

## 4. Gene\_expressions\_analysis - Analyzing differences between field and lab

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2022-07-18

### Aims:

- Compare immune gene expression between lab and field data
- How do eimeria infections affect the expression of various immune genes?
- Does the expression vary between lab and field data?

### load libraries

```
library(ggplot2)
library(tidyverse)

## -- Attaching packages ----- tidyverse 1.3.1 --

## v tibble  3.1.8      v dplyr    1.0.9
## v tidyr   1.2.0      v stringr 1.4.0
## v readr   2.1.2      v forcats 0.5.1
## v purrr   0.3.4

## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()     masks stats::lag()

library(optimx)
```

### Import data:

Here, we have the experimental / field data, including imputed data

```
lab <- read.csv("output_data/gene_expression/data_products/lab_imputed_gene_expression.csv")
field <- read.csv("output_data/gene_expression/data_products/field_imputed_gene_expression.csv")
```

### Selecting genes

```
# vectors for selecting gene columns
Genes_lab <- c("IFNy", "CXCR3", "IL.6", "IL.10", "IL.13", "IL1RN", "CASP1",
              "CXCL9", "IDO1", "IRGM1", "MPO", "MUC2", "MUC5AC",
              "MYD88", "NCR1", "PRF1", "RETNLB", "SOCS1", "TICAM1", "TNF")

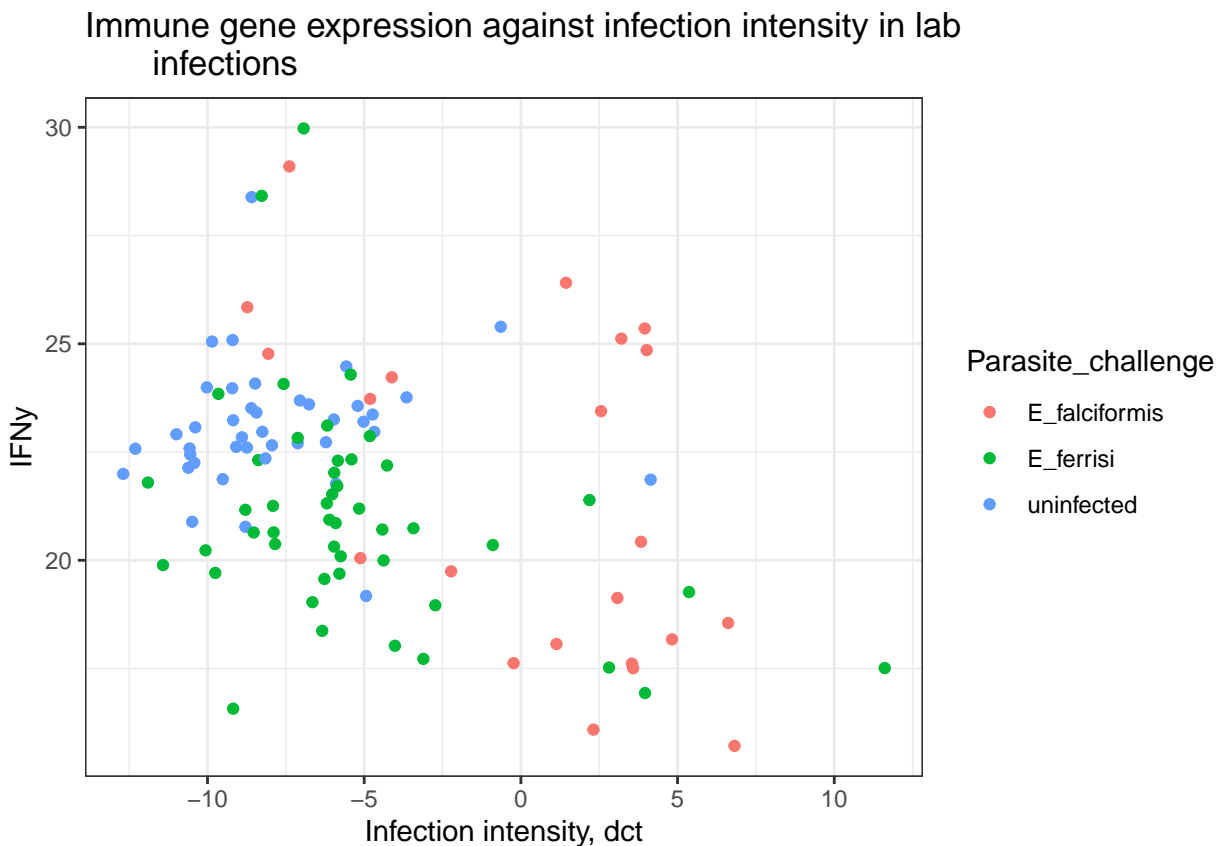
Genes_field <- c("IFNy", "CXCR3", "IL.6", # "GBP2", "IL.12", "IRG6",
                "IL.10", "IL.13", "IL1RN",
                "CXCR3", "CASP1", "CXCL9",
```

```
"IDO1", "IRGM1", "MPO", "MUC2", "MUC5AC", "MYD88",  
"NCR1", "PRF1", "RETNLB", "SOCS1", "TICAM1", "TNF")
```

## 1. IFNy

```
ggplot(lab, aes(x = delta, y = IFNy, color = Parasite_challenge)) +  
  geom_jitter() +  
  geom_abline() +  
  labs(x = "Infection intensity, dct",  
       title = "Immune gene expression against infection intensity in lab  
infections") +  
  theme_bw()
```

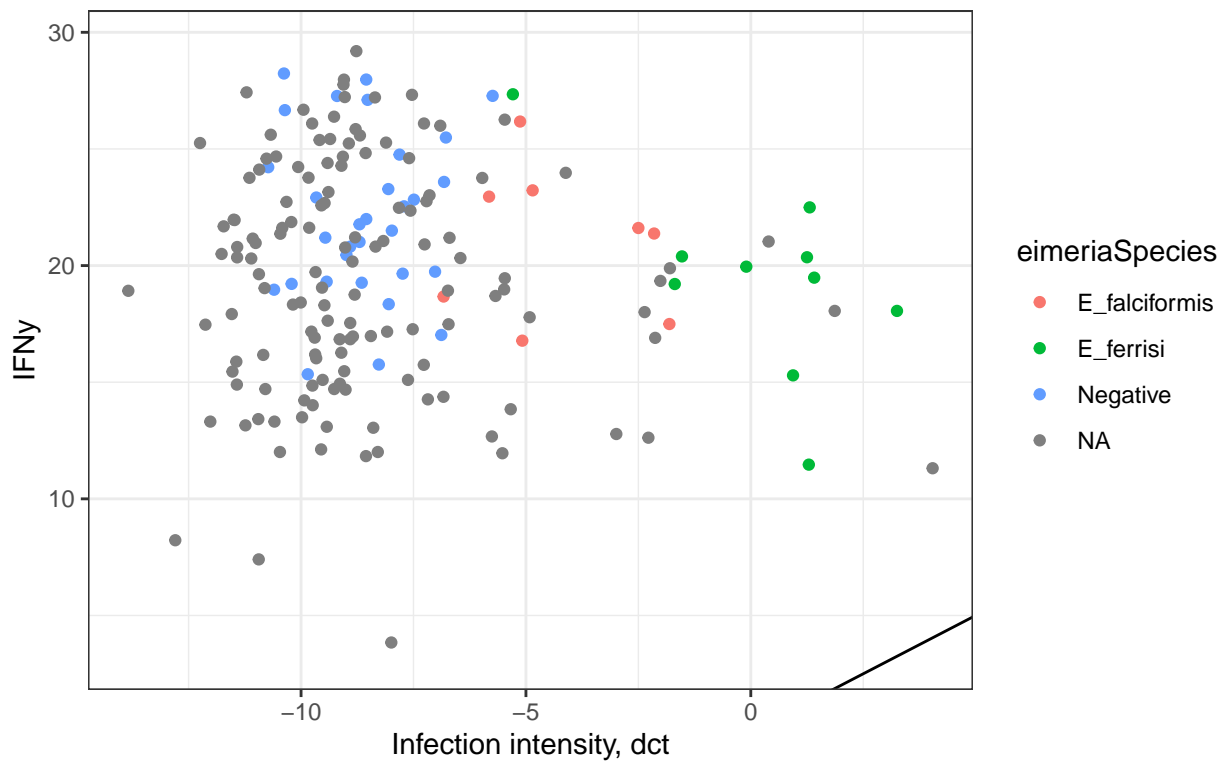
## Warning: Removed 6 rows containing missing values (geom\_point).



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = IFNy, color = eimeriaSpecies)) +  
  geom_jitter() +  
  geom_abline() +  
  labs(x = "Infection intensity, dct",  
       title = "Immune gene expression against infection intensity in field  
samples") +  
  theme_bw()
```

## Warning: Removed 150 rows containing missing values (geom\_point).

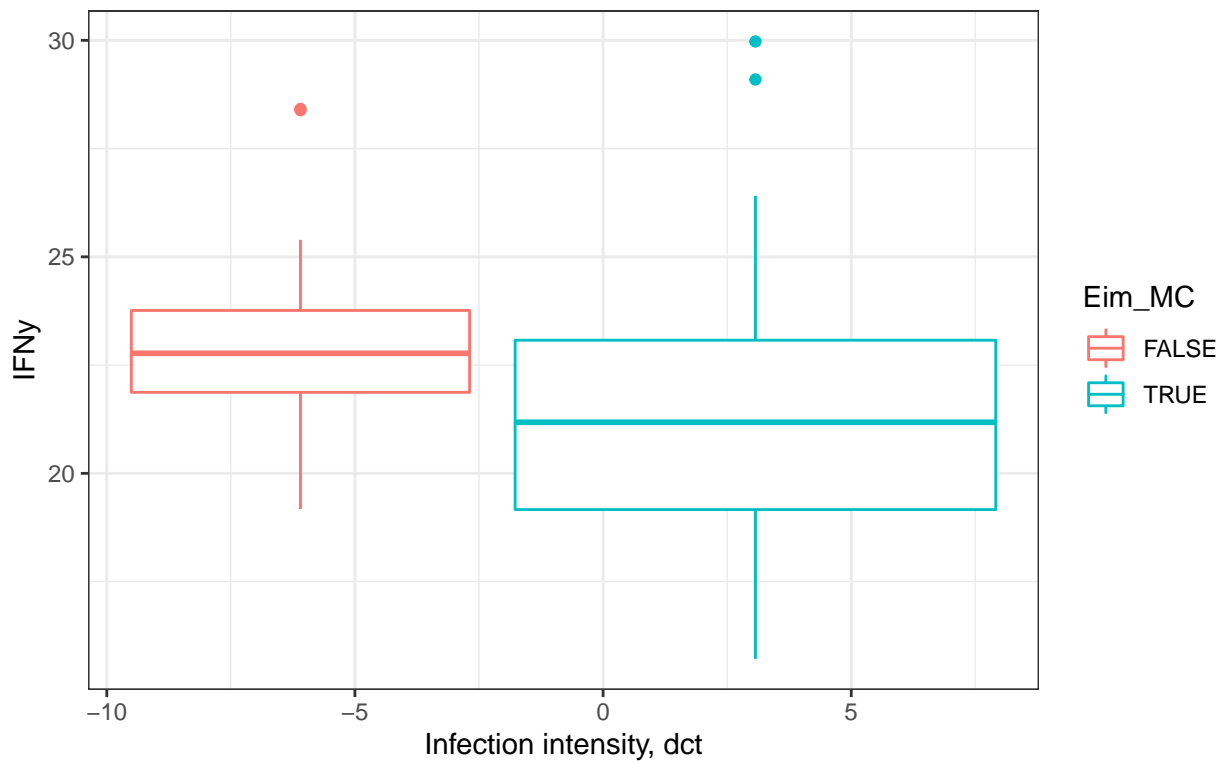
## Immune gene expression against infection intensity in field samples



```
ggplot(lab, aes(x = delta, y = IFNγ, color = Eim_MC)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in lab
infections") +
  theme_bw()
```

## Warning: Removed 6 rows containing missing values (stat\_boxplot).

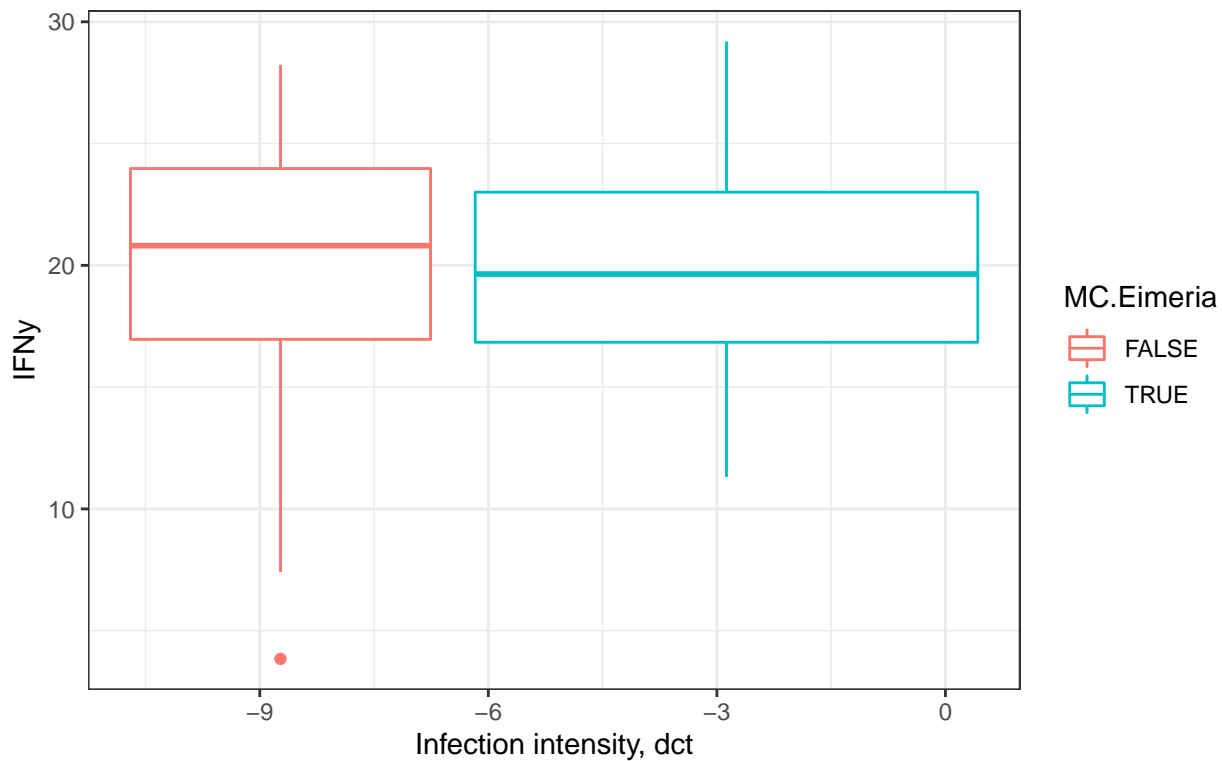
## Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = IFNγ,  
                  color = MC.Eimeria)) +  
  geom_boxplot() +  
  labs(x = "Infection intensity, dct",  
       title = "Immune gene expression against infection intensity in field  
samples") +  
  theme_bw()
```

## Warning: Removed 150 rows containing missing values (stat\_boxplot).

## Immune gene expression against infection intensity in field samples

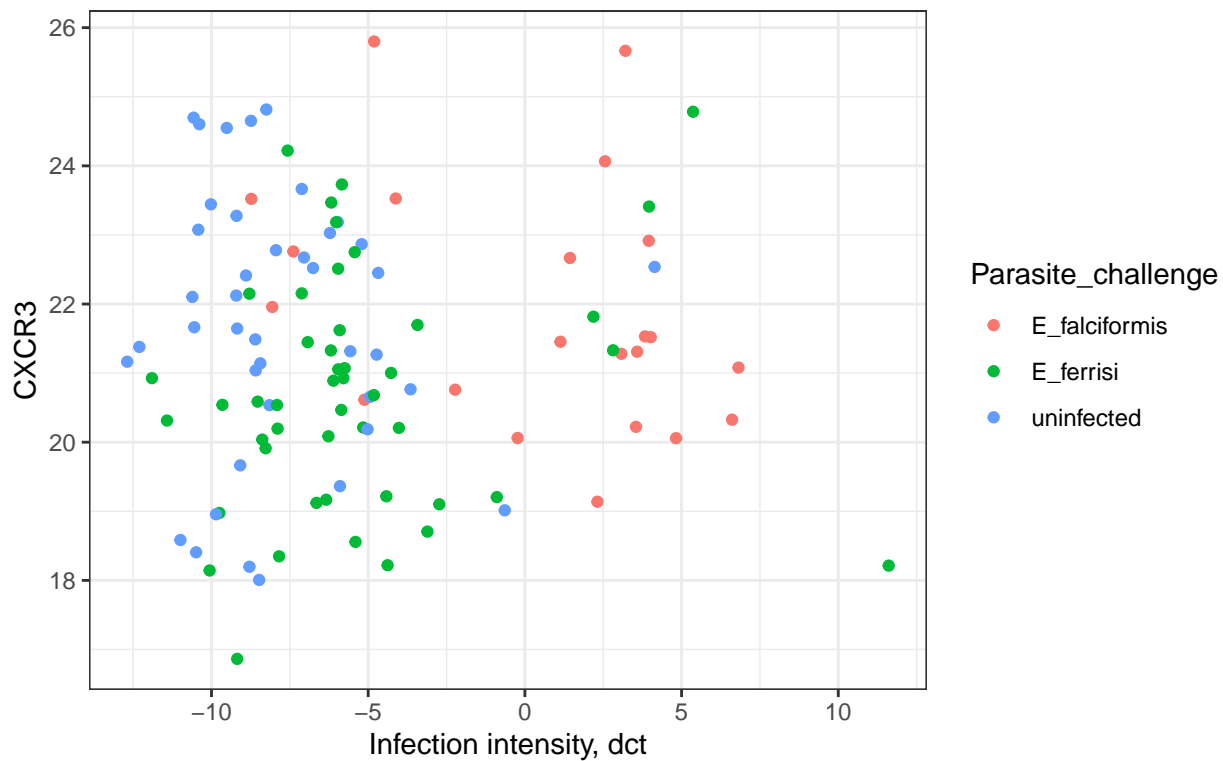


## 2. CXCR3

```
ggplot(lab, aes(x = delta, y = CXCR3_bio, color = Parasite_challenge)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct", y = "CXCR3",
       title = "Immune gene expression against infection intensity in lab
infections") +
  theme_bw()
```

## Warning: Removed 6 rows containing missing values (geom\_point).

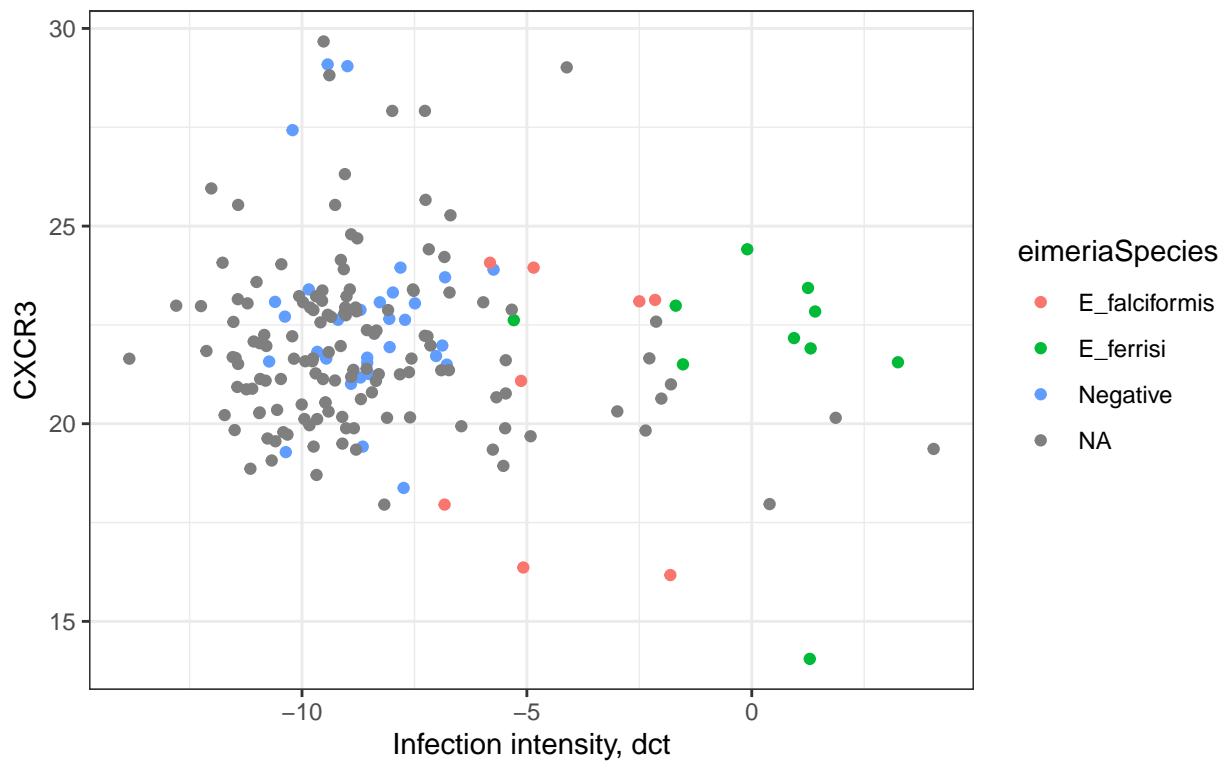
## Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = CXCR3, color = eimeriaSpecies)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in
       field samples") +
  theme_bw()
```

## Warning: Removed 150 rows containing missing values (geom\_point).

## Immune gene expression against infection intensity in field samples

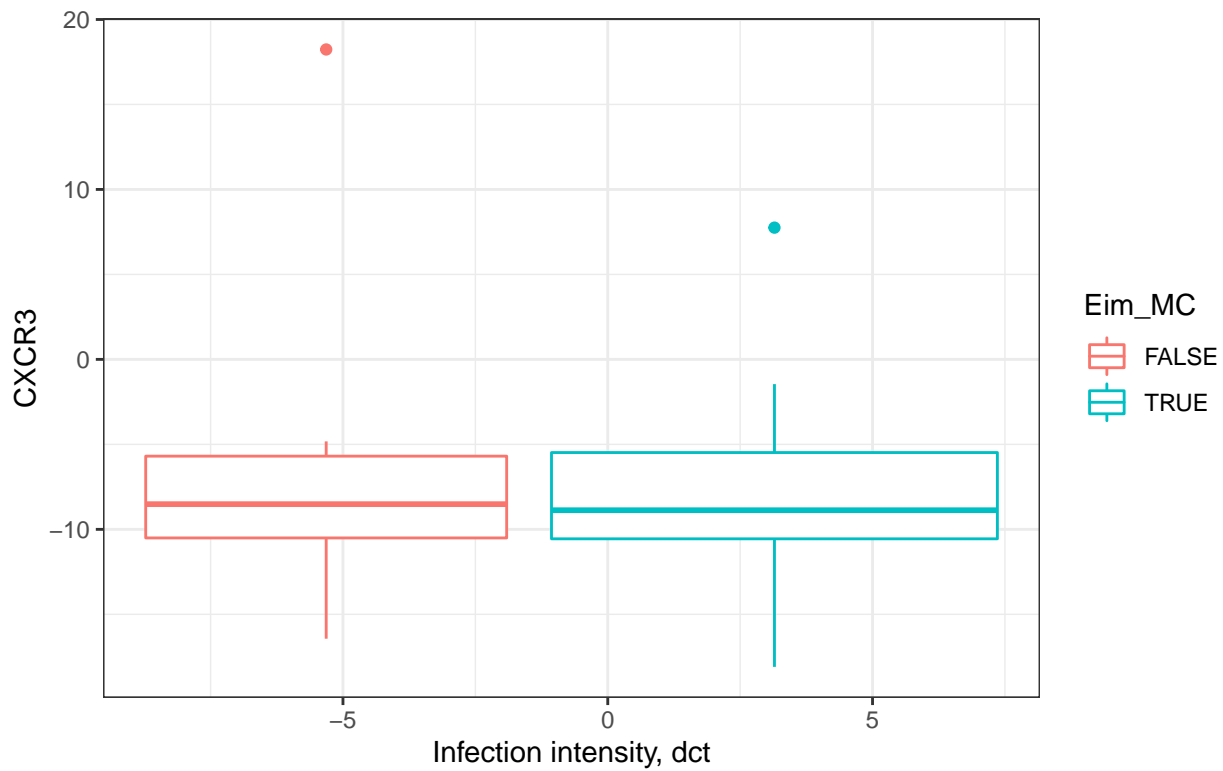


```
ggplot(lab, aes(x = delta, y = CXCR3, color = Eim_MC)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in lab
infections") +
  theme_bw()
```

```
## Warning: Removed 6 rows containing missing values (stat_boxplot).
```

```
## Warning: Removed 49 rows containing non-finite values (stat_boxplot).
```

## Immune gene expression against infection intensity in lab infections

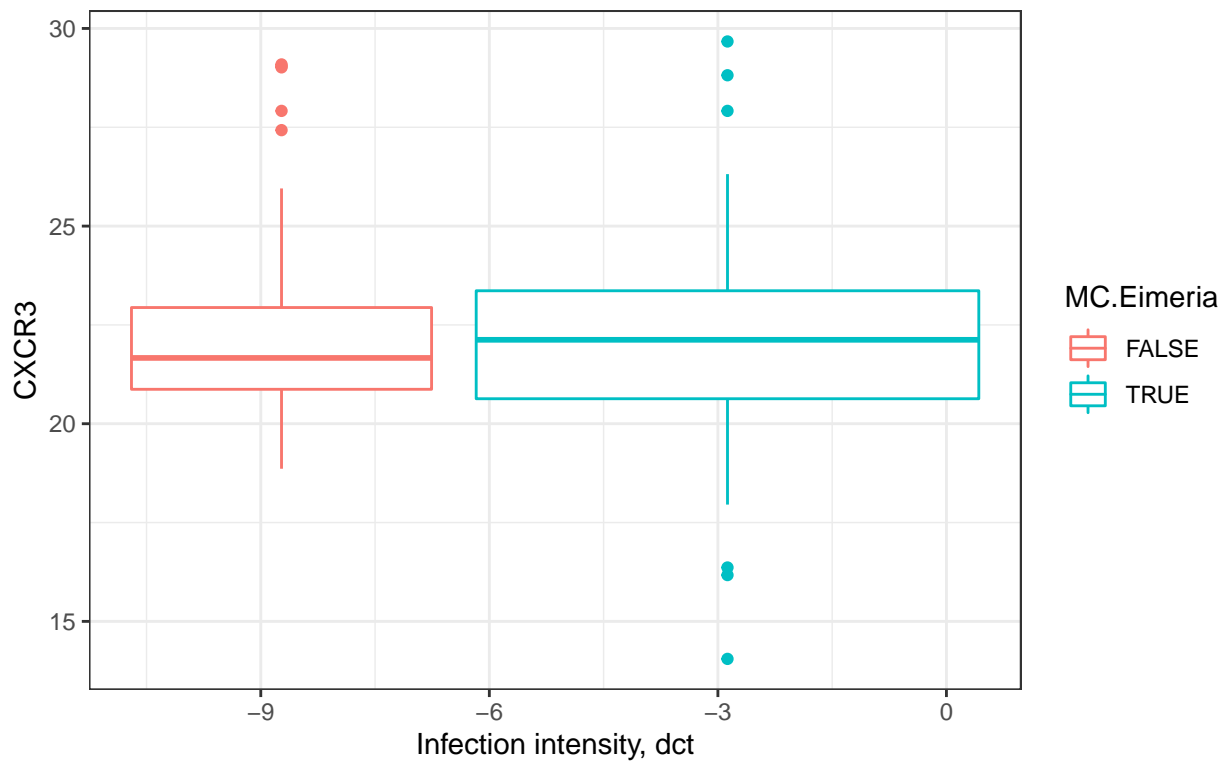


```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = CXCR3,
                  color = MC.Eimeria)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
               samples") +
  theme_bw()
```

## Warning: Removed 150 rows containing missing values (stat\_boxplot).



### Immune gene expression against infection intensity in field samples

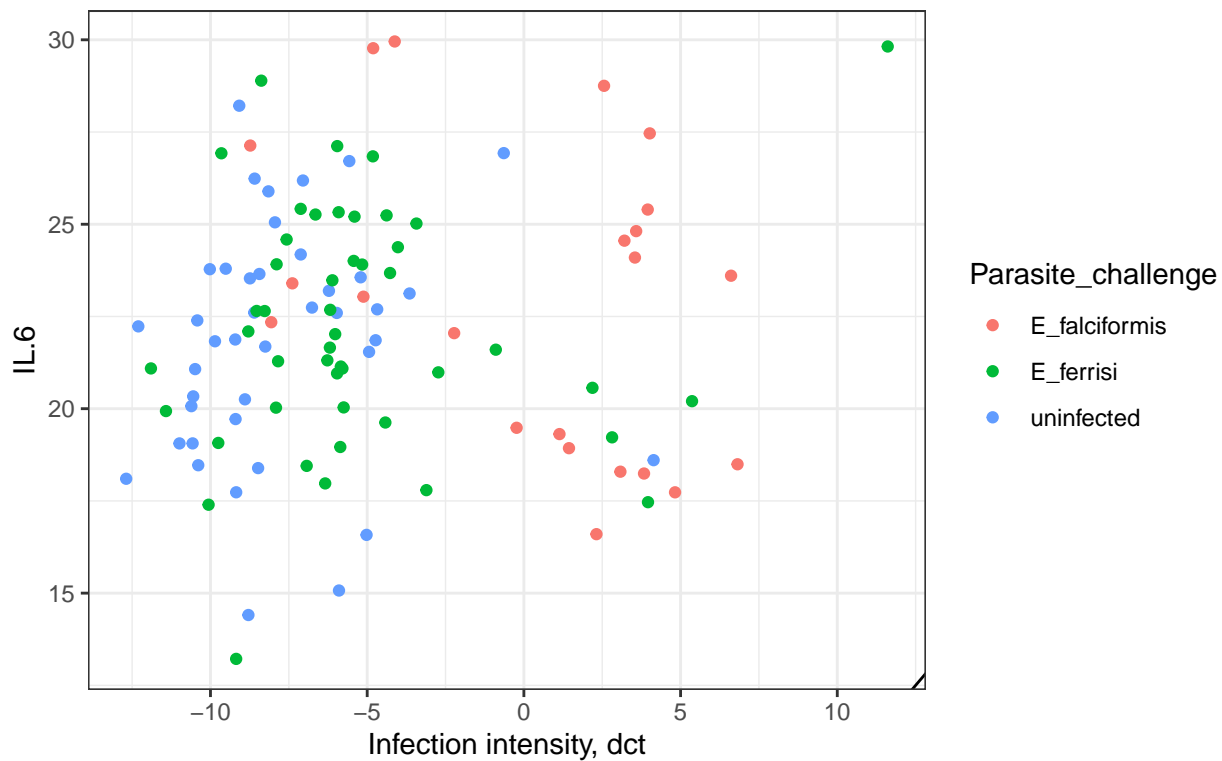


### 3. IL.6

```
ggplot(lab, aes(x = delta, y = IL.6, color = Parasite_challenge)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in lab
infections") +
  theme_bw()
```

## Warning: Removed 6 rows containing missing values (geom\_point).

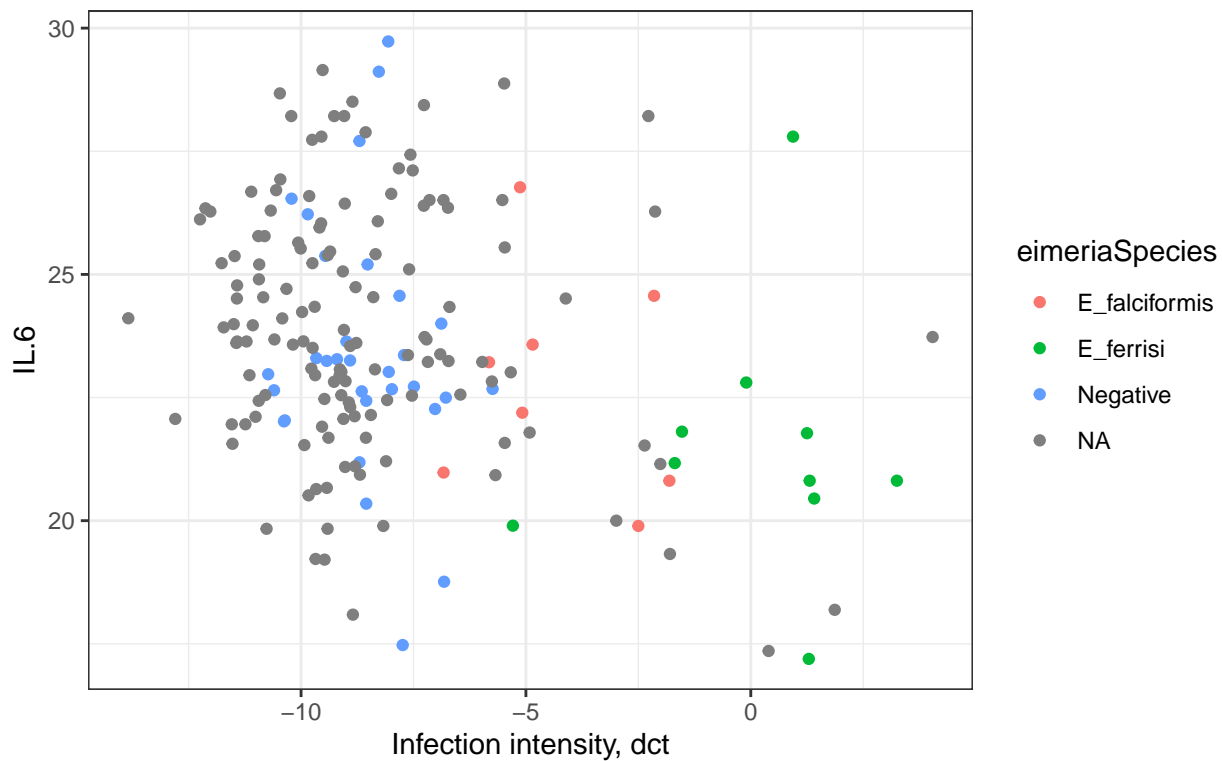
## Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = IL.6, color = eimeriaSpecies)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
samples") +
  theme_bw()
```

