A Regulatory Network Analysis of Orphan Genes in Arabidopsis Thaliana[1] PRAMESH SINGH, TIANLONG CHEN, Department of Physics, University of Houston, ZEBULUN ARENDSEE, Center for Metabolic Biology, Bioinformations and Computational Biology, Iowa State University, EVE S. WURTELE, Center for Metabolic Biology, Iowa State University, KEVIN E. BASSLER, Department of Physics, University of Houston — Orphan genes, which are genes unique to each particular species, have recently drawn significant attention for their potential usefulness for organismal robustness. Their origin and regulatory interaction patterns remain largely undiscovered. Recently, methods that use the context likelihood of relatedness to infer a network followed by modularity maximizing community detection algorithms on the inferred network to find the functional structure of regulatory networks were shown to be effective [PLoS Comput. Biol. 8, e1002391 (2012)]. We apply improved versions of these methods to gene expression data from Arabidopsis thaliana, identify groups (clusters) of interacting genes with related patterns of expression and analyze the structure within those groups. Focusing on clusters that contain orphan genes, we compare the identified clusters to gene ontology (GO) terms, regulons [BMC Plant Biology, 8, 99 (2008)], and pathway designations and analyze their hierarchical structure. We predict new regulatory interactions and unravel the structure of the regulatory interaction patterns of orphan genes.

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