

## 4.Exploration facs data

Fay

2022-10-05

### Import data

```
MICE <- read.csv("output_data/MICE.csv")
```

### Vectors for selecting cells

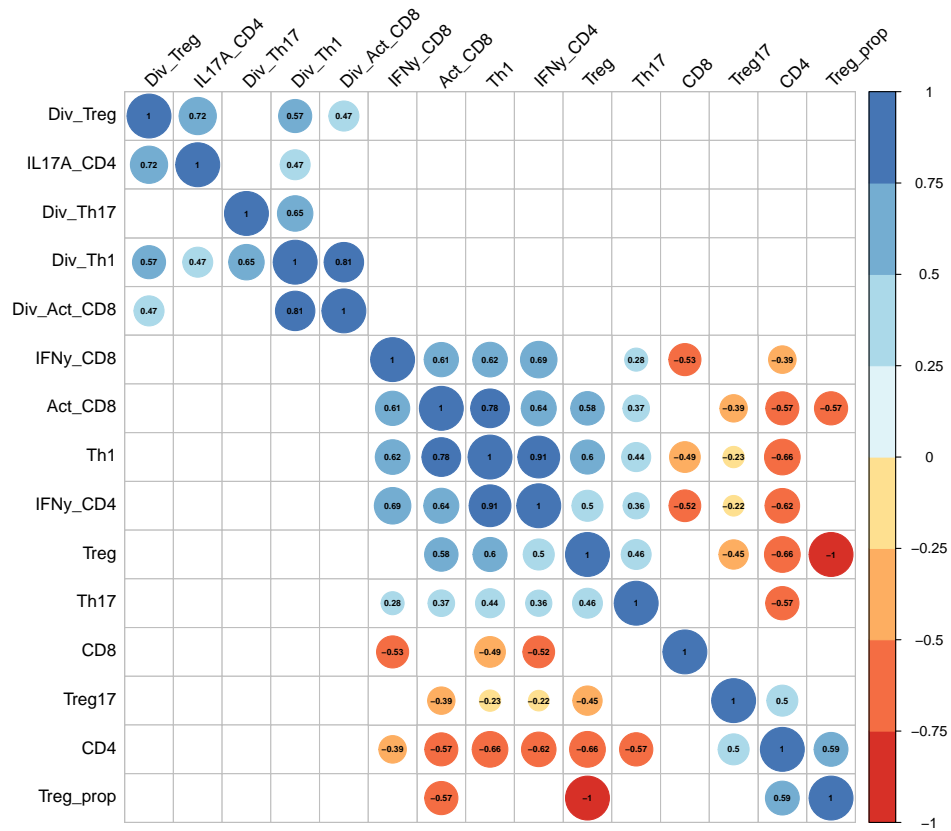
```
Facs_lab <- c("CD4", "Treg", "Div_Treg", "Treg17", "Th1",  
             "Div_Th1", "Th17", "Div_Th17", "CD8", "Act_CD8",  
             "Div_Act_CD8", "IFNy_CD4", "IFNy_CD8", "Treg_prop",  
             "IL17A_CD4")  
  
Facs_wild <- c("Treg", "CD4", "Treg17", "Th1", "Th17", "CD8",  
             "Act_CD8", "IFNy_CD4", "IL17A_CD4", "IFNy_CD8")
```

