N Rate Trial (no topdress)

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Contents

Necessary libraries

Data Organisation

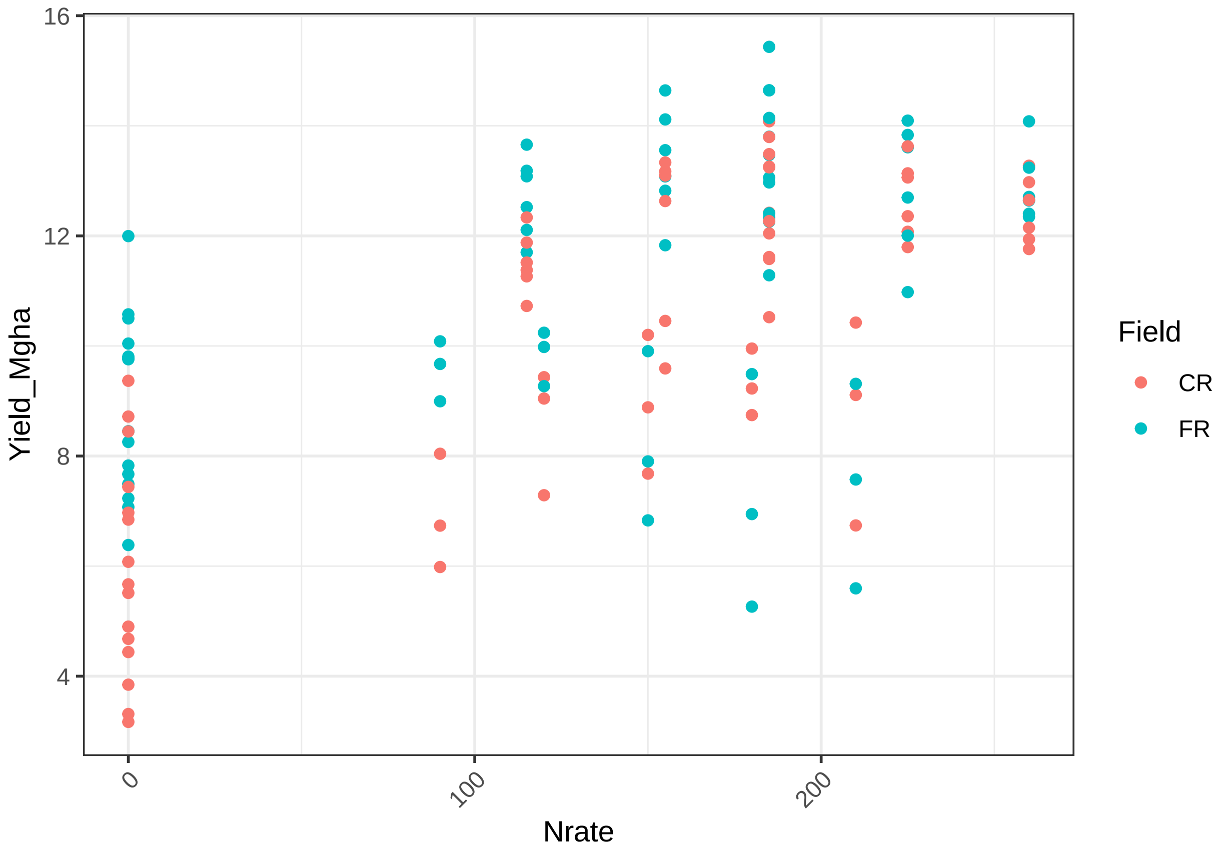
Read from excel

```
master <- read_excel("master_yields.xlsx", sheet = 1)
master$Treatment <- master$Field
master <- mutate_if(master, is.character, as.factor)
master$NrateF <- as.factor(master$Nrate)
master$Year <- as.factor(master$Year)
master$Yield_Mgha <- master$Yield_kgha/1000

str(master)
```

```
## tibble [132 x 11] (S3: tbl_df/tbl/data.frame)
##  $ Year          : Factor w/ 3 levels "2021","2022",..: 3 3 3 3 3 3 3 3 3 3 ...
##  $ Plot          : Factor w/ 132 levels "101","102","103",..: 97 98 99 100 101 102 103 104 105 106 .
##  $ Blk           : num [1:132] 7 7 7 7 7 7 7 7 7 7 ...
##  $ Nrate         : num [1:132] 180 120 150 0 210 90 150 90 120 0 ...
##  $ Field         : Factor w/ 2 levels "CR","FR": 2 2 2 2 2 2 1 1 1 1 ...
##  $ Yield_kgha    : num [1:132] 5264 9982 7902 8451 5596 ...
##  $ Topdress_study: num [1:132] 0 0 0 0 0 0 0 0 0 0 ...
##  $ Topdressed    : Factor w/ 3 levels "0","1","NIL": 3 3 3 3 3 3 3 3 3 3 ...
##  $ Treatment     : Factor w/ 2 levels "CR","FR": 2 2 2 2 2 2 1 1 1 1 ...
##  $ NrateF        : Factor w/ 11 levels "0","90","115",..: 7 4 5 1 9 2 5 2 4 1 ...
##  $ Yield_Mgha    : num [1:132] 5.26 9.98 7.9 8.45 5.6 ...
```

Initial visualisation

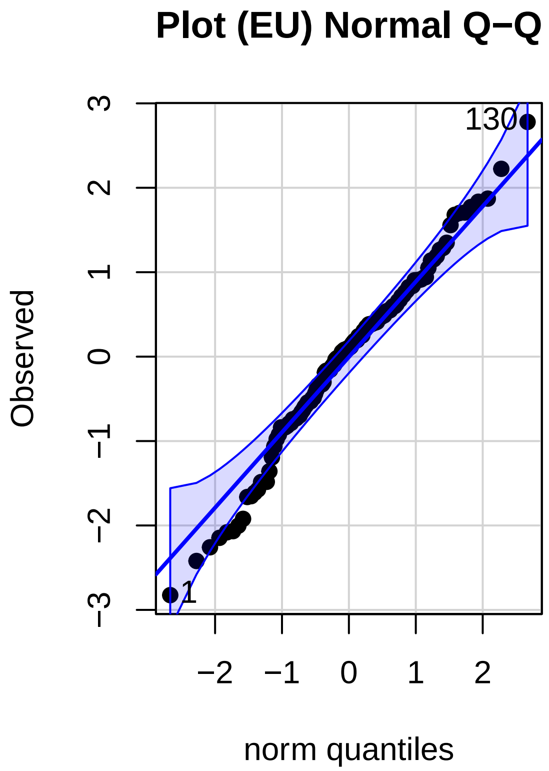
```
ggplot(master, aes(y=Yield_Mgha, x=Nrate, color=Field))+
  geom_point()+
  theme(axis.text.x = element_text(angle = 45, hjust = 1, size= 9))
```

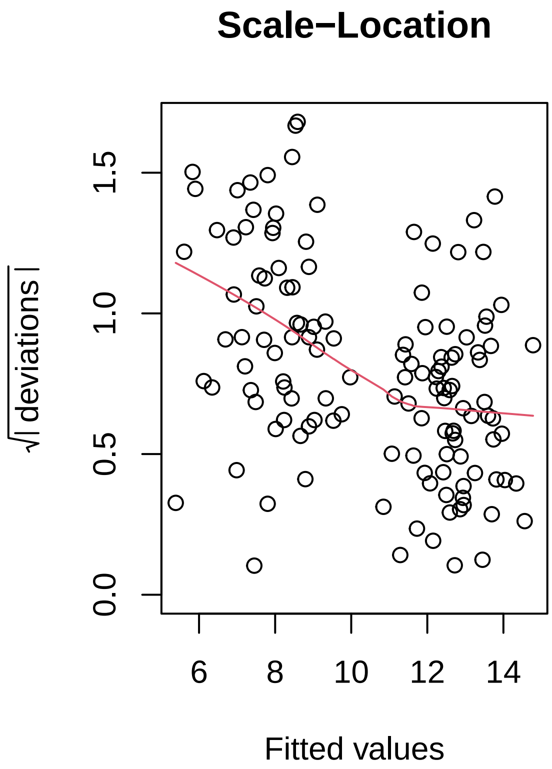


Check for most important variables

Year effect very significant. So analyse data by 3 different years.

```
all_factors_model <- lm(Yield_Mgha~Year+Blk+NrateF+Field+Topdressed, data = master)

pls205_diagnostics(all_factors_model)
```





```r
anova(all_factors_model)
```

```
## Analysis of Variance Table
##
## Response: Yield_Mgha
##              Df Sum Sq Mean Sq F value    Pr(>F)
## Year          2 319.22 159.610 93.6799 < 2.2e-16 ***
## Blk           1   4.30   4.302  2.5248  0.114791
## NrateF       10 483.11  48.311 28.3552 < 2.2e-16 ***
## Field         1  38.87  38.870 22.8141 5.263e-06 ***
## Topdressed    1  14.73  14.734  8.6481  0.003953 **
## Residuals   116 197.64   1.704
## ---
## Signif. codes:  0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1 ’ ’ 1
```

Subset data from the 3 years

```r
#master$main_plot <- paste(master$Blk, master$Treatment, sep="_")
#master$modular <- paste(as.numeric(master$Blk)%%3, master$Treatment, sep = "_")
notopdress <- master %>% filter (Topdressed != 1)

yield_average <- notopdress
```

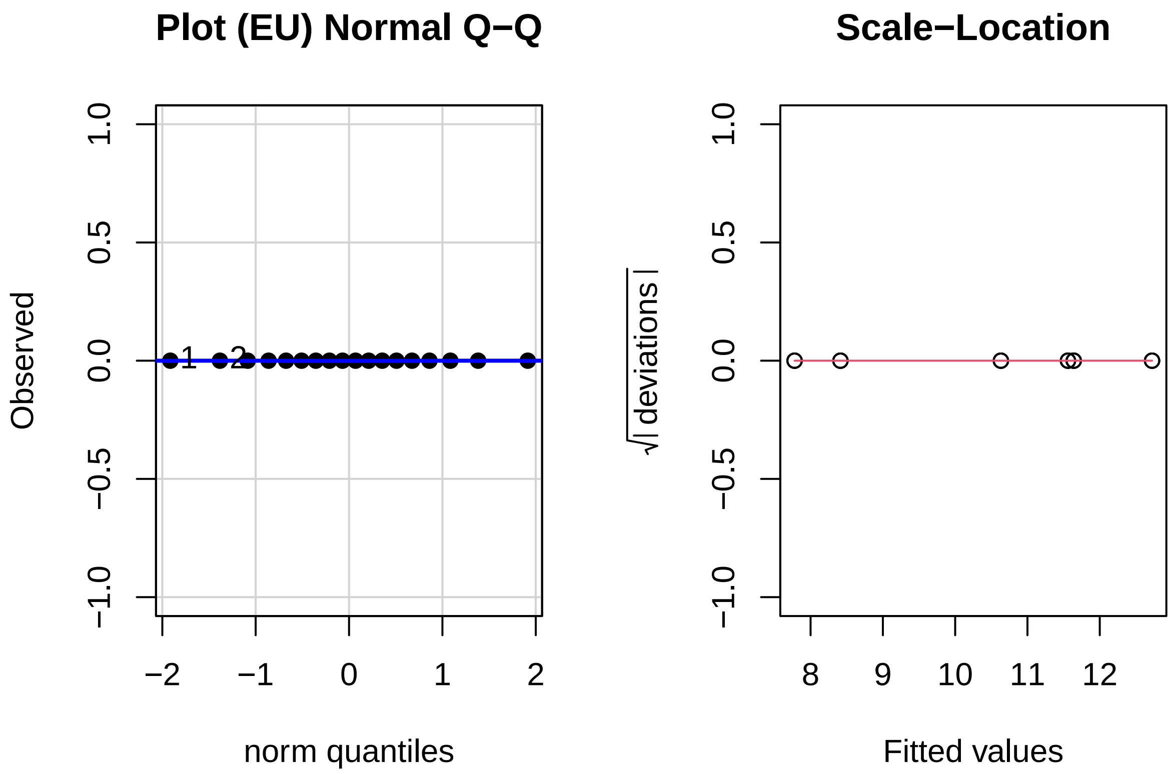
```
yield_2021 <- notopdress %>% filter (Year == "2021")
yield_2022 <- notopdress %>% filter (Year == "2022")
yield_2023 <- notopdress %>% filter (Year == "2023")
#checked datasets, all looks good.
```

