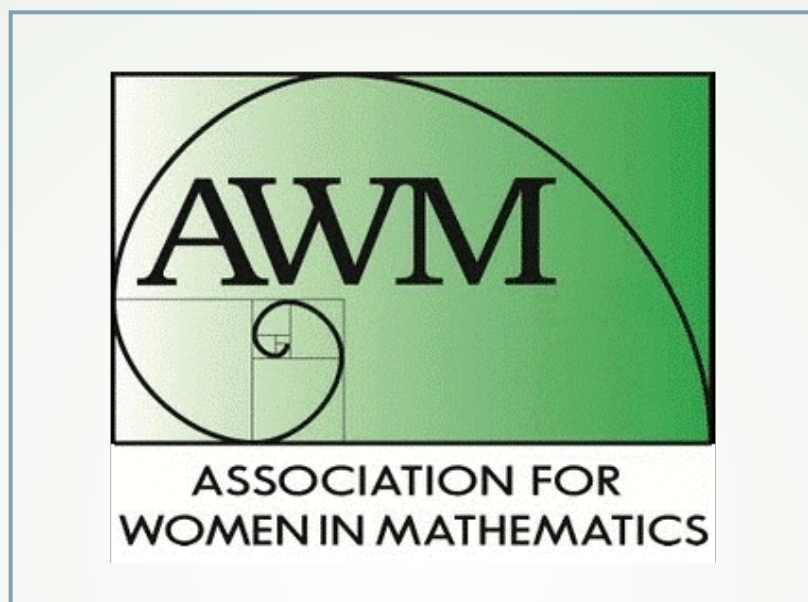


UB's AWM Lecture Series Presents:

# DR. RACHAEL HAGEMAN BLAIR

MONDAY APRIL 18<sup>TH</sup>

AT 5:00PM



Located in Math 250. Pizza will be served following the talk.



## PERTURBING GENETIC NETWORKS

Graphical models have proven to be a valuable tool for connecting genotypes and phenotypes. Structural learning of phenotype-genotype networks has received considerable attention in the post-genome era. In recent years, a dozen different methods have emerged for network inference, which leverage natural variation that arises in certain genetic populations. The structure of the network itself can be used to form hypotheses based on the inferred direct and indirect network relationships, but represents a premature endpoint to the graphical analyses. In this work, we extend this endpoint. We examine the unexplored problem of perturbing a given network structure, and quantifying the system-wide effects on the network in a node-wise manner. We leverage belief propagation methods in Conditional Gaussian Bayesian Networks (CG-BNs), in order to absorb and propagate phenotypic evidence through the network. We show that the modeling assumptions adopted for genotype-phenotype networks represent an important sub-class of CG-BNs, which possess properties that ensure exact inference in the propagation scheme. Applications to kidney and skin cancer expression Quantitative Trait Loci (eQTL) data from different musculus populations are presented. We demonstrate how these predicted system-wide effects can be examined in connection with estimated class probabilities for covariates of interest, e.g., cancer status. Despite the uncertainty in the network structure, we demonstrate the system-wide predictions are stable across an ensemble of highly likely networks. A software package, geneNetBP, which implements our approach, was developed in the R programming language.