

Stem Rot

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Necessary libraries

Data Organisation

Read from excel and getting weighted average score

Each plot had 25 tillers graded for disease severity. Each tiller had a grading from 0-4, where 0 is healthy and 4 is a trainwreck. Total score is the sum of the products of number of tillers at each severity rating. i.e. number of tillers at a rating of 1 x 1 + number of tillers at a rating of 1 x 2.... Weighted average is total score divided by the number of tillers scored i.e. Total_Score/25.

```
master <- read_excel("StemRot_Master.xlsx", sheet = 1)
master <- mutate_if(master, is.character, as.factor)
master$Year <- as.factor(master$Year)
master$Blk <- as.factor(master$Blk)

master$Total_Score <- (master$One*1)+(master$Two*2)+(master$Three*3)+(master$Four*4)+(master$Five*5)
master$Weighted_Average <- master$Total_Score/25
```

```
master$total_plants <- (master$One)+(master$Two)+(master$Three)+(master$Four)+(master$Five)

table(master$total_plants)
```

```
##
## 25
## 18
```

```
#checked that all is okayyyyyy and have 25 tillers
```

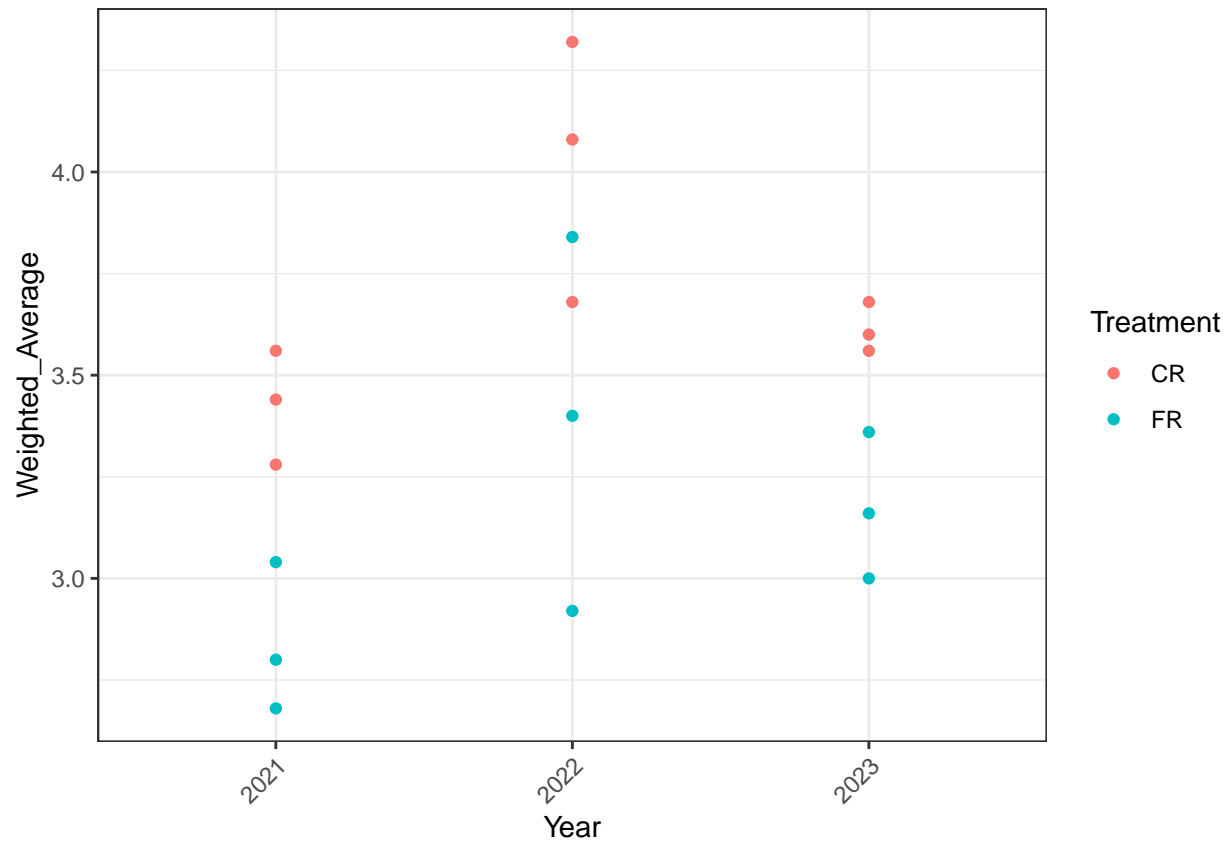
```
str(master)
```

```
## tibble [18 x 12] (S3: tbl_df/tbl/data.frame)
##  $ Plot      : num [1:18] 101 202 303 111 207 308 404 501 604 410 ...
##  $ One       : num [1:18] 0 0 0 0 0 0 0 0 0 0 ...
##  $ Two       : num [1:18] 6 10 13 0 3 3 7 1 0 2 ...
##  $ Three     : num [1:18] 13 11 8 14 13 12 14 16 10 7 ...
##  $ Four      : num [1:18] 5 3 3 8 8 6 3 5 9 13 ...
##  $ Five      : num [1:18] 1 1 1 3 1 4 1 3 6 3 ...
##  $ Treatment  : Factor w/ 2 levels "CR","FR": 2 2 2 1 1 1 2 2 2 1 ...
##  $ Year       : Factor w/ 3 levels "2021","2022",..: 1 1 1 1 1 1 2 2 2 2 ...
##  $ Blk        : Factor w/ 9 levels "1","2","3","4",..: 1 2 3 1 2 3 4 5 6 4 ...
##  $ Total_Score : num [1:18] 76 70 67 89 82 86 73 85 96 92 ...
##  $ Weighted_Average: num [1:18] 3.04 2.8 2.68 3.56 3.28 3.44 2.92 3.4 3.84 3.68 ...
##  $ total_plants : num [1:18] 25 25 25 25 25 25 25 25 25 25 ...
```

