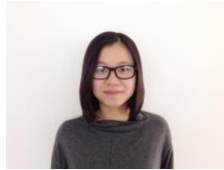




University
of Manitoba

STATISTICS SEMINAR

Thursday, February 17, 2022 at 2:30pm via ZOOM (details below)



QIAN LIU

PhD student (Individual Interdisciplinary Studies)
Department of Biochemistry and Medical Genetics, Statistics and Computer Science
University of Manitoba

“Artificial Intelligence-Empowered Breast Cancer Radiogenomics for Precision Medicine”

Breast cancer (BC) is heterogeneous both genomically and phenotypically. In precise medicine, it is of great significant to develop computational frameworks for identifying prognostic biomarkers which can capture both genomic and phenomic heterogeneity of BC. Radiogenomics is a field where medical images and genomic measurements are integrated and mined to solve challenging clinical problems. There are some limitations in previous radiogenomic studies such as data incompleteness, feature subjectivity and low interpretability. Majority of radiogenomic studies miss one or two of medical imaging data, genomic data, and clinical outcome data, which results in the data incomplete issue. The feature subjectivity comes from the extraction of imaging features with significant human involvement. Although there are some automatic feature extraction methods, such as deep learning (DL), they have limited interpretability. Therefore, there is a pressing need to address the limitations so that fully automatic and transparent radiogenomic prognostic biomarkers could be identified for BC.

In this talk, I will introduce two computational frameworks to address the radiogenomic analysis issues. The first framework mainly focuses on exploring deep learning approaches for automatic medical imaging feature extraction and their association to single type of genomic features and clinical outcomes. The second framework discusses the application of tensor factorization technique to integrate and extract multiple types of omics features, the new deep learning strategy to extract imaging features, and a leverage strategy to take advantage of unpaired imaging, genomic, and clinical outcome data. I will also discuss how to apply statistic mediation analysis for providing further interpretation of identified radiogenomic biomarkers. This work provides a new perspective for conducting a comprehensive radiogenomic study when only limited resources are given. Comparing with traditional radiogenomic biomarkers, the biomarkers identified by the proposed frameworks have significantly higher prognostic value, and their interpretability is guaranteed by different levels of build-in and follow-up analyses.

Seminar at 2:30pm (Join us at 2:00pm for a Meet & Greet)

ZOOM LINK: <https://umanitoba.zoom.us/j/66698742330?pwd=T2laUnUxWFdHbC9QdU1vVXFqTm44QT09>

Meeting ID: 666 9874 2330

Passcode: 103307