



presents Guest Speaker :

## **William Stafford Noble**

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**Associate Professor**

**Department of Genome Sciences**

**Department of Computer Science and Engineering**

**University of Washington**

### *Computational Analyses of Yeast and Human Chromatin*

In the nucleus of the eukaryotic cell, DNA is wrapped into a complex, dynamic molecular structure known as chromatin. Over the past several years, we have collaborated with experimental labs to create and validate a series of computational models of chromatin in human and yeast. In this talk, I will describe three models, which (1) predict local chromatin organization from sequence, (2) delineate larger-scale chromatin domains from high-throughput cleavage data, and (3) identify protein-binding footprints on a genomewide scale.

Student Presentation (10 mins):

**James Taylor, co-supervised by Phil Hieter (MSL, UBC)**

**& Tim Galitski (ISB, Seattle)**

*High-Throughput Microfluidic Technologies for Systems Studies of Cellular Signaling*

**Thursday, October 9, 2008, 6:00 pm**

Gordon and Leslie Diamond Family Theatre,  
BC Cancer Research Centre,  
675 West 10th Avenue



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