

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

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### 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()
```

### 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_bio", "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")
```

## Adding a variable that signifies if sample is infected or not

detection threshold: delta ct = -5 (Jarquin Diaz et al)

```
field <- field %>%
  mutate(
    infected_eimeria =
      case_when(
        delta_ct_cewe_MminusE > -5 ~ "infected",
        delta_ct_cewe_MminusE < -5 ~ "uninfected"
      )
  )

lab <- lab %>%
  mutate(
    infected_eimeria =
      case_when(
        delta > -5 ~ "infected",
        delta < -5 ~ "uninfected"
      )
  )
```

## Compare the differences in uninfected and infected data and field / lab

Write a function which does a t test to quantify the differences of gene expression between uninfected and infected mice in the lab and field infections and also compares the uninfected lab and field and the infected lab and field

```
eimeria_t.test <- function(x, y) {
  # select the uninfected (delta ct under -5 mice)
  lab_uni <- lab %>%
    dplyr::filter(infected_eimeria == "uninfected")
  # select the infected lab mice
  lab_inf <- lab %>%
    dplyr::filter(infected_eimeria == "infected")
  # select the uninfected field mice (delta ct under -5 mice)
  field_uni <- field %>%
    dplyr::filter(infected_eimeria == "uninfected")
  # select the infected lab mice
  field_inf <- field %>%
    dplyr::filter(infected_eimeria == "infected")

  print(c("Testing differences in expression in uninfected and infected lab mice. Gene:", toString(x)))
  print(t.test(lab_uni %>% dplyr::select(all_of(x)), lab_inf %>% dplyr::select(all_of(x))))

  print(c("Testing differences in expression in uninfected and infected field mice. Gene:", toString(x)))
  print(t.test(field_uni %>% dplyr::select(all_of(x)), field_inf %>% dplyr::select(all_of(x))))

  print(c("Testing differences in expression in uninfected lab vs field mice. Gene:", toString(x)))
  print(t.test(lab_uni %>% dplyr::select(all_of(x)), field_uni %>% dplyr::select(all_of(x))))

  print(c("Testing differences in expression in infected lab vs field mice. Gene:", toString(x)))
  print(t.test(lab_inf %>% dplyr::select(all_of(x)), field_inf %>% dplyr::select(all_of(x))))
}
```

### 1. IFNy

```
ggplot(lab, aes(x = delta, y = IFNy, color = Parasite_challenge)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
```

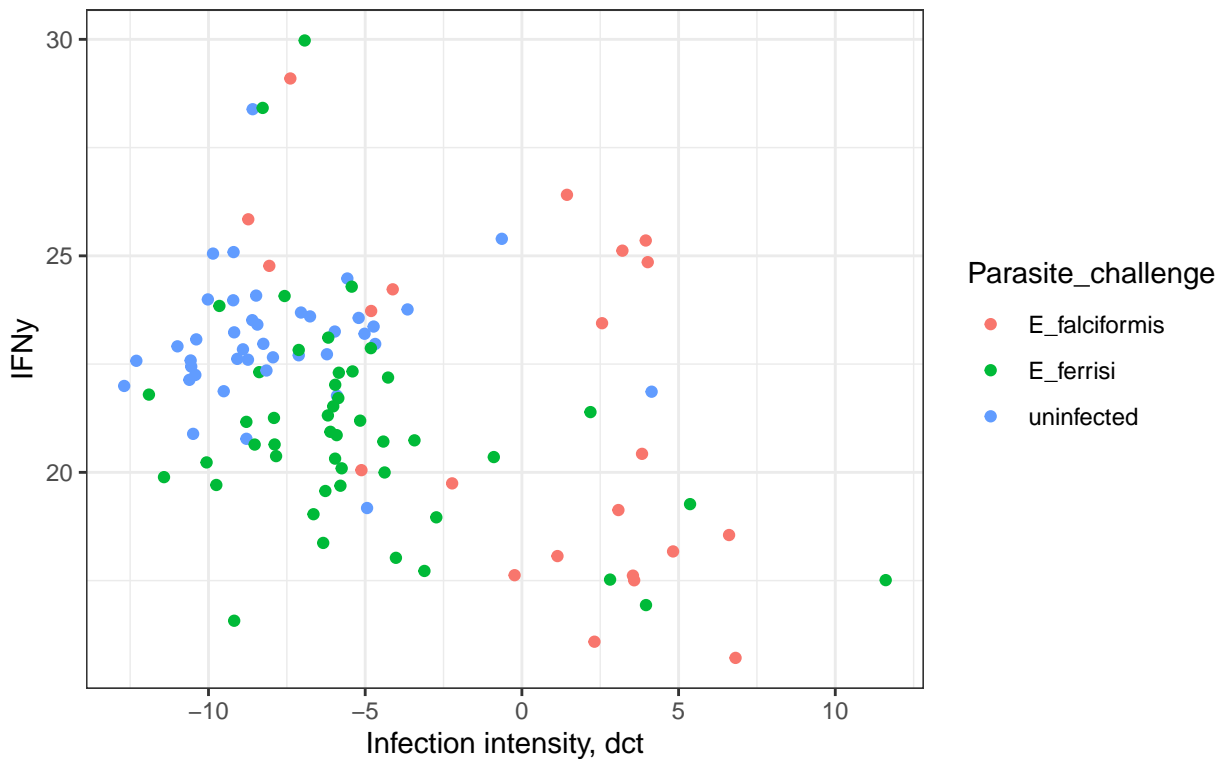
```

    title ="Immune gene expression against infection intensity in lab
infections") +
theme_bw()

```

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

### Immune gene expression against infection intensity in lab infections



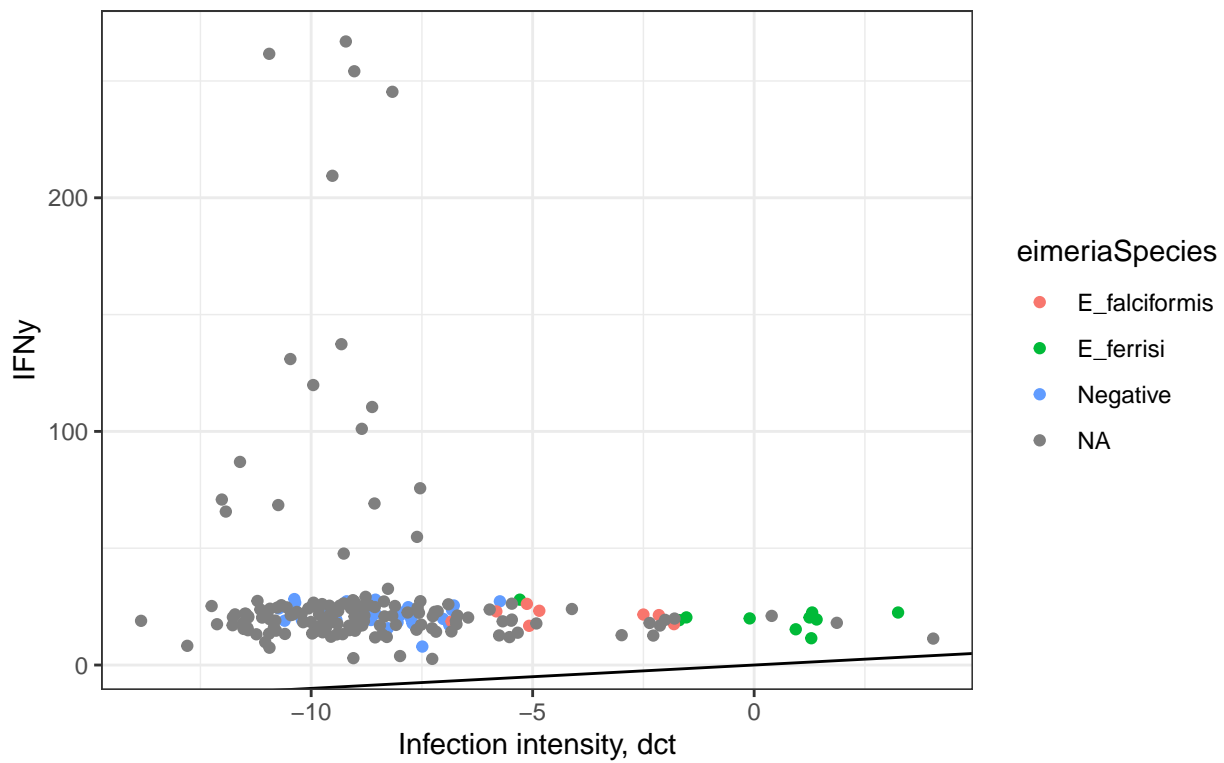
```

ggplot(field, aes(x = delta_ct_cewe_MminusE, y = IFNγ, 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 154 rows containing missing values (geom\_point).

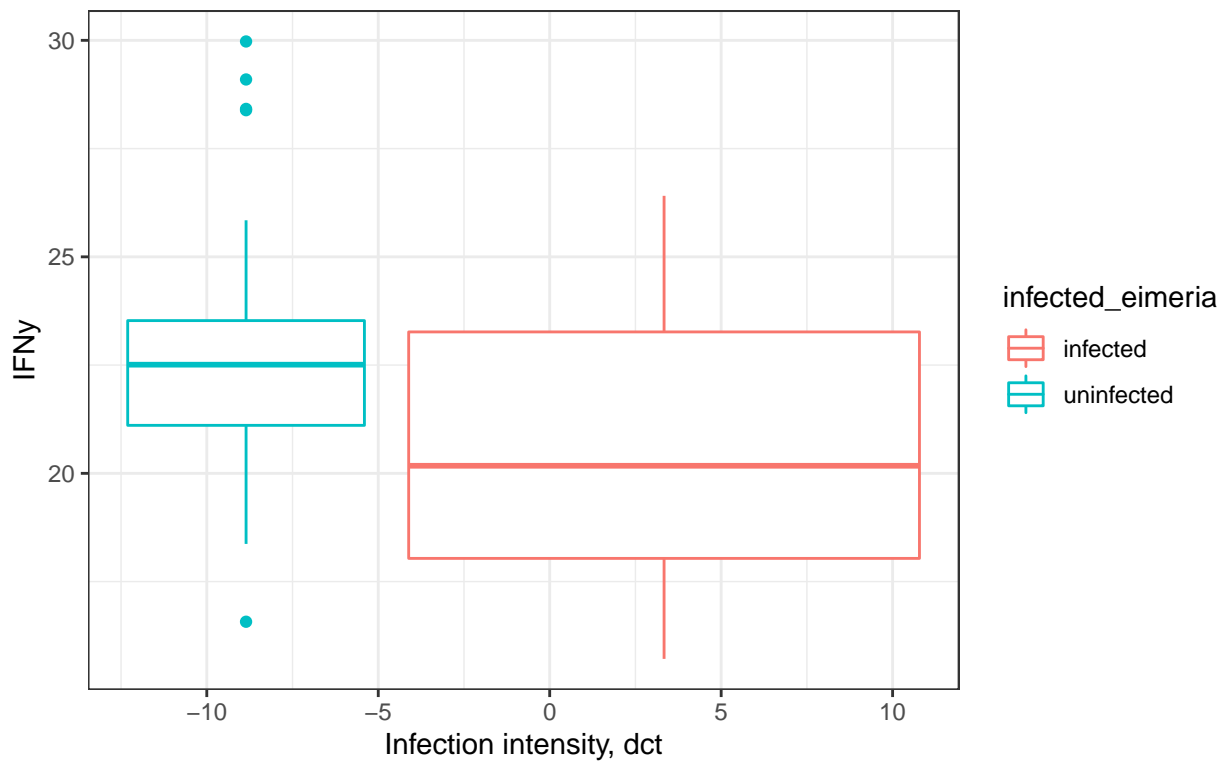
## Immune gene expression against infection intensity in field samples



```
ggplot(lab, aes(x = delta, y = IFN $\gamma$ , color = infected_eimeria)) +  
  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).
```

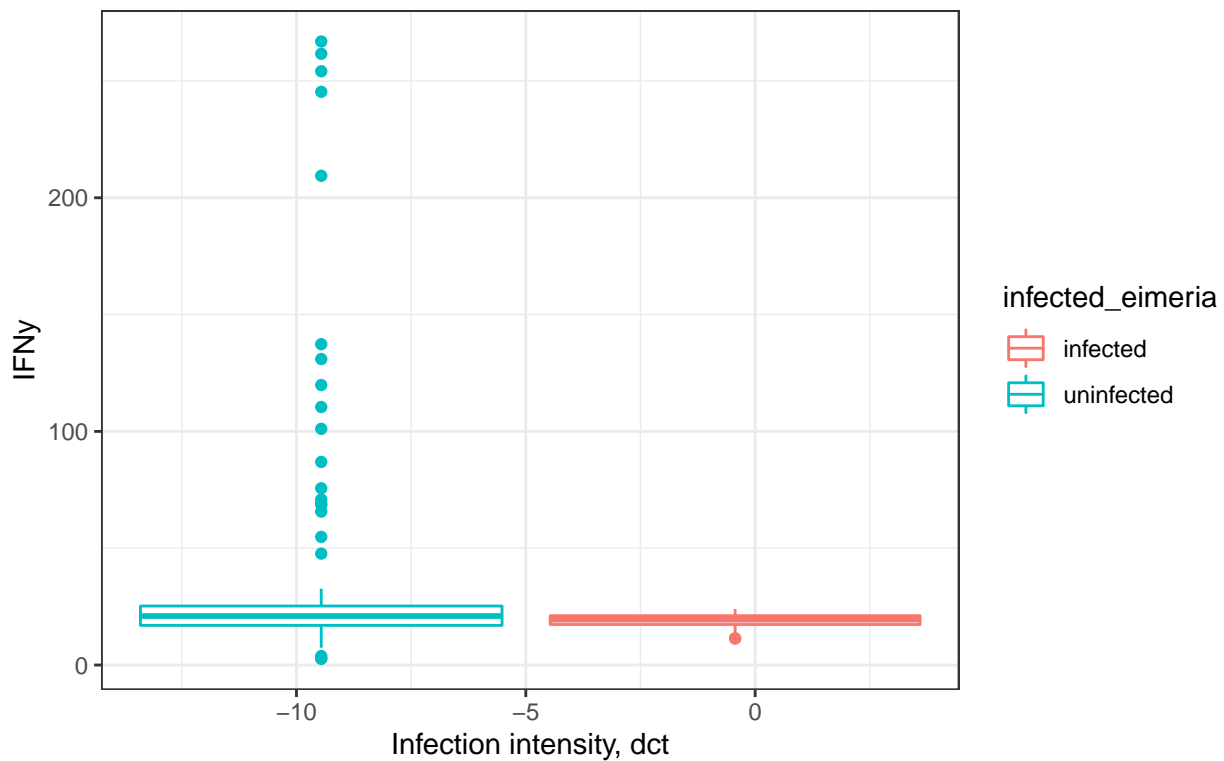
## Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = IFN $\gamma$ ,  
                  color = infected_eimeria)) +  
  geom_boxplot() +  
  labs(x = "Infection intensity, dct",  
       title = "Immune gene expression against infection intensity in field  
samples") +  
  theme_bw()
```

## Warning: Removed 154 rows containing missing values (stat\_boxplot).

## Immune gene expression against infection intensity in field samples

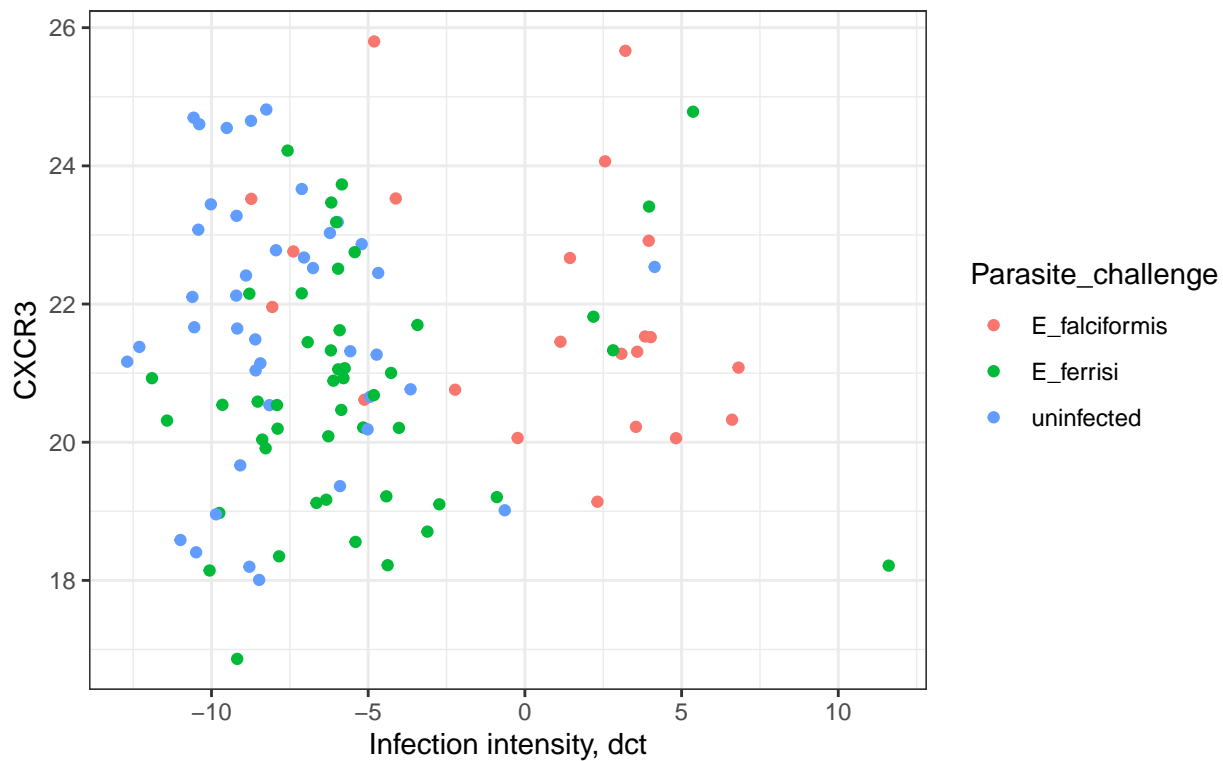


## 2. CXCR3

```
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).

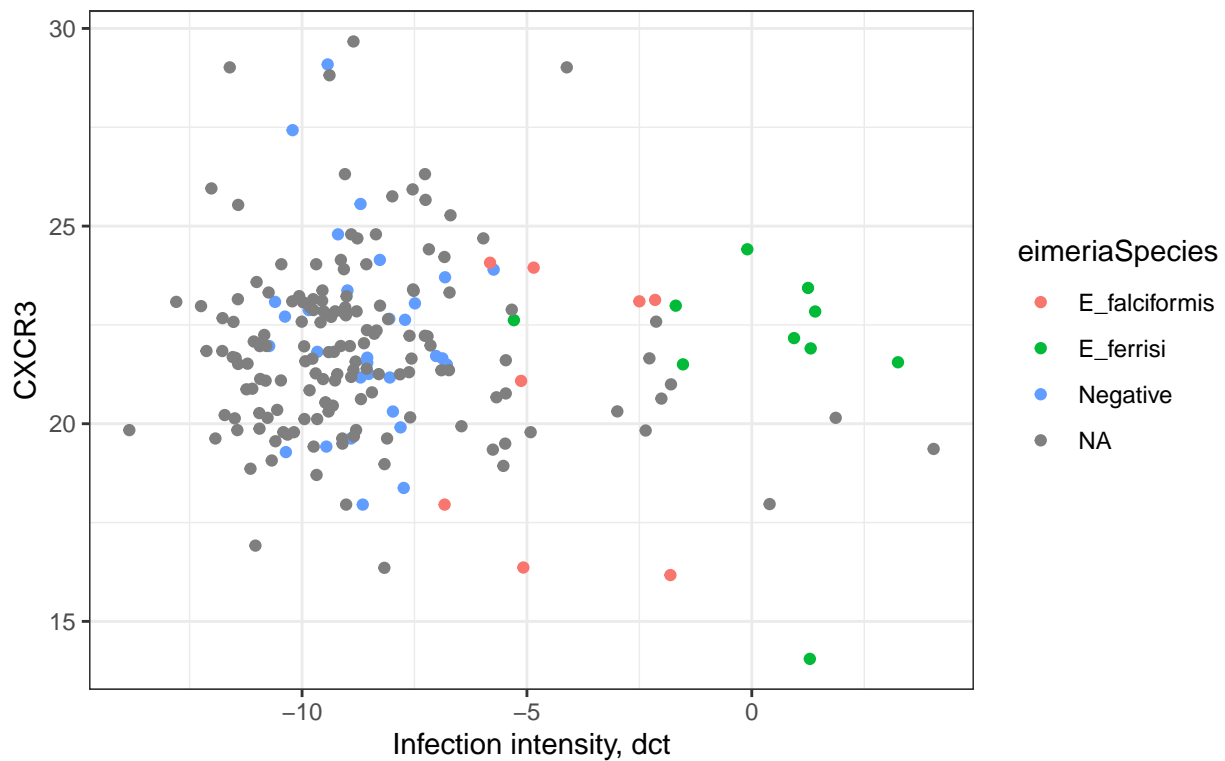
## Immune gene expression against infection intensity in lab infections



```
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 154 rows containing missing values (geom\_point).

## Immune gene expression against infection intensity in field samples



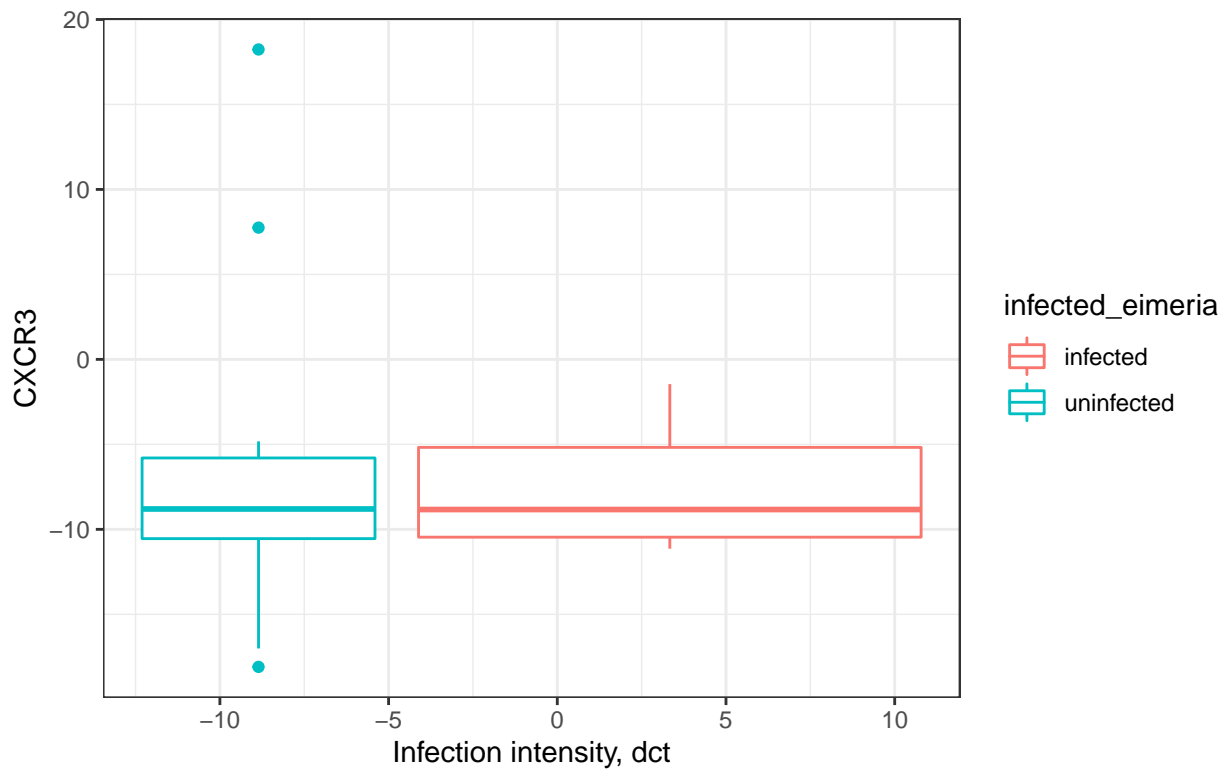
```
ggplot(lab, aes(x = delta, y = CXCR3, color = infected_eimeria)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in lab
infections") +
  theme_bw()
```

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

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



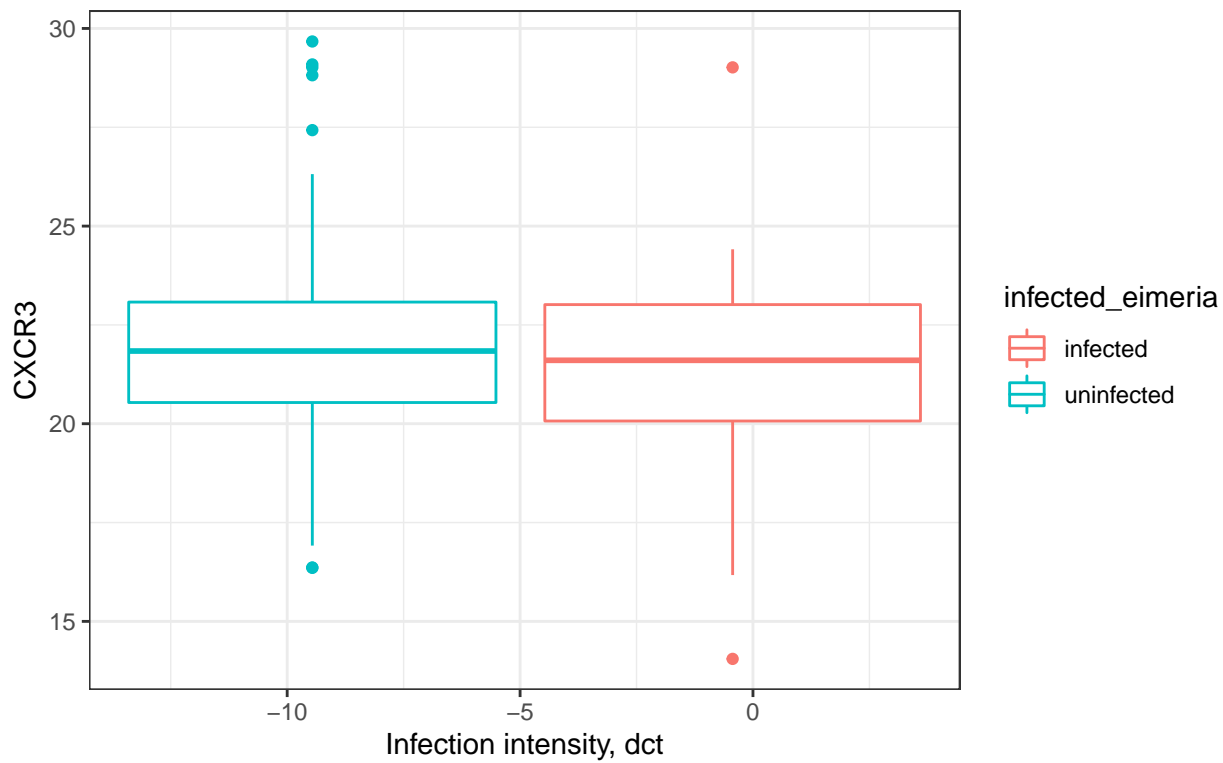
## Immune gene expression against infection intensity in lab infections



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

## Warning: Removed 154 rows containing missing values (stat\_boxplot).

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

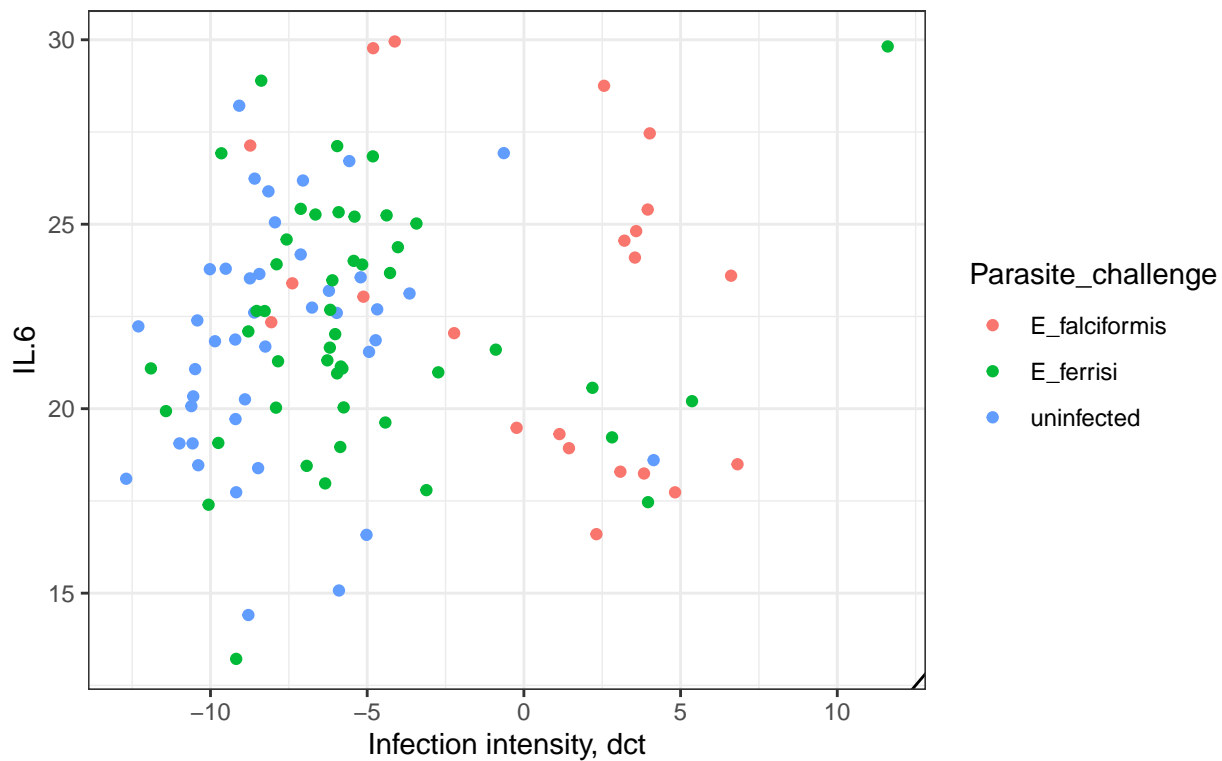


### 3. IL.6

```
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).

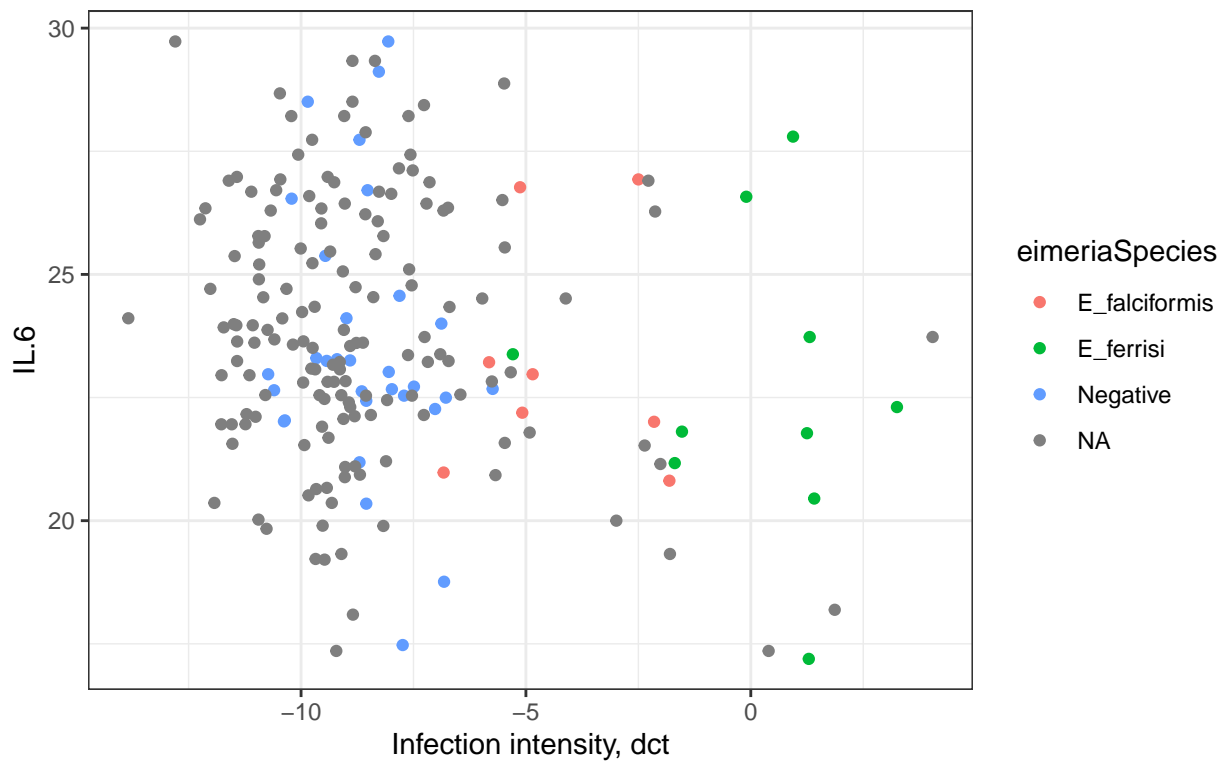
## Immune gene expression against infection intensity in lab infections



```
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 154 rows containing missing values (geom\_point).

