

Weight_problems

Fay

2024-04-24

How many mice went through primary infections?

```
Challenge %>%
  filter(infection == "primary", Mouse_ID %in% lab$Mouse_ID,
         dpi == max_dpi) %>%
  summarise(n())
```

```
##    n()
## 1 136
```

How many mice died in the primary infections?

```
Challenge %>%
  filter(infection == "primary", Mouse_ID %in% lab$Mouse_ID,
         death == "primary", dpi == max_dpi) %>%
  summarise(n())
```

```
##    n()
## 1   20
```

How many mice were in the challenge infections?

```
Challenge %>%
  filter(infection == "challenge", Mouse_ID %in% lab$Mouse_ID,
         dpi == max_dpi, death == "challenge") %>%
  summarise(n())
```

```
##    n()
## 1 148
```

Something is fishy here. Do we have duplicates? Yes, I forgot to remove the spleen measurements. Luke used the spleen for gene expression for some mice. We use here the mesenteric lymph nodes. (?)

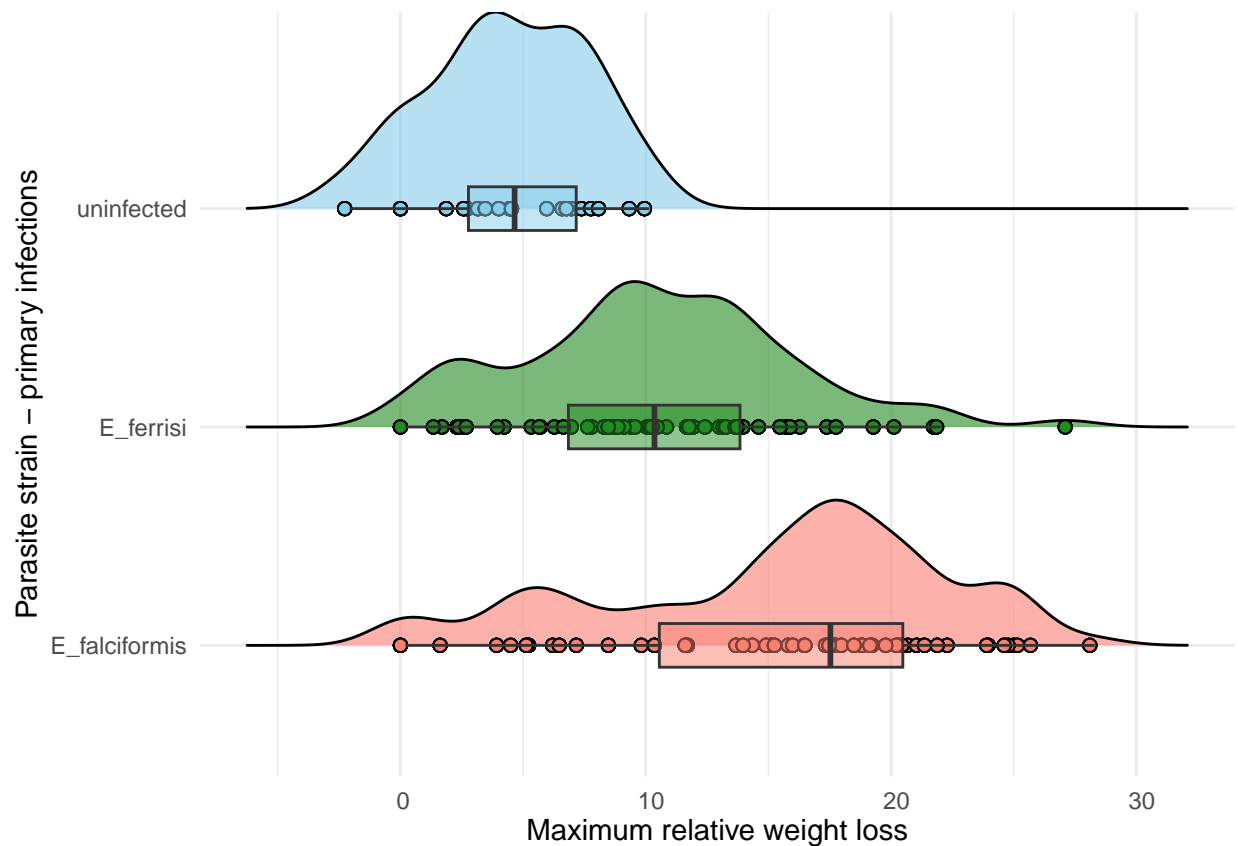
```
Challenge %>%
  filter(infection == "challenge", Mouse_ID %in% lab$Mouse_ID,
         dpi == max_dpi, death == "challenge", Position == "mLN") %>%
  summarize(n())
```

```
##    n()
## 1 116
```

