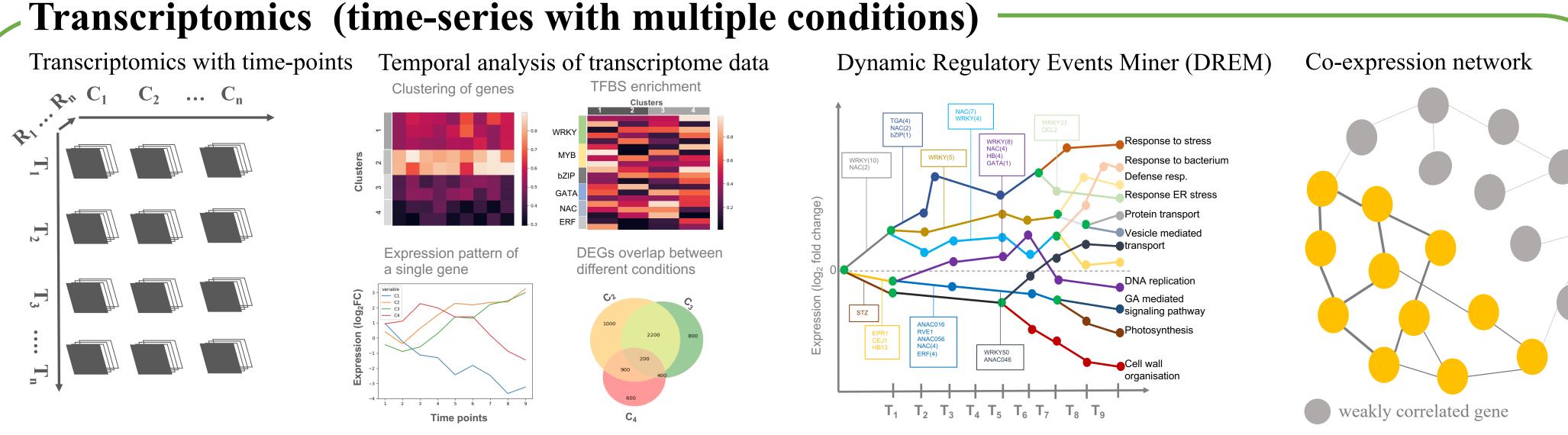
. Investigate transcriptional and metabolic changes that are induced in the roots upon pathogen infection.

- Explore components of plant immune gene regulatory network (GRN) involved in pathogen-induced recruitment of protective endophytes and activation of beneficial microbial biosynthetic gene clusters (BGCs).
- Discover plant biosynthetic pathways and metabolites that are responsible for the underlying interactions with the root microbiome. 3