## Immune gene expression against infection intensity in field samples

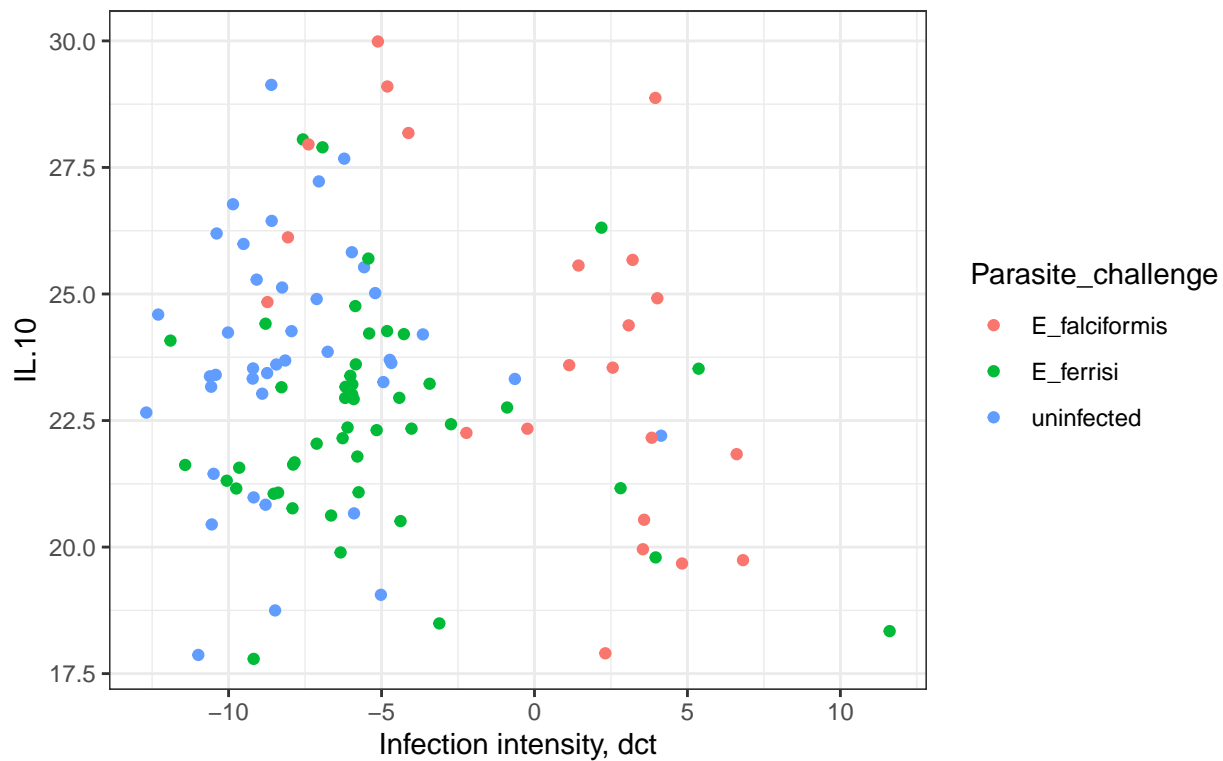


### 4. IL.10

```
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).

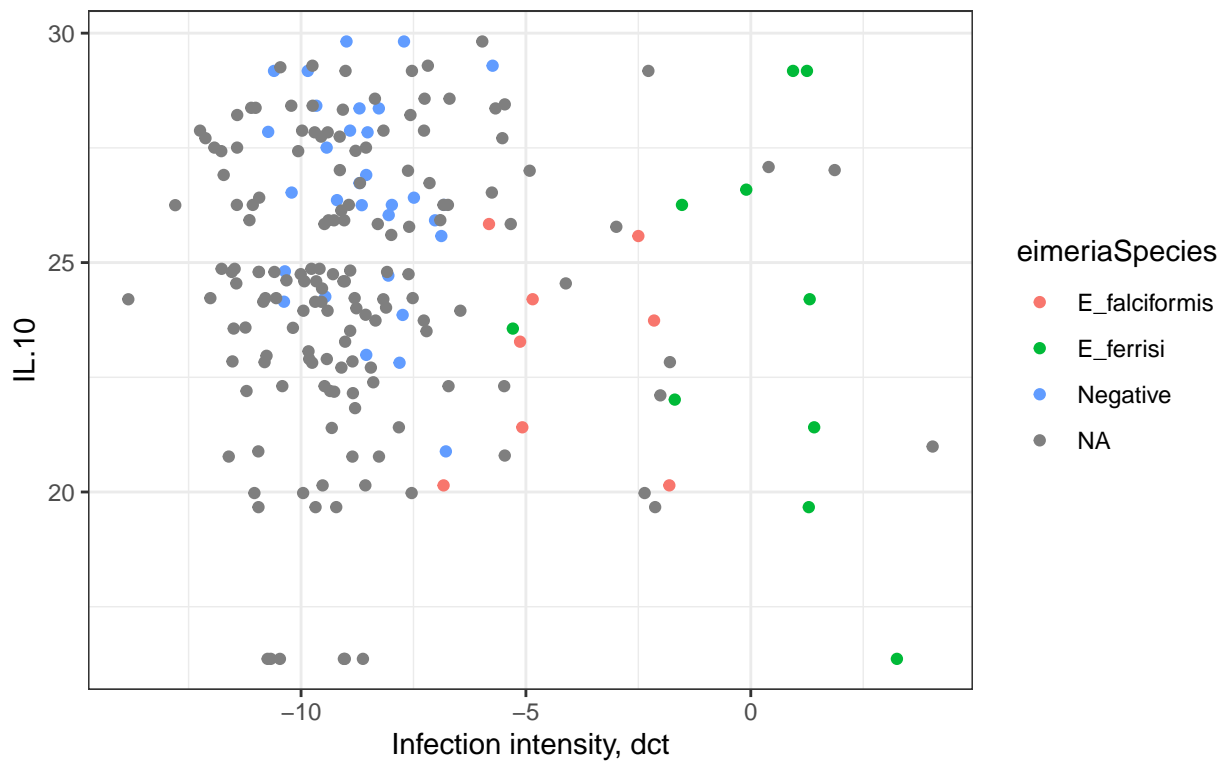
## Immune gene expression against infection intensity in lab infections



```
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 154 rows containing missing values (geom\_point).

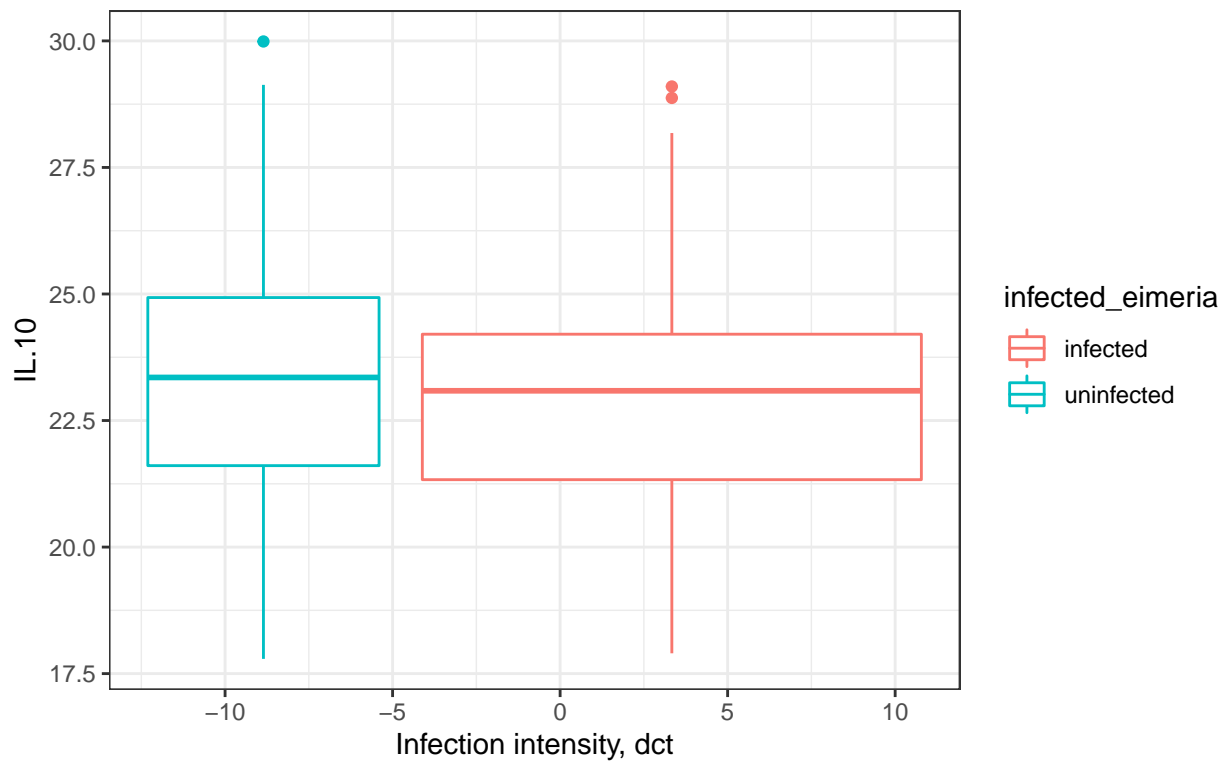
## Immune gene expression against infection intensity in field samples



```
ggplot(lab, aes(x = delta, y = IL.10, color = infected_eimeria)) +
  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).

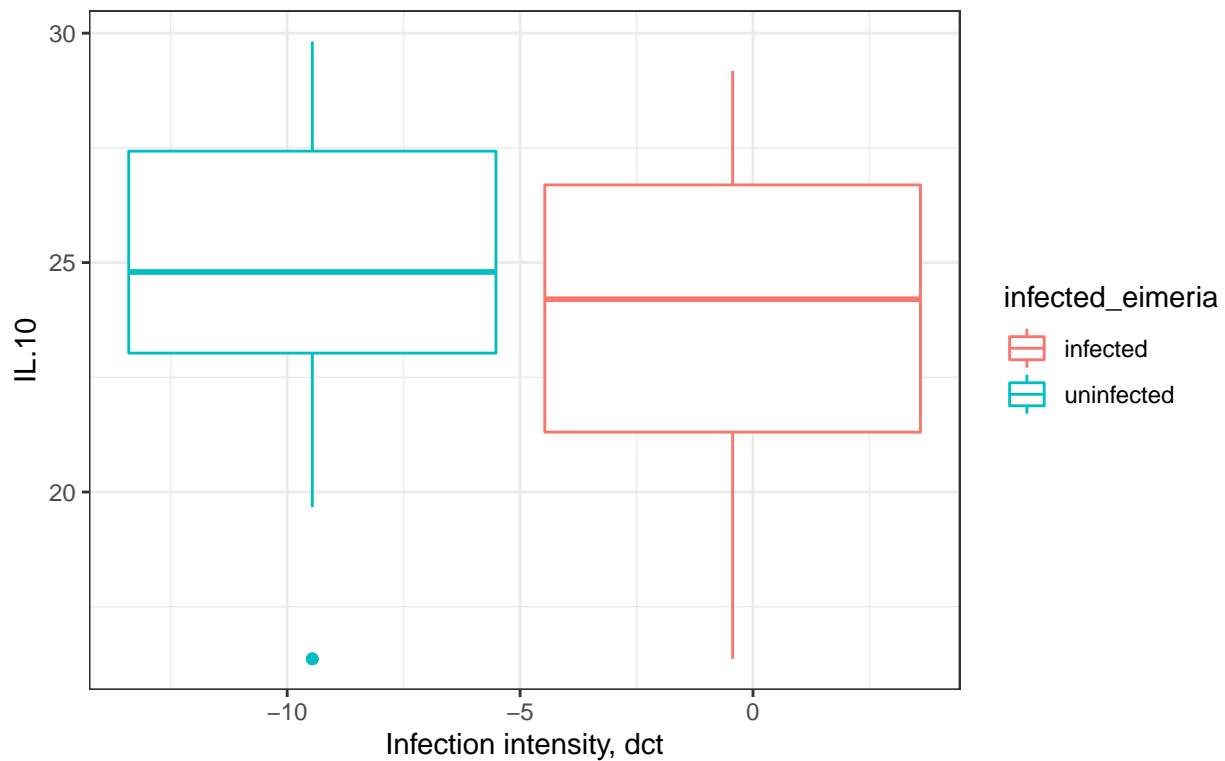
## Immune gene expression against infection intensity in lab infections



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

## Warning: Removed 154 rows containing missing values (stat\_boxplot).

## Immune gene expression against infection intensity in field samples



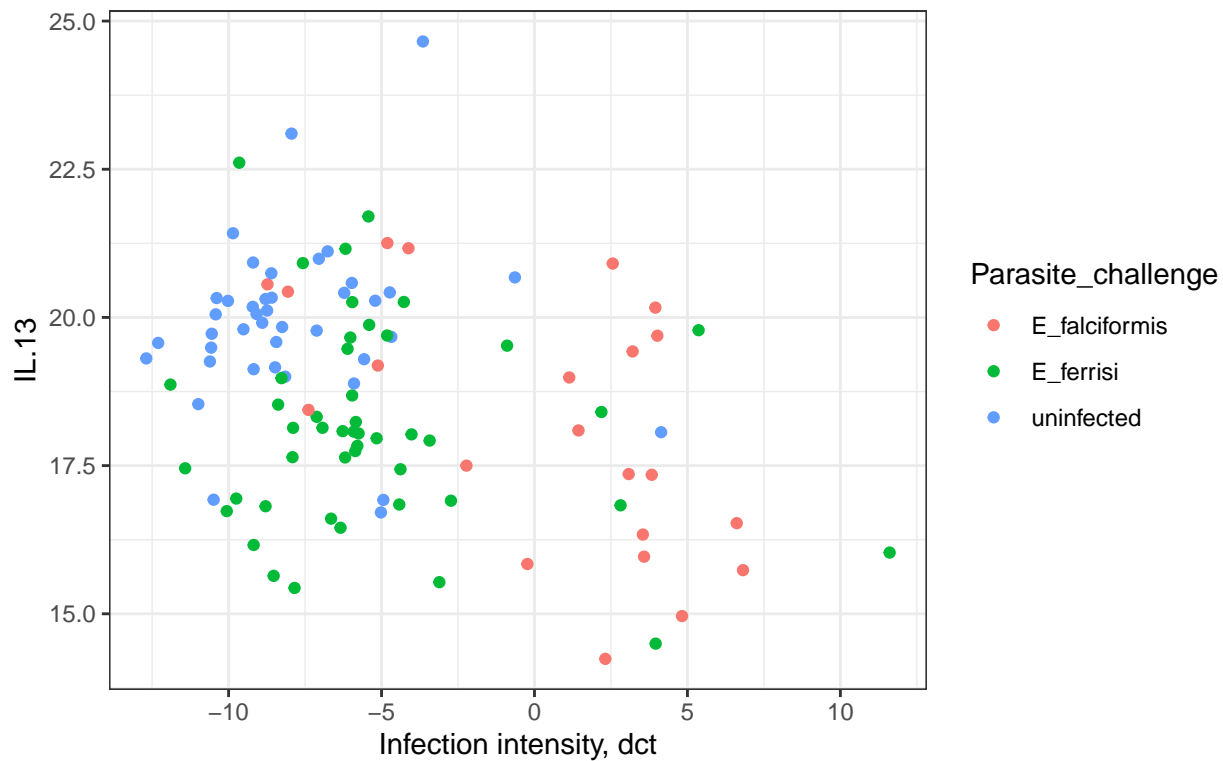
### 5. IL.13

```
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).



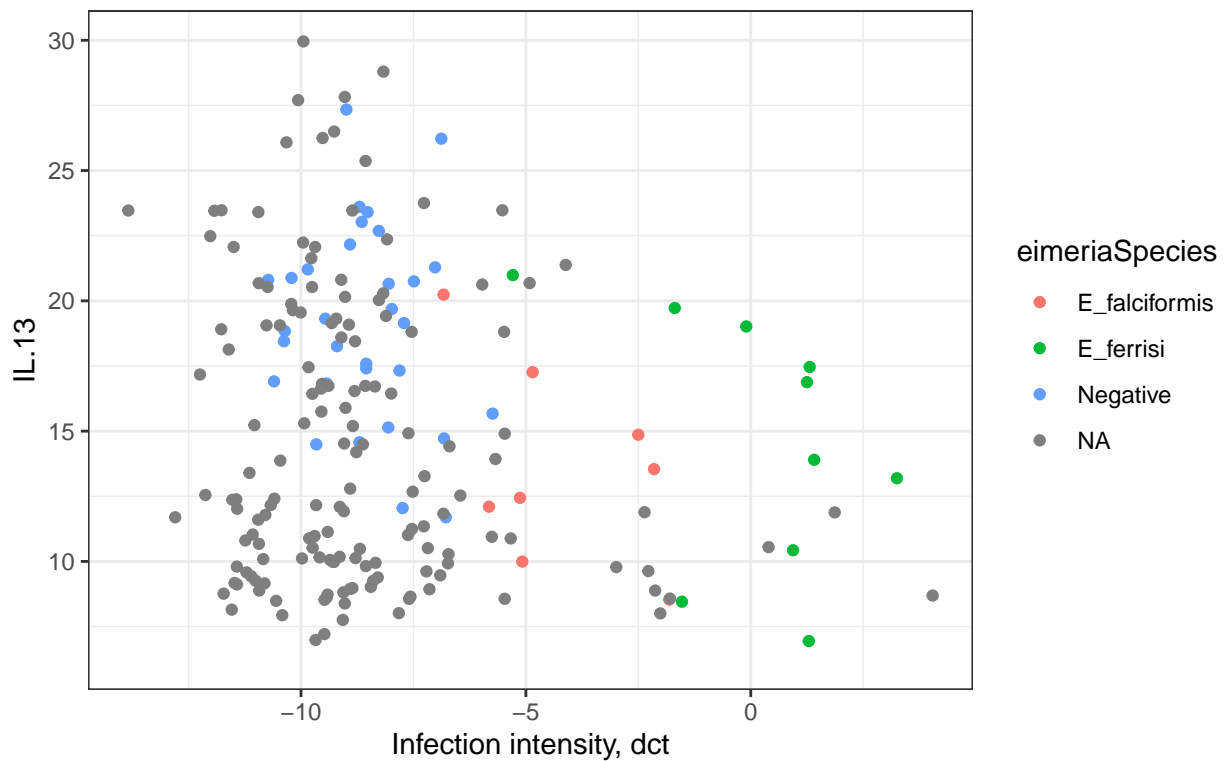
## Immune gene expression against infection intensity in lab infections



```
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 154 rows containing missing values (geom\_point).

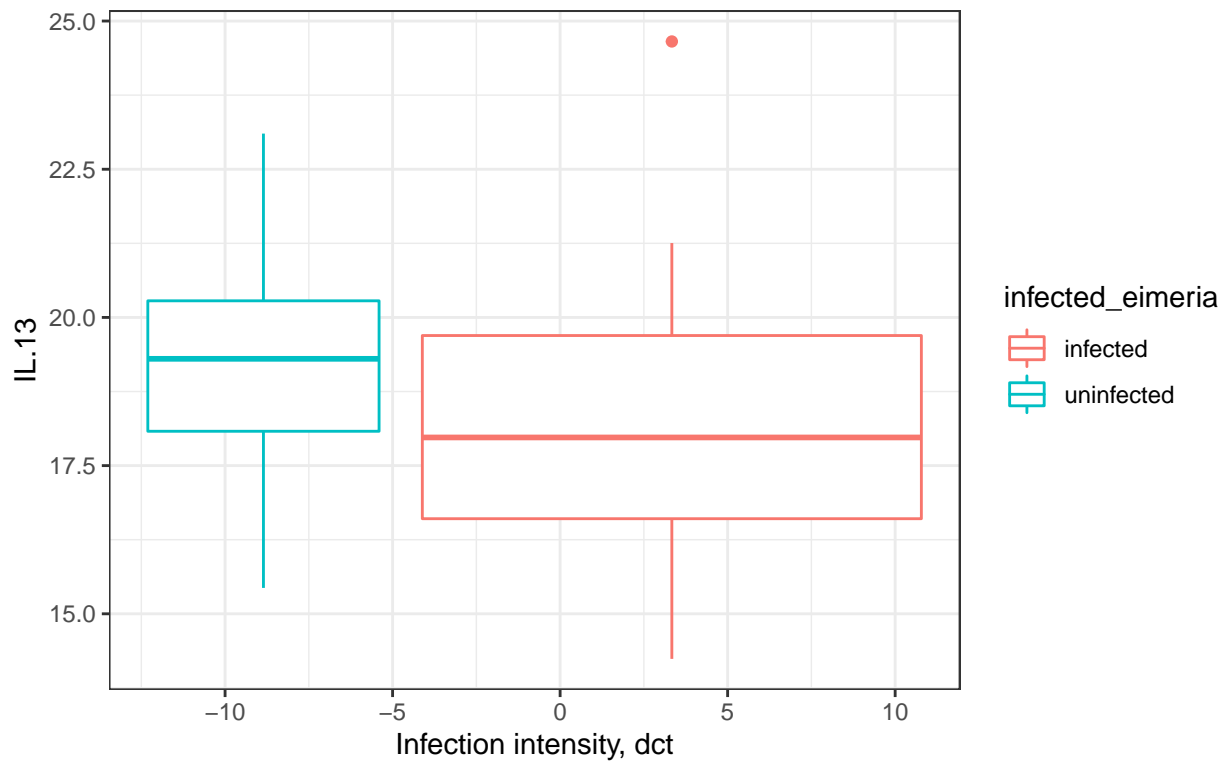
## Immune gene expression against infection intensity in field samples



```
ggplot(lab, aes(x = delta, y = IL.13, color = infected_eimeria)) +
  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).

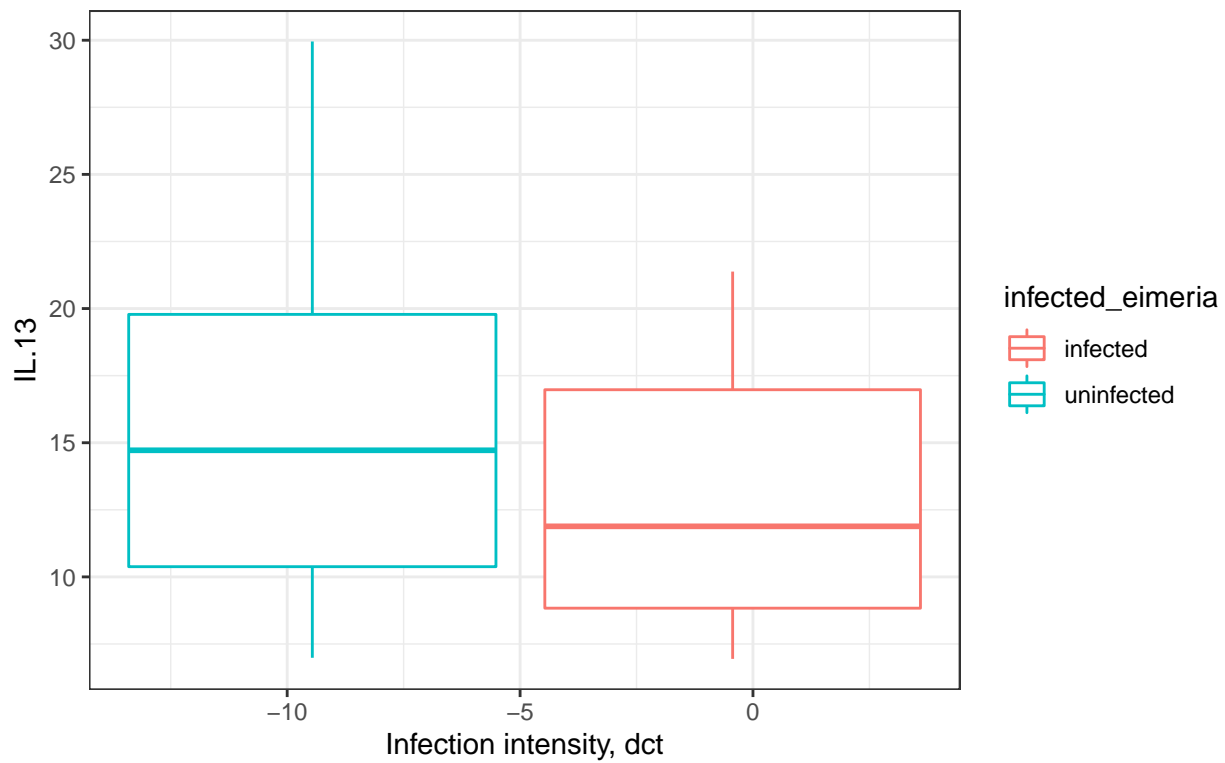
## Immune gene expression against infection intensity in lab infections



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

## Warning: Removed 154 rows containing missing values (stat\_boxplot).

## Immune gene expression against infection intensity in field samples

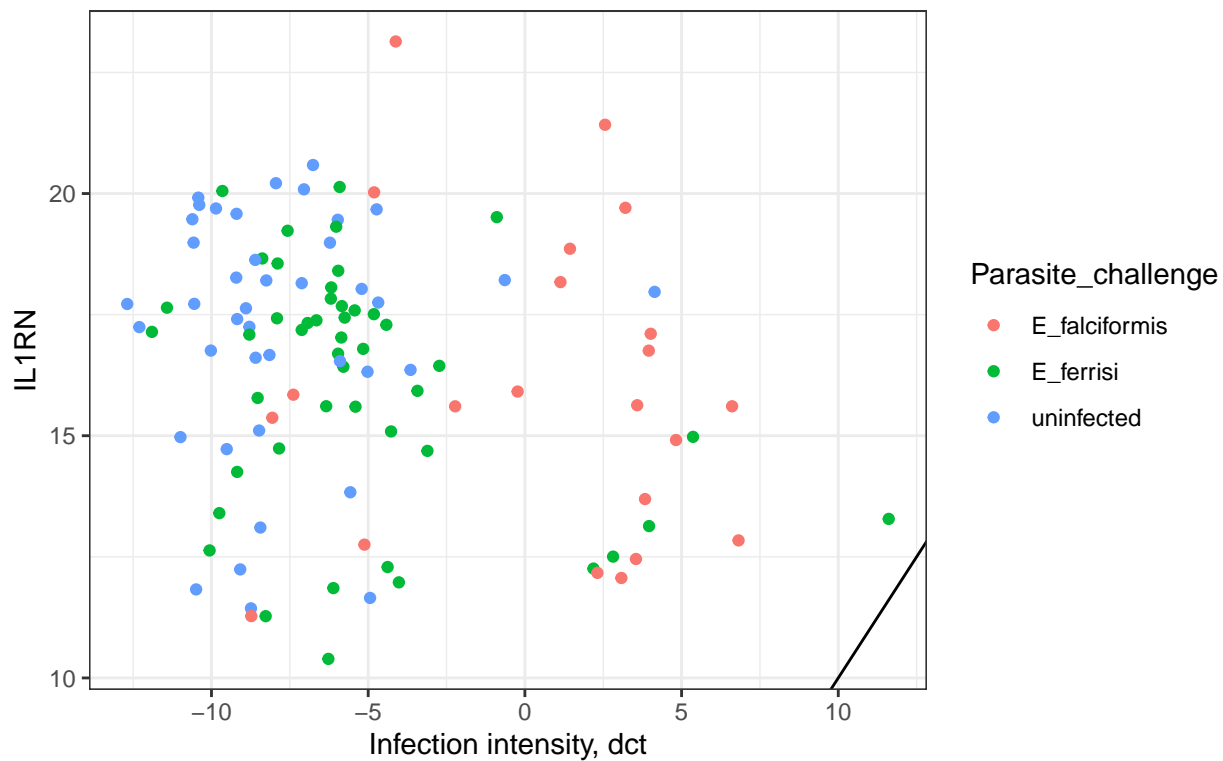


### 6. IL1RN

```
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).

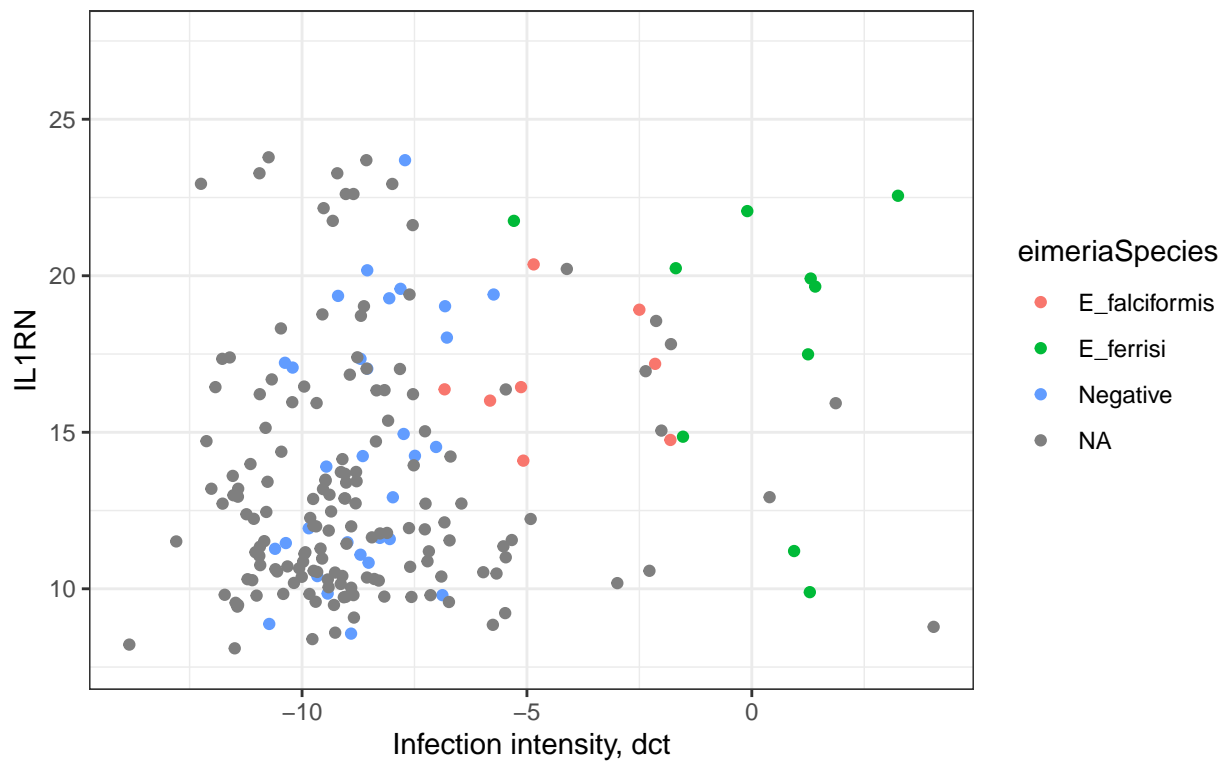
## Immune gene expression against infection intensity in lab infections



```
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 154 rows containing missing values (geom\_point).

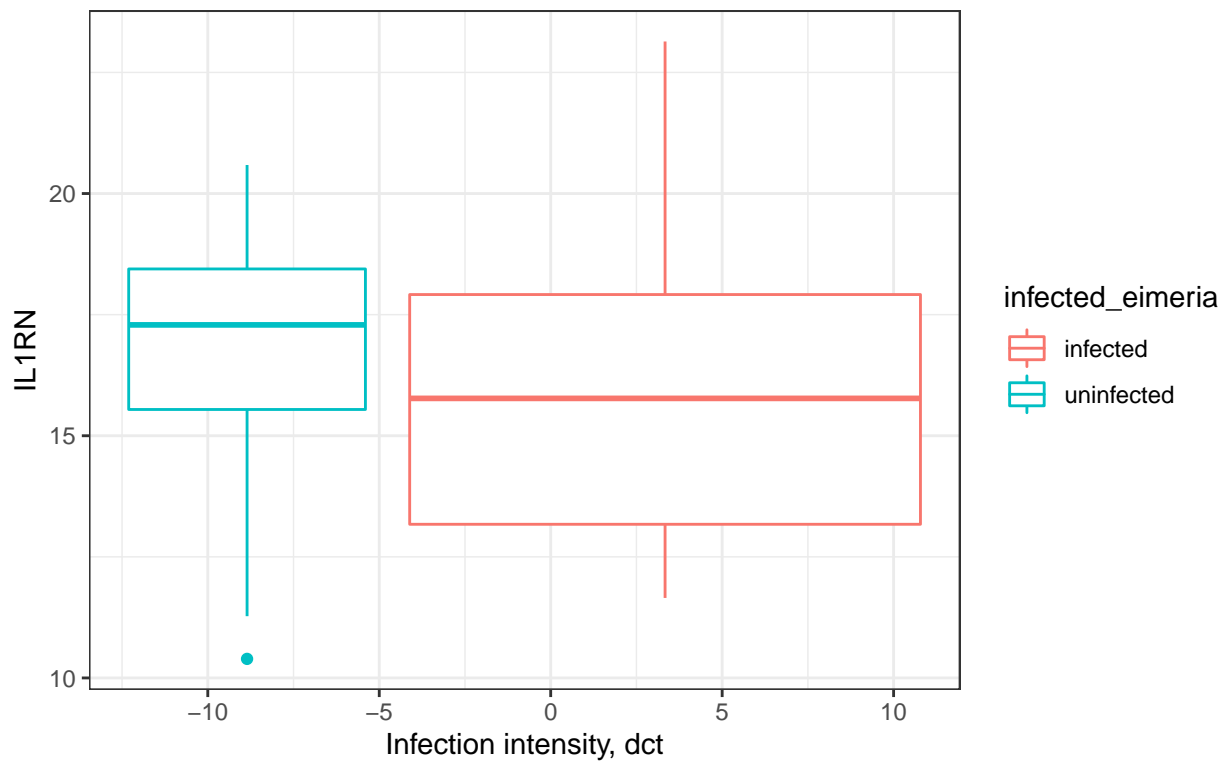
## Immune gene expression against infection intensity in field samples



```
ggplot(lab, aes(x = delta, y = IL1RN, color = infected_eimeria)) +
  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).
```

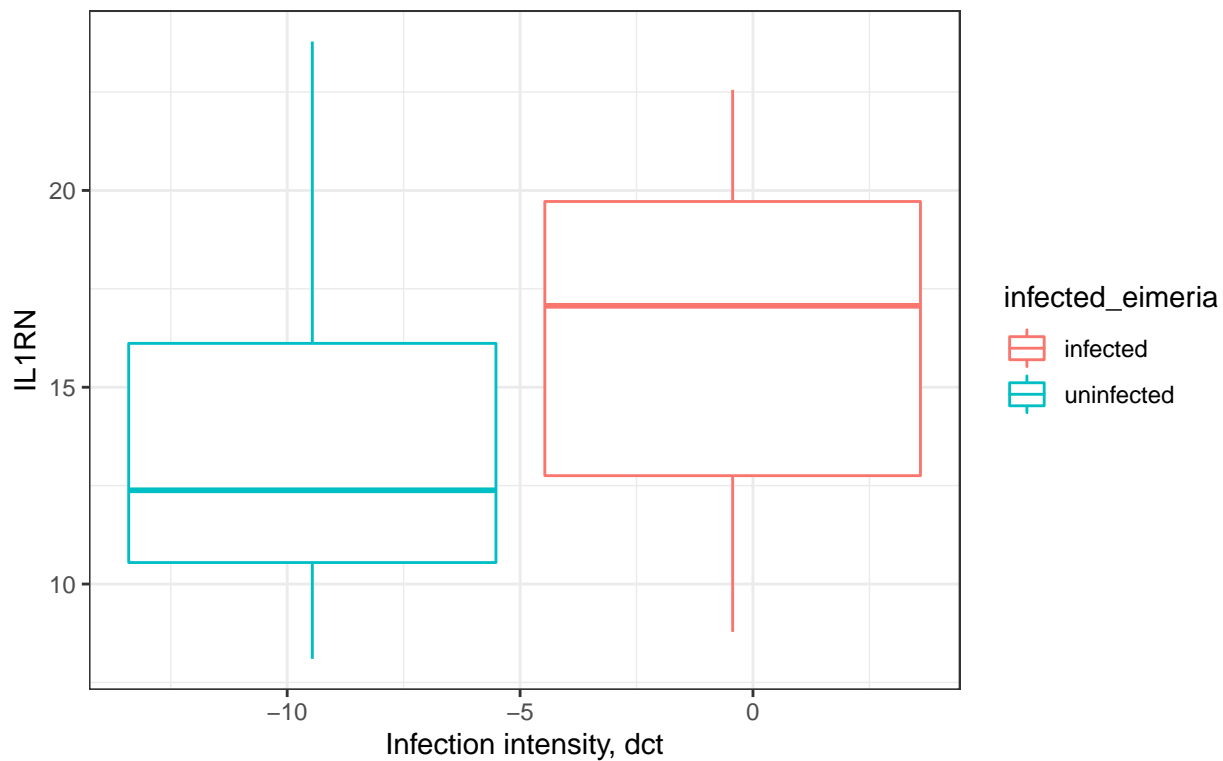
## Immune gene expression against infection intensity in lab infections



