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# STATISTICS SEMINAR

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UW-Department of Statistics

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**Abstract:** Statistical genomics is an emerging field and has played a crucial role in discovering genetic mechanisms behind the complex biological phenomenon. In this talk, I will discuss two statistical methods I have developed to uncover key hidden information from large-scale genomic data. First, I will introduce AIDE, a statistical method that selectively incorporates prior knowledge into the modeling to improve the statistical inference of hidden RNA structures. AIDE is the first method that directly controls false RNA discoveries by implementing the statistical model selection principle. Second, I will introduce MSIQ, a statistical model for robust RNA quantification by integrating multiple biological samples under a Bayesian framework. MSIQ accounts for sample heterogeneity and achieves a more accurate estimation of RNA quantities. Beyond these two methods, I will also summarize my other work in this area, and I will briefly introduce my ongoing work in asymmetric classification.

**TITLE:** Statistical Methods to Uncover Hidden Information from Large-scale Genomic Data

**Speaker:**

**Wei Vivian Li**

Statistics Department  
University of California,  
Los Angeles

**Time & Place:**

Monday, February 4,  
2019 **4pm**, Room  
133 SMI

Cookies & Coffee @  
**3:30**, Rm 1210 MSC