### Lab data

#### Correlations between the cells

#### Corrplot of correlations - Laboratory facs data

Here is a corrplot of the correlations between the cells

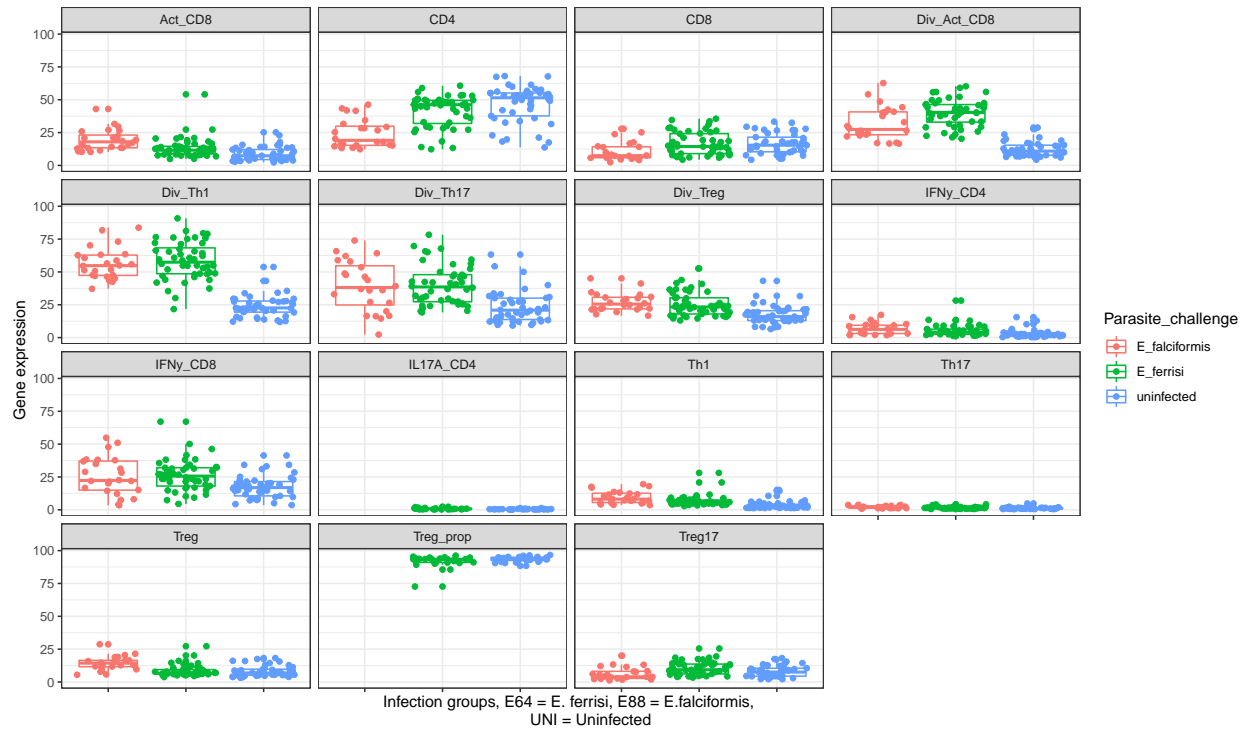


## FACS versus infection intensities - laboratory infections

## Warning: Removed 762 rows containing non-finite values (stat\_boxplot).

## Warning: Removed 762 rows containing missing values (geom\_point).

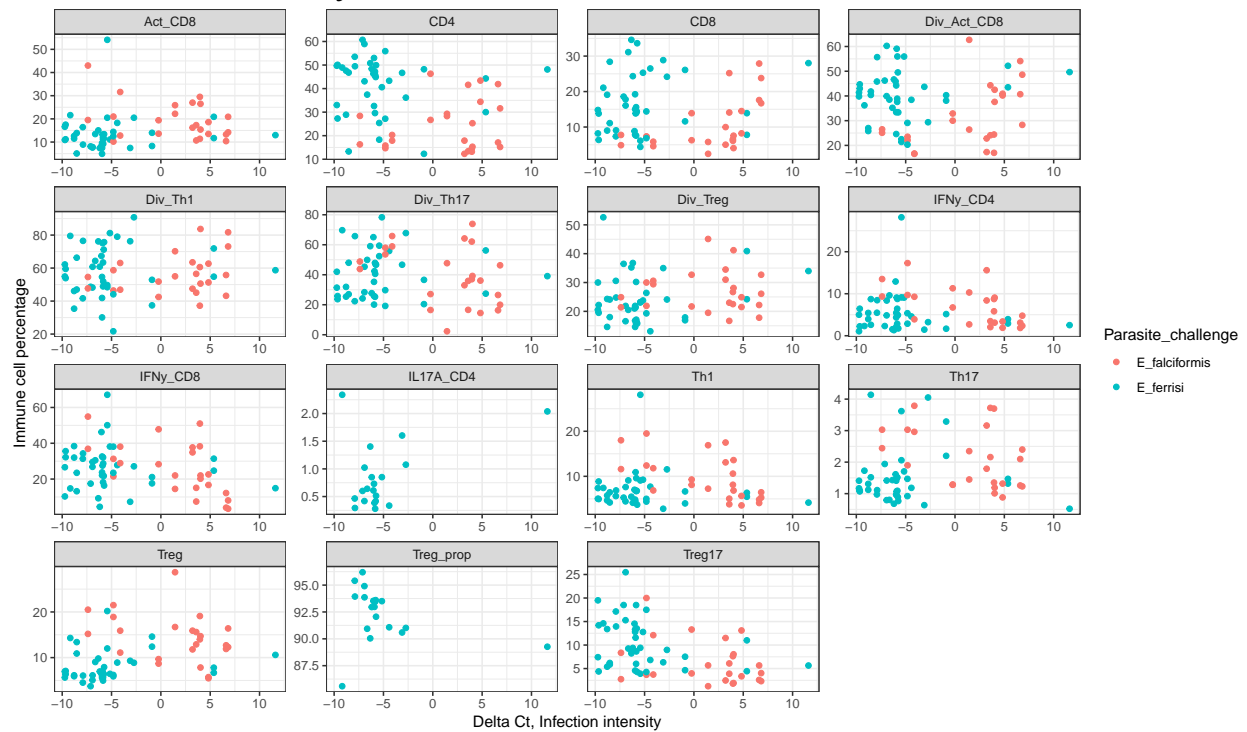
## Immune cell percentages in response to infection group, laboratory infections



```
f %>%
  filter(!Parasite_challenge == "uninfected", MC.Eimeria == "TRUE") %>%