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

## Warning: Removed 154 rows containing missing values (stat\_boxplot).

## Immune gene expression against infection intensity in field samples



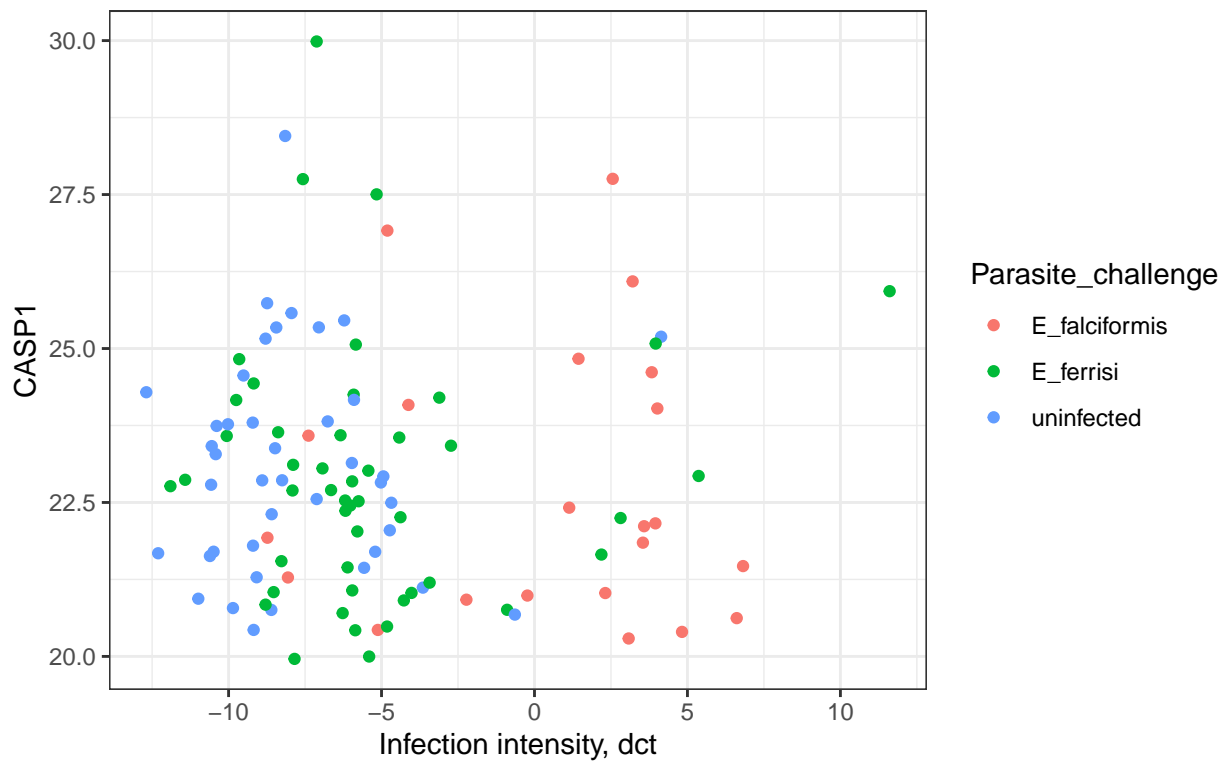
## 7. CASP1

```
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).



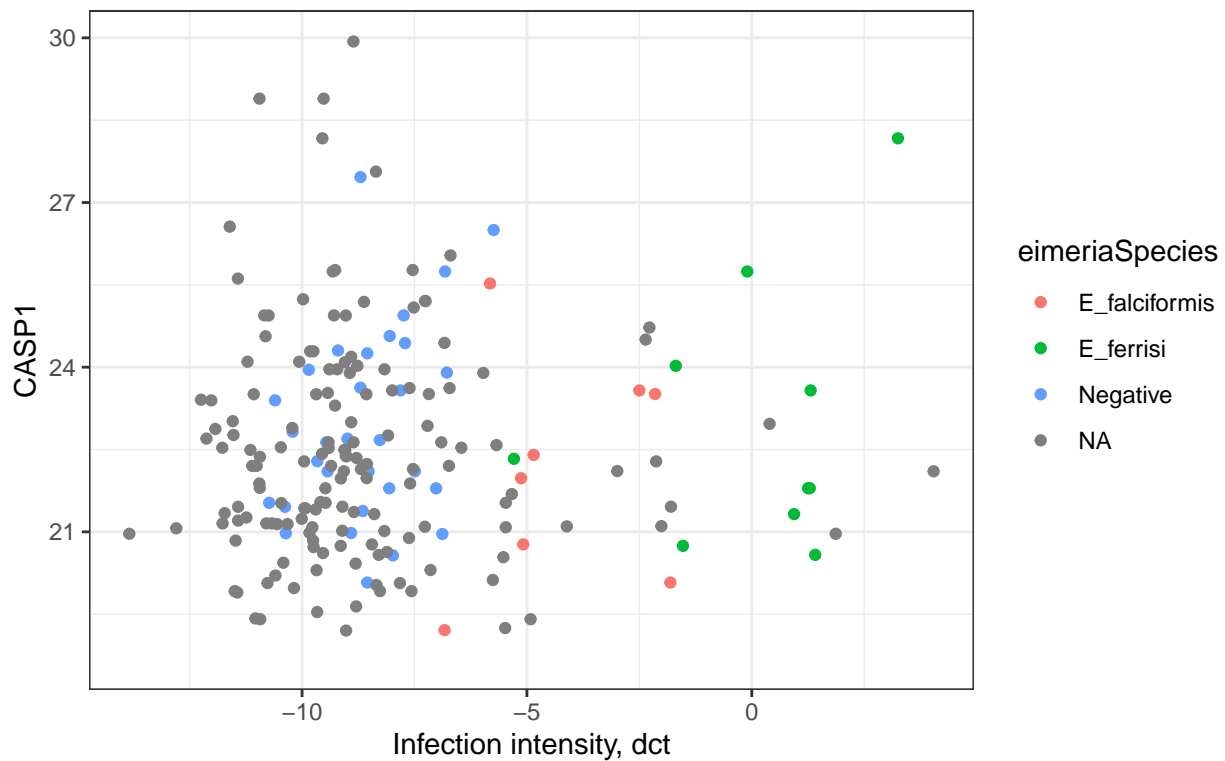
## Immune gene expression against infection intensity in lab infections



```
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 154 rows containing missing values (geom\_point).

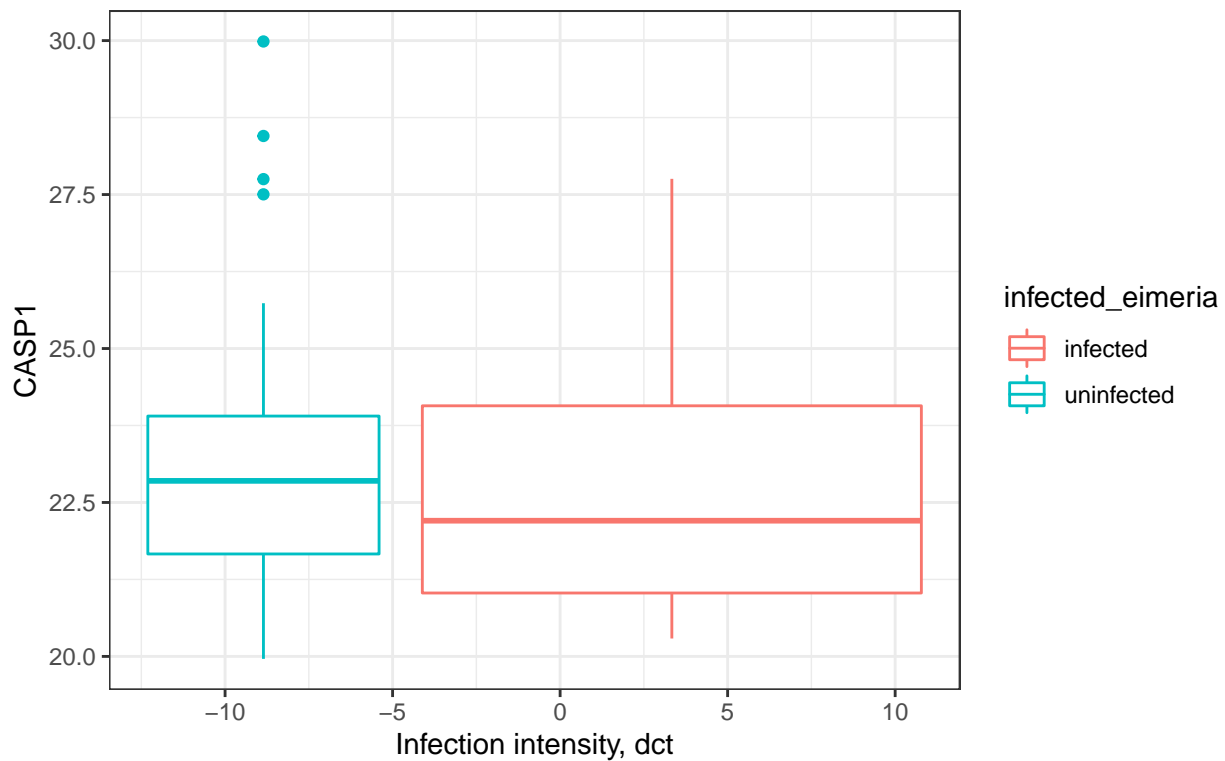
## Immune gene expression against infection intensity in field samples



```
ggplot(lab, aes(x = delta, y = CASP1, color = infected_eimeria)) +
  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).
```

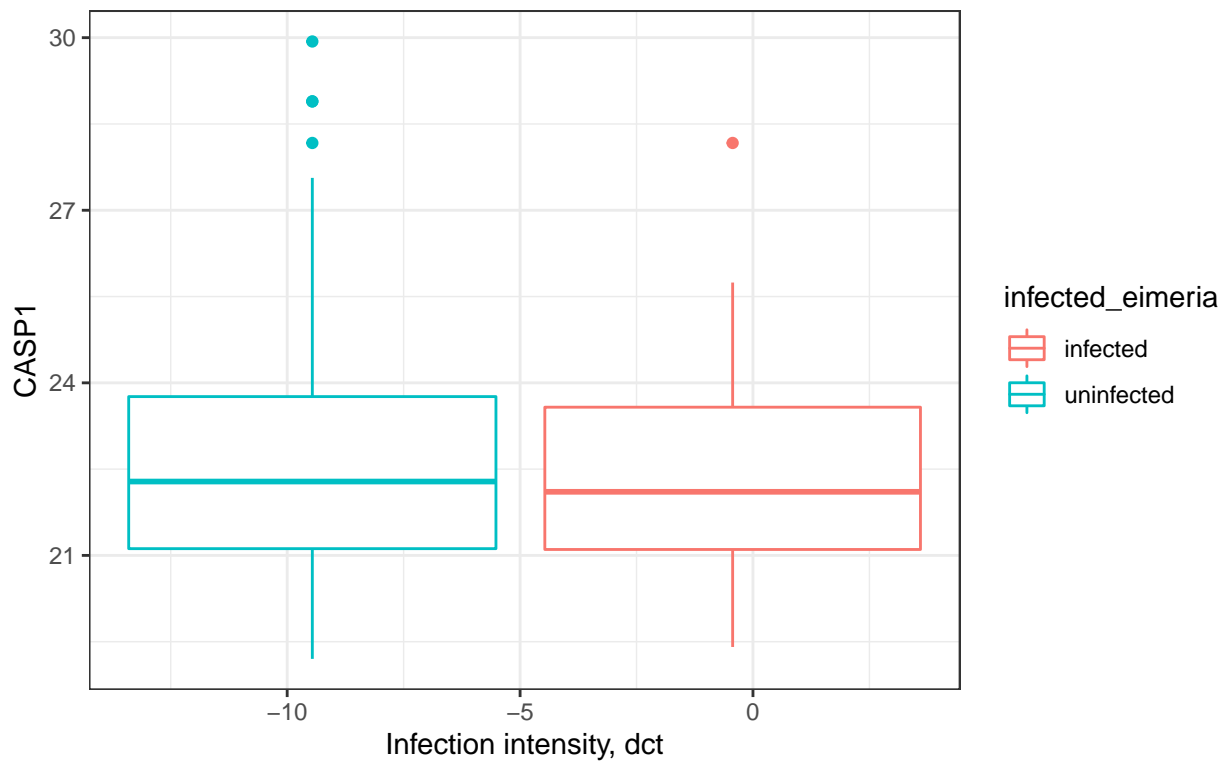
## Immune gene expression against infection intensity in lab infections



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

## Warning: Removed 154 rows containing missing values (stat\_boxplot).

## Immune gene expression against infection intensity in field samples

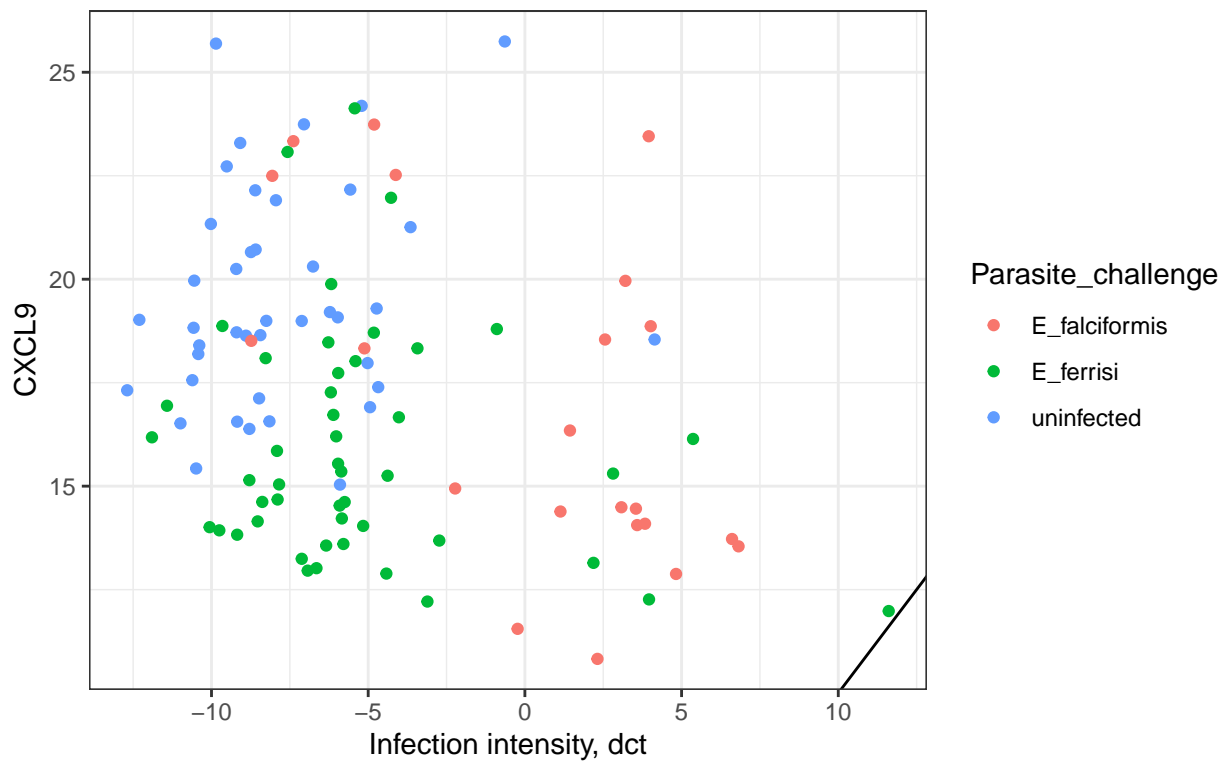


### 8. CXCL9

```
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).

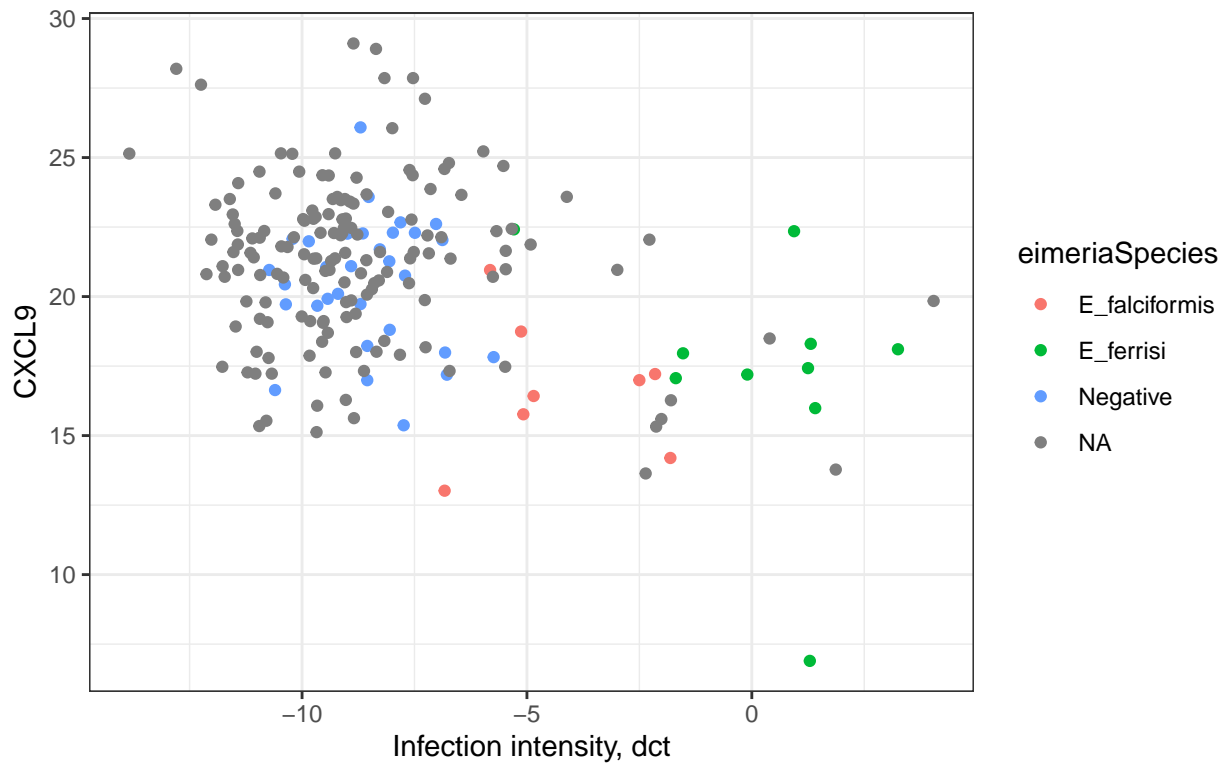
## Immune gene expression against infection intensity in lab infections



```
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 154 rows containing missing values (geom\_point).

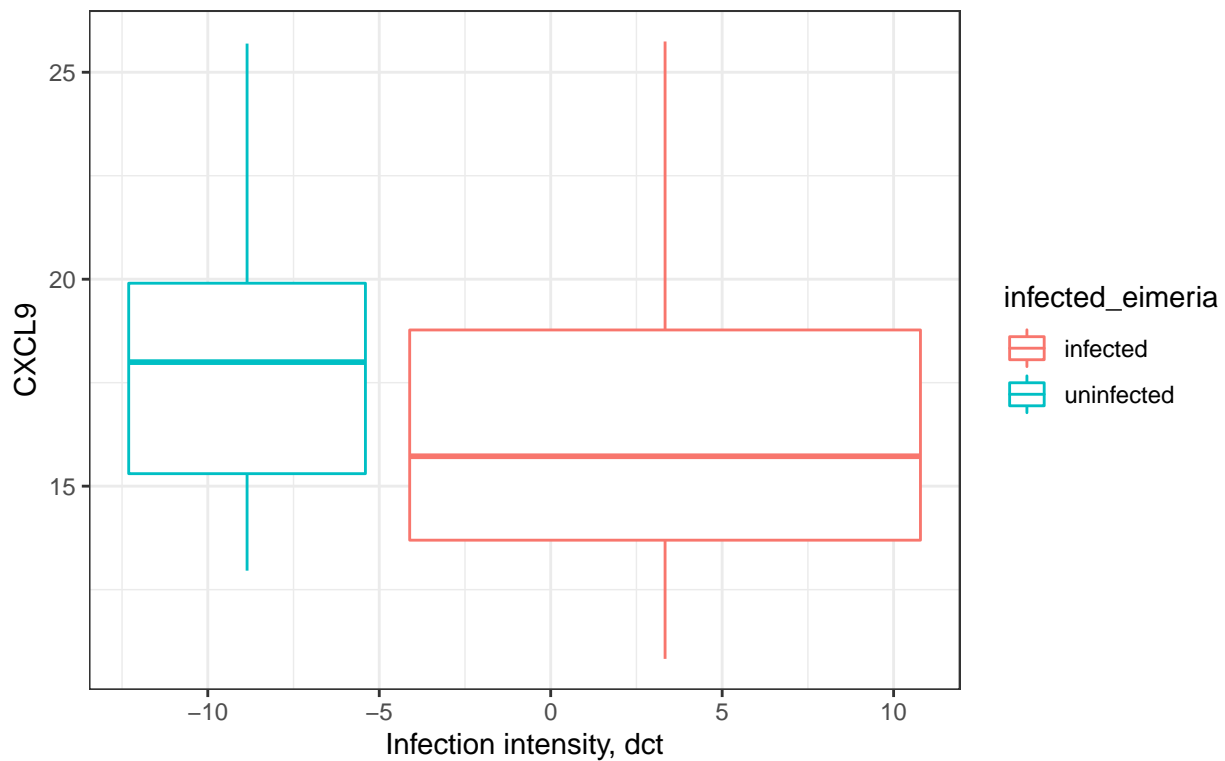
## Immune gene expression against infection intensity in field samples



```
ggplot(lab, aes(x = delta, y = CXCL9, color = infected_eimeria)) +
  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).

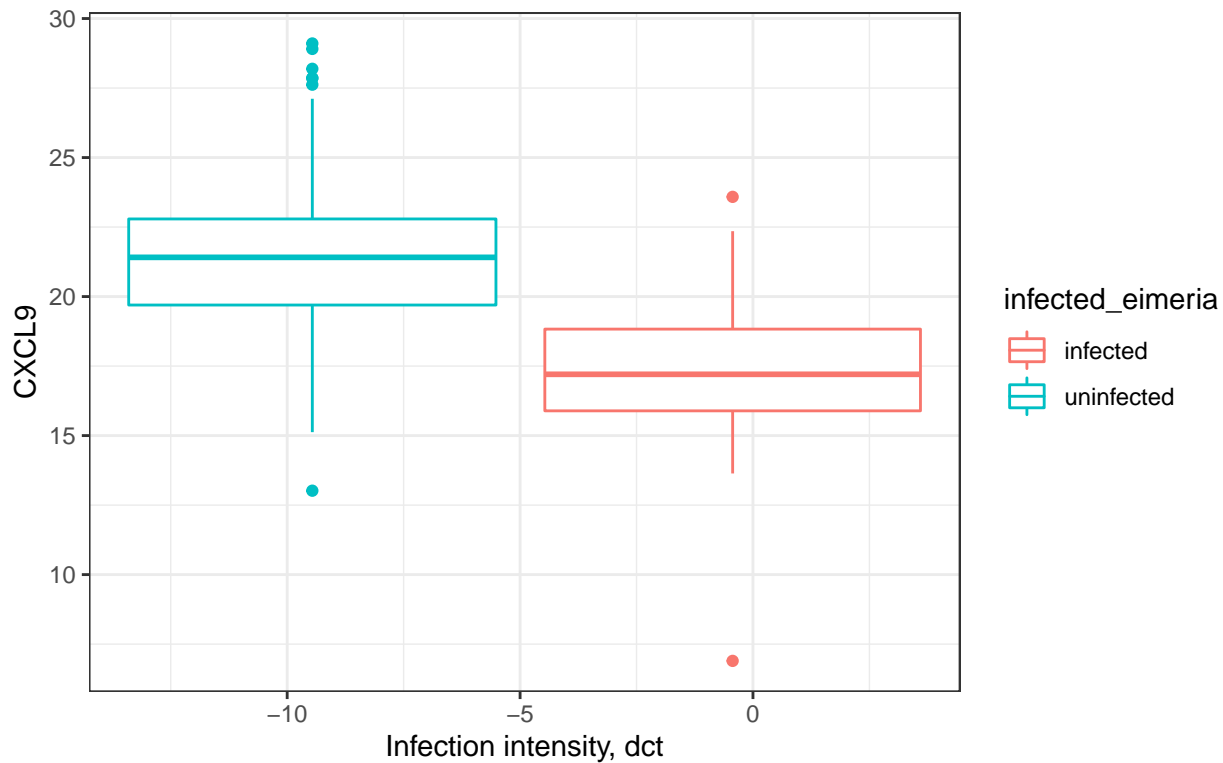
## Immune gene expression against infection intensity in lab infections



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

## Warning: Removed 154 rows containing missing values (stat\_boxplot).

## Immune gene expression against infection intensity in field samples



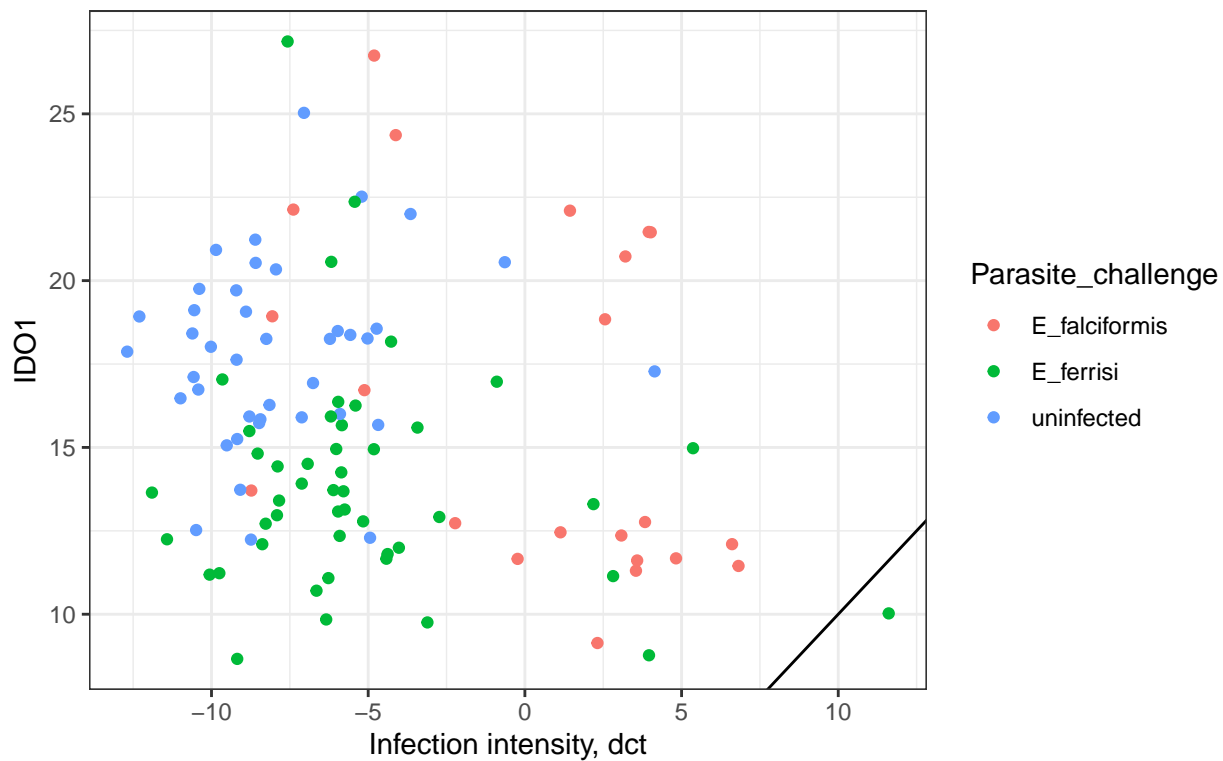
### 9. IDO1

```
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).



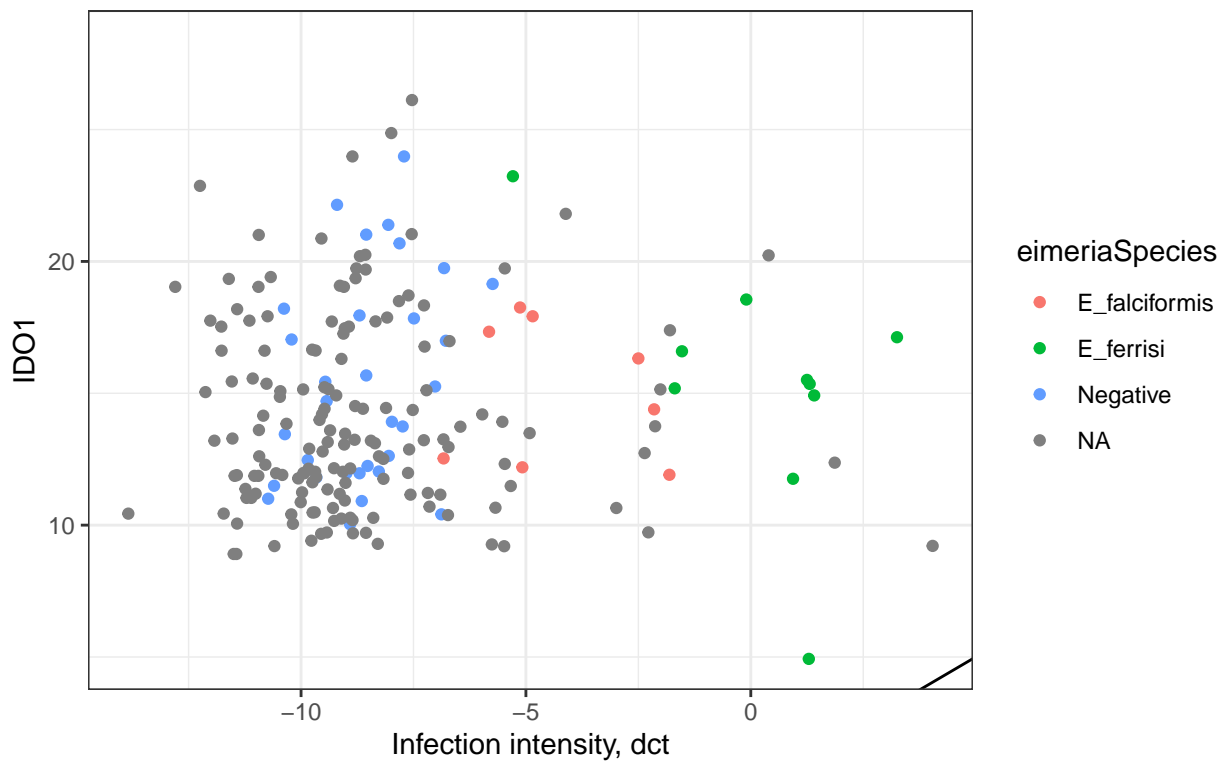
## Immune gene expression against infection intensity in lab infections



```
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 154 rows containing missing values (geom\_point).

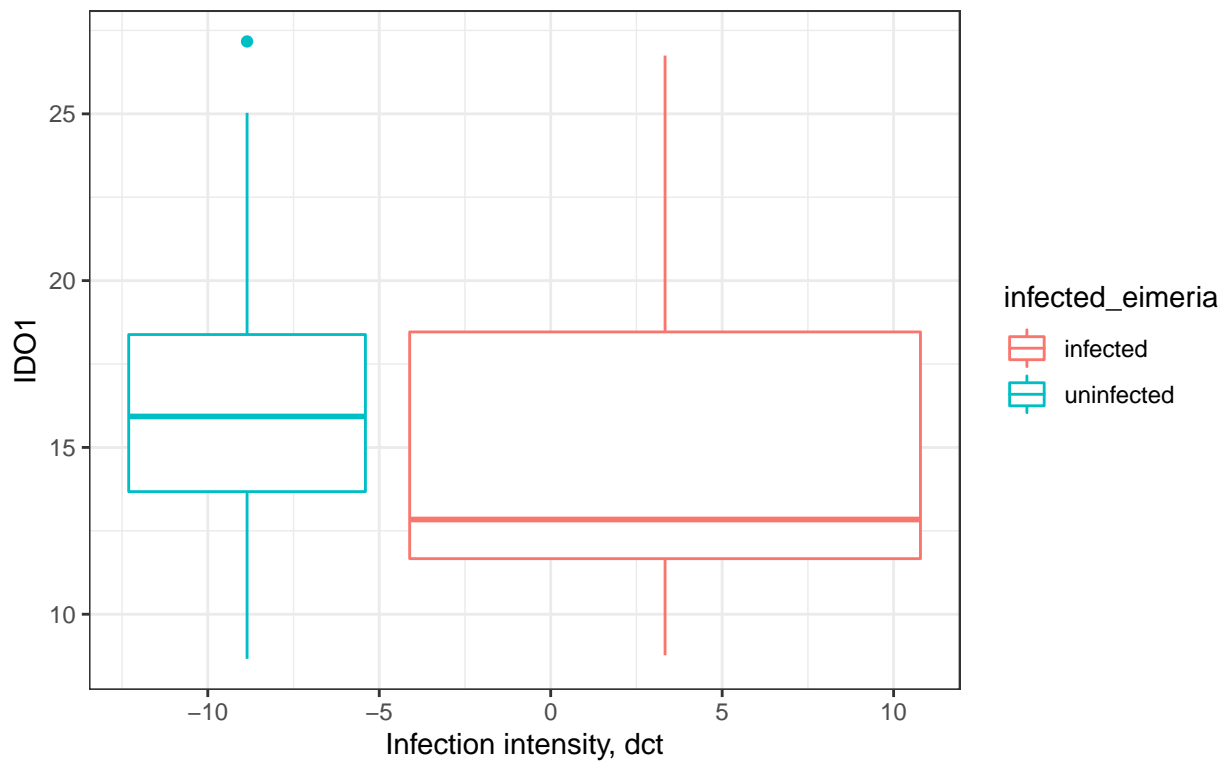
## Immune gene expression against infection intensity in field samples



```
ggplot(lab, aes(x = delta, y = IDO1, color = infected_eimeria)) +
  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).