Treatment and year effect (Corresponds Table 1: ANOVA)

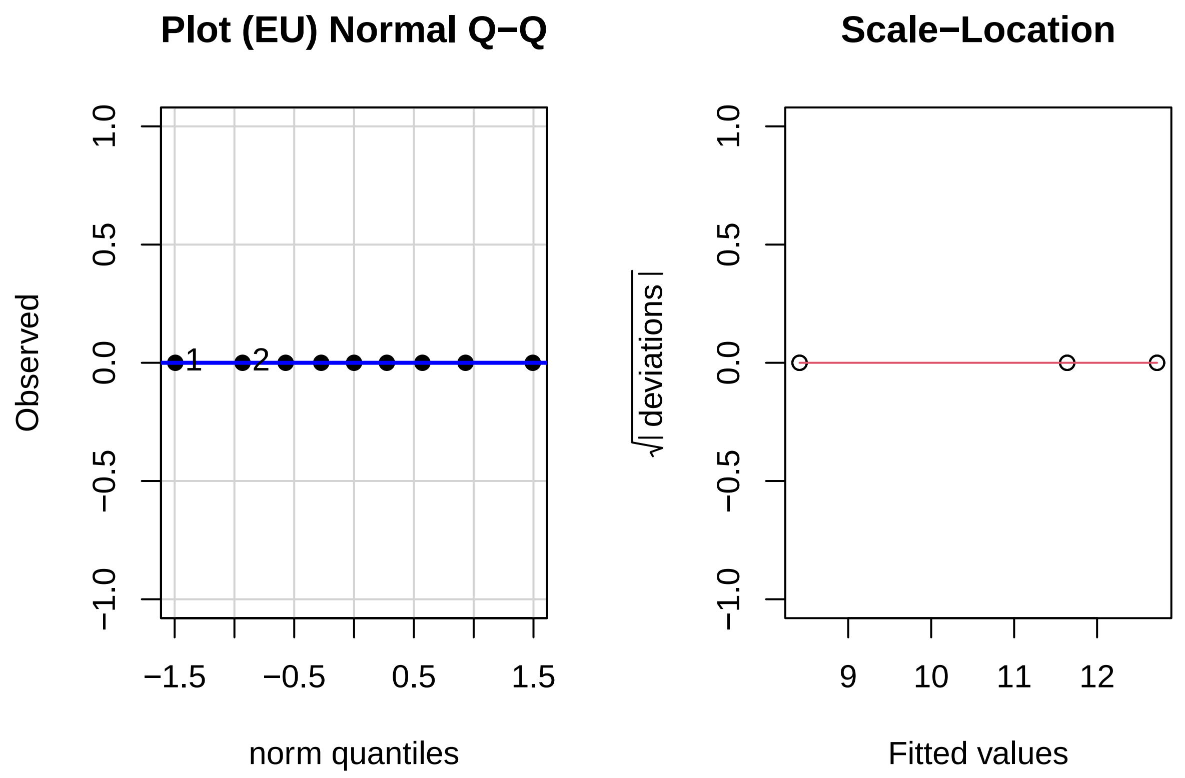
```
model_all_years <- lmer(Yield_Mgha ~ Treatment*Year+(1|Blk:Treatment)+(1|Blk), data = yield_average)
```

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

```
#lm(Yield_Mgha ~ Treatment*Year, data = yield_average)

pls205_diagnostics(model_all_years, EU ="Blk:Treatment")
```



```
pls205_diagnostics(model_all_years, EU ="Blk")
```



```r
anova(model_all_years)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##                 Sum Sq Mean Sq NumDF DenDF F value    Pr(>F)
## Treatment        23.61  23.605     1   102  4.2530   0.04172 *
## Year            319.43 159.717     2   102 28.7766 1.231e-10 ***
## Treatment:Year    1.33   0.664     2   102  0.1197   0.88732
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
field_means_all_years = emmeans(model_all_years,spec = 'Treatment',by = 'Year')
field_effects_all_years = contrast(field_means_all_years, method = 'pairwise', adjust = "Tukey")
summary(field_effects_all_years)
```

```
## Year = 2021:
##  contrast estimate    SE df t.ratio p.value
##  CR - FR    -1.163 0.785  6  -1.481  0.1891
##
## Year = 2022:
##  contrast estimate    SE df t.ratio p.value
##  CR - FR    -1.007 0.785  6  -1.283  0.2469
##
## Year = 2023:
##  contrast estimate    SE df t.ratio p.value
##  CR - FR    -0.634 0.785  6  -0.808  0.4500
##
## Degrees-of-freedom method: kenward-roger
```

```
cld(field_means_all_years)
```

```
## Year = 2021:
##  Treatment emmean    SE df lower.CL upper.CL .group
##  CR         11.56 0.555 12    10.35    12.77  1
##  FR         12.72 0.555 12    11.51    13.93  1
##
## Year = 2022:
##  Treatment emmean    SE df lower.CL upper.CL .group
##  CR         10.63 0.555 12     9.42    11.84  1
##  FR         11.64 0.555 12    10.43    12.85  1
##
## Year = 2023:
##  Treatment emmean    SE df lower.CL upper.CL .group
##  CR          7.78 0.555 12     6.57     8.99  1
##  FR          8.41 0.555 12     7.20     9.62  1
##
## 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.
```

```
anova_results <- as.data.frame(anova(model_all_years))
```

Quadratic models

Automating the process with functions

We will be assuming that the yield-nrate curve will follow a quadratic curve. It will be messy to extract all the coefficients and then compute local maxima of each treatment. So here is a function to do that.

```
#this function automates the extraction of coefficients from quadratic models to calculate optimal N ra

optimal_N <- function(model) {
  # Extract the coefficients
  coefficients <- coef(model)

  # Get the names of the terms to make sure we handle your model's naming conventions
  term_names <- names(coefficients)

  # Identify the names for the intercept, linear, and quadratic terms
  intercept_term <- "(Intercept)"
  linear_term <- term_names[grepl("^Nrate", term_names)]
  quadratic_term <- term_names[grepl("I\\(Nrate\\^2\\)", term_names)]
  # Ensure both linear and quadratic terms are found
  if (length(linear_term) == 0 | length(quadratic_term) == 0) {
    stop("The model must include both Nrate and I(Nrate^2) terms.")
  }

  # Extract individual coefficients
  beta_0 <- coefficients[intercept_term]
  beta_1 <- coefficients[linear_term]
  beta_2 <- coefficients[quadratic_term]

  # Calculate the optimal N rate (x value) where the slope is zero
  x_optimal <- -beta_1 / (2 * beta_2)

  # Calculate the corresponding y value at the optimal N rate
  y_optimal <- beta_0 + beta_1 * x_optimal + beta_2 * x_optimal^2

  # Return both x and y values as a list
  return(list(x_optimal = x_optimal, y_optimal = y_optimal))
}

#this function automates the construction of quadratic models

run_all_models <- function() {
  # Create an empty data frame to store the results
  results <- data.frame(
    Year = character(),
    Treatment = character(),
    Nrate_optimal = numeric(),
    Yield_max = numeric(),
    stringsAsFactors = FALSE
  )

  # Define the years and treatments
  years <- c(2021, 2022, 2023, "average")
  treatments <- c("CR", "FR")

  # Loop through each year and treatment
  for (year in years) {
    for (treatment in treatments) {
      # Construct the model name dynamically
      model_formula <- as.formula(paste0("Yield_Mgha ~ Nrate + I(Nrate^2)"))
      data_name <- paste0("yield_", year)
      model_data <- get(data_name) %>% filter(Treatment == treatment)

      # Fit the model for the current year and treatment
      model <- lm(model_formula, data = model_data)

      # Calculate optimal Nrate and maximum yield using the optimal_N function
      optimal_values <- optimal_N(model)

      # Add the results to the data frame
      results <- rbind(results, data.frame(
        Year = year,
        Treatment = treatment,
        Nrate_optimal = optimal_values$x_optimal,
        Yield_max = optimal_values$y_optimal
      ))
    }
  }

  return(results)
}
```

Quadratic regressions and optimal N rates

```
#Here are all the optimal N rates

optimal_results <- run_all_models()

optimal_results
```

```
##           Year Treatment Nrate_optimal Yield_max
## Nrate     2021        CR     193.27222 13.408929
## Nrate1    2021        FR     188.42729 14.279893
## Nrate2    2022        CR     242.11177 12.336015
## Nrate3    2022        FR     188.44741 12.748488
## Nrate4    2023        CR     200.61488  9.067150
## Nrate5    2023        FR      85.28421  9.402874
## Nrate6 average        CR     280.86405 12.321429
## Nrate7 average        FR     281.63233 12.287842
```

```
optimal_results$Year <- as.factor(optimal_results$Year)

write_xlsx(optimal_results, "C:/Users/zhang/Documents/GitHub/FallowRice_ContinuousRice_AgronomicPerforma
```

Data visualisation and statistical testing (Corresponds to Figure 2)

Graphing dataframes

```
# 2021 dataframe

yield_2021_dataframe <- yield_2021 %>%
    group_by(Treatment, Nrate) %>%
   mutate(Yield_Mgha_se = sd(Yield_Mgha)/sqrt(3)) %>%
  summarise(Yield_Mgha = mean(Yield_Mgha),
            Yield_Mgha_se = mean(Yield_Mgha_se)) %>%
  mutate(Year = "2021")%>%
  left_join(optimal_results %>% select(Year, Treatment, Nrate_optimal), by = c("Year", "Treatment"))%>%
  mutate(Nrate_optimal = round(Nrate_optimal))
```

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

```
# 2022 dataframe

yield_2022_dataframe <- yield_2022 %>%
    group_by(Treatment, Nrate) %>%
   mutate(Yield_Mgha_se = sd(Yield_Mgha)/sqrt(3)) %>%
  summarise(Yield_Mgha = mean(Yield_Mgha),
            Yield_Mgha_se = mean(Yield_Mgha_se)) %>%
  mutate(Year = "2022")%>%
  left_join(optimal_results %>% select(Year, Treatment, Nrate_optimal), by = c("Year", "Treatment"))%>%
  mutate(Nrate_optimal = round(Nrate_optimal))
```

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

```
# 2023 dataframe

yield_2023_dataframe <- yield_2023 %>%
    group_by(Treatment, Nrate) %>%
   mutate(Yield_Mgha_se = sd(Yield_Mgha)/sqrt(3)) %>%
  summarise(Yield_Mgha = mean(Yield_Mgha),
            Yield_Mgha_se = mean(Yield_Mgha_se)) %>%
  mutate(Year = "2023")%>%
  left_join(optimal_results %>% select(Year, Treatment, Nrate_optimal), by = c("Year", "Treatment"))%>%
  mutate(Nrate_optimal = round(Nrate_optimal))
```

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

```
# average dataframe

yield_average_dataframe <- yield_average %>%
    group_by(Treatment, Nrate) %>%
   mutate(Yield_Mgha_se = sd(Yield_Mgha)/sqrt(3)) %>%
  summarise(Yield_Mgha = mean(Yield_Mgha),
            Yield_Mgha_se = mean(Yield_Mgha_se)) %>%
  mutate(Year = "average")%>%
  left_join(optimal_results %>% select(Year, Treatment, Nrate_optimal), by = c("Year", "Treatment"))%>%
  mutate(Nrate_optimal = round(Nrate_optimal))
```

