MAOC and POC

Zhang Zhenglin

Contents

Necessary libraries

```
library(knitr)
library(ggplot2)
theme_set(theme_bw())
library(emmeans)
library(multcomp)
library(PLS205)
library(lme4)
library(lmerTest)
library(multcompView)
library(car)
library(Rmisc)
```

```r
library(dplyr) #https://r4ds.had.co.nz/ (Chapter 3, Chapter 5, look at filter and select)
# https://bookdown.org/ansellbr/WEHI_tidyR_course_book/
library(stringr)
library(data.table)
library(GGally)
library(formatR)
library(readxl)
library(ggpubr)
library(xlsx)
```

Data Organisation

Read from excel

```r
master <- read_excel("MAOC_POC_forR.xlsx", sheet = 2)
str(master)
```

```
## tibble [35 x 10] (S3: tbl_df/tbl/data.frame)
##  $ Sample                  : chr [1:35] "101-106 MAOM" "107-112 MAOM" "201-206 MAOM" "207-212 MAO
##  $ Treatment               : chr [1:35] "RF" "CR" "RF" "CR" ...
##  $ Year                    : num [1:35] 2021 2021 2021 2021 2021 ...
##  $ Blk                     : num [1:35] 1 1 2 2 3 3 4 4 5 5 ...
##  $ Fraction                : chr [1:35] "MAOM" "MAOM" "MAOM" "MAOM" ...
##  $ Post_shaking_total_weight_g: num [1:35] 9.92 9.92 9.84 9.84 9.9 9.92 9.8 9.8 9.86 9.92 ...
##  $ Fraction_weight_g       : num [1:35] 7.88 7.62 7.64 7.56 7.86 7.9 7.24 7.78 7.84 7.56 ...
##  $ Microbalance_Weight_mg  : num [1:35] 30.4 30.4 30 30.2 29.9 ...
##  $ Nitrogen_percent        : num [1:35] 0.14 0.15 0.14 0.14 0.14 0.15 0.13 0.13 0.14 0.14 ...
##  $ Carbon_percent          : num [1:35] 1.44 1.58 1.47 1.41 1.35 1.48 1.27 1.2 1.46 1.37 ...
```

Change variable type

```r
master <- mutate_if(master, is.character, as.factor)
master$Blk <- as.factor(master$Blk)
master$Year <- as.factor(master$Year)

str(master)
```

```
## tibble [35 x 10] (S3: tbl_df/tbl/data.frame)
##  $ Sample                  : Factor w/ 35 levels "101-106 MAOM",..: 1 3 5 7 9 11 13 15 17 19 ...
##  $ Treatment               : Factor w/ 2 levels "CR","RF": 2 1 2 1 2 1 2 1 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 1 2 2 3 3 4 4 5 5 ...
##  $ Fraction                : Factor w/ 2 levels "MAOM","POM": 1 1 1 1 1 1 1 1 1 1 ...
##  $ Post_shaking_total_weight_g: num [1:35] 9.92 9.92 9.84 9.84 9.9 9.92 9.8 9.8 9.86 9.92 ...
##  $ Fraction_weight_g       : num [1:35] 7.88 7.62 7.64 7.56 7.86 7.9 7.24 7.78 7.84 7.56 ...
##  $ Microbalance_Weight_mg  : num [1:35] 30.4 30.4 30 30.2 29.9 ...
##  $ Nitrogen_percent        : num [1:35] 0.14 0.15 0.14 0.14 0.14 0.15 0.13 0.13 0.14 0.14 ...
##  $ Carbon_percent          : num [1:35] 1.44 1.58 1.47 1.41 1.35 1.48 1.27 1.2 1.46 1.37 ...
```

```r
head(master)
```

```
## # A tibble: 6 x 10
##   Sample Treatment Year  Blk   Fraction Post_shaking_total_w~1 Fraction_weight_g
##   <fct>  <fct>     <fct> <fct> <fct>                    <dbl>             <dbl>
## 1 101-1~ RF        2021  1     MAOM                      9.92              7.88
## 2 107-1~ CR        2021  1     MAOM                      9.92              7.62
## 3 201-2~ RF        2021  2     MAOM                      9.84              7.64
## 4 207-2~ CR        2021  2     MAOM                      9.84              7.56
## 5 301-3~ RF        2021  3     MAOM                      9.9               7.86
## 6 307-3~ CR        2021  3     MAOM                      9.92              7.9
## # i abbreviated name: 1: Post_shaking_total_weight_g
## # i 3 more variables: Microbalance_Weight_mg <dbl>, Nitrogen_percent <dbl>,
## #   Carbon_percent <dbl>
```

