

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
```

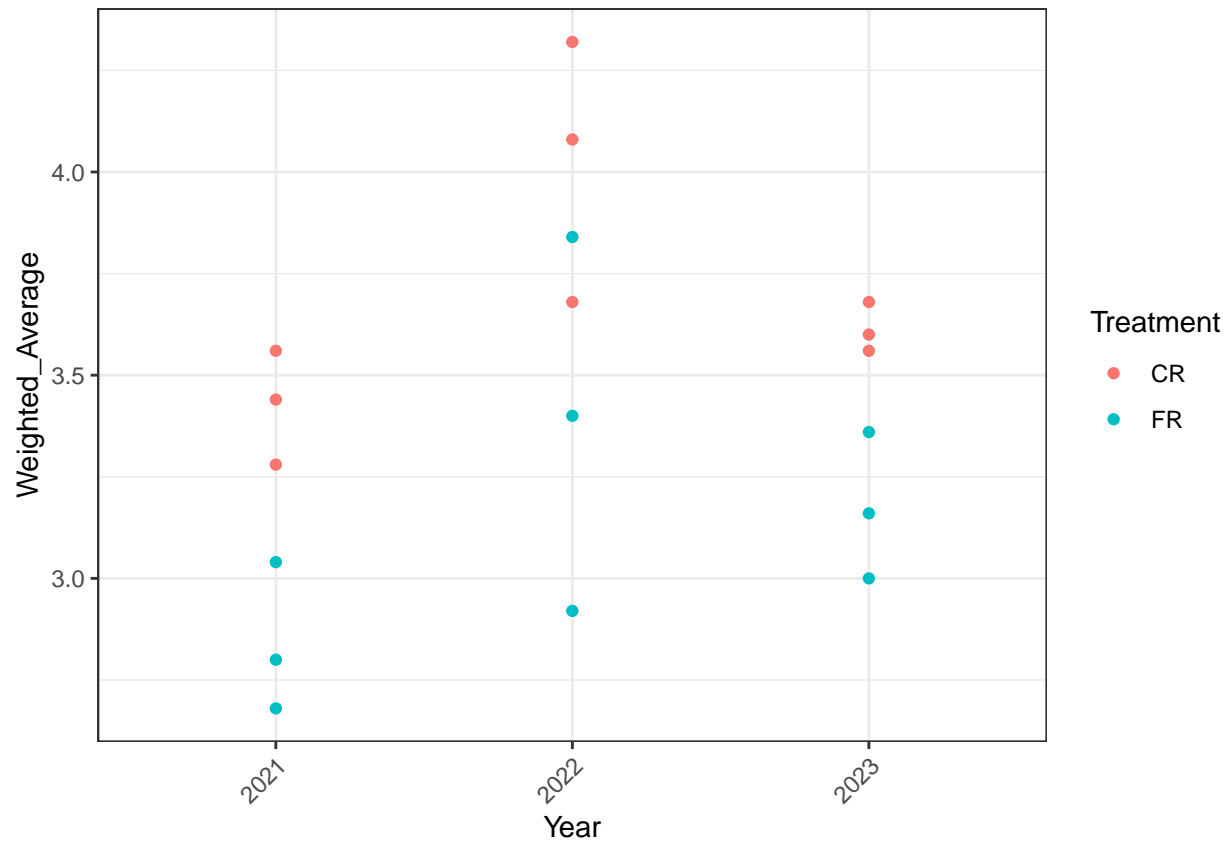
```
str(master)
```

```
## 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

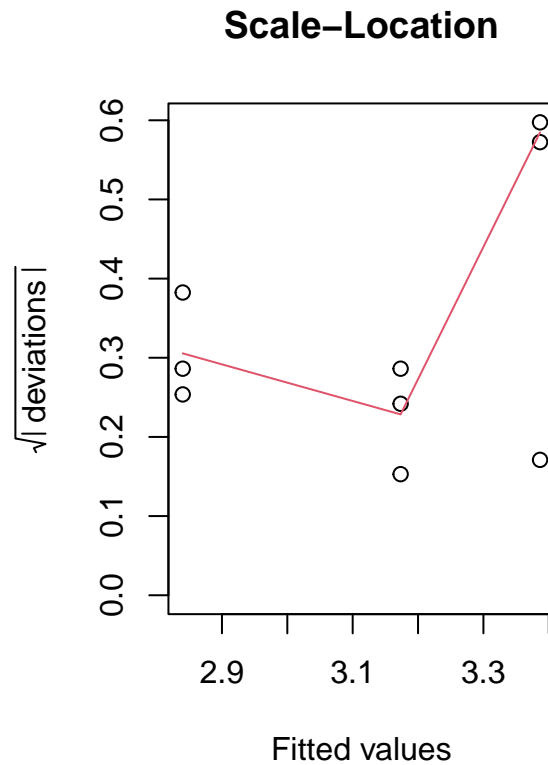
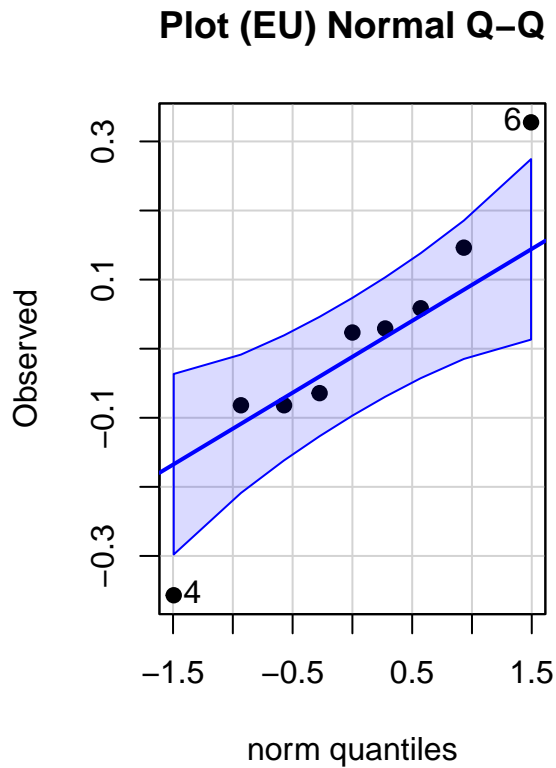
Just purely based on visual inspection, CR has higher disease severity than FR.