## Warning: Removed 150 rows containing missing values (geom\_point).

## Immune gene expression against infection intensity in field samples

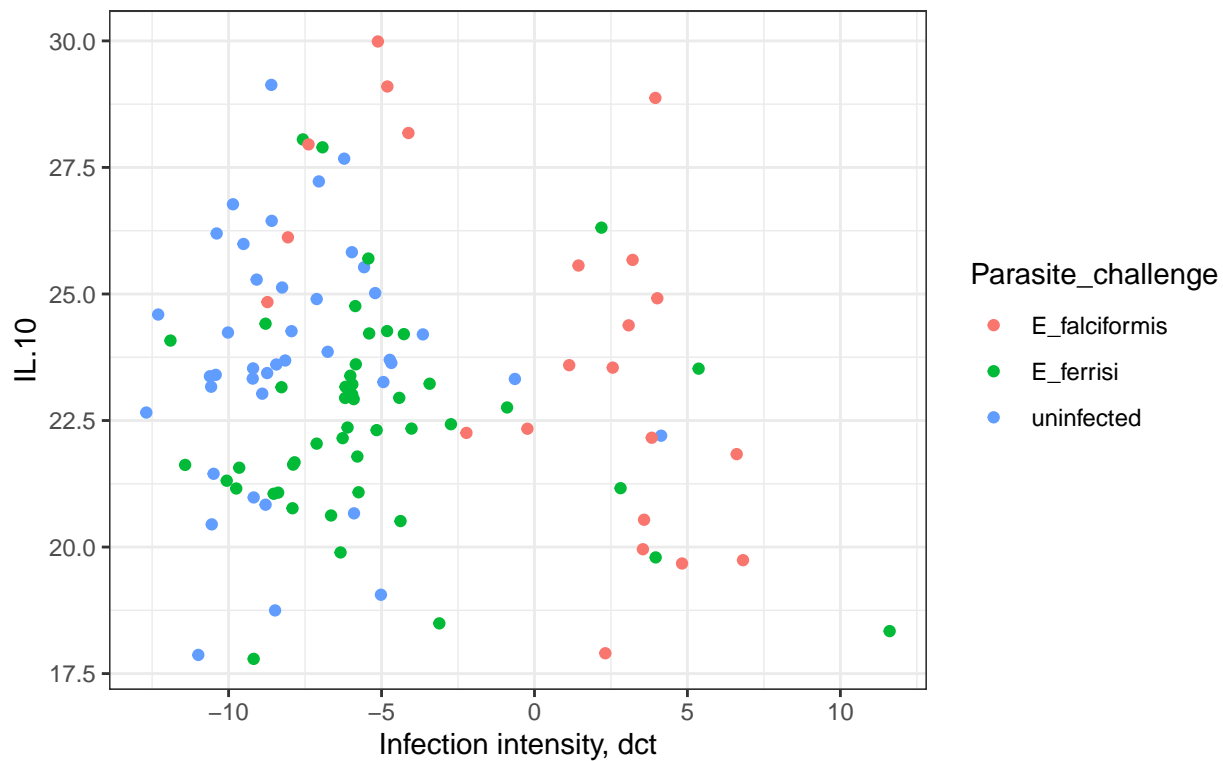


### 4. IL.10

```
ggplot(lab, aes(x = delta, y = IL.10, color = Parasite_challenge)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity
               in lab infections") +
  theme_bw()
```

## Warning: Removed 6 rows containing missing values (geom\_point).

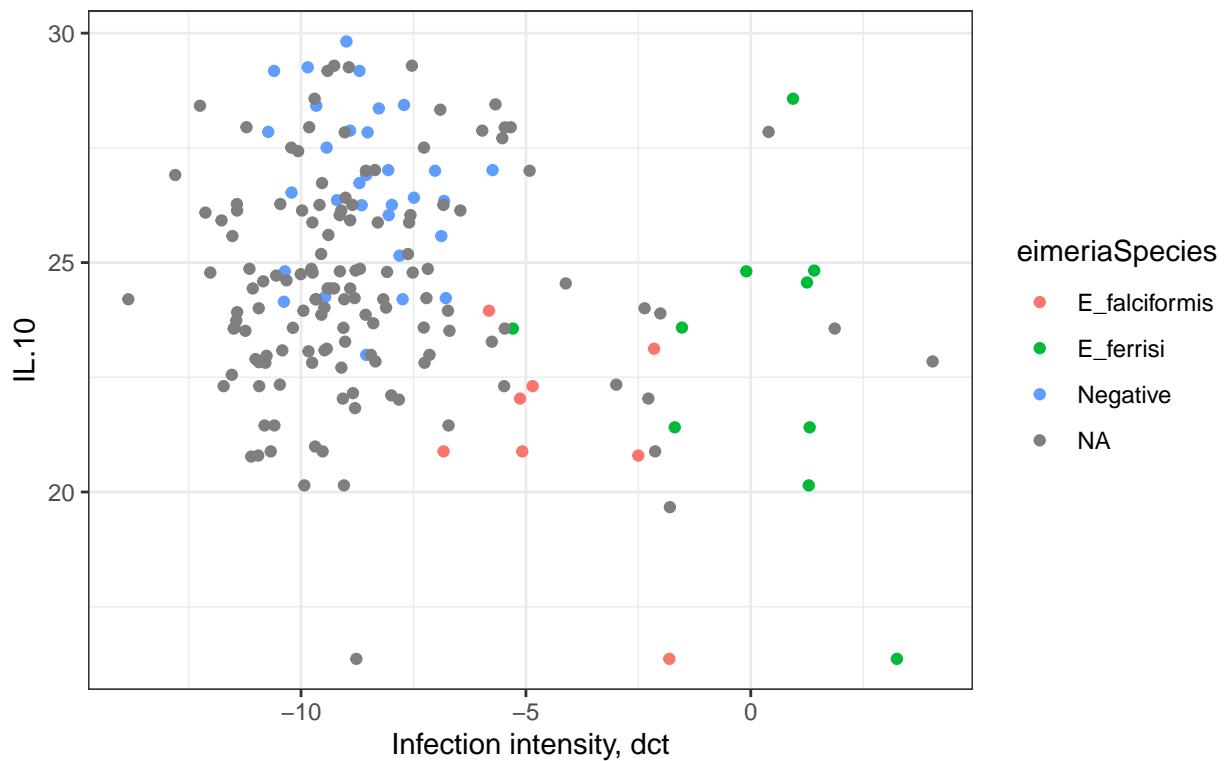
## Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = IL.10, color = eimeriaSpecies)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
samples") +
  theme_bw()
```

## Warning: Removed 150 rows containing missing values (geom\_point).

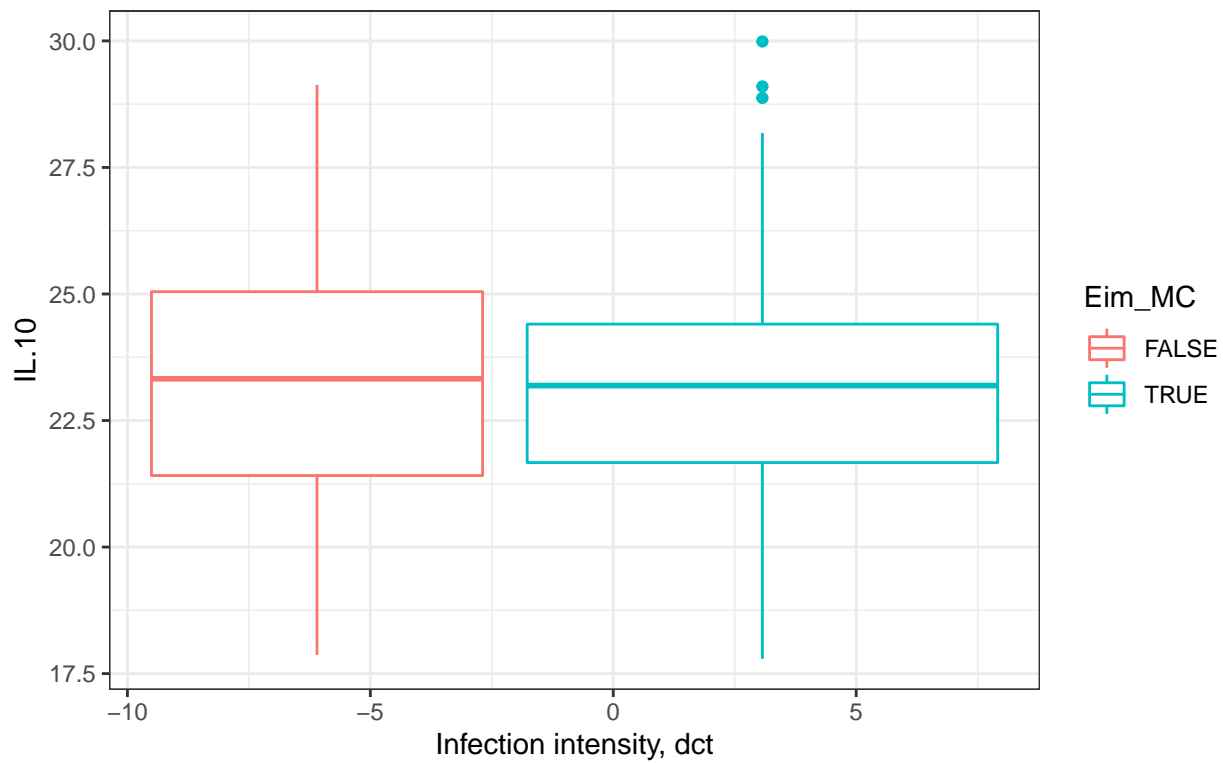
## Immune gene expression against infection intensity in field samples



```
ggplot(lab, aes(x = delta, y = IL.10, color = Eim_MC)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in lab
infections") +
  theme_bw()
```

## Warning: Removed 6 rows containing missing values (stat\_boxplot).

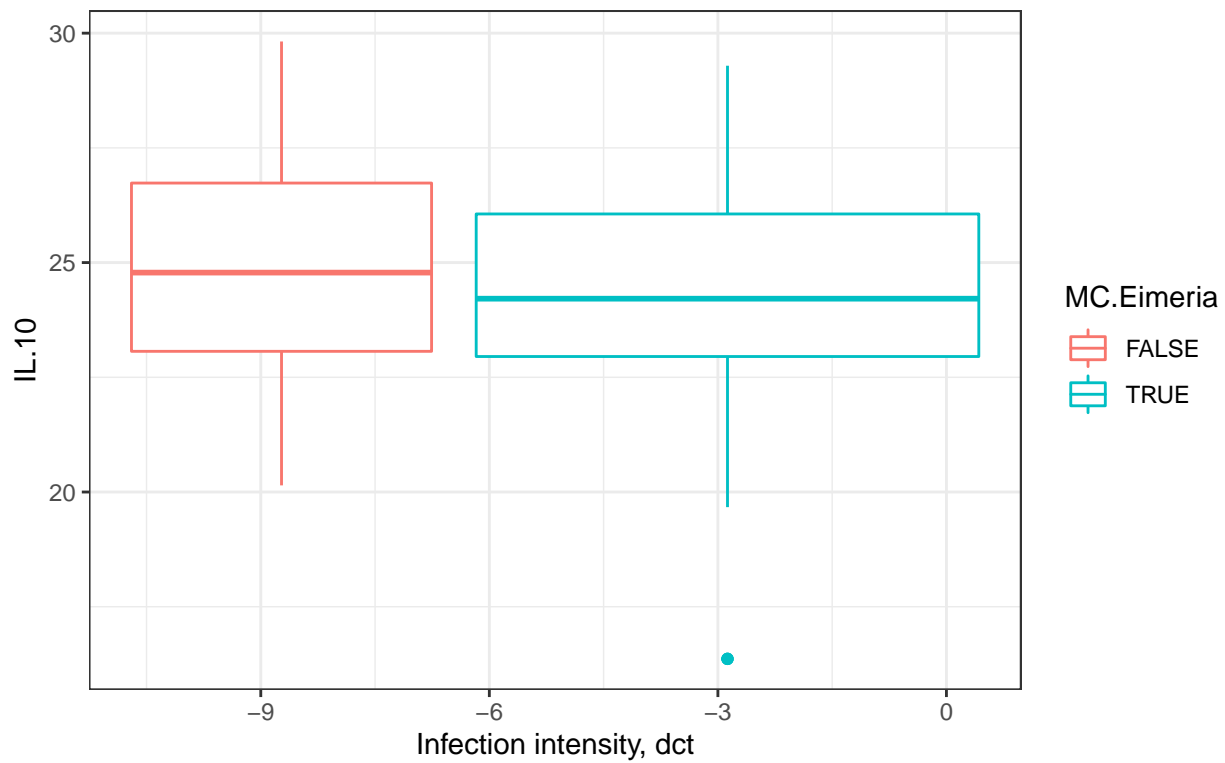
## Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = IL.10,
                  color = MC.Eimeria)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
samples") +
  theme_bw()
```

## Warning: Removed 150 rows containing missing values (stat\_boxplot).

## Immune gene expression against infection intensity in field samples

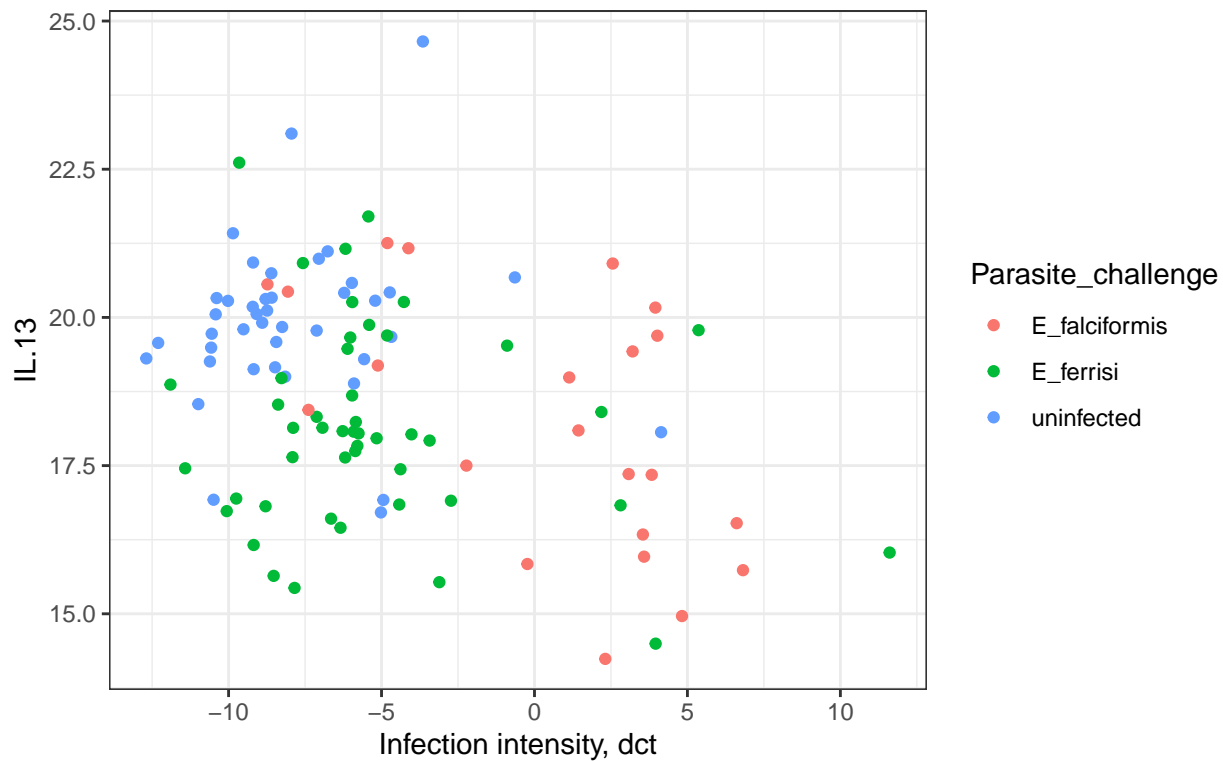


### 5. IL.13

```
ggplot(lab, aes(x = delta, y = IL.13, color = Parasite_challenge)) +  
  geom_jitter() +  
  geom_abline() +  
  labs(x = "Infection intensity, dct",  
       title = "Immune gene expression against infection intensity  
in lab infections") +  
  theme_bw()
```

## Warning: Removed 6 rows containing missing values (geom\_point).

## Immune gene expression against infection intensity in lab infections

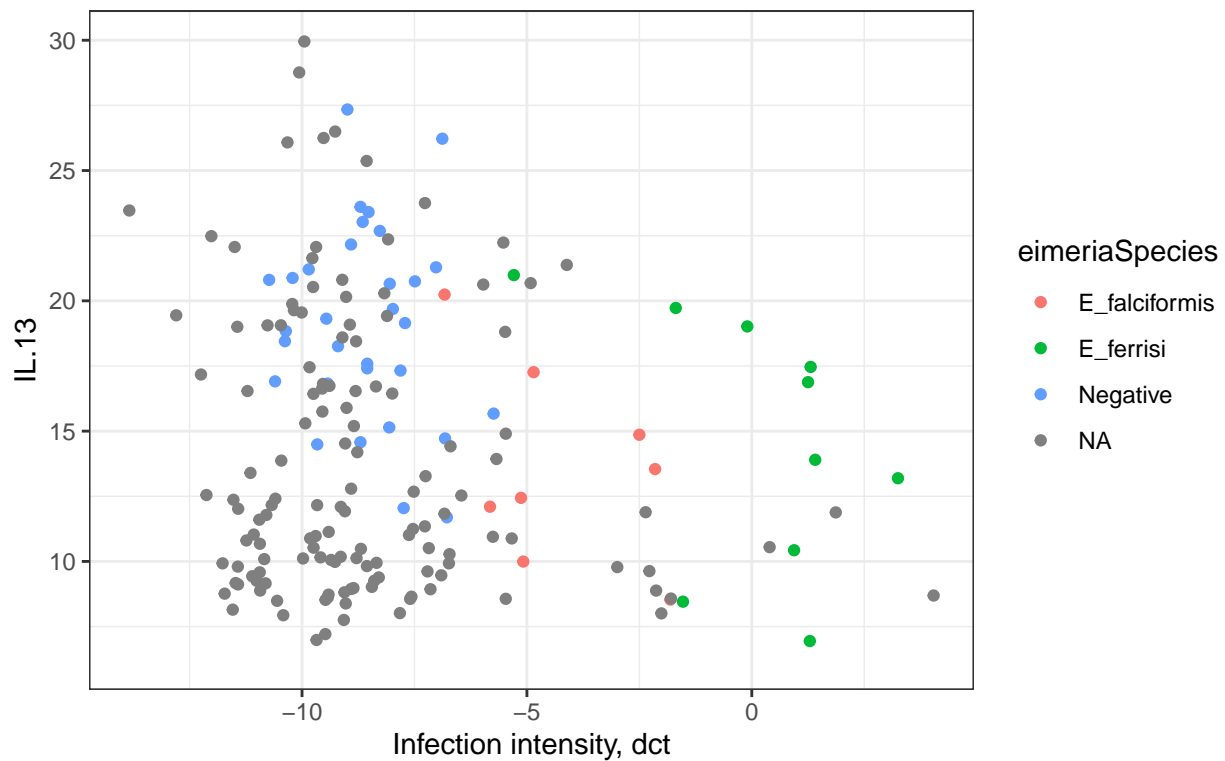


```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = IL.13, color = eimeriaSpecies)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
samples") +
  theme_bw()
```

## Warning: Removed 150 rows containing missing values (geom\_point).



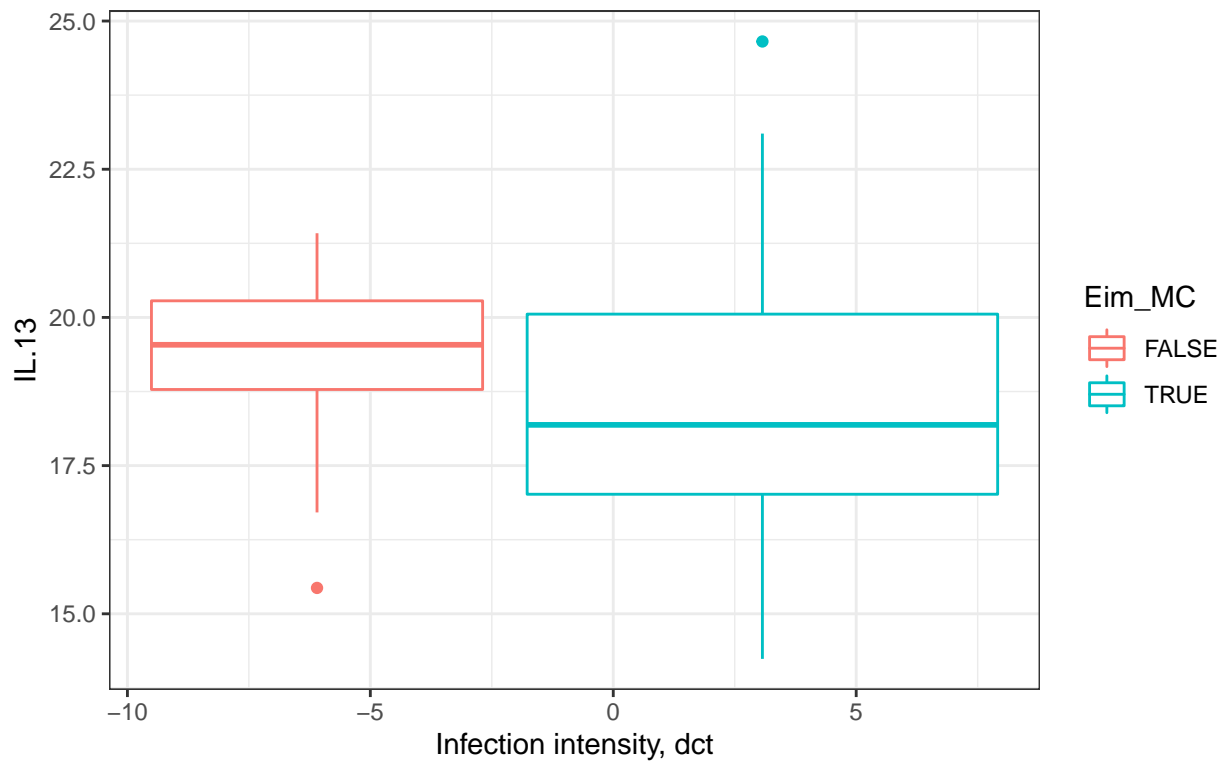
## Immune gene expression against infection intensity in field samples



```
ggplot(lab, aes(x = delta, y = IL.13, color = Eim_MC)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in lab
infections") +
  theme_bw()
```

## Warning: Removed 6 rows containing missing values (stat\_boxplot).

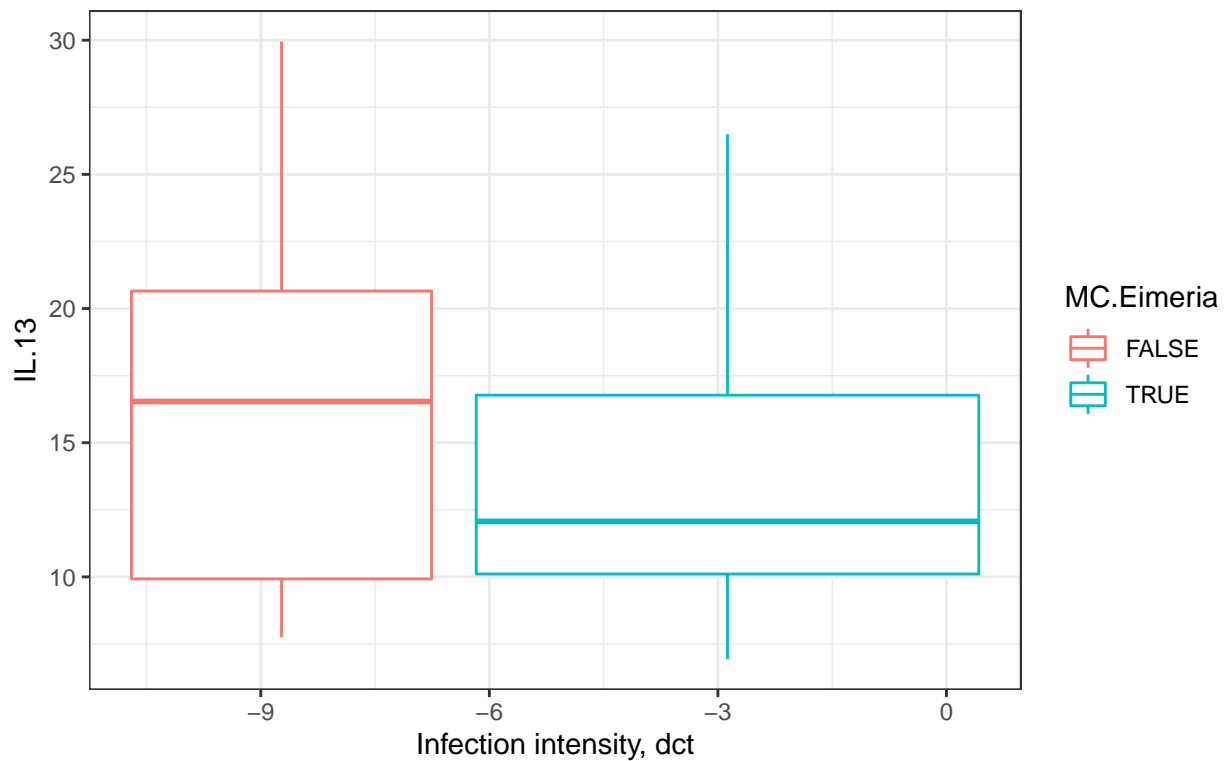
## Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = IL.13,  
                  color = MC.Eimeria)) +  
  geom_boxplot() +  
  labs(x = "Infection intensity, dct",  
       title = "Immune gene expression against infection intensity in field  
samples") +  
  theme_bw()
```

## Warning: Removed 150 rows containing missing values (stat\_boxplot).

## Immune gene expression against infection intensity in field samples

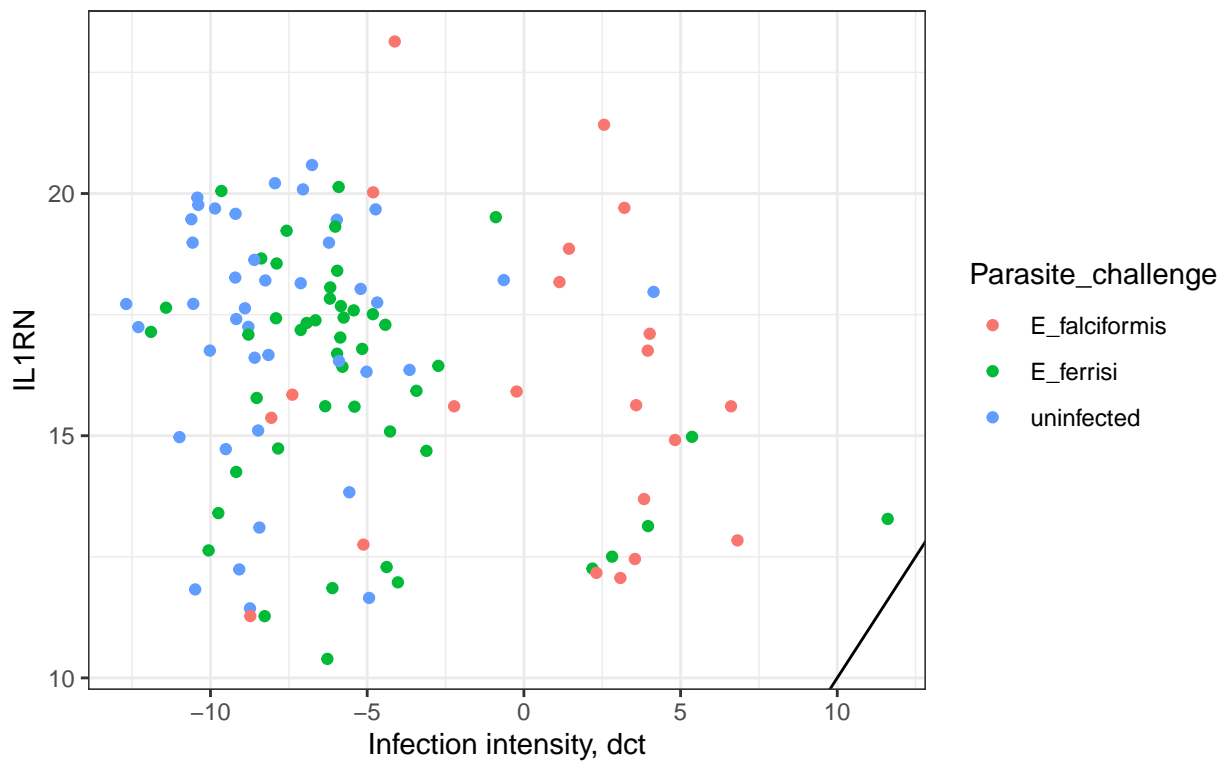


### 6. IL1RN

```
ggplot(lab, aes(x = delta, y = IL1RN, color = Parasite_challenge)) +  
  geom_jitter() +  
  geom_abline() +  
  labs(x = "Infection intensity, dct",  
       title = "Immune gene expression against infection intensity  
in lab infections") +  
  theme_bw()
```

## Warning: Removed 6 rows containing missing values (geom\_point).

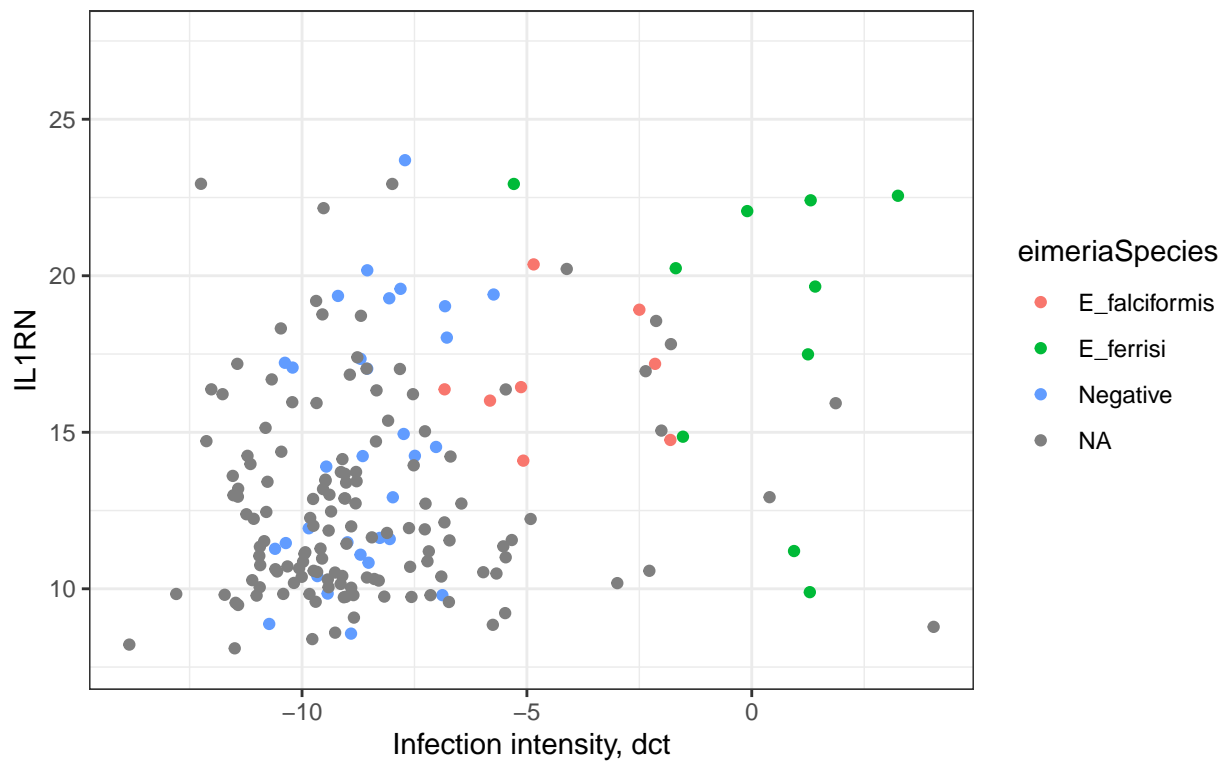
## Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = IL1RN, color = eimeriaSpecies)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
       samples") +
  theme_bw()
```

