Statistical methods for the quantitative genetic analysis of high-throughput phenotyping data

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The advent of phenomics coupled with the wealth of genotypic data generated by next-generation sequencing technologies provides exciting new resources to study and improve complex traits. However, the new technologies also bring about new challenges in quantitative genetics, namely developing robust frameworks that can accommodate these high dimensional data. In this course, we will discuss methods for the statistical analysis of high-throughput phenotyping (HTP) data with the goal of elucidating the genetic interdependencies among HTP data and enhancing the prediction accuracy of genomic selection.

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