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

2021

Statical test, comparisons by N rate and Treatment

```r
model_2021 <- lmer(Yield_Mgha ~ NrateF*Treatment+(1|Blk:Treatment)+(1|Blk), data=yield_2021)
```

```
## boundary (singular) fit: see help(’isSingular’)
```

```r
anova(model_2021)
```

```
## Type III Analysis of Variance Table with Satterthwaite’s method
##                   Sum Sq Mean Sq NumDF DenDF  F value    Pr(>F)    
## NrateF           251.041  50.208     5    22 163.6431 < 2.2e-16 ***
## Treatment         12.176  12.176     1    22  39.6860 2.436e-06 ***
## NrateF:Treatment   2.236   0.447     5    22   1.4574    0.2437    
## ---
## Signif. codes:  0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1 ’ ’ 1
```

```r
field_means_2021 = emmeans(model_2021,spec = 'Treatment',by = 'NrateF')
field_effects_2021 = contrast(field_means_2021, method = 'pairwise', adjust = "Tukey")

summary(field_effects_2021)
```

```
## NrateF = 0:
##  contrast estimate    SE   df t.ratio p.value
##  CR - FR    -2.246 0.452 20.6  -4.965  0.0001
## 
## NrateF = 115:
##  contrast estimate    SE   df t.ratio p.value
##  CR - FR    -1.177 0.452 20.6  -2.603  0.0168
## 
## NrateF = 155:
##  contrast estimate    SE   df t.ratio p.value
##  CR - FR    -0.904 0.452 20.6  -2.000  0.0589
## 
## NrateF = 185:
##  contrast estimate    SE   df t.ratio p.value
##  CR - FR    -0.988 0.452 20.6  -2.184  0.0407
## 
## NrateF = 225:
##  contrast estimate    SE   df t.ratio p.value
##  CR - FR    -0.806 0.452 20.6  -1.781  0.0897
## 
## NrateF = 260:
##  contrast estimate    SE   df t.ratio p.value
##  CR - FR    -0.858 0.452 20.6  -1.897  0.0719
## 
## Degrees-of-freedom method: kenward-roger
```

```r
cld(field_means_2021)
```

```
## NrateF = 0:
##  Treatment emmean    SE   df lower.CL upper.CL .group
##  CR          5.22 0.338 21.5     4.52     5.92  1
##  FR           7.46 0.338 21.5     6.76     8.17   2
## 
## NrateF = 115:
##  Treatment emmean    SE   df lower.CL upper.CL .group
##  CR          11.91 0.338 21.5    11.21    12.61  1    
##  FR          13.09 0.338 21.5    12.39    13.79   2   
## 
## NrateF = 155:
##  Treatment emmean    SE   df lower.CL upper.CL .group
##  CR          13.20 0.338 21.5    12.50    13.90  1    
##  FR          14.10 0.338 21.5    13.40    14.81  1    
## 
## NrateF = 185:
##  Treatment emmean    SE   df lower.CL upper.CL .group
##  CR          13.53 0.338 21.5    12.83    14.23  1    
##  FR          14.52 0.338 21.5    13.82    15.22   2   
## 
## NrateF = 225:
##  Treatment emmean    SE   df lower.CL upper.CL .group
##  CR          13.04 0.338 21.5    12.34    13.74  1    
##  FR          13.85 0.338 21.5    13.14    14.55  1    
## 
## NrateF = 260:
##  Treatment emmean    SE   df lower.CL upper.CL .group
##  CR          12.46 0.338 21.5    11.76    13.16  1    
##  FR          13.32 0.338 21.5    12.62    14.02  1    
## 
## 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.
```

```
emmeans(model_2021, ~ Treatment + NrateF)
```

```
##  Treatment NrateF emmean    SE   df lower.CL upper.CL
##  CR        0        5.22 0.338 21.5     4.52     5.92
##  FR        0        7.46 0.338 21.5     6.76     8.17
##  CR        115     11.91 0.338 21.5    11.21    12.61
##  FR        115     13.09 0.338 21.5    12.39    13.79
##  CR        155     13.20 0.338 21.5    12.50    13.90
##  FR        155     14.10 0.338 21.5    13.40    14.81
##  CR        185     13.53 0.338 21.5    12.83    14.23
##  FR        185     14.52 0.338 21.5    13.82    15.22
##  CR        225     13.04 0.338 21.5    12.34    13.74
##  FR        225     13.85 0.338 21.5    13.14    14.55
##  CR        260     12.46 0.338 21.5    11.76    13.16
##  FR        260     13.32 0.338 21.5    12.62    14.02
## 
## Degrees-of-freedom method: kenward-roger 
## Confidence level used: 0.95
```

```
cld_2021 <- cld(emmeans(model_2021, ~ Treatment + NrateF),adjust = "Sidak")

cld_2021
```

```
##  Treatment NrateF emmean    SE   df lower.CL upper.CL .group
##  CR        0        5.22 0.338 21.5     4.14     6.30  1
##  FR        0        7.46 0.338 21.5     6.39     8.54   2
##  CR        115     11.91 0.338 21.5    10.83    12.99    3
##  CR        260     12.46 0.338 21.5    11.38    13.54    34
##  CR        225     13.04 0.338 21.5    11.96    14.12    345
##  FR        115     13.09 0.338 21.5    12.01    14.17    345
##  CR        155     13.20 0.338 21.5    12.12    14.28    345
##  FR        260     13.32 0.338 21.5    12.24    14.40    345
##  CR        185     13.53 0.338 21.5    12.45    14.61    345
##  FR        225     13.85 0.338 21.5    12.77    14.92     45
##  FR        155     14.10 0.338 21.5    13.03    15.18     45
##  FR        185     14.52 0.338 21.5    13.44    15.59      5
##
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
## Conf-level adjustment: sidak method for 12 estimates
## P value adjustment: sidak method for 66 tests
## 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.
```

```
top_yields_2021 <- cld_2021 %>%
  group_by(Treatment) %>%
  filter(emmean == max(emmean)) %>%
  ungroup()
```

Graph_2021

```
N_response_curve_2021 <-
ggplot(yield_2021_dataframe, aes(x=Nrate, y=Yield_Mgha, color=Treatment))+
  geom_point(data=yield_2021_dataframe, size=2.5)+ #this is the mean values
  geom_point(data=yield_2021, size=1, alpha=0.4)+ #this are the raw values
  scale_color_manual(values=c("#0072B2","#FFCC66"), name = "Treatment", labels = c('Continuous Rice (CR
  scale_x_continuous(name=expression("N rate (kg N ha"^{-1}*")"), limits = c(-20, 320), breaks = seq(0,
  #scale_x_continuous(name=expression("N rate (kg N ha"^{-1}*")"), limits = c(-20, 280), breaks = c(0,
  scale_y_continuous(name= expression("Yield (Mg ha"^{-1}*")"), limits = c(0, 22), breaks = seq(0, 22,
  #geom_errorbar(data=yield_2021_dataframe, aes(ymin=Yield_Mgha-Yield_Mgha_se, ymax=Yield_Mgha+Yield_Mg
  theme_classic()+
  geom_smooth(data = yield_2021, method = "lm", formula = y ~ poly(x, 2), se = FALSE)+
  #geom_vline(xintercept = c(0, 115, 155, 185, 225, 260), linetype = "twodash", color = "black") +
  stat_regline_equation(data=yield_2021,
                        aes(x=Nrate, y=Yield_Mgha, color=Treatment, group = Treatment,
                            label = paste(..rr.label..)),
                        formula = y ~ poly(x, 2, raw = TRUE),
                        show.legend = FALSE, label.x = 0, label.y = c(16.5, 19))+
```

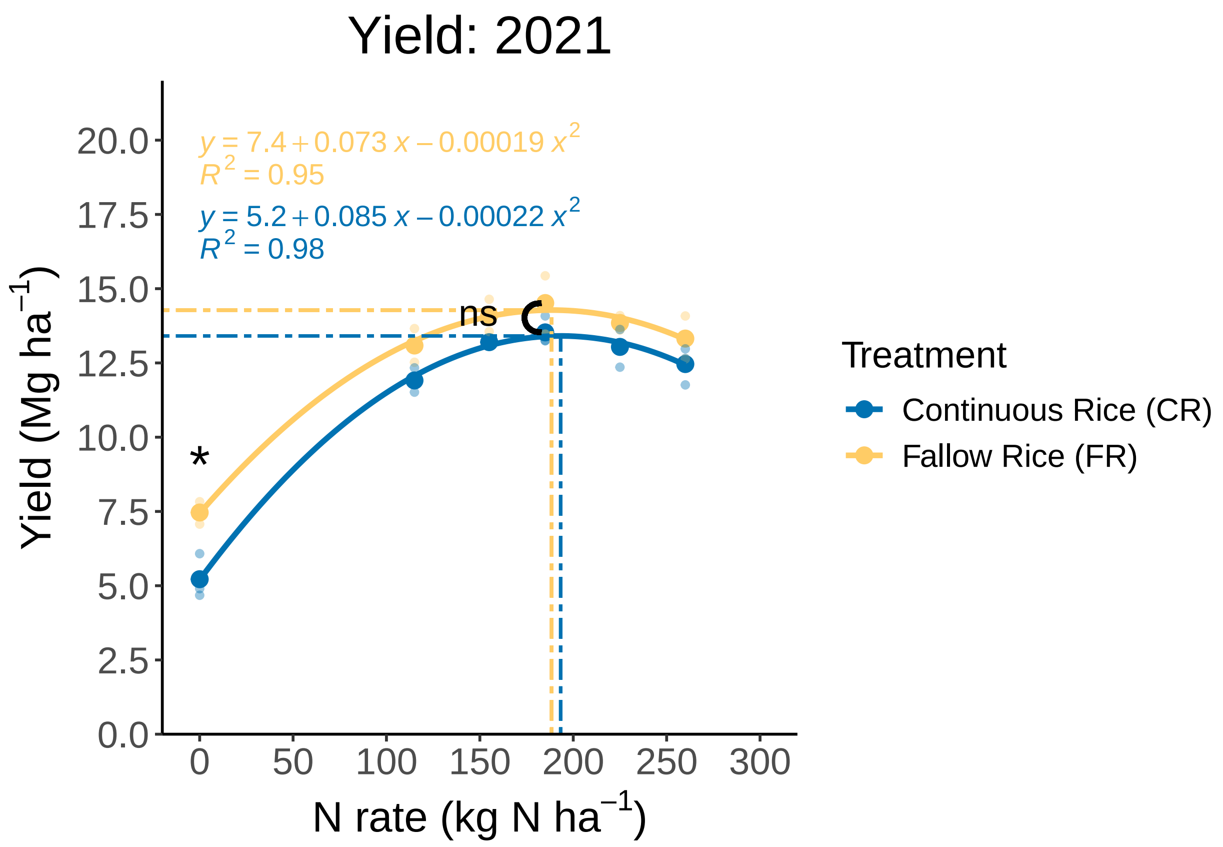
```r
   stat_regline_equation(data=yield_2021,
                      aes(x=Nrate, y=Yield_Mgha, color=Treatment, group = Treatment,
                          label = paste(..eq.label..)),
                      formula = y ~ poly(x, 2, raw = TRUE),
                      show.legend = FALSE, label.x = 0, label.y = c(17.5, 20))+
  theme(axis.text = element_text(size = 14), axis.title = element_text(size=16))+
  theme(legend.text = element_text(size = 12),legend.title = element_text(size = 14))+
  theme(plot.title = element_text(hjust = 0.5, size = 20, face = "bold"))+
  ggtitle(expression("Yield: 2021"))+
  annotate(
  "text",
  x = c(0),
  y = yield_2021_dataframe %>%
       filter(Treatment == "FR", Nrate == 0) %>%
        mutate(Yield_Mgha_plus_higher = Yield_Mgha + 1) %>%
        pull(Yield_Mgha_plus_higher),
  label = "*",
  size = 7,
  vjust = 0
  )+
# Vertical line for CR
geom_segment(
  aes(x = optimal_results %>% filter(Treatment == "CR", Year == "2021") %>% pull(Nrate_optimal),
      xend = optimal_results %>% filter(Treatment == "CR", Year == "2021") %>% pull(Nrate_optimal),
      y = 0,  # Start exactly from 0 on y-axis
      yend = optimal_results %>% filter(Treatment == "CR", Year == "2021") %>% pull(Yield_max)),
  linetype = "twodash", color = "#0072B2", size = 0.6
) +
# Vertical line for FR
geom_segment(
  aes(x = optimal_results %>% filter(Treatment == "FR", Year == "2021") %>% pull(Nrate_optimal),
      xend = optimal_results %>% filter(Treatment == "FR", Year == "2021") %>% pull(Nrate_optimal),
      y = 0,  # Start exactly from 0 on y-axis
      yend = optimal_results %>% filter(Treatment == "FR", Year == "2021") %>% pull(Yield_max)),
  linetype = "twodash", color = "#FFCC66", size = 0.6
) +

# Horizontal line for CR
geom_segment(
  aes(y = optimal_results %>% filter(Treatment == "CR", Year == "2021") %>% pull(Yield_max),
      yend = optimal_results %>% filter(Treatment == "CR", Year == "2021") %>% pull(Yield_max),
      x = -20,  # Start exactly from 0 on x-axis
      xend = optimal_results %>% filter(Treatment == "CR", Year == "2021") %>% pull(Nrate_optimal)),
  linetype = "twodash", color = "#0072B2", size = 0.6
) +
# Horizontal line for FR
geom_segment(
  aes(y = optimal_results %>% filter(Treatment == "FR", Year == "2021") %>% pull(Yield_max),
      yend = optimal_results %>% filter(Treatment == "FR", Year == "2021") %>% pull(Yield_max),
      x = -20,  # Start exactly from 0 on x-axis
      xend = optimal_results %>% filter(Treatment == "FR", Year == "2021") %>% pull(Nrate_optimal)),
  linetype = "twodash", color = "#FFCC66", size = 0.6
)+
      geom_curve(x = top_yields_2021 %>%
                 filter(Treatment == "FR") %>%
                 mutate(NrateF = as.numeric(paste(NrateF))) %>%
                 pull(NrateF)-2,
                 y = top_yields_2021 %>%
                 filter(Treatment == "FR") %>%
                 pull(emmean),
               xend = top_yields_2021 %>%
                 filter(Treatment == "CR") %>%
                 mutate(NrateF = as.numeric(paste(NrateF))) %>%
                 pull(NrateF)-2,
               yend = top_yields_2021 %>%
                 filter(Treatment == "CR") %>%
                 pull(emmean),
               color = 1, size=1,
               curvature = 1.2,)+
  annotate(
  "text",
  x =   (top_yields_2021 %>%
                 filter(Treatment == "FR") %>%
                 mutate(NrateF = as.numeric(paste(NrateF))) %>%
                 pull(NrateF)+
       top_yields_2021 %>%
                 filter(Treatment == "CR") %>%
                 mutate(NrateF = as.numeric(paste(NrateF))) %>%
                 pull(NrateF))/2,
  y = (top_yields_2021 %>%
                 filter(Treatment == "FR") %>%
                 pull(emmean)+
           top_yields_2021 %>%
                 filter(Treatment == "CR") %>%
                 pull(emmean))/2,
  label = "ns",
  size = 5,
  vjust = 0.3,
  hjust = +2.2 )
```

```
## 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.
```

```
N_response_curve_2021
```

```
## Warning: The dot-dot notation (‘..rr.label..‘) was deprecated in ggplot2 3.4.0.
## i Please use ‘after_stat(rr.label)‘ instead.
## This warning is displayed once every 8 hours.
## Call ‘lifecycle::last_lifecycle_warnings()‘ to see where this warning was
## generated.
```

```
## Warning in geom_segment(aes(x = optimal_results %>% filter(Treatment == : All aesthetics have length
## i Please consider using `annotate()` or provide this layer with data containing
##   a single row.

## Warning in geom_segment(aes(x = optimal_results %>% filter(Treatment == : All aesthetics have length
## i Please consider using `annotate()` or provide this layer with data containing
##   a single row.

## Warning in geom_segment(aes(y = optimal_results %>% filter(Treatment == : All aesthetics have length
## i Please consider using `annotate()` or provide this layer with data containing
##   a single row.

## Warning in geom_segment(aes(y = optimal_results %>% filter(Treatment == : All aesthetics have length
## i Please consider using `annotate()` or provide this layer with data containing
##   a single row.
```



