

STUDENT SEMINAR

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Title

Distinguishing
close linkage from
pleiotropy in
multiparental
populations

Speaker

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(PhD student in
Statistics, UW-Madison)

Time & Place

Friday, April 6, 4pm, SMI
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Snacks @ 3:45pm, SMI
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Abstract

Multiparental populations, such as the Diversity Outbred (DO) mouse population, are a new resource for systems genetics studies. Distinguishing close linkage of distinct quantitative trait loci from one pleiotropic locus that associates with multiple traits has implications in biomedical research, plant and animal breeding, and other genetics applications. We develop a likelihood ratio test for the alternative hypothesis of close linkage of two loci against the null hypothesis of pleiotropy for a pair of traits that map to a single genomic region. Unlike previous tests of these competing hypotheses, our test incorporates polygenic random effects to account for complex patterns of relatedness among subjects. Additionally, our test accommodates more than two founder alleles. We use a parametric bootstrap-based method to determine statistical significance. To demonstrate its practical utility, we apply our test to a study of 260 DO mice. We share our methods in a freely available software package (<https://github.com/fboehm/qtL2pleio>) for the R statistical computing environment.