

Subchallenge 1 Report

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load libraries

```
library(knitr)
```

set global options

```
knitr::opts_chunk$set(echo=FALSE,
                      results='markup',
                      comment=NA,
                      message=FALSE,
                      warning=FALSE,
                      error=FALSE,
                      fig.width=8,
                      fig.align='center',
                      fig.path="Figs/",
                      dev="png",
                      dev.args=list(type="cairo"),
                      dpi=96)
```

download data

calculate genesets

```
[1] "H1N1 Predictors With p-value < 0.005"
[1] "H3N2 Predictors With p-value <0.005"
[1] "Rhinovirus Predictors With p-value < 0.005"
[1] "H1N1 H3N2 Intersection"
[1] "H3N2 Rhinovirus Intersection"
[1] "H1N1 Rhinovirus Intersection"
[1] "H1N1 H3N2 Rhinovirus Intersection"
[1] "H1N1 Only"
[1] "H3N2 Only"
[1] "Rhinovirus Only"
```

generate heatmaps

perform pathway analysis