2022

Statical test, comparisons by N rate and Treatment

```
model_2022 <- lmer(Yield_Mgha ~ NrateF*Treatment+(1|Blk:Treatment)+(1|Blk), data=yield_2022)

anova(model_2022)
```

```
## Type III Analysis of Variance Table with Satterthwaite’s method
##                   Sum Sq Mean Sq NumDF DenDF F value    Pr(>F)
## NrateF           155.079 31.0159     5    20 37.7791 1.601e-09 ***
## Treatment          5.857  5.8567     1     2  7.1338    0.1162
## NrateF:Treatment   8.633  1.7265     5    20  2.1030    0.1073
## ---
## Signif. codes:  0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1 ’ ’ 1
```

```r
field_means_2022 = emmeans(model_2022,spec = 'Treatment',by = 'NrateF')
field_effects_2022 = contrast(field_means_2022, method = 'pairwise', adjust = "Tukey")

summary(field_effects_2022)
```

```
## NrateF = 0:
##  contrast estimate    SE   df t.ratio p.value
##  CR - FR   -2.5151 0.774 17.4  -3.251  0.0046
##
## NrateF = 115:
##  contrast estimate    SE   df t.ratio p.value
##  CR - FR   -1.2073 0.774 17.4  -1.561  0.1366
##
## NrateF = 155:
##  contrast estimate    SE   df t.ratio p.value
##  CR - FR   -1.6841 0.774 17.4  -2.177  0.0435
##
## NrateF = 185:
##  contrast estimate    SE   df t.ratio p.value
##  CR - FR   -1.0247 0.774 17.4  -1.325  0.2024
##
## NrateF = 225:
##  contrast estimate    SE   df t.ratio p.value
##  CR - FR    0.4174 0.774 17.4   0.540  0.5963
##
## NrateF = 260:
##  contrast estimate    SE   df t.ratio p.value
##  CR - FR   -0.0308 0.774 17.4  -0.040  0.9686
##
## Degrees-of-freedom method: kenward-roger
```

```r
cld(field_means_2022)
```

```
## NrateF = 0:
##  Treatment emmean  SE   df lower.CL upper.CL .group
##  CR          5.28 0.6 16.4     4.01     6.54  1
##  FR          7.79 0.6 16.4     6.52     9.06   2
##
## NrateF = 115:
##  Treatment emmean  SE   df lower.CL upper.CL .group
##  CR         11.12 0.6 16.4     9.85    12.39  1
##  FR         12.33 0.6 16.4    11.06    13.60  1
##
## NrateF = 155:
##  Treatment emmean  SE   df lower.CL upper.CL .group
##  CR          10.89 0.6 16.4     9.62    12.16  1    
##  FR          12.58 0.6 16.4    11.31    13.85   2   
## 
## NrateF = 185:
##  Treatment emmean  SE   df lower.CL upper.CL .group
##  CR          11.74 0.6 16.4    10.47    13.01  1    
##  FR          12.76 0.6 16.4    11.49    14.03  1    
## 
## NrateF = 225:
##  Treatment emmean  SE   df lower.CL upper.CL .group
##  FR          11.89 0.6 16.4    10.62    13.16  1    
##  CR          12.31 0.6 16.4    11.04    13.58  1    
## 
## NrateF = 260:
##  Treatment emmean  SE   df lower.CL upper.CL .group
##  CR          12.45 0.6 16.4    11.18    13.72  1    
##  FR          12.48 0.6 16.4    11.22    13.75  1    
## 
## 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.
```

```
emmeans(model_2022, ~ Treatment + NrateF)
```

```
##  Treatment NrateF emmean  SE   df lower.CL upper.CL
##  CR        0         5.28 0.6 16.4     4.01     6.54
##  FR        0         7.79 0.6 16.4     6.52     9.06
##  CR        115      11.12 0.6 16.4     9.85    12.39
##  FR        115      12.33 0.6 16.4    11.06    13.60
##  CR        155      10.89 0.6 16.4     9.62    12.16
##  FR        155      12.58 0.6 16.4    11.31    13.85
##  CR        185      11.74 0.6 16.4    10.47    13.01
##  FR        185      12.76 0.6 16.4    11.49    14.03
##  CR        225      12.31 0.6 16.4    11.04    13.58
##  FR        225      11.89 0.6 16.4    10.62    13.16
##  CR        260      12.45 0.6 16.4    11.18    13.72
##  FR        260      12.48 0.6 16.4    11.22    13.75
## 
## Degrees-of-freedom method: kenward-roger 
## Confidence level used: 0.95
```

```
cld_2022 <- cld(emmeans(model_2022, ~ Treatment + NrateF),adjust = "Sidak")

cld_2022
```

```
##  Treatment NrateF emmean  SE   df lower.CL upper.CL .group
##  CR        0         5.28 0.6 16.4     3.29     7.26  1   
##  FR        0         7.79 0.6 16.4     5.80     9.78  12  
##  CR        155      10.89 0.6 16.4     8.90    12.88   23 
##  CR        115      11.12 0.6 16.4     9.14    13.11    3 
##  CR        185    11.74 0.6 16.4     9.75    13.73    3
##  FR        225    11.89 0.6 16.4     9.91    13.88    3
##  CR        225    12.31 0.6 16.4    10.32    14.30    3
##  FR        115    12.33 0.6 16.4    10.34    14.32    3
##  CR        260    12.45 0.6 16.4    10.47    14.44    3
##  FR        260    12.48 0.6 16.4    10.50    14.47    3
##  FR        155    12.58 0.6 16.4    10.59    14.56    3
##  FR        185    12.76 0.6 16.4    10.77    14.75    3
##
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
## Conf-level adjustment: sidak method for 12 estimates
## P value adjustment: sidak method for 66 tests
## 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.
```

```
top_yields_2022 <- cld_2022 %>%
  group_by(Treatment) %>%
  filter(emmean == max(emmean)) %>%
  ungroup()

top_yields_2022
```