  ggplot(aes(x = delta_ct_cewe_MminusE, y = Percentage,
             color = Parasite_challenge)) +
  geom_jitter() +
  facet_wrap(~ Cells, scales = "free") +
  theme_light() +
  labs(x = "Delta Ct, Infection intensity", y = "Immune cell percentage",
       title = "Immune cells in response to infection intensity -
               laboratory infections") +
  theme_bw() +
  theme(plot.title = element_text(size= 30))
```

```
## Warning: Removed 463 rows containing missing values (geom_point).
```

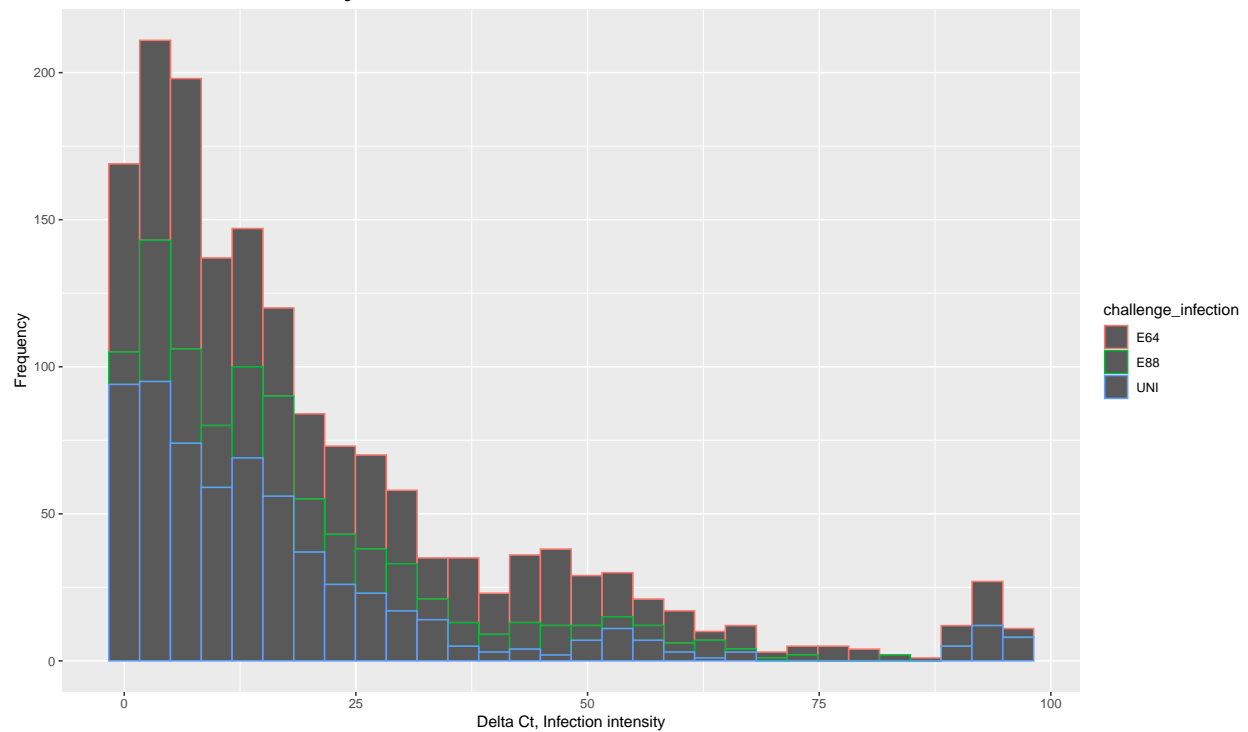
## Immune cells in response to infection intensity – laboratory infections