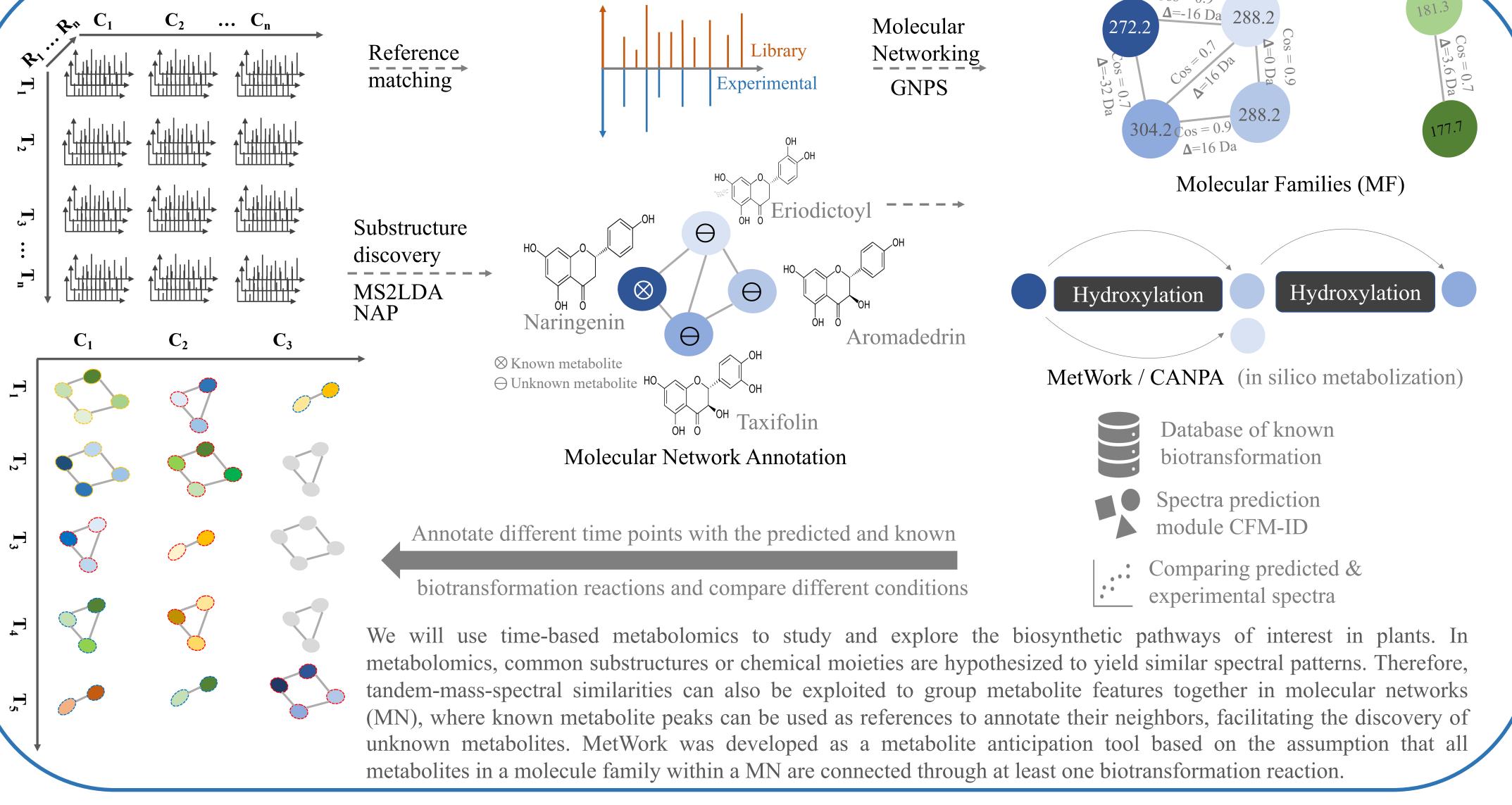
Pathogen

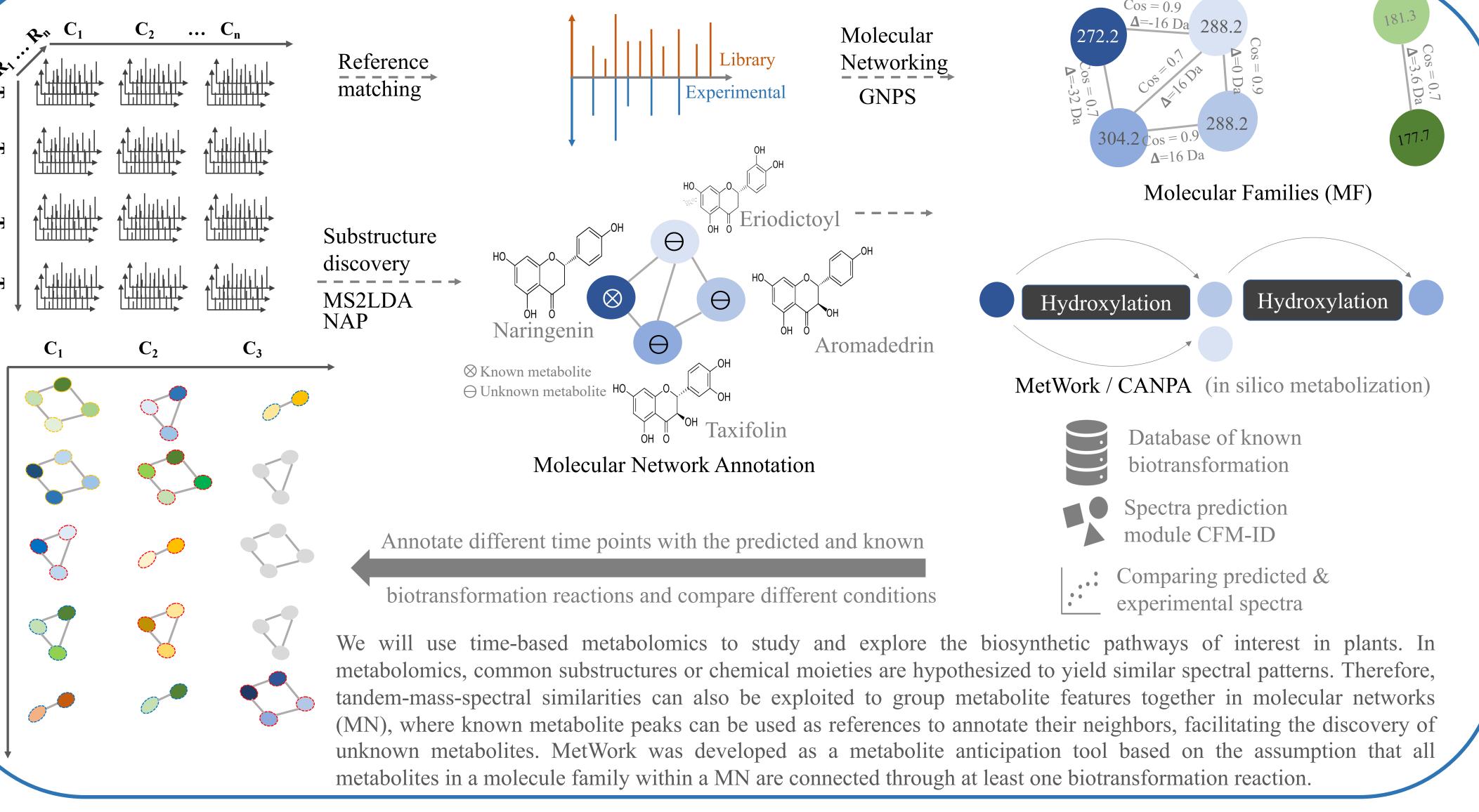
infection

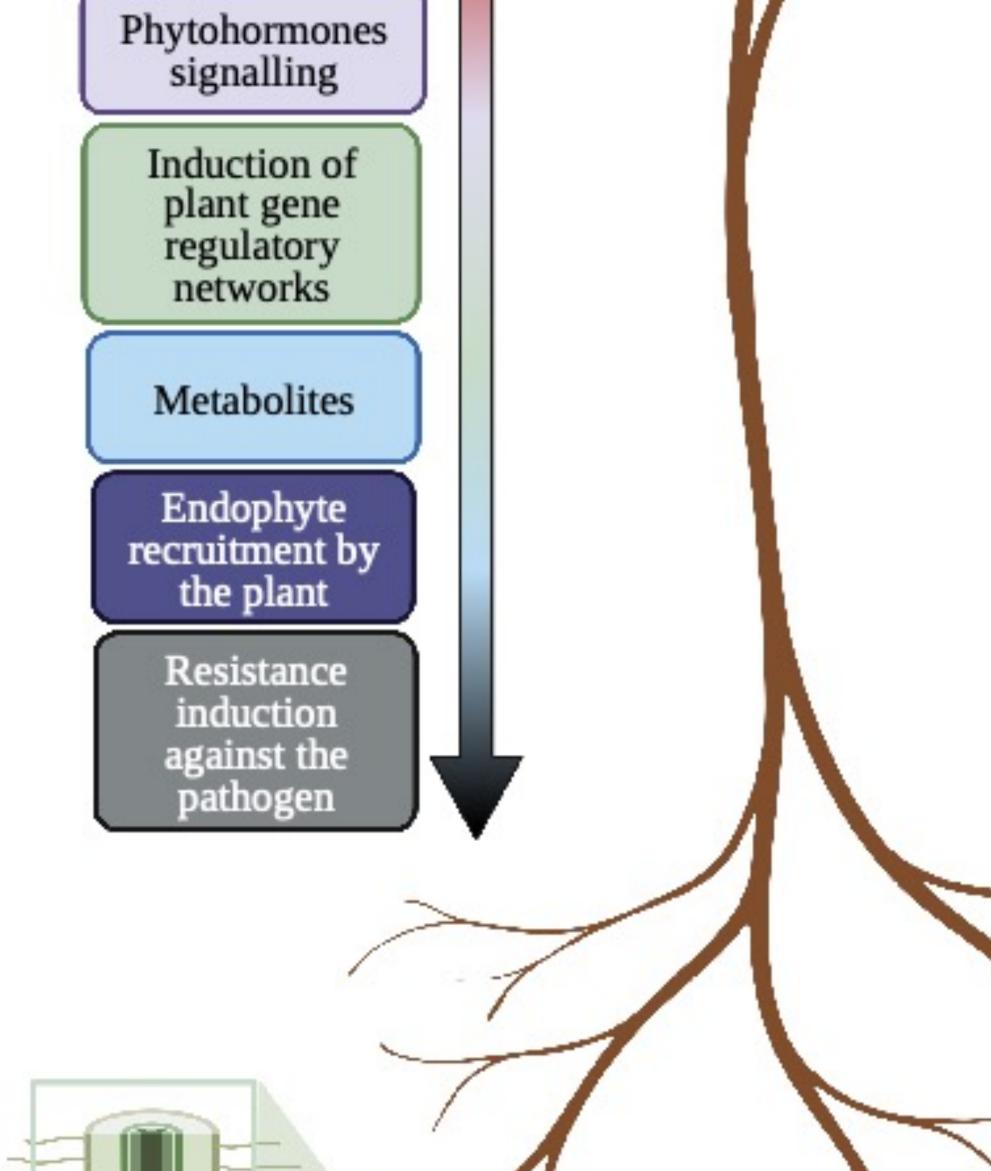


Dynamic transcriptional responses in plants are achieved by a combined action of multiple transcription factors (TFs) working synergistically to cause a genome-wide transcriptional cascade. We will use state-of-the-art methods to capture TF-target gene interactions that are focused not only on stable TF-target interactions but also the transient ones. Time-based analysis of TF-target binding is an effective method to capture such TF-target interactions. Time-based studies will further