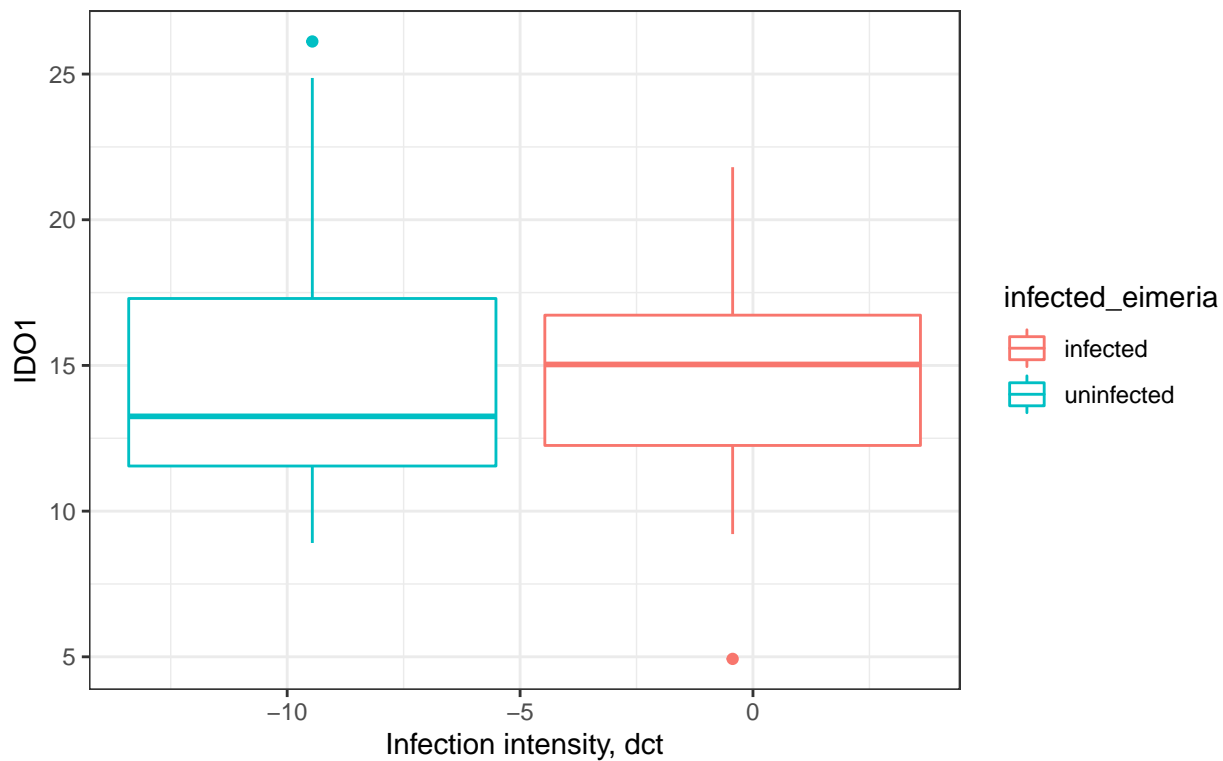
## Immune gene expression against infection intensity in lab infections



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

## Warning: Removed 154 rows containing missing values (stat\_boxplot).

## Immune gene expression against infection intensity in field samples

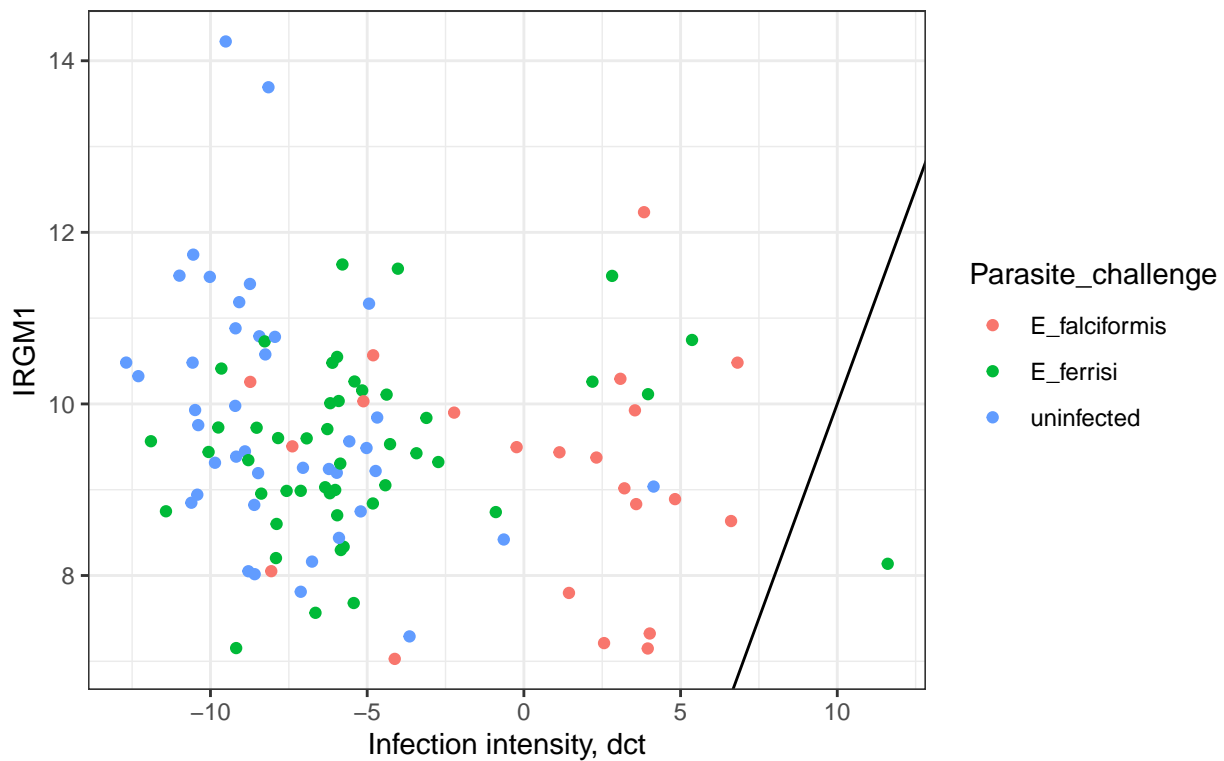


### 10. IRGM1

```
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).

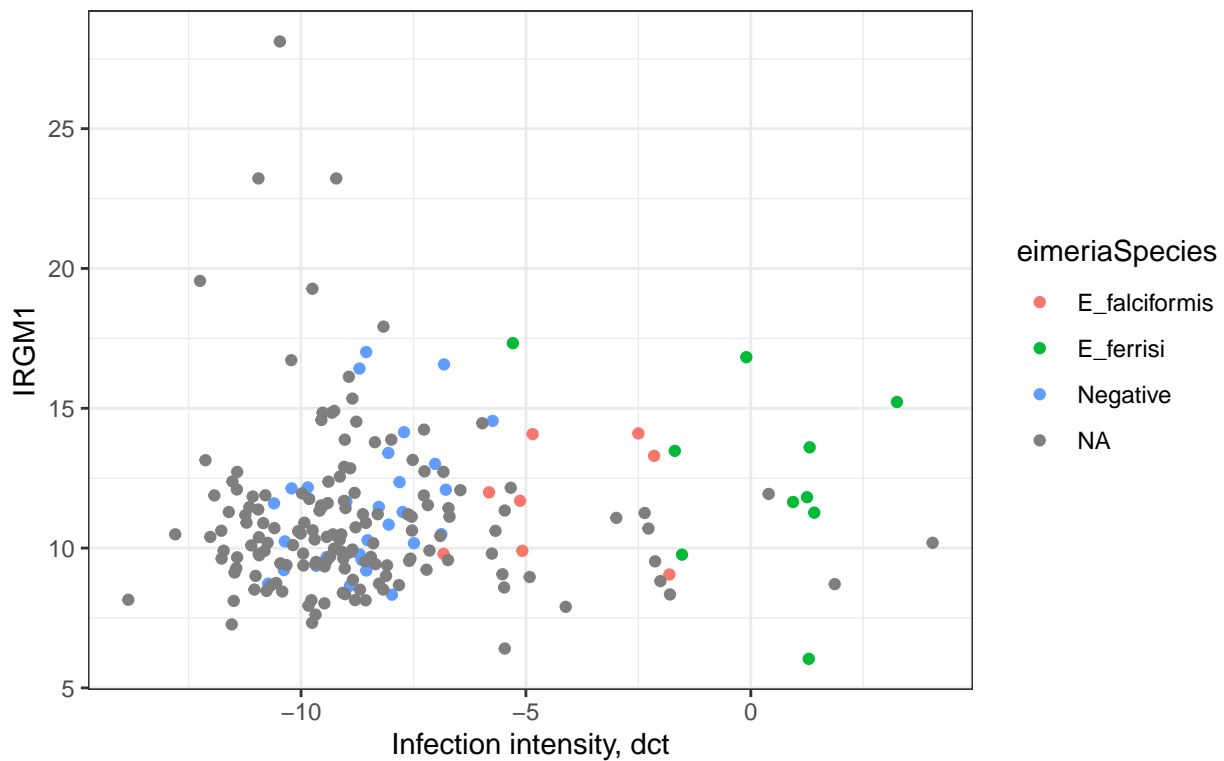
## Immune gene expression against infection intensity in lab infections



```
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 154 rows containing missing values (geom\_point).

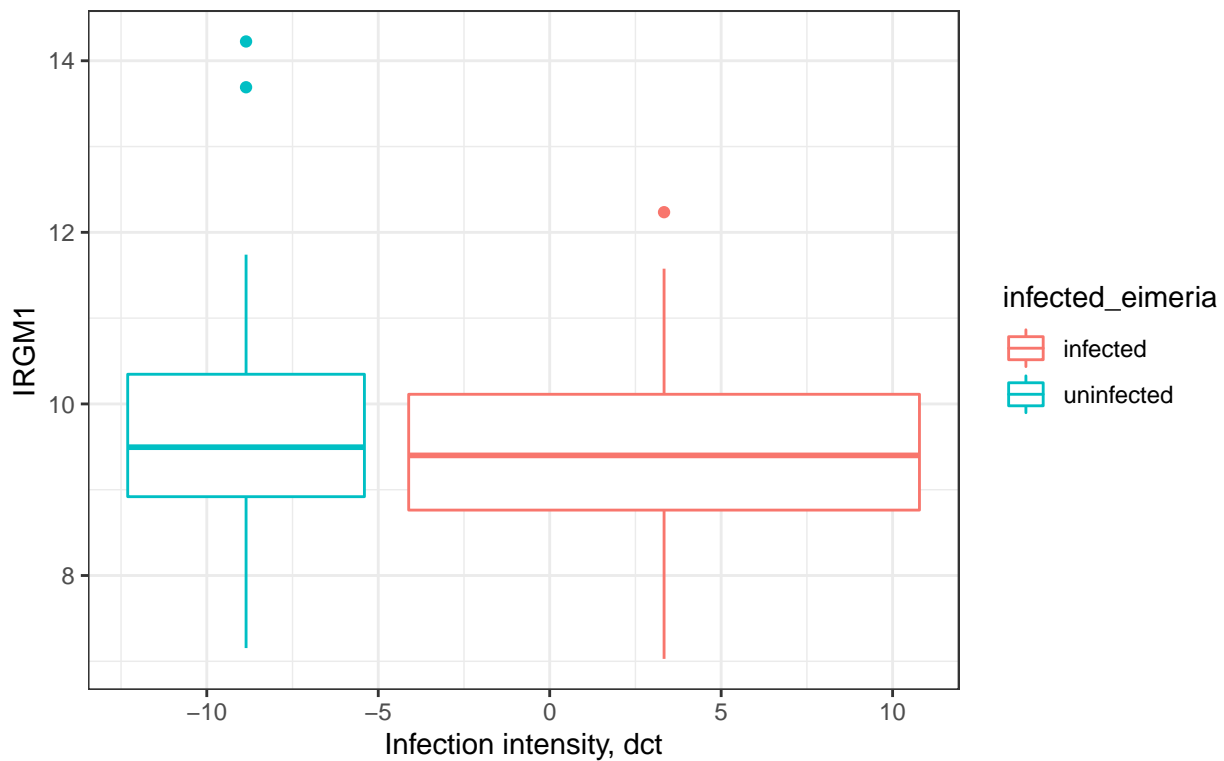
## Immune gene expression against infection intensity in field samples



```
ggplot(lab, aes(x = delta, y = IRGM1, color = infected_eimeria)) +
  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).

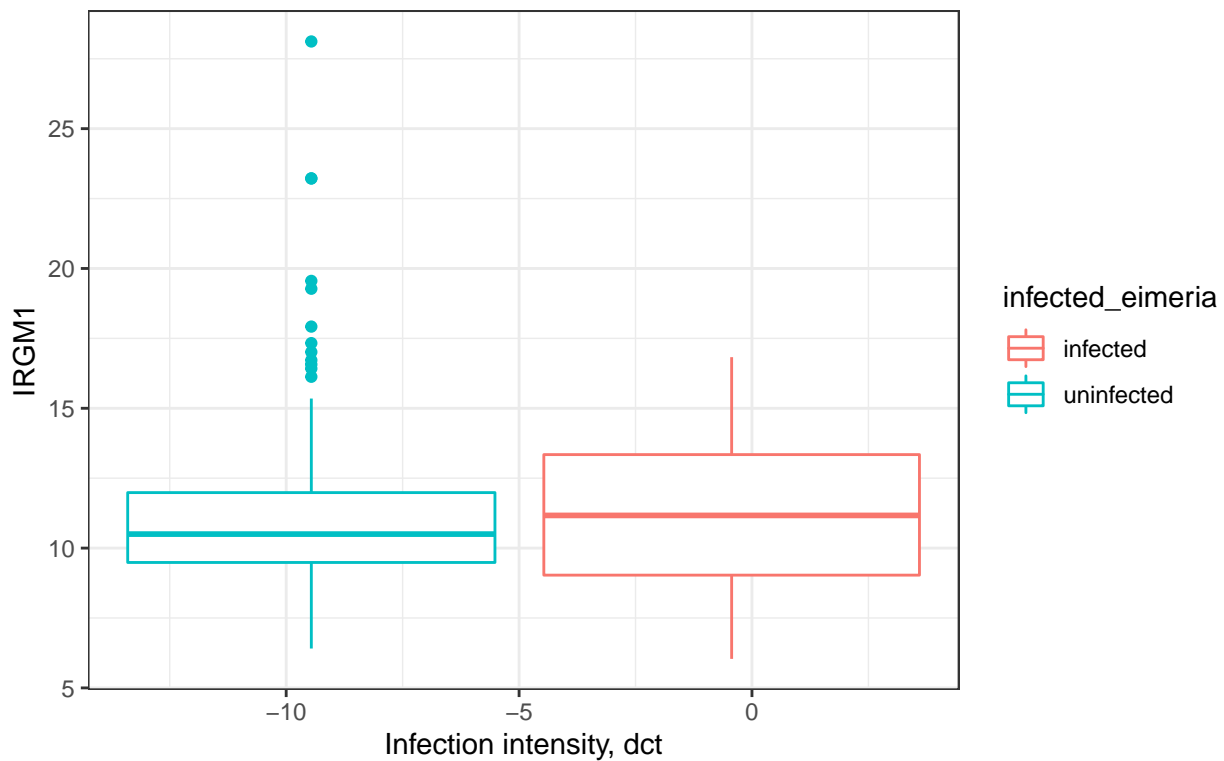
## Immune gene expression against infection intensity in lab infections



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

## Warning: Removed 154 rows containing missing values (stat\_boxplot).

## Immune gene expression against infection intensity in field samples



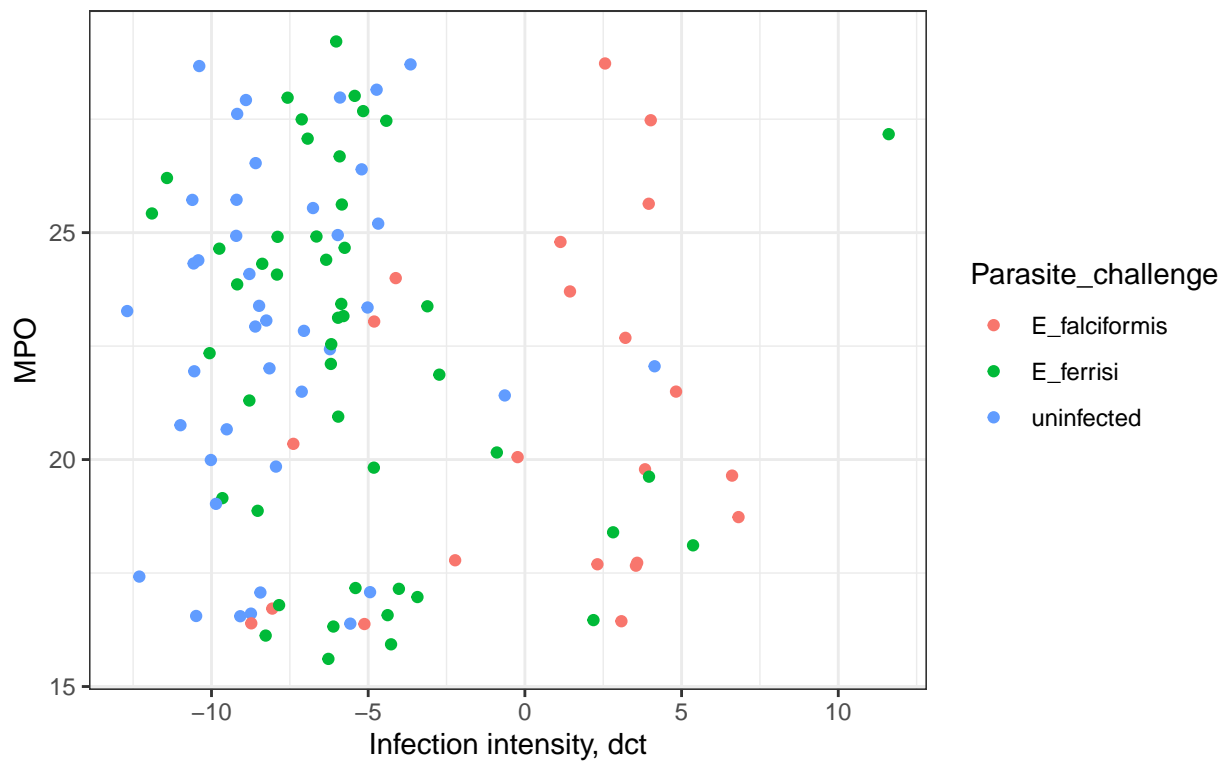
### 11. MPO

```
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).
```



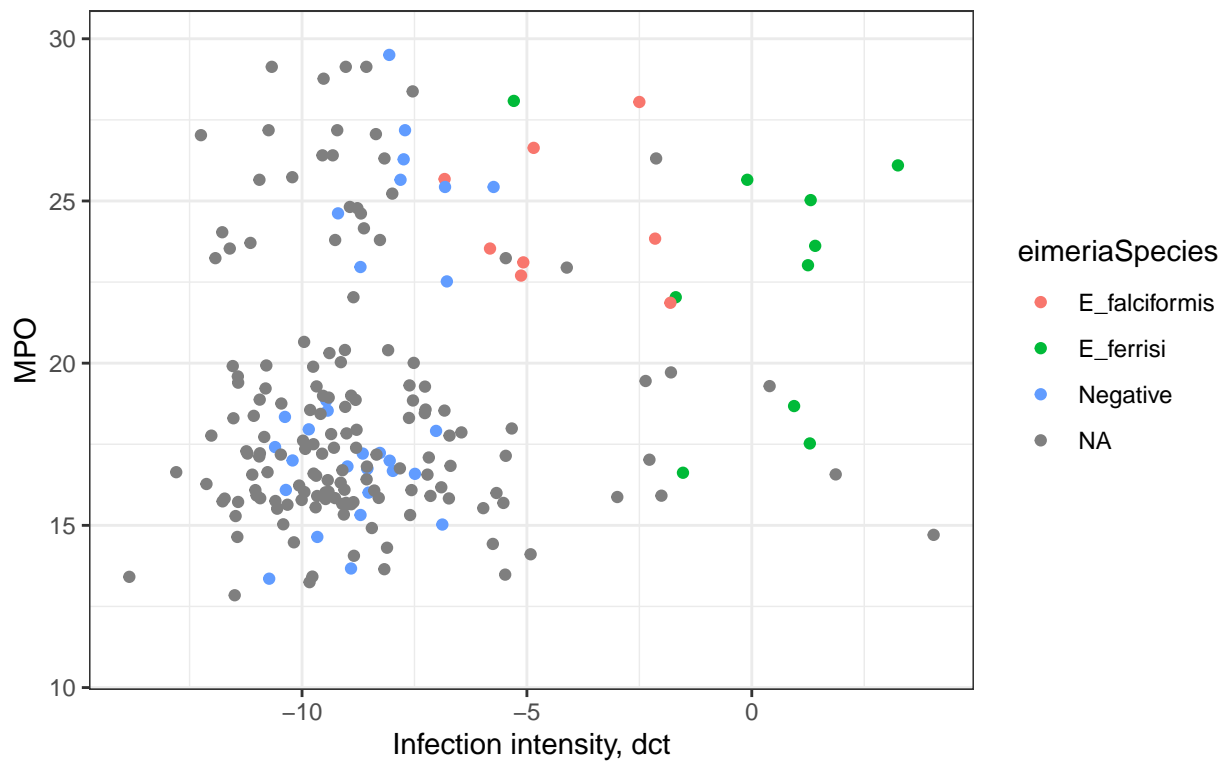
## Immune gene expression against infection intensity in lab infections



```
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 154 rows containing missing values (geom\_point).

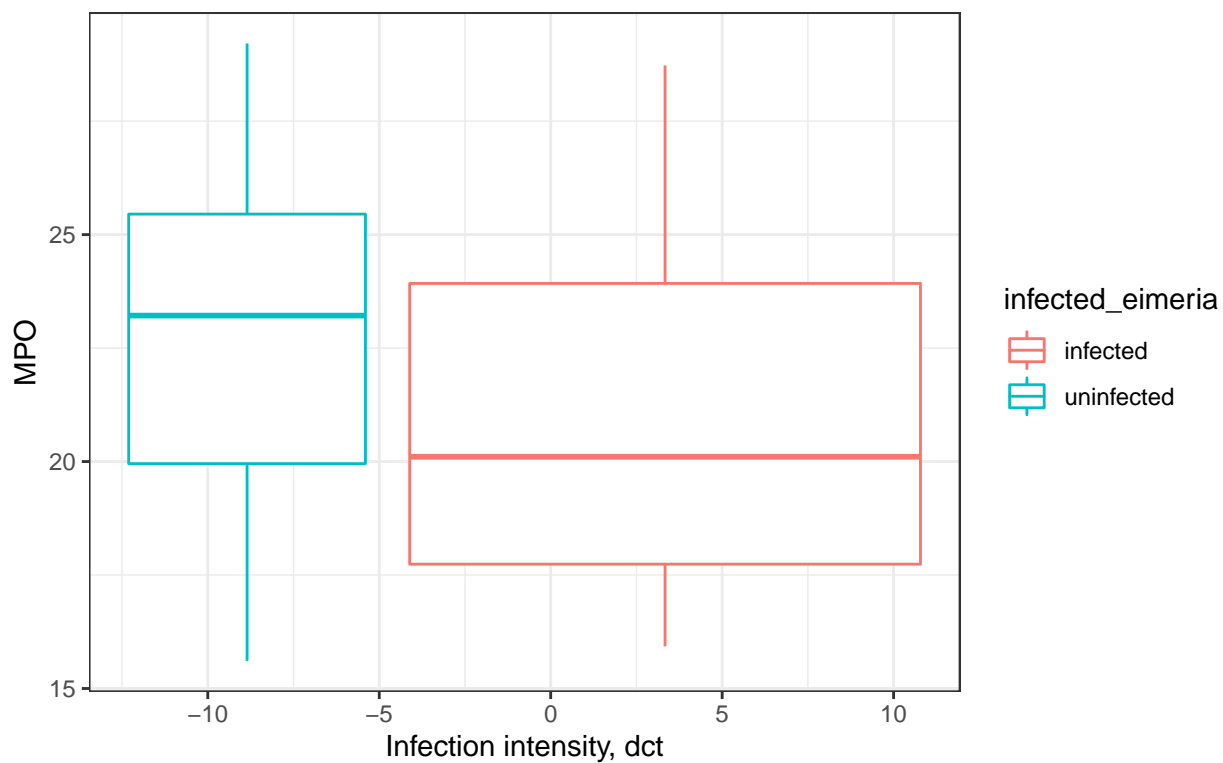
## Immune gene expression against infection intensity in field samples



```
ggplot(lab, aes(x = delta, y = MPO, color = infected_eimeria)) +
  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).

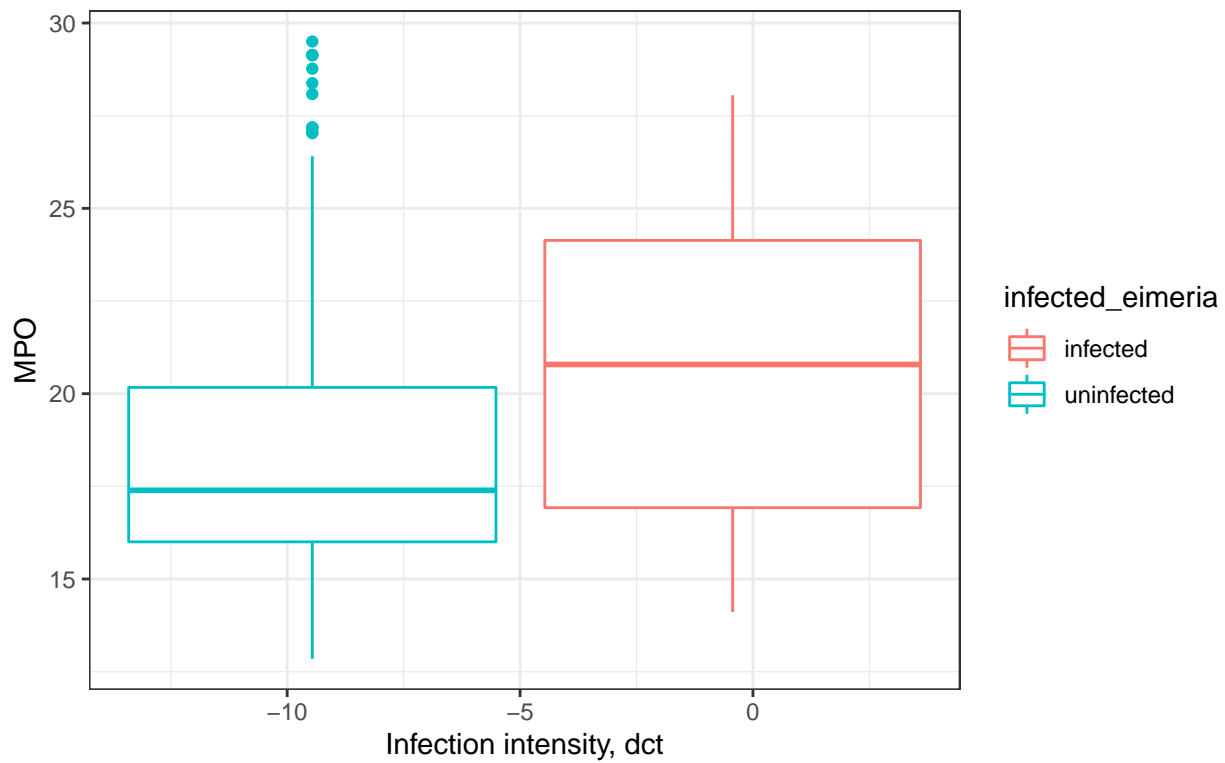
## Immune gene expression against infection intensity in lab infections



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

## Warning: Removed 154 rows containing missing values (stat\_boxplot).

## Immune gene expression against infection intensity in field samples

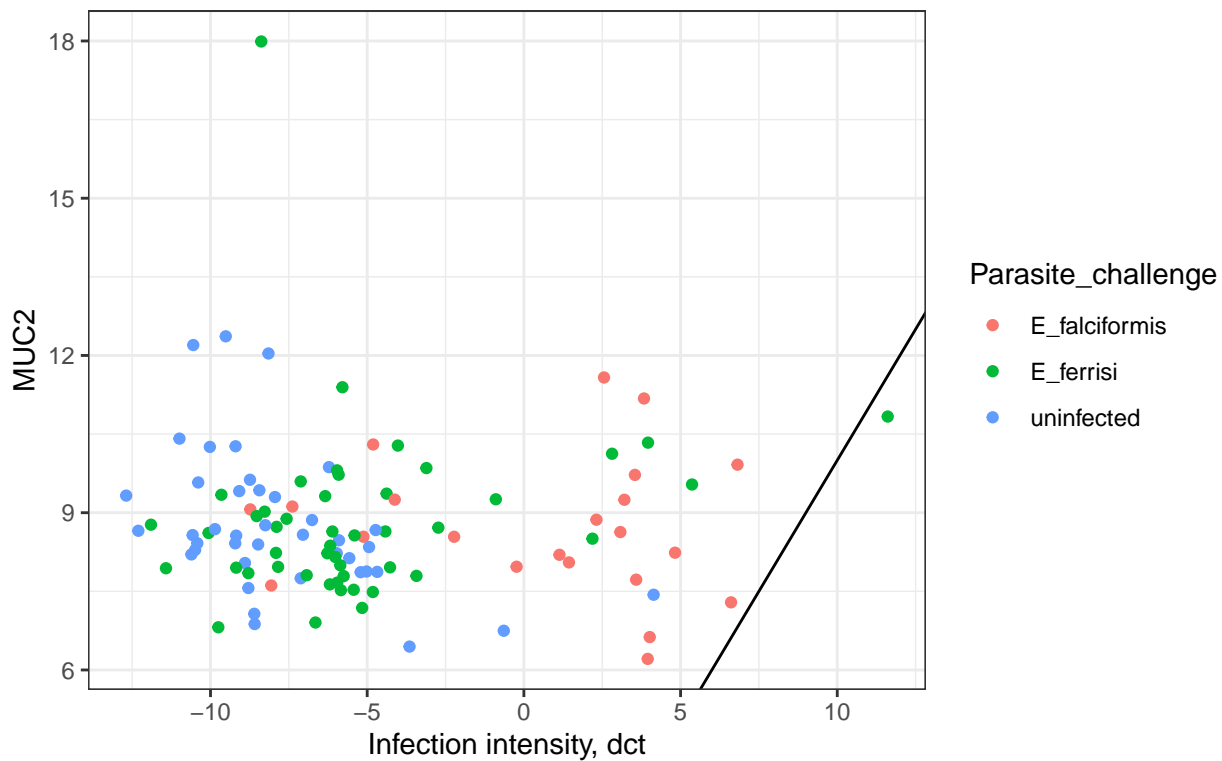


## 12. MUC2

```
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).

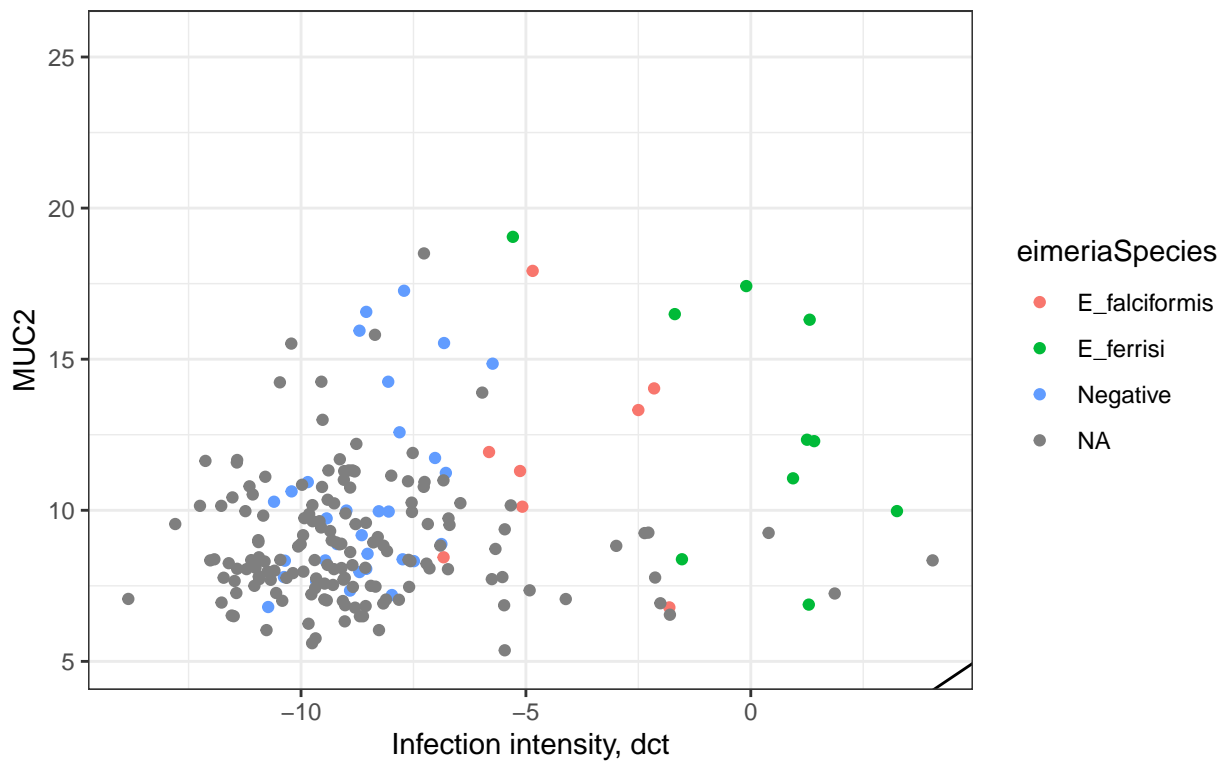
## Immune gene expression against infection intensity in lab infections



```
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 154 rows containing missing values (geom\_point).

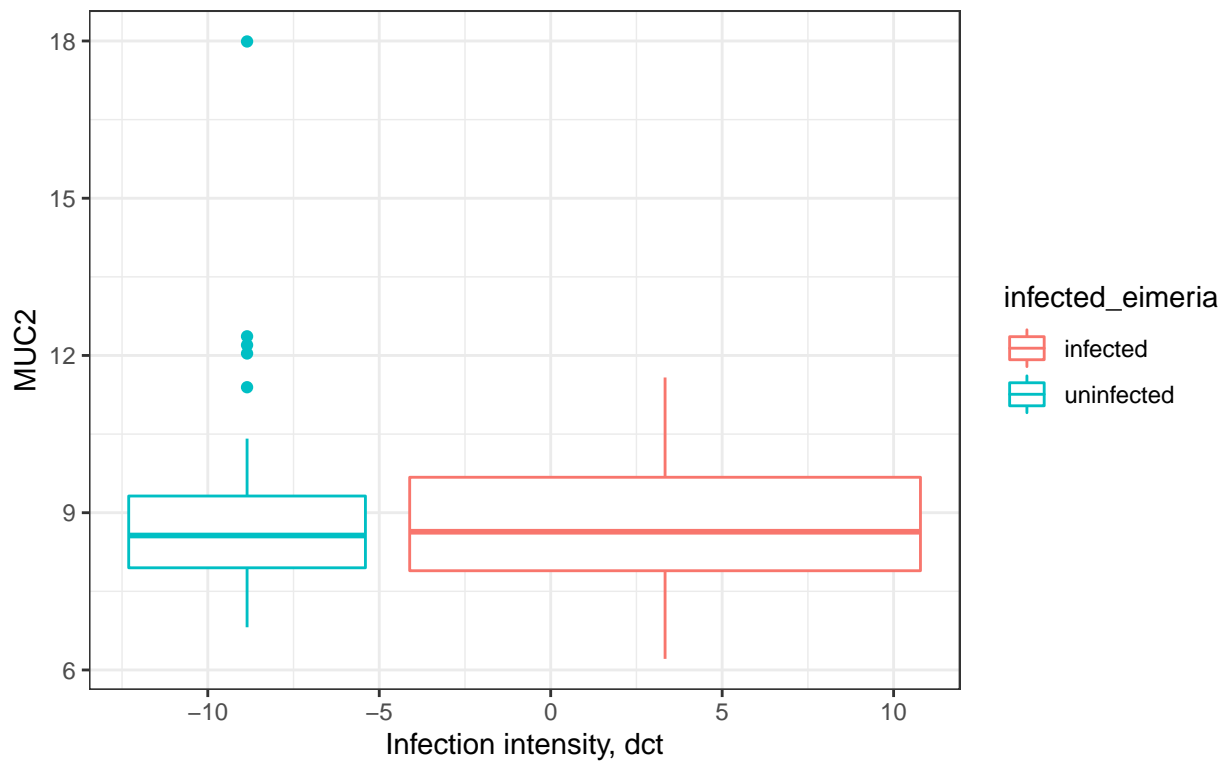
## Immune gene expression against infection intensity in field samples



```
ggplot(lab, aes(x = delta, y = MUC2, color = infected_eimeria)) +
  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).