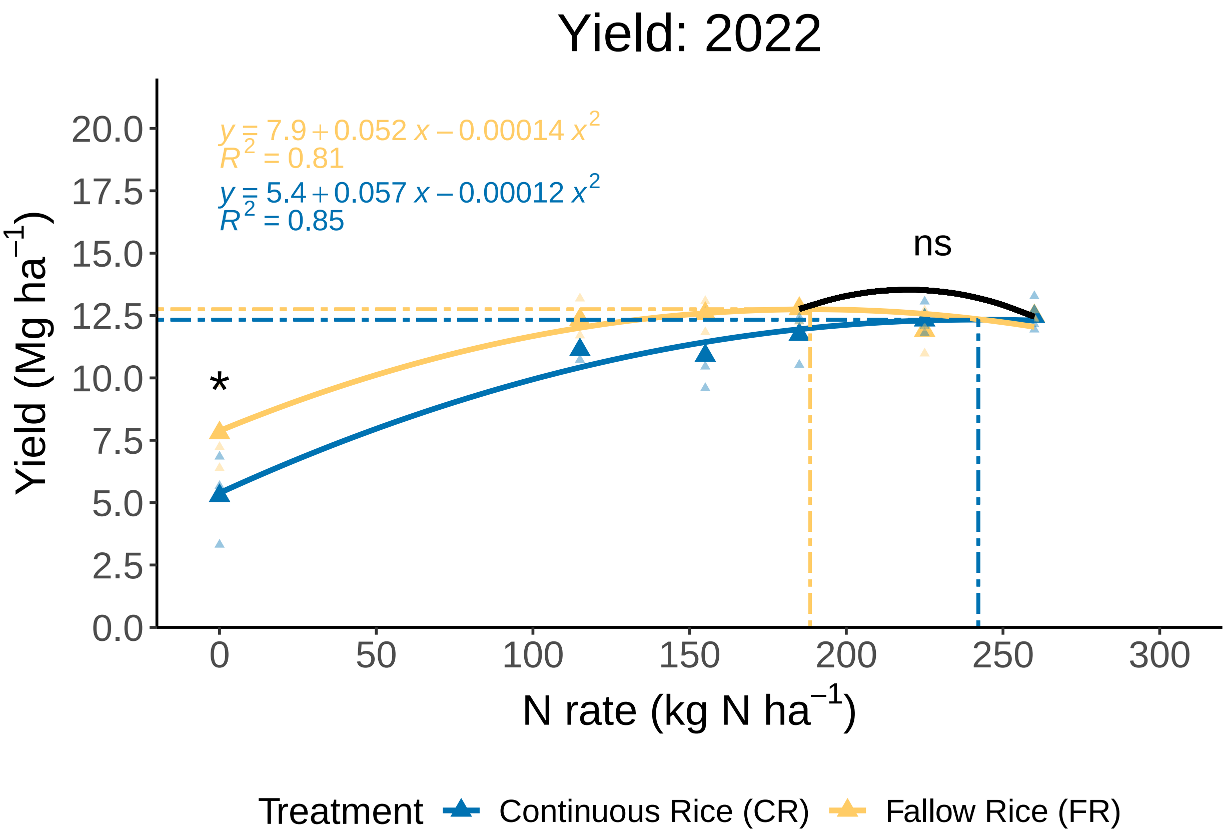
```
## # A tibble: 2 x 8
##   Treatment NrateF emmean    SE    df lower.CL upper.CL .group
##   <fct>     <fct>   <dbl> <dbl> <dbl>    <dbl>    <dbl> <chr>
## 1 CR        260      12.5 0.600  16.4     10.5     14.4 "   3"
## 2 FR        185      12.8 0.600  16.4     10.8     14.8 "   3"
```

Graph_2022

```
N_response_curve_2022 <-
ggplot(yield_2022_dataframe, aes(x=Nrate, y=Yield_Mgha, color=Treatment))+
  geom_point(data=yield_2022_dataframe %>% filter(Treatment == "FR"),
             aes(x=Nrate, y=Yield_Mgha, color="FR"), size=2.5, shape ="triangle") +
  geom_point(data=yield_2022_dataframe %>% filter(Treatment == "CR"),
             aes(x=Nrate, y=Yield_Mgha, color="CR"), size=2.5, shape ="triangle") +
  #geom_point(data=yield_2022_dataframe, size=2.5, shape ="triangle")+ #this is the mean values
  geom_point(data=yield_2022, size=1, alpha=0.4, shape ="triangle")+ #this are the raw values
  scale_color_manual(values=c("#0072B2","#FFCC66"), name = "Treatment", labels = c('Continuous Rice (CR
  scale_x_continuous(name=expression("N rate (kg N ha"^{-1}*")"), limits = c(-20, 320), breaks = seq(0,
  #scale_x_continuous(name=expression("N rate (kg N ha"^{-1}*")"), limits = c(-20, 280), breaks = c(0,
  scale_y_continuous(name= expression("Yield (Mg ha"^{-1}*")"), limits = c(0, 22), breaks = seq(0, 22,
  #geom_errorbar(data=yield_2022_dataframe, aes(ymin=Yield_Mgha-Yield_Mgha_se, ymax=Yield_Mgha+Yield_Mg
  theme_classic()+
  geom_smooth(data = yield_2022, method = "lm", formula = y ~ poly(x, 2), se = FALSE)+
  #geom_vline(xintercept = c(0, 115, 155, 185, 225, 260), linetype = "twodash", color = "black") +
  theme(axis.text = element_text(size = 14), axis.title = element_text(size=16))+
  theme(legend.text = element_text(size = 12),legend.title = element_text(size = 14))+
  theme(plot.title = element_text(hjust = 0.5, size = 20, face = "bold"))+
  theme(legend.position = "bottom")+
  ggtitle(expression("Yield: 2022"))+
  annotate(
  "text",
  x = c(0),
  y = yield_2022_dataframe %>%
       filter(Treatment == "FR", Nrate == 0) %>%
        mutate(Yield_Mgha_plus_higher = Yield_Mgha + 1) %>%
        pull(Yield_Mgha_plus_higher),
  label = "*",
  size = 7,
  vjust = 0
  )+
# Vertical line for CR
geom_segment(
  aes(x = optimal_results %>% filter(Treatment == "CR", Year == "2022") %>% pull(Nrate_optimal),
      xend = optimal_results %>% filter(Treatment == "CR", Year == "2022") %>% pull(Nrate_optimal),
      y = 0,  # Start exactly from 0 on y-axis
      yend = optimal_results %>% filter(Treatment == "CR", Year == "2022") %>% pull(Yield_max)),
  linetype = "twodash", color = "#0072B2", size = 0.6
) +
# Vertical line for FR
geom_segment(
  aes(x = optimal_results %>% filter(Treatment == "FR", Year == "2022") %>% pull(Nrate_optimal),
      xend = optimal_results %>% filter(Treatment == "FR", Year == "2022") %>% pull(Nrate_optimal),
      y = 0,  # Start exactly from 0 on y-axis
      yend = optimal_results %>% filter(Treatment == "FR", Year == "2022") %>% pull(Yield_max)),
  linetype = "twodash", color = "#FFCC66", size = 0.6
) +

# Horizontal line for CR
geom_segment(
  aes(y = optimal_results %>% filter(Treatment == "CR", Year == "2022") %>% pull(Yield_max),
      yend = optimal_results %>% filter(Treatment == "CR", Year == "2022") %>% pull(Yield_max),
      x = -20,  # Start exactly from 0 on x-axis
      xend = optimal_results %>% filter(Treatment == "CR", Year == "2022") %>% pull(Nrate_optimal)),
  linetype = "twodash", color = "#0072B2", size = 0.6
) +
# Horizontal line for FR
geom_segment(
  aes(y = optimal_results %>% filter(Treatment == "FR", Year == "2022") %>% pull(Yield_max),
      yend = optimal_results %>% filter(Treatment == "FR", Year == "2022") %>% pull(Yield_max),
      x = -20,  # Start exactly from 0 on x-axis
      xend = optimal_results %>% filter(Treatment == "FR", Year == "2022") %>% pull(Nrate_optimal)),
  linetype = "twodash", color = "#FFCC66", size = 0.6
)+
  stat_regline_equation(data=yield_2022,
                      aes(x=Nrate, y=Yield_Mgha, color=Treatment, group = Treatment,
                          label = paste(..rr.label..)),
                      formula = y ~ poly(x, 2, raw = TRUE),
                      show.legend = FALSE, label.x = 0, label.y = c(16.5, 19))+
   stat_regline_equation(data=yield_2022,
                      aes(x=Nrate, y=Yield_Mgha, color=Treatment, group = Treatment,
                          label = paste(..eq.label..)),
                      formula = y ~ poly(x, 2, raw = TRUE),
                      show.legend = FALSE, label.x = 0, label.y = c(17.5, 20))+
    geom_curve(x = top_yields_2022 %>%
                 filter(Treatment == "FR") %>%
                 mutate(NrateF = as.numeric(paste(NrateF))) %>%
                 pull(NrateF),
                 y = top_yields_2022 %>%
                 filter(Treatment == "FR") %>%
                 pull(emmean),
               xend = top_yields_2022 %>%
                 filter(Treatment == "CR") %>%
                 mutate(NrateF = as.numeric(paste(NrateF))) %>%
                 pull(NrateF),
               yend = top_yields_2022 %>%
                 filter(Treatment == "CR") %>%
                 pull(emmean),
               color = 1, size=1,
               curvature = -0.2)+
  annotate(
  "text",
  x =   (top_yields_2022 %>%
                 filter(Treatment == "FR") %>%
                 mutate(NrateF = as.numeric(paste(NrateF))) %>%
                 pull(NrateF)+
       top_yields_2022 %>%
                 filter(Treatment == "CR") %>%
                 mutate(NrateF = as.numeric(paste(NrateF))) %>%
                 pull(NrateF))/2,
  y = mean(top_yields_2022 %>%
                 filter(Treatment == "FR") %>%
                 pull(emmean),
           top_yields_2022 %>%
                 filter(Treatment == "CR") %>%
                 pull(emmean)),
  label = "ns",
  size = 5,
  vjust = -2,
  hjust = 0.1 )


N_response_curve_2022
```

```
## Warning in geom_segment(aes(x = optimal_results %>% filter(Treatment == : All aesthetics have length
## i Please consider using `annotate()` or provide this layer with data containing
##   a single row.

## Warning in geom_segment(aes(x = optimal_results %>% filter(Treatment == : All aesthetics have length
## i Please consider using `annotate()` or provide this layer with data containing
##   a single row.

## Warning in geom_segment(aes(y = optimal_results %>% filter(Treatment == : All aesthetics have length
## i Please consider using `annotate()` or provide this layer with data containing
##   a single row.
```

```
## Warning in geom_segment(aes(y = optimal_results %>% filter(Treatment == : All aesthetics have length
## i Please consider using `annotate()` or provide this layer with data containing
##   a single row.
```



2023

Statical test, comparisons by N rate and Treatment

```r
model_2023 <- lmer(Yield_Mgha ~ NrateF*Treatment+(1|Blk:Treatment)+(1|Blk), data=yield_2023)
```

