

Supplementary Material: Instructions for running DeCovid.

DeCovid: A tool for conducting a Wide-spread transcriptional analysis for COVID-19 Disease Map genes

How to Run DeCovid

There are two main options to run DeCovid:

1. Run DeCovid Docker image
2. Install and run as *R package*.

Run DeCovid Docker Image

1. Requirements:
 - Docker engine.
2. Run Docker image in **terminal** (Mac/Linux) **PowerShell** (Win):

```
docker run --rm -p 3838:3838 conesalab/decovid:decovid
```
3. Open the URL that the **terminal** (**PowerShell**) will return (typically [http://\[::\]:3838](http://[::]:3838)) in a **web browser**.

```
[2020-09-25T12:29:21.932] [INFO] shiny-server - Starting listener on http://[::]:3838
```

Run DeCovid Shiny App

1. Requirements:
 - RStudio
 - Install following R packages:

```
install.packages("shinydashboard")
install.packages("shiny")
install.packages("pheatmap")
install.packages("ggplot2")
install.packages("png")
install.packages("grid")
install.packages("DT")
install.packages("scales")
BiocManager::install("edgeR")
BiocManager::install("clusterProfiler")
BiocManager::install("org.Hs.eg.db")
```
2. Download Code and files in GitHub:
 - <https://github.com/ConesaLab/DeCovid>
3. Open **app.R** file and click Run App