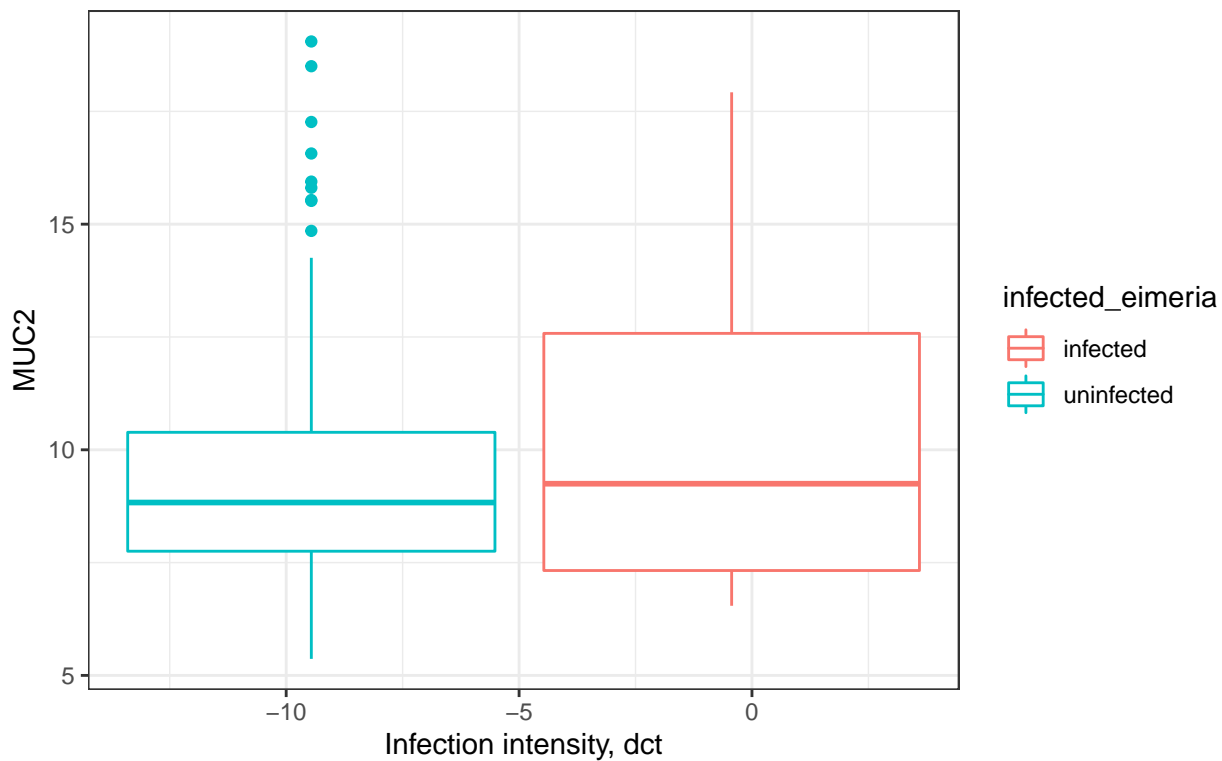
## Immune gene expression against infection intensity in lab infections



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

## Warning: Removed 154 rows containing missing values (stat\_boxplot).

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



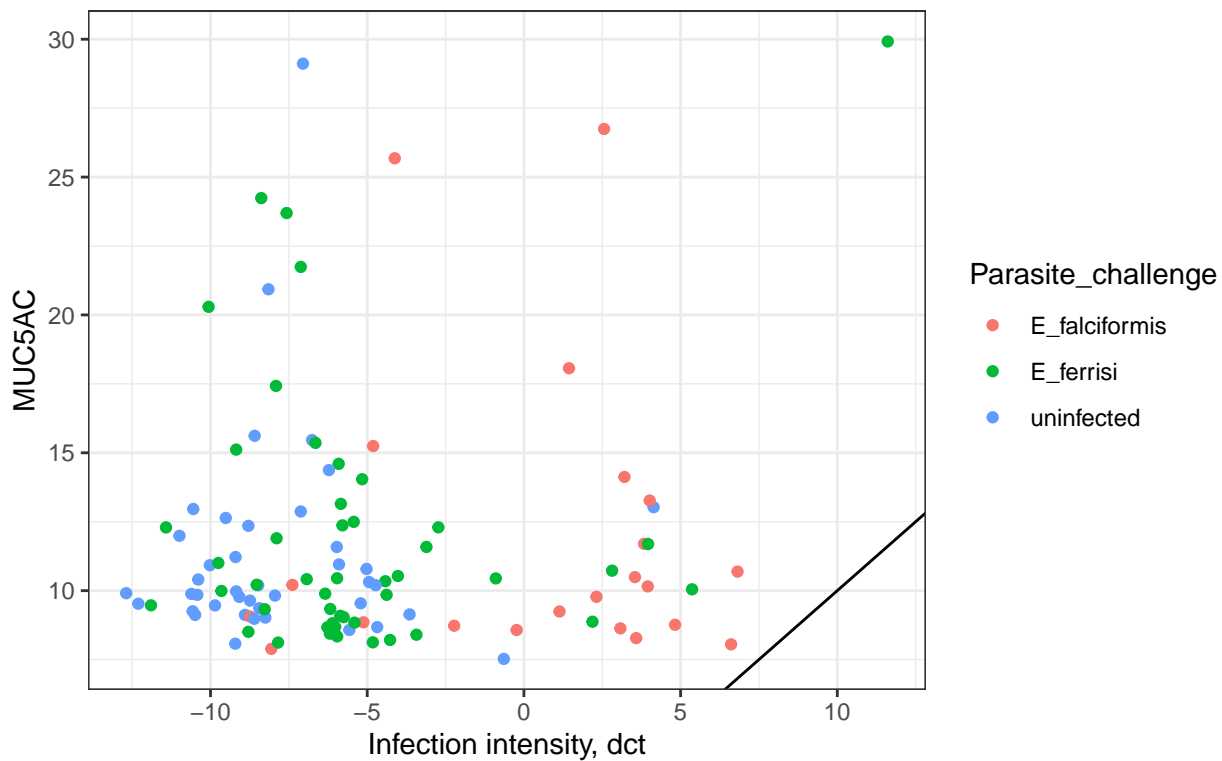
### 13. MUC5AC

```
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).



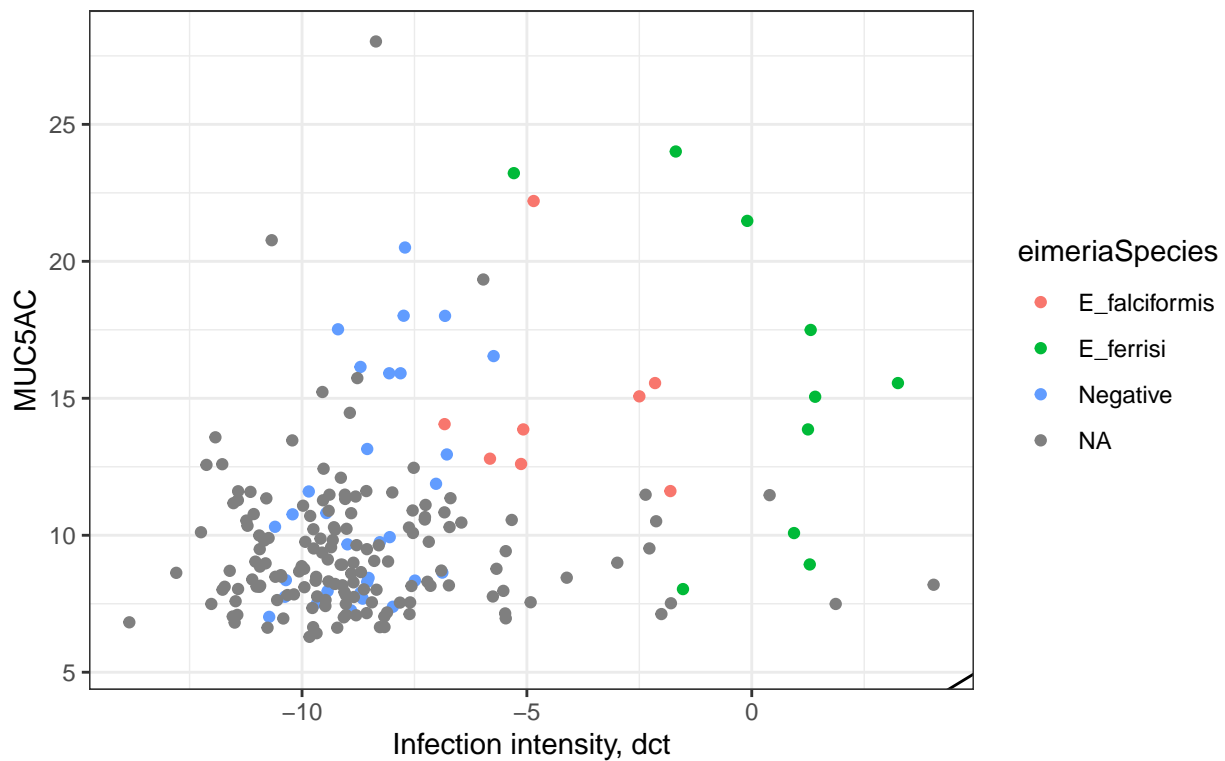
## Immune gene expression against infection intensity in lab infections



```
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 154 rows containing missing values (geom\_point).

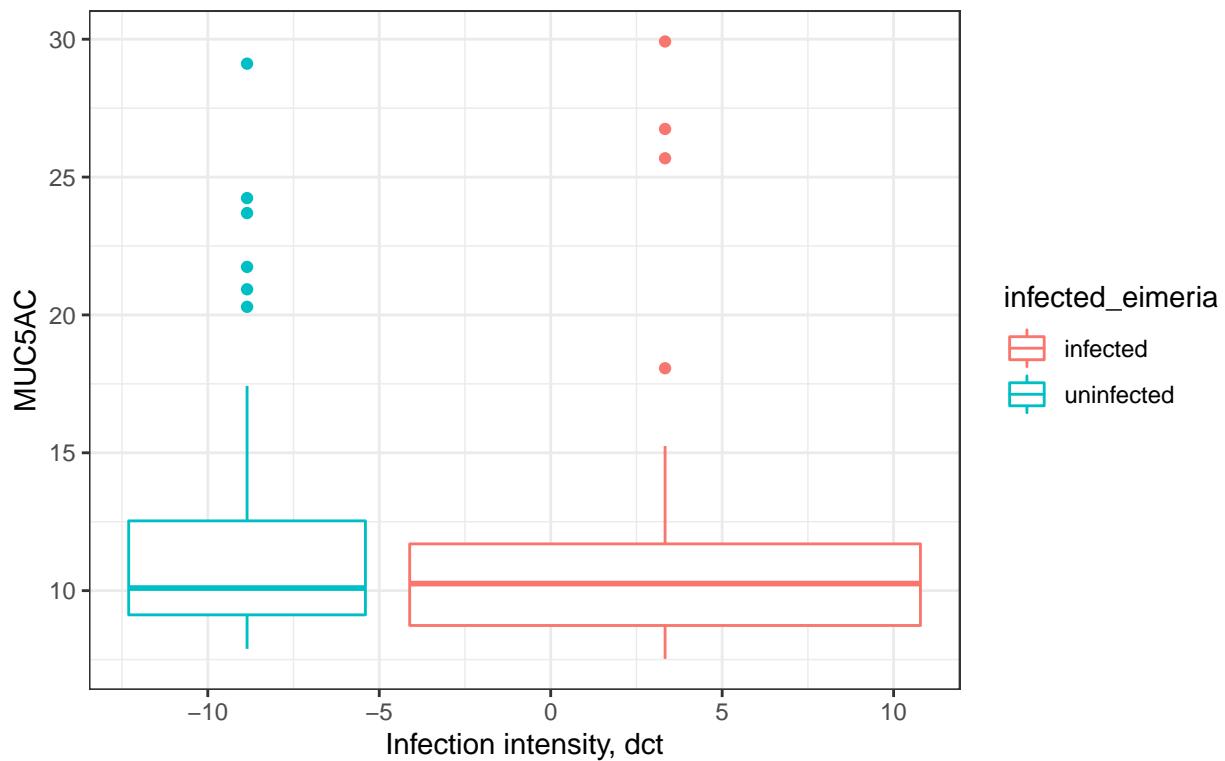
## Immune gene expression against infection intensity in field samples



```
ggplot(lab, aes(x = delta, y = MUC5AC, color = infected_eimeria)) +
  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).

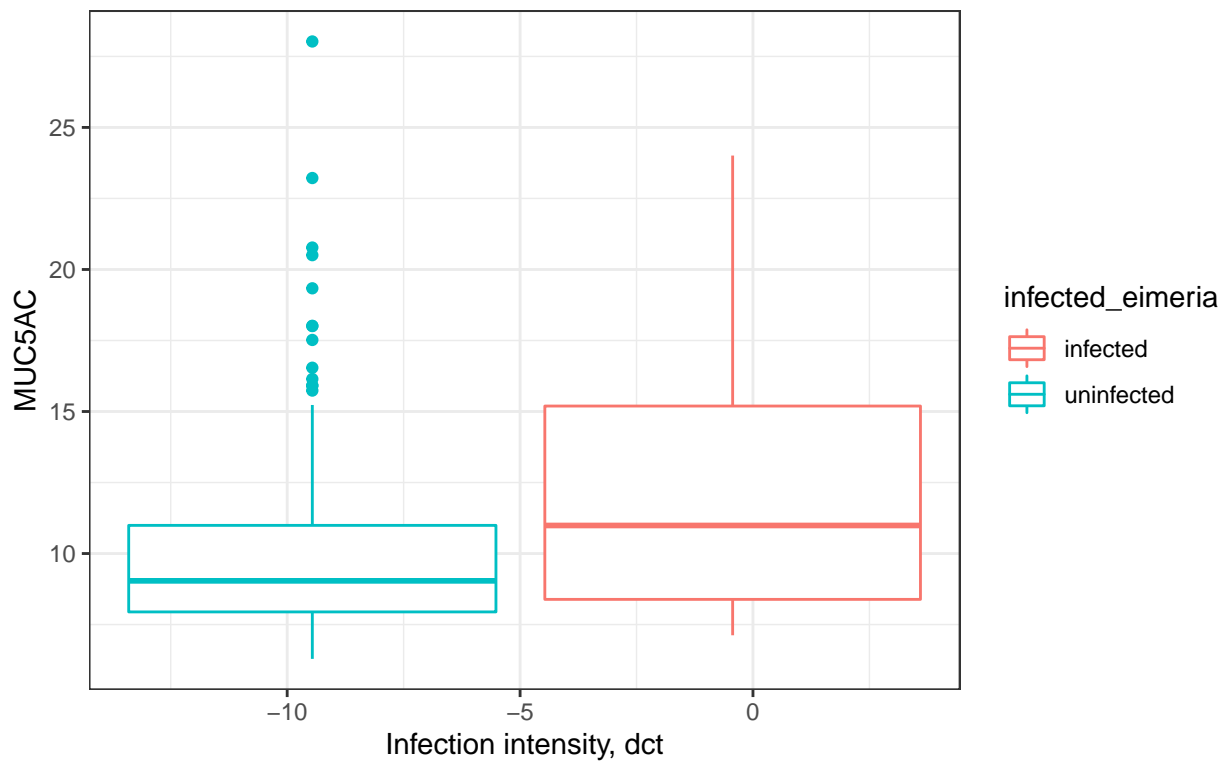
## Immune gene expression against infection intensity in lab infections



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

## Warning: Removed 154 rows containing missing values (stat\_boxplot).

## Immune gene expression against infection intensity in field samples

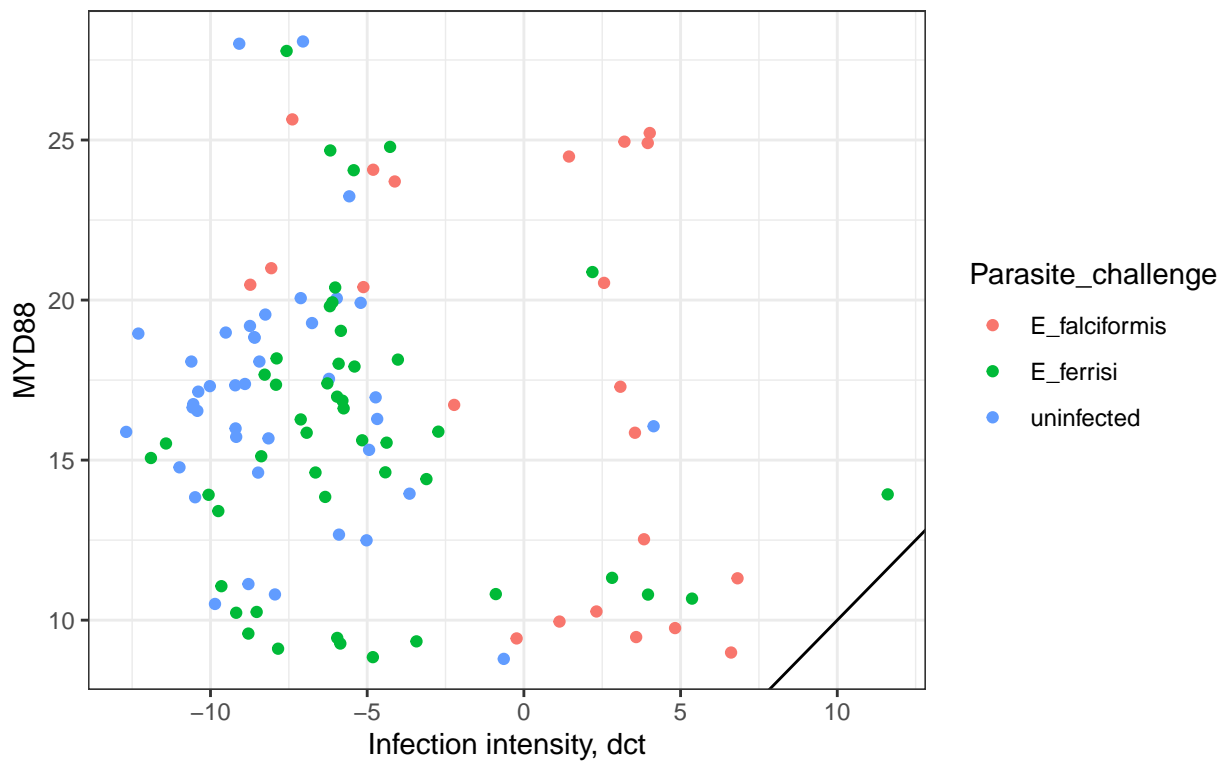


### 14. MYD88

```
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).

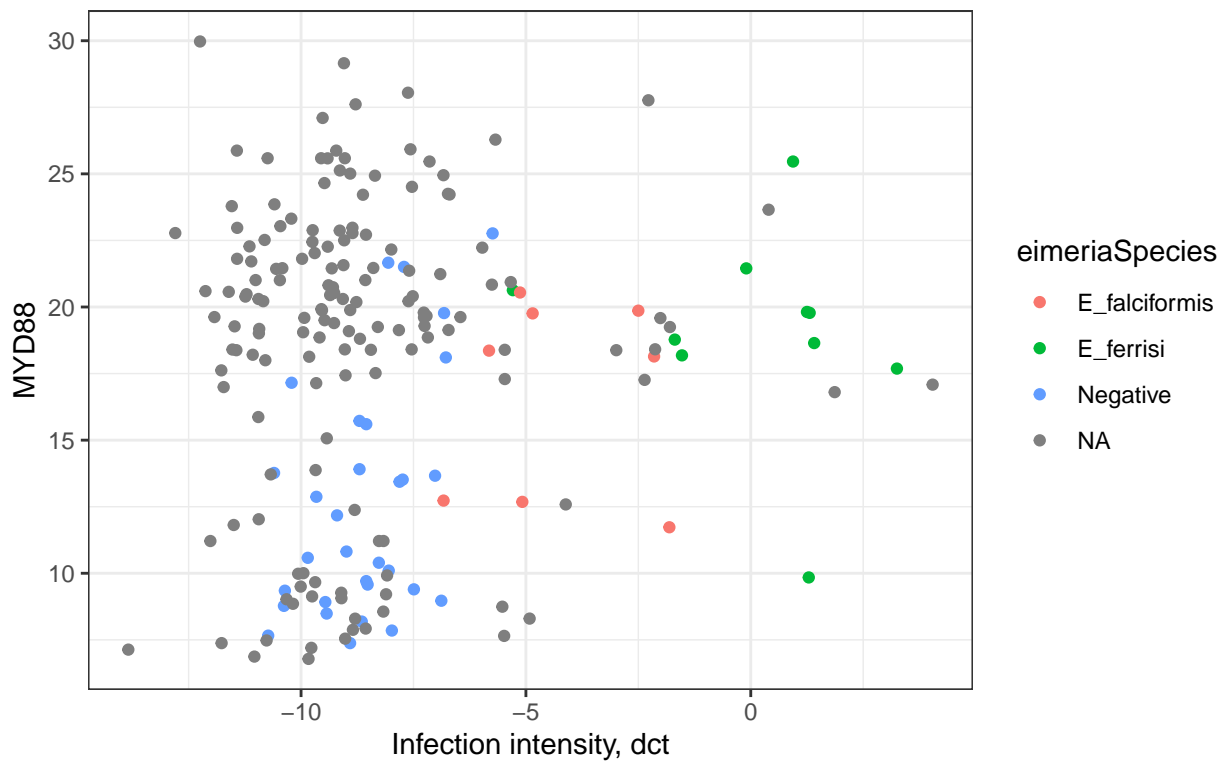
## Immune gene expression against infection intensity in lab infections



```
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 154 rows containing missing values (geom\_point).

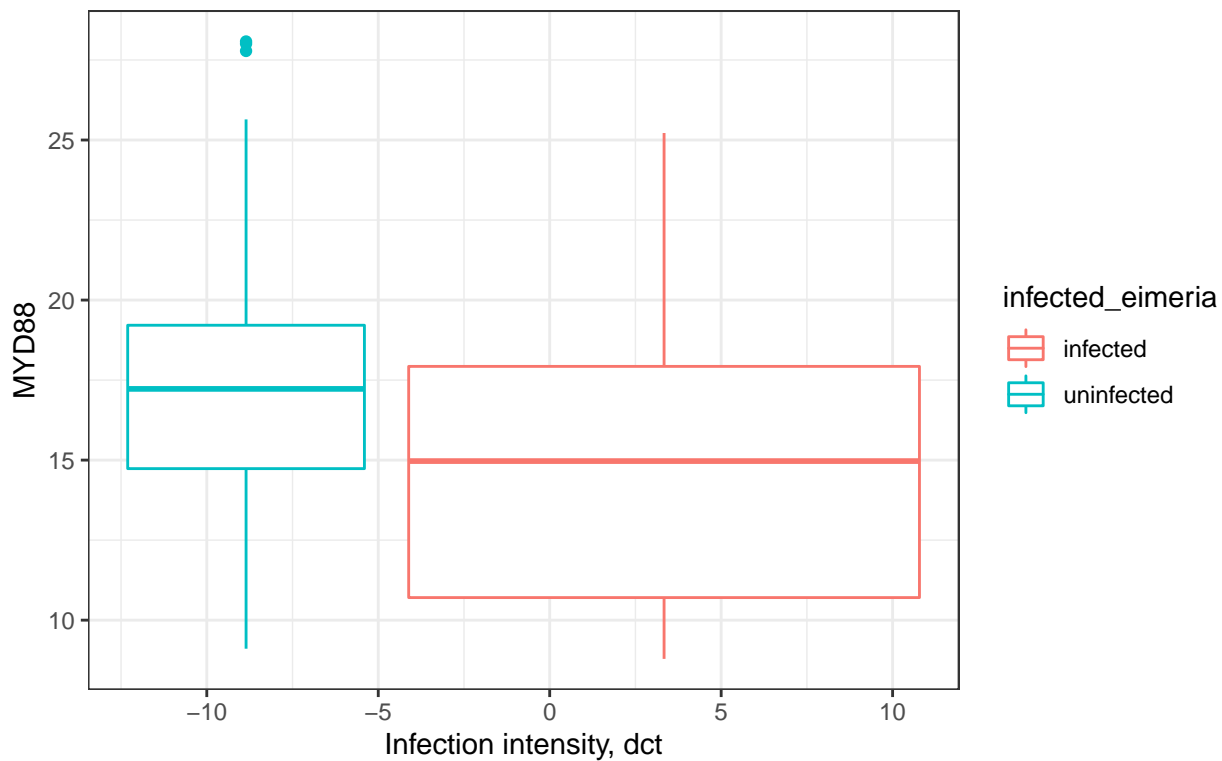
## Immune gene expression against infection intensity in field samples



```
ggplot(lab, aes(x = delta, y = MYD88, color = infected_eimeria)) +
  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).
```

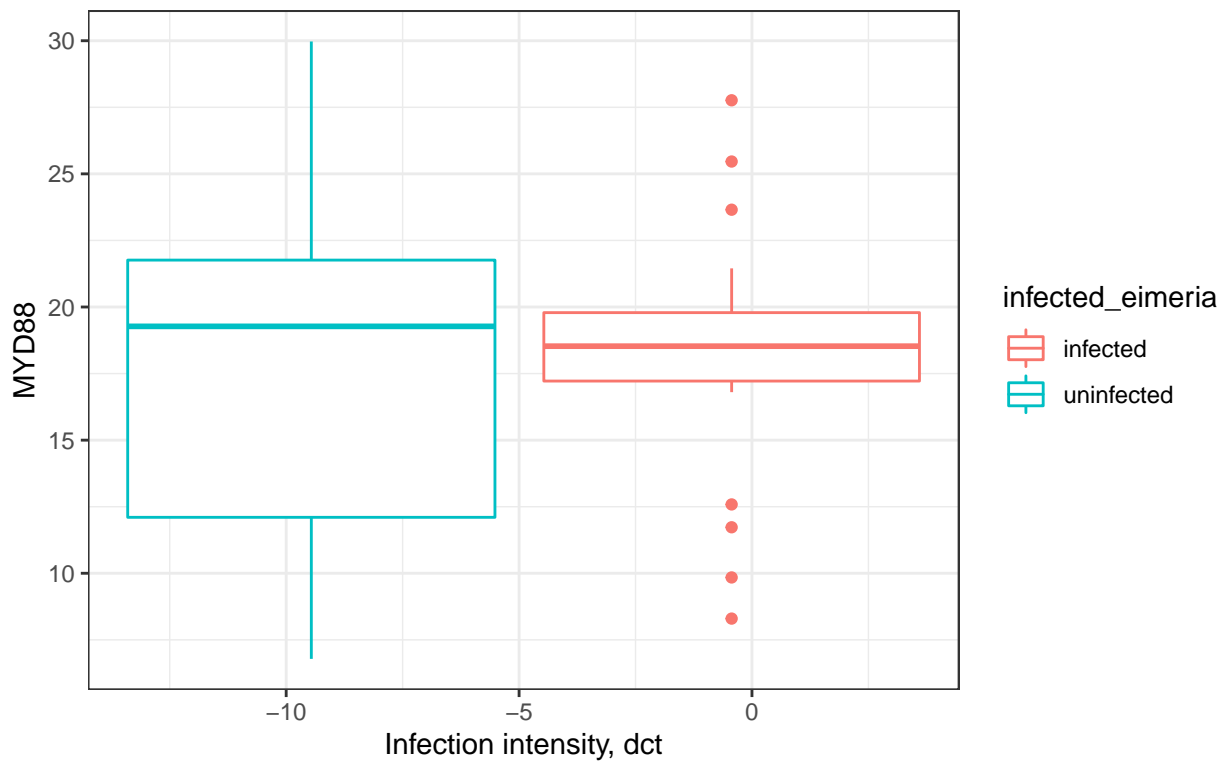
## Immune gene expression against infection intensity in lab infections



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

## Warning: Removed 154 rows containing missing values (stat\_boxplot).

## Immune gene expression against infection intensity in field samples



## 15.

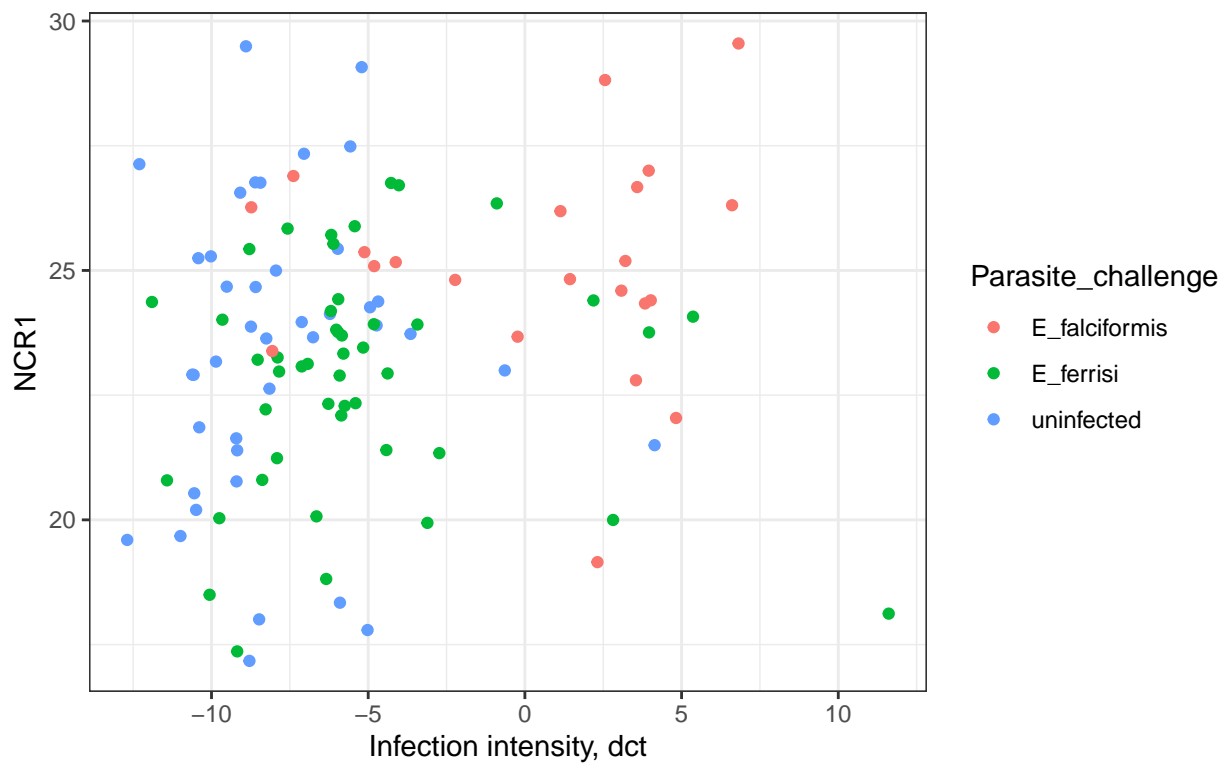
NCR1

```
ggplot(lab, aes(x = delta, y = NCR1, 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).



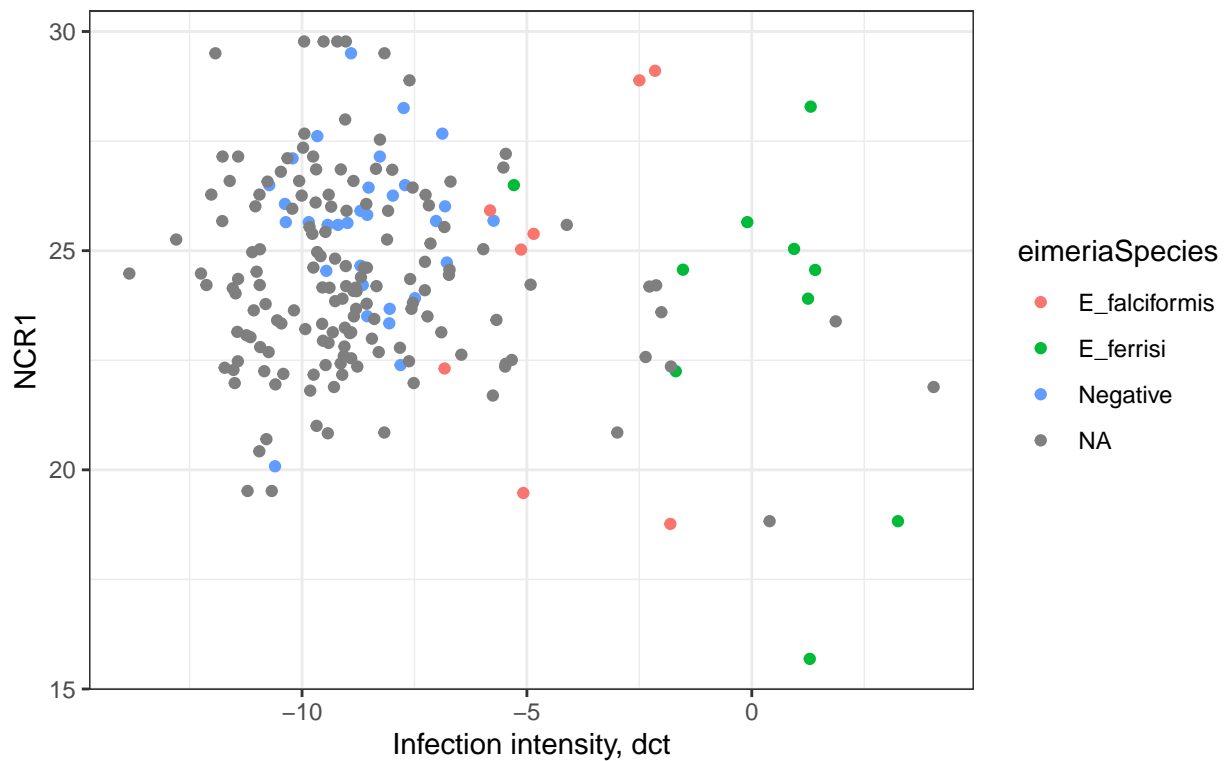
## Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = 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 154 rows containing missing values (geom\_point).

