

Descriptive_immune_parameters

Fay

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R Markdown

How does our immune experimental data look like?

```
#### Read the file
```

```
CI <- read.csv("https://raw.githubusercontent.com/derele/Eimeria_Lab/master/data_products/Challenge_inf
```

Let's add a column with the parasite names

Summary statistics on experimental design

Summarizing data by each mouse

How many mice do we have in each infection ? (primary or challenge infection)

```
## # A tibble: 2 x 2
##   infection total_mice
##   <chr>         <int>
## 1 challenge      132
## 2 primary       153
```

For How many mice do we have Oocyst data?

```
CIMouse_gene %>%
  dplyr::group_by(infection) %>%
  drop_na(max_OOC) %>%
  dplyr::summarise(Total_mice = length(EH_ID))
```

```
## # A tibble: 2 x 2
##   infection Total_mice
##   <chr>         <int>
## 1 challenge      132
## 2 primary       153
```

For how many mice do we have data on weight?

```
CIMouse_gene %>%
  dplyr::group_by(infection) %>%
  drop_na(max_WL) %>%
  dplyr::summarise(Total_mice = length(EH_ID))
```

```
## # A tibble: 2 x 2
##   infection Total_mice
##   <chr>         <int>
## 1 challenge      132
## 2 primary       153
```

For how many mice do we have gene expression data?

```
#Primary:
CIMouse_gene %>%
  dplyr::group_by(infection) %>%
  dplyr::summarise(
    IFNy = length(na.omit(IFNy)),
    CXCR3_bio = length(na.omit(CXCR3_bio)),
    IL.6 = length(na.omit(IL.6)),
    IL.10 = length(na.omit(IL.10)),
    IL.13 = length(na.omit(IL.13)),
    IL1RN = length(na.omit(IL1RN)),
    CASP1 = length(na.omit(CASP1)),
    CXCL9 = length(na.omit(CXCL9)),
    IDO1 = length(na.omit(IDO1)),
    IRGM1 = length(na.omit(IRGM1)),
    MPO = length(na.omit(MPO)),
    MUC2 = length(na.omit(MUC2)),
    MUC5AC = length(na.omit(MUC5AC)),
    MYD88 = length(na.omit(MYD88)),
    NCR1 = length(na.omit(NCR1)),
    PRF1 = length(na.omit(PRF1)),
    RETNLB = length(na.omit(RETNLB)),
    SOCS1 = length(na.omit(SOCS1)),
    TICAM1 = length(na.omit(TICAM1)),
    TNF = length(na.omit(TNF)))

## # A tibble: 2 x 21
##   infection IFNy CXCR3_bio IL.6 IL.10 IL.13 IL1RN CASP1 CXCL9 IDO1 IRGM1
##   <chr>     <int>    <int> <int> <int> <int> <int> <int> <int> <int> <int>
## 1 challenge    89      116  106  106   30  116   114   116   116   116
## 2 primary     109      136  124  123   40  136   133   136   136   136
## # ... with 10 more variables: MPO <int>, MUC2 <int>, MUC5AC <int>, MYD88 <int>,
## #   NCR1 <int>, PRF1 <int>, RETNLB <int>, SOCS1 <int>, TICAM1 <int>, TNF <int>
```

For how many mice do we have facs data?

```
CIMouse_facs %>%
  dplyr::group_by(infection) %>%
  dplyr::summarise(
    CD4 = length(na.omit(CD4)),
    Treg = length(na.omit(Treg)),
    Div_Treg = length(na.omit(Div_Treg)),
    Treg17 = length(na.omit(Treg17)),
    Th1 = length(na.omit(Th1)),
    Div_Th1 = length(na.omit(Div_Th1)),
    Th17 = length(na.omit(Th17)),
    Div_Th17 = length(na.omit(Div_Th17)),
    CD8 = length(na.omit(CD8)),
    Act_CD8 = length(na.omit(Act_CD8)),
    Div_Act_CD8 = length(na.omit(Div_Act_CD8)),
    IFNy_CD4 = length(na.omit(IFNy_CD4)),
    IFNy_CD8 = length(na.omit(IFNy_CD8)),
    Treg_prop = length(na.omit(Treg_prop)),
    IL17A_CD4 = length(na.omit(IL17A_CD4)))

## # A tibble: 2 x 16
##   infection CD4 Treg Div_Treg Treg17 Th1 Div_Th1 Th17 Div_Th17 CD8
```

```
##   <chr>      <int> <int>      <int> <int> <int>      <int> <int>      <int> <int>
## 1 challenge    85    85        85    85    85        85    85        85    85
## 2 primary      0     0         0     0     0         0     0         0     0
## # ... with 6 more variables: Act_CD8 <int>, Div_Act_CD8 <int>, IFNy_CD4 <int>,
## #   IFNy_CD8 <int>, Treg_prop <int>, IL17A_CD4 <int>
```