Statistical quantitative genetic modeling for image-based high-throughput phenotyping data

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The development of phenomics coupled with increased output from sequencing technologies has the potential to further increase the tolerance of agricultural species to abiotic stresses in the face of rapid climate change. In particular, image-based high-throughput phenotyping (HTP) enables researchers to produce large-scale data with temporal resolution, capturing dynamic growth, development, and stress responses. However, the development of statistical methodologies to analyze image-based longitudinal phenotypes has not progressed at the same pace as our ability to generate HTP data and understanding the genetic interdependencies among high-dimensional traits in a statistically robust manner remains a major challenge. In this talk, we show how a random regression model and a Bayesian network coupled with factor analysis can be used to model changes in growth over time and elucidate the genetic interdependencies among diverse traits. In addition, we discuss our recent progress on detecting and understanding the role of variance quantitative trait loci.

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