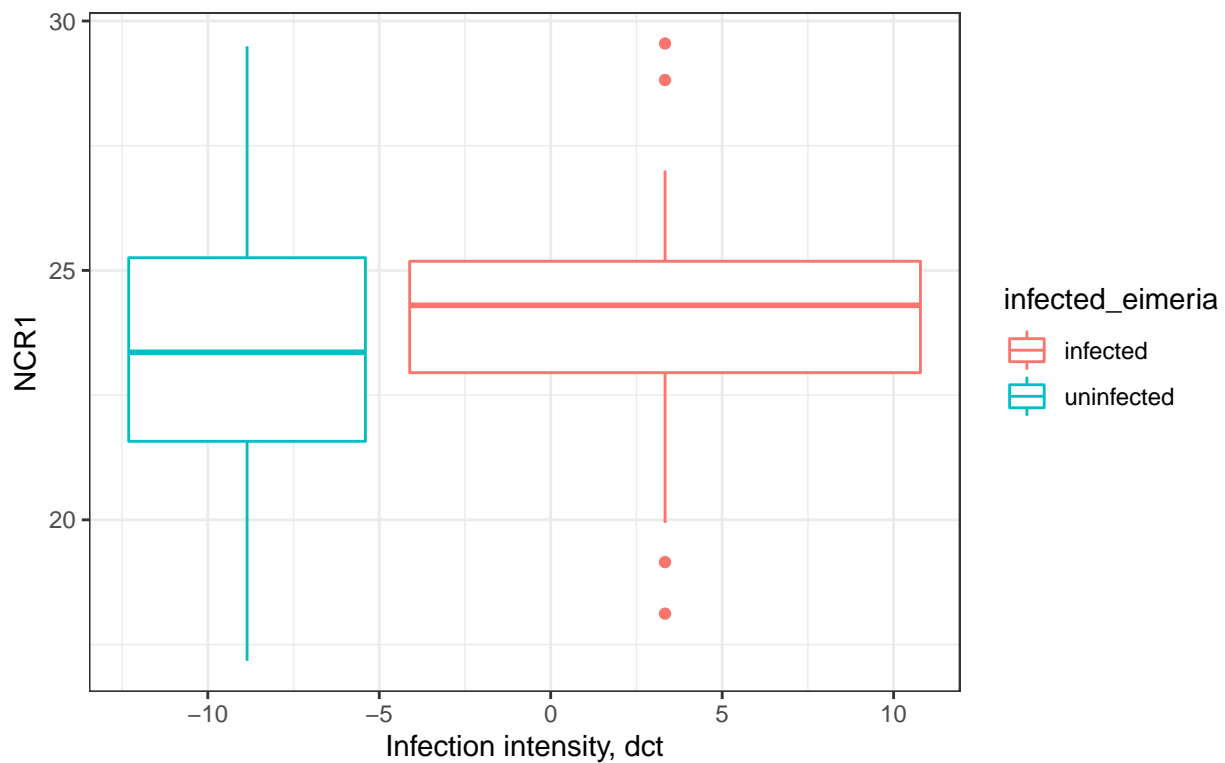
## Immune gene expression against infection intensity in field samples



```
ggplot(lab, aes(x = delta, y = NCR1, color = infected_eimeria)) +
  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).

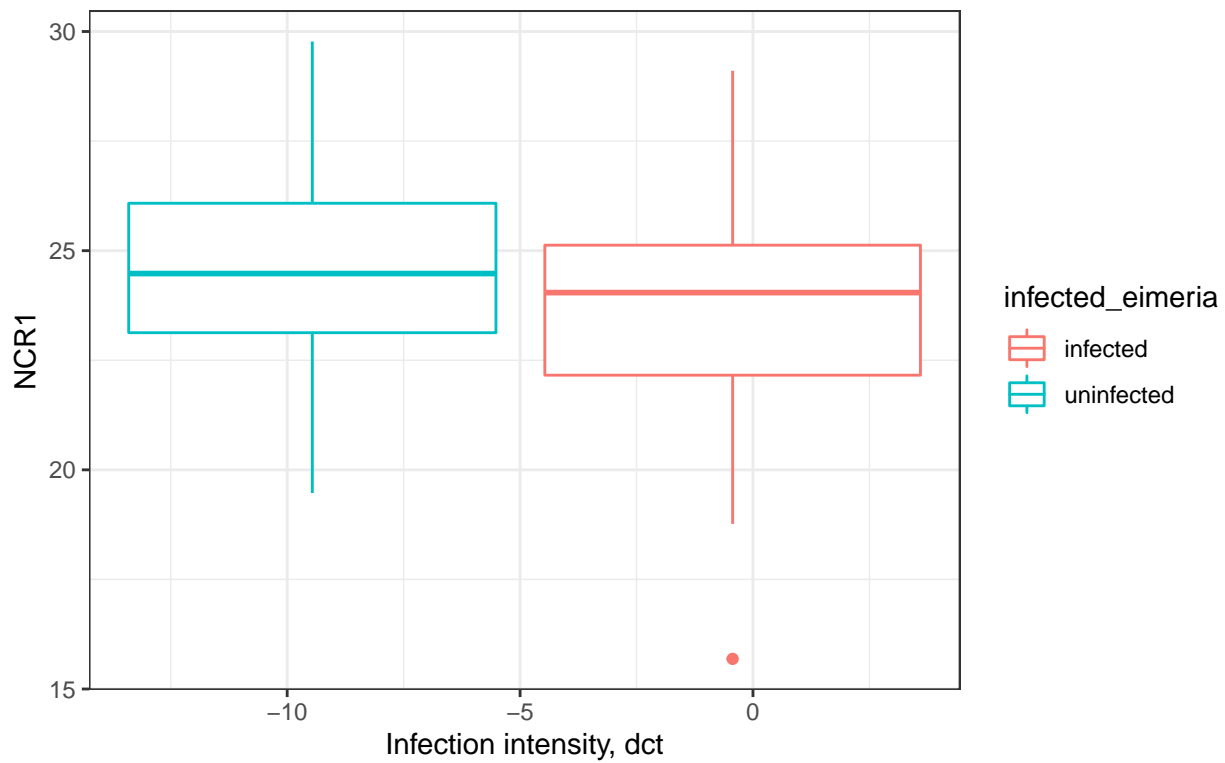
## Immune gene expression against infection intensity in lab infections



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

## Warning: Removed 154 rows containing missing values (stat\_boxplot).

## Immune gene expression against infection intensity in field samples

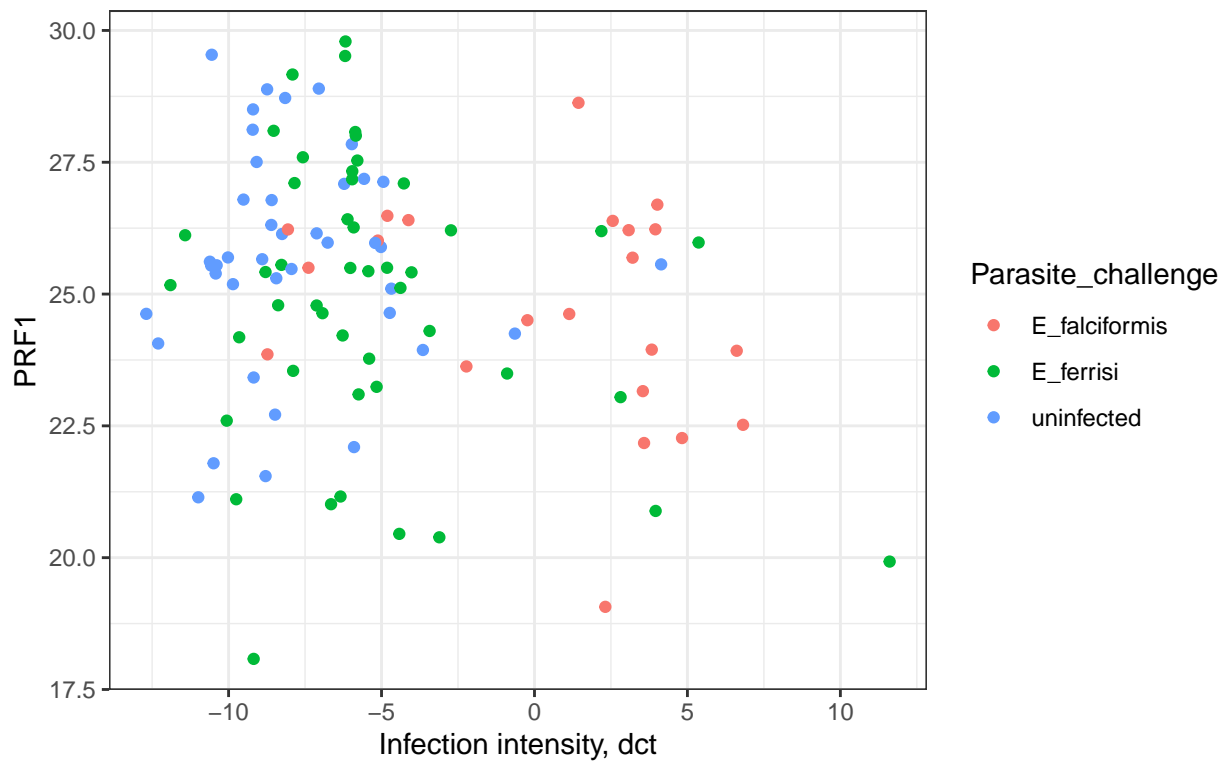


### 16. PRF1

```
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).

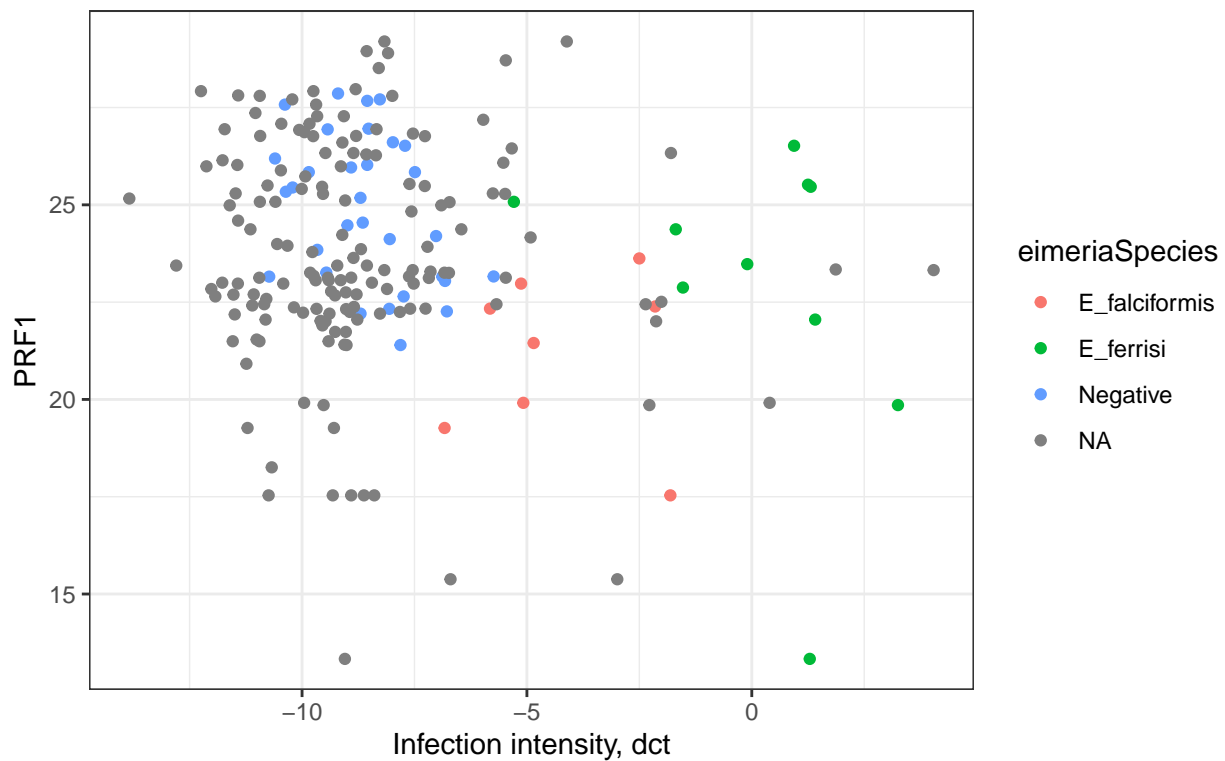
## Immune gene expression against infection intensity in lab infections



```
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 154 rows containing missing values (geom\_point).

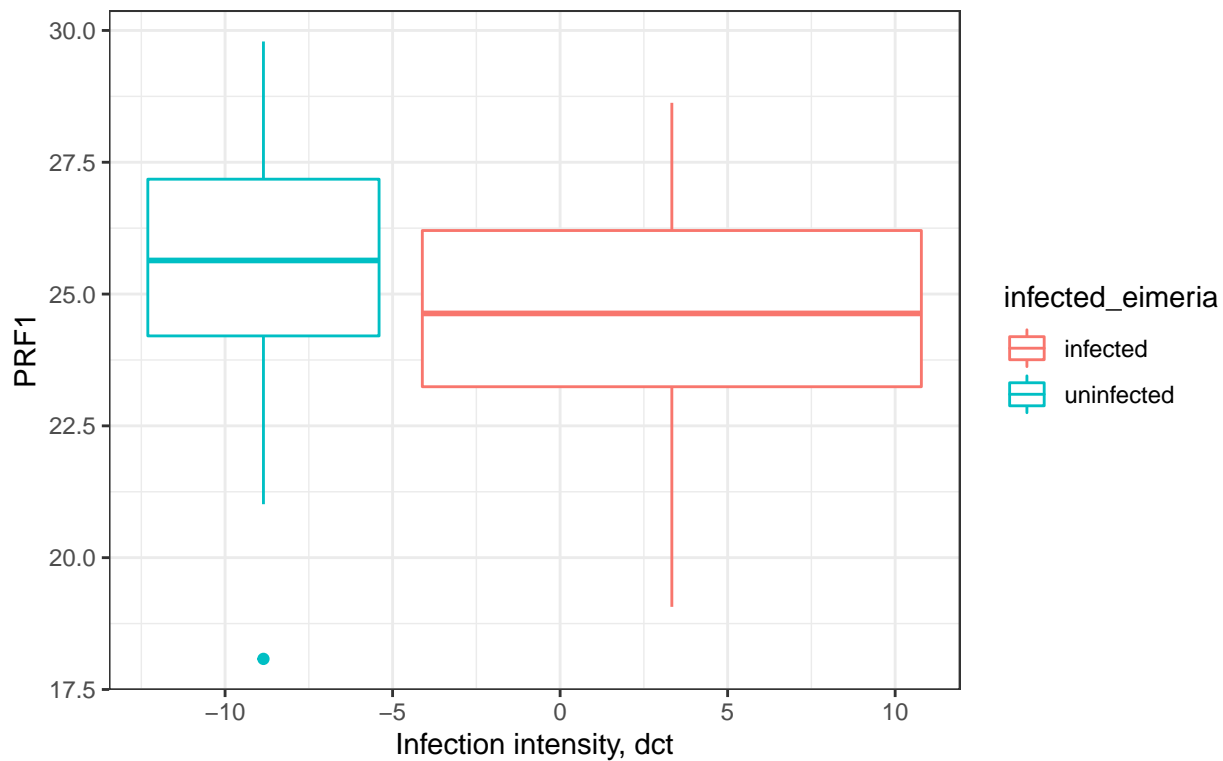
## Immune gene expression against infection intensity in field samples



```
ggplot(lab, aes(x = delta, y = PRF1, color = infected_eimeria)) +
  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).

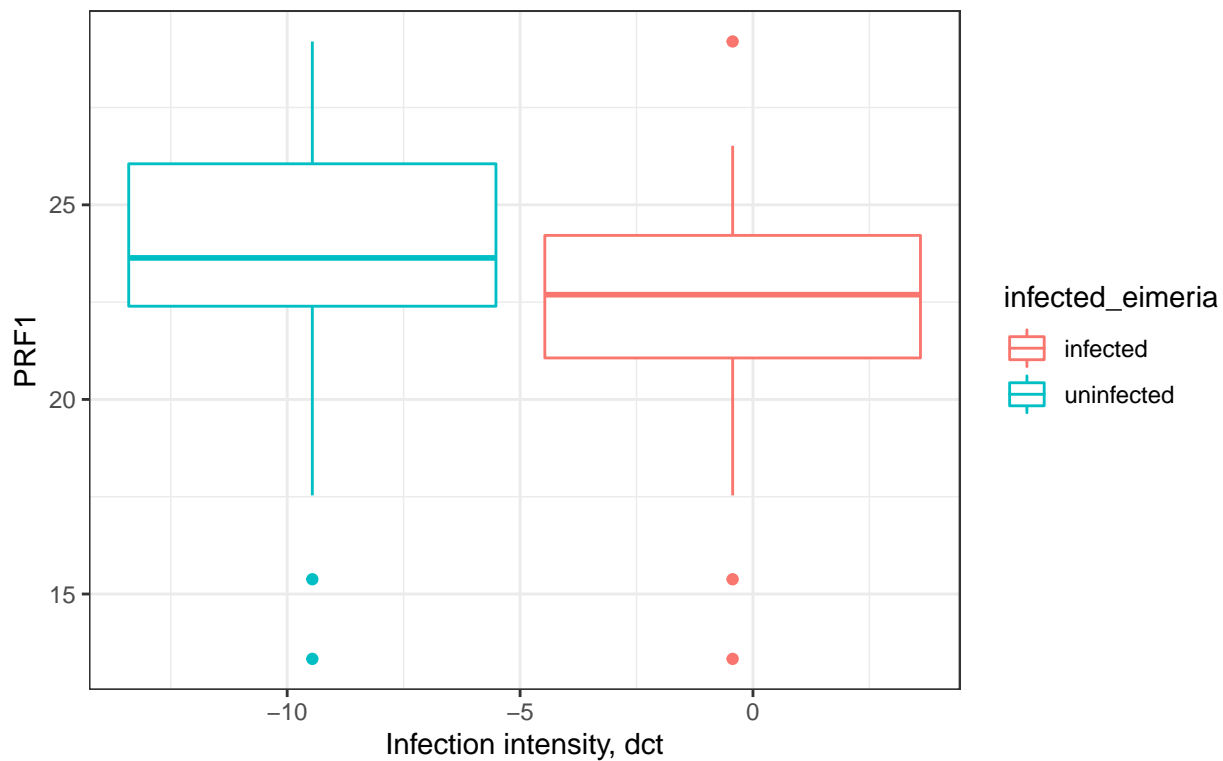
## Immune gene expression against infection intensity in lab infections



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

## Warning: Removed 154 rows containing missing values (stat\_boxplot).

## Immune gene expression against infection intensity in field samples



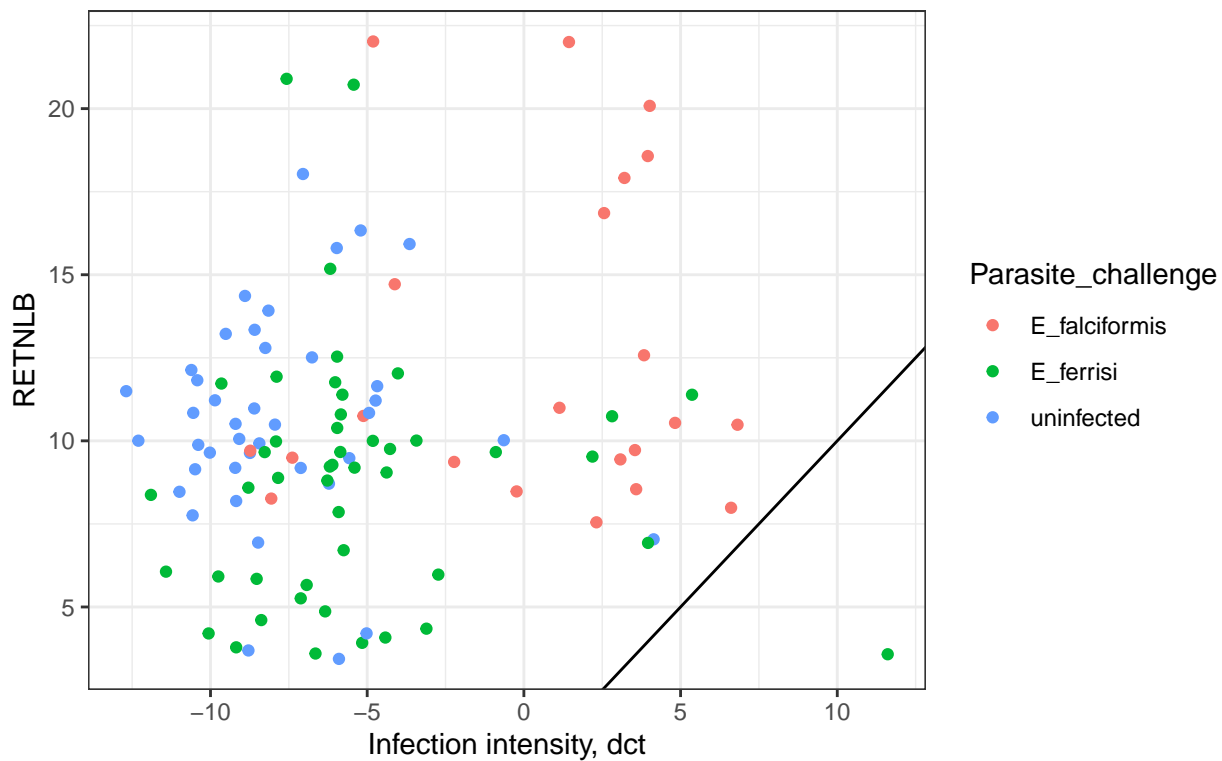
### 17. RETNLB

```
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).



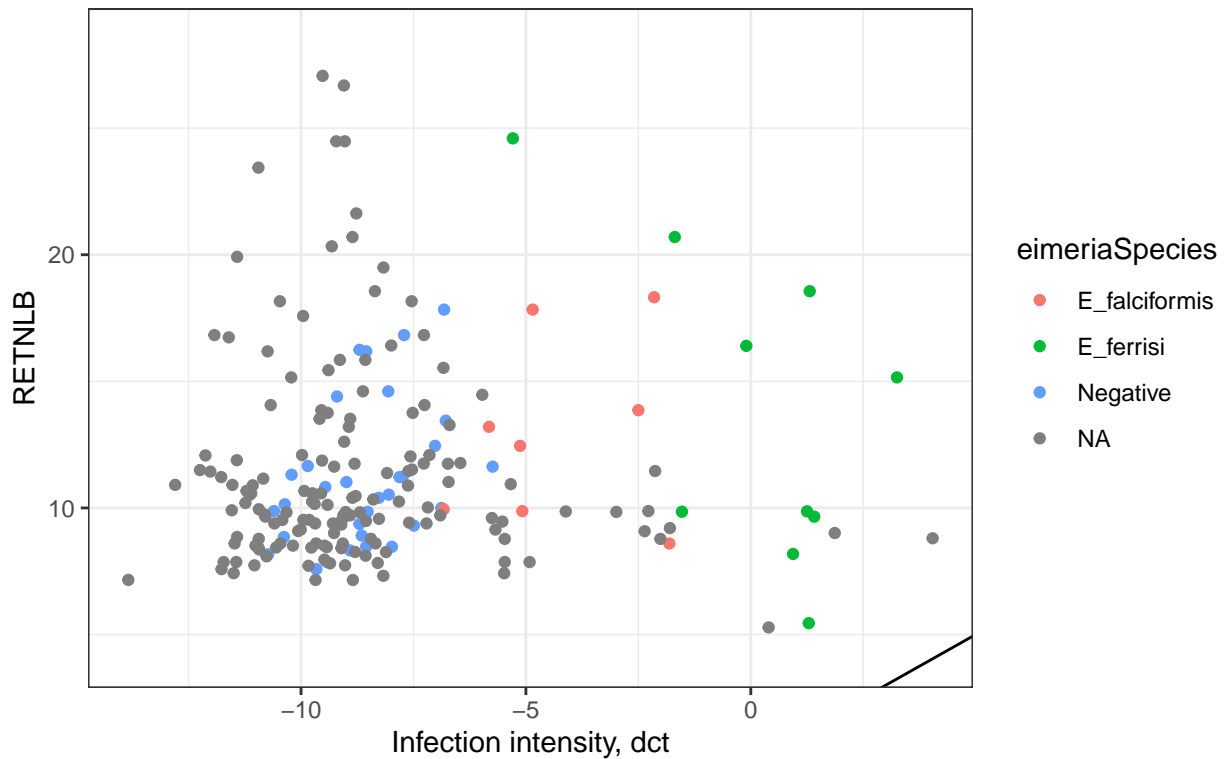
## Immune gene expression against infection intensity in lab infections



```
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 154 rows containing missing values (geom\_point).

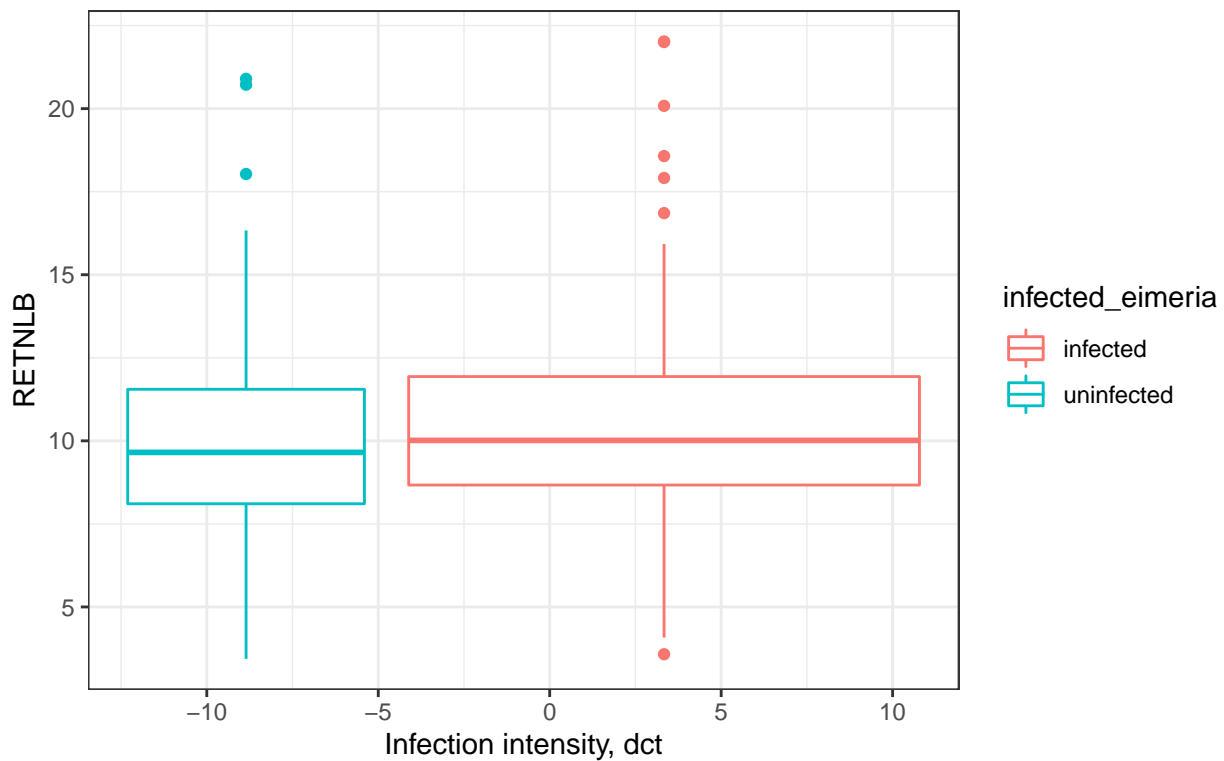
## Immune gene expression against infection intensity in field samples



```
ggplot(lab, aes(x = delta, y = RETNLB, color = infected_eimeria)) +
  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).

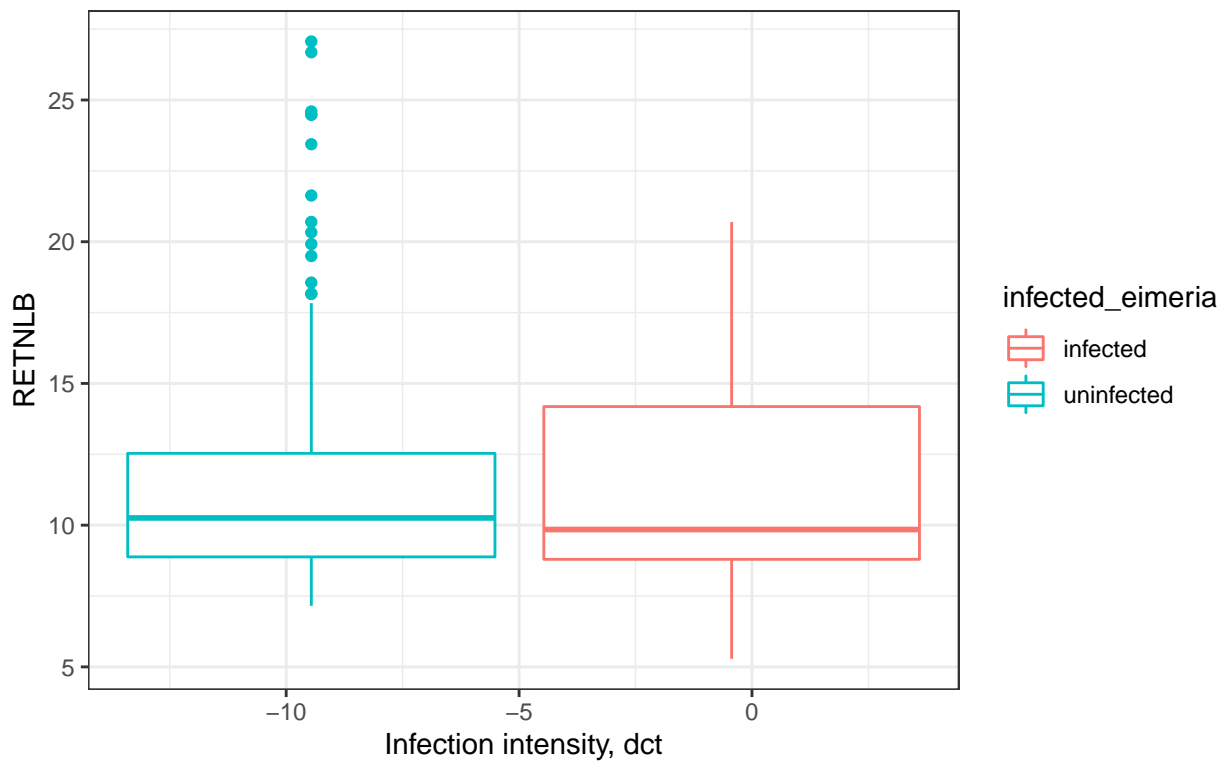
## Immune gene expression against infection intensity in lab infections



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

## Warning: Removed 154 rows containing missing values (stat\_boxplot).

## Immune gene expression against infection intensity in field samples

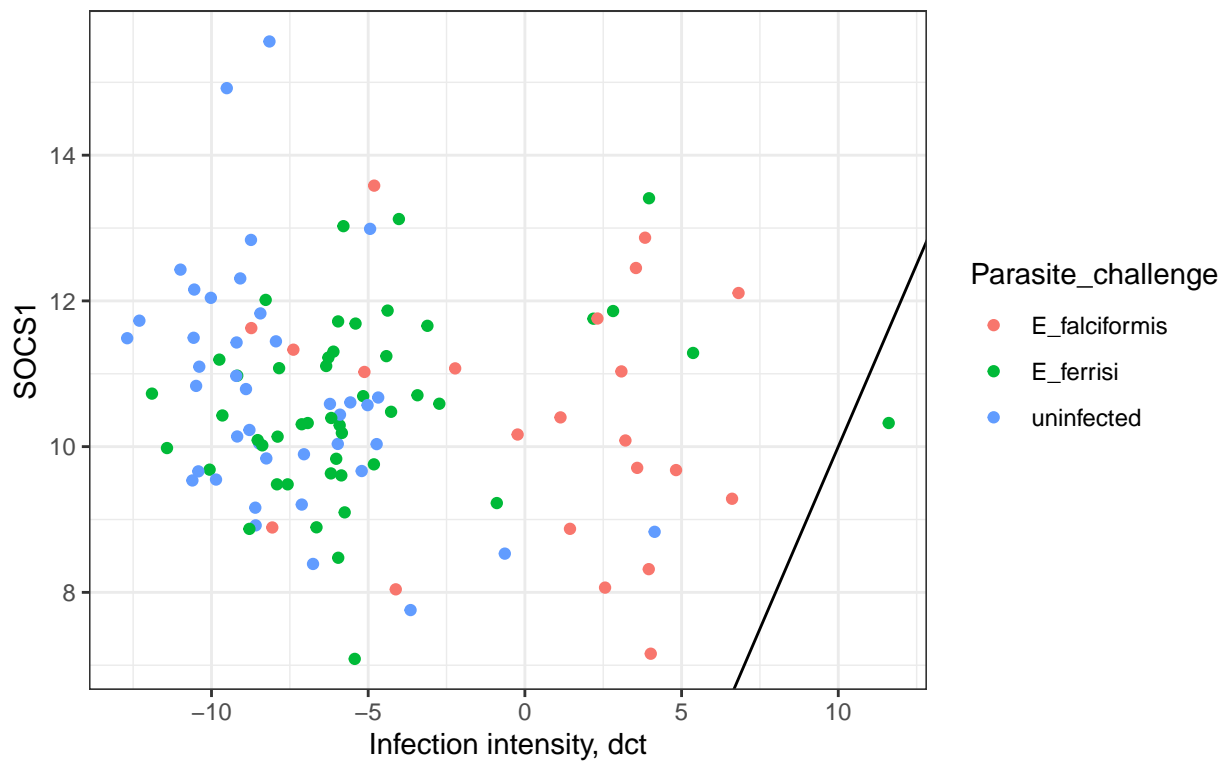


### 18. SOCS1

```
ggplot(lab, aes(x = delta, y = SOCS1, 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).

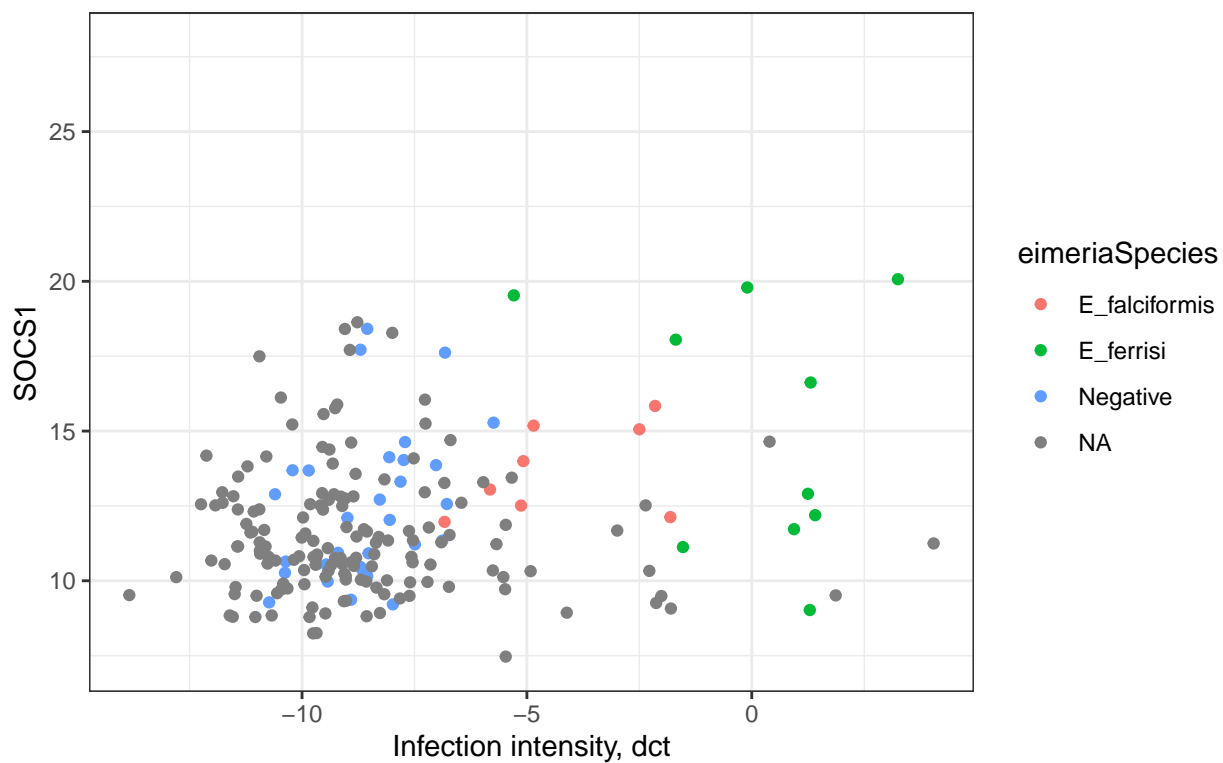
## Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = 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 154 rows containing missing values (geom\_point).

