

## **Project Outline**

### ***What is the name of your project?***

Identification of Consistently Dysregulated Modules and Pathways during Infection by Coronaviruses; Applications to COVID-19

### ***What is the project pitch for recruiting participants? (200 character max)***

We aim to identify consensus gene sets/modules that are consistently dysregulated during infection by coronaviruses with the aim of enhancing the understanding of SARS-CoV-2 infection.

### ***Overview of the main objectives, why they are significant and how you plan to accomplish it.***

Identification of data will be important, as even for previous coronaviruses (MERS,SARS), data is limiting and heterogenous. We will mine OmicsDI, ArrayExpress etc for this data and perform various clustering analyses to remove outliers. This may need to be done prior to the official hackathon. Identification of genes/modules where there is evidence for their dysregulation during SARS-Cov-2019 infection, to compare back to the consensus network predictions. This will be accomplished via a literature search. Construction of network predictions and identification of consensus modules/pathways in order to determine possible pan-coronavirus dysregulated modules/ gene sets, using tools/packages such as WGCNA, ARACNE etc.

## **Data/Papers**

### **SARS-CoV-2**

<https://www.biorxiv.org/content/10.1101/2020.03.12.988865v2.full.pdf> – various nanopore RNA-seq based methods