

# BIOF439 Final Project

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## Overview

In this plot, I am comparing the change in MFI values for several immune cell surface markers and one intracellular phosphoprotein. Peripheral blood mononuclear cells (PBMCs) were collected from whole blood of 9 healthy donors. The PMBCs were stimulated for 20 minutes with IL-10, a cytokine with known action to phosphorylate STAT3. The goal of this experiment was to determine whether stimulation with this cytokine would affect staining for the surface markers to differentiate cell types. The MFIs for each surface marker should be comparable with little to no variance in order to ensure there is no stimulation effect on immunophenotyping. From the graph, we can see that the only condition with an obvious difference between “stim” and “unstim” is the pSTAT3 group, which confirms effective stimulation and that immunophenotyping is not altered by stimulation with IL-10.

## Setup

```
library(rio)
UnstimvStim <- import("Stim vs Unstim DataViz JK.xlsx")
head(UnstimvStim)
```

```
##   Marker Fluorochrome Unstim Stim
## 1   CD3      APC-H7    1300 1382
## 2   CD3      APC-H7    1324 1385
## 3   CD3      APC-H7    1327 1390
## 4   CD3      APC-H7    1302 1362
## 5   CD3      APC-H7    1316 1373
## 6   CD3      APC-H7    1324 1371
```

```
my_theme <- function(){
  labs_pubr() +
    theme(axis.title = element_text(size = 10),
          axis.text = element_text(size = 10),
          strip.text = element_text(size = 10),
          legend.position = "none")
}
```

```
library(ggplot2)
library(ggpubr)
```

```
## Loading required package: magrittr
```

```
library(tidyverse)
```

```
## -- Attaching packages ----- tidyverse 1.2.1 --
```

```
## v tibble  2.0.1      v purrr   0.3.1
## v tidyr   0.8.3      v dplyr   0.8.0.1
## v readr   1.3.1      v stringr 1.4.0
## v tibble  2.0.1      v forcats 0.4.0
```

```
## -- Conflicts ----- tidyverse_conflicts() --
```

```
## x tidyr::extract() masks magrittr::extract()
## x dplyr::filter() masks stats::filter()
## x dplyr::lag() masks stats::lag()
## x purrr::set_names() masks magrittr::set_names()
```

## Some Data Wrangling

```
UnstimvStim1 <- UnstimvStim %>%
  gather(Condition, MFI, Stim, Unstim)
head(UnstimvStim1)
```

```
##   Marker Fluorochrome Condition  MFI
## 1    CD3      APC-H7      Stim 1382
## 2    CD3      APC-H7      Stim 1385
## 3    CD3      APC-H7      Stim 1390
## 4    CD3      APC-H7      Stim 1362
## 5    CD3      APC-H7      Stim 1373
## 6    CD3      APC-H7      Stim 1371
```

## Generate Graph

```
ggplot(UnstimvStim1, aes(x = Condition, y = MFI, color = Condition)) +
  geom_jitter(width = 0.4) +
  my_theme() +
  labs(x = "",
       y = "Median Fluorescent Intensity (MFI)",
       title = "Conditional Comparison of Surface/Intracellular Markers") +
  facet_grid(cols = vars(Marker))
```

Conditional Comparison of Surface/Intracellular Markers