enhance our understanding of the dynamic regulation of phytohormones and gene regulatory network involved in specialized metabolism.

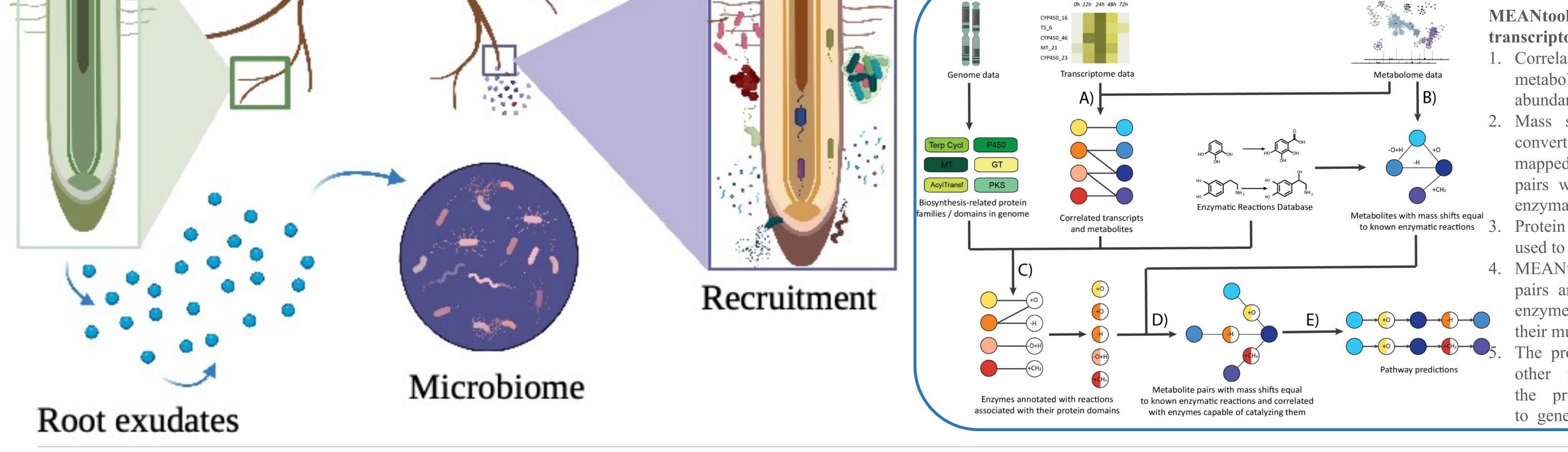
Metabolomics (time-series with multiple conditions)







<u>ME</u>tabolite <u>AN</u>ticipation tools (MEANtools)



 T_3

MEANtools predict metabolic pathways by integrating

- transcriptomic, metabolomic and genomic data 1. Correlations are computed between transcripts and
- metabolites based on gene expression and metabolite abundances.
- 2. Mass signatures from the metabolomic data are converted wo Molecular Families (MF). MFs are then mapped with enzymatic reaction databases to identify pairs with mass differences associated with known enzymatic reactions.
- Protein families/domains encoded by the genes are used to query enzymatic reaction databases.
- 4. MEANtools then identifies cases in which metabolite pairs are correlated to a transcript that encodes an enzyme capable of catalyzing a reaction that explains their mutual mass difference.
- The product of these reactions are then mapped to other mass signatures in the metabolome and the procedure is then repeated multiple times to generate pathway predictions.

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