Hong Kong Institute for
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Online Seminar

HONG KONG INSTITUTE FOR DATA SCIENCE
POSTDOC ASSOCIATES AND STUDENTS SEMINAR

Enabling Single-Cell Drug Response Annotations from Bulk RNA-seq Using SCAD

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Date: 8 January 2024 (Monday)
Time: 3:00pm - 4:00pm
Zoom meeting ID: 985 7555 6083

Seminar link: https://cityu.zoom.us/j/98575556083

Abstract

Bulk RNA sequencing (Bulk RNA-seq) and single-cell RNA sequencing (scRNA-seq) techniques are practical tools for measuring gene expression levels from biopsy samples. The scRNA-seq quantifies the gene expression levels of individual cells, while the bulk RNA-seq measures the average transcriptional profiling of a population of cells. The inference of drug response sensitivities for individual cells can provide detailed and novel insights to understand the mechanism of heterogenous anti-cancer responses and drug resistance at cellular resolution. Unfortunately, the pharmacogenomic information associated with their corresponding single cell is often limited. In contrast, cancer cell lines are still the most widely applied laboratory models for oncology study and anti-cancer drug discovery so far. Therefore, we proposed a transfer learning framework for single-cell drug response inference. This framework integrates domain adaptation strategy to learn cell line bulk pharmacogenomics and transfers the learned knowledge to infer drug response sensitivities at single cells prior to treatment. We have also adopted a widely used model interpretability algorithm (for machine learning models) to infer the subset of genes that contribute the most to drug sensitivity prediction. In addition, our model offers a new perspective on anti-cancer drug combinations. The identified drug sensitivity biomarkers reveal insights into the tumor heterogeneity and treatment at cellular resolution.

Biography

Zetian ZHENG is a Ph.D. candidate at the Department of Computer Science, City University of Hong Kong, under the supervision of Prof. Ka-Chun Wong. He is interested in understanding tumor heterogeneity and pathology informatics by employing computational biology methods on multi-omics data, such as genomics, transcriptomics, and proteomics. Currently, he is focusing on constructing and adopting machine-learning models to explore the clinical translation value of single-cell sequencing data. He has published several journal papers, including IEEE Journal of Biomedical and Health Informatics, and Advanced Science.

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