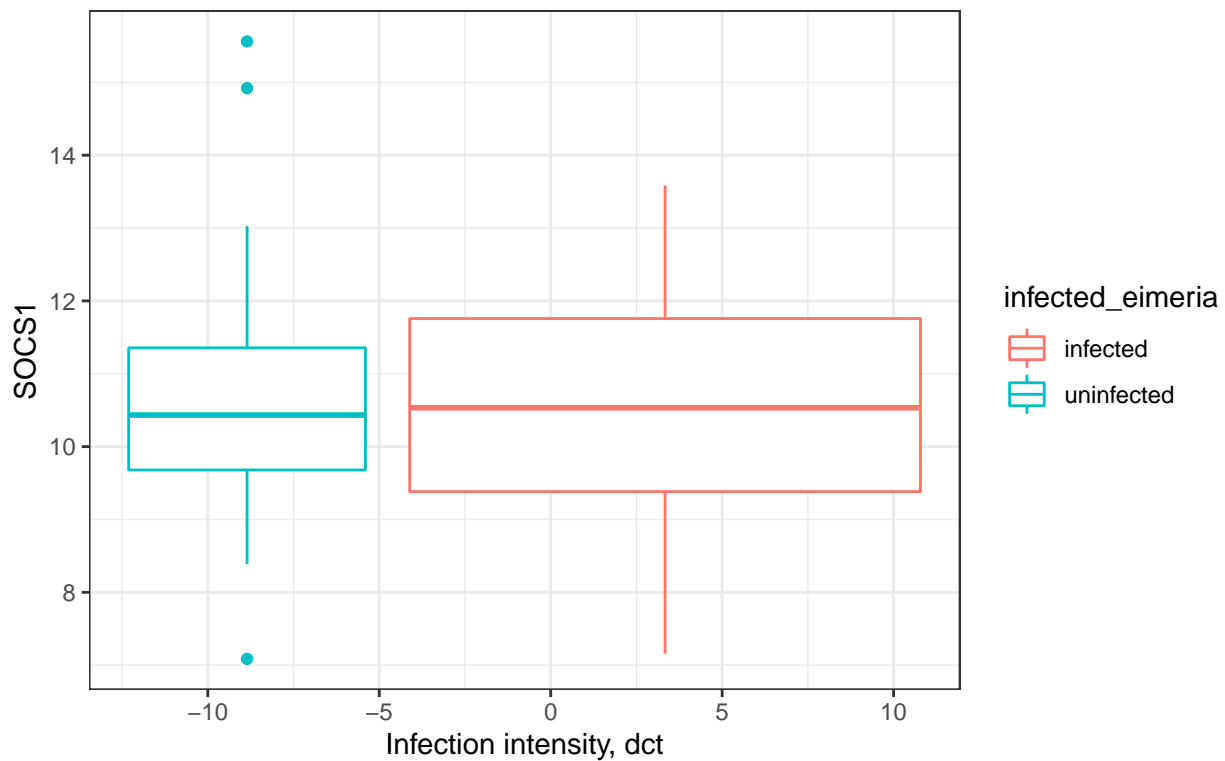
## Immune gene expression against infection intensity in field samples



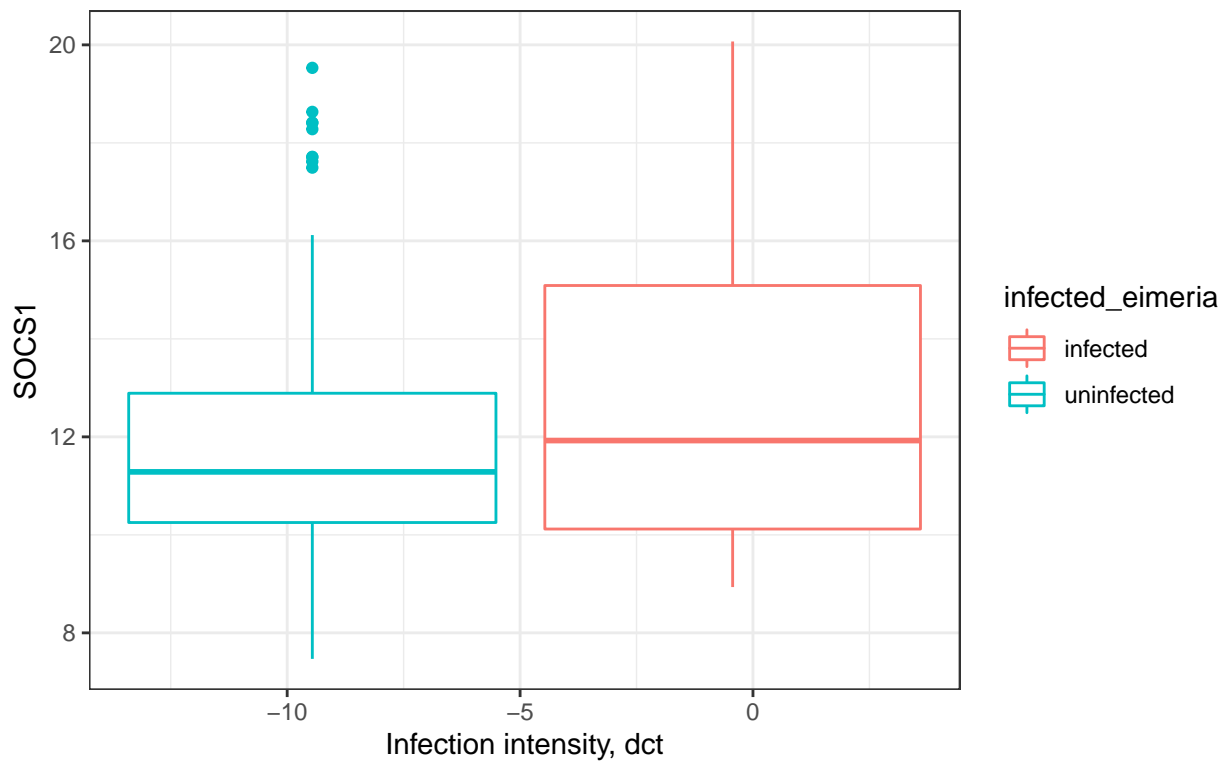
```
ggplot(lab, aes(x = delta, y = SOCS1, color = infected_eimeria)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in lab
infections") +
  theme_bw()
```

## 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



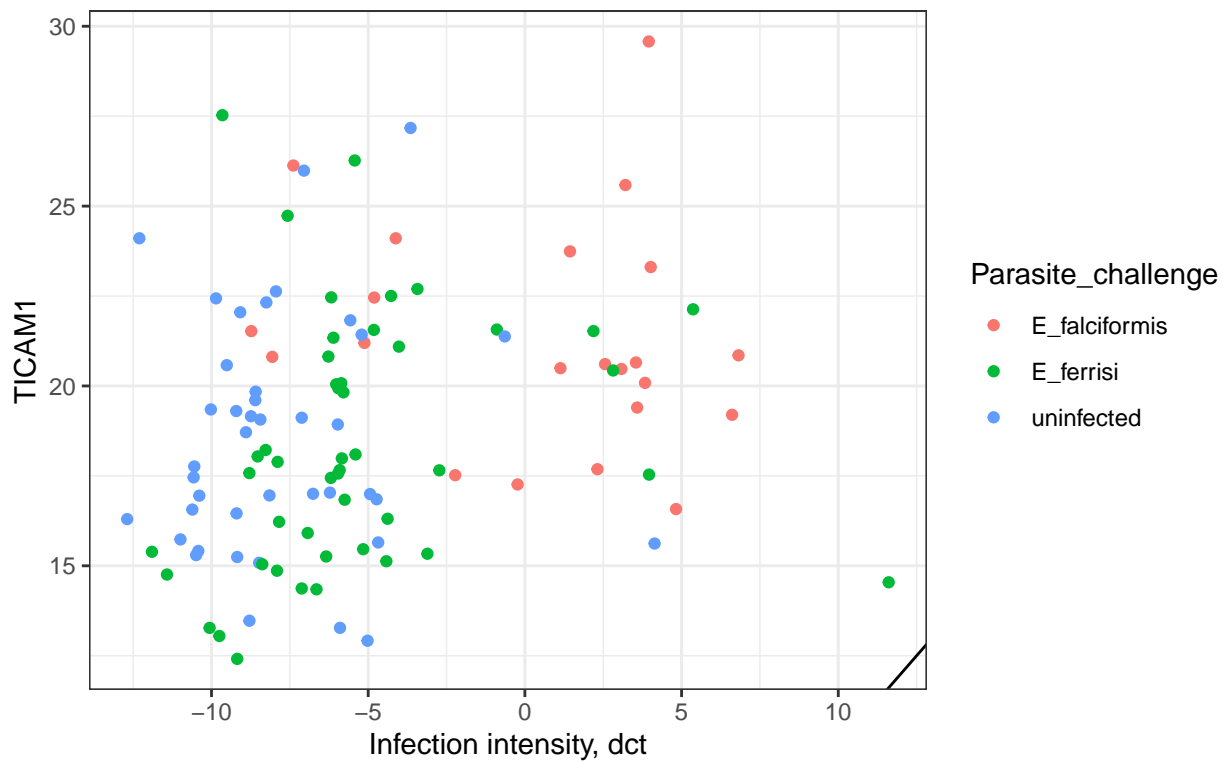
### 19. TICAM1

```
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).



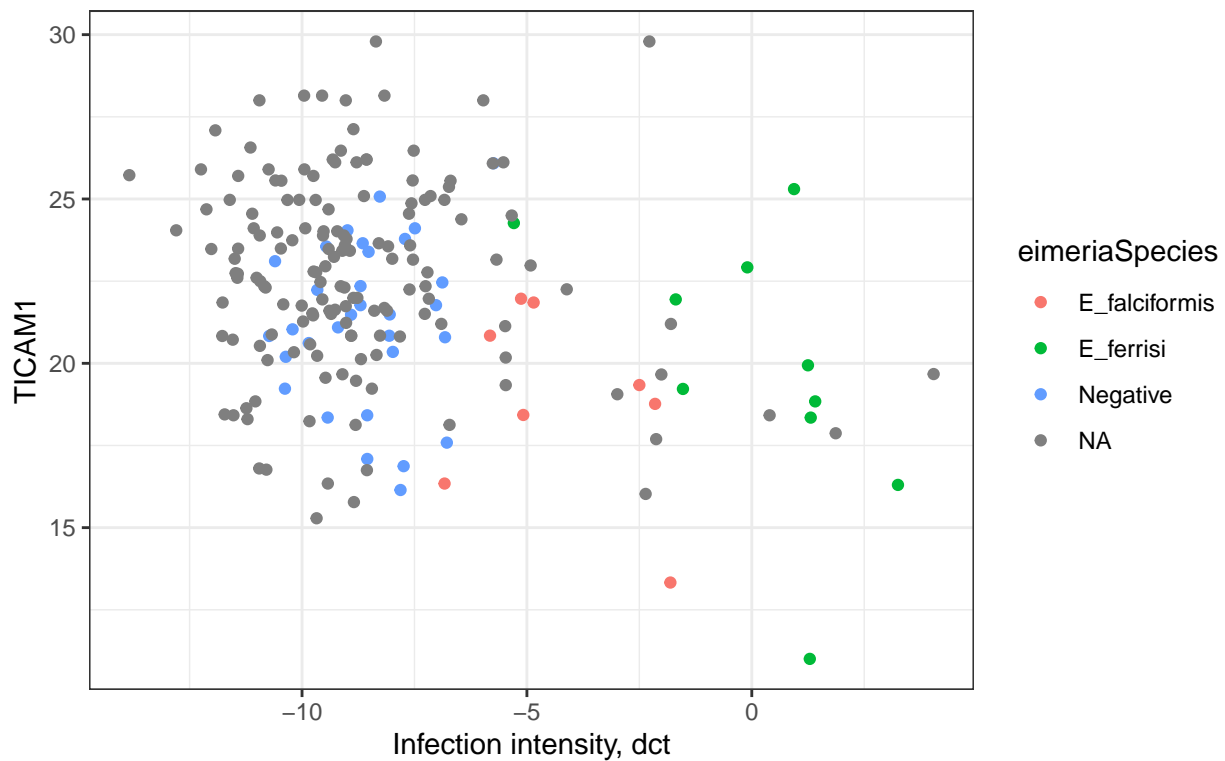
## Immune gene expression against infection intensity in lab infections



```
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 154 rows containing missing values (geom\_point).

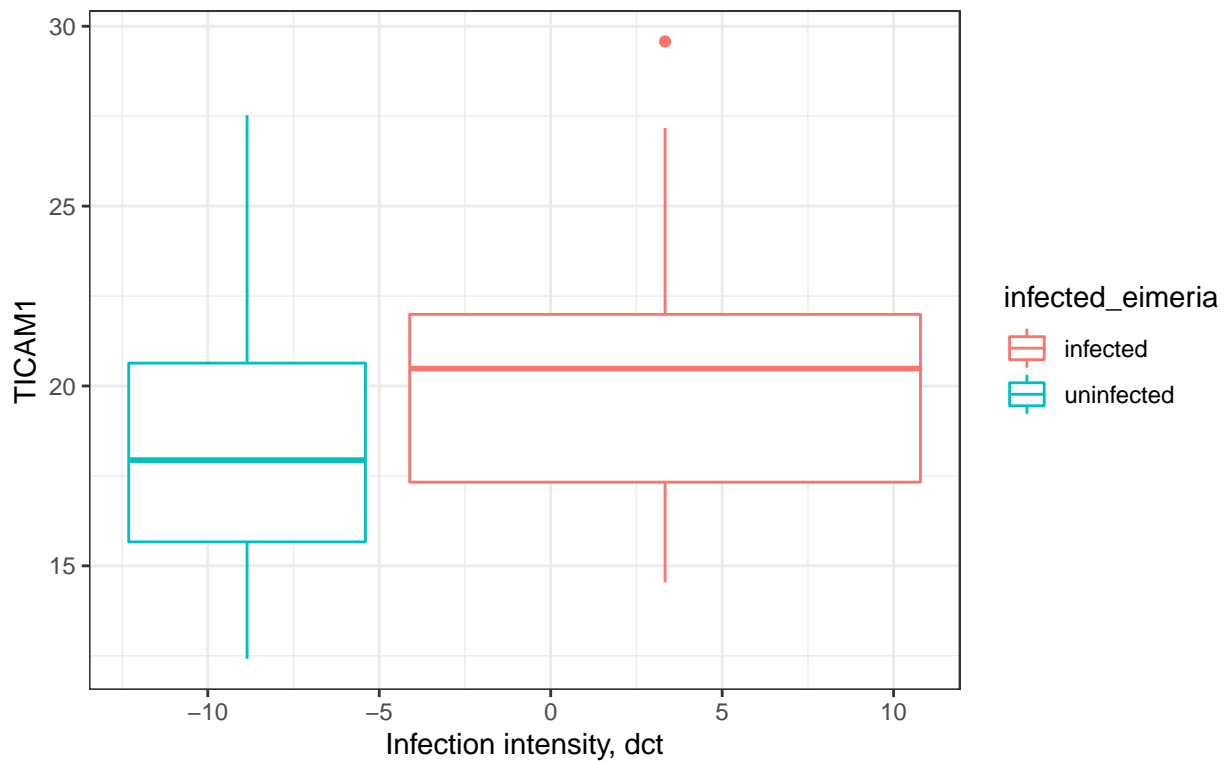
## Immune gene expression against infection intensity in field samples



```
ggplot(lab, aes(x = delta, y = TICAM1, color = infected_eimeria)) +
  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).

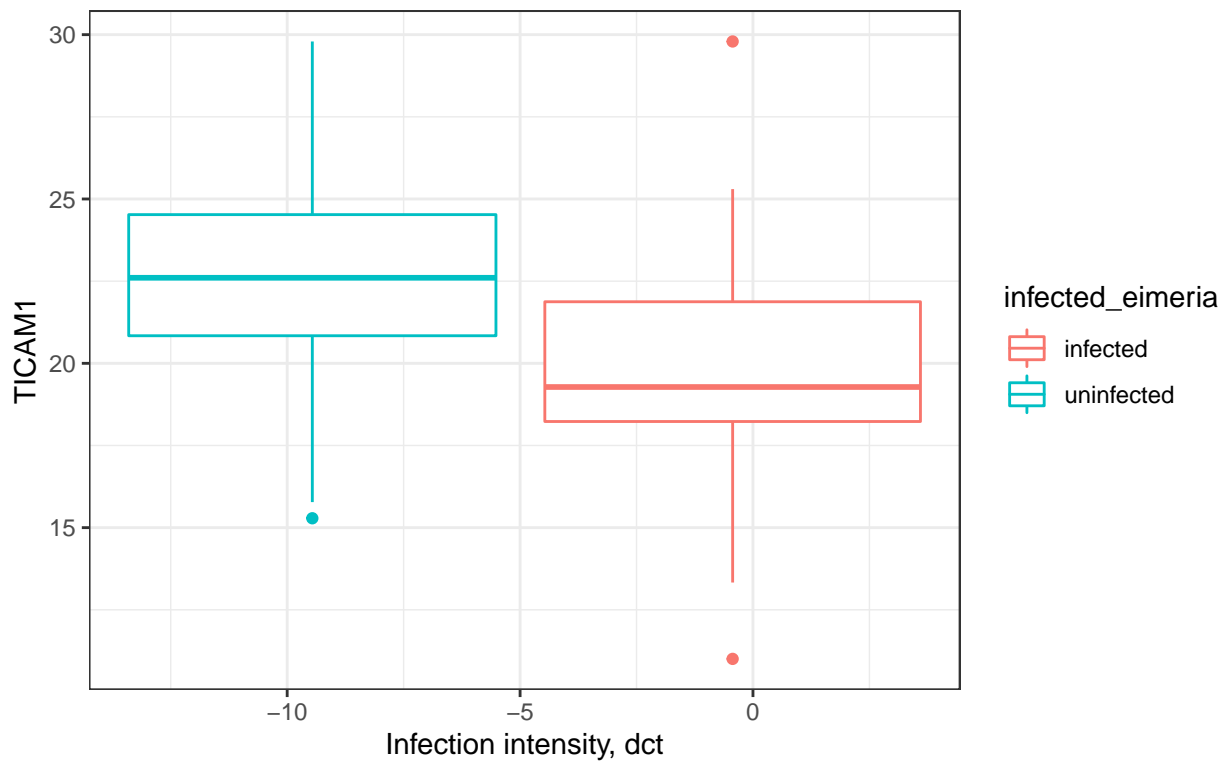
## Immune gene expression against infection intensity in lab infections



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

## Warning: Removed 154 rows containing missing values (stat\_boxplot).

## Immune gene expression against infection intensity in field samples

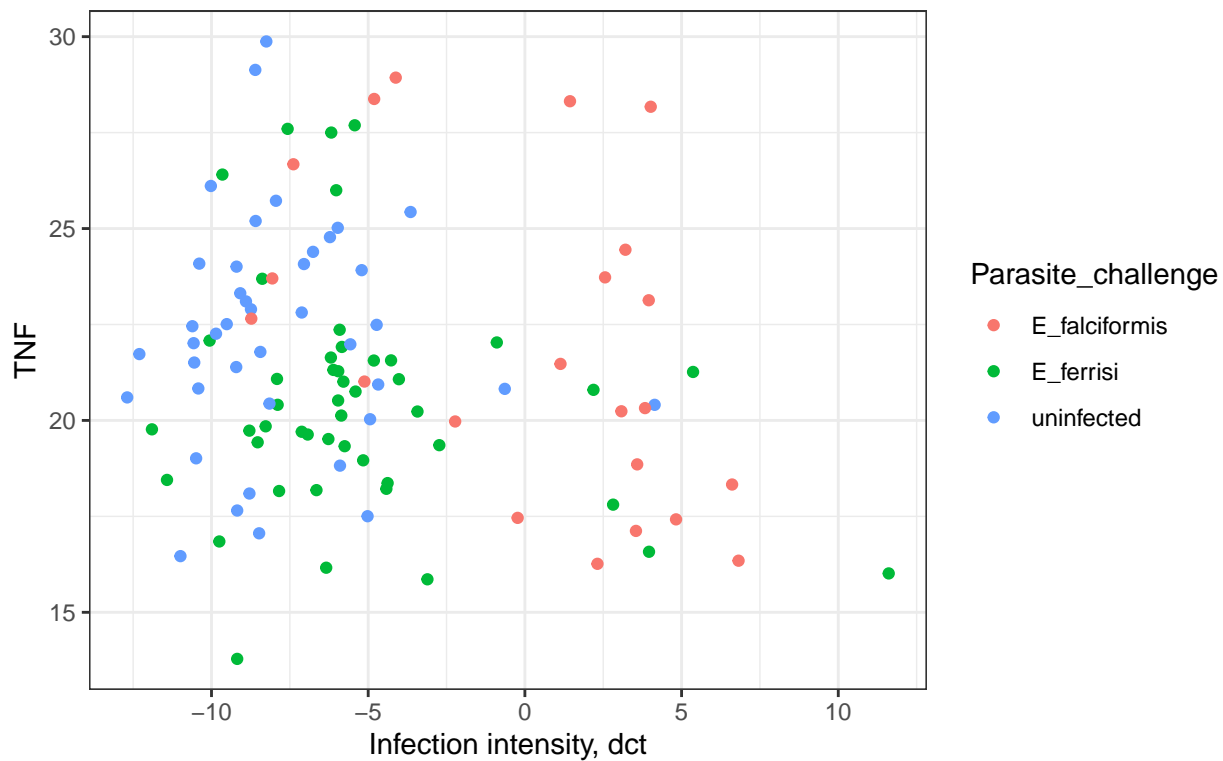


## 20. TNF

```
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).

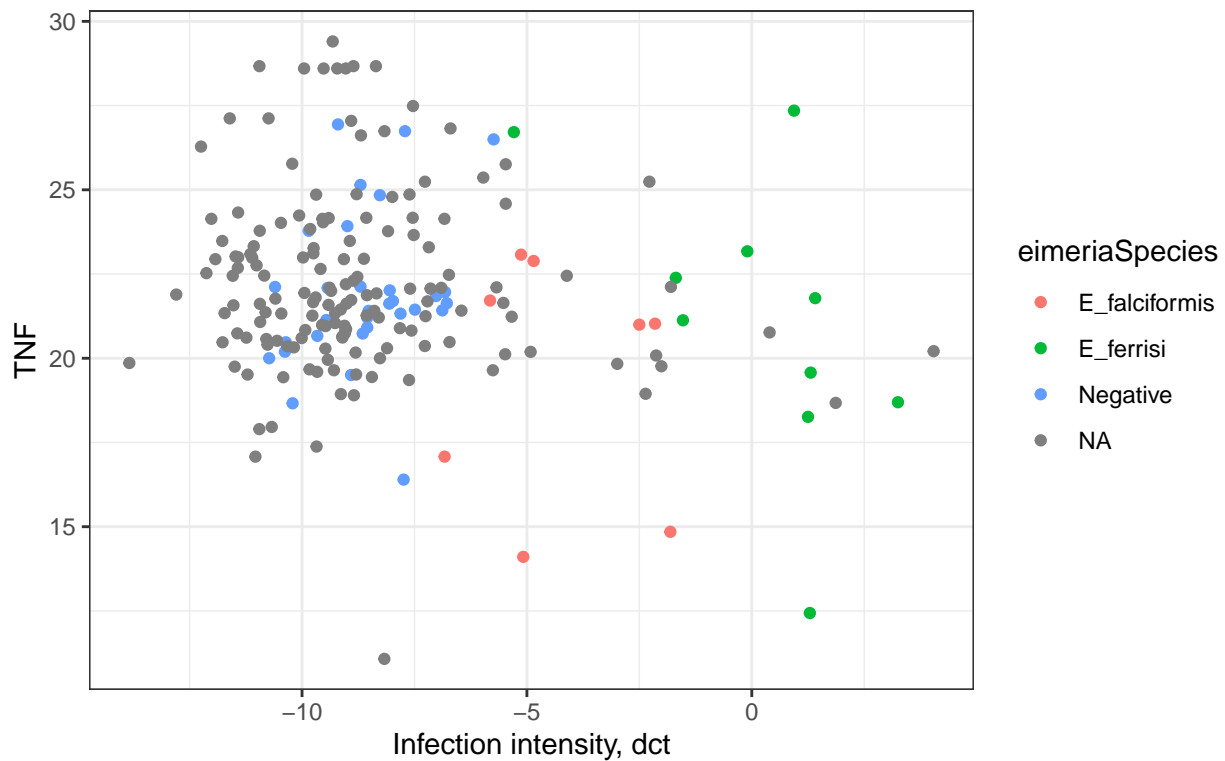
## Immune gene expression against infection intensity in lab infections



```
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 154 rows containing missing values (geom\_point).

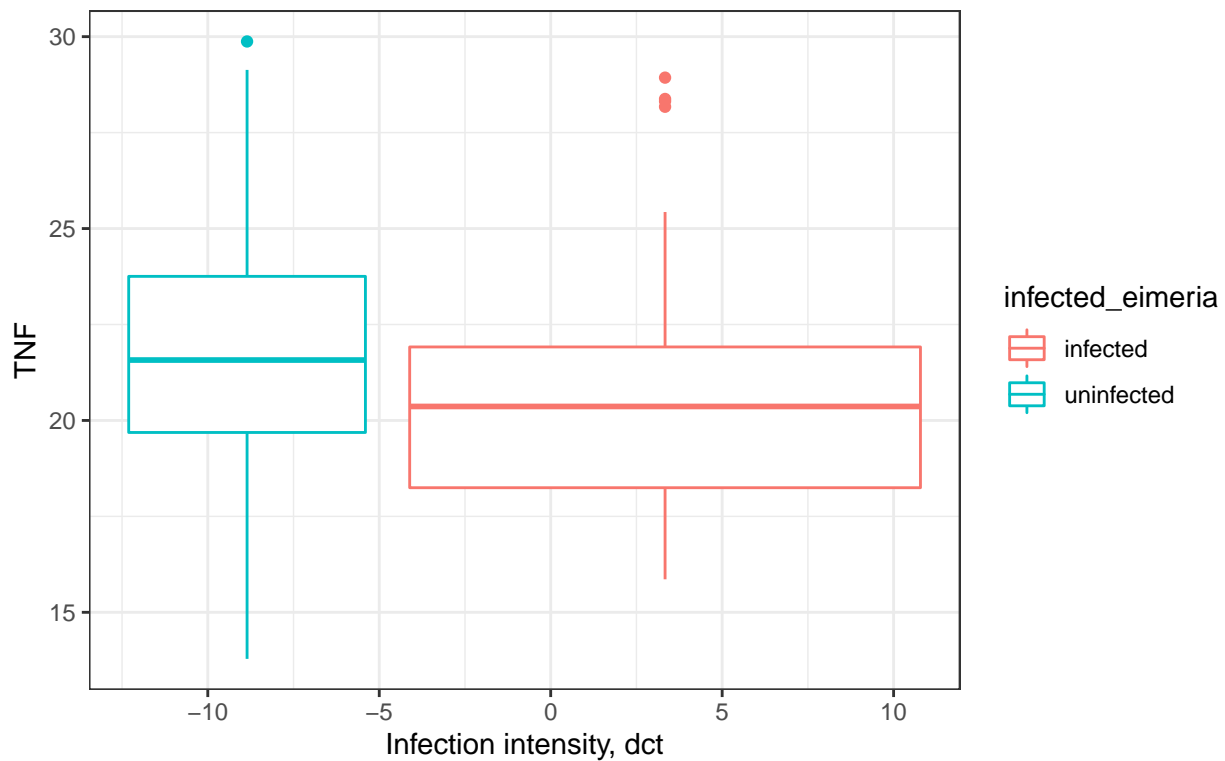
## Immune gene expression against infection intensity in field samples



```
ggplot(lab, aes(x = delta, y = TNF, color = infected_eimeria)) +
  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).

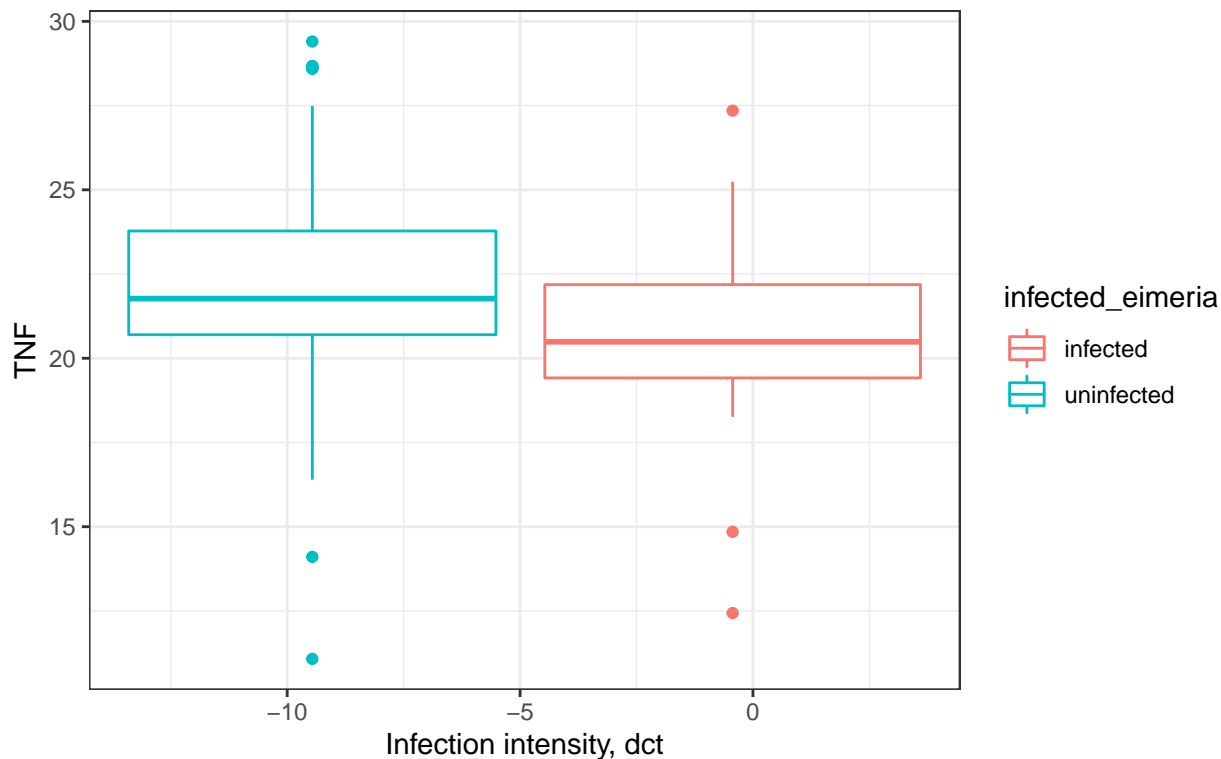
## Immune gene expression against infection intensity in lab infections



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

## Warning: Removed 154 rows containing missing values (stat\_boxplot).

## Immune gene expression against infection intensity in field samples



Compare the differences in uninfected and infected data and field / lab

Write a function which does a t test to quantify the differences of gene expression between uninfected and infected mice in the lab and field infections and also compares the uninfected lab and field and the infected lab and field

```
eimeria_t.test <- function(x) {
  # select the uninfected (delta ct under -5 mice)
  lab_uni <- lab %>%
    dplyr::filter(
      infected_eimeria == "uninfected"
    )
  # select the infected lab mice
  lab_inf <- lab %>%
    dplyr::filter(
      infected_eimeria == "infected"
    )
  # select the uninfected field mice (delta ct under -5 mice)
  field_uni <- field %>%
    dplyr::filter(
      infected_eimeria == "uninfected"
    )
  # select the infected lab mice
  field_inf <- field %>%
    dplyr::filter(
      infected_eimeria == "infected"
    )

  print(c("Testing differences in expression in uninfected and infected lab mice. Gene:", toString(x)))
  print(t.test(lab_uni %>% dplyr::select(all_of(x)), lab_inf %>% dplyr::select(all_of(x))))

  print(c("Testing differences in expression in uninfected and infected field mice. Gene:", toString(x)))
  print(t.test(field_uni %>% dplyr::select(all_of(x)), field_inf %>% dplyr::select(all_of(x))))

  print(c("Testing differences in expression in uninfected lab vs field mice. Gene:", toString(x)))
}
```



```

print(t.test(lab_uni %>% dplyr::select(all_of(x)), field_uni %>% dplyr::select(all_of(x))))

print(c("Testing differences in expression in infected lab vs field mice. Gene:", toString(x)))
print(t.test(lab_inf %>% dplyr::select(all_of(x)), field_inf %>% dplyr::select(all_of(x))))
}

print(lapply(intersect(Genes_field, Genes_lab), eimeria_t.test))

## [1] "Testing differences in expression in uninfected and infected lab mice. Gene:"
## [2] "IFNy"
##
## Welch Two Sample t-test
##
## data: lab_uni %>% dplyr::select(all_of(x)) and lab_inf %>% dplyr::select(all_of(x))
## t = 3.484, df = 60.838, p-value = 0.0009217
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## 0.8212122 3.0339674
## sample estimates:
## mean of x mean of y
## 22.51974 20.59215
##
## [1] "Testing differences in expression in uninfected and infected field mice. Gene:"
## [2] "IFNy"
##
## Welch Two Sample t-test
##
## data: field_uni %>% dplyr::select(all_of(x)) and field_inf %>% dplyr::select(all_of(x))
## t = 3.8789, df = 193.82, p-value = 0.0001437
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## 6.142502 18.850501
## sample estimates:
## mean of x mean of y
## 31.10189 18.60539
##
## [1] "Testing differences in expression in uninfected lab vs field mice. Gene:"
## [2] "IFNy"
##
## Welch Two Sample t-test
##
## data: lab_uni %>% dplyr::select(all_of(x)) and field_uni %>% dplyr::select(all_of(x))
## t = -2.7275, df = 180.64, p-value = 0.007011
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -14.790780 -2.373531
## sample estimates:
## mean of x mean of y
## 22.51974 31.10189
##
## [1] "Testing differences in expression in infected lab vs field mice. Gene:"
## [2] "IFNy"
##
## Welch Two Sample t-test
##
## data: lab_inf %>% dplyr::select(all_of(x)) and field_inf %>% dplyr::select(all_of(x))

```

```

## t = 2.2428, df = 41.863, p-value = 0.03026
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## 0.1989204 3.7745931
## sample estimates:
## mean of x mean of y
## 20.59215 18.60539
##
## [1] "Testing differences in expression in uninfected and infected lab mice. Gene:"
## [2] "IL.6"
##
## Welch Two Sample t-test
##
## data: lab_uni %>% dplyr::select(all_of(x)) and lab_inf %>% dplyr::select(all_of(x))
## t = -0.64224, df = 64.617, p-value = 0.523
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -1.916076 0.983682
## sample estimates:
## mean of x mean of y
## 22.02651 22.49271
##
## [1] "Testing differences in expression in uninfected and infected field mice. Gene:"
## [2] "IL.6"
##
## Welch Two Sample t-test
##
## data: field_uni %>% dplyr::select(all_of(x)) and field_inf %>% dplyr::select(all_of(x))
## t = 2.4988, df = 27.656, p-value = 0.01868
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## 0.2885725 2.9214658
## sample estimates:
## mean of x mean of y
## 23.95024 22.34522
##
## [1] "Testing differences in expression in uninfected lab vs field mice. Gene:"
## [2] "IL.6"
##
## Welch Two Sample t-test
##
## data: lab_uni %>% dplyr::select(all_of(x)) and field_uni %>% dplyr::select(all_of(x))
## t = -4.5589, df = 109.5, p-value = 1.346e-05
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -2.760019 -1.087436
## sample estimates:
## mean of x mean of y
## 22.02651 23.95024
##
## [1] "Testing differences in expression in infected lab vs field mice. Gene:"
## [2] "IL.6"
##
## Welch Two Sample t-test
##
## data: lab_inf %>% dplyr::select(all_of(x)) and field_inf %>% dplyr::select(all_of(x))

