# H5N1 Data Analysis Workflow

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# Environment Setup

## 

## Build and Activate Conda Environment

conda env create --file=env.yaml  
conda activate h5n1  
  
# Install eNetXlporer through install.packages()  
install.packages("eNetXplorer")

Most of the scripts initialize the environment at the very beginning however, if not then run:  
source("SCRIPTS/0\_initialize.r")

To run a script using singularity container:

$ Rscript --vanilla <script path>

## Singularity container

Singularity container with the R packages that were used for the analysis can be downloaded from:

<https://cloud.sylabs.io/library/_container/5d728283cb093ee1142b8810>

or

$ singularity pull library://rohitfarmer/default/h5n1\_workflow:sha256.240542df22ff14f6e49b58f43065e26b1d2d8a1103840d869f6034a5426eaeca

To run a script using singularity container:

$ singularity exec h5n1-container.sif Rscript –vanilla <script path>

*Note: Singularity container also has Neovim installed that can be used with Nvim-R plugin installed on the host system. Recipe file to build the singularity container is available at* <https://github.com/rohitfarmer/singularity-defs/tree/master/H5N1>

*Note: For both conda environment and Singularity container project folder is working directory. Therefore, all the scripts executes relative to the project folder.*

# Titers

## 

## Figure 1A

URL to the Shinyapp that produces figure 1A H5N1/MANUSCRIPT/Figures/Figure1\_url\_180322.txt

## Figure 1B

Rscript --vanilla SCRIPTS/titers/mn\_titer\_profiles.r

## Supplemental Figure 1

Fig 1A.

Rscript --vanilla SCRIPTS/titers/titer\_response\_rate.r

Fig 1B.

Rscript --vanilla SCRIPTS/titers/hai\_titer\_profiles.r

Fig 1C.

Rscript --vanilla SCRIPTS/titers/mn\_titer\_peak.r

# 

# Pattern profiles of clinical CBC data and Luminex

## 

## Figures 1 C,D,E

Fig 1C, D.

Rscript --vanilla SCRIPTS/profiles/Monocytes\_figure.r  
Rscript --vanilla SCRIPTS/profiles/Neutrophils\_figure.r

Fig 1E.

Rscript --vanilla SCRIPTS/profiles/IP10\_figure.r

# Pattern simulation (Figure 2A)

Rscript --vanilla SCRIPTS/pattern\_sim/pattern\_simulation.r

Gene Expression PBMC data processing. First, the CEL files were processed with Power Tools RNA-sketch algorithm.

Rscript --vanilla SCRIPTS/MA/processing\_pbmc/apt.config.r  
Rscript --vanilla SCRIPTS/MA/processing\_pbmc/apt.call.r

*Note: Power Tools are not included in the singularity container or in the conda environment file.*

## 

## Create ExpressionSet from APT output

Rscript --vanilla SCRIPTS/MA/processing\_pbmc/eset.config.r

Rscript --vanilla SCRIPTS/MA/processing\_pbmc/eset.call.r

## 

## Probesets to genes mapping

### 

### Convert the table to probeset-gene mapping

Rscript --vanilla SCRIPTS/MA/annotation/affy\_hugene-2\_1-st\_annotation.r

### 

### Select the best probeset for a gene

Rscript --vanilla SCRIPTS/MA/annotation/generate\_ps2gene\_map.config.r  
Rscript --vanilla SCRIPTS/MA/annotation/generate\_ps2gene\_map.call.r

## Data post processing

### 

### We found that two samples were switched. This is to correct it.

Rscript --vanilla SCRIPTS/MA/filtering\_pbmc/switch.samples/switch.samples.call.r

### Apply different filtering to samples and genes. The probesets mapped to genes.

Rscript --vanilla SCRIPTS/MA/filtering\_pbmc/samples.clean\_genes.all/filtering.r  
Rscript --vanilla SCRIPTS/MA/filtering\_pbmc/samples.clean\_genes.iqr/filtering.r  
Rscript --vanilla SCRIPTS/MA/filtering\_pbmc/samples.all\_genes.all/filtering.r  
Rscript --vanilla SCRIPTS/MA/filtering\_pbmc/samples.all\_genes.iqr/filtering.r