Original in article of primary infections: I include mice that died in primary infections, but also the mice that went on to be challenged.

```
ggplot(Challenge %>%
  filter(infection == "primary", Mouse_ID %in% lab$Mouse_ID) %>%
  group_by(Mouse_ID),
  aes(x = WL_max, y = Parasite_primary, fill = Parasite_primary)) +
  geom_density_ridges(jittered_points = TRUE,
    position = position_points_jitter(height = 0),
    scale = 0.9, alpha = 0.6, point_shape = 21,
    point_size = 2, point_alpha = 1) +
  geom_boxplot(width = 0.2, outlier.shape = NA, alpha = 0.5,
    position = position_nudge(x = 0.2)) +
  # coord_flip() +
  theme_minimal() +
  scale_fill_manual(values = color_mapping) +
  theme(legend.position = "none",
    axis.text.x = element_text(angle = 0, vjust = 0.5, hjust=0.3)) +
  xlab("Maximum relative weight loss") +
  ylab("Parasite strain - primary infections")
```

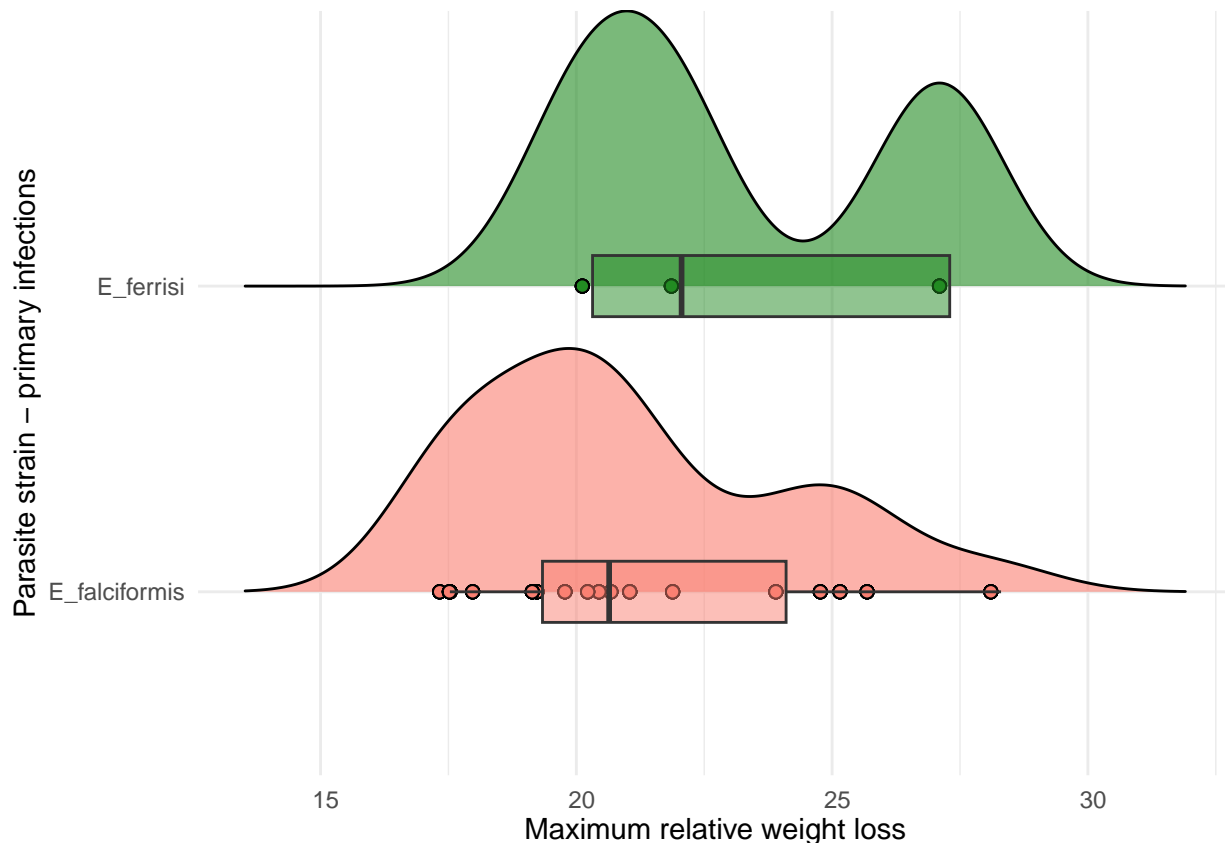
Picking joint bandwidth of 1.33



What happens, if I remove the mice that were challenged. Here, including just the mice that died in the primary infections.

```
ggplot(Challenge %>%
  filter(infection == "primary", Mouse_ID %in% lab$Mouse_ID,
    death == "primary") %>%
  group_by(Mouse_ID),
  aes(x = WL_max, y = Parasite_primary, fill = Parasite_primary)) +
  geom_density_ridges(jittered_points = TRUE,
    position = position_points_jitter(height = 0),
    scale = 0.9, alpha = 0.6, point_shape = 21,
    point_size = 2, point_alpha = 1) +
  geom_boxplot(width = 0.2, outlier.shape = NA, alpha = 0.5,
    position = position_nudge(x = 0.2)) +
  # coord_flip() +
  theme_minimal() +
  scale_fill_manual(values = color_mapping) +
  theme(legend.position = "none",
    axis.text.x = element_text(angle = 0, vjust = 0.5, hjust=0.3)) +
  xlab("Maximum relative weight loss") +
  ylab("Parasite strain - primary infections")
```

Picking joint bandwidth of 1.27



Where are the uninfected mice? Did we just have infected mice? I remember reaching the same conclusion before.

