THE UNIVERSITY OF CHICAGO

Department of Statistics
MASTER'S THESIS PRESENTATION

ISABELA KERNIN

Department of Statistics
The University of Chicago

Exploring Host Response to SARS-CoV-2 Through Differential Expression Analysis

TUESDAY, February 23, 2021, at 2:00 PM
ZOOM Meeting

ABSTRACT

RNA sequencing enables the comparison of gene expression levels between biological conditions, and genes identified through RNA-seq data have been used to classify infection and risk of severity in multiple diseases. Covid-19, caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), was declared a pandemic in March 2020. However, many factors related to the severity and progression of the disease remain unknown. This project explores how differential expression (DE) analysis of RNA-seq data may be useful in piecing apart the complexities of host response to SARS-CoV-2. Using a publicly available dataset, DE analysis is used to determine genes that change in expression due to infection by the virus. These genes are then used in downstream analysis to identify effected biological processes through over-representation analysis (ORA) and gene set enrichment analysis (GSEA). Since risk of disease severity has been linked to patient age and sex, DE analysis is also performed to identify genes effected by the respective interactions of these two factors and viral infection.