## Warning: Removed 150 rows containing missing values (geom\_point).

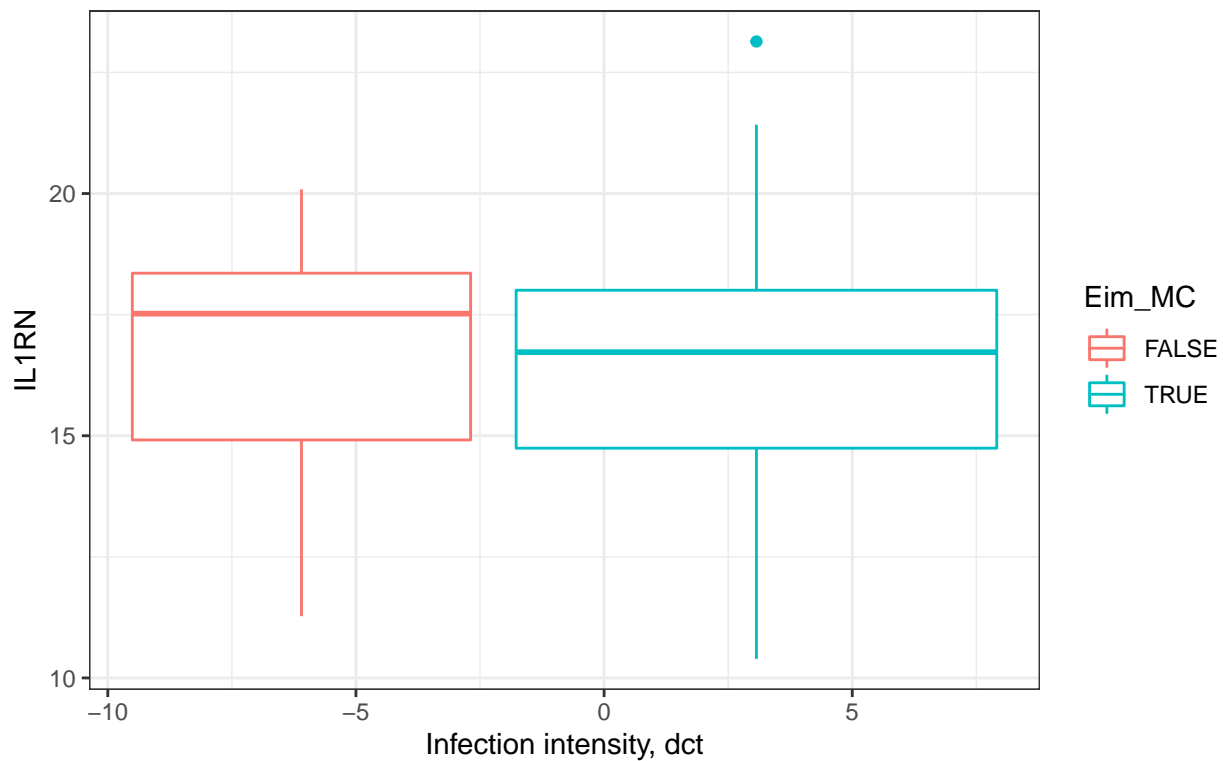
## Immune gene expression against infection intensity in field samples



```
ggplot(lab, aes(x = delta, y = IL1RN, color = Eim_MC)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in lab
infections") +
  theme_bw()
```

## Warning: Removed 6 rows containing missing values (stat\_boxplot).

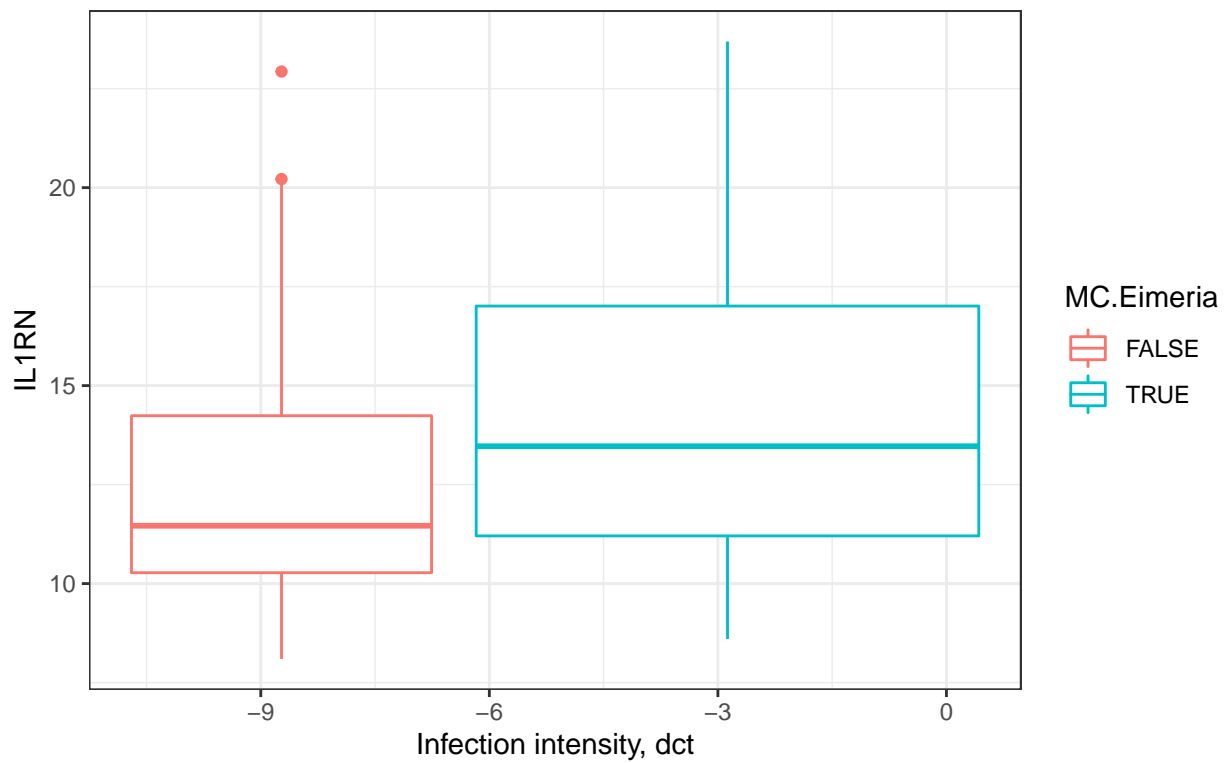
## Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = IL1RN,  
                  color = MC.Eimeria)) +  
  geom_boxplot() +  
  labs(x = "Infection intensity, dct",  
       title = "Immune gene expression against infection intensity in field  
samples") +  
  theme_bw()
```

## Warning: Removed 150 rows containing missing values (stat\_boxplot).

## Immune gene expression against infection intensity in field samples

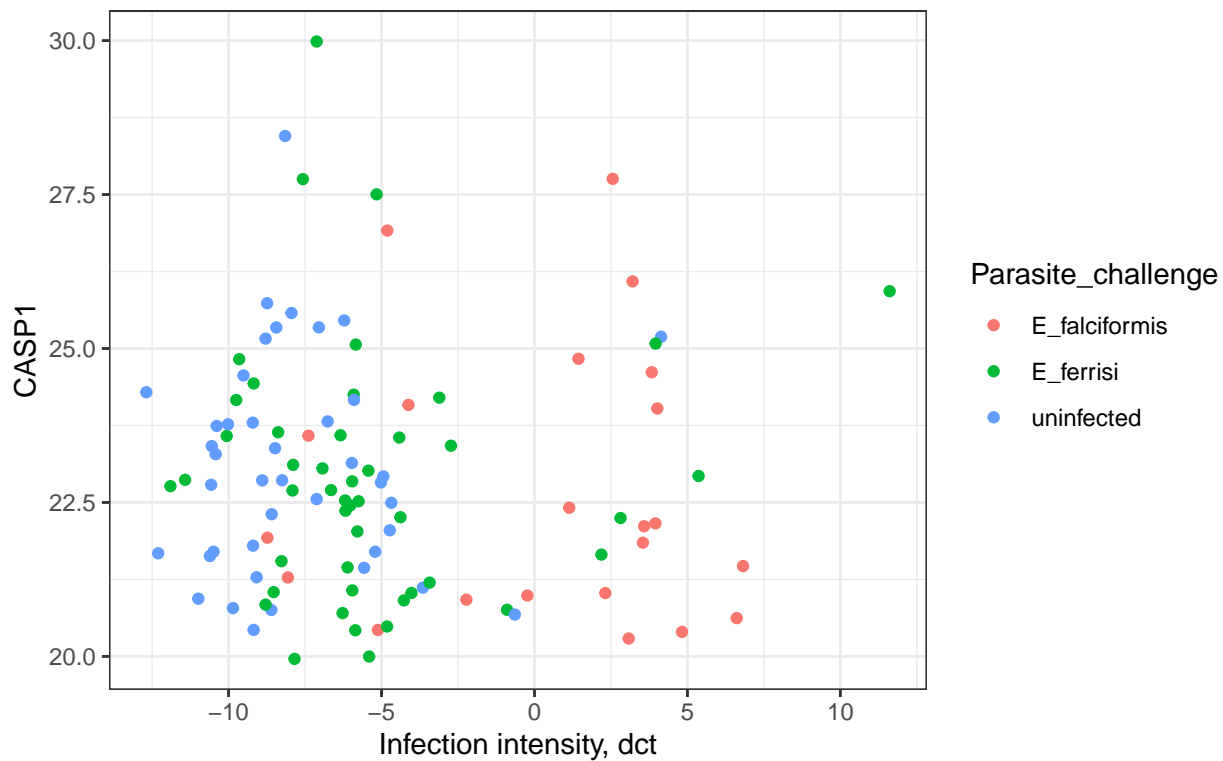


### 7. CASP1

```
ggplot(lab, aes(x = delta, y = CASP1, color = Parasite_challenge)) +  
  geom_jitter() +  
  geom_abline() +  
  labs(x = "Infection intensity, dct",  
       title = "Immune gene expression against infection intensity  
in lab infections") +  
  theme_bw()
```

## Warning: Removed 6 rows containing missing values (geom\_point).

## Immune gene expression against infection intensity in lab infections

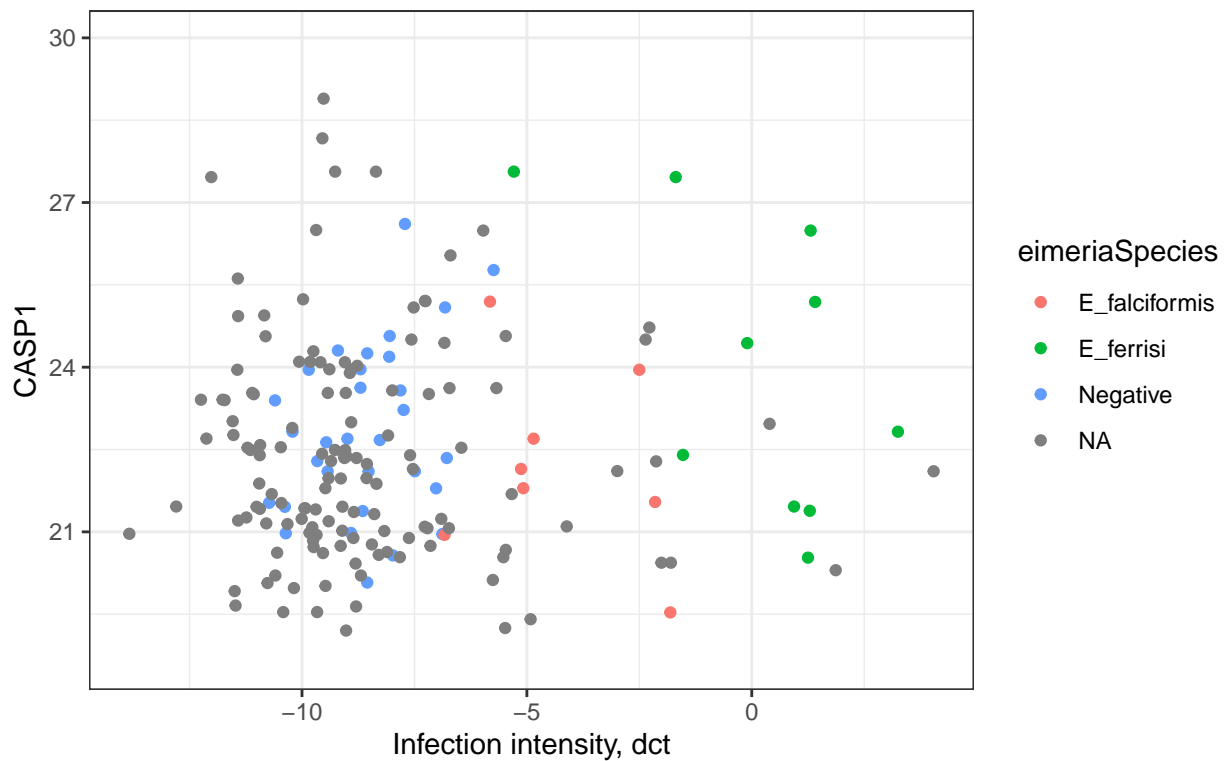


```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = CASP1, color = eimeriaSpecies)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
samples") +
  theme_bw()
```

## Warning: Removed 150 rows containing missing values (geom\_point).



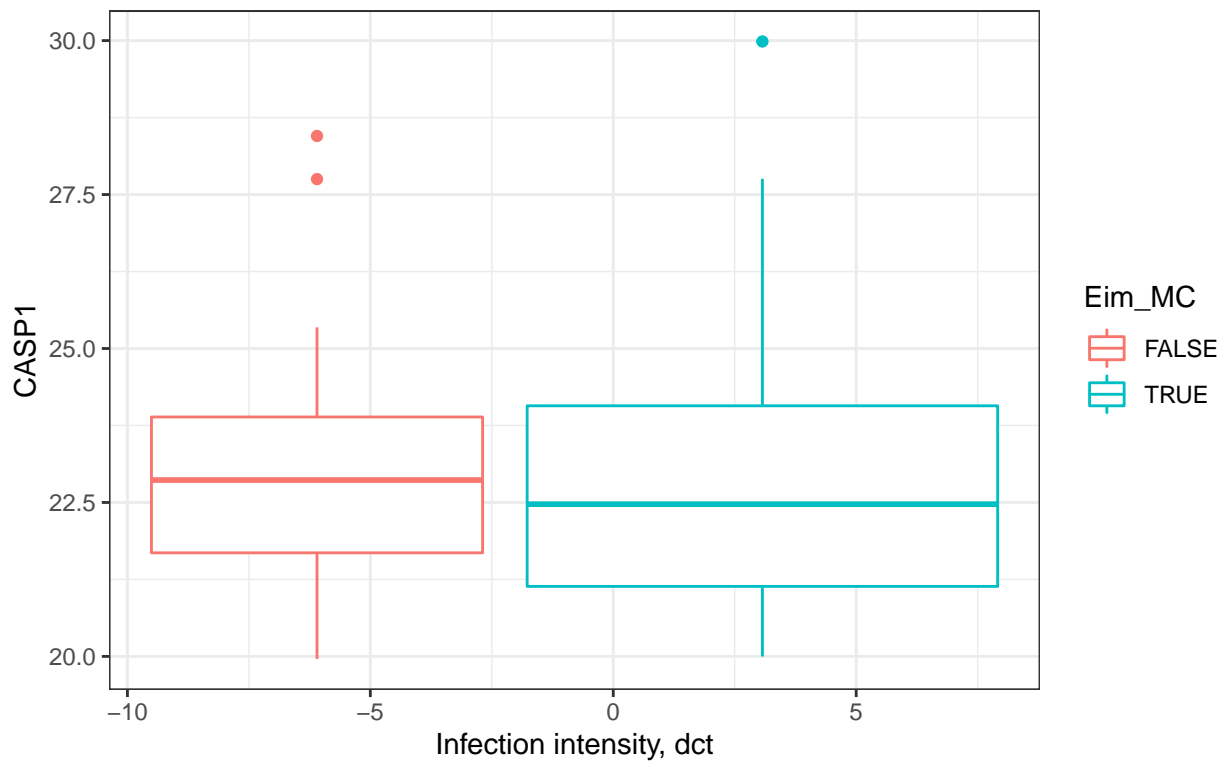
## Immune gene expression against infection intensity in field samples



```
ggplot(lab, aes(x = delta, y = CASP1, color = Eim_MC)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in lab
infections") +
  theme_bw()
```

## Warning: Removed 6 rows containing missing values (stat\_boxplot).

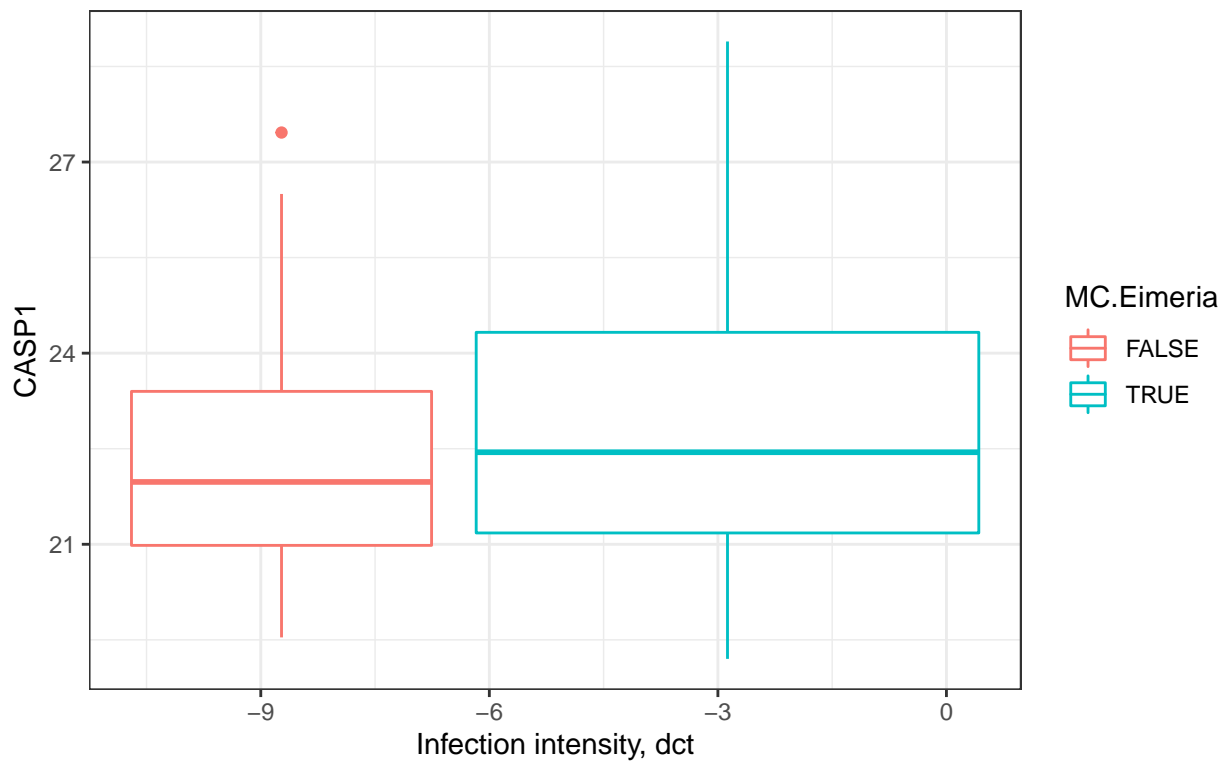
## Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = CASP1,
                  color = MC.Eimeria)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
               samples") +
  theme_bw()
```

## Warning: Removed 150 rows containing missing values (stat\_boxplot).

## Immune gene expression against infection intensity in field samples

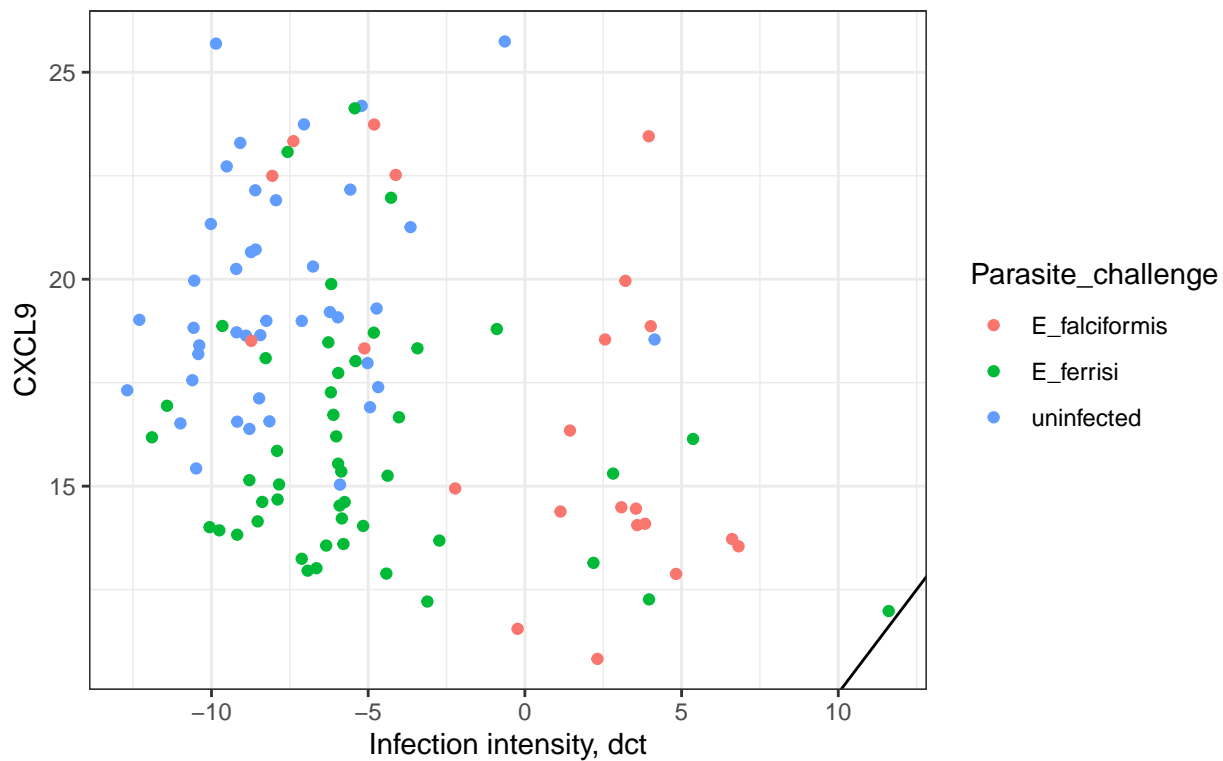


### 8. CXCL9

```
ggplot(lab, aes(x = delta, y = CXCL9, color = Parasite_challenge)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity
in lab infections") +
  theme_bw()
```

## Warning: Removed 6 rows containing missing values (geom\_point).

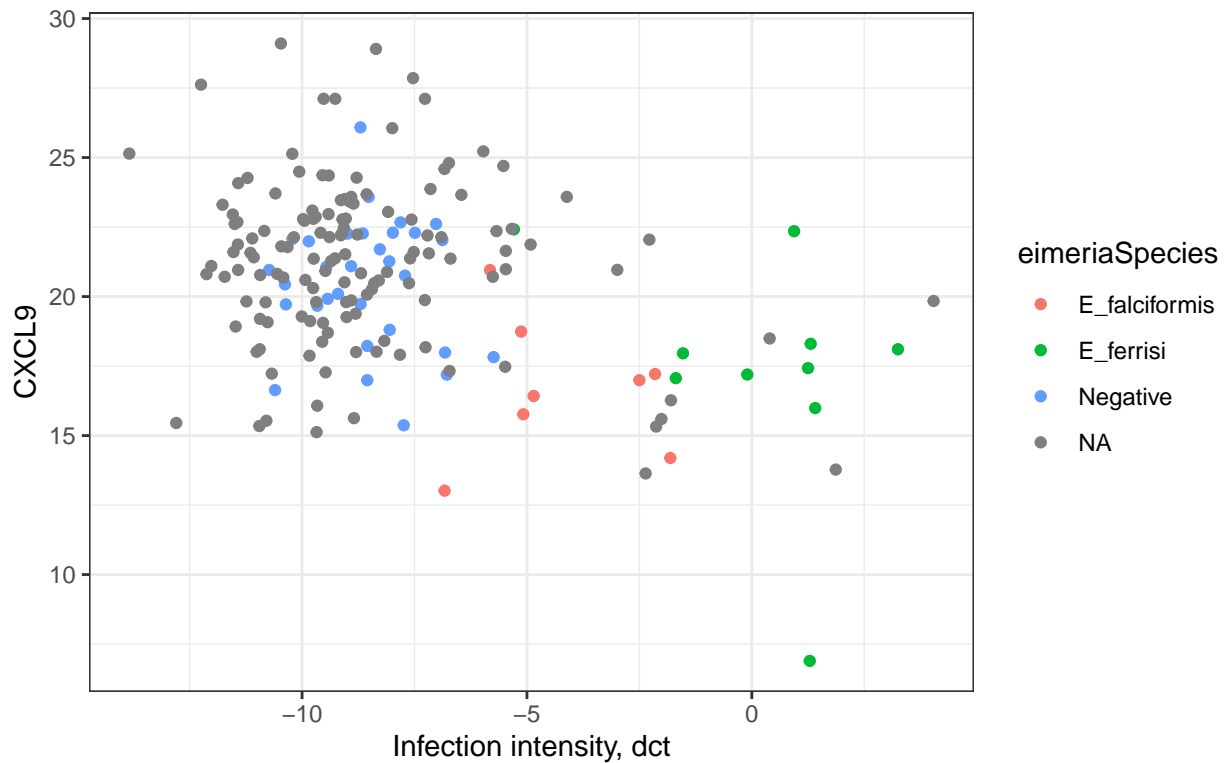
## Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = CXCL9, color = eimeriaSpecies)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
               samples") +
  theme_bw()
```

## Warning: Removed 150 rows containing missing values (geom\_point).

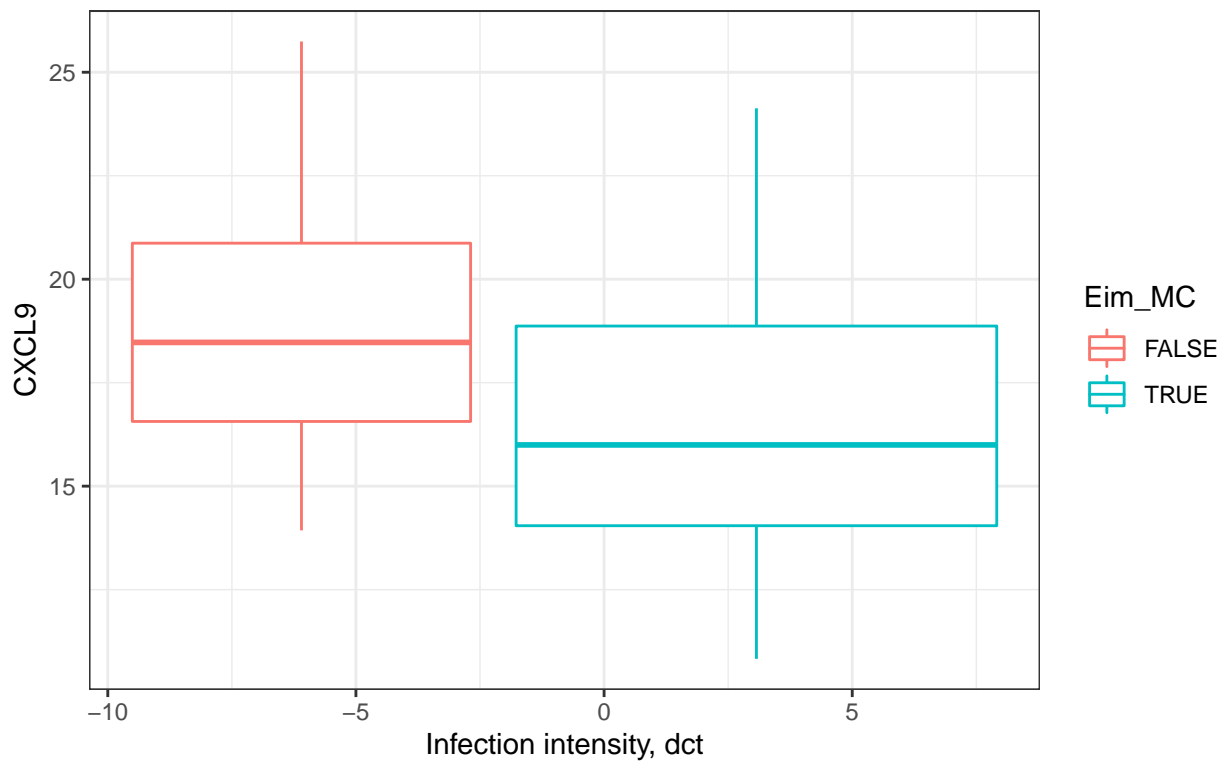
## Immune gene expression against infection intensity in field samples



```
ggplot(lab, aes(x = delta, y = CXCL9, color = Eim_MC)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in lab
infections") +
  theme_bw()
```

## Warning: Removed 6 rows containing missing values (stat\_boxplot).

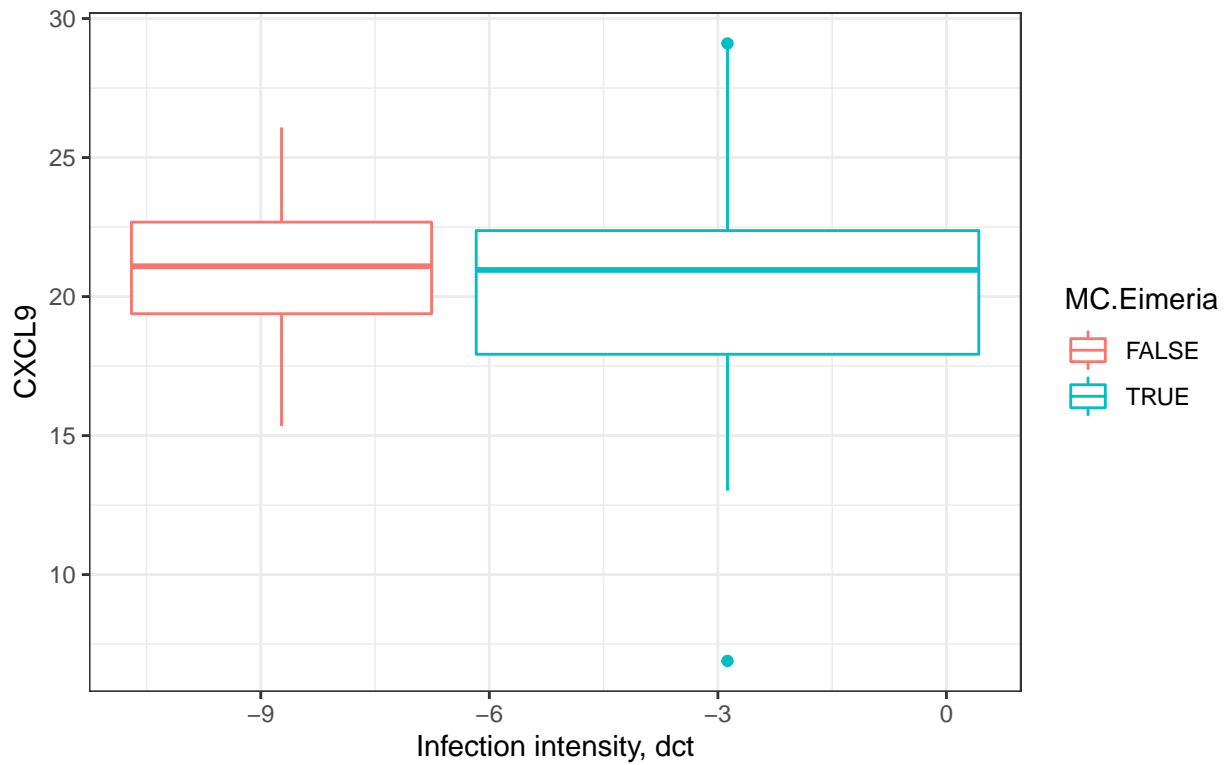
## Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = CXCL9,  
                  color = MC.Eimeria)) +  
  geom_boxplot() +  
  labs(x = "Infection intensity, dct",  
       title = "Immune gene expression against infection intensity in field  
samples") +  
  theme_bw()
```