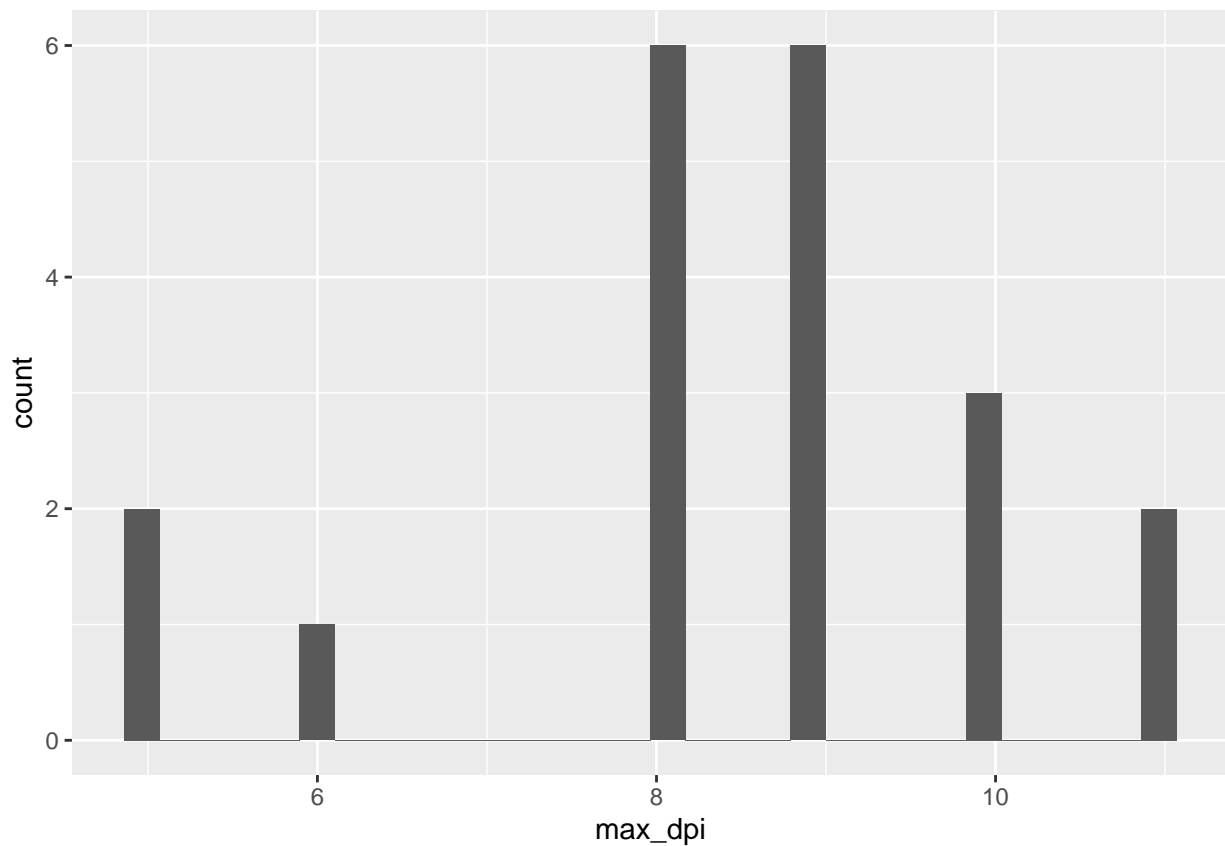
How many mice died on each day in the primary infections?

```
Challenge %>%
  filter(infection == "primary", Mouse_ID %in% lab$Mouse_ID,
         death == "primary", dpi == max_dpi) %>%
  group_by(max_dpi) %>%
  summarise(n())
```

```
## # A tibble: 6 x 2
##   max_dpi `n()`
##   <int> <int>
## 1     5     2
## 2     6     1
## 3     8     6
## 4     9     6
## 5    10     3
## 6    11     2
```