Calculating (g C kg-1 soil for each fraction)

```r
master$C_soil_g_per_kg <- (master$Fraction_weight_g/master$Post_shaking_total_weight_g)*master$Carbon_pe

write.xlsx(master, file = "MAOC_POC_Levels.xlsx", sheetName = "1")

POC <- master %>% filter(Fraction == "POM")
str(POC)
```

```
## tibble [17 x 11] (S3: tbl_df/tbl/data.frame)
##  $ Sample                 : Factor w/ 35 levels "101-106 MAOM",..: 2 4 6 8 10 12 14 16 18 20 ...
##  $ Treatment              : Factor w/ 2 levels "CR","RF": 2 1 2 1 2 1 2 1 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 1 2 2 3 3 4 4 5 5 ...
##  $ Fraction               : Factor w/ 2 levels "MAOM","POM": 2 2 2 2 2 2 2 2 2 2 ...
##  $ Post_shaking_total_weight_g: num [1:17] 9.92 9.92 9.84 9.84 9.9 9.92 9.8 9.8 9.86 9.92 ...
##  $ Fraction_weight_g      : num [1:17] 2.04 2.3 2.2 2.28 2.04 ...
##  $ Microbalance_Weight_mg : num [1:17] 29.5 29.9 29.9 30.2 30.3 ...
##  $ Nitrogen_percent       : num [1:17] 0.1 0.1 0.07 0.12 0.1 0.14 0.05 0.1 0.12 0.1 ...
##  $ Carbon_percent         : num [1:17] 1.74 1.98 1.43 2.71 1.7 3 0.93 2.32 2.29 2.15 ...
##  $ C_soil_g_per_kg        : num [1:17] 3.58 4.59 3.2 6.28 3.5 ...
```

```r
MAOC <- master %>% filter(Fraction == "MAOM")
