ABSTRACT

Precision cancer medicine leverages advances in genomics and computational methods towards a better life. The genomic data has to be integrated with diverse biomedical information and analyzed through biologically interpretable computational methods, before they can lead to biomedical discoveries.

In this talk, I will discuss my research on integrating diverse biomedical data types to understand cancer. First, I will describe a genome-to-disease bioinformatic pipeline that identifies the underlying cause of ovarian cancer initiation and development. Next, I will present a probabilistic model that predicts gene’s expression and provides experimentally testable hypotheses in embryonic development. These knowledge-guided probabilistic frameworks explore fundamental aspects of cancer biology and transform the way of scientific discovery. Finally, I will address promising directions for catalyzing a new era of data-driven precision cancer medicine.

BIOGRAPHY

Pei-Chen Peng (http://www.peichenpeng.com/) is a postdoctoral scientist at Cedars-Sinai Medical Center, working with Dr. Simon Gayther. Her research focuses on machine learning and statistical modeling of heterogenous multi-omics data to improve the prevention and treatment of cancer and other diseases.

She obtained her Ph.D. in Computer Science from University of Illinois at Urbana-Champaign in 2018, advised by Prof. Saurabh Sinha. She holds a M.S. and a B.S. in Computer Science from National Taiwan University. She received an NIH/NCI Early K99/R00 Pathway to Independence Award in 2021 and a Google Anita Borg Award in 2012. She was also recognized as a Rising Star in Electrical Engineering and Computer Sciences in 2019.