CHINESE-AMERICAN LUNG ASSOCIATION

CALA Happy Friday Seminar

March 4th, 2022

Time: EST 10:30 am; PST: 7:30 am; Beijing time: 11:30pm

Zoom: 849 9682 9273 (Password: 654321)

A Brief Introduction on Nanopore Sequencing

Hongxu Ding, PhD

Assistant Professor

College of Pharmacy, University of Arizona

Bio: Dr. Ding finished his undergraduate at Tsinghua University in 2013, where he was initially trained as a physicist and later switched to the field of life sciences. He finished his PhD at Columbia University under the instruction of Dr. Andrea Califano in 2018, where he worked on single-cell systems biology. After that, he joined UCSC Genomics Institute as a postdoctoral scholar. Under the supervision of Dr. Joshua Stuart and Dr. Benedict Paten, he continued his work on single-cell analysis, as well as expanded his research to the field of nanopore sequencing. Dr. Ding joined the University of Arizona, College of Pharmacy in 2021 as an assistant professor. The Ding lab (http://dinghongxulab.org/) develops computational biology approaches to interpret single-cell omics profiles and nanopore sequencing readouts.

Abstract: Nanopore sequencing has several prominent advantages, which promise to revolutionize life science research. Specifically, nanopore sequencing is able to 1) generate ultra-long sequencing reads, which greatly facilitate, e.g. *de novo* genome assembly, genome structural variation detection and RNA splicing isoform detection; 2) profile native DNA/RNA molecules, which opens up possibilities for routinely detecting nucleotide modifications; 3) perform real-time sequencing, which could be used for, e.g. field sequencing and diagnostics.

In my presentation, I will first introduce how does nanopore sequencing work. I will then describe the above-mentioned prominent advantages of nanopore sequencing with basic and clinical research examples. At the end of the presentation, I will report my recent work on nanopore sequencing-based *de novo* nucleotide modification analysis.