str(MAOC)
```

```
## tibble [18 x 11] (S3: tbl_df/tbl/data.frame)
##  $ Sample                 : Factor w/ 35 levels "101-106 MAOM",..: 1 3 5 7 9 11 13 15 17 19 ...
##  $ Treatment              : Factor w/ 2 levels "CR","RF": 2 1 2 1 2 1 2 1 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 1 2 2 3 3 4 4 5 5 ...
##  $ Fraction               : Factor w/ 2 levels "MAOM","POM": 1 1 1 1 1 1 1 1 1 1 ...
##  $ Post_shaking_total_weight_g: num [1:18] 9.92 9.92 9.84 9.84 9.9 9.92 9.8 9.8 9.86 9.92 ...
##  $ Fraction_weight_g      : num [1:18] 7.88 7.62 7.64 7.56 7.86 7.9 7.24 7.78 7.84 7.56 ...
##  $ Microbalance_Weight_mg : num [1:18] 30.4 30.4 30 30.2 29.9 ...
```

```
##  $ Nitrogen_percent          : num [1:18] 0.14 0.15 0.14 0.14 0.14 0.15 0.13 0.13 0.14 0.14 ...
##  $ Carbon_percent            : num [1:18] 1.44 1.58 1.47 1.41 1.35 1.48 1.27 1.2 1.46 1.37 ...
##  $ C_soil_g_per_kg           : num [1:18] 11.4 12.1 11.4 10.8 10.7 ...
```

```r
ggplot(POC, aes(y=C_soil_g_per_kg, x=Year, color=Treatment)) + geom_boxplot()
```
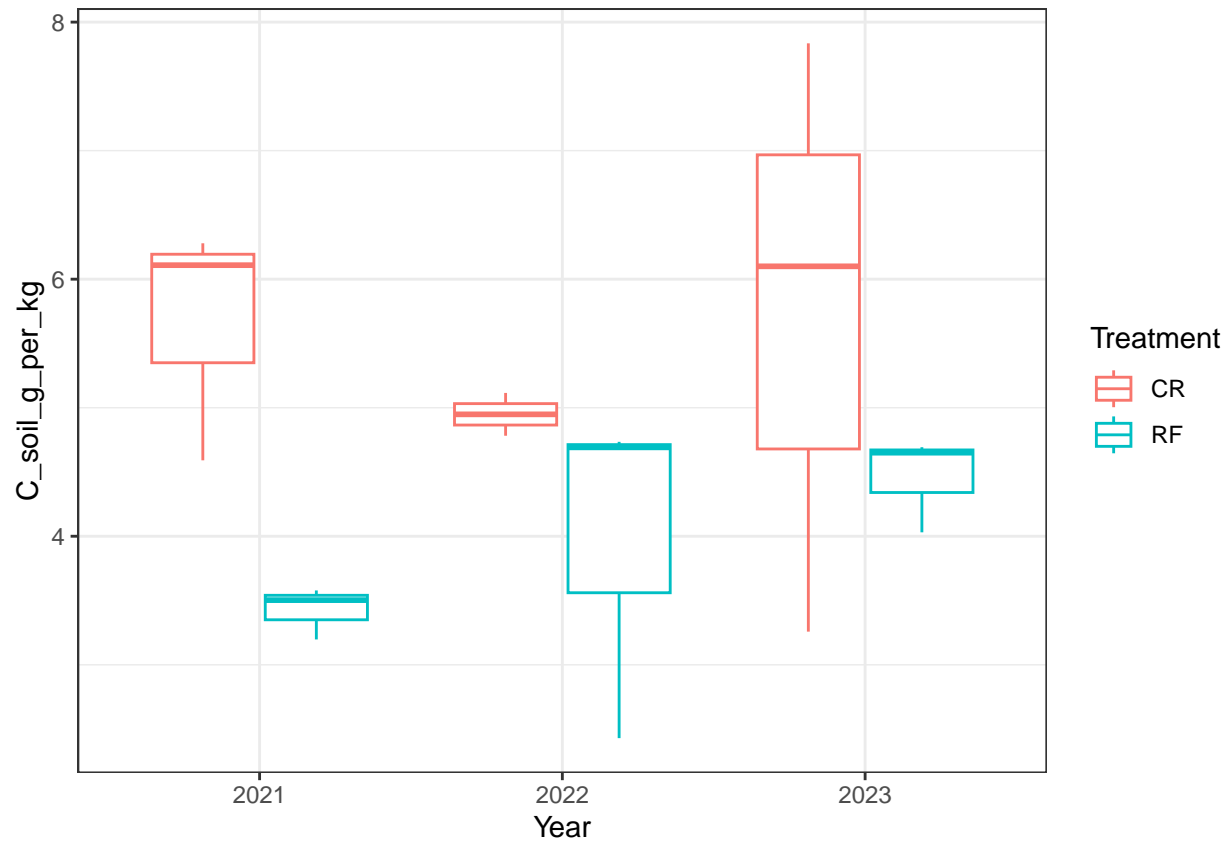


```r
ggplot(MAOC, aes(y=C_soil_g_per_kg, x=Year, color=Treatment)) + geom_boxplot()
```
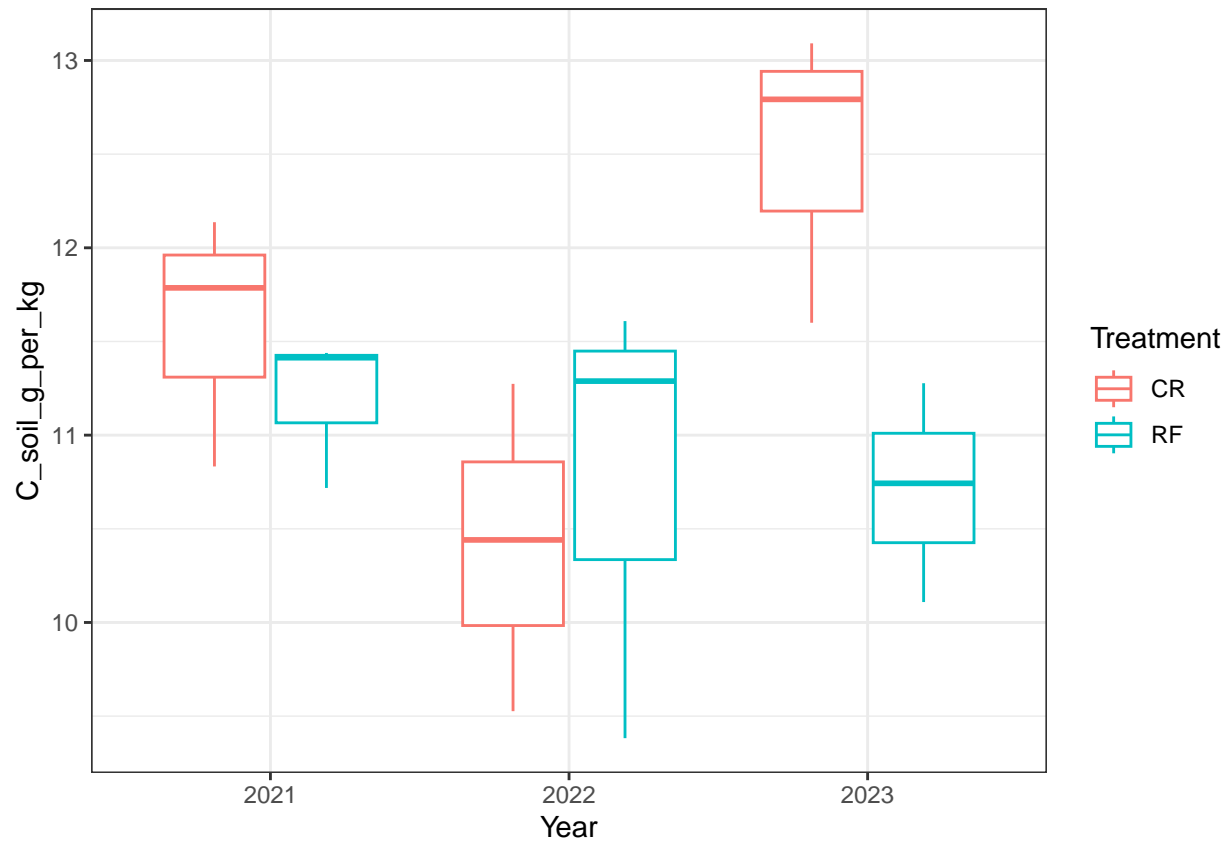
POC