Initial visualisation

Just purely based on visual inspection, CR has higher disease severity than FR.

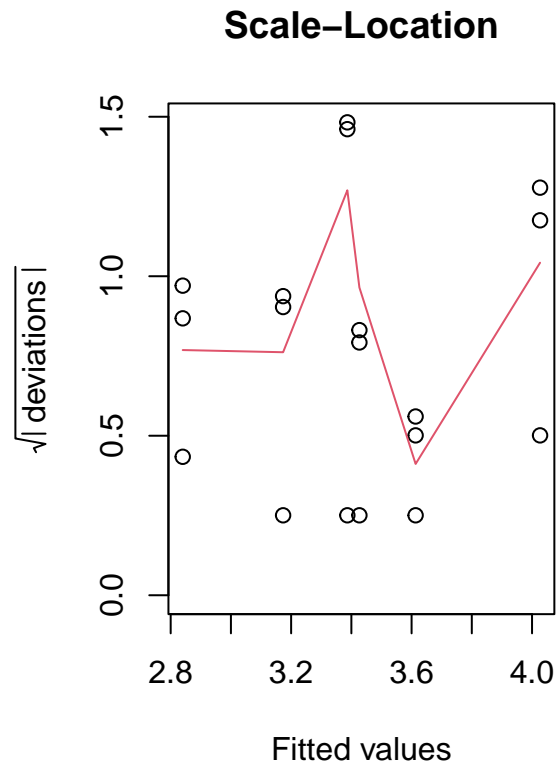
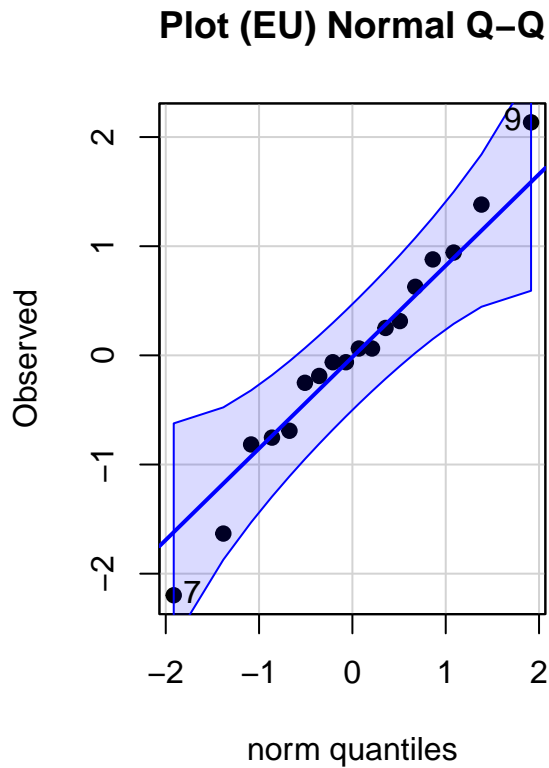
```
ggplot(master, aes(y=Weighted_Average, x=Year, color=Treatment))+
  geom_point()+
  theme(axis.text.x = element_text(angle = 45, hjust = 1, size= 9))
```



