



RNA Expression of Lung Cells Infected with COVID-19

Michael Mezzina, Zhiqing Qu

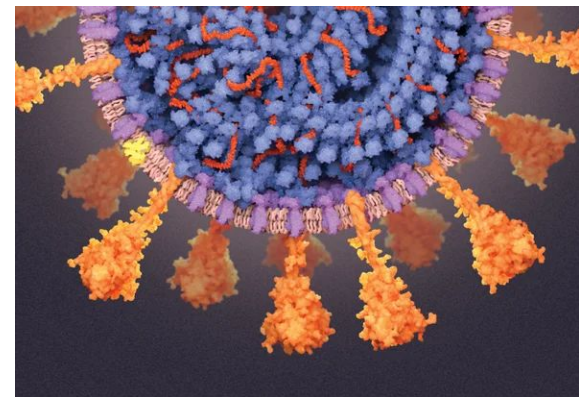
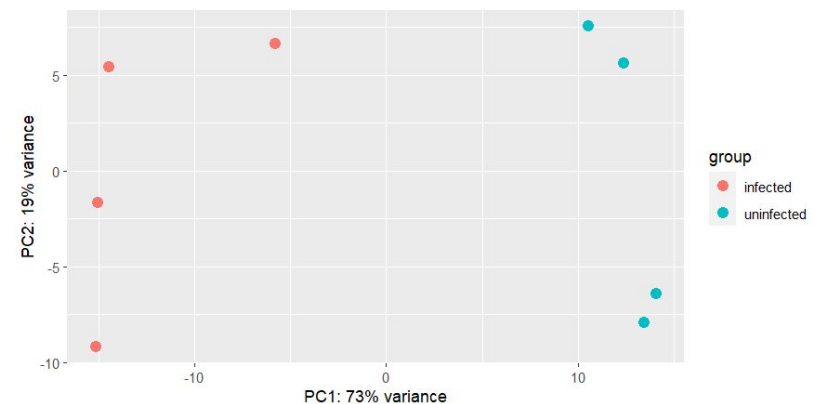
November 23

Team 2

Introduction

General description of our approach:

- General background about coronavirus family
 - Middle East Respiratory Syndrome (MERS)
 - Caused by Middle East Respiratory Syndrome Coronavirus (MERS-CoV).
 - Severe Acute Respiratory Syndrome (SARS)
 - Caused by SARS-associated Coronavirus.
 - Ongoing Coronavirus Disease 19 (COVID-19) pandemic
 - Caused by Severe Acute Respiratory Syndrome coronavirus 2 (SARS-CoV-2).
- COVID-19 causes respiratory symptoms
 - Cold
 - Flu
 - Pneumonia
- COVID-19 may attack more than your lungs and respiratory system. Other parts of your body may also be affected by the disease.
- PCA plot (on the right).
 - No similarities.
- Differential expression analysis and unsupervised analysis will be used to analyze the data.



Hypothesis

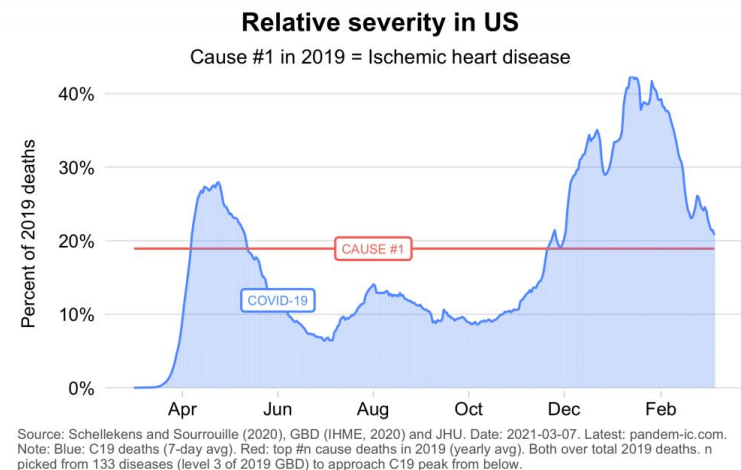
Our hypothesis: To identify the difference in RNA expression between infected and uninfected lung cells.

The reason we chose this question:

- Severity of COVID-19.
- Picture on the right.

How we used data to answer it:

- Data used: Calu3 cells infected and uninfected and sampled at different hours.
- Differential expression analysis
 - PCA plot
 - biological processes ontology
 - dotplot
- Unsupervised analysis
 - Clustering methods
 - heatmaps
 - chi-squared tests

