BCB Thesis Seminar

From pathway to regulon in Arabidopsiss

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Abstract:
I apply combined bioinformatic approaches using genomic and transcriptomic data to investigate the fatty acid biosynthesis pathway, at the molecular level, and in the context of the system biology of Arabidopsis. Fatty acids are essential components of all known bacterial and eukaryotic cells with critical role in cells as energy reserves and the metabolic precursors for biological membranes. The pathway for fatty acid synthesis seems to be conserved across all living systems. Acetyl-CoA carboxylase, a member of a superfamily of biotin-dependent enzymes, catalyzes the first committed step of the fatty acid biosynthesis pathway. Phylogenetic study exposed complex and intertwined evolutionary histories of this family, with multiple domain fusions and rearrangements. As revealed by meta-analysis of a wide array of Arabidopsis transcriptomic data, fatty acid biosynthesis is transcriptionally regulated, and this regulation not only extends across all pathway reactions, but also some substrate- and cofactor-producing reactions, thus defining a major transcriptionally co-regulated pathway. I extend the meta-analysis of the transcriptome to find groups of coexpressed genes (also called modules, or regulons) in the Arabidopsis genome. Major functionally-coherent gene groups were identified. These comprise development, information processing, defense, and metabolism, as well as tissue- and organelle- specific processes.