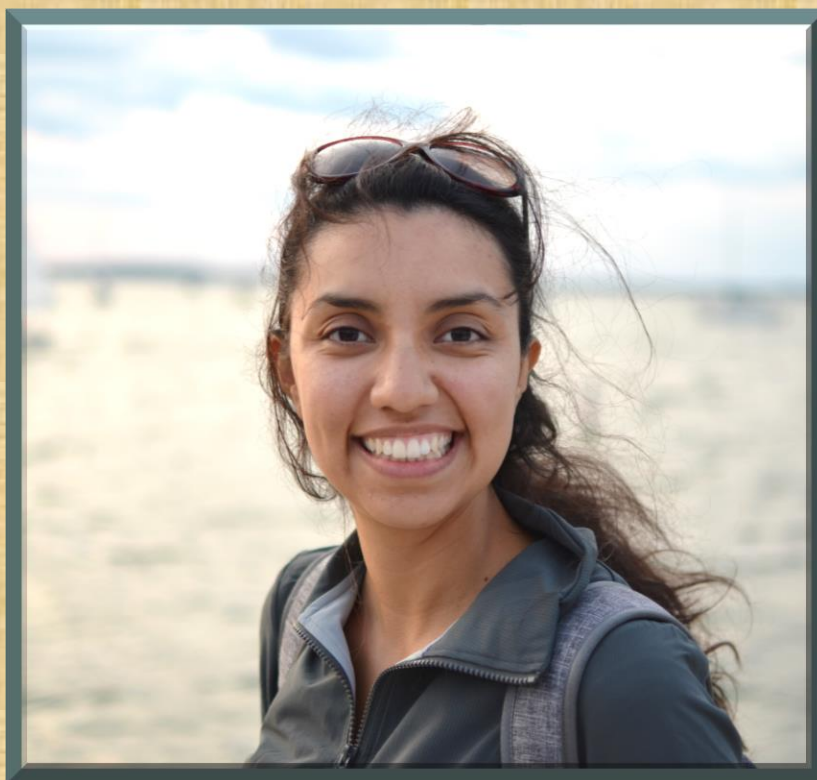


Department of Mathematics Colloquium

Friday, October 26, 2018 | 4:30 p.m. | HLSB 522

*“Statistical Methods to Identify Genes
Associated with Disease”*



**Presented by Claudia Solis-Lemus, Emory University Postdoctoral Fellow
in the Department of Human Genetics**

Genome-Wide Association Studies (GWAS) have been used for over a decade to elucidate ties between genes and diseases. Standard analytic methods for GWAS typically consist of a regression of an individual genetic variant on a given phenotype, like presence or absence of a given symptom, or continuous measures like BMI. These standard approaches face numerous challenges including small individual genetic effects, low statistical power due to improper modeling of genetic correlation patterns, and potential type-I error inflation due to unmodeled population structure or kinship. In summary, typical GWAS approaches involve single regression models followed by multiple test corrections, thus yielding very stringent cutoffs for significance so that very few genes are found to be associated with the disease.