

1st setting-R&D tunnel

```
library(readxl)
library(skimr)
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  1.9.3      v tidyr      1.3.1
v purrr      1.0.2
```

```
-- 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(ggplot2)
library(knitr)
```

```
Hedge_tunnel_sand_beds <- read_excel("Y:/Technical Division/Nursery/R&D Nursery/Hedge tunnel
```

```
Hedge_tunnel_sand_beds |>
  kable()
```

Table	Treatment	Ecotype	Female	Male	Quantity
1	No heat	PTL	BP012	16-059	727
1	No heat	PTL	BP026	16-022	441
1	No heat	PTL	BP002	16-059	196
2	No heat	PTH	BP002	13-324	462
2	No heat	PTH	BP012	13-324	504

Table	Treatment	Ecotype	Female	Male	Quantity
3	Close space	PTH	PTH 365	NA	607
4	Closer spacing	PTL	BP002	16-022	882
4	Closer spacing	PTL	BP002	16-023	165
5	Heat	PTL	BP012	16-022	537
5	Heat	PTL	BP012	16-277	509
5	Heat	PTL	BP012	16-278	826
6	Heat	PTH	BP002	13-008	1323
7	Heat	PTH	BP002	13-008	392
7	Heat	PTH	GAP272	13-012	251
7	Heat	PTH	BP026	13-067	343
8	No heat	PTL	BP026	16-277	966
8	No heat	PTL	BP002	16-023	578
9	Closer spacing	PTL	BP012	16-040	330
9	Closer spacing	PTL	GAP267	16-040	1761
10	Normal spacing	PTL	BP002	16-040	1148
11	Heat	PTL	BP026	16-060	686
11	Heat	PTL	BP024	16-022	315
11	Heat	PTL	BP012	16-023	339
11	Heat	PTL	BP026	16-059	325
11	Heat	PTL	BP012	16-022	242
12	Close space	PTH	PTH 365	NA	488
13	Heat	PTL	BP026	16-040	284
13	Heat	PTL	BP026	16-059	192
13	Heat	PTL	BP026	16-022	259
13	Heat	PTL	BP026	16-060	223
14	Heat	PTH	BP002	13-324	805
15	Normal spacing	PTL	BP002	16-040	1498
16	Wide space	PTH	PTH 365	NA	557
17	Wide space	PTH	PTH 365	NA	762
18	No heat	PTH	GAP267	13-324	1406
19	No heat	PTL	BP002	16-060	245
19	No heat	PTL	BP002	16-023	196
19	No heat	PTL	BP002	16-059	518
19	No heat	PTL	BP024	16-060	392
20	No heat	PTH	BP024	13-324	464
20	No heat	PTH	GAP263	13-324	490
20	No heat	PTH	BP026	13-067	308

Data analysis

```
Hedge_tunnel_sand_beds |>
  skim()
```

Table 2: Data summary

Name	Hedge_tunnel_sand_beds
Number of rows	42
Number of columns	6
Column type frequency:	
character	4
numeric	2
Group variables	None

Variable type: character

skim_variable	n_missing	complete_rate	min	max	empty	n_unique	whitespace
Treatment	0	1.0	4	14	0	6	0
Ecotype	0	1.0	3	3	0	2	0
Female	0	1.0	5	7	0	8	0
Male	4	0.9	6	6	0	11	0

Variable type: numeric

skim_variable	n_missing	complete_rate	mean	sd	p0	p25	p50	p75	p100	hist
Table	0	1	10.45	5.99	1	5.25	11	14.75	20	
Quantity	0	1	570.05	383.05	165	309.75	476	716.75	1761	

```
Hedge_tunnel_sand_beds |>
  summary()
```

Table	Treatment	Ecotype	Female
Min. : 1.00	Length:42	Length:42	Length:42
1st Qu.: 5.25	Class :character	Class :character	Class :character
Median :11.00	Mode :character	Mode :character	Mode :character
Mean :10.45			
3rd Qu.:14.75			

```

Max.      :20.00
      Male      Quantity
Length:42      Min.      : 165.0
Class :character 1st Qu.: 309.8
Mode  :character Median : 476.0
                        Mean  : 570.0
                        3rd Qu.: 716.8
                        Max.   :1761.0