## Warning: Ignoring unknown parameters: echo

## Warning: Removed 762 rows containing non-finite values (stat\_bin).

## Immune cells in response to infecting parasite – laboratory infections



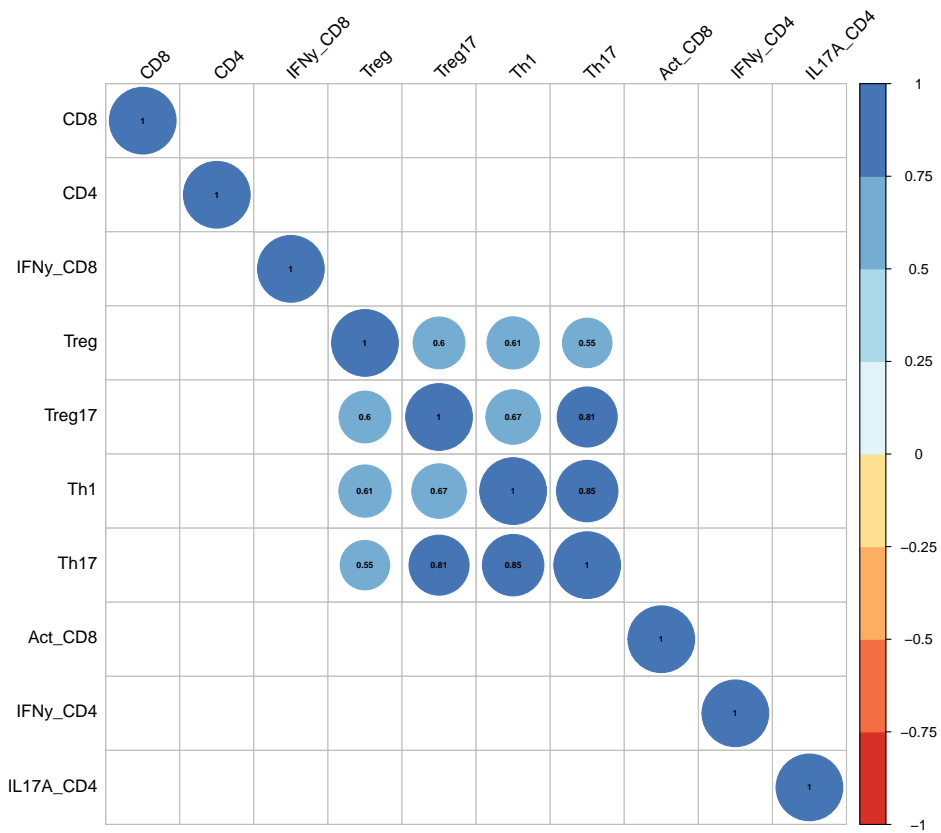
## Repeating for field infections

### Field data

#### Correlations between the cells

#### Corrplot of correlations - Field facs data

Here is a corrplot of the correlations between the cells

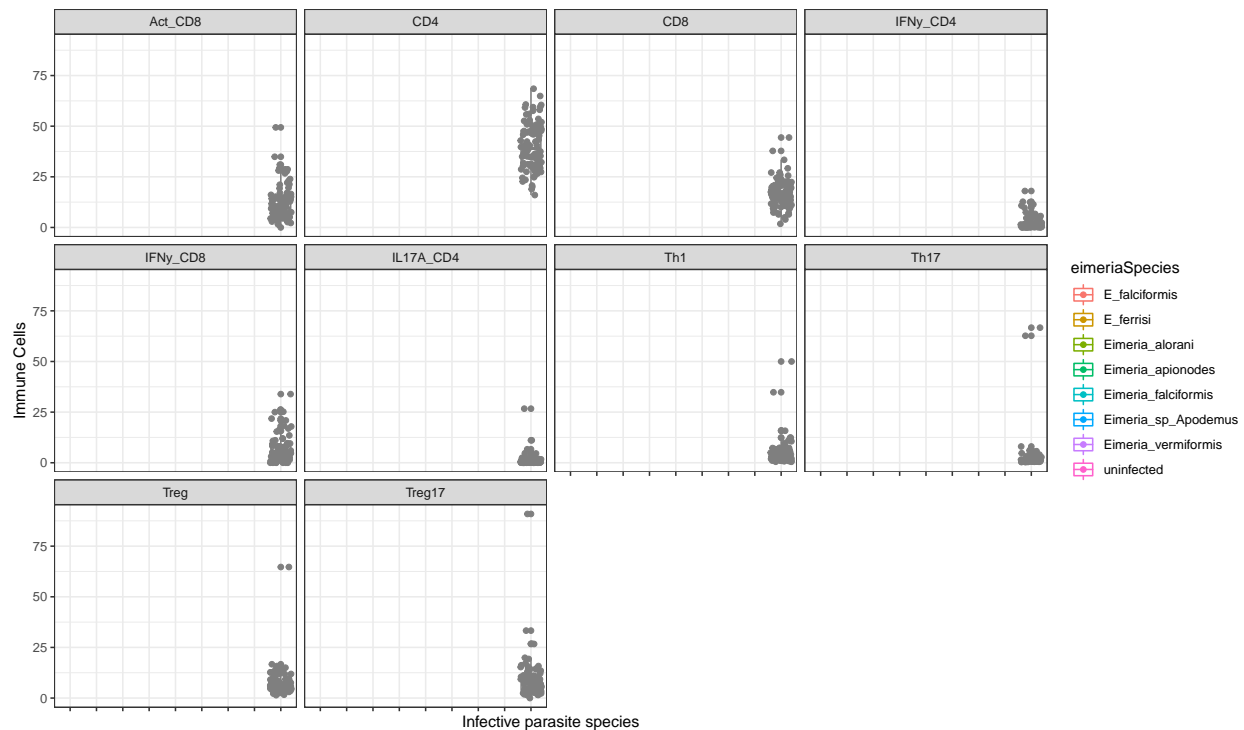


## Immune cells versus infection intensities - Field infections

## Warning: Removed 18260 rows containing non-finite values (stat\_boxplot).

## Warning: Removed 18260 rows containing missing values (geom\_point).

