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### **Surrogate variable analysis using Partial Least Squares (SVA-PLS) in Gene Expression Studies**

**Friday, Feb 10, 11A.M. – 12 P.M. SPHIS Room 103**

#### **Abstract:**

In a typical gene expression profiling study, our prime objective is to identify the genes that are differentially expressed between the samples from two different tissue types. Commonly, standard ANOVA/regression is implemented to identify the relative effects of these genes over the two types of samples from their respective arrays of expression levels. But, this technique becomes fundamentally flawed when there are unaccounted sources of variability in these arrays (latent variables attributable to different biological, environmental or other factors relevant in the context). These factors distort the true picture of differential gene expression between the two tissue types and introduce spurious signals of expression heterogeneity. As a result many genes, which are actually differentially expressed, are not detected, whereas many others are falsely identified as positives. Moreover, these distortions can be different for different genes. Thus, it is also not possible to get rid of these variations by simple array normalizations. This both-way error can lead to a serious loss in sensitivity and specificity, thereby causing a severe inefficiency in the underlying multiple testing problem. In this work, we attempt to identify the hidden effects of the underlying latent factors in a gene-expression profiling study by Partial Least Squares (PLS) and apply ANCOVA technique with the PLS-identified signatures of these hidden effects as covariates, in order to identify the genes that are truly differentially expressed between the two concerned tissue types.

**Department of Bioinformatics and Biostatistics**

**Spring 2012 Seminar Series**

**Every Friday**

**11AM-12PM**

**SPHIS Building Room 103**

Seminar Attendance for Feb 10, 2012

**STUDENTS**

**FACULTY/STAFF**