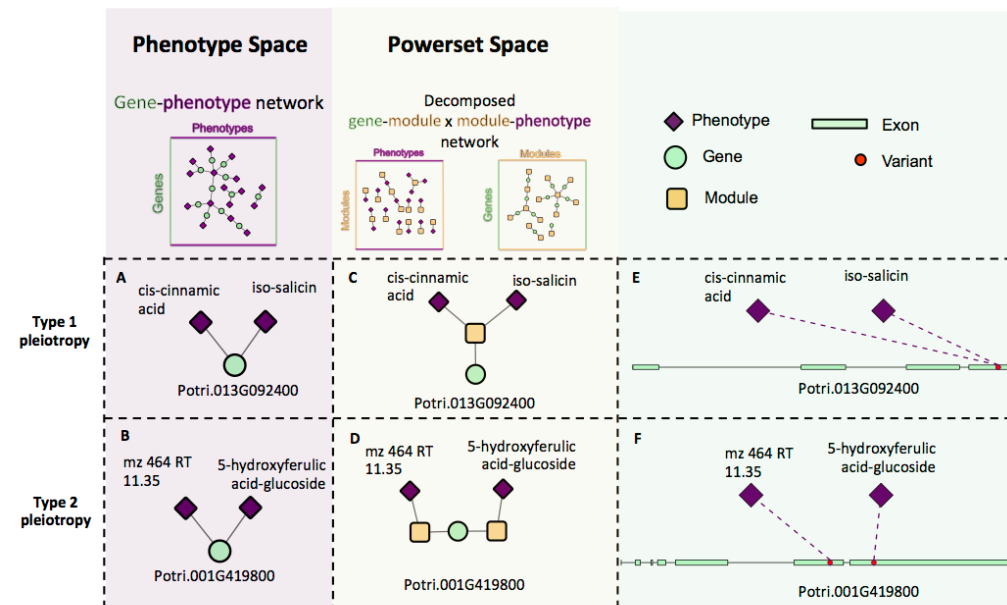


Novel approach: Multi-Phenotype Association Decomposition: Unraveling Complex Gene-Phenotype Relationships.

Objective	<ul style="list-style-type: none"> Identify pleiotropic signatures from genome-wide association studies (GWAS).
New science	<ul style="list-style-type: none"> Developed MPA Decomposition, a new network-based approach which unravels the multi phenotype signatures of thousands of genes on a genome-wide scale. The decomposition involves the construction of a phenotype powerset space, and subsequent mapping of genes into this new space. Clustering of genes in this powerset space groups genes based on their detailed MPA signatures.
Impact	<ul style="list-style-type: none"> This method should prove invaluable in the interpretation of large GWAS datasets and aid in future synthetic biology efforts designed to optimize phenotypes of interest.



Signature decomposition example. Two genes, Potri.013G092400 (A) and Potri.001G419800 (B) have the same surrounding network topology in the gene-phenotype network in that they are both connected to two phenotypes. Projecting the genes into powerset space through MPA decomposition of the gene-phenotype network indicates that they exhibit different MPA signatures in that Potri.013G092400 exhibits a type 1 MPA signature (C), containing a SNP associating with two phenotypes (E) and Potri.001G419800 exhibits a type 2 MPA signature. (D) containing two SNPs, each with a different phenotype association (F).