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DSICCR Tuesday Seminar Series

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Identifying Viruses from Host Genomes and Predicting Virus-host Interactions and Disease Severity

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Viral infections are commonly observed in nature. Recently, SARS-CoV-2 has caused a global pandemic which has infected over 200 million individuals worldwide (as of August 2021). Effective and efficient detection of viruses in host genomes, together with tracking how viruses interact with host genomes, are major challenges. In this talk, I will first introduce our computational approaches for detecting viruses and their integration sites in host genomes from next-generation sequencing data. Then, based on our recently developed Viral Integration Site DataBase (VISDB), we have developed a deep learning method, DeepVISP, for virus site integration prediction and motif discovery. To study COVID-19, we developed a deep learning method, DrivAER: Identification of Driving transcriptional programs with AutoEncoder derived Relevance scores from single-cell RNA sequencing (scRNA-seq) data. We applied DrivAER to COVID-19 scRNA-seq data and also for integrative analysis of COVID-19 genome-wide association studies (GWAS) and transcriptome-wide association studies (TWAS). Our investigation identified a number of genes, regulatory factors, and cellular trajectories that may be relevant in COVID-19 disease severity.

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