```
Challenge %>%
  filter(infection == "primary", Mouse_ID %in% lab$Mouse_ID,
         death == "primary", dpi == max_dpi) %>%
  ggplot(aes(x = max_dpi)) +
  geom_histogram()
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



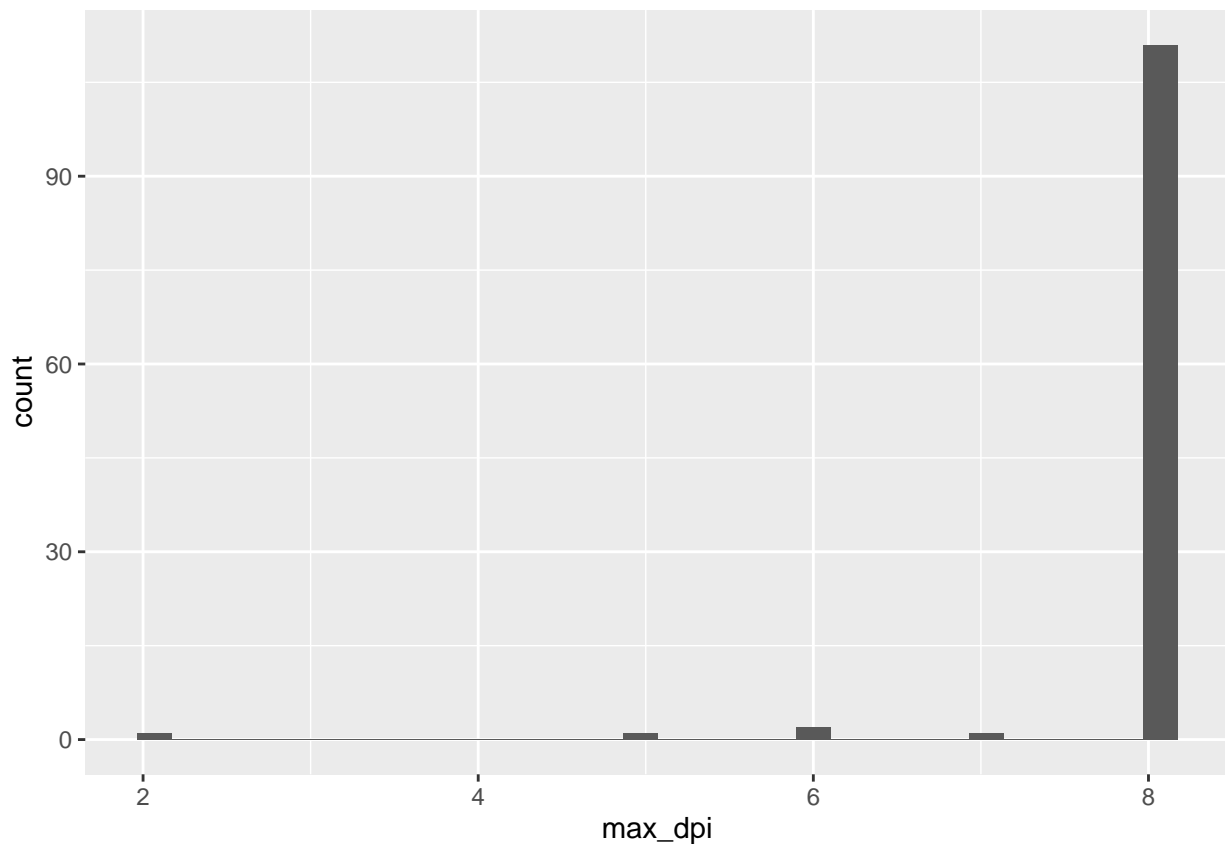
What about the challenge infections? How many mice died on each day in the primary infections?