```

Analysis

```

#anova_model <- aov(Outcome ~ Treatment, data = data)
anova_model <- aov(Quantity~Treatment , data = Hedge_tunnel_sand_beds)
summary (anova_model)

```

```

              Df  Sum Sq Mean Sq F value Pr(>F)
Treatment      5 1562805  312561    2.527 0.0464 *
Residuals     36 4452985  123694
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

The F Value is the ratio of the Mean Square for Treatment to the Mean Square for Residuals. It tests whether the variability between groups is significantly greater than the variability within groups.

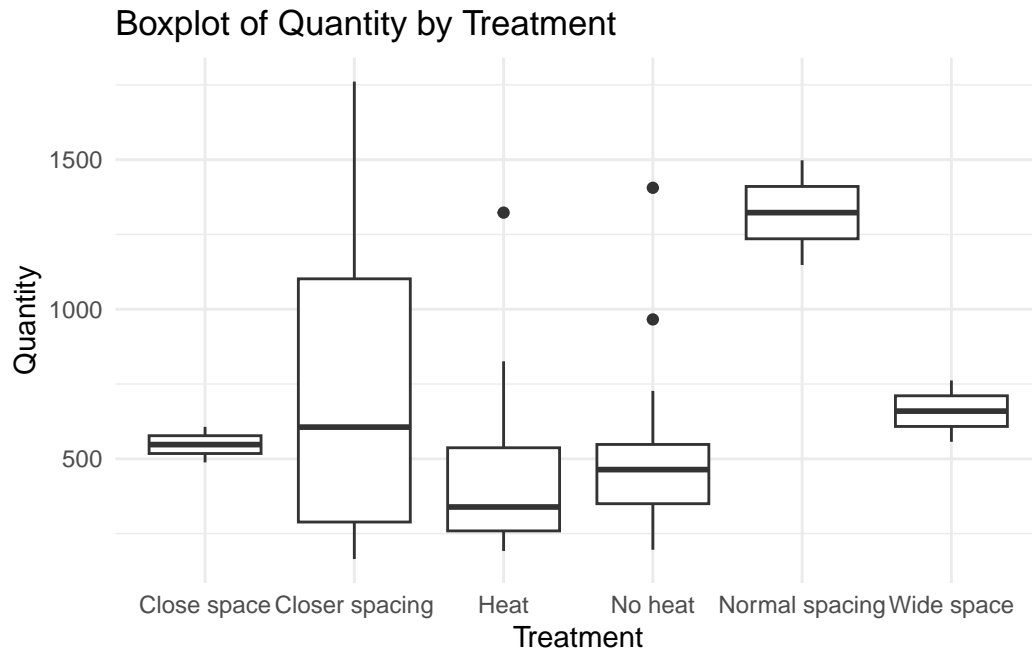
This is the p-value associated with the F statistic. It indicates the probability of observing an F value at least as extreme as the one obtained, assuming the null hypothesis is true (i.e., that there are no differences between the treatment groups).

The p-value for Treatment is 0.0464. This is typically compared to a significance level (alpha), often set at 0.05. Since 0.0464 is less than 0.05, you can reject the null hypothesis and conclude that there are statistically significant differences among the treatment groups.

