

# **Science at the Edge Seminar Series**

**Quantitative Biology Graduate Program/  
Gene Expression in Development and Disease**

**Dr. Shirley Liu**

**School of Public Health  
Harvard University**

## **“Using Epigenetic Profiling and CRISPR Screens to Understand Cancer Progression and Drug Response”**

With the recent exciting development of high throughput sequencing applications, epigenetic profiling and CRISPR screens have become important tool boxes for cancer research. I will introduce the following two projects in the lab.

First, I will discuss how to utilize H3K27ac ChIP-seq data to better model gene regulation. By distant-weighting the H3K27ac ChIP-seq reads and integrating publicly available H3K27ac ChIP-seq data, we found an effective method to better identify genes activated or repressed by the BET inhibitor JQ1. We discovered that when given a list of differential genes between cell conditions, we could use a regression method to extract relevant public H3K27ac ChIP-seq and identify relevant enhancers that might regulate the differential expression of the genes of interests.

In the second part, I will discuss our computational work on facilitating genome-wide CRISPR/Cas9 knockout screens. We developed a sequence model to identify efficient sgRNAs for CRISPR screens and built MAGeCK / VISPR to analyze and visualize CRISPR screen results. We also designed a network analysis method to predict essential genes in a cell and prioritize CRISPR screen results. Finally I will demonstrate how we use CRISPR screens to study breast and prostate cancer progression into hormone independence.

**Friday, October 23, 2015 at 11:30a.m.**

**Room 1400 BPS**

*Refreshments at 11:15*