BIOSTATISTICS SEMINAR

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Computational Analysis of 3'UTR Usages in Human Cancers from RNA-Seq

Abstract

The transcriptome undergoes dramatic but highly orchestrated remodeling during diverse physiological state changes such as development and differentiation. This controlled process is perturbed under pathological conditions, such as cancer, leading alterations in transcriptome levels and content. The advent of the RNA-sequencing technology has provided an unprecedented resolution in profiling different aspects of the transcriptome including gene expression, alternative splicing, alternative polyadenylation (APA) and long non-coding RNAs. This form of deep profiling has brought new insights, many of which have been both biologically and clinically relevant.

Recent studies have demonstrated that APA is regulating more than 70% of human genes and accumulating evidences have indicated that APA is implicated in human diseases like cancers. Though compelling, it remains to be determined to what extent APA occurs in large clinical cohorts as well as its clinical utilities, functional consequences, and molecular mechanisms. In order to identify APA events retrospectively from the existing large-scale RNA-seq datasets in The Cancer Genome Atlas (TCGA), based on a sparse regression model, I developed a bioinformatics tool for the *de novo* Dynamic analysis of Alternative PolyAdenylation from RNA-Seq (DaPars). By applying DaPars to hundreds of tumor-normal matched RNA-seq samples from TCGA, I revealed a global 3'UTR shortening landscape, which can facilitate up-regulation of oncogenes during tumorigenesis by escaping miRNA repression (Xia et al., Nature Communications, 2014). Furthermore, through computational big-data analysis of TCGA RNA-seq using DaPars, I identified a pivotal function of CFIm25 as a tumor suppressor in glioblastoma through APA regulation (Masamha and Xia et al., Nature, 2014). Finally, I developed a sparse low-rank regression framework to identify more APA regulators from large-scale public RNA-seq data.

Date: Thursday, February 25, 2016
Time: 3:30 - 4:30 PM
Place: Blue Cross Blue Shield Memorial Auditorium
0001 Michael Hooker Research Center