## Warning: Removed 150 rows containing missing values (stat\_boxplot).

## Immune gene expression against infection intensity in field samples

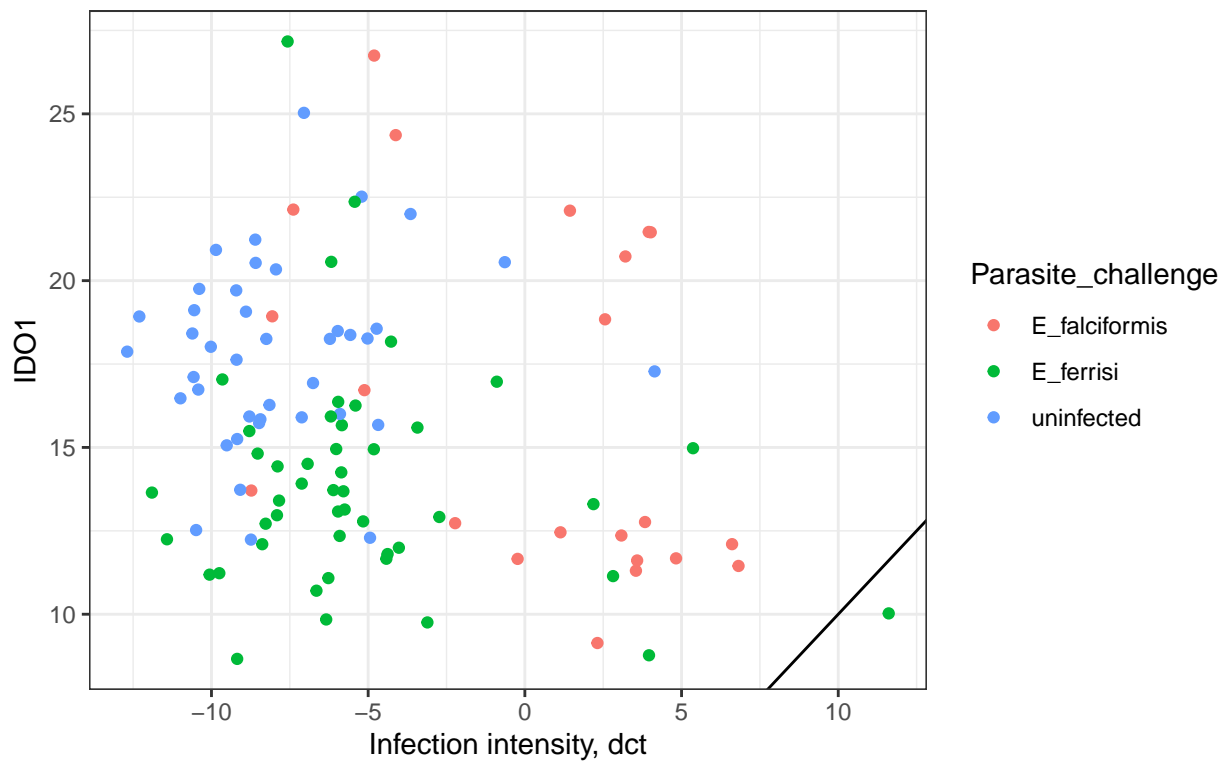


### 9. IDO1

```
ggplot(lab, aes(x = delta, y = IDO1, color = Parasite_challenge)) +  
  geom_jitter() +  
  geom_abline() +  
  labs(x = "Infection intensity, dct",  
       title = "Immune gene expression against infection intensity  
in lab infections") +  
  theme_bw()
```

## Warning: Removed 6 rows containing missing values (geom\_point).

## Immune gene expression against infection intensity in lab infections

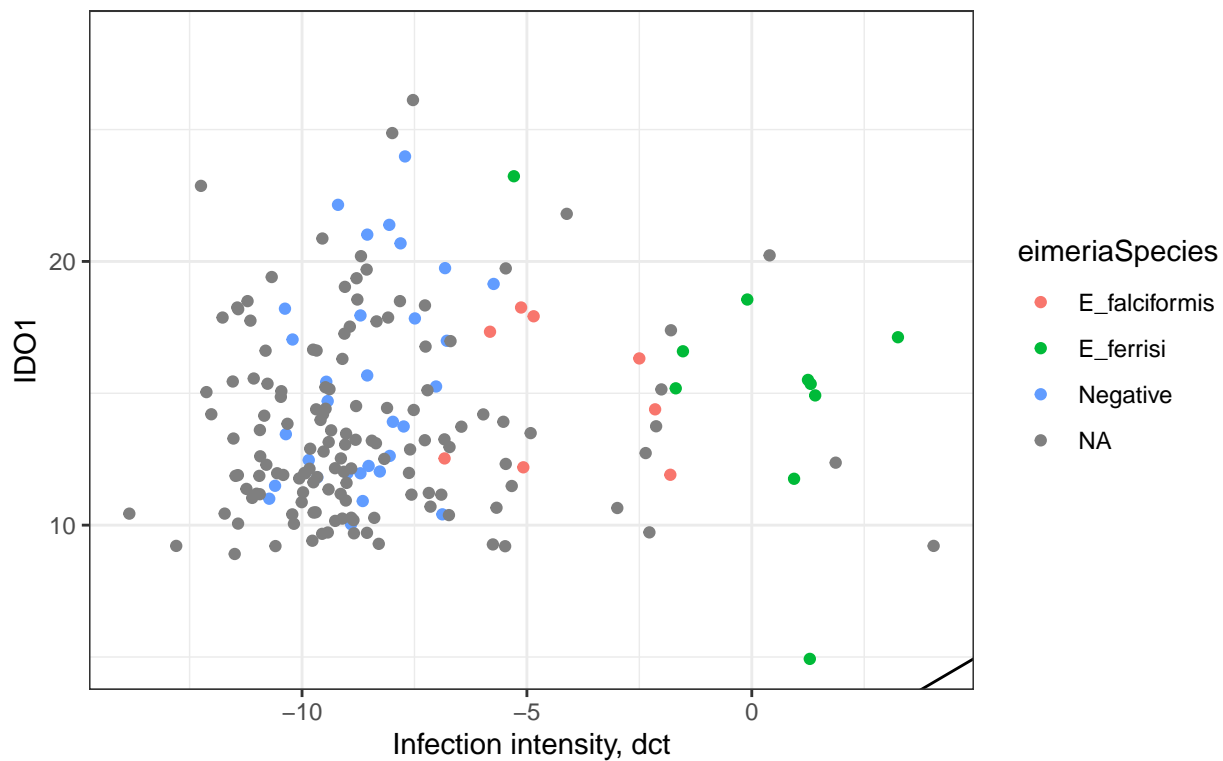


```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = IDO1, color = eimeriaSpecies)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
       samples") +
  theme_bw()
```

## Warning: Removed 150 rows containing missing values (geom\_point).



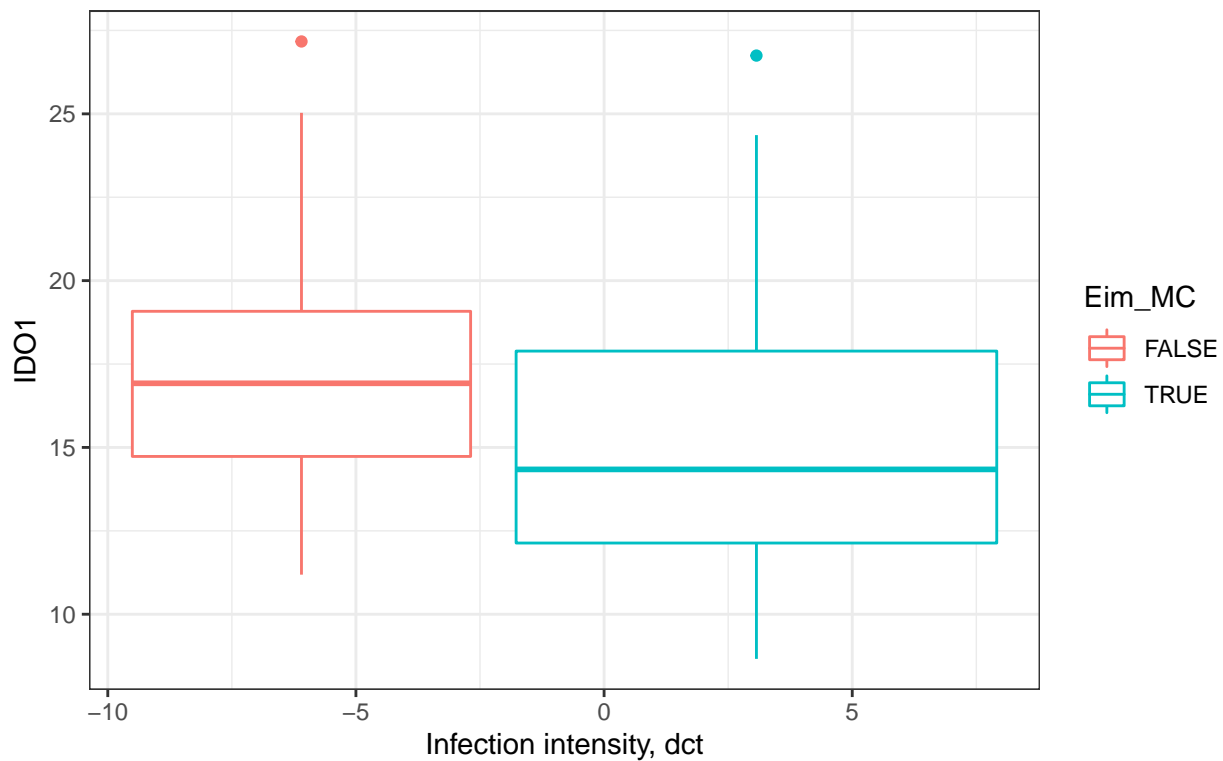
## Immune gene expression against infection intensity in field samples



```
ggplot(lab, aes(x = delta, y = IDO1, color = Eim_MC)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in lab
infections") +
  theme_bw()
```

## Warning: Removed 6 rows containing missing values (stat\_boxplot).

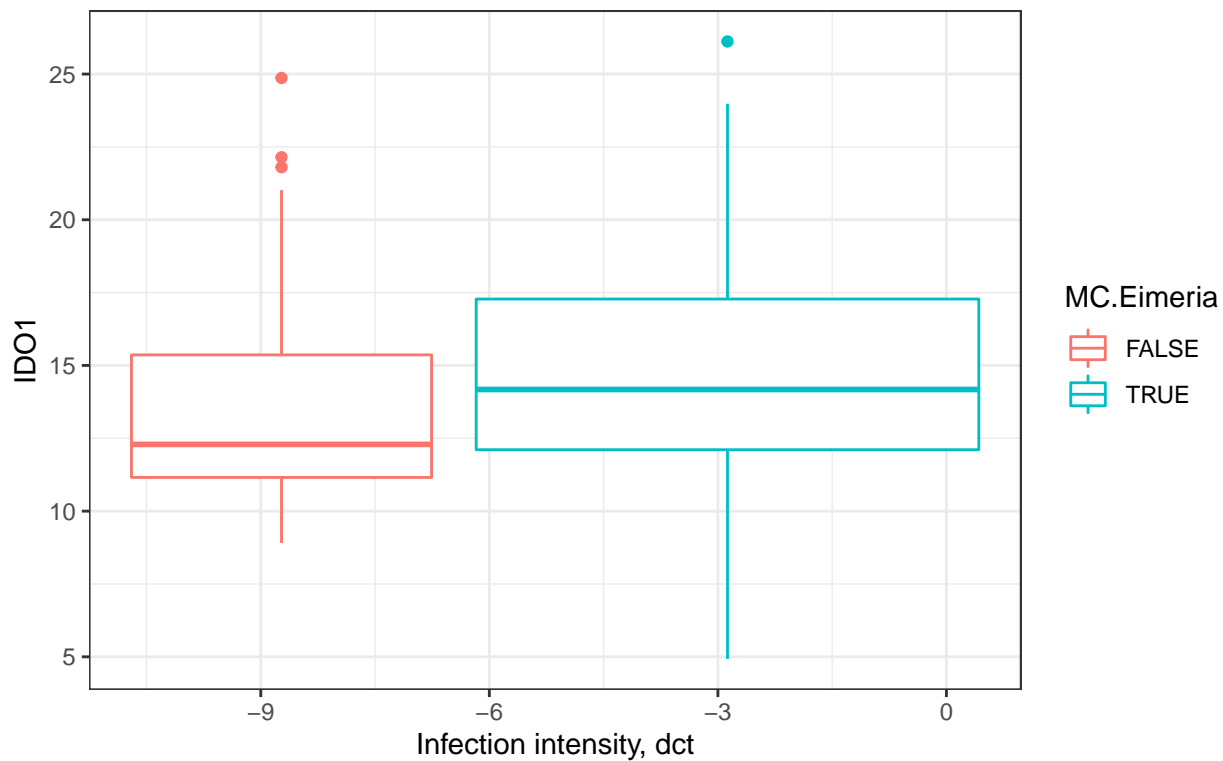
## Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = IDO1,
                  color = MC.Eimeria)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
               samples") +
  theme_bw()
```

## Warning: Removed 150 rows containing missing values (stat\_boxplot).

## Immune gene expression against infection intensity in field samples

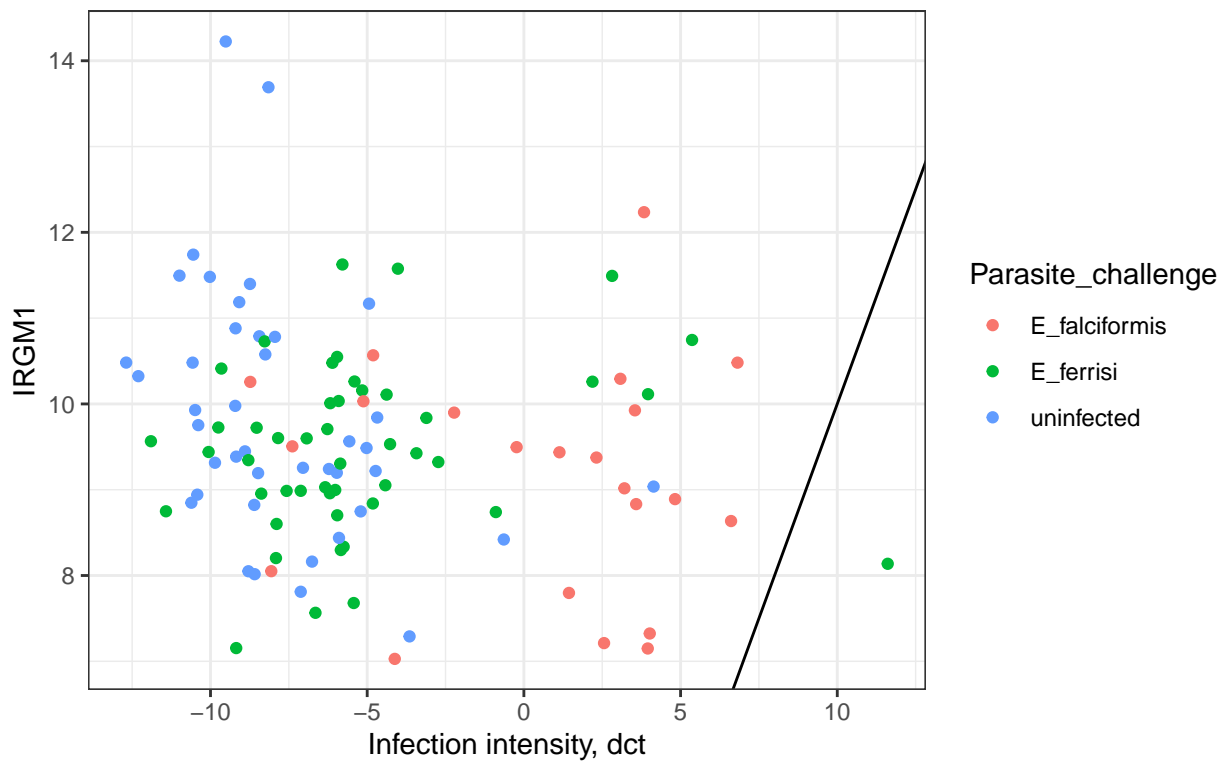


### 10. IRGM1

```
ggplot(lab, aes(x = delta, y = IRGM1, color = Parasite_challenge)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity
               in lab infections") +
  theme_bw()
```

## Warning: Removed 6 rows containing missing values (geom\_point).

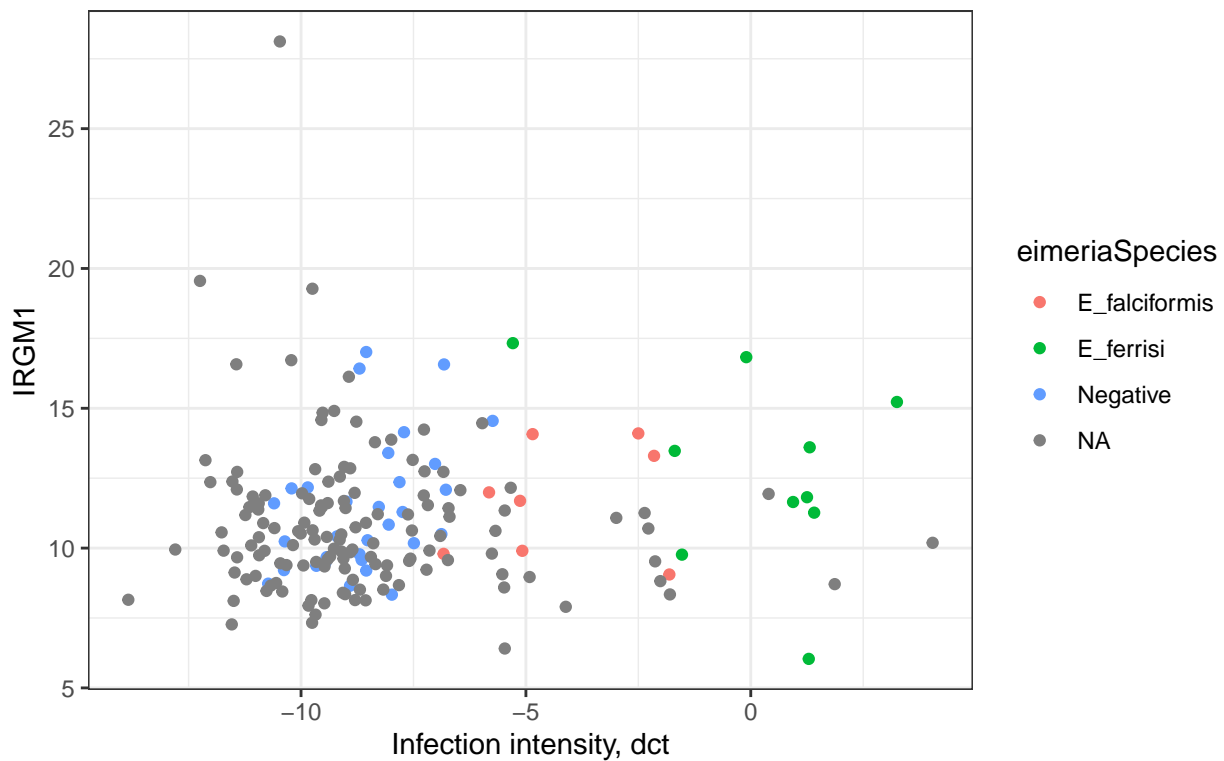
## Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = IRGM1, color = eimeriaSpecies)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
samples") +
  theme_bw()
```

## Warning: Removed 150 rows containing missing values (geom\_point).

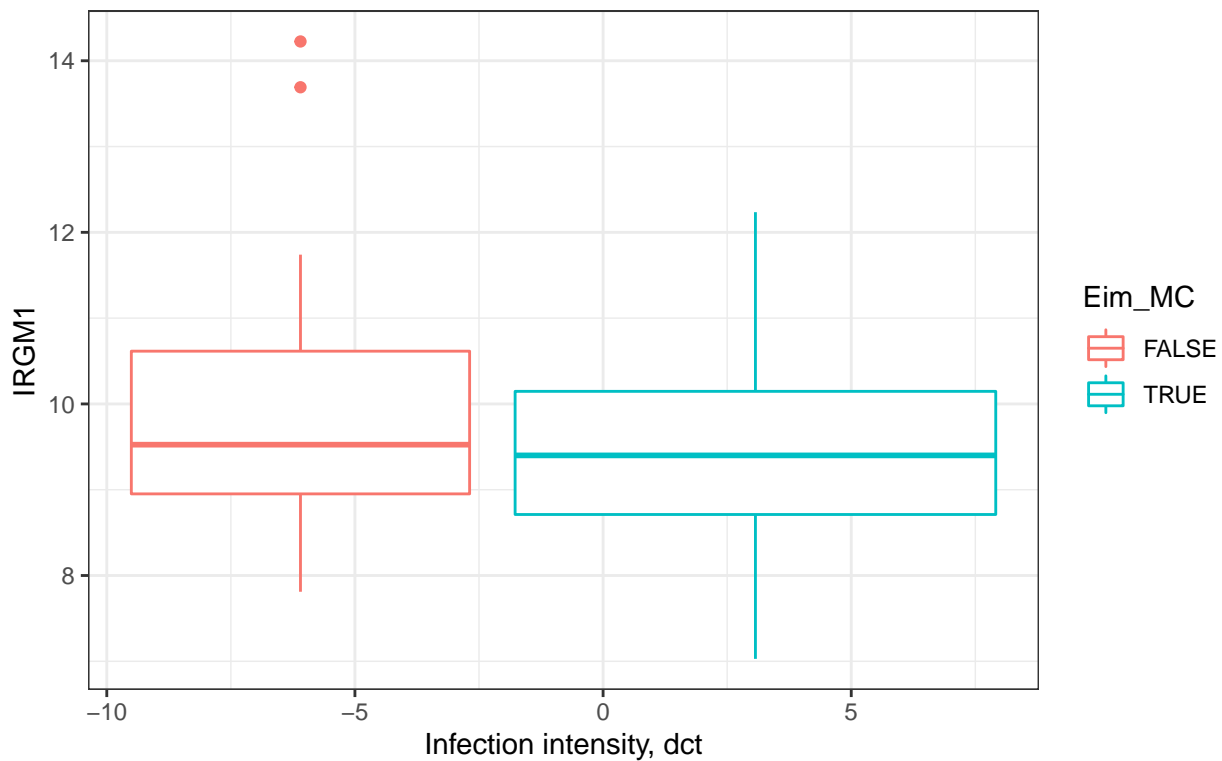
## Immune gene expression against infection intensity in field samples



```
ggplot(lab, aes(x = delta, y = IRGM1, color = Eim_MC)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in lab
infections") +
  theme_bw()
```

## Warning: Removed 6 rows containing missing values (stat\_boxplot).

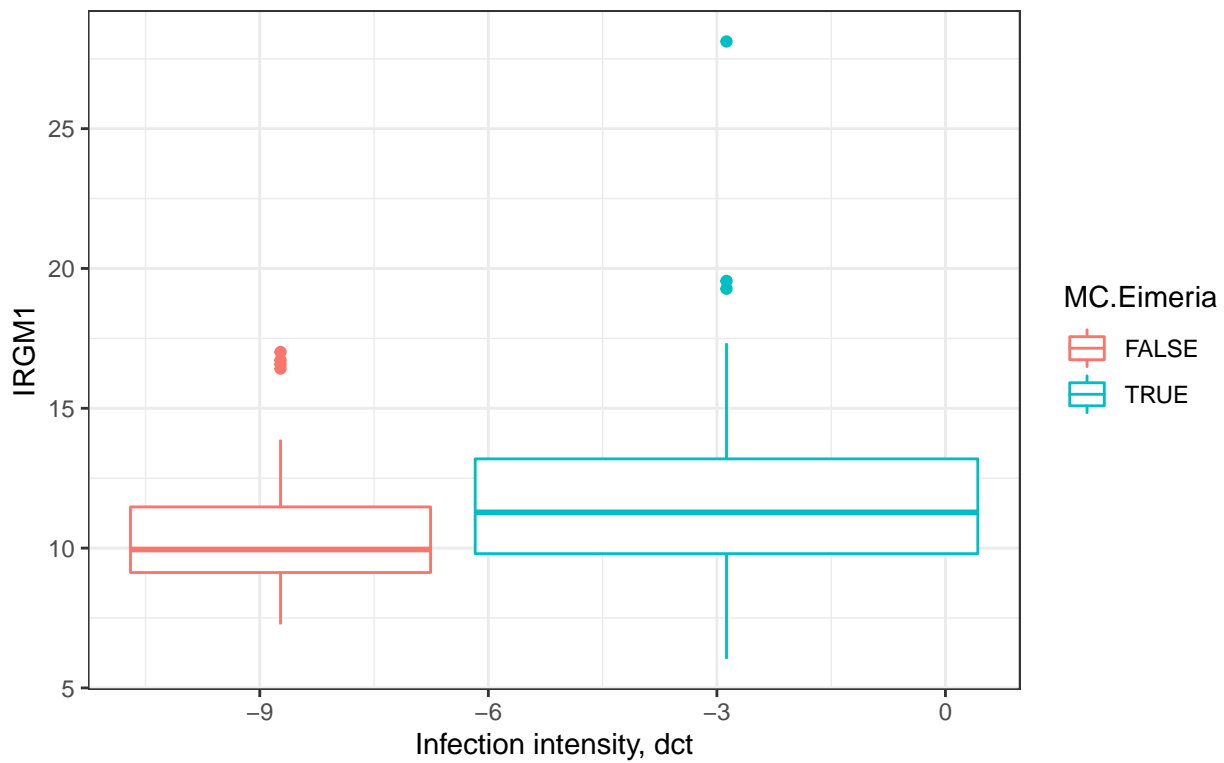
## Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = IRGM1,
                  color = MC.Eimeria)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
samples") +
  theme_bw()
```

## Warning: Removed 150 rows containing missing values (stat\_boxplot).

## Immune gene expression against infection intensity in field samples

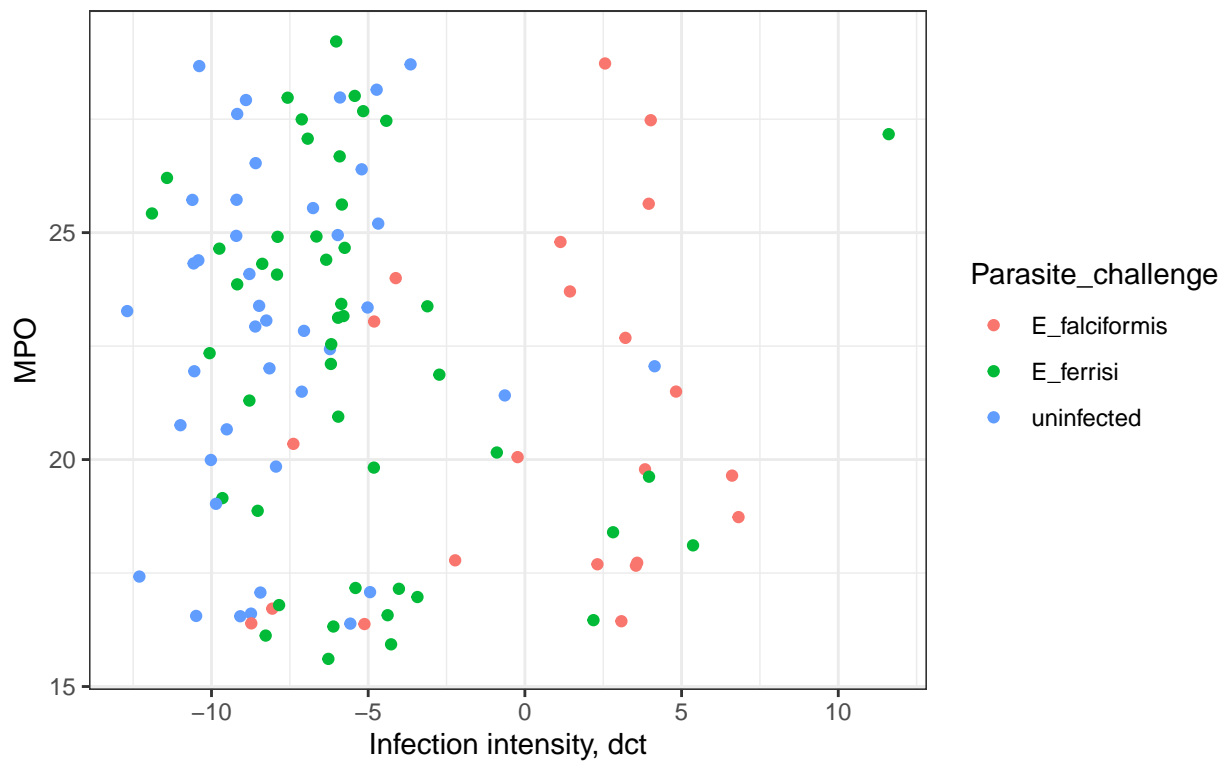


## 11. MPO

```
ggplot(lab, aes(x = delta, y = MPO, color = Parasite_challenge)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity
in lab infections") +
  theme_bw()
```

## Warning: Removed 6 rows containing missing values (geom\_point).

## Immune gene expression against infection intensity in lab infections

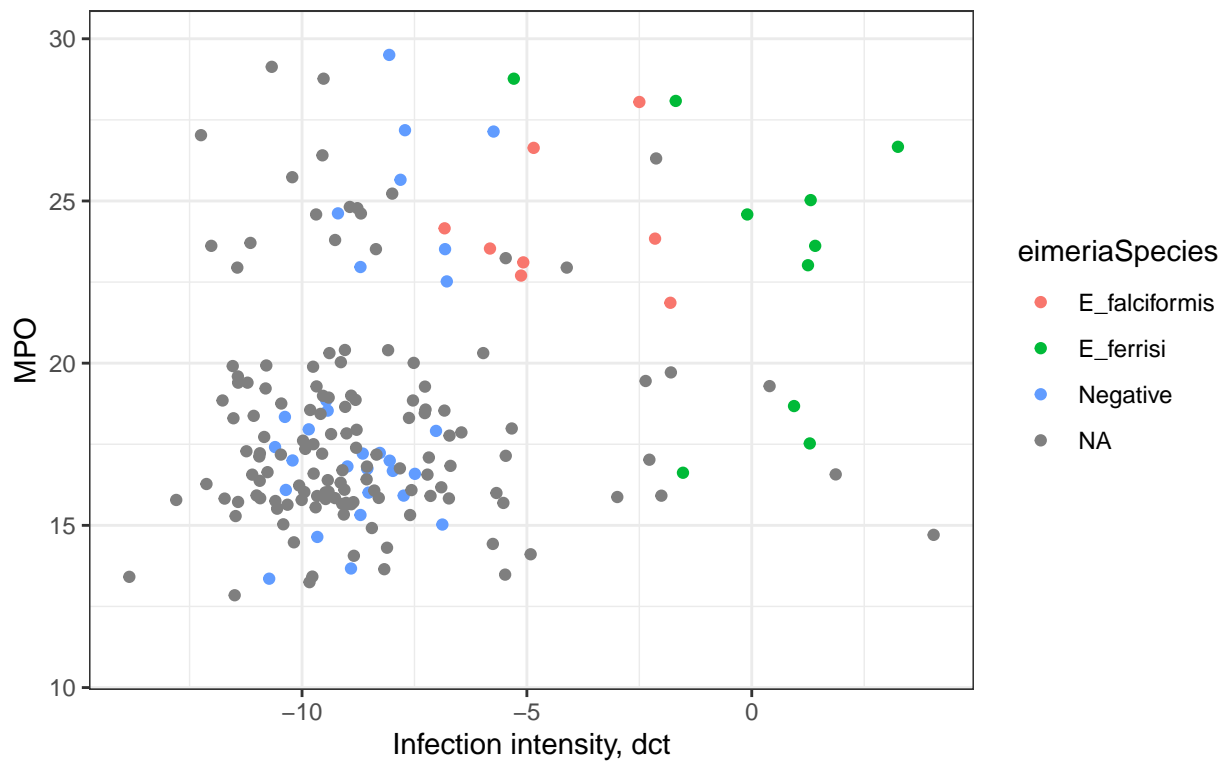


