

# Pathway-based Analysis of Large-Scale Association Studies

**Dr. Iryna Lobach**

Yale University School of Medicine

Agricultural and Biosystems Engineering

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**Shantz Building – Room 440**

## **Abstract:**

A central problem in genetic epidemiology is to identify and rank genes involved in a disease. Genome-Wide Association studies are increasingly used to detect disease-gene associations. Information about gene regulatory dependence (1) is collected using biomedical experiments in pathway databases; (2) can be inferred via statistical methodology e.g., gene co-expression networks. We propose a Bayesian methodology that can be used to rank disease-gene associations with ability to incorporate prior biological information about gene regulatory dependence and integrate various types of data. This approach is based on a prior distribution that is defined by a Markov Random Field (MRF). In the context of pathway-based association analysis the a priori knowledge induced by a MRF is that whether or not a gene is associated with disease directly depends on an association status of genes within the same pathway. We conducted simulation experiments to illustrate performance of our method. An application of the proposed methodology is illustrated using an association study of Crohn's disease.

If you have questions, contact: Dr. Mark Riley, ABE Dept., 626-9120, [riley@ag.arizona.edu](mailto:riley@ag.arizona.edu)