```
Challenge %>%
  filter(infection == "challenge", Mouse_ID %in% lab$Mouse_ID,
         death == "challenge", dpi == max_dpi, Position == "mLN") %>%
  group_by(max_dpi) %>%
  summarise(n())
```

```
## # A tibble: 5 x 2
##   max_dpi `n()`
##   <int> <int>
## 1     2     1
## 2     5     1
## 3     6     2
## 4     7     1
## 5     8    111
```

```
Challenge %>%
  filter(infection == "challenge", Mouse_ID %in% lab$Mouse_ID,
         death == "challenge", dpi == max_dpi, Position == "mLN") %>%
  ggplot(aes(x = max_dpi)) +
  geom_histogram()
```

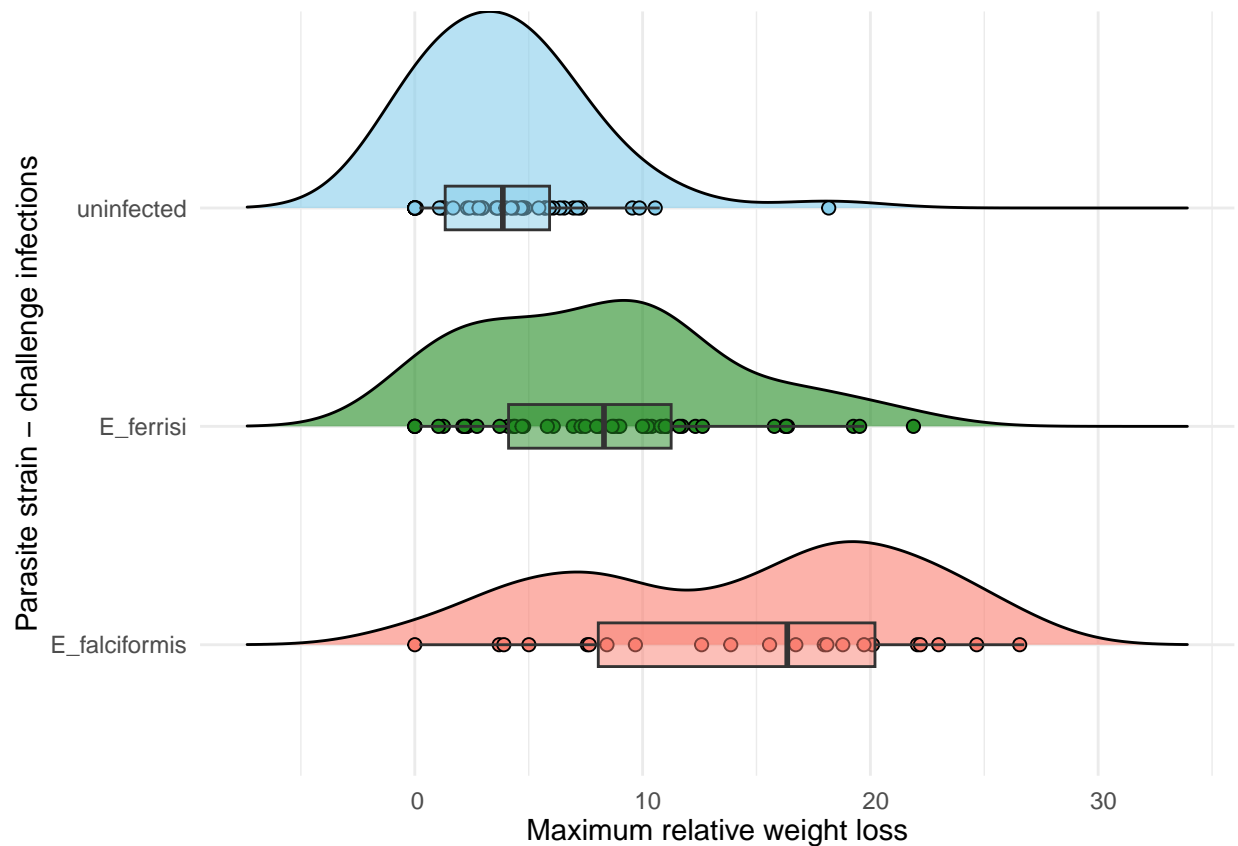
```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



Challenge infections remains the same

```
ggplot(lab %>%  
  filter(infection == "challenge") %>%  
  group_by(Mouse_ID),  
  aes(x = WL_max, y = Parasite_challenge, fill = Parasite_challenge)) +  
  geom_density_ridges(jittered_points = TRUE, position =  
    position_points_jitter(height = 0),  
    scale = 0.9, alpha = 0.6, point_shape = 21,  
    point_size = 2, point_alpha = 1) +  
  geom_boxplot(width = 0.2, outlier.shape = NA, alpha = 0.5,  
    position = position_nudge(x = 0.2)) +  
  # coord_flip() +  
  theme_minimal() +  
  scale_fill_manual(values = color_mapping) +  
  theme(legend.position = "none",  
    axis.text.x = element_text(angle = 0, vjust = 0.5, hjust=0.3)) +  
  xlab("Maximum relative weight loss") +  
  ylab("Parasite strain - challenge infections")
```

