

# BIOSTATISTICS SEMINAR



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## **Knockoff genotypes: value in counterfeit**

The framework of knockoffs has been recently proposed to perform variable selection under rigorous type-I error control, without relying on strong modeling assumptions. We extend the methodology of knockoffs to a rich family of problems where the distribution of the covariates can be described by a hidden Markov model. We develop an exact and efficient algorithm to sample knockoff variables in this setting and then argue that, combined with the existing selective framework, this provides a natural and powerful tool for performing principled inference in genome-wide association studies with guaranteed false discovery rate control. To handle the high level of dependence that can exist between SNPs in linkage disequilibrium, we propose a multi-resolution analysis, that simultaneously identifies loci of importance and provides results analogous to those obtained in fine mapping.

This is joint work with Matteo Sesia, Eugene Katsevich, Stephen Bates and Emmanuel Candès.

**Thursday January 9, 2020**

**3:30 pm - 4:30 pm**

**Blue Cross and Blue Shield of North Carolina Foundation Auditorium**



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