### 

### Calculate fold change from day 0

Rscript --vanilla SCRIPTS/MA/calculate\_d0\_fc/calculate\_d0\_fc\_pbmc.r

# Pattern discovery in post-vaccination profiles of gene expression

## 

## Profiles clustering with DIANA

Rscript --vanilla SCRIPTS/MA/pattern\_discovery/pattern\_discovery.r

## Cut the dendrogram tree at different levels and detect stable clusters

Rscript --vanilla SCRIPTS/MA/pattern\_discovery/patterns\_cutTree\_stable.r

## 

## Filter the patterns

Rscript --vanilla SCRIPTS/MA/pattern\_discovery/pattern\_filter.r

## 

## Summarize patterns stats

Rscript --vanilla SCRIPTS/MA/pattern\_discovery/patterns\_stats.r

## 

## Figure 2B - patterns profile plot

Rscript --vanilla SCRIPTS/MA/pattern\_discovery/plot\_patterns.r

## 

## Expand list of pattern signature genes

Rscript --vanilla SCRIPTS/MA/pattern\_discovery/pattern\_filter\_expanded.r

## 

## Compute correlations and clean up the genes

### 

### Supplemental Figure 2A

Rscript --vanilla SCRIPTS/MA/pattern\_discovery/pattern\_expanded\_genes\_cor.r  
Rscript --vanilla SCRIPTS/MA/pattern\_discovery/pattern\_expanded\_genes\_clean.r

## 

## Compute subject scores for each pattern

Rscript --vanilla SCRIPTS/MA/pattern\_discovery/patterns\_to\_subjects.r

## Output the table of genes (with annotations) for each pattern

Rscript --vanilla SCRIPTS/MA/pattern\_discovery/pattern\_genes\_output.r

## 

## BTM enrichment in patterns genes.

## Figure 2C

Rscript --vanilla SCRIPTS/MA/pattern\_discovery/pattern\_BTM\_enrichment.r

## 

## Add data for subject s10 and update the score matrix

Rscript --vanilla SCRIPTS/MA/pattern\_discovery/s10\_peaks\_assessment.r  
Rscript --vanilla SCRIPTS/MA/pattern\_discovery/pattern\_scores\_in\_samples\_GE\_incl.s10.r

# 

# Pattern discovery in post-vaccination profiles of flow cytometry data

FlowJo software was used to export flow data.

## 

## Generate Trajectory Matrix

Rscript --vanilla SCRIPTS/Flow\_10c/Flow\_10c\_TrajMatrix\_v2.R  
Rscript --vanilla SCRIPTS/Flow\_10c/Flow\_10c\_TrajMatrix\_v3.R

## Genetrate Trajectory Clusters

Rscript --vanilla SCRIPTS/Flow\_10c/Flow\_10c\_TrajCluster\_v2.R  
Rscript --vanilla SCRIPTS/Flow\_10c/Flow\_10c\_TrajCluster\_v3.R

## Figure 2D

Rscript --vanilla SCRIPTS/Flow/pattern\_figures/plot\_flow\_patters\_only.r

## 

## Figure 2E

Rscript --vanilla SCRIPTS/Flow/pattern\_figures/pattern\_flow\_ann\_heatmap.r

## Figure 2F

Rscript --vanilla SCRIPTS/MA/pattern\_discovery/pattern\_scores\_GE\_flow\_heatmap.r

## 

## Supplemental Figure 3

Rscript --vanilla SCRIPTS/Flow\_10c/Flow\_10c\_TrajCluster\_QM.R

# 

# Find signature for adjuvant status prediction

## 

## Figure 3C

Rscript --vanilla SCRIPTS/adjuvant\_prediction/2peaks\_pca\_2clusters.r

## 

## Figure 3D

Rscript --vanilla SCRIPTS/adjuvant\_prediction/ip10\_2clusters\_compare.r

## 

## Supplemental Figure 4B

Rscript --vanilla SCRIPTS/adjuvant\_prediction/cytokines\_2clusters\_compare.r

## 

## Supplemental Figure 4C

Rscript --vanilla SCRIPTS/MA/baseline/Gb13\_vs\_GbWB11.r

## 

## Figure 3E

Rscript --vanilla SCRIPTS/adjuvant\_prediction/ip10\_2peak\_scores.r  
Rscript --vanilla SCRIPTS/adjuvant\_prediction/2peaks\_pca\_final\_heamap.r

### 

### Generate input data:

Rscript --vanilla SCRIPTS/eNetXplorer/eNet\_input\_r1.r