Picking joint bandwidth of 2.45



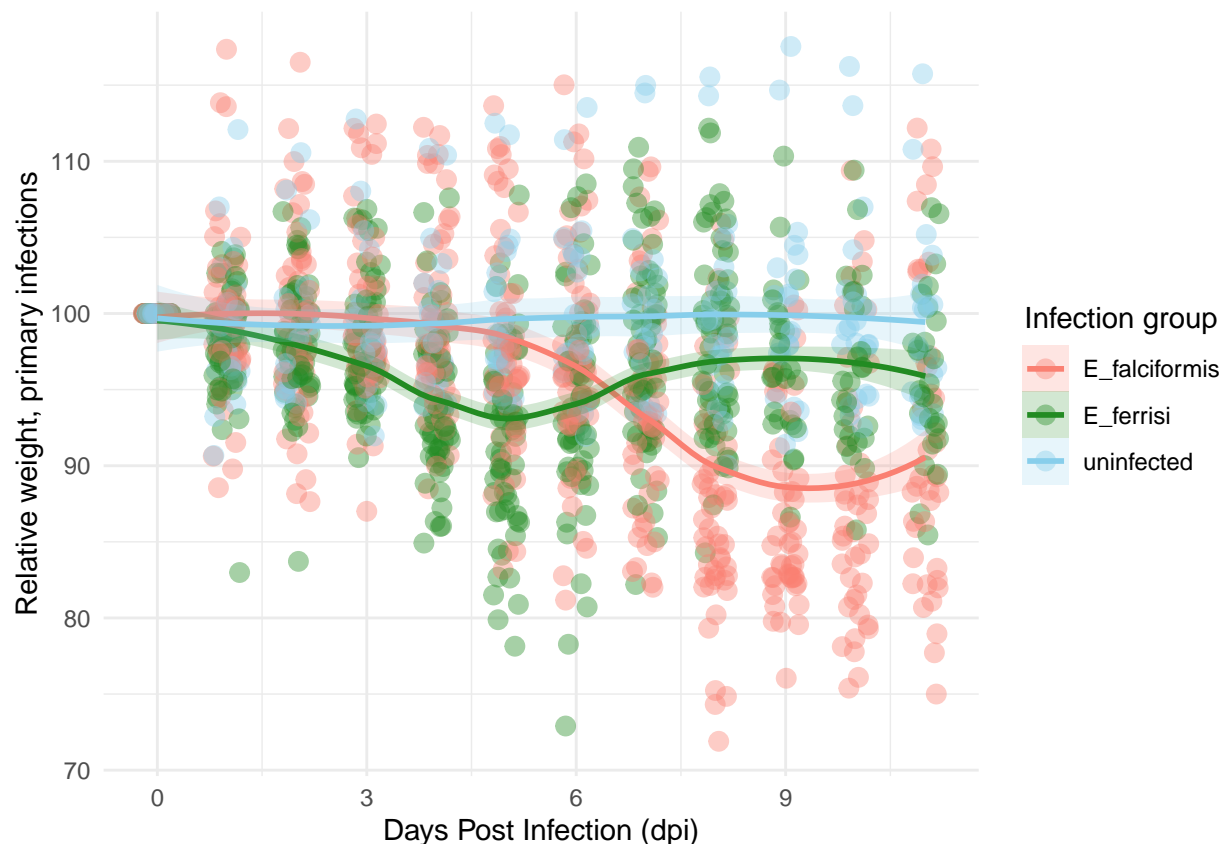
So what about the weight loss per dpi. Here is what I originally plotted:

```

#relative weight loss per day - primary
Challenge %>%
  filter(infection == "primary", Mouse_ID %in% lab$Mouse_ID) %>%
  ggplot(aes(x = dpi, y = relative_weight, color = Parasite_primary,
             fill = Parasite_primary)) +
  geom_jitter(width = 0.2, height = 0, alpha = 0.4,
             shape = 21, stroke = 0.5, size = 3) + # Adjusted for outlines
  geom_smooth(aes(fill = Parasite_primary),
             method = "loess", se = TRUE, alpha = 0.2) +
  # Add smooth line with confidence intervals
  scale_color_manual(values = color_mapping) + # Apply custom color mapping
  scale_fill_manual(values = color_mapping) +
  # Ensure fills match colors for confidence intervals
  labs(#title = "Relative Weight by Days Post Infection",
       x = "Days Post Infection (dpi)",
       y = "Relative weight, primary infections",
       color = "Infection group",
       fill = "Infection group") + # Added for consistency with the legend
  theme_minimal() + # Use a minimal theme for a cleaner look
  theme(legend.position = "right", # Adjust legend position
        plot.title = element_text(hjust = 0.5), # Center the plot title
        legend.title.align = 0.5)

