

MICHIGAN STATE UNIVERSITY
Department of Statistics and Probability

COLLOQUIUM

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Better Genotyping for Polyploids

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10:20 AM - 11:10 AM

Refreshments 10:00 AM

C405 Wells Hall

Abstract

Modern genomics has revolutionized how we answer questions about evolution, population dynamics, medicine, and plant and animal breeding. To answer these questions, we must first be able to detect and quantify (or "genotype") differences in individual genomes. Many scientists have used next generation sequencing technologies to genotype diploid individuals (those with two copies of their genomes). However, methods to genotype polyploids (those with more than two copies of their genomes) are just emerging. We present two main contributions: (i) many datasets feature related individuals, and so we use the structure of Mendelian segregation to borrow strength between polyploid siblings to improve genotyping; (ii) we additionally draw attention to and then model common aspects of next generation sequencing data: sequencing error, allele bias, overdispersion, and outlying observations. We apply our method to a dataset of hexaploid sweet potatoes and discuss future extensions.

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