Look at a basic linear model

Seems that there is a strong year effect and also a strong Treatment effect. Proceed with testings by year.

```
all_factors_model <- lm(Weighted_Average~Treatment*Year, data = master)
pls205_diagnostics(all_factors_model)
```

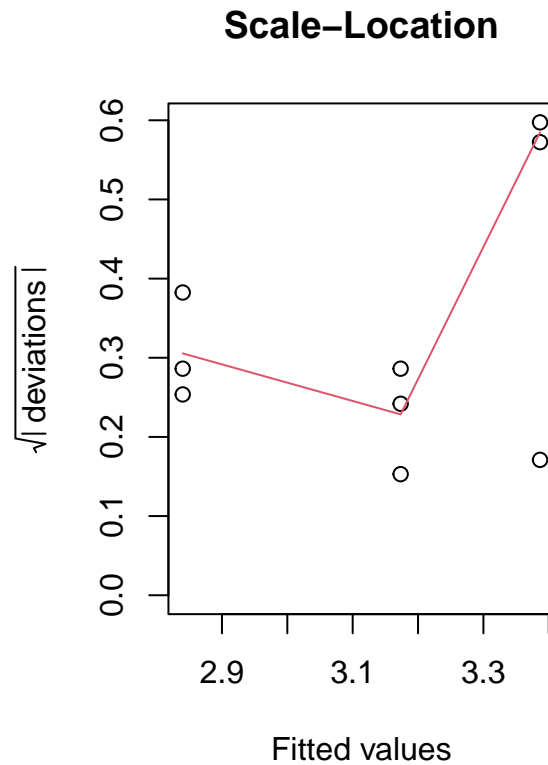
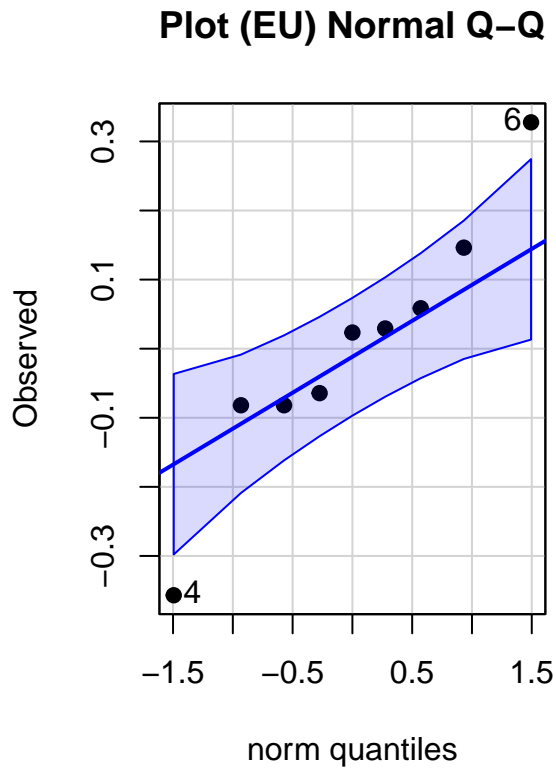


```
anova(all_factors_model)
```

```
## Analysis of Variance Table
##
## Response: Weighted_Average
##          Df Sum Sq Mean Sq F value    Pr(>F)
## Treatment  1  1.38889  1.38889  20.5322 0.0006882 ***
## Year       2   0.98898  0.49449   7.3101 0.0083910 **
## Treatment:Year  2  0.03218  0.01609   0.2378 0.7919542
## Residuals   12  0.81173  0.06764
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Testing by year (Main text results taken from here)