ANOVA and Tukey

```
POC_model <-lm(C_soil_g_per_kg~Treatment*Year, data = POC)
anova(POC_model)
```

```
## Analysis of Variance Table
##
## Response: C_soil_g_per_kg
##                Df  Sum Sq Mean Sq F value  Pr(>F)
## Treatment       1 10.3512 10.3512  6.9877 0.02285 *
## Year            2  1.2586  0.6293  0.4248 0.66418
## Treatment:Year  2  1.1824  0.5912  0.3991 0.68026
## Residuals      11 16.2948  1.4813
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#all pooled
```

```
POC_means_all <- emmeans(POC_model, spec ='Treatment')
```

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

```r
POC_effects_all <- contrast(POC_means_all, method = 'pairwise', adjust = "tukey")
summary(POC_effects_all)
```

```
##  contrast estimate    SE df t.ratio p.value
##  CR - RF       1.5 0.597 11   2.514  0.0288
##
## Results are averaged over the levels of: Year
```

```r
cld(POC_means_all)
```

```
##  Treatment emmean    SE df lower.CL upper.CL .group
##  RF          3.95 0.406 11     3.05     4.84  1
##  CR          5.45 0.438 11     4.48     6.41   2
##
## Results are averaged over the levels of: Year
## 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.
```

```r
#by year
POC_means <- emmeans(POC_model, spec ='Treatment', by = 'Year')
POC_effects <- contrast(POC_means, method = 'pairwise', adjust = "tukey")
summary(POC_effects)
```

```
## Year = 2021:
##  contrast estimate    SE df t.ratio p.value
##  CR - RF     2.233 0.994 11   2.248  0.0461
##
## Year = 2022:
##  contrast estimate    SE df t.ratio p.value
##  CR - RF     0.997 1.111 11   0.897  0.3889
##
## Year = 2023:
##  contrast estimate    SE df t.ratio p.value
##  CR - RF     1.273 0.994 11   1.281  0.2265
```

```r
cld(POC_means)
```

```
## Year = 2021:
##  Treatment emmean    SE df lower.CL upper.CL .group
##  RF          3.43 0.703 11     1.88     4.97  1
##  CR          5.66 0.703 11     4.11     7.21   2
##
## Year = 2022:
##  Treatment emmean    SE df lower.CL upper.CL .group
##  RF          3.95 0.703 11     2.41     5.50  1
##  CR          4.95 0.861 11     3.05     6.84  1
##
## Year = 2023:
```

```
##   Treatment emmean     SE df lower.CL upper.CL .group
##   RF          4.46 0.703 11     2.91     6.00  1
##   CR          5.73 0.703 11     4.18     7.28  1
##
## 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.
```

POC Graph

```
POC_graphing <- POC %>% group_by(Treatment, Year) %>%
mutate(C_soil_g_per_kg_se = sd(C_soil_g_per_kg)/sqrt(3)) %>%
  summarise(C_soil_g_per_kg = mean(C_soil_g_per_kg),
            C_soil_g_per_kg_se = mean(C_soil_g_per_kg_se))
```

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

```
POC_all <- POC %>% group_by(Treatment) %>%
mutate(C_soil_g_per_kg_se = sd(C_soil_g_per_kg)/sqrt(9)) %>%
  summarise(C_soil_g_per_kg = mean(C_soil_g_per_kg),
            C_soil_g_per_kg_se = mean(C_soil_g_per_kg_se)) %>%
  mutate(Year = "Average")

POC_graphing <- rbind(POC_graphing, POC_all)

POC_graph <-
ggplot(POC_graphing, aes(x= Year, y = C_soil_g_per_kg, fill = Treatment))+
  geom_bar(stat = "identity", position = "dodge", width = 0.7) +
  labs(x = "Year", y = "C_soil_g_per_kg", fill = "Treatment") +
  scale_fill_manual(values = c("#0072B2","#FFCC66"),labels = c("Continuous rice (CR)", "Fallow rice (FR)
  geom_errorbar(aes(ymin=C_soil_g_per_kg-C_soil_g_per_kg_se, ymax=C_soil_g_per_kg+C_soil_g_per_kg_se), w
  scale_y_continuous(name=expression("POC (g C kg"^{-1}*")"), limits = c(0, 22), expand = c(0, 0))+
  scale_x_discrete(name="")+
  theme_classic()+
  theme(axis.text = element_text(size = 12), axis.title = element_text(size=14))+
  theme(legend.position = "bottom",legend.text = element_text(size = 12))+
  theme(legend.title = element_blank(),
        legend.text = element_text(size = 16),
        axis.text.x = element_text(size = 14),  # Increase size of x-axis text
        axis.text.y = element_text(size = 14),  # Increase size of y-axis text
        axis.title.y = element_text(size = 14), # Increase size of y-axis title
        ) +
  annotate(
  "text",
  x = c(1,4),  # X-axis positions for annotations
  y = c(6.5,7),  # Y-axis positions for annotations
  label = "*",
  size = 10,
```

```r
    vjust = 0   # Adjust vertical position of asterisks
)+
  annotate(
  "text",
  x = c(1),   # X-axis positions for annotations
  y = c(20),   # Y-axis positions for annotations
  label = "POC",
  size = 8,
  vjust = 0
)+
  geom_segment(aes(x = 3.5, xend = 3.5, y = 0, yend = 20.5), color = "black", linetype = "dashed", size=
```

```
## Warning: Using 'size' aesthetic for lines was deprecated in ggplot2 3.4.0.
## i Please use 'linewidth' instead.
## This warning is displayed once every 8 hours.
## Call 'lifecycle::last_lifecycle_warnings()' to see where this warning was
## generated.
```

```r
ggsave(POC_graph, filename = "POC_graph.png", height = 15, width = 20, units = "cm", dpi=1000)
```

