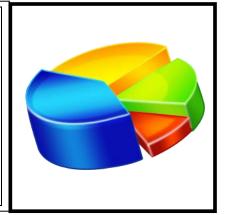# STATISTICS SEMINAR
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Thursday, September 18, 2014
Dickens Hall, Room 207, 4:00-5:00 pm
Refreshments: Dickens 108, 3:30-4:00 pm

Great Needs for Statistical Approaches in Modern Genomics

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DNA is the genetic basis to control biological traits. Understanding the sequence of DNA, the order of nucleotides, in genomes is critical for the discovery of genes and their relationship with traits. The new genome technologies, next-generation sequencing (NGS) technologies, provide tremendous tools to rapidly obtain DNA sequence. With the great power of NGS, lots of novel applications were developed. These applications would usually be leveraged with sound statistical approaches. NGS generates large amount of sequence reads and can be converted to counts data for further statistical analyses. Statisticians have developed many useful software packages for some general studies, such as DESeq for gene expression studies. However, more statistical approaches are needed to mine NGS data and answer biological questions. This talk will provide overview of NGS and an application of NGS in mapping genes, identifying genomic loci containing causal genes that control phenotypes/traits in plant. To suppress background noises, a Bayesian method was developed in this study to reliably determine genomic loci responsible for the traits of interest.