```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = MPO, color = eimeriaSpecies)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
samples") +
  theme_bw()
```

## Warning: Removed 150 rows containing missing values (geom\_point).



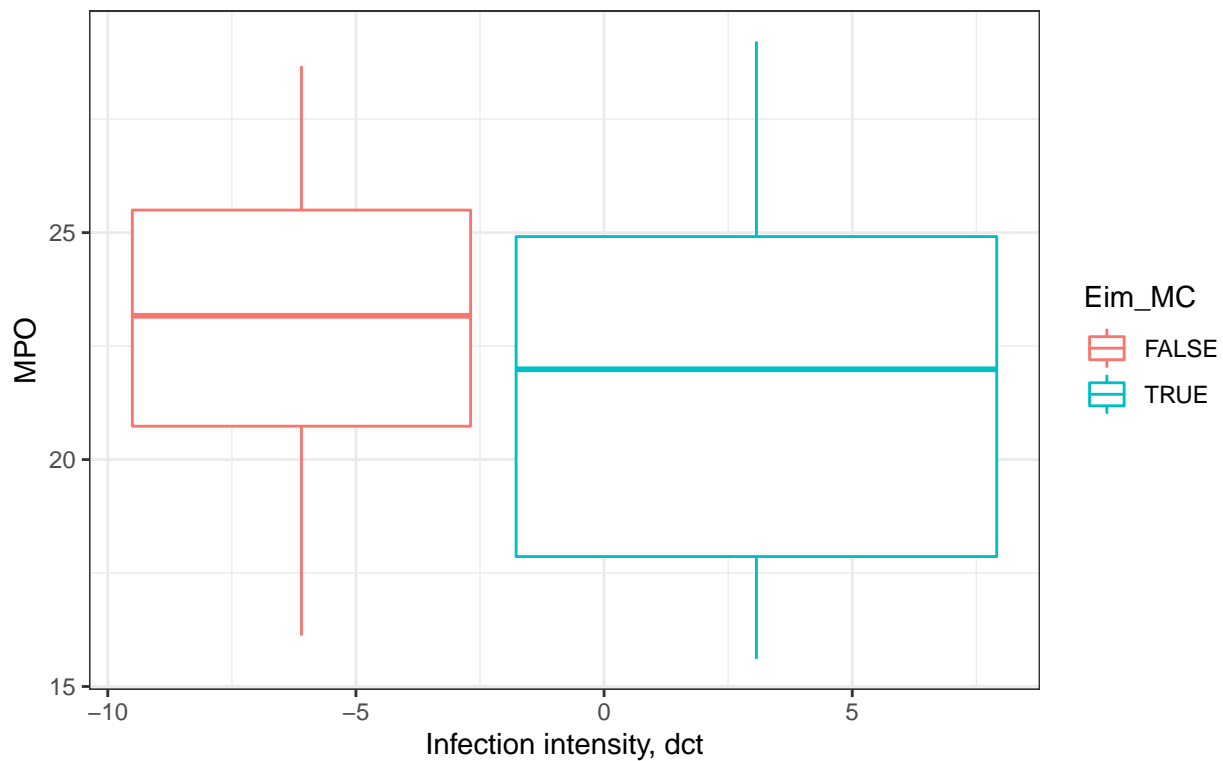
## Immune gene expression against infection intensity in field samples



```
ggplot(lab, aes(x = delta, y = MPO, color = Eim_MC)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in lab
infections") +
  theme_bw()
```

## Warning: Removed 6 rows containing missing values (stat\_boxplot).

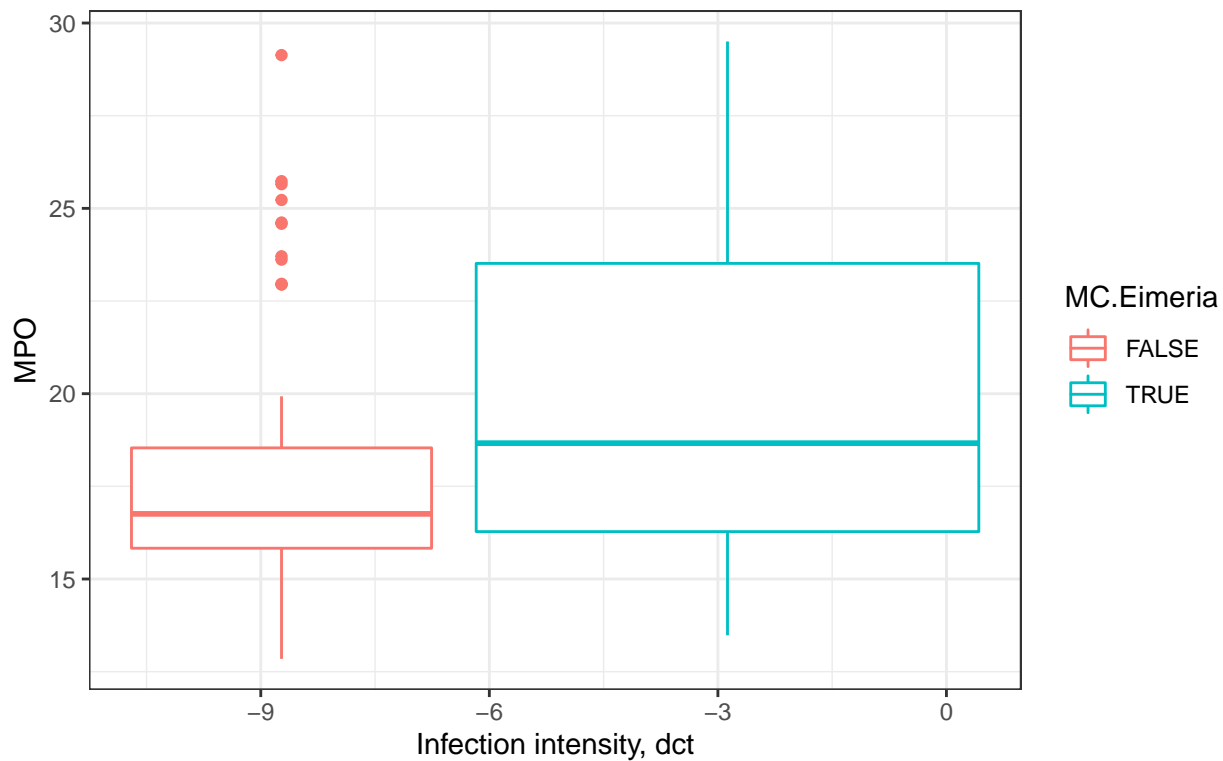
## Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = MPO,
                  color = MC.Eimeria)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
samples") +
  theme_bw()
```

## Warning: Removed 150 rows containing missing values (stat\_boxplot).

## Immune gene expression against infection intensity in field samples

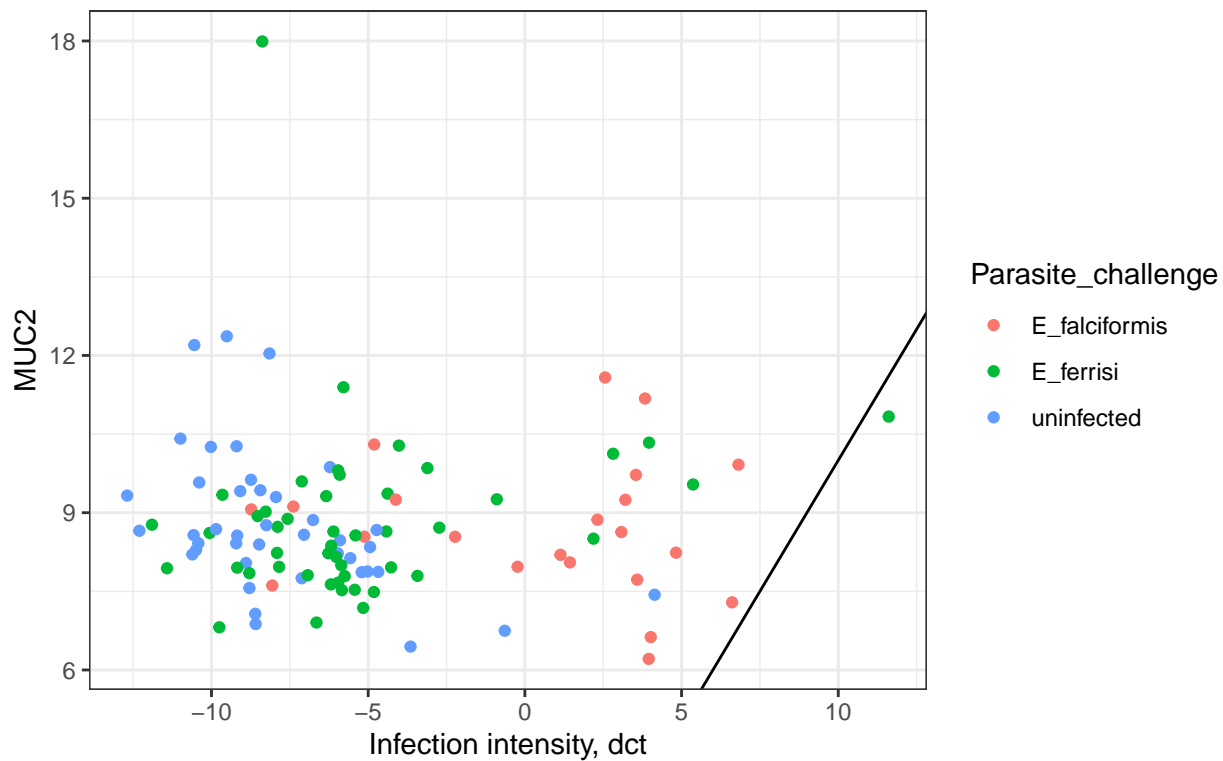


## 12. MUC2

```
ggplot(lab, aes(x = delta, y = MUC2, color = Parasite_challenge)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity
in lab infections") +
  theme_bw()
```

## Warning: Removed 6 rows containing missing values (geom\_point).

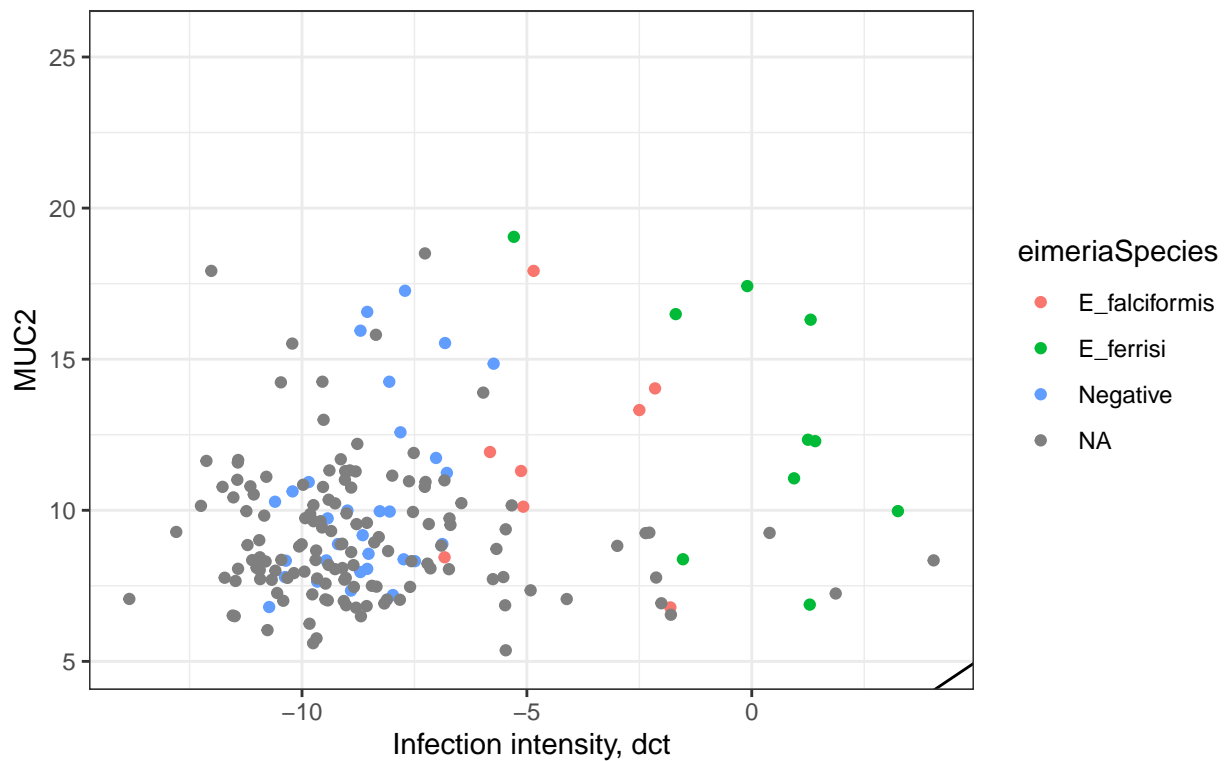
## Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = MUC2, color = eimeriaSpecies)) +  
  geom_jitter() +  
  geom_abline() +  
  labs(x = "Infection intensity, dct",  
        title = "Immune gene expression against infection intensity in field  
        samples") +  
  theme_bw()
```

```
## Warning: Removed 150 rows containing missing values (geom_point).
```

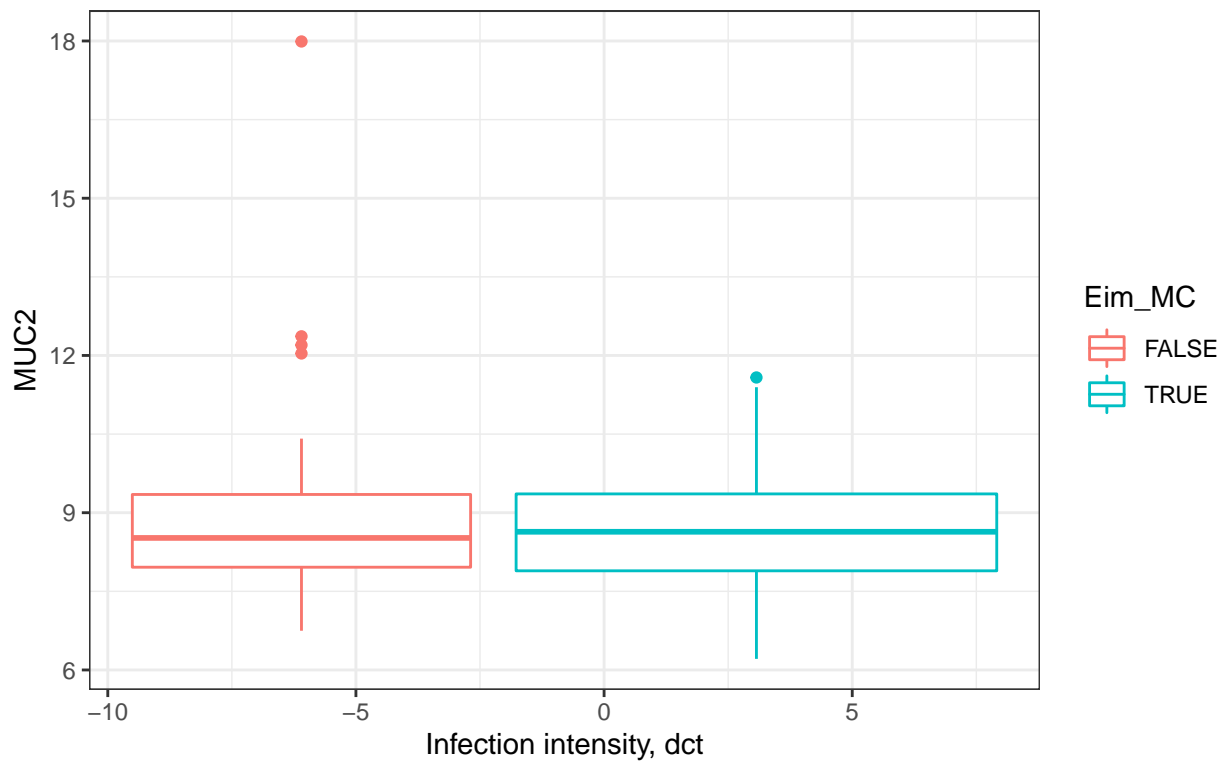
## Immune gene expression against infection intensity in field samples



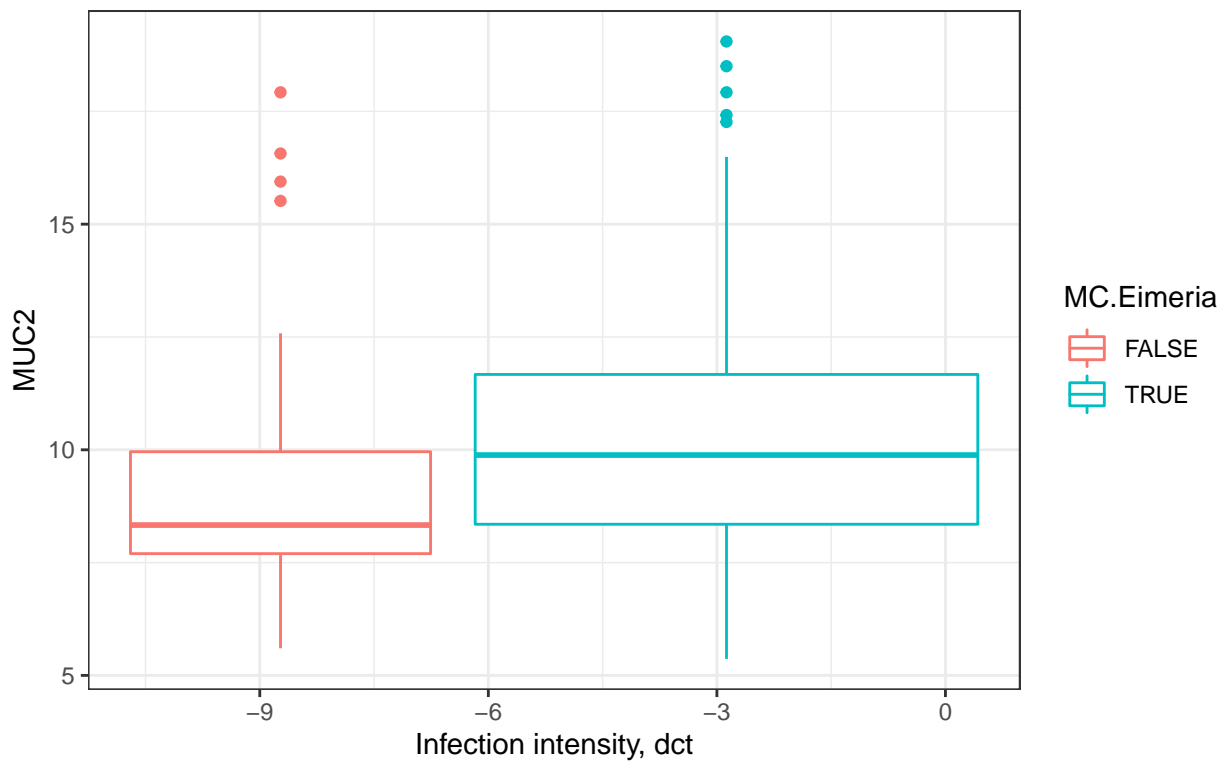
```
ggplot(lab, aes(x = delta, y = MUC2, color = Eim_MC)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in lab
infections") +
  theme_bw()
```

## Warning: Removed 6 rows containing missing values (stat\_boxplot).

## Immune gene expression against infection intensity in lab infections



## Immune gene expression against infection intensity in field samples

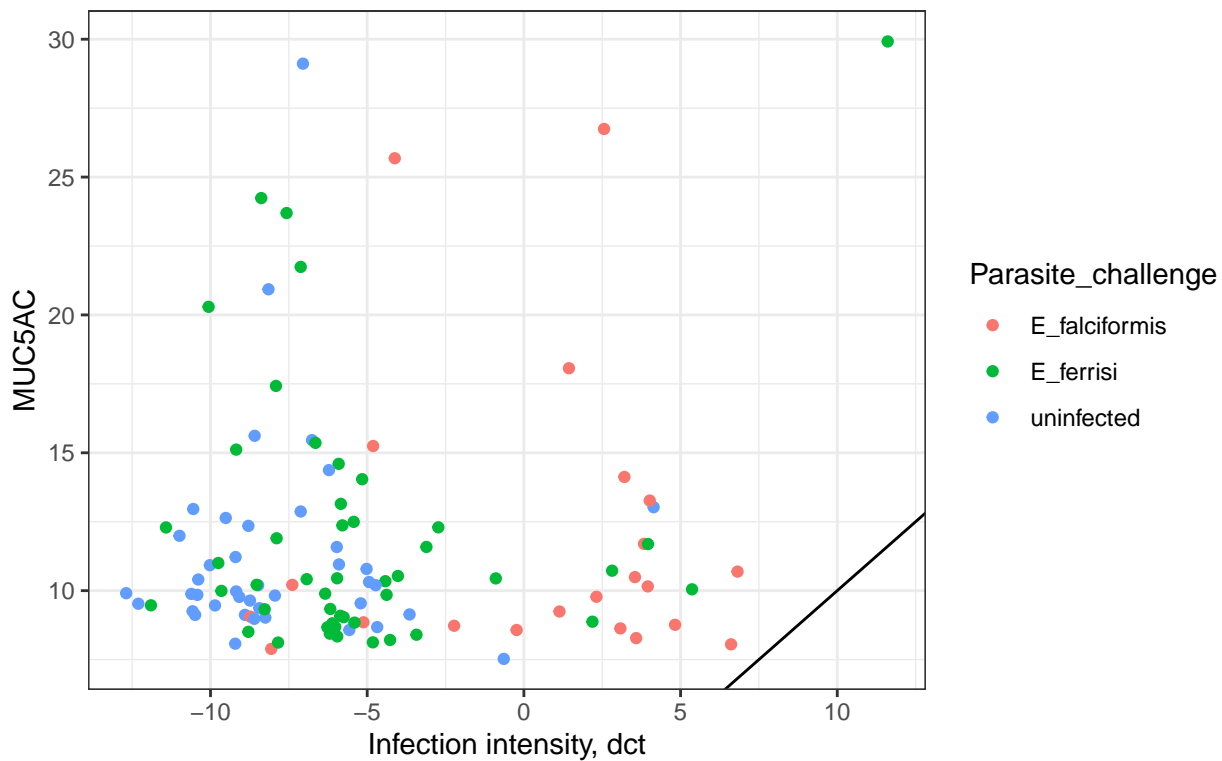


### 13. MUC5AC

```
ggplot(lab, aes(x = delta, y = MUC5AC, color = Parasite_challenge)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity
in lab infections") +
  theme_bw()
```

## Warning: Removed 6 rows containing missing values (geom\_point).

## Immune gene expression against infection intensity in lab infections

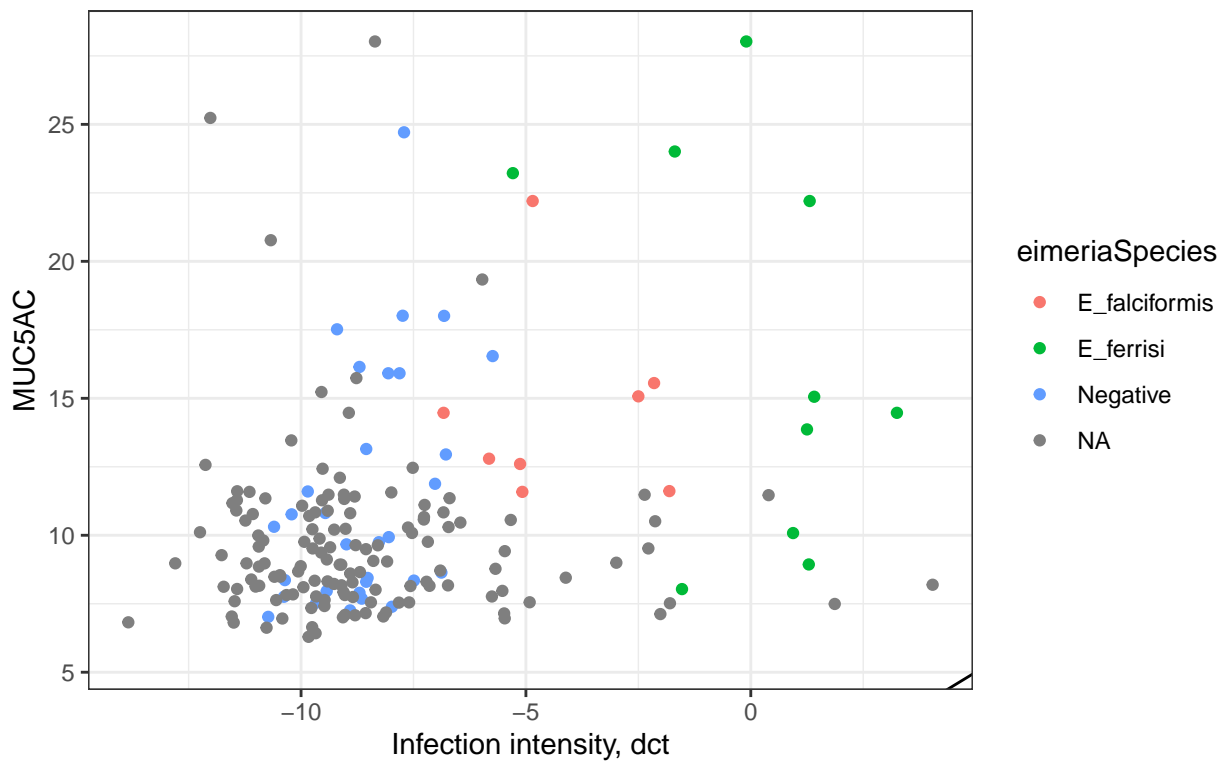


```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = MUC5AC, color = eimeriaSpecies)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
       samples") +
  theme_bw()
```

## Warning: Removed 150 rows containing missing values (geom\_point).



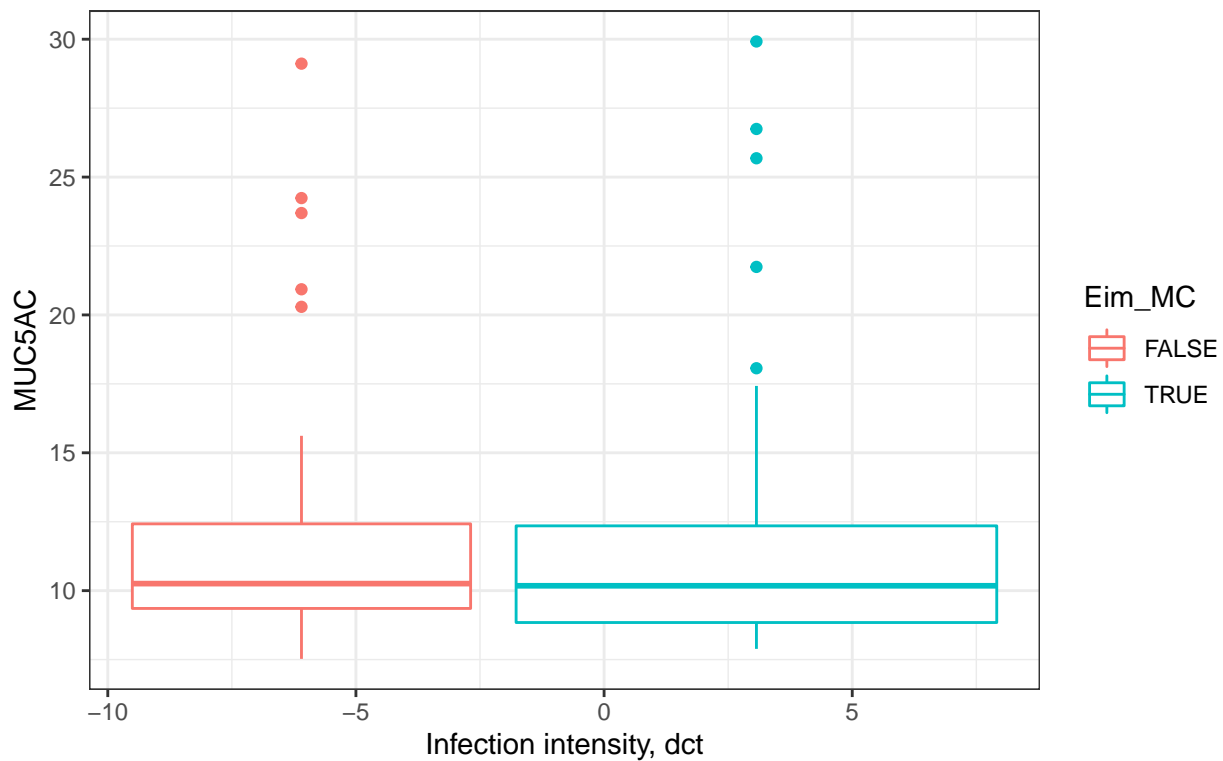
## Immune gene expression against infection intensity in field samples



```
ggplot(lab, aes(x = delta, y = MUC5AC, color = Eim_MC)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in lab
infections") +
  theme_bw()
```

## Warning: Removed 6 rows containing missing values (stat\_boxplot).

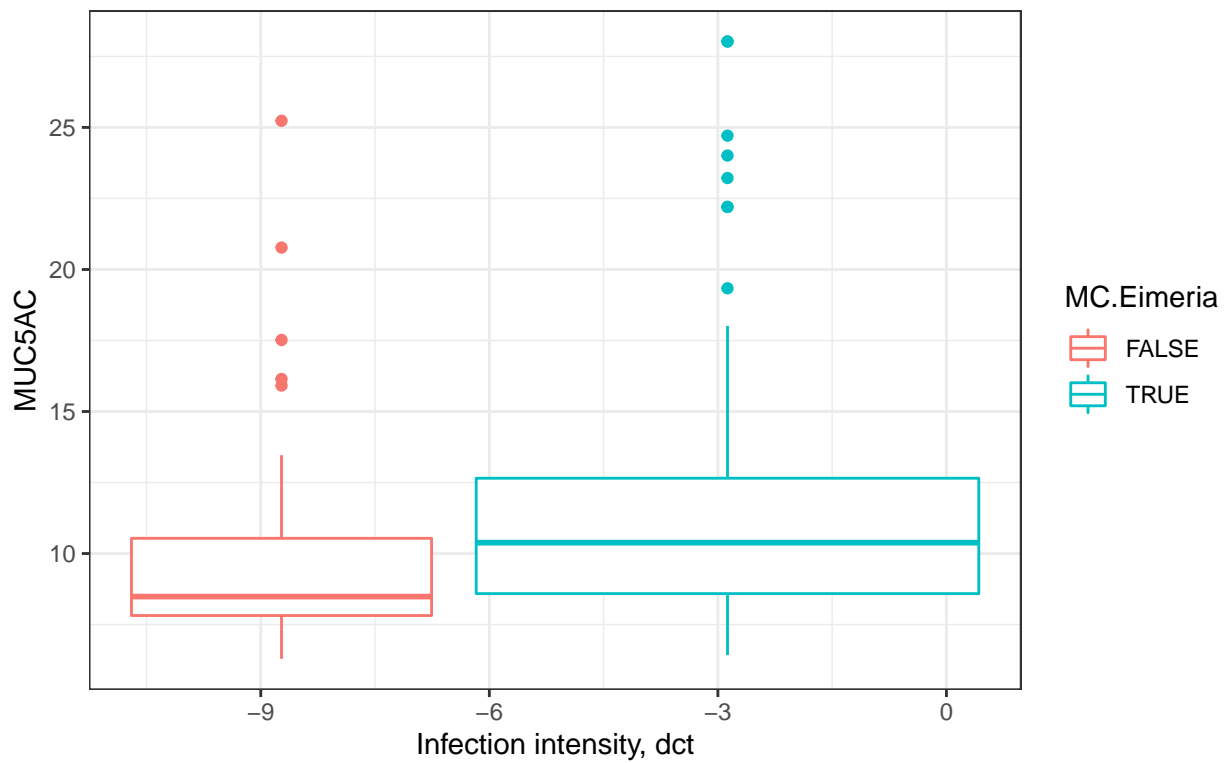
## Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = MUC5AC,
                  color = MC.Eimeria)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
               samples") +
  theme_bw()
```

## Warning: Removed 150 rows containing missing values (stat\_boxplot).

## Immune gene expression against infection intensity in field samples

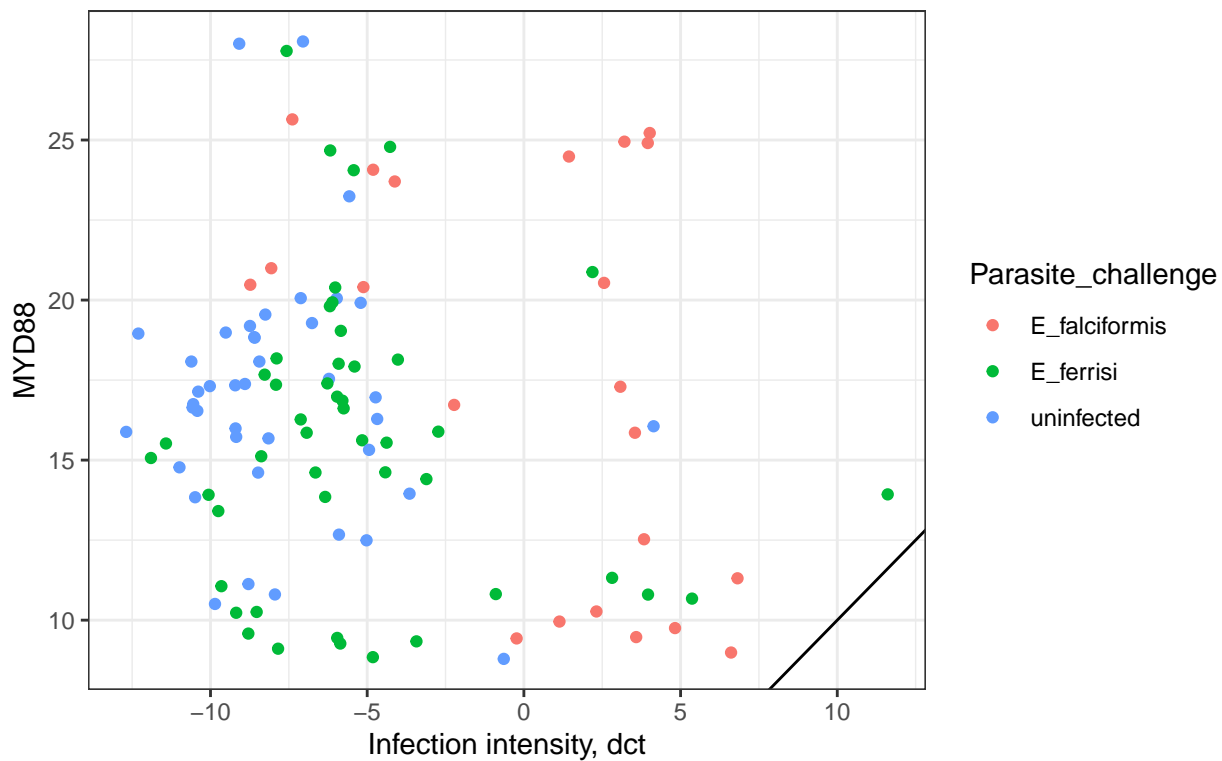


### 14. MYD88

```
ggplot(lab, aes(x = delta, y = MYD88, color = Parasite_challenge)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity
in lab infections") +
  theme_bw()
```