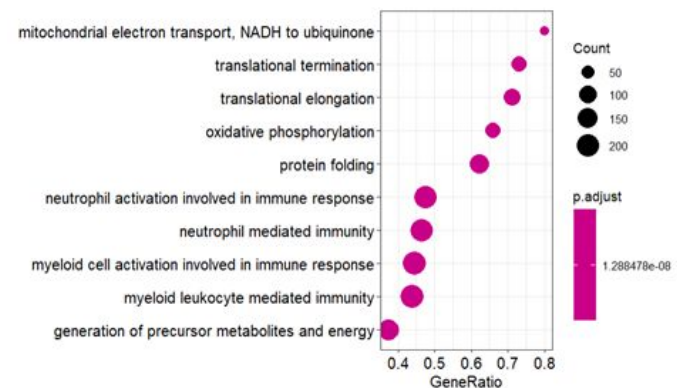
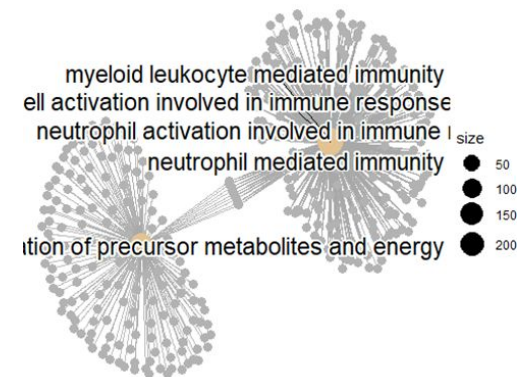
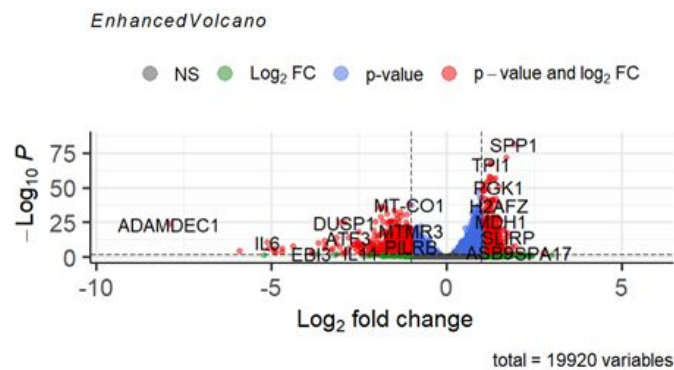


Differential Expression and Enrichment Analysis

Findings from GSEA

Infected cells

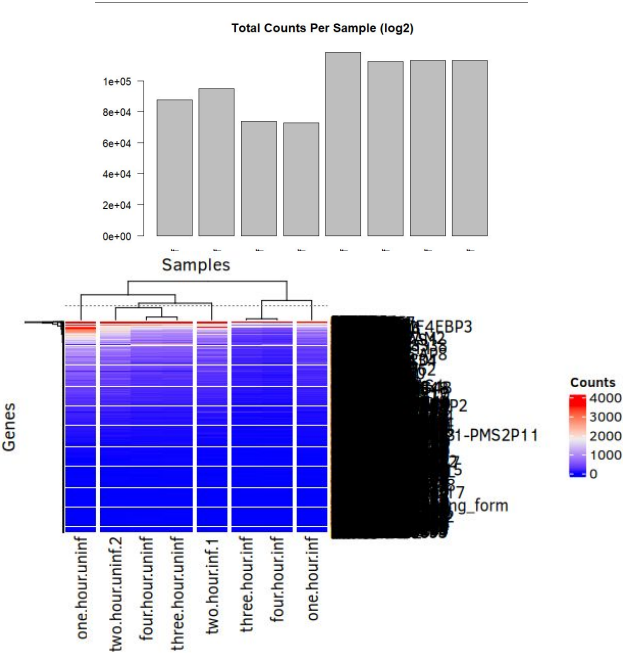
- signal to neutrophils and leukocytes
 - Cytokine increases
 - interleukin expression in volcano plot
- have reduced oxidative glutamine metabolism



Clustering & Enrichment Analysis

Findings

- Expression of host genes in lung cells is reduced
- Infected and uninfected cell samples are clustered together.
- Clustered samples don't align with infected vs uninfected groups



Chi Squared Tests

	Starting Group	Consensus Cluster
Cluster 1 / Infected	4	6
Cluster 2 / Not Infected	4	2

$$\chi^2 = 0.266$$

$$P\text{-value} = 0.6956$$

	Starting Group	KMeans
Cluster 1 / Infected	4	5
Cluster 2 / Not Infected	4	3

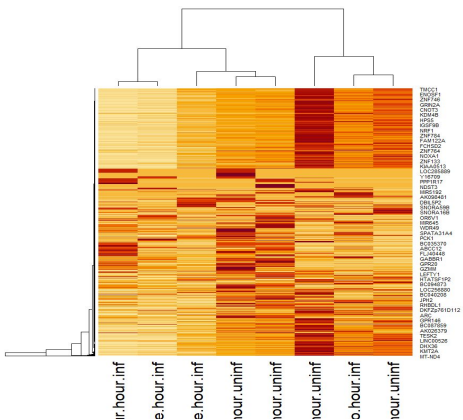
$$\chi^2 = 0$$

$$P\text{-value} = 1$$

	Consensus Cluster	KMeans
Cluster 1 / Infected	6	5
Cluster 2 / Not Infected	2	3

$$\chi^2 = 0.266$$

$$P\text{-value} = 0.6956$$



Conclusions & Future Work

Some of our main findings about lung cells infected with Sars-CoV-2:

- Gene expression from the host cells is reduced. The original paper for our dataset examined this in depth.
- Host cells signal immune cells and begin an immune response. Cytokines are released by infected cells. The strong immune response caused by cytokines has been linked to damage in the lungs and death from COVID-19.
- Metabolism of infected cells changes. Other research has found that mitochondria and cellular metabolism play an important role in COVID-19 progression and virus replication. This may be related why some groups, like diabetes and elderly, have worse outcomes when infected.