```

```
## `geom_smooth()` using formula = 'y ~ x'
```



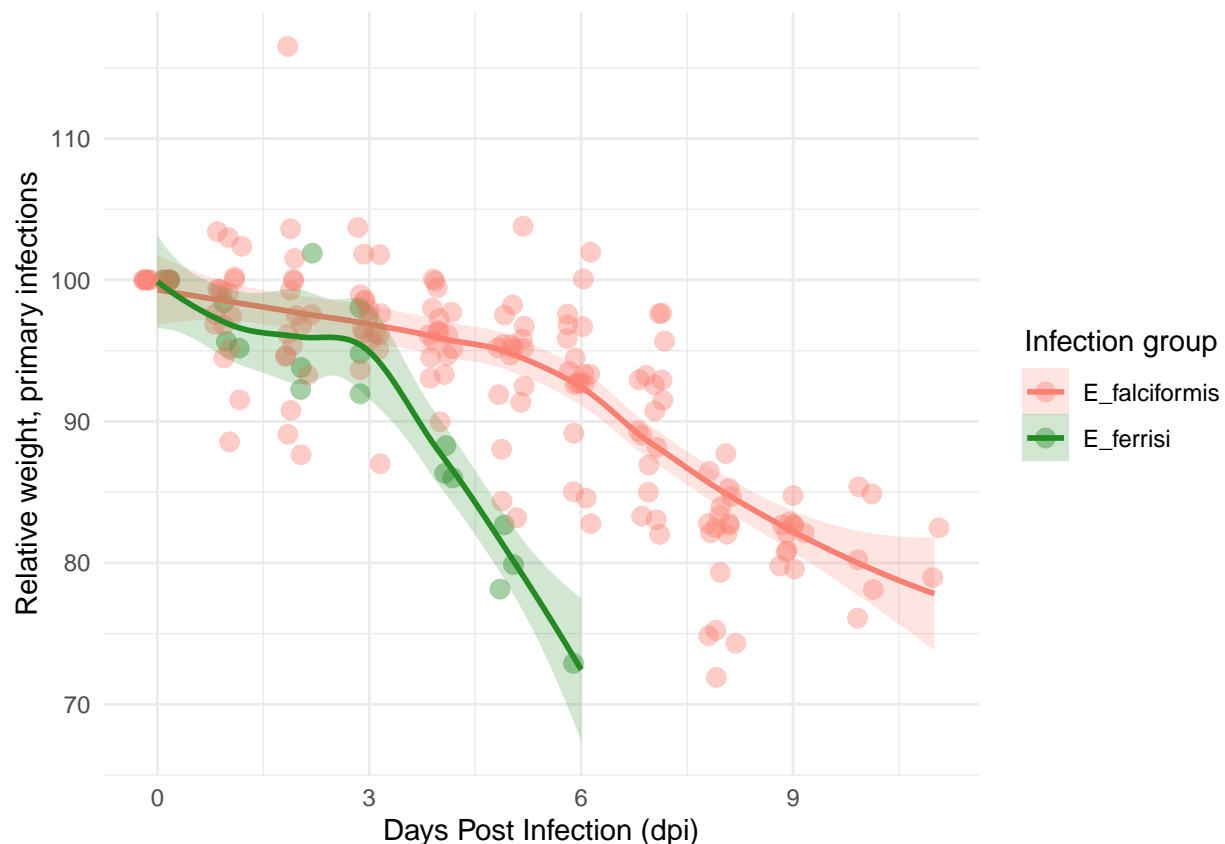
Should I include ONLY the 20 mice that were solely subjected to primary infections?

```

#relative weight loss per day - primary
Challenge %>%
  filter(infection == "primary", Mouse_ID %in% lab$Mouse_ID, death == "primary") %>%
  ggplot(aes(x = dpi, y = relative_weight, color = Parasite_primary,
             fill = Parasite_primary)) +
  geom_jitter(width = 0.2, height = 0, alpha = 0.4,
             shape = 21, stroke = 0.5, size = 3) + # Adjusted for outlines
  geom_smooth(aes(fill = Parasite_primary),
             method = "loess", se = TRUE, alpha = 0.2) +
  # Add smooth line with confidence intervals
  scale_color_manual(values = color_mapping) + # Apply custom color mapping
  scale_fill_manual(values = color_mapping) +
  # Ensure fills match colors for confidence intervals
  labs(#title = "Relative Weight by Days Post Infection",
       x = "Days Post Infection (dpi)",
       y = "Relative weight, primary infections",
       color = "Infection group",
       fill = "Infection group") + # Added for consistency with the legend
  theme_minimal() + # Use a minimal theme for a cleaner look
  theme(legend.position = "right", # Adjust legend position
        plot.title = element_text(hjust = 0.5), # Center the plot title
        legend.title.align = 0.5)