## Immune cells in response to parasite species – field data

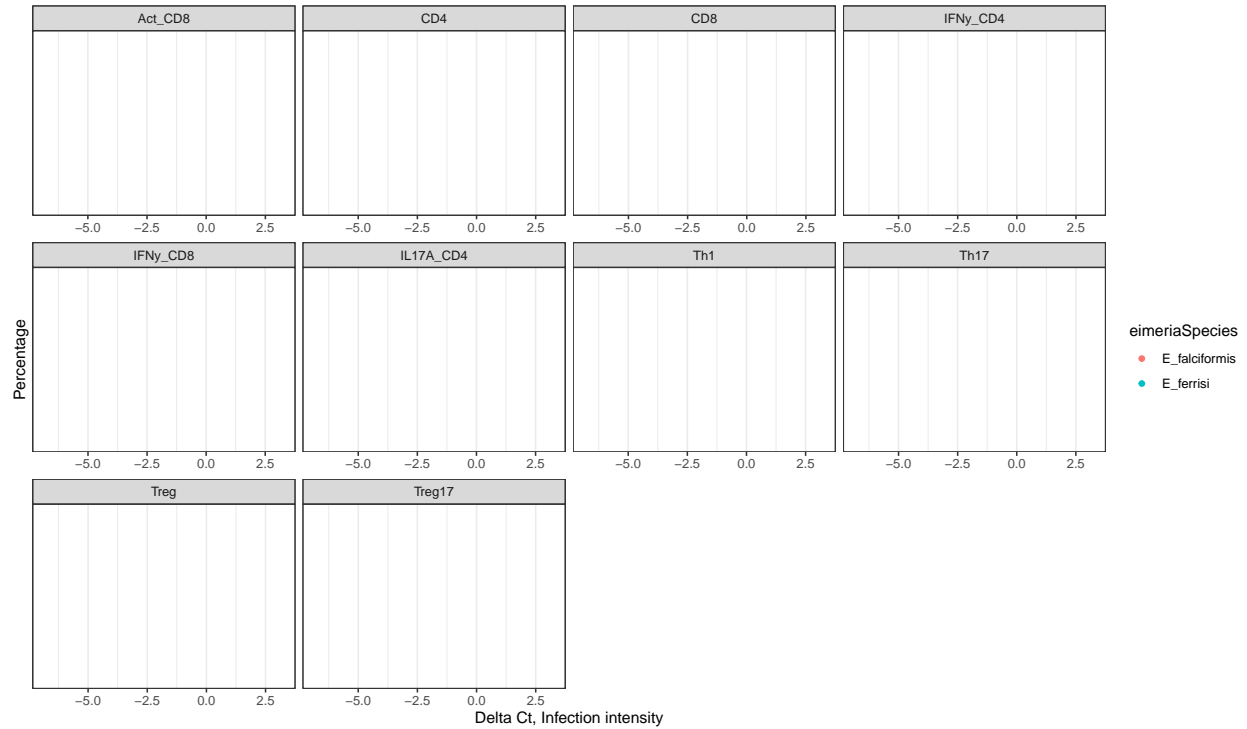


```
f %>%
  filter(!eimeriaSpecies == "uninfected", MC.Eimeria == "TRUE") %>%
  ggplot(aes(x = delta_ct_cewe_MminusE, y = Percentage,
             color = eimeriaSpecies)) +
  geom_jitter() +
  facet_wrap(~ Cells, scales = "free") +
  theme_light() +
  labs(x = "Delta Ct, Infection intensity", y = "Percentage",
       title = "Immune cells in response to infection intensity -
               field data") +
  theme_bw() +
  theme(plot.title = element_text(size= 30))
```

```
## Warning in min(x): no non-missing arguments to min; returning Inf
## Warning in max(x): no non-missing arguments to max; returning -Inf
## Warning in min(diff(sort(x))): no non-missing arguments to min; returning Inf
## Warning in min(x): no non-missing arguments to min; returning Inf
## Warning in max(x): no non-missing arguments to max; returning -Inf
## Warning in stats::runif(length(x), -amount, amount): NAs produced
```

```
## Warning: Removed 180 rows containing missing values (geom_point).
```

## Immune cells in response to infection intensity – field data



## FACS correlations in lab and field data

### Corrplot of correlations - *Laboratory and field* gene expression data

Here is a corrplot of the correlations between the genes.