## Warning: Removed 6 rows containing missing values (geom\_point).

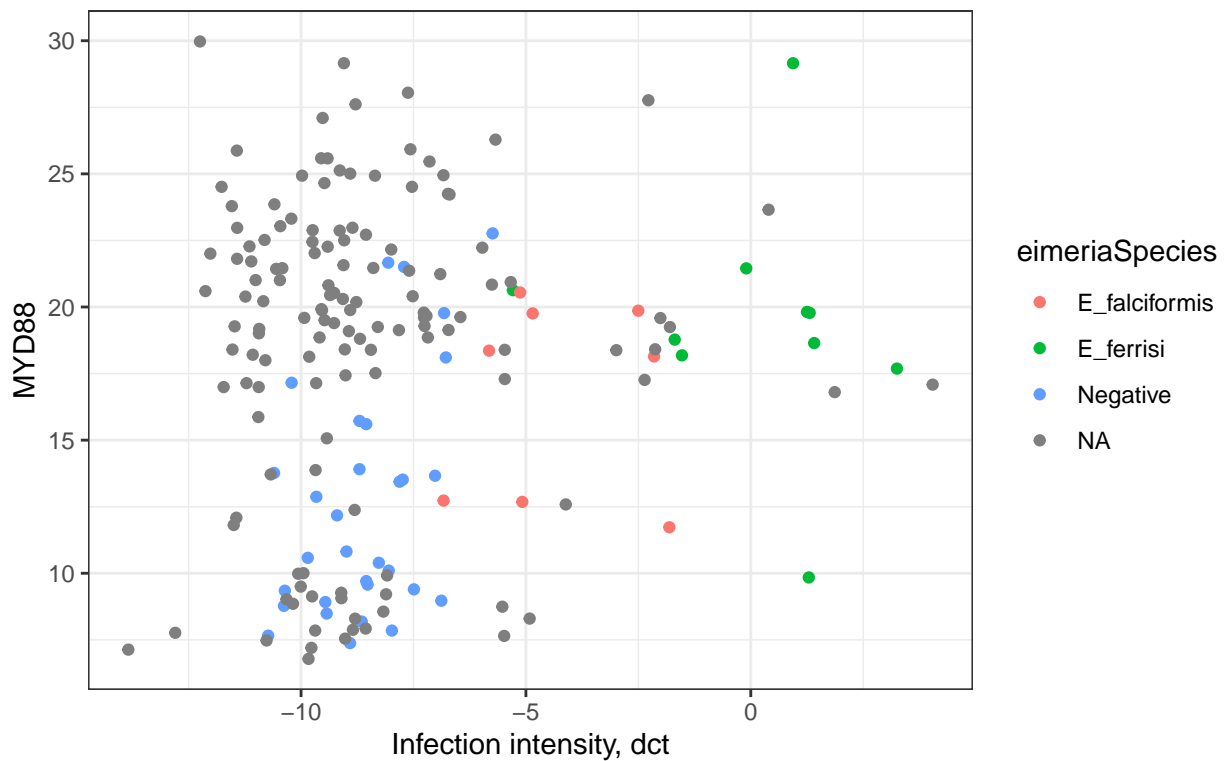
## Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = MYD88, color = eimeriaSpecies)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
       samples") +
  theme_bw()
```

## Warning: Removed 150 rows containing missing values (geom\_point).

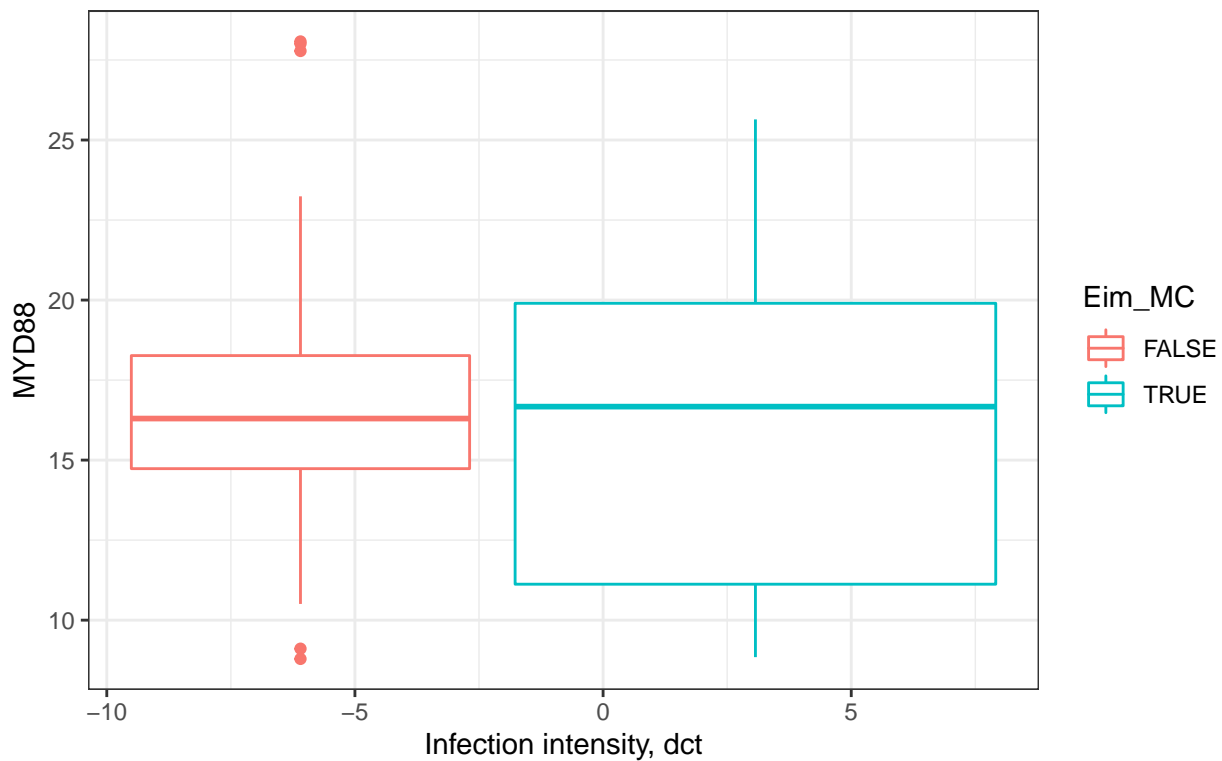
## Immune gene expression against infection intensity in field samples



```
ggplot(lab, aes(x = delta, y = MYD88, color = Eim_MC)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in lab
infections") +
  theme_bw()
```

## Warning: Removed 6 rows containing missing values (stat\_boxplot).

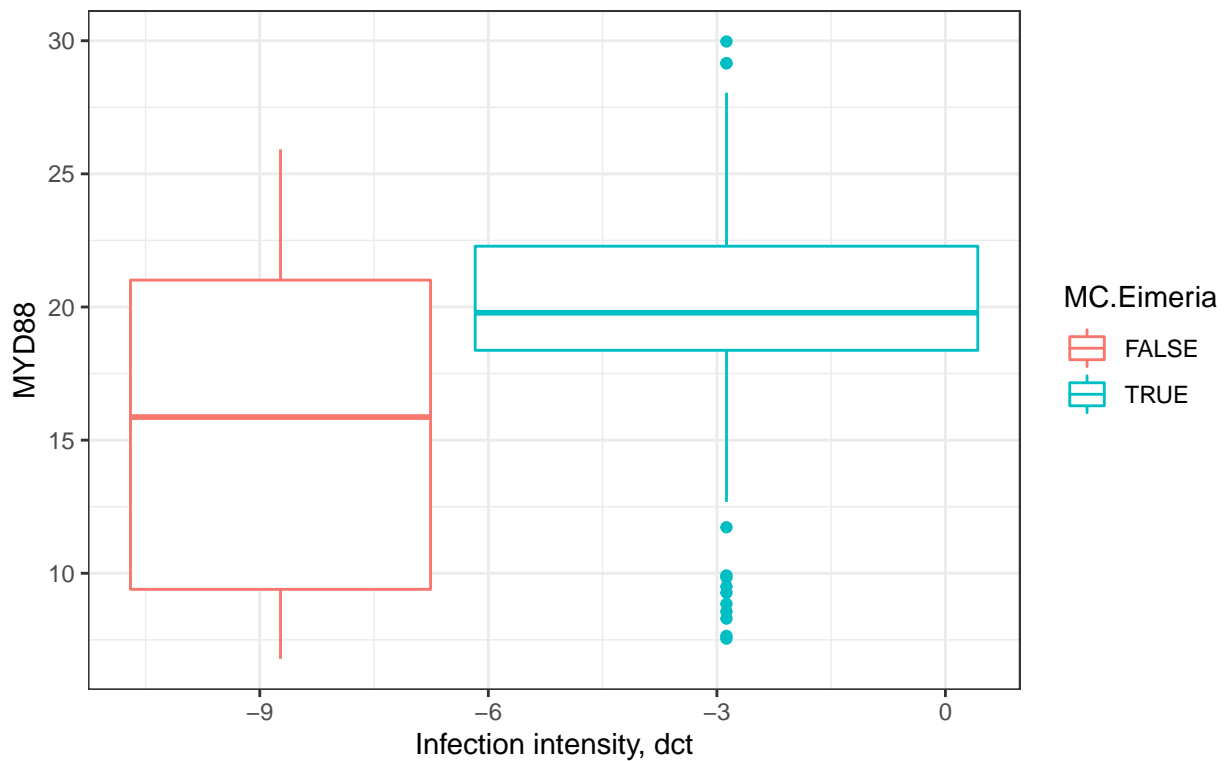
## Immune gene expression against infection intensity in lab infections



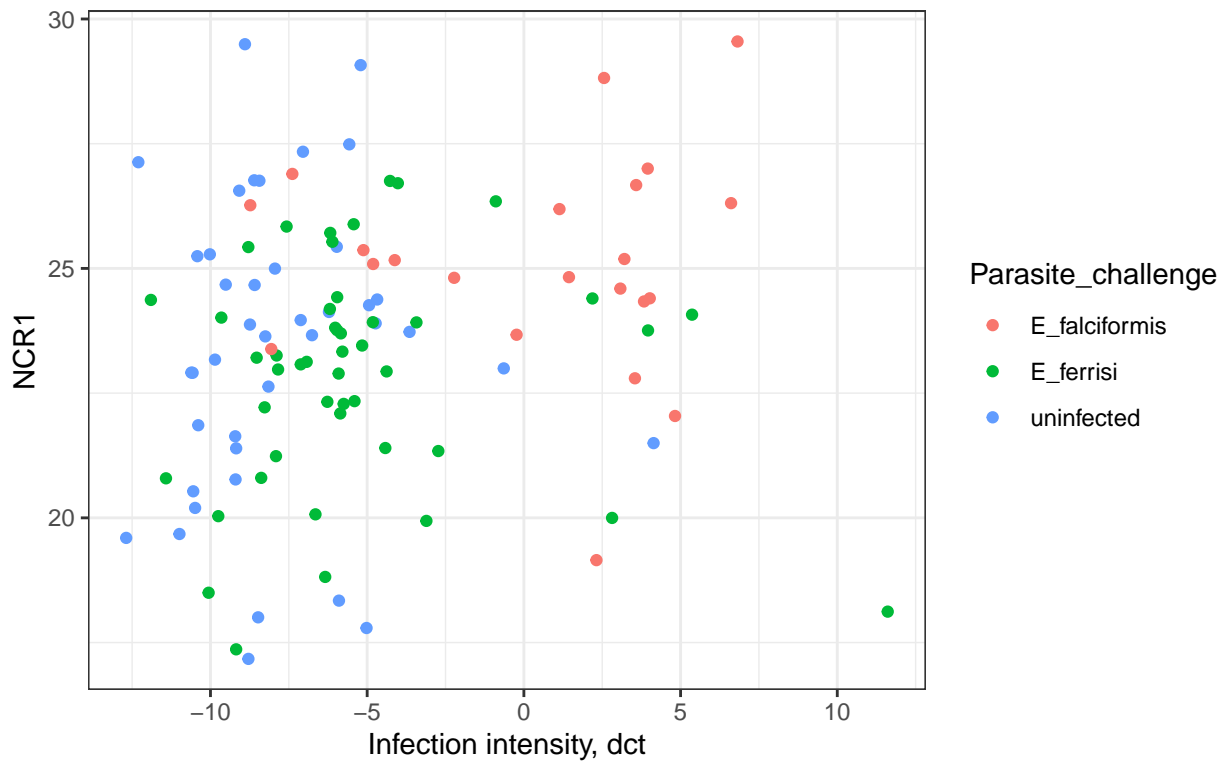
```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = MYD88,
                  color = MC.Eimeria)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
samples") +
  theme_bw()
```

## Warning: Removed 150 rows containing missing values (stat\_boxplot).

## Immune gene expression against infection intensity in field samples



## Immune gene expression against infection intensity in lab infections

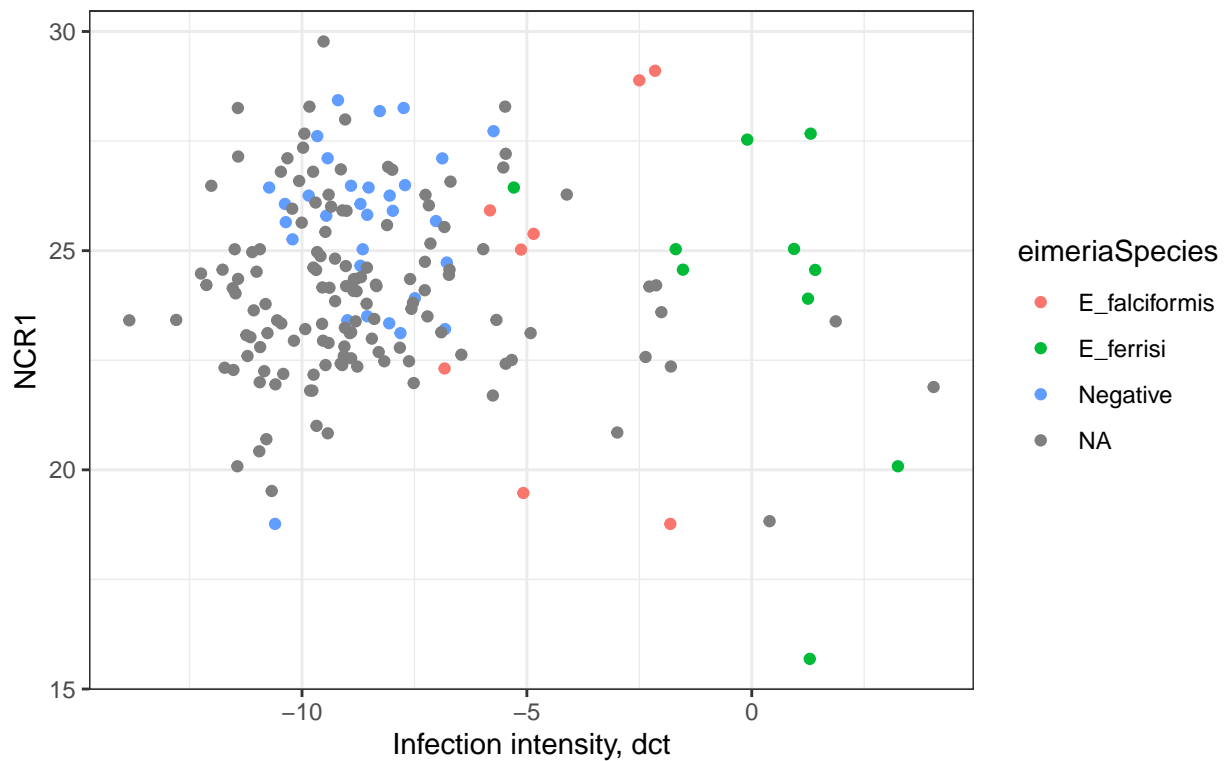


```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = NCR1, color = eimeriaSpecies)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
               samples") +
  theme_bw()
```

## Warning: Removed 150 rows containing missing values (geom\_point).



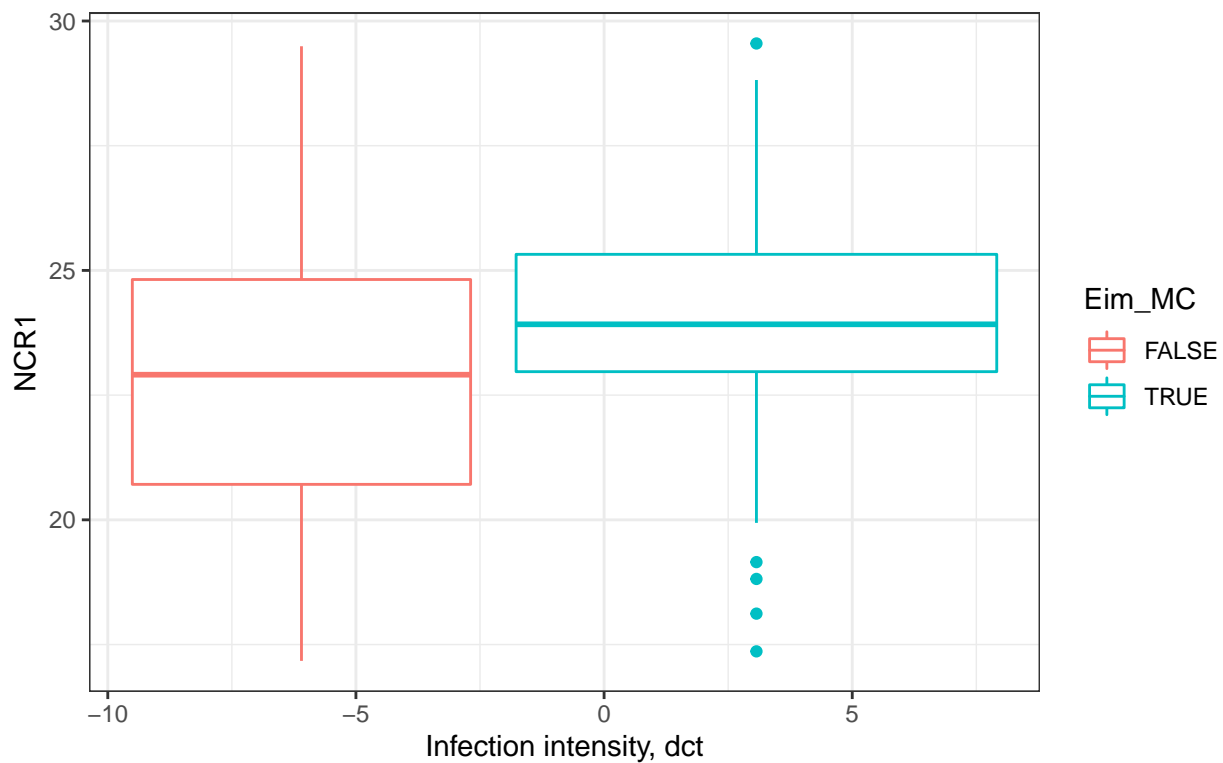
## Immune gene expression against infection intensity in field samples



```
ggplot(lab, aes(x = delta, y = NCR1, color = Eim_MC)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in lab
infections") +
  theme_bw()
```

## Warning: Removed 6 rows containing missing values (stat\_boxplot).

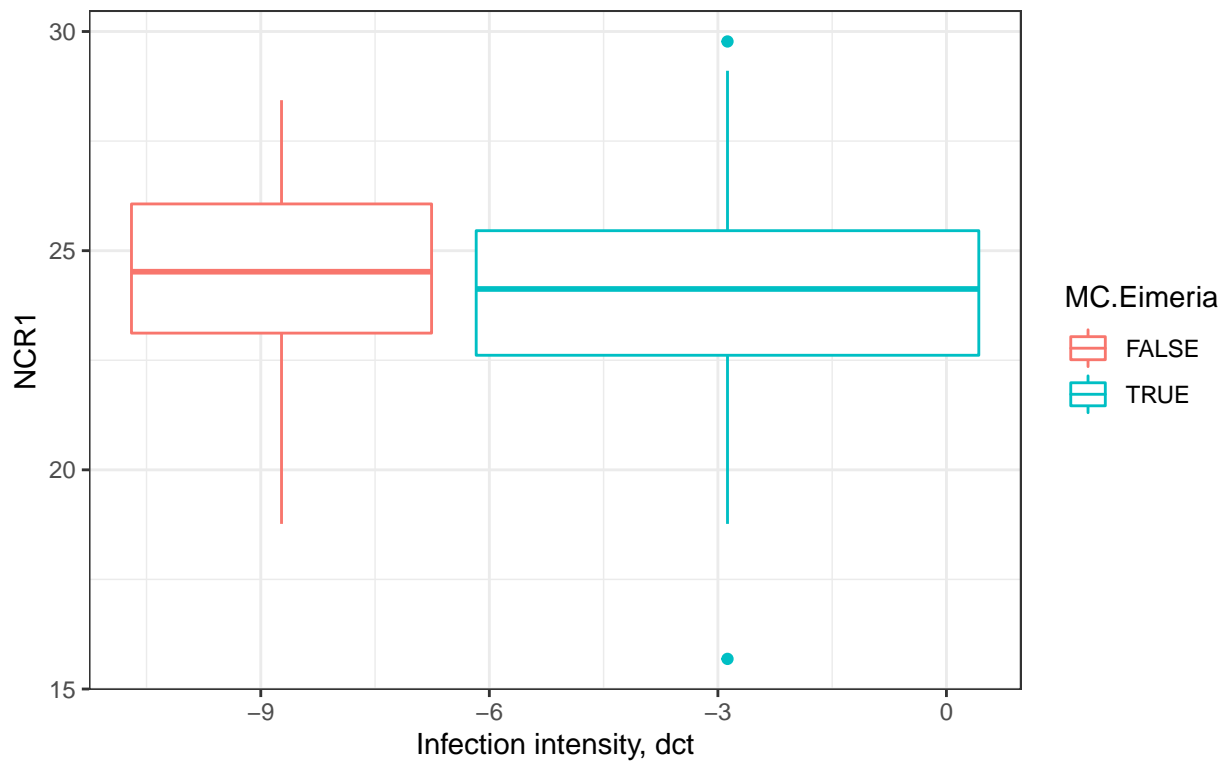
## Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = NCR1,
                  color = MC.Eimeria)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
               samples") +
  theme_bw()
```

## Warning: Removed 150 rows containing missing values (stat\_boxplot).

## Immune gene expression against infection intensity in field samples

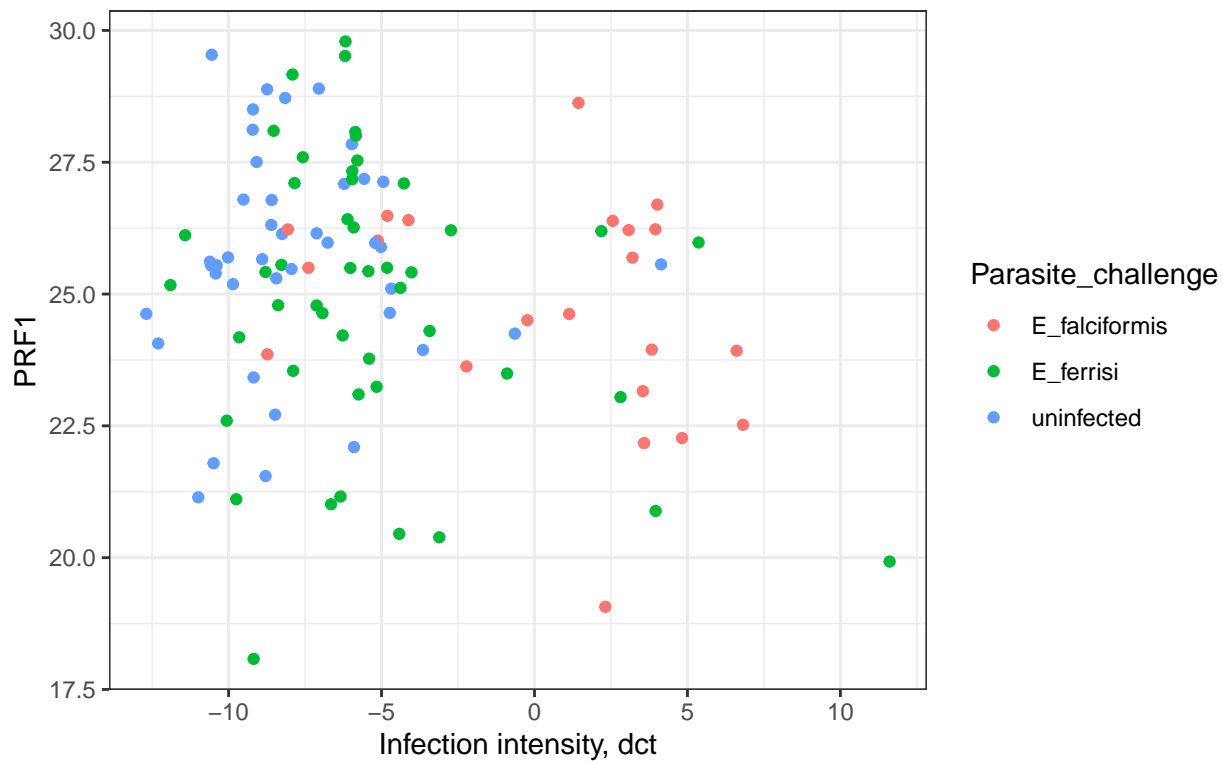


### 16. PRF1

```
ggplot(lab, aes(x = delta, y = PRF1, color = Parasite_challenge)) +  
  geom_jitter() +  
  geom_abline() +  
  labs(x = "Infection intensity, dct",  
       title = "Immune gene expression against infection intensity  
in lab infections") +  
  theme_bw()
```

## Warning: Removed 6 rows containing missing values (geom\_point).

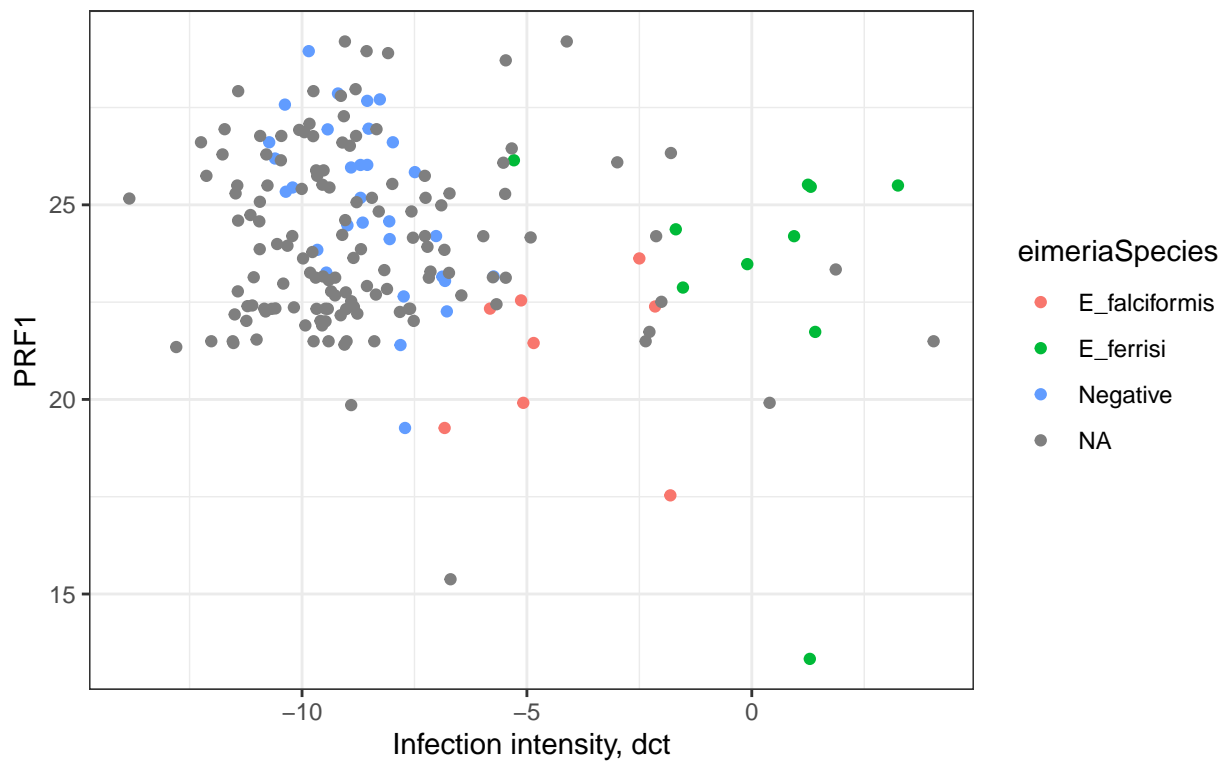
## Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = PRF1, color = eimeriaSpecies)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
               samples") +
  theme_bw()
```

## Warning: Removed 150 rows containing missing values (geom\_point).

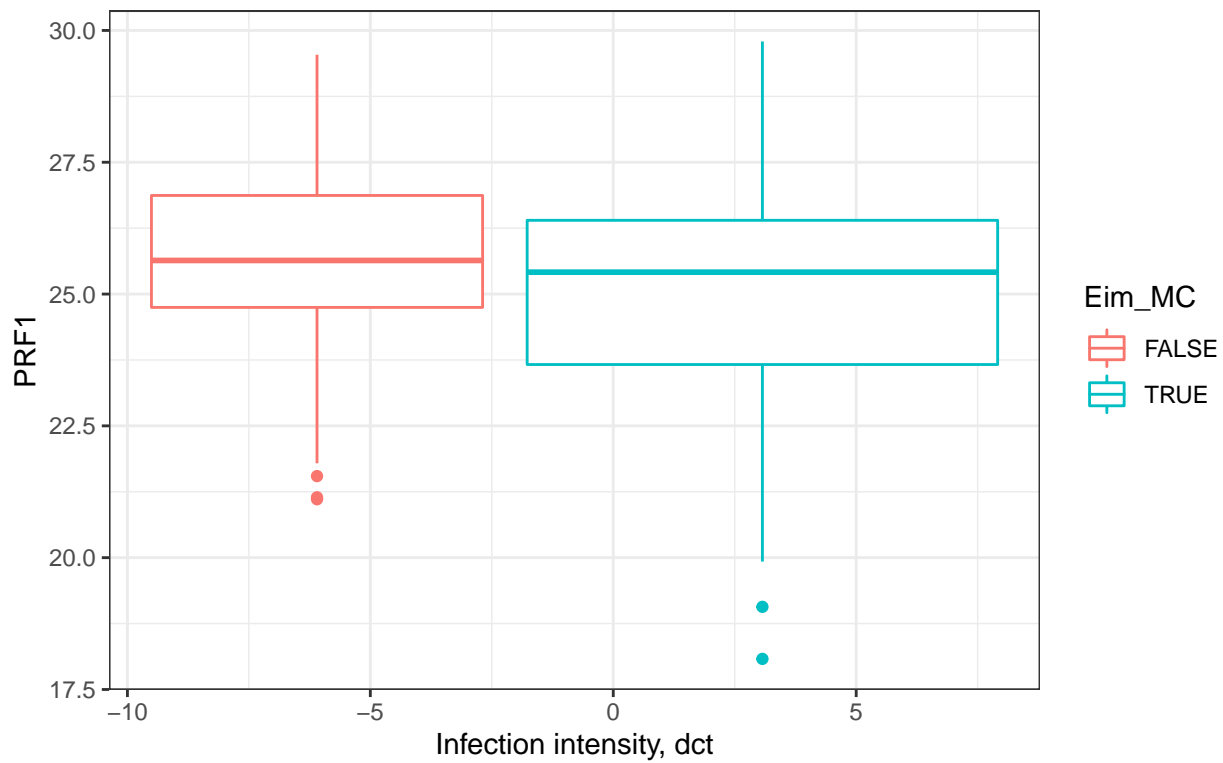
## Immune gene expression against infection intensity in field samples