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

```r
anova(model_2023)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##                  Sum Sq Mean Sq NumDF DenDF F value  Pr(>F)
## NrateF           31.805  6.3610     5    20  4.0251 0.01088 *
## Treatment         2.477  2.4772     1     4  1.5675 0.27878
## NrateF:Treatment 42.351  8.4702     5    20  5.3597 0.00276 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
field_means_2023 = emmeans(model_2023,spec = 'Treatment',by = 'NrateF')
field_effects_2023 = contrast(field_means_2023, method = 'pairwise', adjust = "Tukey")

summary(field_effects_2023)
```

```
## NrateF = 0:
##  contrast estimate   SE df t.ratio p.value
##  CR - FR    -3.950 1.07 18  -3.708  0.0016
##
## NrateF = 90:
##  contrast estimate   SE df t.ratio p.value
##  CR - FR    -2.664 1.07 18  -2.501  0.0223
##
## NrateF = 120:
##  contrast estimate   SE df t.ratio p.value
##  CR - FR    -1.242 1.07 18  -1.166  0.2589
##
## NrateF = 150:
##  contrast estimate   SE df t.ratio p.value
##  CR - FR     0.709 1.07 18   0.666  0.5139
##
## NrateF = 180:
##  contrast estimate   SE df t.ratio p.value
##  CR - FR     2.076 1.07 18   1.948  0.0671
##
## NrateF = 210:
##  contrast estimate   SE df t.ratio p.value
##  CR - FR     1.264 1.07 18   1.187  0.2508
##
## Degrees-of-freedom method: kenward-roger
```

```r
cld(field_means_2023)
```

```
## NrateF = 0:
##  Treatment emmean    SE   df lower.CL upper.CL .group
##  CR          4.18 0.753 23.4     2.62     5.73  1
##  FR          8.13 0.753 23.4     6.57     9.68   2
##
## NrateF = 90:
##  Treatment emmean    SE   df lower.CL upper.CL .group
##  CR          6.92 0.753 23.4     5.36     8.48  1
##  FR          9.58 0.753 23.4     8.03    11.14   2
##
## NrateF = 120:
##  Treatment emmean    SE   df lower.CL upper.CL .group
##  CR          8.59 0.753 23.4     7.03    10.15  1
##  FR          9.83 0.753 23.4     8.27    11.39  1
##
## NrateF = 150:
##  Treatment emmean    SE   df lower.CL upper.CL .group
##  FR          8.21 0.753 23.4     6.66     9.77  1
##  CR          8.92 0.753 23.4     7.37    10.48  1
```

```
## 
## NrateF = 180:
##  Treatment emmean    SE   df lower.CL upper.CL .group
##  FR          7.23 0.753 23.4     5.68     8.79  1    
##  CR          9.31 0.753 23.4     7.75    10.86  1    
## 
## NrateF = 210:
##  Treatment emmean    SE   df lower.CL upper.CL .group
##  FR          7.49 0.753 23.4     5.94     9.05  1    
##  CR          8.76 0.753 23.4     7.20    10.31  1    
## 
## 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.
```

```r
emmeans(model_2023, ~ Treatment + NrateF)
```

```
##  Treatment NrateF emmean    SE   df lower.CL upper.CL
##  CR        0        4.18 0.753 23.4     2.62     5.73
##  FR        0        8.13 0.753 23.4     6.57     9.68
##  CR        90       6.92 0.753 23.4     5.36     8.48
##  FR        90       9.58 0.753 23.4     8.03    11.14
##  CR        120      8.59 0.753 23.4     7.03    10.15
##  FR        120      9.83 0.753 23.4     8.27    11.39
##  CR        150      8.92 0.753 23.4     7.37    10.48
##  FR        150      8.21 0.753 23.4     6.66     9.77
##  CR        180      9.31 0.753 23.4     7.75    10.86
##  FR        180      7.23 0.753 23.4     5.68     8.79
##  CR        210      8.76 0.753 23.4     7.20    10.31
##  FR        210      7.49 0.753 23.4     5.94     9.05
## 
## Degrees-of-freedom method: kenward-roger 
## Confidence level used: 0.95
```

```r
cld_2023 <- cld(emmeans(model_2023, ~ Treatment + NrateF),adjust = "Sidak")

cld_2023
```

```
##  Treatment NrateF emmean    SE   df lower.CL upper.CL .group
##  CR        0        4.18 0.753 23.4     1.79     6.56  1    
##  CR        90       6.92 0.753 23.4     4.54     9.30  12   
##  FR        180      7.23 0.753 23.4     4.85     9.62  12   
##  FR        210      7.49 0.753 23.4     5.11     9.88  12   
##  FR        0        8.13 0.753 23.4     5.74    10.51  12   
##  FR        150      8.21 0.753 23.4     5.83    10.60  12   
##  CR        120      8.59 0.753 23.4     6.20    10.97   2   
##  CR        210      8.76 0.753 23.4     6.37    11.14   2   
##  CR        150      8.92 0.753 23.4     6.54    11.31   2   
##  CR        180      9.31 0.753 23.4     6.92    11.69   2   
##  FR        90       9.58 0.753 23.4     7.20    11.97   2   
##  FR        120      9.83 0.753 23.4     7.45    12.21   2
##
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
## Conf-level adjustment: sidak method for 12 estimates
## P value adjustment: sidak method for 66 tests
## 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.
```

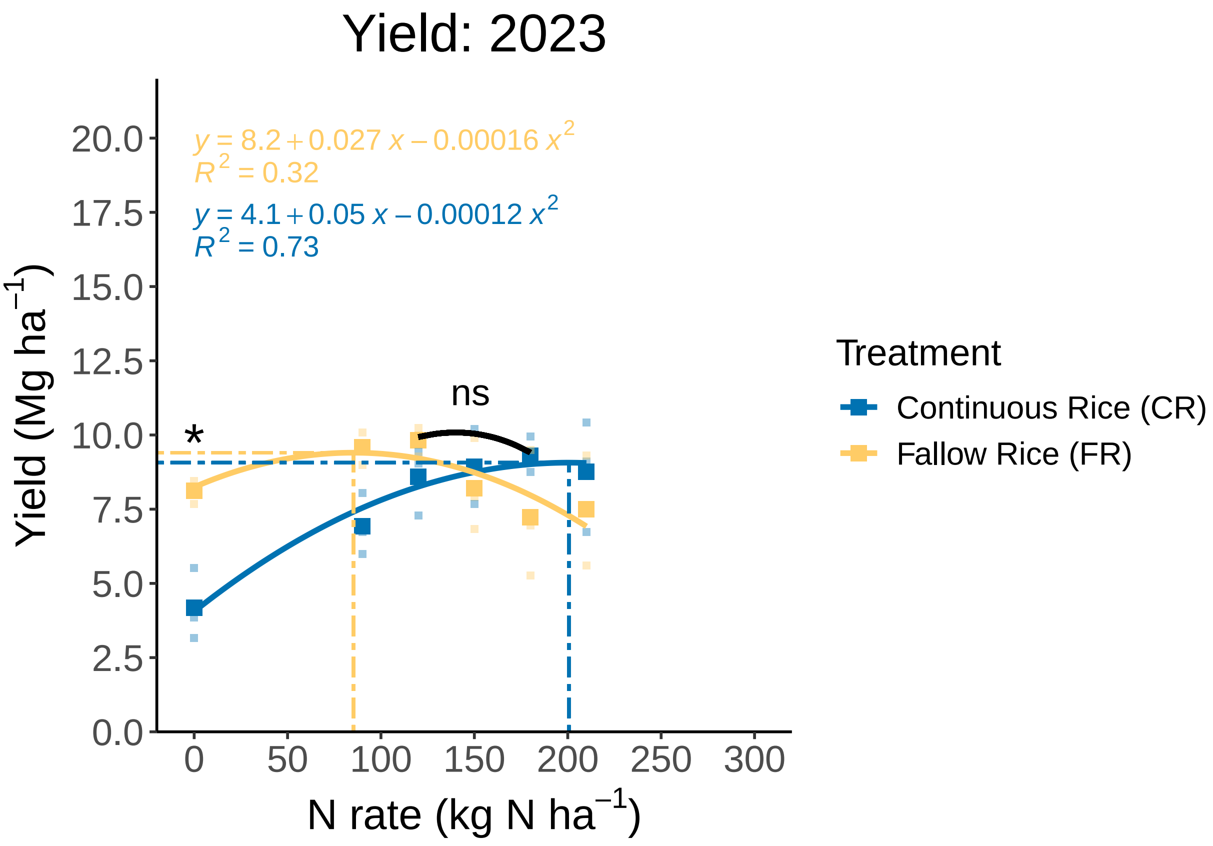
```
top_yields_2023 <- cld_2023 %>%
  group_by(Treatment) %>%
  filter(emmean == max(emmean)) %>%
  ungroup()
```

Graph_2023

```
N_response_curve_2023 <-
ggplot(yield_2023_dataframe, aes(x=Nrate, y=Yield_Mgha, color=Treatment))+
  geom_point(data=yield_2023_dataframe, size=2.5, shape ="square")+ #this is the mean values
  geom_point(data=yield_2023, size=1, alpha=0.4, shape ="square")+ #this are the raw values
  scale_color_manual(values=c("#0072B2","#FFCC66"), name = "Treatment", labels = c('Continuous Rice (CR)
  scale_x_continuous(name=expression("N rate (kg N ha"^{-1}*")"), limits = c(-20, 320), breaks = seq(0,
  #scale_x_continuous(name=expression("N rate (kg N ha"^{-1}*")"), limits = c(-20, 280), breaks = c(0,
  scale_y_continuous(name= expression("Yield (Mg ha"^{-1}*")"), limits = c(0, 22), breaks = seq(0, 22,
  #geom_errorbar(data=yield_2023_dataframe, aes(ymin=Yield_Mgha-Yield_Mgha_se, ymax=Yield_Mgha+Yield_Mg
  theme_classic()+
  geom_smooth(data = yield_2023, method = "lm", formula = y ~ poly(x, 2), se = FALSE)+
  #geom_vline(xintercept = c(0, 115, 155, 185, 225, 260), linetype = "twodash", color = "black") +
  theme(axis.text = element_text(size = 14), axis.title = element_text(size=16))+
  theme(legend.text = element_text(size = 12),legend.title = element_text(size = 14))+
  theme(plot.title = element_text(hjust = 0.5, size = 20, face = "bold"))+
  ggtitle(expression("Yield: 2023"))+
annotate(
  "text",
  x = c(0),
  y = yield_2023_dataframe %>%
       filter(Treatment == "FR", Nrate == 0) %>%
        mutate(Yield_Mgha_plus_higher = Yield_Mgha + 1) %>%
        pull(Yield_Mgha_plus_higher),
  label = "*",
  size = 7,
  vjust = 0
  )+
# Vertical line for CR
geom_segment(
  aes(x = optimal_results %>% filter(Treatment == "CR", Year == "2023") %>% pull(Nrate_optimal),
      xend = optimal_results %>% filter(Treatment == "CR", Year == "2023") %>% pull(Nrate_optimal),
      y = 0,  # Start exactly from 0 on y-axis
      yend = optimal_results %>% filter(Treatment == "CR", Year == "2023") %>% pull(Yield_max)),
  linetype = "twodash", color = "#0072B2", size = 0.6
```

```
) +
# Vertical line for FR
geom_segment(
  aes(x = optimal_results %>% filter(Treatment == "FR", Year == "2023") %>% pull(Nrate_optimal),
      xend = optimal_results %>% filter(Treatment == "FR", Year == "2023") %>% pull(Nrate_optimal),
      y = 0,  # Start exactly from 0 on y-axis
      yend = optimal_results %>% filter(Treatment == "FR", Year == "2023") %>% pull(Yield_max)),
  linetype = "twodash", color = "#FFCC66", size = 0.6
) +

# Horizontal line for CR
geom_segment(
  aes(y = optimal_results %>% filter(Treatment == "CR", Year == "2023") %>% pull(Yield_max),
      yend = optimal_results %>% filter(Treatment == "CR", Year == "2023") %>% pull(Yield_max),
      x = -20,  # Start exactly from 0 on x-axis
      xend = optimal_results %>% filter(Treatment == "CR", Year == "2023") %>% pull(Nrate_optimal)),
  linetype = "twodash", color = "#0072B2", size = 0.6
) +
# Horizontal line for FR
geom_segment(
  aes(y = optimal_results %>% filter(Treatment == "FR", Year == "2023") %>% pull(Yield_max),
      yend = optimal_results %>% filter(Treatment == "FR", Year == "2023") %>% pull(Yield_max),
      x = -20,  # Start exactly from 0 on x-axis
      xend = optimal_results %>% filter(Treatment == "FR", Year == "2023") %>% pull(Nrate_optimal)),
  linetype = "twodash", color = "#FFCC66", size = 0.6
)+
    geom_curve(x = top_yields_2023 %>%
                 filter(Treatment == "FR") %>%
                 mutate(NrateF = as.numeric(paste(NrateF))) %>%
                 pull(NrateF),
                 y = top_yields_2023 %>%
                 filter(Treatment == "FR") %>%
                 pull(emmean)+0.1,
               xend = top_yields_2023 %>%
                 filter(Treatment == "CR") %>%
                 mutate(NrateF = as.numeric(paste(NrateF))) %>%
                 pull(NrateF),
               yend = top_yields_2023 %>%
                 filter(Treatment == "CR") %>%
                 pull(emmean)+0.1,
               color = 1, size=1,
               curvature = -0.2)+
  stat_regline_equation(data=yield_2023,
                      aes(x=Nrate, y=Yield_Mgha, color=Treatment, group = Treatment,
                          label = paste(..rr.label..)),
                      formula = y ~ poly(x, 2, raw = TRUE),
                      show.legend = FALSE, label.x = 0, label.y = c(16.5, 19))+
   stat_regline_equation(data=yield_2023,
                      aes(x=Nrate, y=Yield_Mgha, color=Treatment, group = Treatment,
                          label = paste(..eq.label..)),
                      formula = y ~ poly(x, 2, raw = TRUE),
                      show.legend = FALSE, label.x = 0, label.y = c(17.5, 20))+
  annotate(
  "text",
  x =   (top_yields_2023 %>%
                 filter(Treatment == "FR") %>%
                 mutate(NrateF = as.numeric(paste(NrateF))) %>%
                 pull(NrateF)+
       top_yields_2023 %>%
                 filter(Treatment == "CR") %>%
                 mutate(NrateF = as.numeric(paste(NrateF))) %>%
                 pull(NrateF))/2,
  y = mean(top_yields_2023 %>%
                 filter(Treatment == "FR") %>%
                 pull(emmean),
           top_yields_2023 %>%
                 filter(Treatment == "CR") %>%
                 pull(emmean)),
  label = "ns",
  size = 5,
  vjust = -1.3,
  hjust = 0.6)


N_response_curve_2023
```

```
## Warning in geom_segment(aes(x = optimal_results %>% filter(Treatment == : All aesthetics have length
## i Please consider using ‘annotate()‘ or provide this layer with data containing
##   a single row.

## Warning in geom_segment(aes(x = optimal_results %>% filter(Treatment == : All aesthetics have length
## i Please consider using ‘annotate()‘ or provide this layer with data containing
##   a single row.

## Warning in geom_segment(aes(y = optimal_results %>% filter(Treatment == : All aesthetics have length
## i Please consider using ‘annotate()‘ or provide this layer with data containing
##   a single row.

## Warning in geom_segment(aes(y = optimal_results %>% filter(Treatment == : All aesthetics have length
## i Please consider using ‘annotate()‘ or provide this layer with data containing
##   a single row.
```