```
disease_model <- lmer(Weighted_Average~Treatment*Year+(1|Blk), data = master)
pls205_diagnostics(disease_model, EU = "Blk")
```



```
anova(disease_model)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##              Sum Sq Mean Sq NumDF DenDF F value    Pr(>F)
## Treatment      1.38889  1.38889     1     6 94.1265 6.881e-05 ***
## Year            0.12107  0.06053     2     6  4.1025  0.07536 .
## Treatment:Year  0.03218  0.01609     2     6  1.0904  0.39453
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Treatment_means = emmeans(disease_model, spec = 'Treatment', by = 'Year')
Treatment_effects = contrast(Treatment_means, method = 'pairwise', adjust = "Tukey")

summary(Treatment_effects)
```

```
## Year = 2021:
## contrast estimate      SE df t.ratio p.value
## CR - FR      0.587 0.0992  6   5.915  0.0010
##
## Year = 2022:
## contrast estimate      SE df t.ratio p.value
## CR - FR      0.640 0.0992  6   6.453  0.0007
##
## Year = 2023:
## contrast estimate      SE df t.ratio p.value
```

```
## CR - FR      0.440 0.0992  6   4.436  0.0044
##
## Degrees-of-freedom method: kenward-roger
```

```
cld(Treatment_means)
```

```
## Year = 2021:
## Treatment emmean   SE    df lower.CL upper.CL .group
## FR          2.84 0.15 7.45     2.49     3.19  1
## CR          3.43 0.15 7.45     3.08     3.78  2
##
## Year = 2022:
## Treatment emmean   SE    df lower.CL upper.CL .group
## FR          3.39 0.15 7.45     3.04     3.74  1
## CR          4.03 0.15 7.45     3.68     4.38  2
##
## Year = 2023:
## Treatment emmean   SE    df lower.CL upper.CL .group
## FR          3.17 0.15 7.45     2.82     3.52  1
## CR          3.61 0.15 7.45     3.26     3.96  2
##
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
## significance level used: alpha = 0.05
## NOTE: If two or more means share the same grouping symbol,
##       then we cannot show them to be different.
##       But we also did not show them to be the same.
```

```
Treatment_effects_summary <-
  as.data.frame(summary(Treatment_effects)) %>%
  mutate(
    p_value = case_when(
      p.value < 0.05 ~ "*",          # For p-values less than 0.01
      TRUE ~ sprintf("%.2f", p.value) # Force two decimal places for all other p-values
    )
  )
```

Pairwise pooled

```
Treatment_means_average = emmeans(disease_model, spec = 'Treatment')
```

```
## NOTE: Results may be misleading due to involvement in interactions
```

```
Treatment_effects_average = contrast(Treatment_means_average, method = 'pairwise', adjust = "Tukey")
summary(Treatment_effects_average)
```

```
## contrast estimate      SE df t.ratio p.value
## CR - FR          0.556 0.0573  6   9.702  0.0001
```