MAOC

ANOVA and Tukey

```r
MAOC_model <-lm(C_soil_g_per_kg~Treatment*Year, data = MAOC)
anova(MAOC_model)
```

```
## Analysis of Variance Table
##
## Response: C_soil_g_per_kg
##                Df Sum Sq Mean Sq F value Pr(>F)
## Treatment       1 1.6816 1.68158  2.6553 0.1292
## Year            2 3.4368 1.71839  2.7135 0.1066
## Treatment:Year  2 3.5116 1.75580  2.7725 0.1024
## Residuals      12 7.5994 0.63329
```

```r
#all pooled
```

```r
MAOC_means_all <- emmeans(MAOC_model, spec ='Treatment')
```

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

```r
MAOC_effects_all <- contrast(MAOC_means_all, method = 'pairwise', adjust = "tukey")
summary(MAOC_effects_all)
```

```
##  contrast estimate    SE df t.ratio p.value
##  CR - RF     0.611 0.375 12   1.630  0.1292
##
## Results are averaged over the levels of: Year
```

```
cld(MAOC_means_all)
```

```
##  Treatment emmean    SE df lower.CL upper.CL .group
##  RF          10.9 0.265 12     10.3     11.5  1
##  CR          11.5 0.265 12     10.9     12.1  1
##
## Results are averaged over the levels of: Year
## 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.
```

```
#by year
```

```
MAOC_means <- emmeans(MAOC_model, spec ='Treatment', by = 'Year')
MAOC_effects <- contrast(MAOC_means, method = 'pairwise', adjust = "tukey")
summary(MAOC_effects)
```

```
## Year = 2021:
##  contrast estimate   SE df t.ratio p.value
##  CR - RF     0.395 0.65 12   0.608  0.5544
##
## Year = 2022:
##  contrast estimate   SE df t.ratio p.value
##  CR - RF    -0.346 0.65 12  -0.533  0.6038
##
## Year = 2023:
##  contrast estimate   SE df t.ratio p.value
##  CR - RF     1.785 0.65 12   2.747  0.0177
```

```
cld(MAOC_means)
```

```
## Year = 2021:
##  Treatment emmean    SE df lower.CL upper.CL .group
##  RF          11.2 0.459 12    10.19     12.2  1
##  CR          11.6 0.459 12    10.58     12.6  1
##
## Year = 2022:
##  Treatment emmean    SE df lower.CL upper.CL .group
##  CR          10.4 0.459 12     9.41     11.4  1
##  RF          10.8 0.459 12     9.76     11.8  1
##
## Year = 2023:
##  Treatment emmean    SE df lower.CL upper.CL .group
##  RF          10.7 0.459 12     9.71     11.7  1
##  CR          12.5 0.459 12    11.49     13.5   2
##
## 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.
```

MAOC Graph

```r
MAOC_graphing <- MAOC %>% group_by(Treatment, Year) %>%
mutate(C_soil_g_per_kg_se = sd(C_soil_g_per_kg)/sqrt(3)) %>%
  summarise(C_soil_g_per_kg = mean(C_soil_g_per_kg),
            C_soil_g_per_kg_se = mean(C_soil_g_per_kg_se))
```