```

```

## t = 0.16902, df = 57.054, p-value = 0.8664
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -1.599821 1.894798
## sample estimates:
## mean of x mean of y
## 22.49271 22.34522
##
## [1] "Testing differences in expression in uninfected and infected lab mice. Gene:"
## [2] "IL.10"
##
## Welch Two Sample t-test
##
## data: lab_uni %>% dplyr::select(all_of(x)) and lab_inf %>% dplyr::select(all_of(x))
## t = 0.96483, df = 72.305, p-value = 0.3378
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.5424635 1.5602329
## sample estimates:
## mean of x mean of y
## 23.42632 22.91743
##
## [1] "Testing differences in expression in uninfected and infected field mice. Gene:"
## [2] "IL.10"
##
## Welch Two Sample t-test
##
## data: field_uni %>% dplyr::select(all_of(x)) and field_inf %>% dplyr::select(all_of(x))
## t = 1.2187, df = 27.741, p-value = 0.2332
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.6172094 2.4285355
## sample estimates:
## mean of x mean of y
## 24.85136 23.94569
##
## [1] "Testing differences in expression in uninfected lab vs field mice. Gene:"
## [2] "IL.10"
##
## Welch Two Sample t-test
##
## data: lab_uni %>% dplyr::select(all_of(x)) and field_uni %>% dplyr::select(all_of(x))
## t = -3.8107, df = 152.44, p-value = 0.0002006
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -2.1638425 -0.6862312
## sample estimates:
## mean of x mean of y
## 23.42632 24.85136
##
## [1] "Testing differences in expression in infected lab vs field mice. Gene:"
## [2] "IL.10"
##
## Welch Two Sample t-test
##
## data: lab_inf %>% dplyr::select(all_of(x)) and field_inf %>% dplyr::select(all_of(x))

```

```

## t = -1.2374, df = 39.958, p-value = 0.2232
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -2.7078599 0.6513429
## sample estimates:
## mean of x mean of y
## 22.91743 23.94569
##
## [1] "Testing differences in expression in uninfected and infected lab mice. Gene:"
## [2] "IL.13"
##
## Welch Two Sample t-test
##
## data: lab_uni %>% dplyr::select(all_of(x)) and lab_inf %>% dplyr::select(all_of(x))
## t = 2.4547, df = 57.363, p-value = 0.01716
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## 0.1841028 1.8134243
## sample estimates:
## mean of x mean of y
## 19.14649 18.14773
##
## [1] "Testing differences in expression in uninfected and infected field mice. Gene:"
## [2] "IL.13"
##
## Welch Two Sample t-test
##
## data: field_uni %>% dplyr::select(all_of(x)) and field_inf %>% dplyr::select(all_of(x))
## t = 2.5297, df = 33.292, p-value = 0.01633
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## 0.498436 4.587285
## sample estimates:
## mean of x mean of y
## 15.46584 12.92298
##
## [1] "Testing differences in expression in uninfected lab vs field mice. Gene:"
## [2] "IL.13"
##
## Welch Two Sample t-test
##
## data: lab_uni %>% dplyr::select(all_of(x)) and field_uni %>% dplyr::select(all_of(x))
## t = 8.0723, df = 233.41, p-value = 3.65e-14
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## 2.782331 4.578972
## sample estimates:
## mean of x mean of y
## 19.14649 15.46584
##
## [1] "Testing differences in expression in infected lab vs field mice. Gene:"
## [2] "IL.13"
##
## Welch Two Sample t-test
##
## data: lab_inf %>% dplyr::select(all_of(x)) and field_inf %>% dplyr::select(all_of(x))

```

```

## t = 5.3101, df = 30.271, p-value = 9.452e-06
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## 3.216075 7.233421
## sample estimates:
## mean of x mean of y
## 18.14773 12.92298
##
## [1] "Testing differences in expression in uninfected and infected lab mice. Gene:"
## [2] "IL1RN"
##
## Welch Two Sample t-test
##
## data: lab_uni %>% dplyr::select(all_of(x)) and lab_inf %>% dplyr::select(all_of(x))
## t = 1.4677, df = 66.301, p-value = 0.1469
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.2977368 1.9509204
## sample estimates:
## mean of x mean of y
## 16.73620 15.90961
##
## [1] "Testing differences in expression in uninfected and infected field mice. Gene:"
## [2] "IL1RN"
##
## Welch Two Sample t-test
##
## data: field_uni %>% dplyr::select(all_of(x)) and field_inf %>% dplyr::select(all_of(x))
## t = -3.0051, df = 28.667, p-value = 0.005468
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -4.4787733 -0.8501397
## sample estimates:
## mean of x mean of y
## 13.51544 16.17990
##
## [1] "Testing differences in expression in uninfected lab vs field mice. Gene:"
## [2] "IL1RN"
##
## Welch Two Sample t-test
##
## data: lab_uni %>% dplyr::select(all_of(x)) and field_uni %>% dplyr::select(all_of(x))
## t = 7.7718, df = 196.31, p-value = 4.237e-13
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## 2.403476 4.038033
## sample estimates:
## mean of x mean of y
## 16.73620 13.51544
##
## [1] "Testing differences in expression in infected lab vs field mice. Gene:"
## [2] "IL1RN"
##
## Welch Two Sample t-test
##
## data: lab_inf %>% dplyr::select(all_of(x)) and field_inf %>% dplyr::select(all_of(x))

```

```

## t = -0.28004, df = 37.854, p-value = 0.781
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -2.224451 1.683864
## sample estimates:
## mean of x mean of y
## 15.90961 16.17990
##
## [1] "Testing differences in expression in uninfected and infected lab mice. Gene:"
## [2] "CASP1"
##
## Welch Two Sample t-test
##
## data: lab_uni %>% dplyr::select(all_of(x)) and lab_inf %>% dplyr::select(all_of(x))
## t = 0.9175, df = 74.897, p-value = 0.3618
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.425971 1.153338
## sample estimates:
## mean of x mean of y
## 23.06600 22.70232
##
## [1] "Testing differences in expression in uninfected and infected field mice. Gene:"
## [2] "CASP1"
##
## Welch Two Sample t-test
##
## data: field_uni %>% dplyr::select(all_of(x)) and field_inf %>% dplyr::select(all_of(x))
## t = 0.1352, df = 29.721, p-value = 0.8934
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.8209311 0.9372816
## sample estimates:
## mean of x mean of y
## 22.56004 22.50186
##
## [1] "Testing differences in expression in uninfected lab vs field mice. Gene:"
## [2] "CASP1"
##
## Welch Two Sample t-test
##
## data: lab_uni %>% dplyr::select(all_of(x)) and field_uni %>% dplyr::select(all_of(x))
## t = 1.833, df = 133.51, p-value = 0.06903
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.03999533 1.05192535
## sample estimates:
## mean of x mean of y
## 23.06600 22.56004
##
## [1] "Testing differences in expression in infected lab vs field mice. Gene:"
## [2] "CASP1"
##
## Welch Two Sample t-test
##
## data: lab_inf %>% dplyr::select(all_of(x)) and field_inf %>% dplyr::select(all_of(x))

```

```

## t = 0.38862, df = 49.18, p-value = 0.6992
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.8360302 1.2369434
## sample estimates:
## mean of x mean of y
## 22.70232 22.50186
##
## [1] "Testing differences in expression in uninfected and infected lab mice. Gene:"
## [2] "CXCL9"
##
## Welch Two Sample t-test
##
## data: lab_uni %>% dplyr::select(all_of(x)) and lab_inf %>% dplyr::select(all_of(x))
## t = 1.9516, df = 65.086, p-value = 0.05529
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.03268334 2.83665525
## sample estimates:
## mean of x mean of y
## 17.95081 16.54883
##
## [1] "Testing differences in expression in uninfected and infected field mice. Gene:"
## [2] "CXCL9"
##
## Welch Two Sample t-test
##
## data: field_uni %>% dplyr::select(all_of(x)) and field_inf %>% dplyr::select(all_of(x))
## t = 5.1726, df = 27.072, p-value = 1.901e-05
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## 2.339810 5.415883
## sample estimates:
## mean of x mean of y
## 21.27463 17.39679
##
## [1] "Testing differences in expression in uninfected lab vs field mice. Gene:"
## [2] "CXCL9"
##
## Welch Two Sample t-test
##
## data: lab_uni %>% dplyr::select(all_of(x)) and field_uni %>% dplyr::select(all_of(x))
## t = -7.7354, df = 118.12, p-value = 3.826e-12
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -4.174717 -2.472923
## sample estimates:
## mean of x mean of y
## 17.95081 21.27463
##
## [1] "Testing differences in expression in infected lab vs field mice. Gene:"
## [2] "CXCL9"
##
## Welch Two Sample t-test
##
## data: lab_inf %>% dplyr::select(all_of(x)) and field_inf %>% dplyr::select(all_of(x))

```

```

## t = -0.89709, df = 51.598, p-value = 0.3738
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -2.745060 1.049142
## sample estimates:
## mean of x mean of y
## 16.54883 17.39679
##
## [1] "Testing differences in expression in uninfected and infected lab mice. Gene:"
## [2] "ID01"
##
## Welch Two Sample t-test
##
## data: lab_uni %>% dplyr::select(all_of(x)) and lab_inf %>% dplyr::select(all_of(x))
## t = 1.2877, df = 60.617, p-value = 0.2027
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.6138799 2.8339873
## sample estimates:
## mean of x mean of y
## 16.19718 15.08712
##
## [1] "Testing differences in expression in uninfected and infected field mice. Gene:"
## [2] "ID01"
##
## Welch Two Sample t-test
##
## data: field_uni %>% dplyr::select(all_of(x)) and field_inf %>% dplyr::select(all_of(x))
## t = -0.10101, df = 29.594, p-value = 0.9202
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -1.741861 1.577775
## sample estimates:
## mean of x mean of y
## 14.37506 14.45710
##
## [1] "Testing differences in expression in uninfected lab vs field mice. Gene:"
## [2] "ID01"
##
## Welch Two Sample t-test
##
## data: lab_uni %>% dplyr::select(all_of(x)) and field_uni %>% dplyr::select(all_of(x))
## t = 3.6045, df = 137.54, p-value = 0.0004362
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## 0.8225371 2.8216913
## sample estimates:
## mean of x mean of y
## 16.19718 14.37506
##
## [1] "Testing differences in expression in infected lab vs field mice. Gene:"
## [2] "ID01"
##
## Welch Two Sample t-test
##
## data: lab_inf %>% dplyr::select(all_of(x)) and field_inf %>% dplyr::select(all_of(x))

```



```

## t = 0.58818, df = 56.389, p-value = 0.5588
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -1.515375 2.775411
## sample estimates:
## mean of x mean of y
## 15.08712 14.45710
##
## [1] "Testing differences in expression in uninfected and infected lab mice. Gene:"
## [2] "IRGM1"
##
## Welch Two Sample t-test
##
## data: lab_uni %>% dplyr::select(all_of(x)) and lab_inf %>% dplyr::select(all_of(x))
## t = 1.1119, df = 75.133, p-value = 0.2697
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.2239697 0.7898970
## sample estimates:
## mean of x mean of y
## 9.644743 9.361779
##
## [1] "Testing differences in expression in uninfected and infected field mice. Gene:"
## [2] "IRGM1"
##
## Welch Two Sample t-test
##
## data: field_uni %>% dplyr::select(all_of(x)) and field_inf %>% dplyr::select(all_of(x))
## t = 0.087281, df = 31.343, p-value = 0.931
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -1.115779 1.215595
## sample estimates:
## mean of x mean of y
## 11.20121 11.15131
##
## [1] "Testing differences in expression in uninfected lab vs field mice. Gene:"
## [2] "IRGM1"
##
## Welch Two Sample t-test
##
## data: lab_uni %>% dplyr::select(all_of(x)) and field_uni %>% dplyr::select(all_of(x))
## t = -5.8981, df = 247.57, p-value = 1.201e-08
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -2.076238 -1.036706
## sample estimates:
## mean of x mean of y
## 9.644743 11.201215
##
## [1] "Testing differences in expression in infected lab vs field mice. Gene:"
## [2] "IRGM1"
##
## Welch Two Sample t-test
##
## data: lab_inf %>% dplyr::select(all_of(x)) and field_inf %>% dplyr::select(all_of(x))

```

```

## t = -3.1532, df = 30.094, p-value = 0.003644
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -2.9484074 -0.6306483
## sample estimates:
## mean of x mean of y
## 9.361779 11.151307
##
## [1] "Testing differences in expression in uninfected and infected lab mice. Gene:"
## [2] "MPO"
##
## Welch Two Sample t-test
##
## data: lab_uni %>% dplyr::select(all_of(x)) and lab_inf %>% dplyr::select(all_of(x))
## t = 1.7025, df = 72.981, p-value = 0.09292
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.2274392 2.8929142
## sample estimates:
## mean of x mean of y
## 22.61581 21.28308
##
## [1] "Testing differences in expression in uninfected and infected field mice. Gene:"
## [2] "MPO"
##
## Welch Two Sample t-test
##
## data: field_uni %>% dplyr::select(all_of(x)) and field_inf %>% dplyr::select(all_of(x))
## t = -2.1723, df = 28.941, p-value = 0.03816
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -3.8793283 -0.1167495
## sample estimates:
## mean of x mean of y
## 18.85906 20.85709
##
## [1] "Testing differences in expression in uninfected lab vs field mice. Gene:"
## [2] "MPO"
##
## Welch Two Sample t-test
##
## data: lab_uni %>% dplyr::select(all_of(x)) and field_uni %>% dplyr::select(all_of(x))
## t = 6.929, df = 139.49, p-value = 1.435e-10
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## 2.684807 4.828708
## sample estimates:
## mean of x mean of y
## 22.61581 18.85906
##
## [1] "Testing differences in expression in infected lab vs field mice. Gene:"
## [2] "MPO"
##
## Welch Two Sample t-test
##
## data: lab_inf %>% dplyr::select(all_of(x)) and field_inf %>% dplyr::select(all_of(x))

```

```

## t = 0.39469, df = 46.38, p-value = 0.6949
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -1.745993 2.597955
## sample estimates:
## mean of x mean of y
## 21.28308 20.85709
##
## [1] "Testing differences in expression in uninfected and infected lab mice. Gene:"
## [2] "MUC2"
##
## Welch Two Sample t-test
##
## data: lab_uni %>% dplyr::select(all_of(x)) and lab_inf %>% dplyr::select(all_of(x))
## t = 0.3433, df = 88.5, p-value = 0.7322
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.4655075 0.6599413
## sample estimates:
## mean of x mean of y
## 8.827395 8.730178
##
## [1] "Testing differences in expression in uninfected and infected field mice. Gene:"
## [2] "MUC2"
##
## Welch Two Sample t-test
##
## data: field_uni %>% dplyr::select(all_of(x)) and field_inf %>% dplyr::select(all_of(x))
## t = -1.4279, df = 25.747, p-value = 0.1653
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -2.6942056 0.4860873
## sample estimates:
## mean of x mean of y
## 9.354584 10.458643
##
## [1] "Testing differences in expression in uninfected lab vs field mice. Gene:"
## [2] "MUC2"
##
## Welch Two Sample t-test
##
## data: lab_uni %>% dplyr::select(all_of(x)) and field_uni %>% dplyr::select(all_of(x))
## t = -2.0251, df = 197.99, p-value = 0.0442
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -1.04056315 -0.01381481
## sample estimates:
## mean of x mean of y
## 8.827395 9.354584
##
## [1] "Testing differences in expression in infected lab vs field mice. Gene:"
## [2] "MUC2"
##
## Welch Two Sample t-test
##
## data: lab_inf %>% dplyr::select(all_of(x)) and field_inf %>% dplyr::select(all_of(x))

```

```

## t = -2.2125, df = 26.733, p-value = 0.03566
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -3.3321377 -0.1247923
## sample estimates:
## mean of x mean of y
## 8.730178 10.458643
##
## [1] "Testing differences in expression in uninfected and infected lab mice. Gene:"
## [2] "MUC5AC"
##
## Welch Two Sample t-test
##
## data: lab_uni %>% dplyr::select(all_of(x)) and lab_inf %>% dplyr::select(all_of(x))
## t = -0.0098852, df = 63.103, p-value = 0.9921
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -1.951604 1.932390
## sample estimates:
## mean of x mean of y
## 11.73079 11.74040
##
## [1] "Testing differences in expression in uninfected and infected field mice. Gene:"
## [2] "MUC5AC"
##
## Welch Two Sample t-test
##
## data: field_uni %>% dplyr::select(all_of(x)) and field_inf %>% dplyr::select(all_of(x))
## t = -2.2961, df = 25.656, p-value = 0.0301
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -4.547387 -0.249950
## sample estimates:
## mean of x mean of y
## 9.986871 12.385540
##
## [1] "Testing differences in expression in uninfected lab vs field mice. Gene:"
## [2] "MUC5AC"
##
## Welch Two Sample t-test
##
## data: lab_uni %>% dplyr::select(all_of(x)) and field_uni %>% dplyr::select(all_of(x))
## t = 3.1783, df = 106.7, p-value = 0.001939
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## 0.6561499 2.8316963
## sample estimates:
## mean of x mean of y
## 11.730794 9.986871
##
## [1] "Testing differences in expression in infected lab vs field mice. Gene:"
## [2] "MUC5AC"
##
## Welch Two Sample t-test
##
## data: lab_inf %>% dplyr::select(all_of(x)) and field_inf %>% dplyr::select(all_of(x))

```

```

## t = -0.48983, df = 50.4, p-value = 0.6264
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -3.290046  1.999769
## sample estimates:
## mean of x mean of y
## 11.74040 12.38554
##
## [1] "Testing differences in expression in uninfected and infected lab mice. Gene:"
## [2] "MYD88"
##
## Welch Two Sample t-test
##
## data:  lab_uni %>% dplyr::select(all_of(x)) and lab_inf %>% dplyr::select(all_of(x))
## t = 1.5858, df = 61.768, p-value = 0.1179
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.4214675  3.6558341
## sample estimates:
## mean of x mean of y
## 17.05906 15.44188
##
## [1] "Testing differences in expression in uninfected and infected field mice. Gene:"
## [2] "MYD88"
##
## Welch Two Sample t-test
##
## data:  field_uni %>% dplyr::select(all_of(x)) and field_inf %>% dplyr::select(all_of(x))
## t = -0.6244, df = 35.337, p-value = 0.5364
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -2.654930  1.405607
## sample estimates:
## mean of x mean of y
## 17.63426 18.25892
##
## [1] "Testing differences in expression in uninfected lab vs field mice. Gene:"
## [2] "MYD88"
##
## Welch Two Sample t-test
##
## data:  lab_uni %>% dplyr::select(all_of(x)) and field_uni %>% dplyr::select(all_of(x))
## t = -0.85443, df = 179.38, p-value = 0.394
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -1.9035732  0.7531882
## sample estimates:
## mean of x mean of y
## 17.05906 17.63426
##
## [1] "Testing differences in expression in infected lab vs field mice. Gene:"
## [2] "MYD88"
##
## Welch Two Sample t-test
##
## data:  lab_inf %>% dplyr::select(all_of(x)) and field_inf %>% dplyr::select(all_of(x))

```

```

## t = -2.2357, df = 56.374, p-value = 0.02935
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -5.3407522 -0.2933225
## sample estimates:
## mean of x mean of y
## 15.44188 18.25892
##
## [1] "Testing differences in expression in uninfected and infected lab mice. Gene:"
## [2] "NCR1"
##
## Welch Two Sample t-test
##
## data: lab_uni %>% dplyr::select(all_of(x)) and lab_inf %>% dplyr::select(all_of(x))
## t = -1.6757, df = 82.837, p-value = 0.09757
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -1.8864489 0.1612932
## sample estimates:
## mean of x mean of y
## 23.21552 24.07810
##
## [1] "Testing differences in expression in uninfected and infected field mice. Gene:"
## [2] "NCR1"
##
## Welch Two Sample t-test
##
## data: field_uni %>% dplyr::select(all_of(x)) and field_inf %>% dplyr::select(all_of(x))
## t = 1.7395, df = 25.738, p-value = 0.0939
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.216197 2.588161
## sample estimates:
## mean of x mean of y
## 24.62785 23.44186
##
## [1] "Testing differences in expression in uninfected lab vs field mice. Gene:"
## [2] "NCR1"
##
## Welch Two Sample t-test
##
## data: lab_uni %>% dplyr::select(all_of(x)) and field_uni %>% dplyr::select(all_of(x))
## t = -3.9109, df = 107.22, p-value = 0.0001616
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -2.1281963 -0.6964553
## sample estimates:
## mean of x mean of y
## 23.21552 24.62785
##
## [1] "Testing differences in expression in infected lab vs field mice. Gene:"
## [2] "NCR1"
##
## Welch Two Sample t-test
##
## data: lab_inf %>% dplyr::select(all_of(x)) and field_inf %>% dplyr::select(all_of(x))

```

```

## t = 0.82176, df = 39.551, p-value = 0.4161
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.9291034 2.2015714
## sample estimates:
## mean of x mean of y
## 24.07810 23.44186
##
## [1] "Testing differences in expression in uninfected and infected lab mice. Gene:"
## [2] "PRF1"
##
## Welch Two Sample t-test
##
## data: lab_uni %>% dplyr::select(all_of(x)) and lab_inf %>% dplyr::select(all_of(x))
## t = 2.5434, df = 79.405, p-value = 0.01292
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## 0.2520221 2.0659080
## sample estimates:
## mean of x mean of y
## 25.55788 24.39892
##
## [1] "Testing differences in expression in uninfected and infected field mice. Gene:"
## [2] "PRF1"
##
## Welch Two Sample t-test
##
## data: field_uni %>% dplyr::select(all_of(x)) and field_inf %>% dplyr::select(all_of(x))
## t = 2.1862, df = 26.752, p-value = 0.03773
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## 0.09961136 3.16272430
## sample estimates:
## mean of x mean of y
## 24.00283 22.37166
##
## [1] "Testing differences in expression in uninfected lab vs field mice. Gene:"
## [2] "PRF1"
##
## Welch Two Sample t-test
##
## data: lab_uni %>% dplyr::select(all_of(x)) and field_uni %>% dplyr::select(all_of(x))
## t = 4.5252, df = 148.94, p-value = 1.225e-05
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## 0.8760135 2.2340970
## sample estimates:
## mean of x mean of y
## 25.55788 24.00283
##
## [1] "Testing differences in expression in infected lab vs field mice. Gene:"
## [2] "PRF1"
##
## Welch Two Sample t-test
##
## data: lab_inf %>% dplyr::select(all_of(x)) and field_inf %>% dplyr::select(all_of(x))

```

```

## t = 2.5218, df = 34.705, p-value = 0.01642
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## 0.3947802 3.6597358
## sample estimates:
## mean of x mean of y
## 24.39892 22.37166
##
## [1] "Testing differences in expression in uninfected and infected lab mice. Gene:"
## [2] "RETNLB"
##
## Welch Two Sample t-test
##
## data: lab_uni %>% dplyr::select(all_of(x)) and lab_inf %>% dplyr::select(all_of(x))
## t = -1.5579, df = 63.147, p-value = 0.1242
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -3.0423806 0.3766941
## sample estimates:
## mean of x mean of y
## 9.761624 11.094467
##
## [1] "Testing differences in expression in uninfected and infected field mice. Gene:"
## [2] "RETNLB"
##
## Welch Two Sample t-test
##
## data: field_uni %>% dplyr::select(all_of(x)) and field_inf %>% dplyr::select(all_of(x))
## t = 0.2748, df = 28.583, p-value = 0.7854
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -1.632392 2.138765
## sample estimates:
## mean of x mean of y
## 11.56502 11.31184
##
## [1] "Testing differences in expression in uninfected lab vs field mice. Gene:"
## [2] "RETNLB"
##
## Welch Two Sample t-test
##
## data: lab_uni %>% dplyr::select(all_of(x)) and field_uni %>% dplyr::select(all_of(x))
## t = -3.4297, df = 140.62, p-value = 0.0007933
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -2.842930 -0.763871
## sample estimates:
## mean of x mean of y
## 9.761624 11.565025
##
## [1] "Testing differences in expression in infected lab vs field mice. Gene:"
## [2] "RETNLB"
##
## Welch Two Sample t-test
##
## data: lab_inf %>% dplyr::select(all_of(x)) and field_inf %>% dplyr::select(all_of(x))

```



```

## t = -0.19033, df = 51.318, p-value = 0.8498
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -2.509826  2.075083
## sample estimates:
## mean of x mean of y
## 11.09447 11.31184
##
## [1] "Testing differences in expression in uninfected and infected lab mice. Gene:"
## [2] "SOCS1"
##
## Welch Two Sample t-test
##
## data: lab_uni %>% dplyr::select(all_of(x)) and lab_inf %>% dplyr::select(all_of(x))
## t = 0.19509, df = 63.6, p-value = 0.8459
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.5683438  0.6913425
## sample estimates:
## mean of x mean of y
## 10.60761 10.54611
##
## [1] "Testing differences in expression in uninfected and infected field mice. Gene:"
## [2] "SOCS1"
##
## Welch Two Sample t-test
##
## data: field_uni %>% dplyr::select(all_of(x)) and field_inf %>% dplyr::select(all_of(x))
## t = -1.3517, df = 25.879, p-value = 0.1882
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -2.434232  0.503112
## sample estimates:
## mean of x mean of y
## 11.81475 12.78031
##
## [1] "Testing differences in expression in uninfected lab vs field mice. Gene:"
## [2] "SOCS1"
##
## Welch Two Sample t-test
##
## data: lab_uni %>% dplyr::select(all_of(x)) and field_uni %>% dplyr::select(all_of(x))
## t = -5.1349, df = 213.54, p-value = 6.344e-07
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -1.6705250 -0.7437603
## sample estimates:
## mean of x mean of y
## 10.60761 11.81475
##
## [1] "Testing differences in expression in infected lab vs field mice. Gene:"
## [2] "SOCS1"
##
## Welch Two Sample t-test
##
## data: lab_inf %>% dplyr::select(all_of(x)) and field_inf %>% dplyr::select(all_of(x))

```

```

## t = -3.0007, df = 30.125, p-value = 0.005368
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -3.7545577 -0.7138464
## sample estimates:
## mean of x mean of y
## 10.54611 12.78031
##
## [1] "Testing differences in expression in uninfected and infected lab mice. Gene:"
## [2] "TICAM1"
##
## Welch Two Sample t-test
##
## data: lab_uni %>% dplyr::select(all_of(x)) and lab_inf %>% dplyr::select(all_of(x))
## t = -2.4137, df = 75.428, p-value = 0.01822
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -3.0526991 -0.2922873
## sample estimates:
## mean of x mean of y
## 18.41316 20.08565
##
## [1] "Testing differences in expression in uninfected and infected field mice. Gene:"
## [2] "TICAM1"
##
## Welch Two Sample t-test
##
## data: field_uni %>% dplyr::select(all_of(x)) and field_inf %>% dplyr::select(all_of(x))
## t = 3.6098, df = 26.609, p-value = 0.00125
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## 1.243060 4.522493
## sample estimates:
## mean of x mean of y
## 22.53816 19.65539
##
## [1] "Testing differences in expression in uninfected lab vs field mice. Gene:"
## [2] "TICAM1"
##
## Welch Two Sample t-test
##
## data: lab_uni %>% dplyr::select(all_of(x)) and field_uni %>% dplyr::select(all_of(x))
## t = -8.9812, df = 111.51, p-value = 7.61e-15
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -5.035075 -3.214933
## sample estimates:
## mean of x mean of y
## 18.41316 22.53816
##
## [1] "Testing differences in expression in infected lab vs field mice. Gene:"
## [2] "TICAM1"
##
## Welch Two Sample t-test
##
## data: lab_inf %>% dplyr::select(all_of(x)) and field_inf %>% dplyr::select(all_of(x))

```

```

## t = 0.4518, df = 45.841, p-value = 0.6535
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -1.486848 2.347379
## sample estimates:
## mean of x mean of y
## 20.08565 19.65539
##
## [1] "Testing differences in expression in uninfected and infected lab mice. Gene:"
## [2] "TNF"
##
## Welch Two Sample t-test
##
## data: lab_uni %>% dplyr::select(all_of(x)) and lab_inf %>% dplyr::select(all_of(x))
## t = 1.4346, df = 68.806, p-value = 0.1559
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.3858507 2.3610054
## sample estimates:
## mean of x mean of y
## 21.77046 20.78288
##
## [1] "Testing differences in expression in uninfected and infected field mice. Gene:"
## [2] "TNF"
##
## Welch Two Sample t-test
##
## data: field_uni %>% dplyr::select(all_of(x)) and field_inf %>% dplyr::select(all_of(x))
## t = 2.6667, df = 28.344, p-value = 0.01252
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## 0.4007401 3.0499092
## sample estimates:
## mean of x mean of y
## 22.25946 20.53414
##
## [1] "Testing differences in expression in uninfected lab vs field mice. Gene:"
## [2] "TNF"
##
## Welch Two Sample t-test
##
## data: lab_uni %>% dplyr::select(all_of(x)) and field_uni %>% dplyr::select(all_of(x))
## t = -1.1411, df = 115.06, p-value = 0.2562
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -1.3378190 0.3598145
## sample estimates:
## mean of x mean of y
## 21.77046 22.25946
##
## [1] "Testing differences in expression in infected lab vs field mice. Gene:"
## [2] "TNF"
##
## Welch Two Sample t-test
##
## data: lab_inf %>% dplyr::select(all_of(x)) and field_inf %>% dplyr::select(all_of(x))

```

```

## t = 0.29544, df = 54.901, p-value = 0.7688
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -1.438643 1.936133
## sample estimates:
## mean of x mean of y
## 20.78288 20.53414
##
## [[1]]
##
## Welch Two Sample t-test
##
## data: lab_inf %>% dplyr::select(all_of(x)) and field_inf %>% dplyr::select(all_of(x))
## t = 2.2428, df = 41.863, p-value = 0.03026
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## 0.1989204 3.7745931
## sample estimates:
## mean of x mean of y
## 20.59215 18.60539
##
##
## [[2]]
##
## Welch Two Sample t-test
##
## data: lab_inf %>% dplyr::select(all_of(x)) and field_inf %>% dplyr::select(all_of(x))
## t = 0.16902, df = 57.054, p-value = 0.8664
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -1.599821 1.894798
## sample estimates:
## mean of x mean of y
## 22.49271 22.34522
##
##
## [[3]]
##
## Welch Two Sample t-test
##
## data: lab_inf %>% dplyr::select(all_of(x)) and field_inf %>% dplyr::select(all_of(x))
## t = -1.2374, df = 39.958, p-value = 0.2232
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -2.7078599 0.6513429
## sample estimates:
## mean of x mean of y
## 22.91743 23.94569
##
##
## [[4]]
##
## Welch Two Sample t-test
##
## data: lab_inf %>% dplyr::select(all_of(x)) and field_inf %>% dplyr::select(all_of(x))
## t = 5.3101, df = 30.271, p-value = 9.452e-06

```

```

## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  3.216075 7.233421
## sample estimates:
## mean of x mean of y
##  18.14773  12.92298
##
##
## [[5]]
##
## Welch Two Sample t-test
##
## data:  lab_inf %>% dplyr::select(all_of(x)) and field_inf %>% dplyr::select(all_of(x))
## t = -0.28004, df = 37.854, p-value = 0.781
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -2.224451  1.683864
## sample estimates:
## mean of x mean of y
##  15.90961  16.17990
##
##
## [[6]]
##
## Welch Two Sample t-test
##
## data:  lab_inf %>% dplyr::select(all_of(x)) and field_inf %>% dplyr::select(all_of(x))
## t = 0.38862, df = 49.18, p-value = 0.6992
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.8360302  1.2369434
## sample estimates:
## mean of x mean of y
##  22.70232  22.50186
##
##
## [[7]]
##
## Welch Two Sample t-test
##
## data:  lab_inf %>% dplyr::select(all_of(x)) and field_inf %>% dplyr::select(all_of(x))
## t = -0.89709, df = 51.598, p-value = 0.3738
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -2.745060  1.049142
## sample estimates:
## mean of x mean of y
##  16.54883  17.39679
##
##
## [[8]]
##
## Welch Two Sample t-test
##
## data:  lab_inf %>% dplyr::select(all_of(x)) and field_inf %>% dplyr::select(all_of(x))
## t = 0.58818, df = 56.389, p-value = 0.5588

```

```

## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -1.515375 2.775411
## sample estimates:
## mean of x mean of y
## 15.08712 14.45710
##
##
## [[9]]
##
## Welch Two Sample t-test
##
## data: lab_inf %>% dplyr::select(all_of(x)) and field_inf %>% dplyr::select(all_of(x))
## t = -3.1532, df = 30.094, p-value = 0.003644
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -2.9484074 -0.6306483
## sample estimates:
## mean of x mean of y
## 9.361779 11.151307
##
##
## [[10]]
##
## Welch Two Sample t-test
##
## data: lab_inf %>% dplyr::select(all_of(x)) and field_inf %>% dplyr::select(all_of(x))
## t = 0.39469, df = 46.38, p-value = 0.6949
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -1.745993 2.597955
## sample estimates:
## mean of x mean of y
## 21.28308 20.85709
##
##
## [[11]]
##
## Welch Two Sample t-test
##
## data: lab_inf %>% dplyr::select(all_of(x)) and field_inf %>% dplyr::select(all_of(x))
## t = -2.2125, df = 26.733, p-value = 0.03566
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -3.3321377 -0.1247923
## sample estimates:
## mean of x mean of y
## 8.730178 10.458643
##
##
## [[12]]
##
## Welch Two Sample t-test
##
## data: lab_inf %>% dplyr::select(all_of(x)) and field_inf %>% dplyr::select(all_of(x))
## t = -0.48983, df = 50.4, p-value = 0.6264

```

```

## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -3.290046 1.999769
## sample estimates:
## mean of x mean of y
## 11.74040 12.38554
##
##
## [[13]]
##
## Welch Two Sample t-test
##
## data: lab_inf %>% dplyr::select(all_of(x)) and field_inf %>% dplyr::select(all_of(x))
## t = -2.2357, df = 56.374, p-value = 0.02935
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -5.3407522 -0.2933225
## sample estimates:
## mean of x mean of y
## 15.44188 18.25892
##
##
## [[14]]
##
## Welch Two Sample t-test
##
## data: lab_inf %>% dplyr::select(all_of(x)) and field_inf %>% dplyr::select(all_of(x))
## t = 0.82176, df = 39.551, p-value = 0.4161
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.9291034 2.2015714
## sample estimates:
## mean of x mean of y
## 24.07810 23.44186
##
##
## [[15]]
##
## Welch Two Sample t-test
##
## data: lab_inf %>% dplyr::select(all_of(x)) and field_inf %>% dplyr::select(all_of(x))
## t = 2.5218, df = 34.705, p-value = 0.01642
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## 0.3947802 3.6597358
## sample estimates:
## mean of x mean of y
## 24.39892 22.37166
##
##
## [[16]]
##
## Welch Two Sample t-test
##
## data: lab_inf %>% dplyr::select(all_of(x)) and field_inf %>% dplyr::select(all_of(x))
## t = -0.19033, df = 51.318, p-value = 0.8498

```

```

## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -2.509826  2.075083
## sample estimates:
## mean of x mean of y
## 11.09447 11.31184
##
##
## [[17]]
##
## Welch Two Sample t-test
##
## data: lab_inf %>% dplyr::select(all_of(x)) and field_inf %>% dplyr::select(all_of(x))
## t = -3.0007, df = 30.125, p-value = 0.005368
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -3.7545577 -0.7138464
## sample estimates:
## mean of x mean of y
## 10.54611 12.78031
##
##
## [[18]]
##
## Welch Two Sample t-test
##
## data: lab_inf %>% dplyr::select(all_of(x)) and field_inf %>% dplyr::select(all_of(x))
## t = 0.4518, df = 45.841, p-value = 0.6535
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -1.486848  2.347379
## sample estimates:
## mean of x mean of y
## 20.08565 19.65539
##
##
## [[19]]
##
## Welch Two Sample t-test
##
## data: lab_inf %>% dplyr::select(all_of(x)) and field_inf %>% dplyr::select(all_of(x))
## t = 0.29544, df = 54.901, p-value = 0.7688
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -1.438643  1.936133
## sample estimates:
## mean of x mean of y
## 20.78288 20.53414

```