```
ggplot(lab, aes(x = delta, y = PRF1, color = Eim_MC)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in lab
infections") +
  theme_bw()
```

## Warning: Removed 6 rows containing missing values (stat\_boxplot).

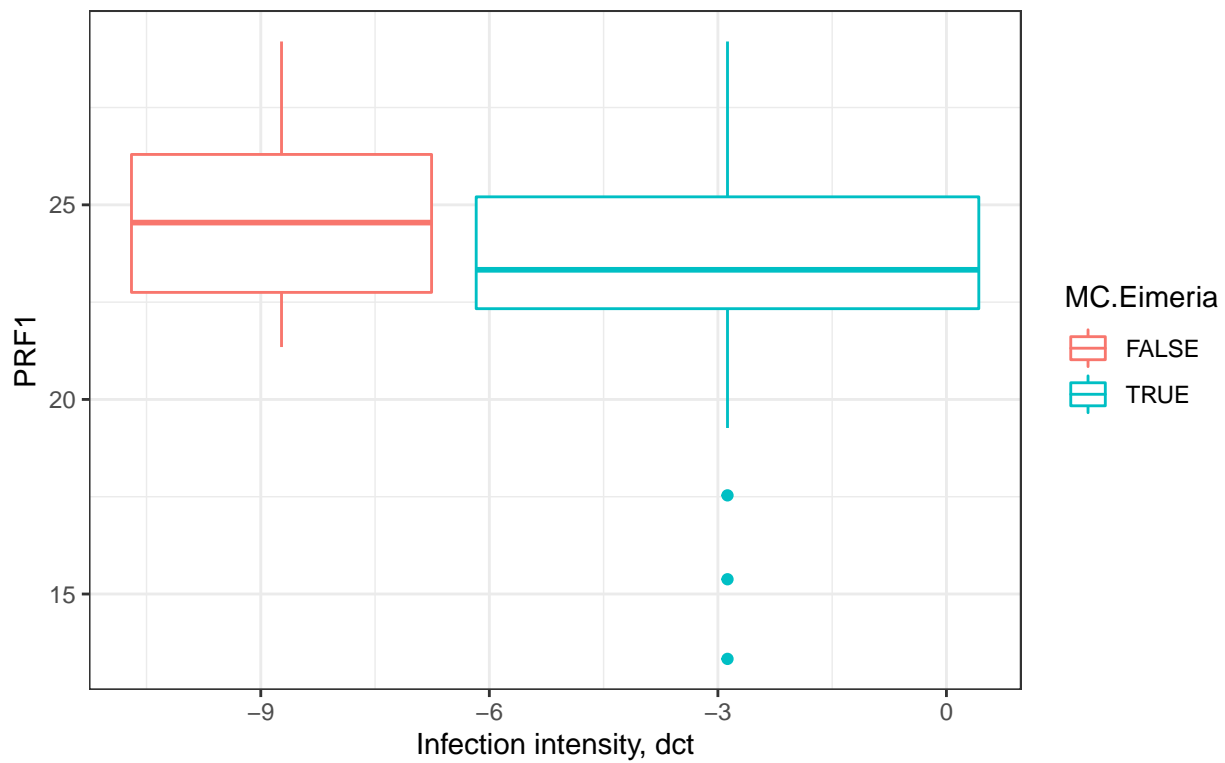
## Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = PRF1,
                  color = MC.Eimeria)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
               samples") +
  theme_bw()
```

## Warning: Removed 150 rows containing missing values (stat\_boxplot).

## Immune gene expression against infection intensity in field samples

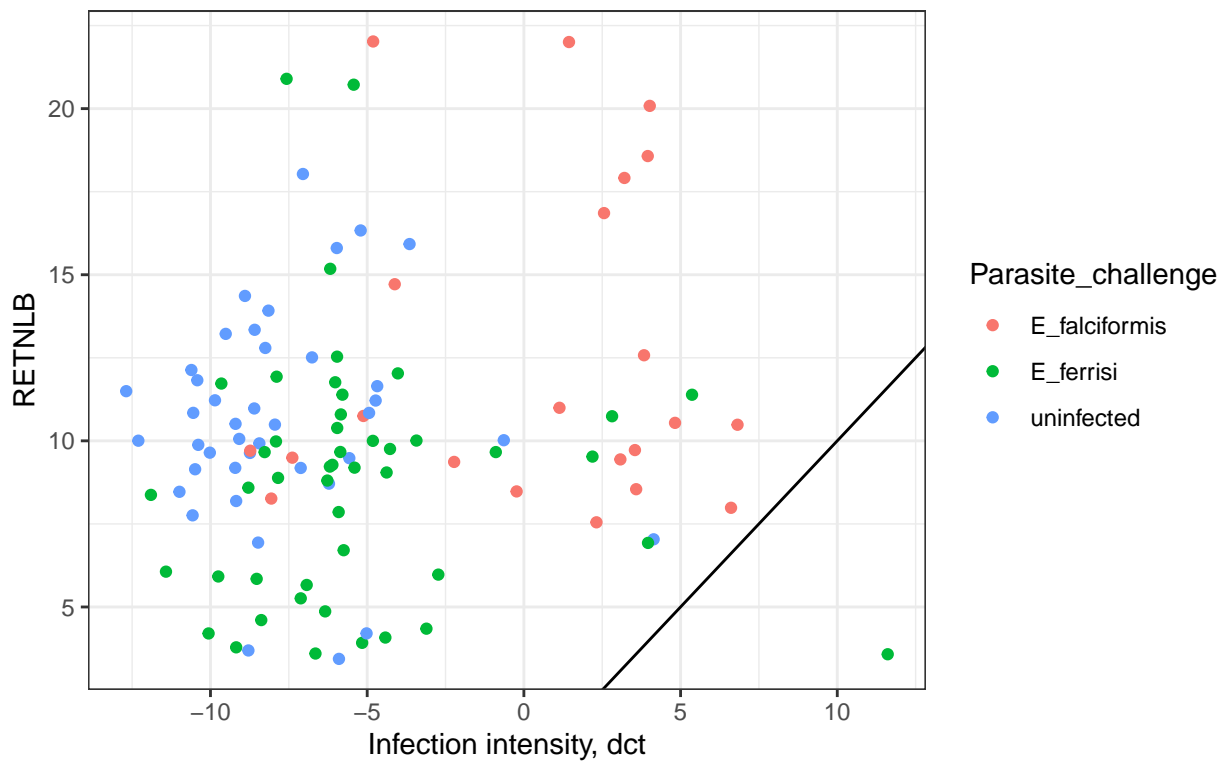


### 17. RETNLB

```
ggplot(lab, aes(x = delta, y = RETNLB, color = Parasite_challenge)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity
               in lab infections") +
  theme_bw()
```

## Warning: Removed 6 rows containing missing values (geom\_point).

## Immune gene expression against infection intensity in lab infections

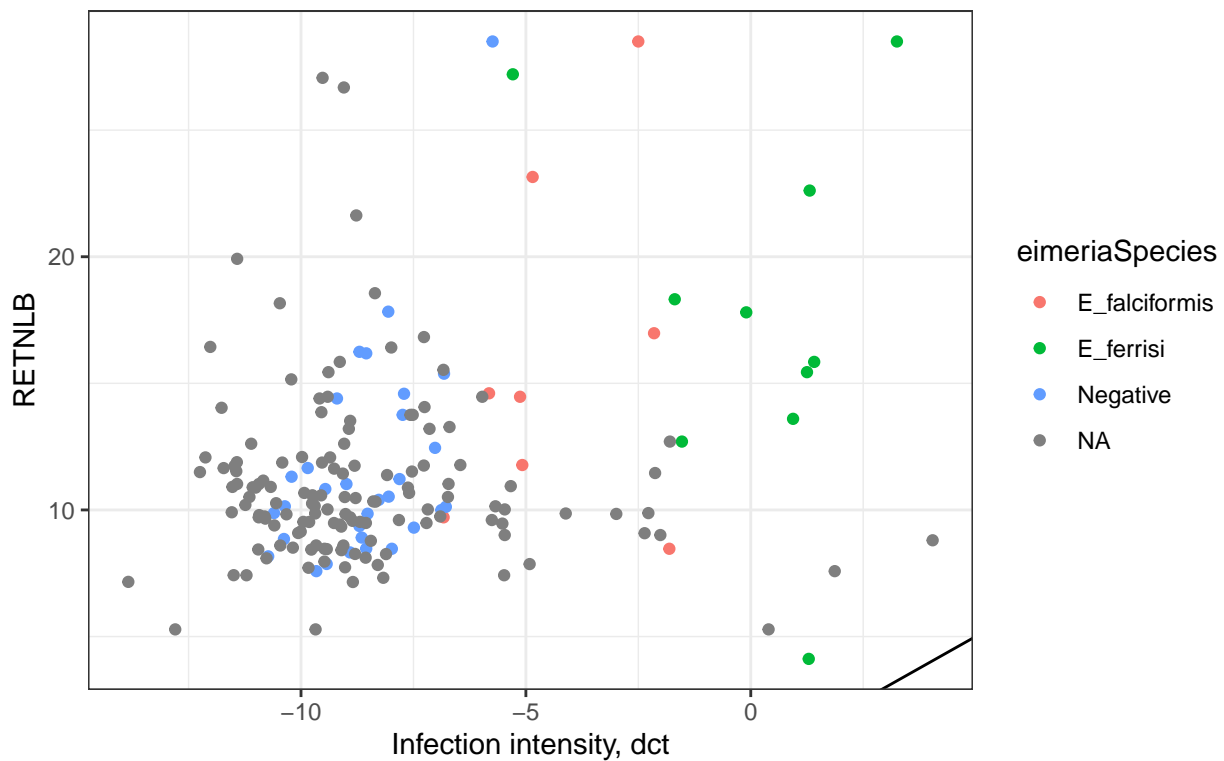


```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = RETNLB, color = eimeriaSpecies)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
       samples") +
  theme_bw()
```

## Warning: Removed 150 rows containing missing values (geom\_point).



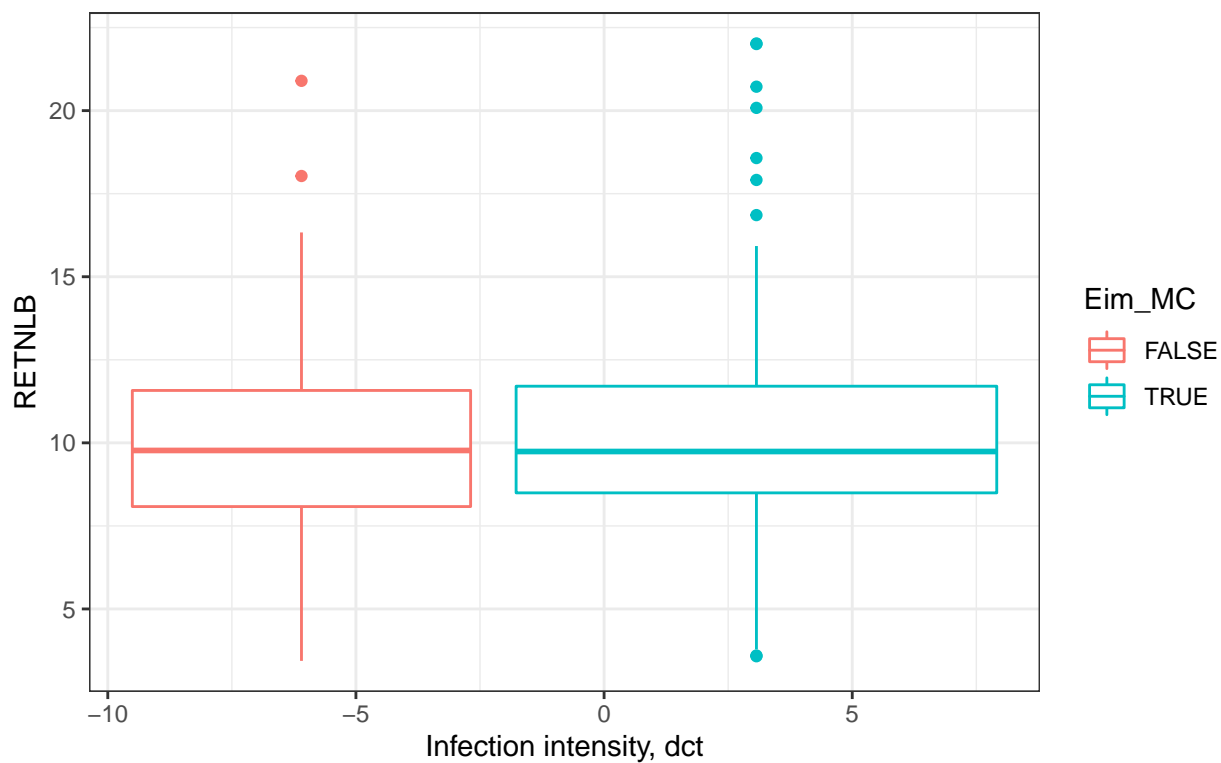
## Immune gene expression against infection intensity in field samples



```
ggplot(lab, aes(x = delta, y = RETNLB, color = Eim_MC)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in lab
infections") +
  theme_bw()
```

## Warning: Removed 6 rows containing missing values (stat\_boxplot).

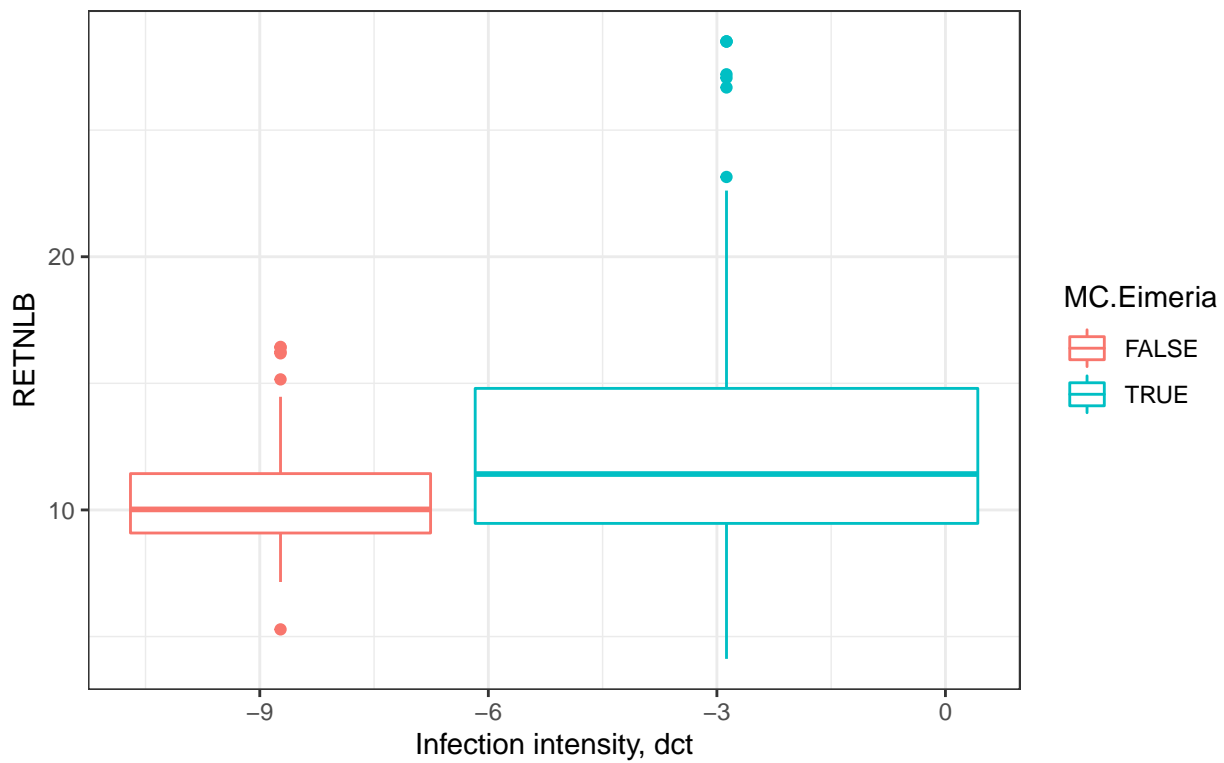
## Immune gene expression against infection intensity in lab infections



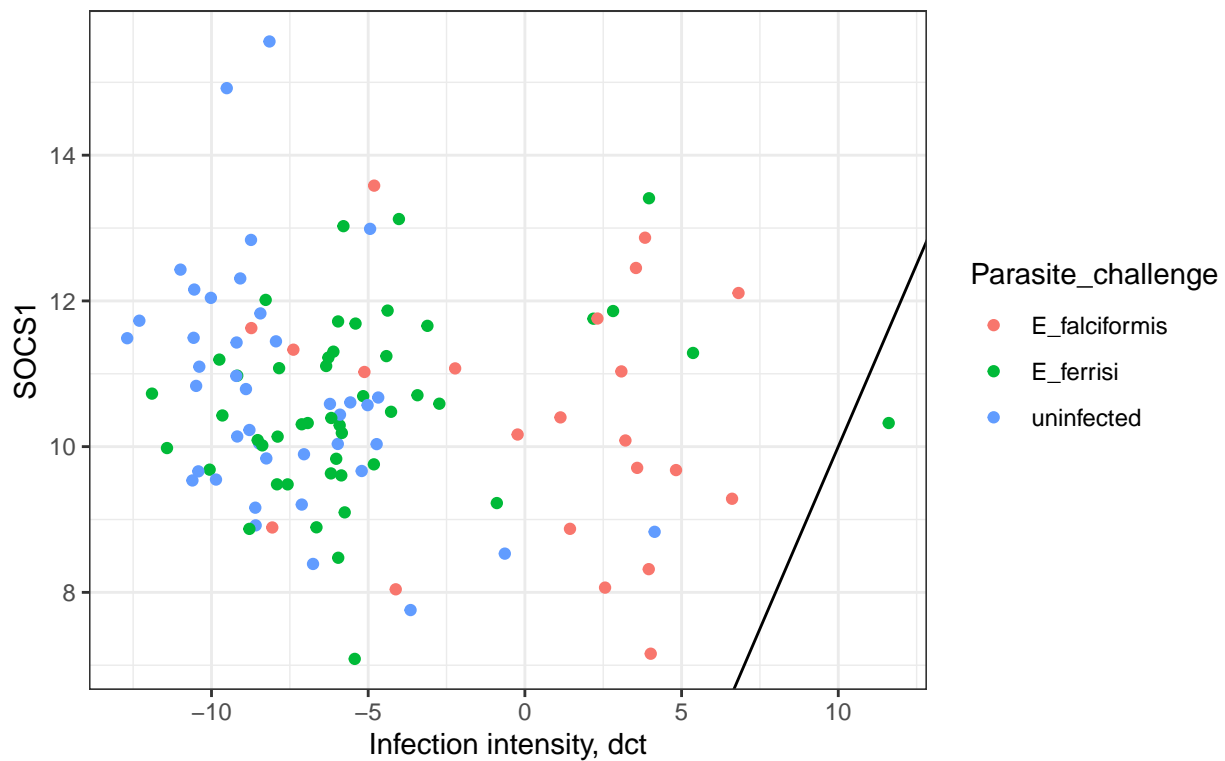
```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = RETNLB,
                  color = MC.Eimeria)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
               samples") +
  theme_bw()
```

## Warning: Removed 150 rows containing missing values (stat\_boxplot).

## Immune gene expression against infection intensity in field samples



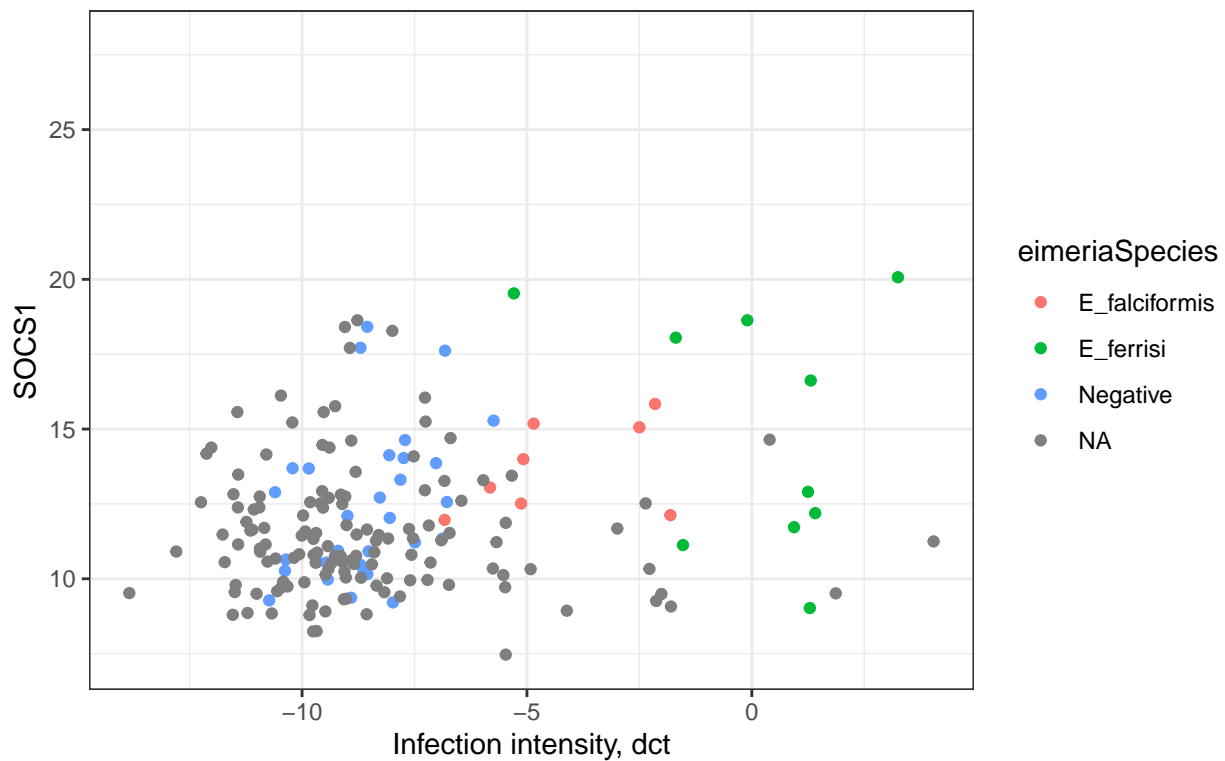
## Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = SOCS1, color = eimeriaSpecies)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
       samples") +
  theme_bw()
```

## Warning: Removed 150 rows containing missing values (geom\_point).

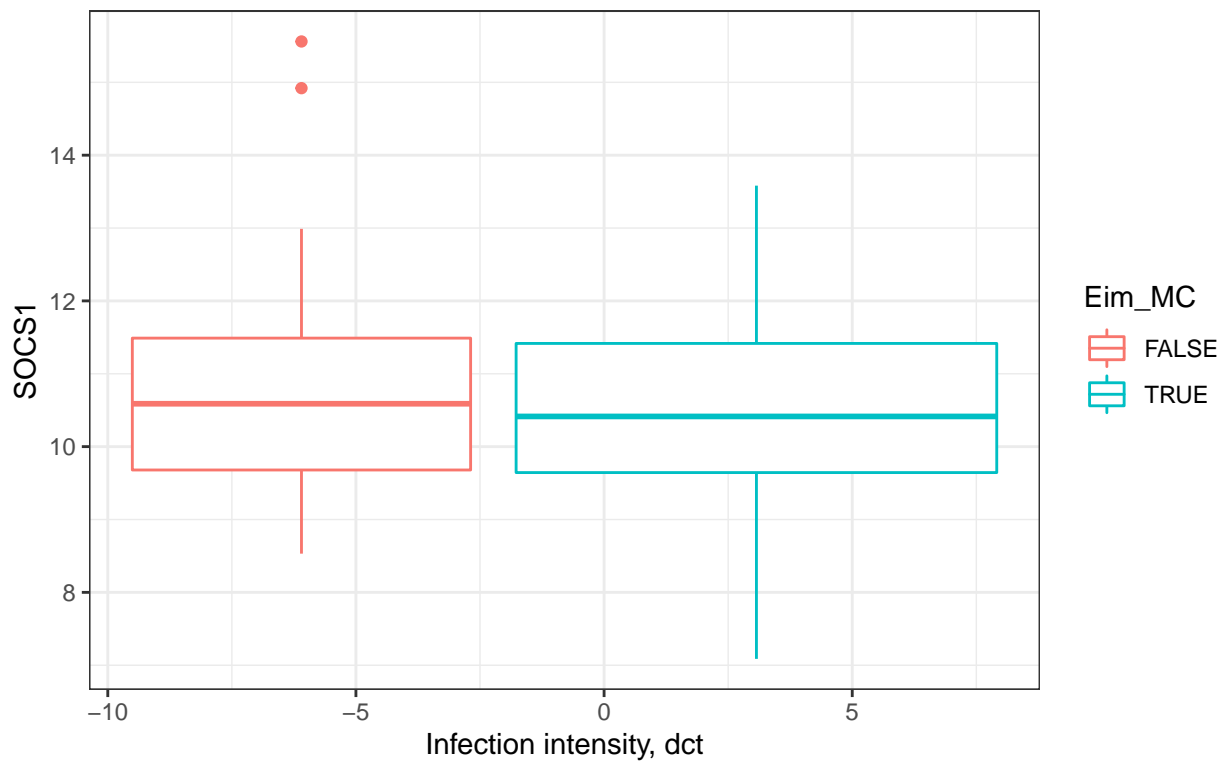
## Immune gene expression against infection intensity in field samples



```
ggplot(lab, aes(x = delta, y = SOCS1, color = Eim_MC)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in lab
infections") +
  theme_bw()
```

## Warning: Removed 6 rows containing missing values (stat\_boxplot).

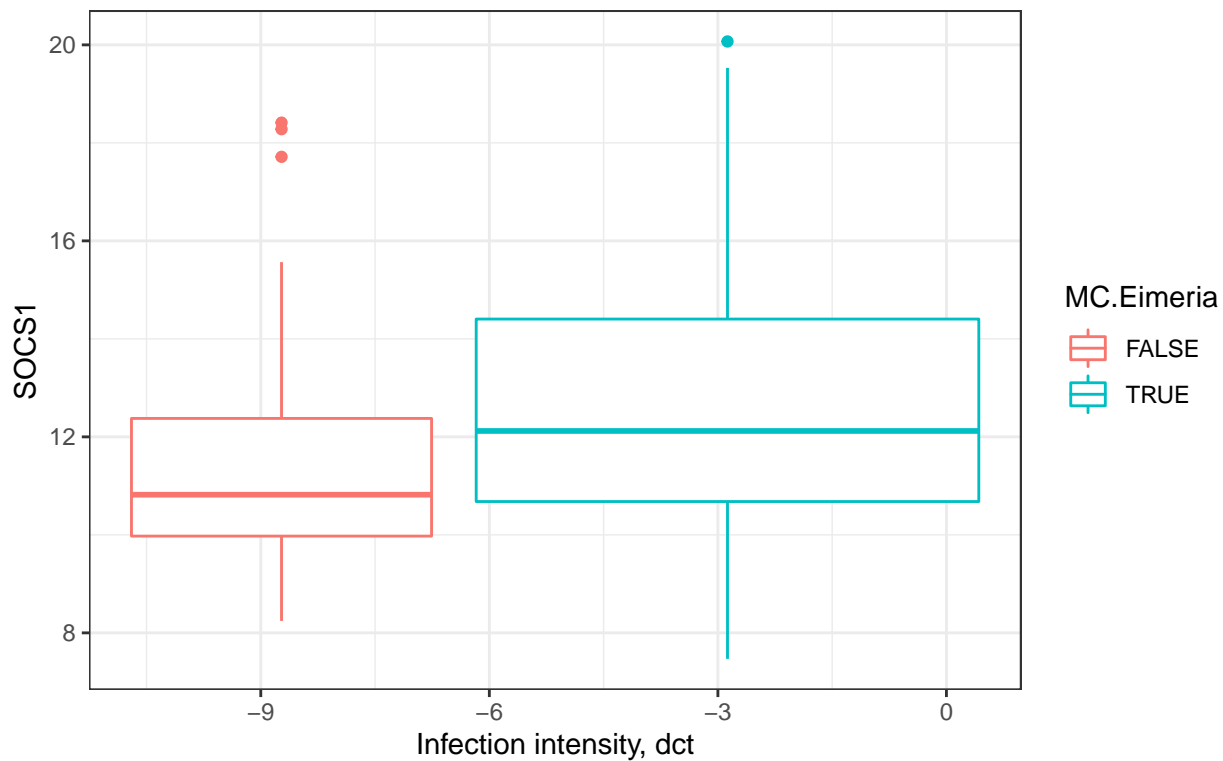
## Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = SOCS1,
                  color = MC.Eimeria)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
               samples") +
  theme_bw()
```

## Warning: Removed 150 rows containing missing values (stat\_boxplot).

## Immune gene expression against infection intensity in field samples

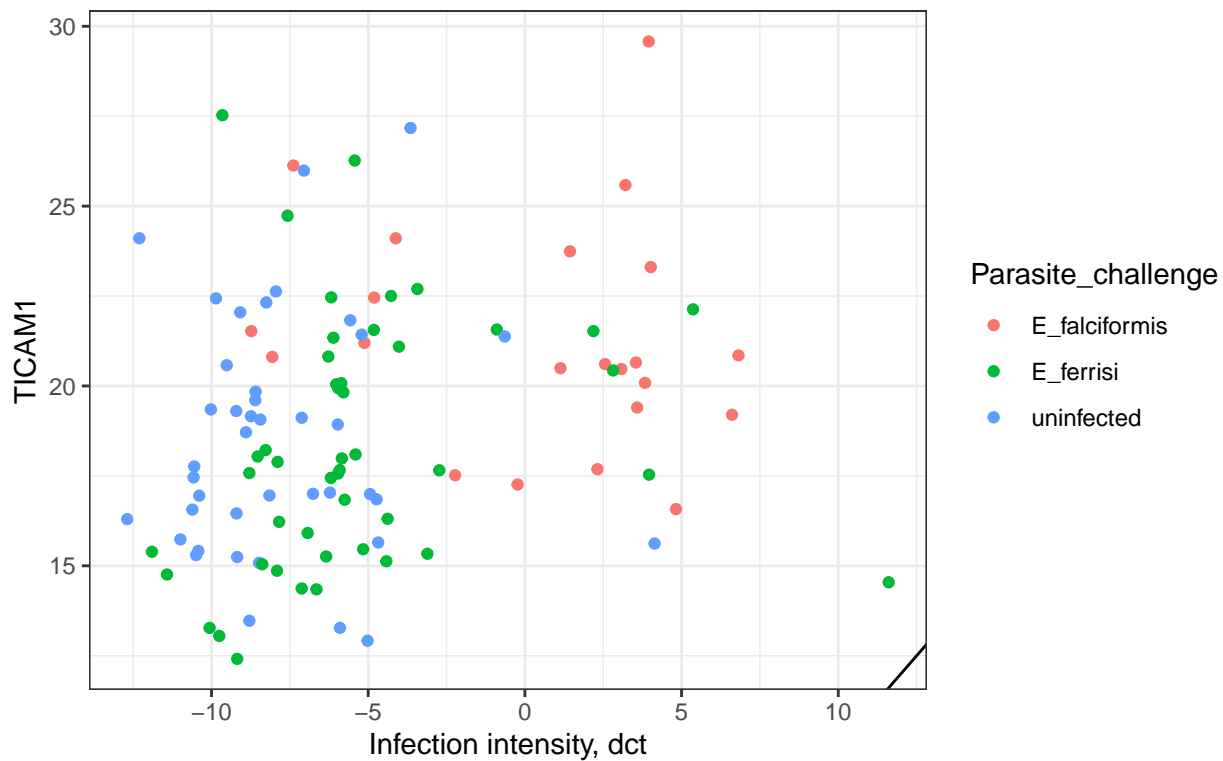


### 19. TICAM1

```
ggplot(lab, aes(x = delta, y = TICAM1, color = Parasite_challenge)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity
               in lab infections") +
  theme_bw()
```