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

```r
MAOC_all <- MAOC %>% group_by(Treatment) %>%
mutate(C_soil_g_per_kg_se = sd(C_soil_g_per_kg)/sqrt(9)) %>%
  summarise(C_soil_g_per_kg = mean(C_soil_g_per_kg),
            C_soil_g_per_kg_se = mean(C_soil_g_per_kg_se)) %>%
  mutate(Year = "Average")

MAOC_graphing <- rbind(MAOC_graphing, MAOC_all)

MAOC_graph <-
ggplot(MAOC_graphing, aes(x= Year, y = C_soil_g_per_kg, fill = Treatment))+
  geom_bar(stat = "identity", position = "dodge", width = 0.7) +
  labs(x = "Year", y = "C_soil_g_per_kg", fill = "Treatment") +
  scale_fill_manual(values = c("#0072B2","#FFCC66"),labels = c("Continuous rice (CR)", "Fallow rice (FR)
  geom_errorbar(aes(ymin=C_soil_g_per_kg-C_soil_g_per_kg_se, ymax=C_soil_g_per_kg+C_soil_g_per_kg_se),
  scale_y_continuous(name=expression("MAOC (g C kg"^{-1}*")"), limits = c(0, 22), expand = c(0, 0))+
  scale_x_discrete(name="")+
  theme_classic()+
  theme(axis.text = element_text(size = 12), axis.title = element_text(size=14))+
  theme(legend.position = "bottom",legend.text = element_text(size = 12))+
  theme(legend.title = element_blank(),
        legend.text = element_text(size = 16),
        axis.text.x = element_text(size = 14),  # Increase size of x-axis text
        axis.text.y = element_text(size = 14),  # Increase size of y-axis text
        axis.title.y = element_text(size = 14), # Increase size of y-axis title
        ) +
  annotate(
  "text",
  x = c(3),  # X-axis positions for annotations
  y = c(13),  # Y-axis positions for annotations
  label = "*",
  size = 10,
  vjust = 0  # Adjust vertical position of asterisks
)+
  annotate(
  "text",
  x = c(1),  # X-axis positions for annotations
  y = c(20),  # Y-axis positions for annotations
  label = "MAOC",
  size = 8,
  vjust = 0
)+
  geom_segment(aes(x = 3.5, xend = 3.5, y = 0, yend = 20.5), color = "black", linetype = "dashed", size=
```
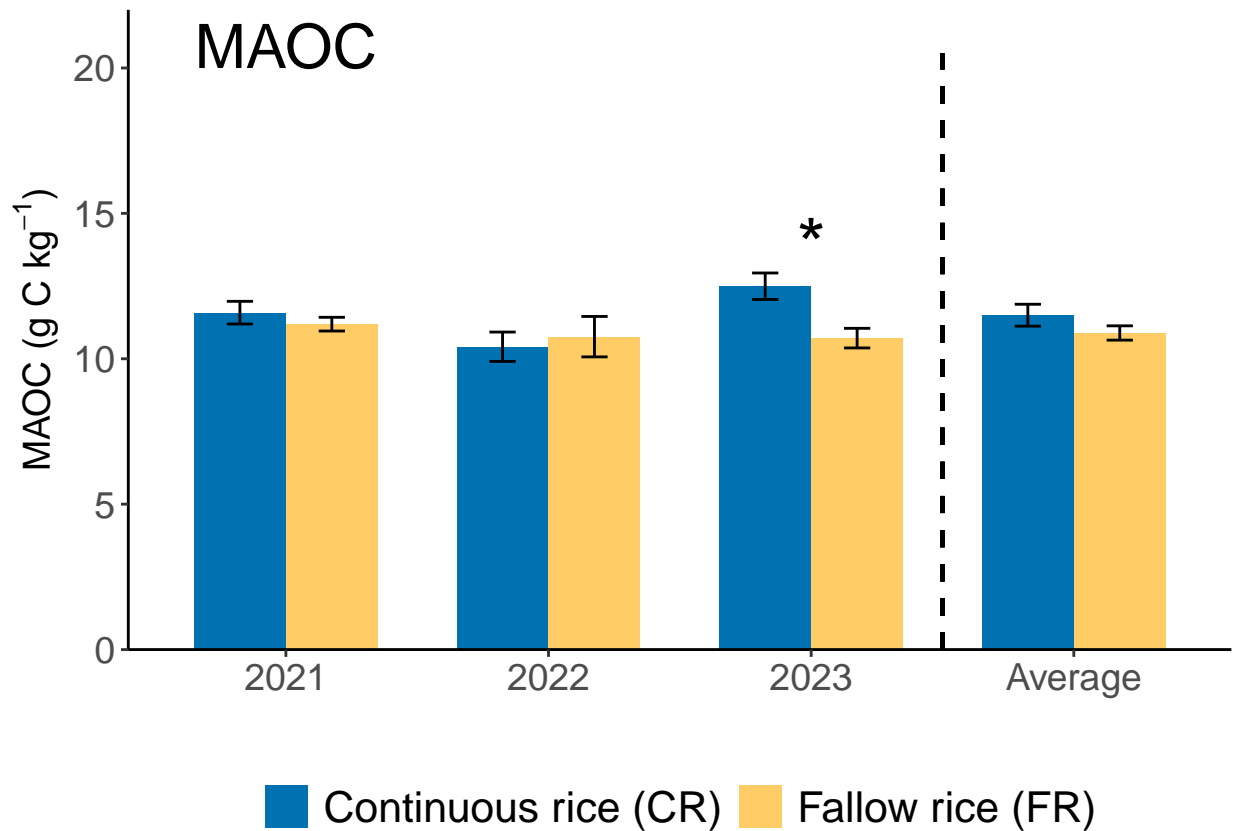
```
ggsave(MAOC_graph, filename = "MAOC_graph.png", height = 15, width = 20, units = "cm", dpi=1000)
```