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



ANOVA (Main text results taken from here: Figure 5)

```
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
    )
  )
```

Graphing dataframe

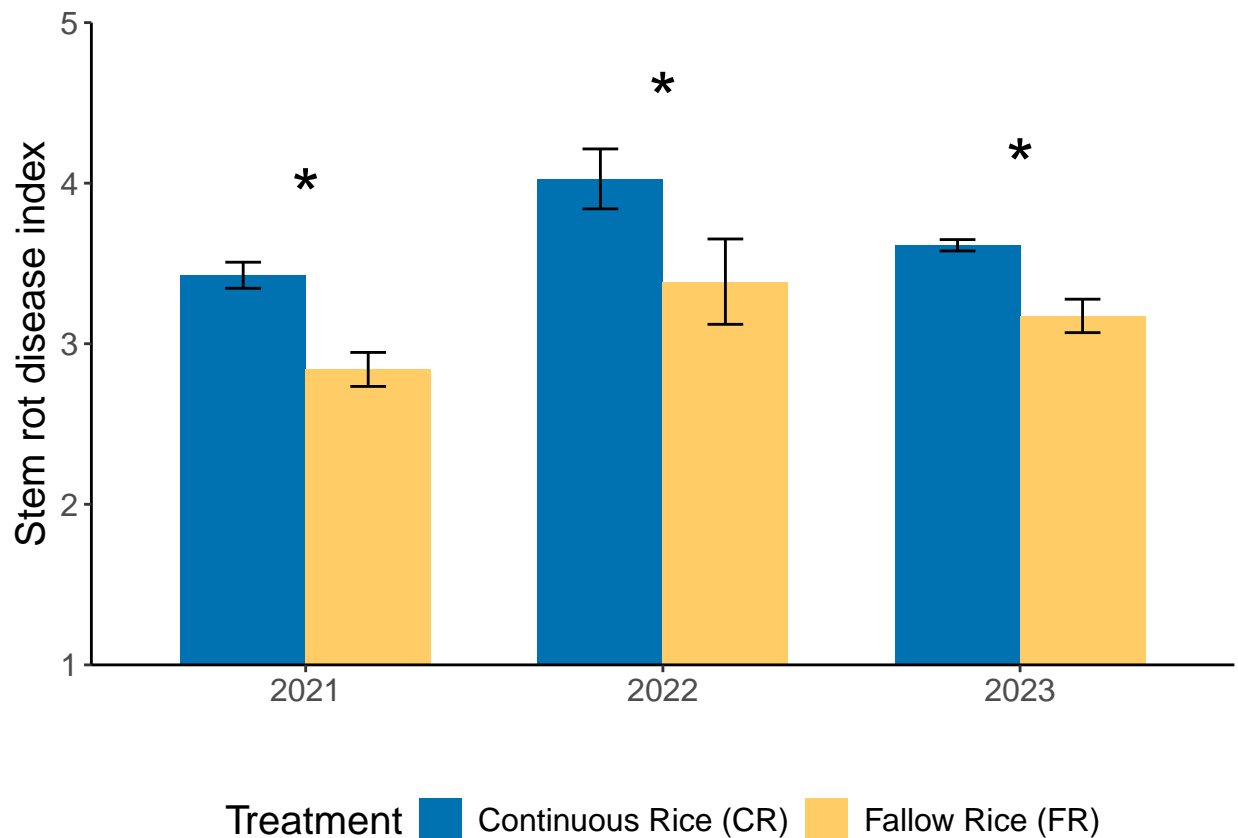
```
graphing <- master %>%
  group_by(Treatment, Year) %>%
  mutate(Weighted_Average_se = sd(Weighted_Average)/sqrt(3)) %>%
  summarise(Weighted_Average = mean(Weighted_Average),
            Weighted_Average_se = mean(Weighted_Average_se)) %>%
  left_join(Treatment_effects_summary %>% select(Year, p_value),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

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

Graph

```
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/Linguist 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
    )
  )
```