Average

Statical test, comparisons by N rate and Treatment

```
model_average <- lmer(Yield_Mgha ~ NrateF*Treatment+(1|Blk:Treatment)+(1|Blk), data=yield_average)

anova(model_average)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##                  Sum Sq Mean Sq NumDF  DenDF F value    Pr(>F)
## NrateF           498.78  49.878    10 63.464 51.7315 < 2.2e-16 ***
## Treatment          6.70   6.697     1  7.259  6.9463   0.03256 *
## NrateF:Treatment  49.76   4.976    10 44.320  5.1615 5.542e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
field_means_average = emmeans(model_average,spec = 'Treatment',by = 'NrateF')
field_effects_average = contrast(field_means_average, method = 'pairwise', adjust = "Tukey")

summary(field_effects_average)
```

```
## NrateF = 0:
```

```
##  contrast estimate    SE   df t.ratio p.value
##  CR - FR    -2.904 0.475 67.0  -6.110  <.0001
##
## NrateF = 90:
##  contrast estimate    SE   df t.ratio p.value
##  CR - FR    -2.610 0.829 69.2  -3.148  0.0024
##
## NrateF = 115:
##  contrast estimate    SE   df t.ratio p.value
##  CR - FR    -1.219 0.584 68.1  -2.087  0.0406
##
## NrateF = 120:
##  contrast estimate    SE   df t.ratio p.value
##  CR - FR    -1.188 0.829 69.2  -1.433  0.1563
##
## NrateF = 150:
##  contrast estimate    SE   df t.ratio p.value
##  CR - FR     0.763 0.829 69.2   0.920  0.3606
##
## NrateF = 155:
##  contrast estimate    SE   df t.ratio p.value
##  CR - FR    -1.321 0.584 68.1  -2.262  0.0269
##
## NrateF = 180:
##  contrast estimate    SE   df t.ratio p.value
##  CR - FR     2.129 0.829 69.2   2.568  0.0124
##
## NrateF = 185:
##  contrast estimate    SE   df t.ratio p.value
##  CR - FR    -1.033 0.584 68.1  -1.768  0.0815
##
## NrateF = 210:
##  contrast estimate    SE   df t.ratio p.value
##  CR - FR     1.318 0.829 69.2   1.589  0.1166
##
## NrateF = 225:
##  contrast estimate    SE   df t.ratio p.value
##  CR - FR    -0.221 0.584 68.1  -0.378  0.7065
##
## NrateF = 260:
##  contrast estimate    SE   df t.ratio p.value
##  CR - FR    -0.471 0.584 68.1  -0.807  0.4226
##
## Degrees-of-freedom method: kenward-roger
```

```
cld(field_means_average)
```

```
## NrateF = 0:
##  Treatment emmean    SE   df lower.CL upper.CL .group
##  CR          4.89 0.373 59.1     4.14     5.64  1
##  FR          7.79 0.373 59.1     7.05     8.54   2
##
## NrateF = 90:
##  Treatment emmean    SE   df lower.CL upper.CL .group
##  CR          7.01 0.639 77.8     5.74     8.29  1 
##  FR          9.62 0.639 77.8     8.35    10.90   2
## 
## NrateF = 115:
##  Treatment emmean    SE   df lower.CL upper.CL .group
##  CR         11.47 0.454 68.6    10.56    12.38  1 
##  FR         12.69 0.454 68.6    11.78    13.59   2
## 
## NrateF = 120:
##  Treatment emmean    SE   df lower.CL upper.CL .group
##  CR          8.68 0.639 77.8     7.41     9.95  1 
##  FR          9.87 0.639 77.8     8.60    11.14  1 
## 
## NrateF = 150:
##  Treatment emmean    SE   df lower.CL upper.CL .group
##  FR          8.25 0.639 77.8     6.98     9.52  1 
##  CR          9.02 0.639 77.8     7.74    10.29  1 
## 
## NrateF = 155:
##  Treatment emmean    SE   df lower.CL upper.CL .group
##  CR         12.00 0.454 68.6    11.09    12.91  1 
##  FR         13.32 0.454 68.6    12.41    14.23   2
## 
## NrateF = 180:
##  Treatment emmean    SE   df lower.CL upper.CL .group
##  FR          7.27 0.639 77.8     6.00     8.54  1 
##  CR          9.40 0.639 77.8     8.13    10.67   2
## 
## NrateF = 185:
##  Treatment emmean    SE   df lower.CL upper.CL .group
##  CR         12.59 0.454 68.6    11.68    13.49  1 
##  FR         13.62 0.454 68.6    12.71    14.53  1 
## 
## NrateF = 210:
##  Treatment emmean    SE   df lower.CL upper.CL .group
##  FR          7.53 0.639 77.8     6.26     8.81  1 
##  CR          8.85 0.639 77.8     7.58    10.12  1 
## 
## NrateF = 225:
##  Treatment emmean    SE   df lower.CL upper.CL .group
##  CR         12.63 0.454 68.6    11.72    13.53  1 
##  FR         12.85 0.454 68.6    11.94    13.76  1 
## 
## NrateF = 260:
##  Treatment emmean    SE   df lower.CL upper.CL .group
##  CR         12.41 0.454 68.6    11.51    13.32  1 
##  FR         12.88 0.454 68.6    11.98    13.79  1 
## 
## 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.
```

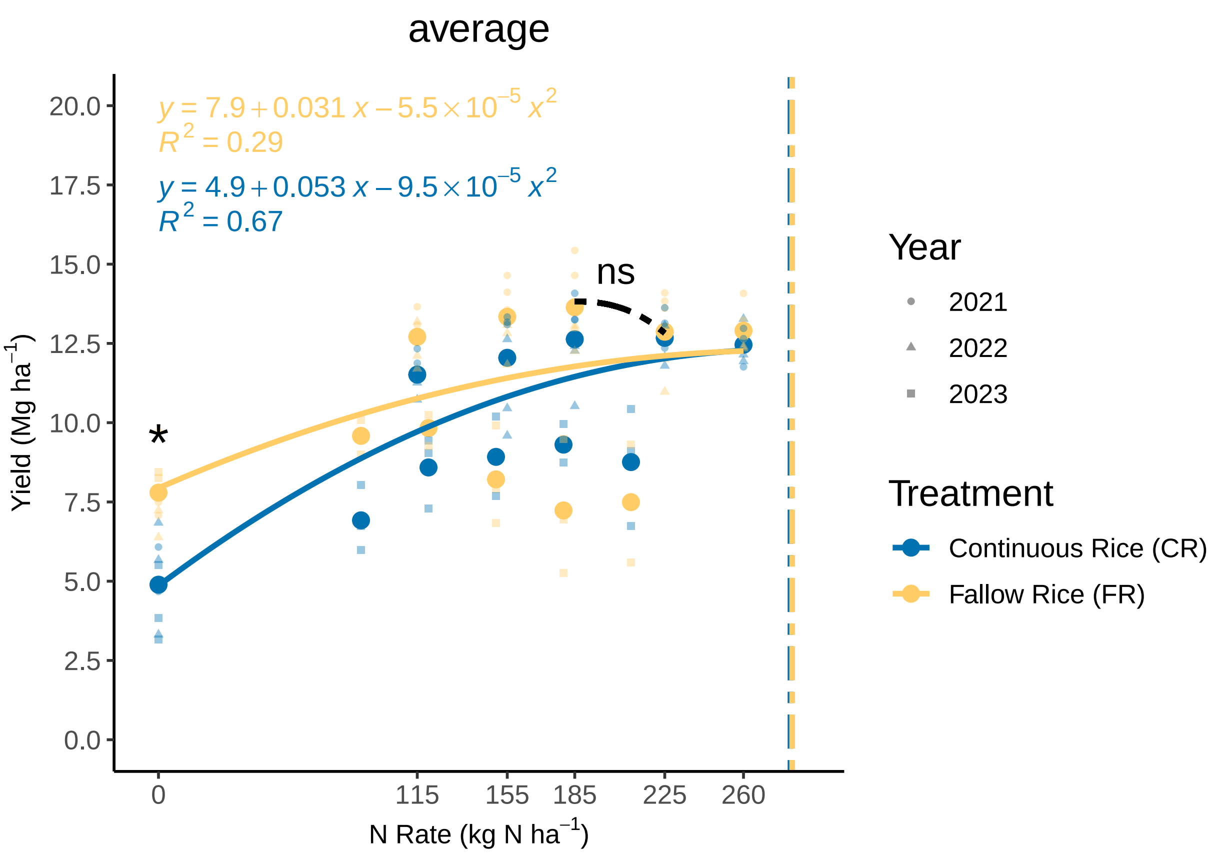
```
emmeans(model_average, ~ Treatment + NrateF)
```

```
##  Treatment NrateF emmean    SE   df lower.CL upper.CL
##  CR        0        4.89 0.373 59.1     4.14     5.64
##  FR        0        7.79 0.373 59.1     7.05     8.54
##  CR        90       7.01 0.639 77.8     5.74     8.29
##  FR        90       9.62 0.639 77.8     8.35    10.90
##  CR        115     11.47 0.454 68.6    10.56    12.38
##  FR        115     12.69 0.454 68.6    11.78    13.59
##  CR        120      8.68 0.639 77.8     7.41     9.95
##  FR        120      9.87 0.639 77.8     8.60    11.14
##  CR        150      9.02 0.639 77.8     7.74    10.29
##  FR        150      8.25 0.639 77.8     6.98     9.52
##  CR        155     12.00 0.454 68.6    11.09    12.91
##  FR        155     13.32 0.454 68.6    12.41    14.23
##  CR        180      9.40 0.639 77.8     8.13    10.67
##  FR        180      7.27 0.639 77.8     6.00     8.54
##  CR        185     12.59 0.454 68.6    11.68    13.49
##  FR        185     13.62 0.454 68.6    12.71    14.53
##  CR        210      8.85 0.639 77.8     7.58    10.12
##  FR        210      7.53 0.639 77.8     6.26     8.81
##  CR        225     12.63 0.454 68.6    11.72    13.53
##  FR        225     12.85 0.454 68.6    11.94    13.76
##  CR        260     12.41 0.454 68.6    11.51    13.32
##  FR        260     12.88 0.454 68.6    11.98    13.79
##
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
```

```
cld_average <- cld(emmeans(model_average, ~ Treatment + NrateF),adjust = "Sidak")

top_yields_average <- cld_average %>%
  group_by(Treatment) %>%
  filter(emmean == max(emmean)) %>%
  ungroup()
```