SOC

ANOVA and Tukey

```
SOC <- read_excel("MAOC_POC_Levels_total_carbon_summed.xlsx", sheet = 1) %>% filter(Fraction=="All")
```

```
## New names:
## * `` -> `...1`
```

```
SOC <- mutate_if(SOC, is.character, as.factor)
SOC$Blk <- as.factor(SOC$Blk)
SOC$Year <- as.factor(SOC$Year)

SOC_model <-lm(C_soil_g_per_kg~Treatment*Year, data = SOC)
anova(SOC_model)
```

```
## Analysis of Variance Table
##
## Response: C_soil_g_per_kg
##              Df  Sum Sq Mean Sq F value  Pr(>F)
## Treatment    1 14.7572 14.7572  5.9311 0.03142 *
## Year         2 13.7162  6.8581  2.7563 0.10351
## Treatment:Year  2  9.7326  4.8663  1.9558 0.18399
## Residuals   12 29.8575  2.4881
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#all pooled

SOC_means_all <- emmeans(SOC_model, spec ='Treatment')
```

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

```
SOC_effects_all <- contrast(SOC_means_all, method = 'pairwise', adjust = "tukey")
summary(SOC_effects_all)
```

```
##  contrast estimate    SE df t.ratio p.value
##  CR - RF      1.81 0.744 12   2.435  0.0314
##
## Results are averaged over the levels of: Year
```

```
cld(SOC_means_all)
```

```
##  Treatment emmean    SE df lower.CL upper.CL .group
##  RF          14.8 0.526 12     13.7     16.0  1
##  CR          16.6 0.526 12     15.5     17.8   2
##
## Results are averaged over the levels of: Year
## 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.
```

```
#by year

SOC_means <- emmeans(SOC_model, spec ='Treatment', by = 'Year')
SOC_effects <- contrast(SOC_means, method = 'pairwise', adjust = "tukey")
summary(SOC_effects)
```

```
## Year = 2021:
##  contrast estimate   SE df t.ratio p.value
##  CR - RF     2.629 1.29 12   2.041  0.0639
##
## Year = 2022:
##  contrast estimate   SE df t.ratio p.value
##  CR - RF    -0.254 1.29 12  -0.197  0.8469
```

```
##
## Year = 2023:
##  contrast estimate   SE df t.ratio p.value
##  CR - RF      3.058 1.29 12   2.374  0.0351
```

```r
cld(SOC_means)
```

```
## Year = 2021:
##  Treatment emmean    SE df lower.CL upper.CL .group
##  RF          14.6 0.911 12     12.6     16.6  1
##  CR          17.2 0.911 12     15.3     19.2  1
##
## Year = 2022:
##  Treatment emmean    SE df lower.CL upper.CL .group
##  CR          14.5 0.911 12     12.5     16.4  1
##  RF          14.7 0.911 12     12.7     16.7  1
##
## Year = 2023:
##  Treatment emmean    SE df lower.CL upper.CL .group
##  RF          15.2 0.911 12     13.2     17.2  1
##  CR          18.2 0.911 12     16.2     20.2   2
##
## 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.
```

SOC Graph

```r
SOC_graphing <- SOC %>% group_by(Treatment, Year) %>%
mutate(C_soil_g_per_kg_se = sd(C_soil_g_per_kg)/sqrt(3)) %>%
  summarise(C_soil_g_per_kg = mean(C_soil_g_per_kg),
            C_soil_g_per_kg_se = mean(C_soil_g_per_kg_se))
```