```

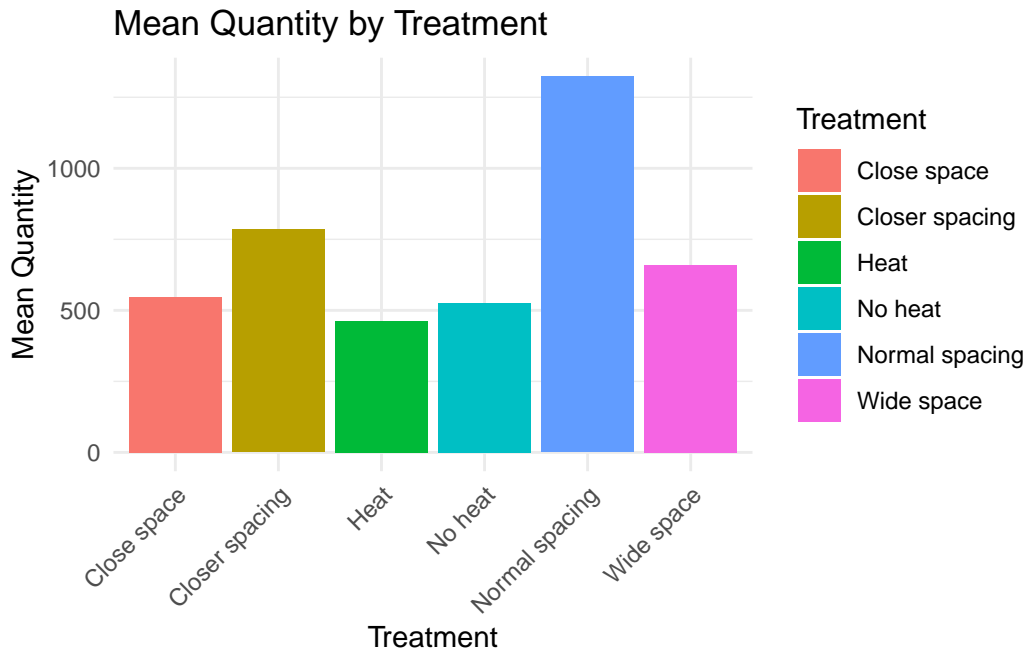
# Create a boxplot to visualize the distribution of Quantity by Treatment
ggplot(Hedge_tunnel_sand_beds, aes(x = Treatment, y = Quantity)) +
  geom_boxplot() +
  theme_minimal() +
  labs(title = "Boxplot of Quantity by Treatment", x = "Treatment", y = "Quantity")

```



```
# Calculate the mean Quantity for each Treatment
mean_quantity <- aggregate(Quantity ~ Treatment, data = Hedge_tunnel_sand_beds, FUN = mean)

# Create the bar graph
ggplot(mean_quantity, aes(x = Treatment, y = Quantity, fill = Treatment)) +
  geom_bar(stat = "identity") +
  theme_minimal() +
  labs(title = "Mean Quantity by Treatment", x = "Treatment", y = "Mean Quantity") +
  theme(axis.text.x = element_text(angle = 45, hjust = 1))
```



```
# Fit the ANOVA model with Treatment, Ecotype, and their interaction
anova_model <- aov(Quantity ~ Treatment * Ecotype, data = Hedge_tunnel_sand_beds)

# Display the ANOVA table
summary(anova_model)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Treatment	5	1562805	312561	2.526	0.0476 *
Ecotype	1	230413	230413	1.862	0.1813
Treatment:Ecotype	1	16290	16290	0.132	0.7189
Residuals	34	4206282	123714		

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

- **Treatment:** Significant ($p = 0.0476$). This indicates that the mean quantities are different among the different treatments.
- **Ecotype:** Not significant ($p = 0.1813$). This suggests that ecotype alone does not have a significant effect on the quantity.
- **Treatment** Not significant ($p = 0.7189$). This suggests that there is no significant interaction between treatment and ecotype.

```
# Mean Quantity
mean_quantity_ecotype <- aggregate(Quantity ~ Treatment + Ecotype, data = Hedge_tunnel_sand_L

# grouped bar graph
ggplot(mean_quantity_ecotype, aes(x = Treatment, y = Quantity, fill = Ecotype)) +
  geom_bar(stat = "identity", position = "dodge") +
  theme_minimal() +
  labs(title = "Mean Quantity by Treatment and Ecotype", x = "Treatment", y = "Mean Quantity") +
  theme(axis.text.x = element_text(angle = 45, hjust = 1)) +
  scale_fill_brewer(palette = "Set1")
```

