DATE: January 13, 2022

TIME: 1:30-3:00pm

TITLE: Developing and translating liquid biopsies to create a personalized dynamic risk model during cancer therapy

SPEAKER: David Kurtz
Assistant Professor of Medicine (Oncology), Stanford

Abstract:

Predicting an individual’s response to treatment remains a major challenge in the care of patients with cancer. Liquid biopsies – a group of biomarkers to detect cancer from circulating tumor DNA (ctDNA) – are promising tools to measure treatment response and residual disease. Moreover, due to their ease of evaluation, liquid biopsies readily allow serial evaluation over time to monitor response and emerging resistance to therapy.

Despite this promise, current approaches for implementing liquid biopsies are limited in two key ways. First, the sensitivity of current approaches for detecting minimal residual disease are limited. Second, current clinical paradigms for risk stratification largely rely on static features measured at a single point in time. To address these, our group has developed novel molecular and statistical frameworks to improve the performance of liquid biopsies. First, we developed Phased Variant Enrichment and Detection by Sequencing (PhasED-Seq), a novel platform to detect ctDNA in the parts-per-million range. This method allows for measurement of residual disease that is undetectable by other approaches. Later, we developed a framework to integrate serial ctDNA measurements with conventional prognostic features to produce a single personalized prediction of likely outcome to cancer therapy. This method, called the Continuous Individualized Risk Index (CIRI), adds additional information as it is measured throughout a patient’s course of therapy to dynamically update the probability of outcomes for an individual patient. We demonstrate that CIRI can improve on risk predictions from conventional risk tools in diverse cancers, including lymphomas, leukemias, and breast cancer.

Suggested Reading:
- Phased variant enrichment for enhanced disease detection from cell-free DNA
- Dynamic risk profiling using serial tumor biomarkers for personalized outcome prediction