

Homework: Linear Models

PLPA-5820 (Spring 2025)

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Notes

```
library(tidyverse)
```

```
-- Attaching core tidyverse packages ----- tidyverse 2.0.0 --  
v dplyr      1.1.4      v readr      2.1.5  
v forcats    1.0.0      v stringr    1.5.1  
v ggplot2    3.5.1      v tibble     3.2.1  
v lubridate  1.9.4      v tidyr      1.3.1  
v purrr      1.0.4
```

```
-- Conflicts ----- tidyverse_conflicts() --
```

```
x dplyr::filter() masks stats::filter()
```

```
x dplyr::lag()     masks stats::lag()
```

```
i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become
```

```
library(lme4)
```

Loading required package: Matrix

Attaching package: 'Matrix'

The following objects are masked from 'package:tidyr':

expand, pack, unpack

```
library(emmeans)
```

Welcome to emmeans.

Caution: You lose important information if you filter this package's results.
See '? untidy'

```
library(multcomp)
```

```
Loading required package: mvtnorm
Loading required package: survival
Loading required package: TH.data
Loading required package: MASS
```

```
Attaching package: 'MASS'
```

```
The following object is masked from 'package:dplyr':
```

```
select
```

```
Attaching package: 'TH.data'
```

```
The following object is masked from 'package:MASS':
```

```
geyser
```

```
bull.rich <- read_csv("Bull_richness.csv")
```

```
Rows: 287 Columns: 16
```

```
-- Column specification -----
```

```
Delimiter: ","
```

```
chr (13): SampleID, Crop, Objective, Compartment, DateSampled, GrowthStage, ...
```

```
dbl (3): Collection, Year, richness
```

```
i Use `spec()` to retrieve the full column specification for this data.
```

```
i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```
lm.inter <- lm(richness ~ GrowthStage*Fungicide, data = bull.rich)

lsmeans <- emmeans(lm.inter, ~Fungicide|GrowthStage )
Results_lsmeans <- cld(lsmeans, alpha = 0.05, reversed = TRUE, details = TRUE)

lme1 <- lmer(richness ~ GrowthStage*Fungicide + (1|Rep), data = bull.rich)
```

boundary (singular) fit: see help('isSingular')

```
lsmeans_lme1 <- emmeans(lme1, ~Fungicide|GrowthStage )
Results_lsmeans_lme1 <- cld(lsmeans_lme1, alpha = 0.05, reversed = TRUE, details = TRUE)

# add significance level as asterisks
significance <- data.frame(GrowthStage = Results_lsmeans_lme1$comparisons$GrowthStage,
  p.value = Results_lsmeans_lme1$comparisons$p.value) %>%
  mutate(sig = ifelse(p.value < 0.05, ifelse(p.value < 0.01, "***", "*"), NA)) %>%
  mutate(Fungicide = '')

ggplot(bull.rich, aes(x = GrowthStage, y = richness, fill = Fungicide)) +
  geom_boxplot() +
  geom_text(data = significance, aes(x = GrowthStage, label = sig), y = 35, size = 6) +
  theme_minimal()
```

Warning: Removed 2 rows containing missing values or values outside the scale range (`geom_text()`).

