Department of Mathematics, Statistics and Computer Science

**Colloquium Announcement**

***High-dimensional joint Bayesian variable and covariance selection: applications in eQTL analysis and cancer genomics***

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**3:00 PM, Friday, February 7, 2014**

Cudahy Hall, Room 401

We describe a Bayesian technique to (a) perform a sparse joint selection of significant predictor variables and significant inverse covariance matrix elements of the response variables in a high-dimensional linear Gaussian sparse seemingly unrelated regression (SSUR) setting and (b) perform an association analysis between the high-dimensional sets of predictors and responses in such a setting. To search the high-dimensional model space, where boththe number of predictors and the number of possibly correlated responses can be larger than the sample size, we demonstrate that a marginalization-based collapsed Gibbs sampler, in combination with spike and slab type of priors, offers a computationally feasible and efficient solution. We demonstrate our method in an eQTL data set (SNPs as predictors and mRNA as responses) and in a glioblastoma data set (microRNA and copy number aberration as predictors and mRNA as responses). If time permits, we will also describe ongoing work on generalizations to non-linear, non-Gaussian models.

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**For further information: see** [**http://www.marquette.edu/mscs/resources-colloquium.shtml**](http://www.marquette.edu/mscs/resources-colloquium.shtml)

**or contact Dr. Rong Ge #414-288-6344, Rong.Ge@marquette.edu.**

Pre-colloquium refreshments served in Cudahy Hall, Room 342 at 2:30 p.m.