## Warning: Removed 6 rows containing missing values (geom\_point).

## Immune gene expression against infection intensity in lab infections

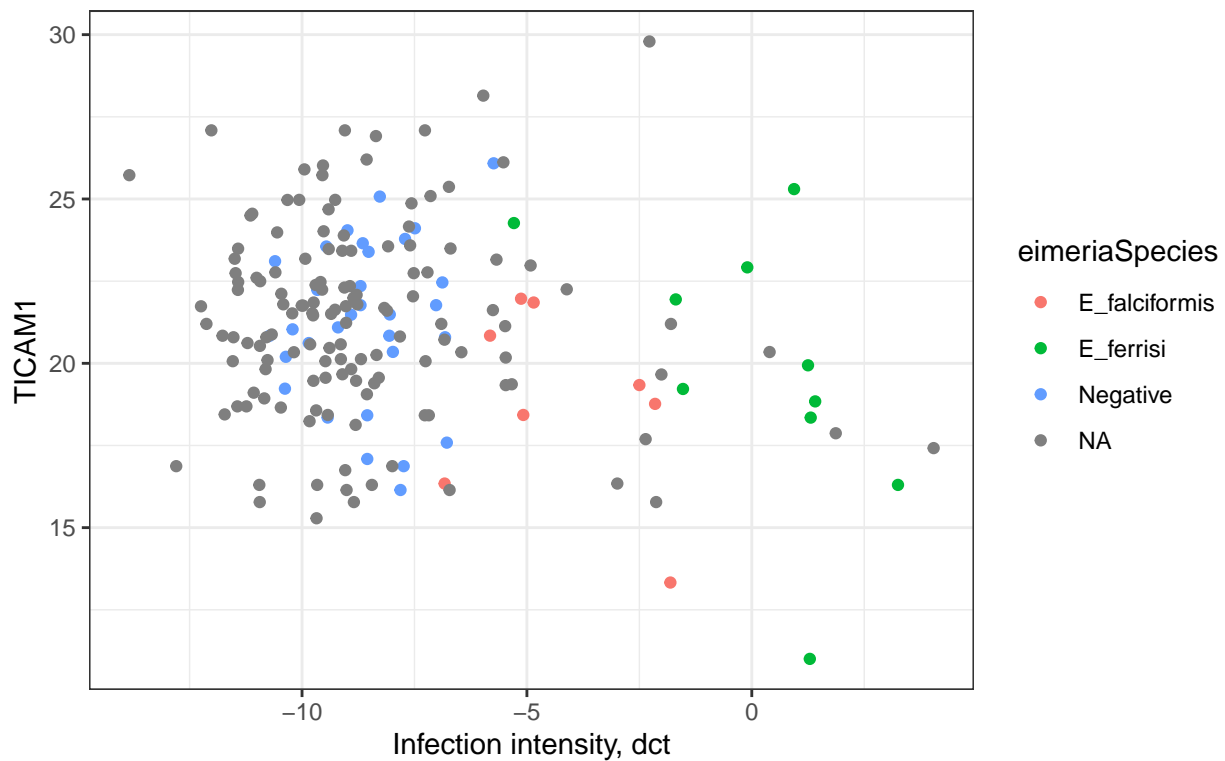


```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = TICAM1, color = eimeriaSpecies)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
               samples") +
  theme_bw()
```

## Warning: Removed 150 rows containing missing values (geom\_point).



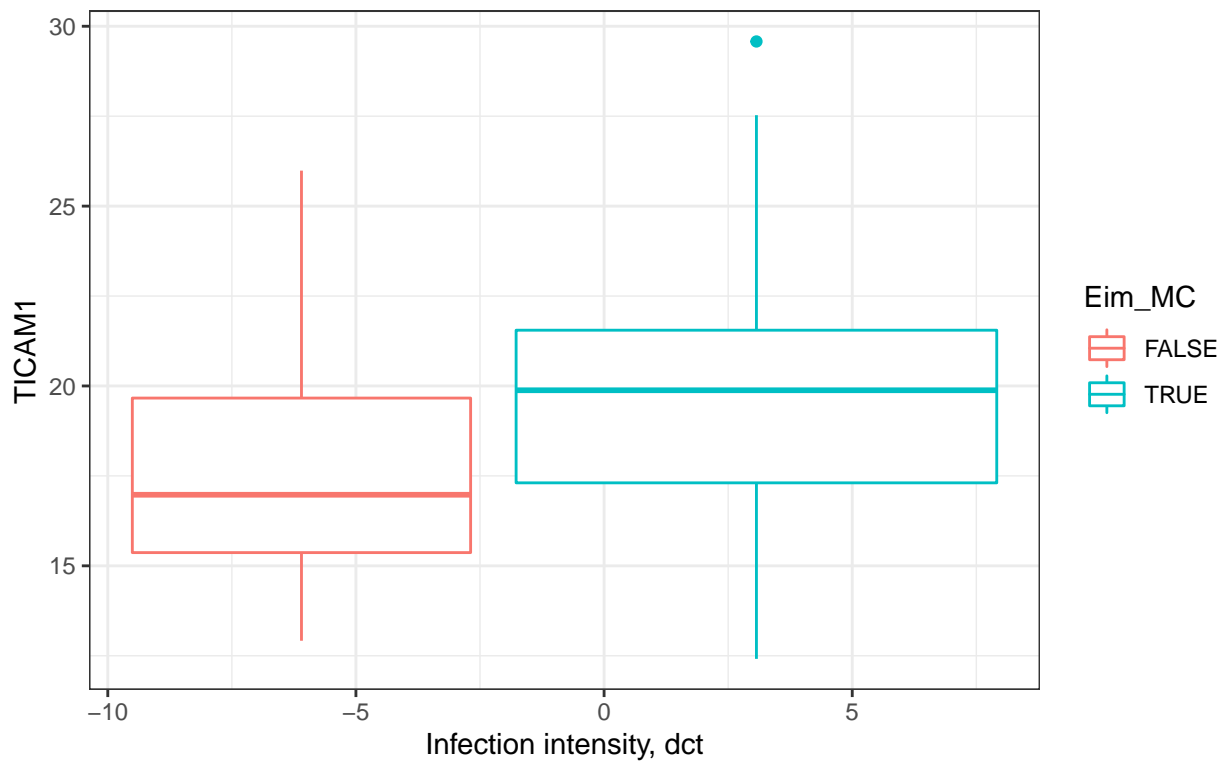
## Immune gene expression against infection intensity in field samples



```
ggplot(lab, aes(x = delta, y = TICAM1, color = Eim_MC)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in lab
infections") +
  theme_bw()
```

## Warning: Removed 6 rows containing missing values (stat\_boxplot).

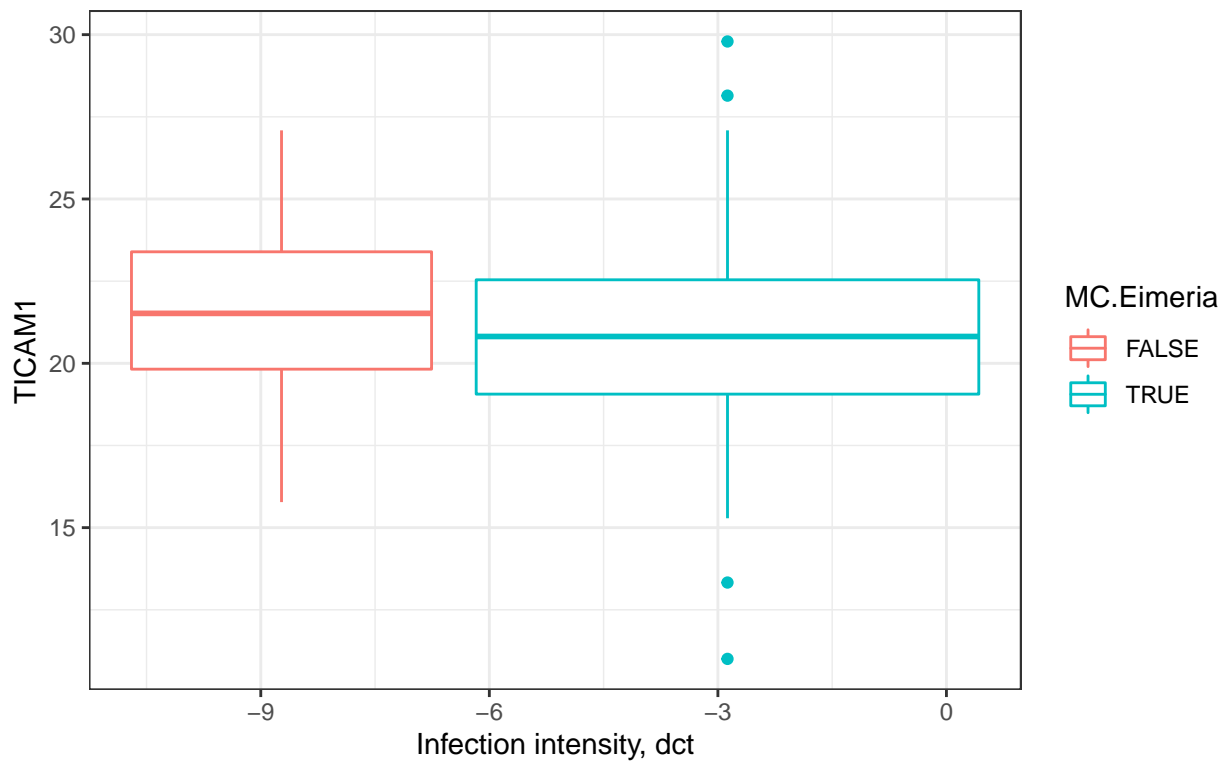
## Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = TICAM1,
                  color = MC.Eimeria)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
               samples") +
  theme_bw()
```

## Warning: Removed 150 rows containing missing values (stat\_boxplot).

## Immune gene expression against infection intensity in field samples

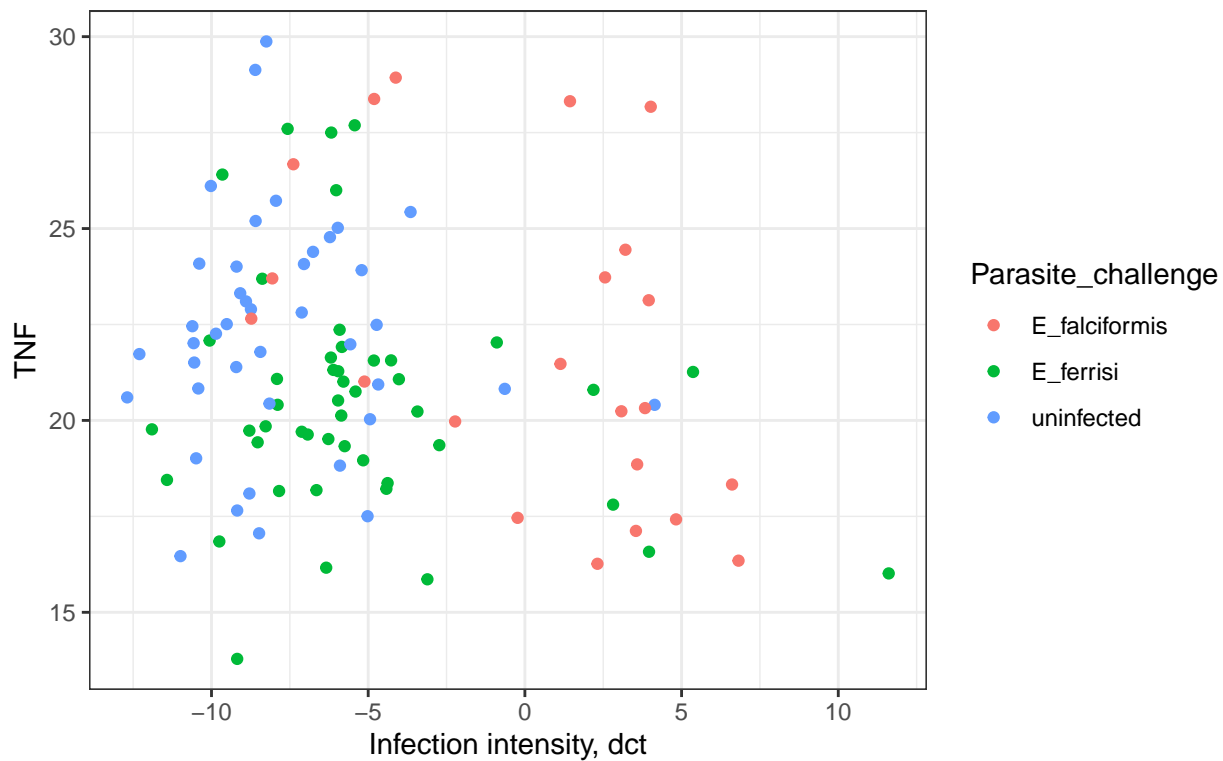


## 20. TNF

```
ggplot(lab, aes(x = delta, y = TNF, color = Parasite_challenge)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity
               in lab infections") +
  theme_bw()
```

## Warning: Removed 6 rows containing missing values (geom\_point).

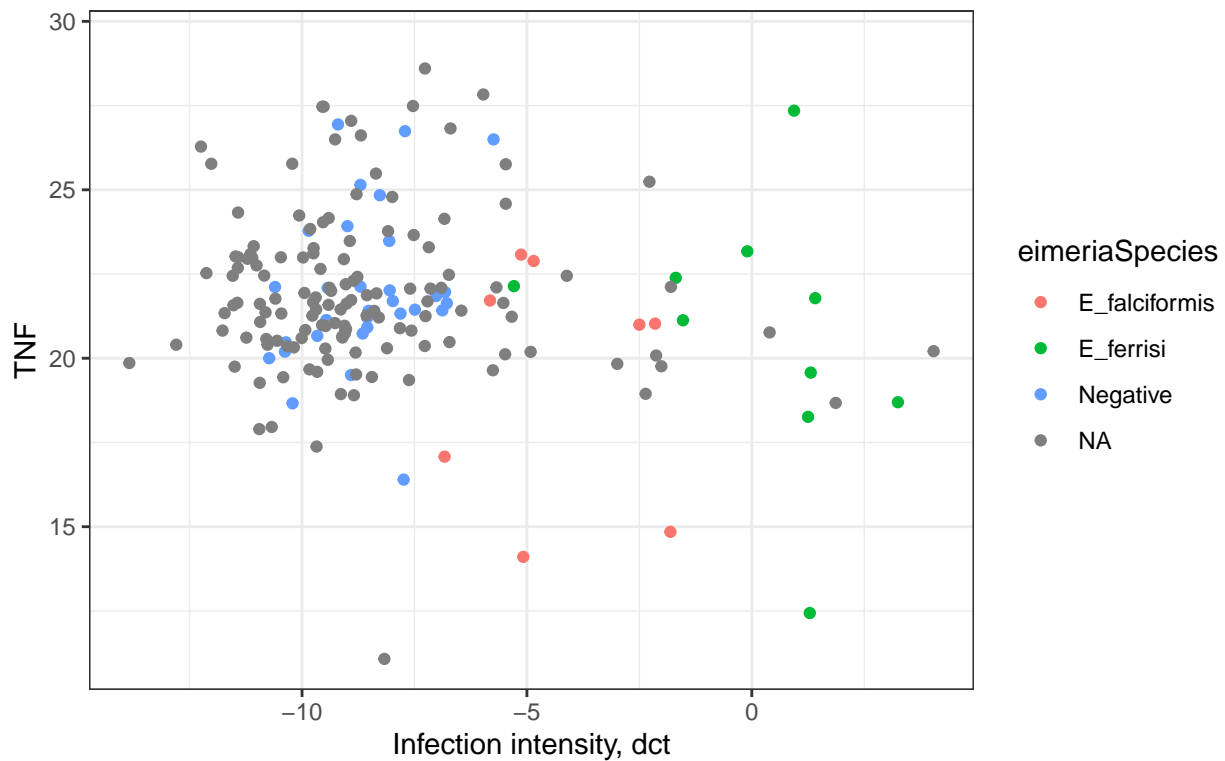
## Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = TNF, color = eimeriaSpecies)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
               samples") +
  theme_bw()
```

## Warning: Removed 150 rows containing missing values (geom\_point).

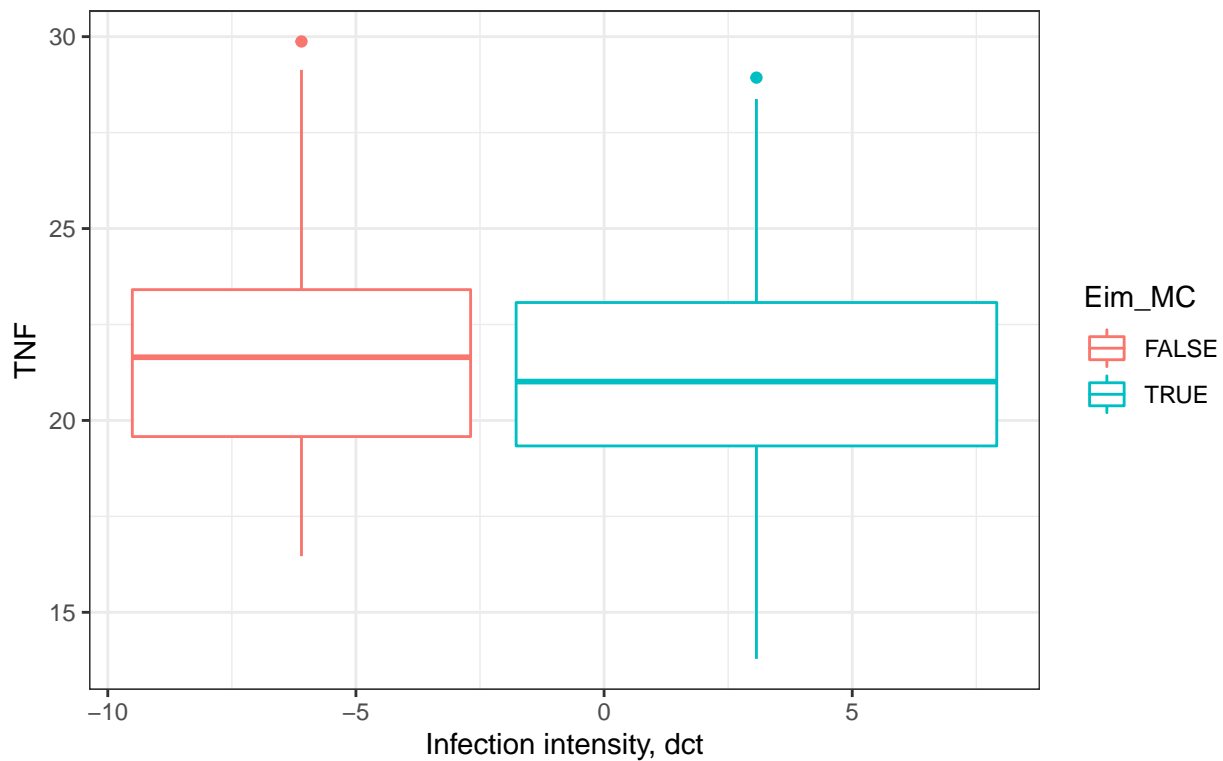
## Immune gene expression against infection intensity in field samples



```
ggplot(lab, aes(x = delta, y = TNF, color = Eim_MC)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in lab
infections") +
  theme_bw()
```

## Warning: Removed 6 rows containing missing values (stat\_boxplot).

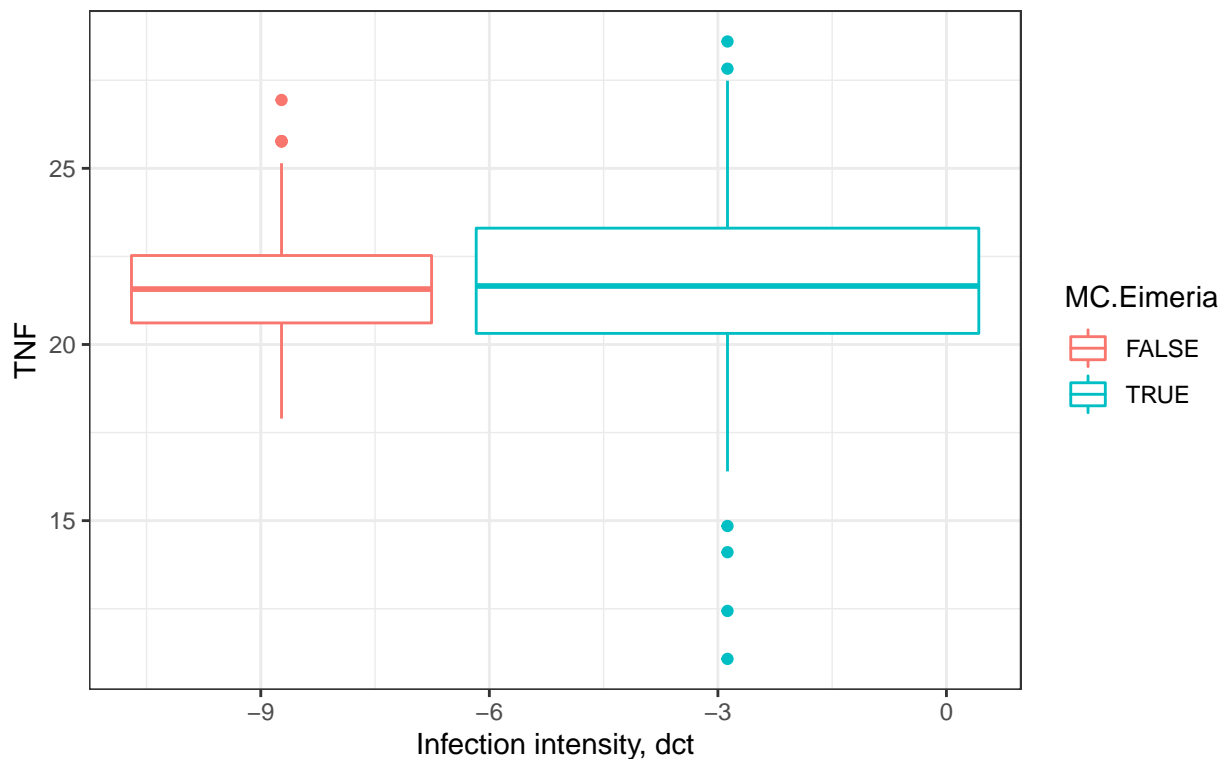
## Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = TNF,
                  color = MC.Eimeria)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
               samples") +
  theme_bw()
```

## Warning: Removed 150 rows containing missing values (stat\_boxplot).

## Immune gene expression against infection intensity in field samples



```

        field_inf %>% dplyr::select(all_of(x)))$p.value

lab.uni_field_uni <- t.test(lab_uni %>% dplyr::select(all_of(x)),
        field_uni %>% dplyr::select(all_of(x)))$p.value

lab.inf_field.inf <- t.test(lab_inf %>% dplyr::select(all_of(x)),
        field_inf %>% dplyr::select(all_of(x)))$p.value

A <- data.frame(lab.uni_lab.inf,field.uni_field.inf,lab.uni_field_uni,
        lab.inf_field.inf)

rownames(A) <- toString(x)

print(A)
}

P <- lapply(intersect(Genes_field, Genes_lab), eimeria_t_test_pvalue)

##      lab.uni_lab.inf field.uni_field.inf lab.uni_field_uni lab.inf_field.inf
## IFNy      0.0008701234      0.8443114      3.898003e-06      0.01489448
##      lab.uni_lab.inf field.uni_field.inf lab.uni_field_uni lab.inf_field.inf
## CXCR3      0.7240836      0.834139      6.110718e-23      8.025602e-31
##      lab.uni_lab.inf field.uni_field.inf lab.uni_field_uni lab.inf_field.inf
## IL.6      0.4569897      0.05500413      0.0009836655      0.1259247
##      lab.uni_lab.inf field.uni_field.inf lab.uni_field_uni lab.inf_field.inf
## IL.10      0.6664722      0.07224988      0.0005858587      0.01284744
##      lab.uni_lab.inf field.uni_field.inf lab.uni_field_uni lab.inf_field.inf
## IL.13      0.01136685      0.003696082      1.797684e-07      4.358343e-16
##      lab.uni_lab.inf field.uni_field.inf lab.uni_field_uni lab.inf_field.inf
## IL1RN      0.7694255      0.0005816463      3.000582e-11      0.0003306339
##      lab.uni_lab.inf field.uni_field.inf lab.uni_field_uni lab.inf_field.inf
## CASP1      0.9965703      0.01341      0.03392336      0.9314781
##      lab.uni_lab.inf field.uni_field.inf lab.uni_field_uni lab.inf_field.inf
## CXCL9      3.645686e-05      0.2722695      0.004333807      2.325014e-10
##      lab.uni_lab.inf field.uni_field.inf lab.uni_field_uni lab.inf_field.inf
## IDO1      0.01723246      0.02809745      1.480942e-06      0.5102659
##      lab.uni_lab.inf field.uni_field.inf lab.uni_field_uni lab.inf_field.inf
## IRGM1      0.03189147      0.0003797562      0.07525817      2.273495e-10
##      lab.uni_lab.inf field.uni_field.inf lab.uni_field_uni lab.inf_field.inf
## MPO      0.6247867      4.431343e-05      7.643367e-10      0.003084519
##      lab.uni_lab.inf field.uni_field.inf lab.uni_field_uni lab.inf_field.inf
## MUC2      0.4783091      0.0004607668      0.8243095      3.134409e-06
##      lab.uni_lab.inf field.uni_field.inf lab.uni_field_uni lab.inf_field.inf
## MUC5AC      0.8906956      0.0002337175      0.005060887      0.871851
##      lab.uni_lab.inf field.uni_field.inf lab.uni_field_uni lab.inf_field.inf
## MYD88      0.6477168      1.336611e-06      0.723573      5.178099e-05
##      lab.uni_lab.inf field.uni_field.inf lab.uni_field_uni lab.inf_field.inf
## NCR1      0.1069354      0.2811749      0.004499826      0.5085016
##      lab.uni_lab.inf field.uni_field.inf lab.uni_field_uni lab.inf_field.inf
## PRF1      0.1370779      0.002647012      0.009069733      0.0004315407
##      lab.uni_lab.inf field.uni_field.inf lab.uni_field_uni lab.inf_field.inf
## RETNLB      0.6017666      6.188518e-05      0.4800438      0.0009378679
##      lab.uni_lab.inf field.uni_field.inf lab.uni_field_uni lab.inf_field.inf
## SOCS1      0.2327638      0.000177738      0.1015706      1.028948e-09

```



```
##      lab.uni_lab.inf field.uni_field.inf lab.uni_field_uni lab.inf_field.inf
## TICAM1      0.04802866      0.1746463      1.082312e-06      0.0307961
##      lab.uni_lab.inf field.uni_field.inf lab.uni_field_uni lab.inf_field.inf
## TNF      0.4766501      0.7745215      0.9639207      0.3303136

t.test.p.value <- reduce(P, rbind)

t.test.p.value <- tibble::rownames_to_column(t.test.p.value, "Genes")

write.csv(t.test.p.value,
          "output_data/gene_expression/data_products/t.test.p.values_gene_exp.csv",
          row.names = FALSE)
```

Which genes are significant to predict weight loss?

```
Lab_wl <- lm(formula = max_WL ~ IFNy + CXCR3 + IL.6 + IL.10 + IL.13 + IL1RN +
              CXCR3 + CASP1 + CXCL9 + IDO1 + IRGM1 + MPO + MUC2 + MUC5AC +
              MYD88 + NCR1 + PRF1 + RETNLB + SOCS1 + TICAM1 + TNF, data = lab)

summary(Lab_wl)
```

```
##
## Call:
## lm(formula = max_WL ~ IFNy + CXCR3 + IL.6 + IL.10 + IL.13 + IL1RN +
##      CXCR3 + CASP1 + CXCL9 + IDO1 + IRGM1 + MPO + MUC2 + MUC5AC +
##      MYD88 + NCR1 + PRF1 + RETNLB + SOCS1 + TICAM1 + TNF, data = lab)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -5.6176 -2.4799  0.1734  1.8098  9.5301
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -3.000006   15.405379  -0.195   0.8466
## IFNy         0.322858    0.428596   0.753   0.4557
## CXCR3        -0.092789    0.140074  -0.662   0.5115
## IL.6         -0.037201    0.319540  -0.116   0.9079
## IL.10        -0.074093    0.412013  -0.180   0.8582
## IL.13         1.304887    0.948274   1.376   0.1765
## IL1RN        -0.797456    0.571481  -1.395   0.1706
## CASP1        -0.616740    0.499440  -1.235   0.2241
## CXCL9        -0.241405    0.574569  -0.420   0.6766
## IDO1         -0.878372    0.464389  -1.891   0.0658
## IRGM1         0.175299    1.221502   0.144   0.8866
## MPO          0.371152    0.359642   1.032   0.3083
## MUC2         -0.074745    0.671834  -0.111   0.9120
## MUC5AC       -0.179853    0.316862  -0.568   0.5735
## MYD88        -0.547750    0.695541  -0.788   0.4356
## NCR1         -0.227017    0.452027  -0.502   0.6183
## PRF1         0.510498    0.381384   1.339   0.1883
## RETNLB       -0.003365    0.350031  -0.010   0.9924
## SOCS1        -0.174075    1.442321  -0.121   0.9045
## TICAM1        0.861394    0.749231   1.150   0.2571
## TNF          0.221457    0.475055   0.466   0.6436
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.214 on 40 degrees of freedom
```

```
## (55 observations deleted due to missingness)
## Multiple R-squared: 0.4005, Adjusted R-squared: 0.1008
## F-statistic: 1.336 on 20 and 40 DF, p-value: 0.213
AIC(Lab_w1)

## [1] 366.853
Lab_MC <- lm(formula = Eim_MC ~ IFNy + CXCR3 + IL.6 + IL.10 + IL.13 + IL1RN +
              CXCR3 + CASP1 + CXCL9 + IDO1 + IRGM1 + MPO + MUC2 + MUC5AC +
              MYD88 + NCR1 + PRF1 + RETNLB + SOCS1 + TICAM1 + TNF, data = lab)

summary(Lab_MC)

##
## Call:
## lm(formula = Eim_MC ~ IFNy + CXCR3 + IL.6 + IL.10 + IL.13 + IL1RN +
##     CXCR3 + CASP1 + CXCL9 + IDO1 + IRGM1 + MPO + MUC2 + MUC5AC +
##     MYD88 + NCR1 + PRF1 + RETNLB + SOCS1 + TICAM1 + TNF, data = lab)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.96381 -0.21804  0.03771  0.22030  0.87795
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -0.5822570   1.5120281  -0.385   0.7022
## IFNy         -0.0009029   0.0420665  -0.021   0.9830
## CXCR3        -0.0103727   0.0137482  -0.754   0.4550
## IL.6          0.0081549   0.0313627   0.260   0.7962
## IL.10         0.0193551   0.0404388   0.479   0.6348
## IL.13         0.0725771   0.0930725   0.780   0.4401
## IL1RN         0.0319357   0.0560905   0.569   0.5723
## CASP1         0.0332448   0.0490198   0.678   0.5016
## CXCL9        -0.0792809   0.0563935  -1.406   0.1675
## IDO1          -0.0899176   0.0455795  -1.973   0.0555
## IRGM1        -0.1607594   0.1198897  -1.341   0.1875
## MPO           -0.0072732   0.0352986  -0.206   0.8378
## MUC2          -0.0175636   0.0659401  -0.266   0.7913
## MUC5AC        -0.0113556   0.0310998  -0.365   0.7169
## MYD88         0.0886323   0.0682669   1.298   0.2016
## NCR1          -0.0240597   0.0443661  -0.542   0.5906
## PRF1          0.0210632   0.0374326   0.563   0.5768
## RETNLB        0.0075148   0.0343553   0.219   0.8280
## SOCS1         0.0706436   0.1415629   0.499   0.6205
## TICAM1        0.0674897   0.0735366   0.918   0.3642
## TNF           -0.0476275   0.0466263  -1.021   0.3132
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4136 on 40 degrees of freedom
## (55 observations deleted due to missingness)
## Multiple R-squared: 0.5502, Adjusted R-squared: 0.3253
## F-statistic: 2.447 on 20 and 40 DF, p-value: 0.007899
AIC(Lab_MC)

## [1] 83.65866
```

## Results

1. Significant difference between means of lab uni and lab inf:
  - IFNy
  - IL.13
  - PRF1
  - TICAM1
2. Significant difference between means of field uni and field inf:
  - IFNy
  - IL.6
  - IL.13
  - IL1RN
  - CXCL9
  - MPO
  - MUC5AC
  - PRF1
  - TICAM1
  - TNF
3. Significant difference between means of lab uni and field uni: IFNy CXCR3 IL.6 IL.10 IL.13 IL1RN CXCL9 IDO1 IRGM1 MPO MUC2 MUC5AC NCR1 PRF1 RETNLB SOCS1 TICAM1
4. No Significant difference between means of lab uni and field uni:
  - CASP1
  - MYD88 -TNF
5. Significant difference between means of lab inf and field inf: IFNy CXCR3 IL.13 IRGM1 MUC2 MYD88 PRF1 SOCS1
6. No Significant difference between means of lab inf and field inf: IL.6 IL.10 IL1RN CASP1 CXCL9 IDO1 MPO MUC5AC NCR1 RETNLB TICAM1 TNF

[https://docs.google.com/spreadsheets/d/1JWjsyzlQxWlSttZ5KwxYSsZapjZCgMCO1OcF0Yz9\\_ZQ/edit?usp=sharing](https://docs.google.com/spreadsheets/d/1JWjsyzlQxWlSttZ5KwxYSsZapjZCgMCO1OcF0Yz9_ZQ/edit?usp=sharing)

## It is time to apply the package of Alice Balard et al. on our predictions!

Let's see if we indeed have differences across the hybrid index with our predicted weight loss.

### Install the package

```
##
## * checking for file '/tmp/RtmpdMPgGf/remotes33bb7d41b7f8ce/alicebalard-parasiteLoad-1b43216/DESCRIPTION' ... OK
## * preparing 'parasiteLoad':
## * checking DESCRIPTION meta-information ... OK
## * checking for LF line-endings in source and make files and shell scripts
## * checking for empty or unneeded directories
## * building 'parasiteLoad_0.1.0.tar.gz'
```