```

```
## `geom_smooth()` using formula = 'y ~ x'
```



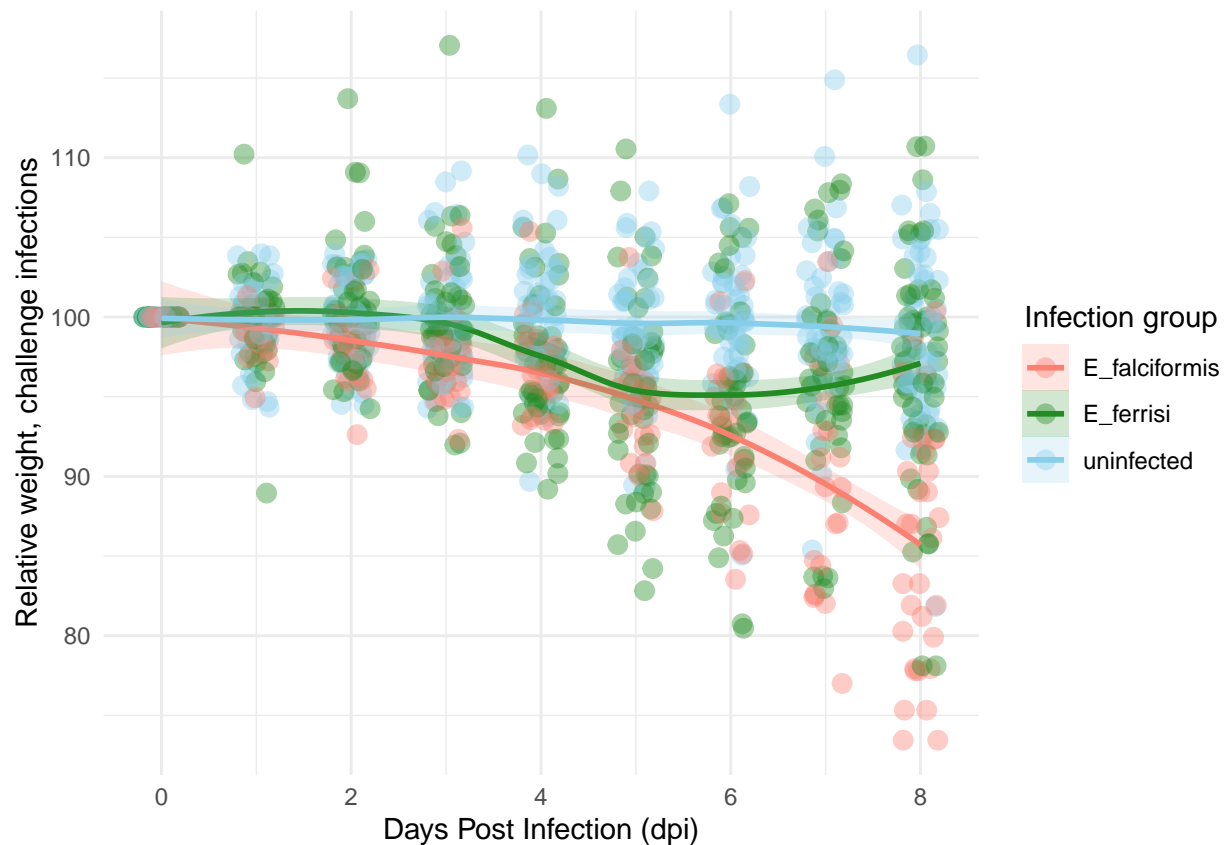
Why do the ferrisi mice loose more weight? They probably died on day 6 naturally? Many mice fall under

the 80% relative weight.

Back to the challenge infections:

```
#relative weight loss per day - challenge
Challenge %>%
  filter(infection == "challenge", Mouse_ID %in% lab$Mouse_ID) %>%
  ggplot(aes(x = dpi, y = relative_weight, color = Parasite_challenge,
             fill = Parasite_challenge)) +
  geom_jitter(width = 0.2, height = 0, alpha = 0.4,
             shape = 21, stroke = 0.5, size = 3) + # Adjusted for outlines
  geom_smooth(aes(fill = Parasite_challenge),
             method = "loess", se = TRUE, alpha = 0.2) +
  #Add smooth line with confidence intervals
  scale_color_manual(values = color_mapping) + # Apply custom color mapping
  scale_fill_manual(values = color_mapping) +
  # Ensure fills match colors for confidence intervals
  labs(#title = "Relative Weight by Days Post Infection",
       x = "Days Post Infection (dpi)",
       y = "Relative weight, challenge infections",
       color = "Infection group",
       fill = "Infection group") + # Added for consistency with the legend
  theme_minimal() + # Use a minimal theme for a cleaner look
  theme(legend.position = "right", # Adjust legend position
        plot.title = element_text(hjust = 0.5), # Center the plot title
        legend.title.align = 0.5)
```

```
## `geom_smooth()` using formula = 'y ~ x'
```



Falciformis mice falling under 80%, but only on day 8.

Mouse strains:

```
# transform mouse strain into factor
lab$mouse_strain <- as.factor(lab$mouse_strain)

lab$mouse_strain <- gsub(pattern = "_", " ", lab$mouse_strain)

#Numbers of each mouse strain
ggplot(lab, aes(x = WL_max, y = mouse_strain, fill = mouse_strain)) +
  geom_density_ridges(jittered_points = TRUE, position =
    position_points_jitter(height = 0),
    scale = 0.9, alpha = 0.6, point_shape = 21,
    point_size = 2, point_alpha = 1) +
  geom_boxplot(width = 0.2, outlier.shape = NA, alpha = 0.5,
    position = position_nudge(x = 0.2)) +
  coord_flip() +
  theme_minimal() +
  theme(legend.position = "none",
    axis.text.x = element_text(angle = 70, vjust = 0.5, hjust=0.3)) +
  xlab("Maximum relative weight loss") +
  ylab("Mouse Strain") +
  facet_grid(~infection)
```

```
## Picking joint bandwidth of 2.02
```

```
## Picking joint bandwidth of 1.64
```