```
##
## Results are averaged over the levels of: Year
## Degrees-of-freedom method: kenward-roger
```

```
cld(Treatment_means_average)
```

```
## Treatment emmean SE df lower.CL upper.CL .group
## FR 3.13 0.0867 7.45 2.93 3.34 1
## CR 3.69 0.0867 7.45 3.49 3.89 2
##
## Results are averaged over the levels of: Year
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
## significance level used: alpha = 0.05
## NOTE: If two or more means share the same grouping symbol,
## then we cannot show them to be different.
## But we also did not show them to be the same.
```

```
Treatment_effects_summary_average <-
  as.data.frame(summary(Treatment_effects_average)) %>%
  mutate(
    p_value = case_when(
      p.value < 0.05 ~ "*", # For p-values less than 0.01
      TRUE ~ sprintf("%.2f", p.value) # Force two decimal places for all other p-values
    )
  )
```

Graphing dataframe

```
graphing <- master %>%
  group_by(Treatment, Year) %>%
  mutate(Weighted_Average_se = sd(Weighted_Average)/sqrt(3)) %>%
  summarise(Weighted_Average = mean(Weighted_Average),
            Weighted_Average_se = mean(Weighted_Average_se)) %>%
  left_join(Treatment_effects_summary %>% select(Year, p_value), by = "Year")
```

```
## 'summarise()' has grouped output by 'Treatment'. You can override using the
## '.groups' argument.
```

Graphs

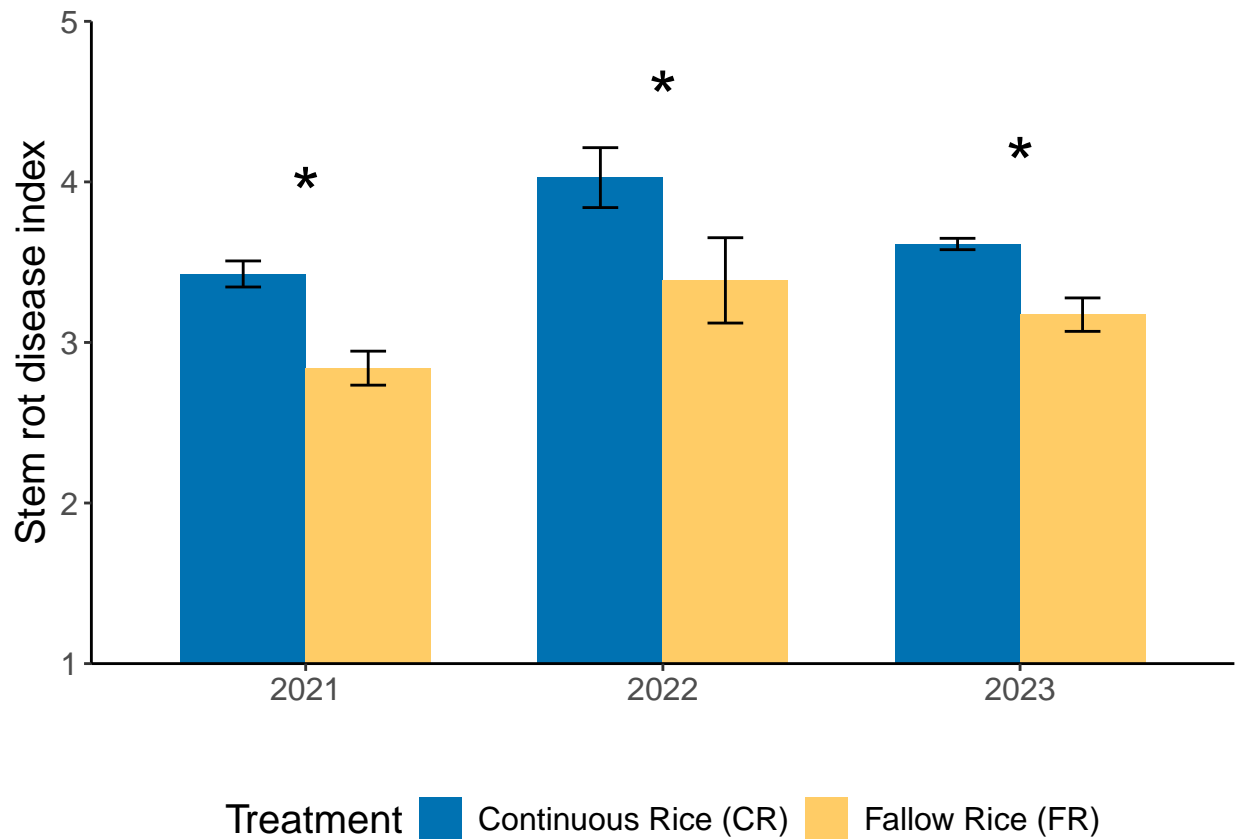
```
Disease_graph_bar <-
  ggplot(graphing, aes(x = Year, y = Weighted_Average, fill = Treatment)) +
  #geom_boxplot()+
  geom_bar(stat = "identity", position = "dodge", width = 0.7) +
  labs(x = "Year", y = "Weighted_Average", fill = "Treatment") +
  scale_fill_manual(values = c("#0072B2", "#FFCC66"), labels = c("Continuous Rice (CR)", "Fallow Rice (FR)"))
```

