VirginiaTech
VIRGINIA POLYTECHNIC INSTITUTE AND STATE UNIVERSITY

# Computer Science Seminar Series, 2012

## National Capital Region

# Asymmetric Independence Model to Identify Interactions in Complex Diseases


**Speaker: Prof. Guoqiang Yu**
**Virginia Tech**


**Friday, November 16, 2012**
**1:00PM- 2:00PM, NVC 325**

### Abstract


It is widely accepted that "interactions" occur in most complex biological systems including, e.g., systems of genetic variants, environmental exposures and behavioral factors that collectively result in specific clinical traits of interest. The identification of interactions could ultimately lead to improved identification of individuals at high risk for disease (for disease domains that include heart disease and diabetes), suggest environmental or behavioral modifications to attenuate that risk, and provide novel insights into underlying disease pathophysiology. The *de facto* standard methodology for addressing this problem is logistic regression with multiplicative interaction terms. We have figured out several fundamental limitations of logistic regression for identifying interactions, including a lack of agreement with established biological models as well as inconsistency under two almost universally occurring scenarios: a) some true causal factors are missing (unmeasured) and b) some measured factors are surrogates of true factors. Accordingly, we propose the Asymmetric Independence Model (AIM), which is consistent with several prominent biological theories and models and, moreover, unlike logistic regression, AIM is a consistent model under unmeasured and surrogate factor scenarios. Both theoretical and experimental supports will be demonstrated in the talk.


### Biography

Guoqiang Yu is an Assistant Professor in the ECE department at Virginia Tech. Previously he was a Postdoctoral Fellow at Stanford University. He obtained his Ph.D. from Virginia Tech, Arlington, VA. His research interest is in machine learning, pattern recognition, signal and image processing, applied statistics, and their applications to developing computational bioinformatics and systems genetics tools, for the integrated modeling and analyses of various human diseases using multiplatform genomic, epigenetic and molecular data.