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

```r
SOC_all <- SOC %>% group_by(Treatment) %>%
mutate(C_soil_g_per_kg_se = sd(C_soil_g_per_kg)/sqrt(9)) %>%
  summarise(C_soil_g_per_kg = mean(C_soil_g_per_kg),
            C_soil_g_per_kg_se = mean(C_soil_g_per_kg_se)) %>%
  mutate(Year = "Average")

SOC_graphing <- rbind(SOC_graphing, SOC_all)

SOC_graph <-
ggplot(SOC_graphing, aes(x= Year, y = C_soil_g_per_kg, fill = Treatment))+
  geom_bar(stat = "identity", position = "dodge", width = 0.7) +
  labs(x = "Year", y = "C_soil_g_per_kg", fill = "Treatment") +
```

```r
scale_fill_manual(values = c("#0072B2","#FFCC66"),labels = c("Continuous rice (CR)", "Fallow rice (FR)
geom_errorbar(aes(ymin=C_soil_g_per_kg-C_soil_g_per_kg_se, ymax=C_soil_g_per_kg+C_soil_g_per_kg_se), 
scale_y_continuous(name=expression("SOC (g C kg"^{-1}*")"), limits = c(0, 22), expand = c(0, 0))+
scale_x_discrete(name="")+
theme_classic()+
theme(axis.text = element_text(size = 12), axis.title = element_text(size=14))+
theme(legend.position = "bottom",legend.text = element_text(size = 12))+
theme(legend.title = element_blank(),
      legend.text = element_text(size = 16),
      axis.text.x = element_text(size = 14),  # Increase size of x-axis text
      axis.text.y = element_text(size = 14),  # Increase size of y-axis text
      axis.title.y = element_text(size = 14), # Increase size of y-axis title
      ) +
annotate(
"text",
x = c(3, 4),  # X-axis positions for annotations
y = c(19, 18),  # Y-axis positions for annotations
label = "*",
size = 10,
vjust = 0  # Adjust vertical position of asterisks
)+
  annotate(
"text",
x = c(1),  # X-axis positions for annotations
y = c(20),  # Y-axis positions for annotations
label = "SOC",
size = 8,
vjust = 0
)+
  geom_segment(aes(x = 3.5, xend = 3.5, y = 0, yend = 20.5), color = "black", linetype = "dashed", size=

SOC_graph
```
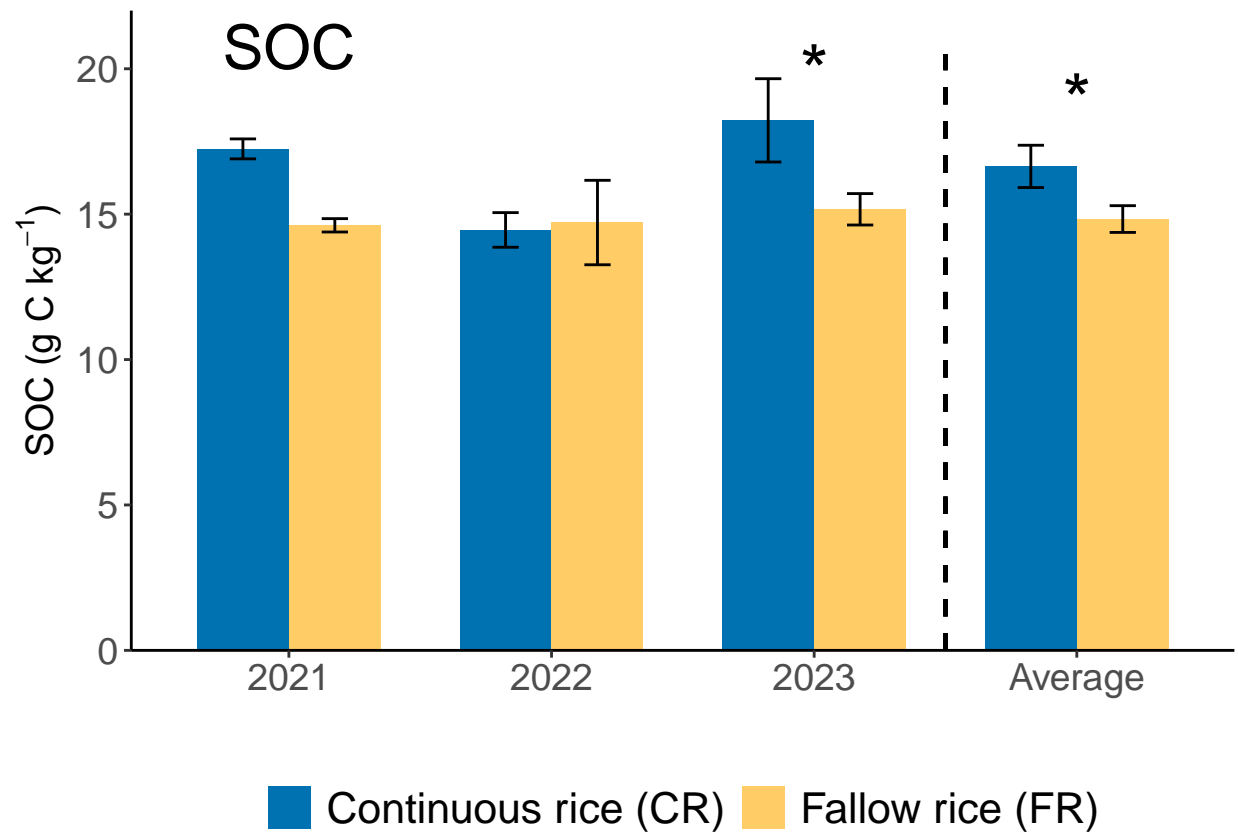
```r
ggsave(SOC_graph, filename = "SOC_graph.png", height = 15, width = 20, units = "cm", dpi=1000)
```

Combine all into 1 figure

```r
c_fractions_horizontal <- ggarrange(SOC_graph,POC_graph, MAOC_graph,
                    #labels = c("2021", "2022", "2023"),
                    ncol = 3,
                    common.legend = TRUE,
                    legend= "bottom")

ggsave(c_fractions_horizontal, filename = "c_fractions_horizontal.jpg", height = 15, width = 50, units =
```