```

geom_errorbar(aes(ymin=Weighted_Average-Weighted_Average_se, ymax=Weighted_Average+Weighted_Average_se,
scale_y_continuous(name="Stem rot disease index", limits = c(0, 5), expand = c(0, 0))+
coord_cartesian(ylim = c(1, 5))+
scale_x_discrete(name="")+
theme_classic()+
theme(axis.text.x = element_text(size= 12),
axis.text.y = element_text(size= 12),
axis.title = element_text(size=15),
legend.title = element_text(size = 15),
legend.text = element_text(size = 12))+
geom_text(data = graphing %>% filter(Treatment == "CR"),
aes(x = Year, y = Weighted_Average+ 0.5, label = p_value), size =10)+
#geom_vline(xintercept = 3.5, linetype = "dashed", color = "black", size = 1.1)+
theme(legend.position = "bottom")

```

Disease_graph_bar



```

ggsave(Disease_graph_bar,
filename = "Disease_graph_bar.png",
path = "D:/Academics/UC Davis/School Work/Linquist Lab/Data/R stats/Agronomic paper/Figures",
height = 15,
width = 15,
units = "cm",
dpi = 300)

```


Pairwise pooled

```
Treatment_means_average = emmeans(disease_model, spec = 'Treatment')
```

```
## NOTE: Results may be misleading due to involvement in interactions
```

```
Treatment_effects_average = contrast(Treatment_means_average, method = 'pairwise', adjust = "Tukey")
summary(Treatment_effects_average)
```

```
## contrast estimate      SE df t.ratio p.value
## CR - FR      0.556 0.0573  6   9.702  0.0001
##
## Results are averaged over the levels of: Year
## Degrees-of-freedom method: kenward-roger
```

```
cld(Treatment_means_average)
```

```
## Treatment emmean      SE   df lower.CL upper.CL .group
## FR          3.13 0.0867 7.45    2.93    3.34    1
## CR          3.69 0.0867 7.45    3.49    3.89    2
##
## Results are averaged over the levels of: Year
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
## significance level used: alpha = 0.05
## NOTE: If two or more means share the same grouping symbol,
##       then we cannot show them to be different.
##       But we also did not show them to be the same.
```

```
Treatment_effects_summary_average <-
  as.data.frame(summary(Treatment_effects_average)) %>%
  mutate(
    p_value = case_when(
      p.value < 0.05 ~ "*",          # For p-values less than 0.01
      TRUE ~ sprintf("%.2f", p.value) # Force two decimal places for all other p-values
    )
  )
```