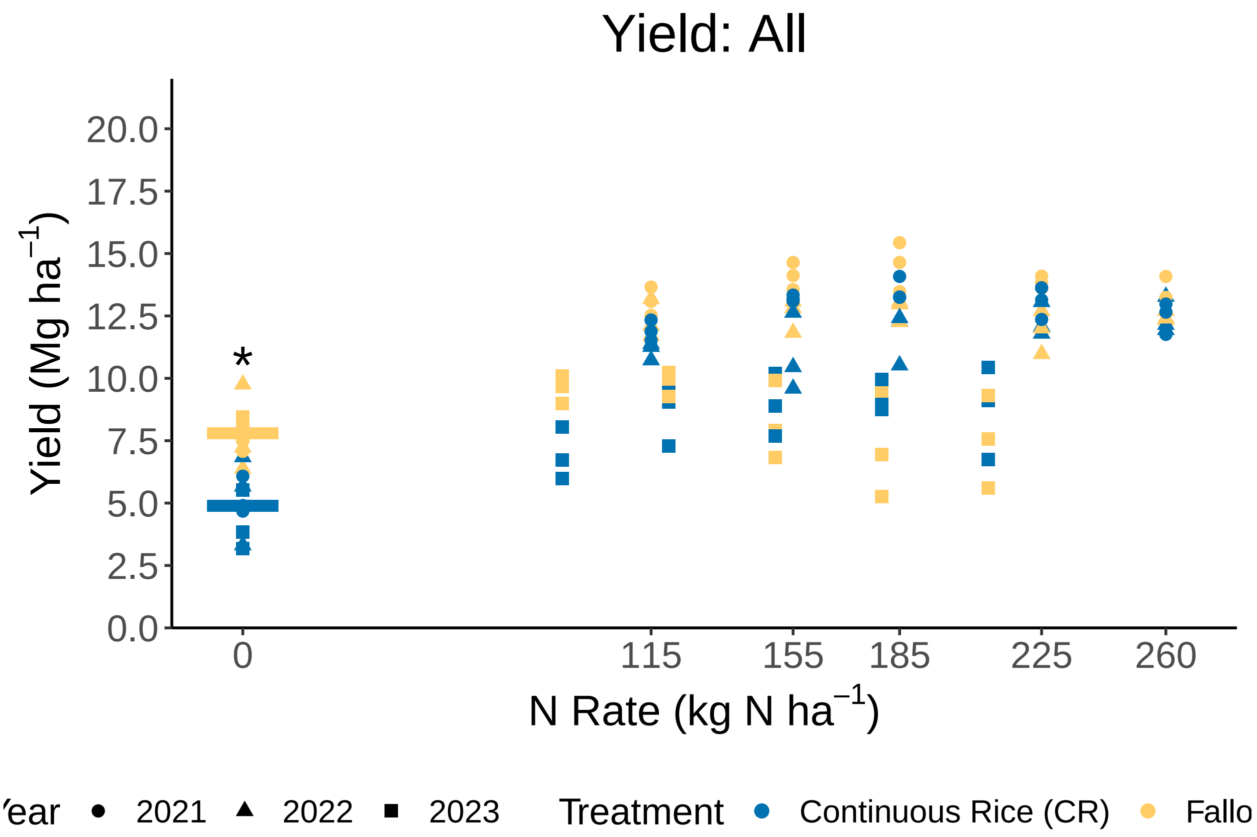
Graph_average_with_equations

```
N_response_curve_average_v1 <-
ggplot(yield_average_dataframe, aes(x=Nrate, y=Yield_Mgha, color=Treatment))+
  geom_point(data=yield_average_dataframe, size=2.5)+ #this is the mean values
  geom_point(data=yield_average, size=1, alpha=0.4, aes(shape=Year))+ #this are the raw values
  scale_color_manual(values=c("#0072B2","#FFCC66"), name = "Treatment", labels = c('Continuous Rice (CR
  scale_x_continuous(name=expression("N Rate (kg N ha"^{-1}*")"), limits = c(-5, 290), breaks = c(0, 115
  scale_y_continuous(name= expression("Yield (Mg ha"^{-1}*")"), limits = c(0, 20), breaks = seq(0, 20,
  #geom_errorbar(data=yield_average_dataframe, aes(ymin=Yield_Mgha-Yield_Mgha_se, ymax=Yield_Mgha+Yield_
  theme_classic()+
  theme(axis.text = element_text(size = 10), axis.title = element_text(size=10))+
  geom_smooth(data = yield_average, method = "lm", formula = y ~ poly(x, 2), se = FALSE)+
  #geom_vline(xintercept = c(0, 115, 155, 185, 225, 260), linetype = "twodash", color = "black") +
  theme(legend.text = element_text(size = 10),legend.title = element_text(size = 14))+
  stat_regline_equation(data=yield_average,
                      aes(x=Nrate, y=Yield_Mgha, color=Treatment, group = Treatment,
                          label = paste(..rr.label..)),
                      formula = y ~ poly(x, 2, raw = TRUE),
                      show.legend = FALSE, label.x = 0, label.y = c(16.5, 19))+
   stat_regline_equation(data=yield_average,
                      aes(x=Nrate, y=Yield_Mgha, color=Treatment, group = Treatment,
                          label = paste(..eq.label..)),
                      formula = y ~ poly(x, 2, raw = TRUE),
                      show.legend = FALSE, label.x = 0, label.y = c(17.5, 20))+

  theme(plot.title = element_text(hjust = 0.5, size = 15))+
  ggtitle(expression("average"))+
  annotate(
  "text",
  x = c(0),
  y = yield_average_dataframe %>%
        filter(Treatment == "FR", Nrate == 0) %>%
        mutate(Yield_Mgha_plus_higher = Yield_Mgha + 1) %>%
        pull(Yield_Mgha_plus_higher),
  label = "*",
  size = 7,
  vjust = 0
  )+
  geom_vline(
    aes(xintercept = optimal_results %>% filter(Treatment == "CR") %>% filter(Year == "average") %>% pul
    linetype = "twodash", color = "#0072B2", size = 1
  )+
  geom_vline(
    aes(xintercept = optimal_results %>% filter(Treatment == "FR") %>% filter(Year == "average") %>% pul
    linetype = "twodash", color = "#FFCC66", size = 1
  )+
    geom_curve(x = top_yields_average %>%
                 filter(Treatment == "FR") %>%
                 mutate(NrateF = as.numeric(paste(NrateF))) %>%
                 pull(NrateF),
                 y = top_yields_average %>%
                 filter(Treatment == "FR") %>%
                 pull(emmean)+0.2,
               xend = top_yields_average %>%
                 filter(Treatment == "CR") %>%
                 mutate(NrateF = as.numeric(paste(NrateF))) %>%
                 pull(NrateF),
               yend = top_yields_average %>%
                 filter(Treatment == "CR") %>%
                 pull(emmean)+0.2,
               color = 1, size=1,
               curvature = -0.2,
               linetype = "twodash")+
  annotate(
  "text",
  x =   (top_yields_average %>%
                 filter(Treatment == "FR") %>%
                 mutate(NrateF = as.numeric(paste(NrateF))) %>%
                 pull(NrateF)+
       top_yields_average %>%
                 filter(Treatment == "CR") %>%
                 mutate(NrateF = as.numeric(paste(NrateF))) %>%
                 pull(NrateF))/2,
  y = mean(top_yields_average %>%
                 filter(Treatment == "FR") %>%
                 pull(emmean),
           top_yields_average %>%
                 filter(Treatment == "CR") %>%
                 pull(emmean)),
  label = "ns",
  size = 5,
  vjust = -0.9,
  hjust = 0.6)


N_response_curve_average_v1
```



Graph_average

```
N_response_curve_average <-
ggplot(yield_average, aes(x=Nrate, y=Yield_Mgha, color=Treatment, shape=Year))+
  geom_point(data=yield_average, size=2)+ #this is the mean values+
    geom_segment(x = -10,
            y = yield_average_dataframe %>%
                 filter(Nrate==0)  %>%
                 filter(Treatment == "FR") %>%
                 pull(Yield_Mgha),
            xend = 10,
            yend = yield_average_dataframe %>%
                 filter(Nrate==0)  %>%
                 filter(Treatment == "FR") %>%
                 pull(Yield_Mgha),
               color = "#FFCC66", size=2)+
  geom_segment(x = -10,
            y = yield_average_dataframe %>%
                 filter(Nrate==0)  %>%
                 filter(Treatment == "CR") %>%
                 pull(Yield_Mgha),
            xend = 10,
            yend = yield_average_dataframe %>%
                 filter(Nrate==0)  %>%
                 filter(Treatment == "CR") %>%
                 pull(Yield_Mgha),
               color = "#0072B2", size=2)+
  #geom_point(data=yield_average, size=1, alpha=0.4)+ #this are the raw values
  scale_color_manual(values=c("#0072B2","#FFCC66"), name = "Treatment", labels = c('Continuous Rice (CR
 scale_x_continuous(name=expression("N Rate (kg N ha"^{-1}*")"), limits = c(-20, 280), breaks = c(0, 115
  scale_y_continuous(name= expression("Yield (Mg ha"^{-1}*")"), limits = c(0, 22), breaks = seq(0, 22,
  theme_classic()+
  #geom_smooth(data = yield_average, aes(group = Treatment), method = "lm", formula = y ~ poly(x, 2), s
  #geom_vline(xintercept = c(0, 115, 155, 185, 225, 260), linetype = "twodash", color = "black") +
  #stat_regline_equation(data=yield_average,
   #                   aes(x=Nrate, y=Yield_Mgha, color=Treatment, group = Treatment,
    #                      label = paste(..rr.label..)),
     #                formula = y ~ poly(x, 2, raw = TRUE),
      #               show.legend = FALSE, label.x = 0, label.y = c(16.5, 19))+
   #stat_regline_equation(data=yield_average,
    #                   aes(x=Nrate, y=Yield_Mgha, color=Treatment, group = Treatment,
     #                      label = paste(..eq.label..)),
      #               formula = y ~ poly(x, 2, raw = TRUE),
       #              show.legend = FALSE, label.x = 0, label.y = c(17.5, 20))+
  theme(axis.text = element_text(size = 14), axis.title = element_text(size=16))+
  theme(legend.text = element_text(size = 12),legend.title = element_text(size = 14))+
  theme(plot.title = element_text(hjust = 0.5, size = 20, face = "bold"))+
  ggtitle(expression("Yield: All"))+
  annotate(
  "text",
  x = c(0),
  y = yield_average_dataframe %>%
        filter(Treatment == "FR", Nrate == 0) %>%
        mutate(Yield_Mgha_plus_higher = Yield_Mgha + 2) %>%
        pull(Yield_Mgha_plus_higher),
  label = "*",
  size = 7,
  vjust = 0
  )+
  theme(legend.position = "bottom")



N_response_curve_average
```



Combine all plots

```
Yields <- ggarrange(N_response_curve_2021,
                    N_response_curve_2022,
                    N_response_curve_2023,
                    #N_response_curve_average,
                               nrow = 1,
                               ncol = 3,
                               common.legend = TRUE,
                               #legend.grob = get_legend(N_response_curve_average),
                               legend= "bottom")
```

```
## Warning in geom_segment(aes(x = optimal_results %>% filter(Treatment == : All aesthetics have length
## i Please consider using ‘annotate()‘ or provide this layer with data containing
##   a single row.

## Warning in geom_segment(aes(x = optimal_results %>% filter(Treatment == : All aesthetics have length
## i Please consider using ‘annotate()‘ or provide this layer with data containing
##   a single row.

## Warning in geom_segment(aes(y = optimal_results %>% filter(Treatment == : All aesthetics have length
## i Please consider using ‘annotate()‘ or provide this layer with data containing
##   a single row.

## Warning in geom_segment(aes(y = optimal_results %>% filter(Treatment == : All aesthetics have length
## i Please consider using ‘annotate()‘ or provide this layer with data containing
##   a single row.

## Warning in geom_segment(aes(x = optimal_results %>% filter(Treatment == : All aesthetics have length
## i Please consider using ‘annotate()‘ or provide this layer with data containing
##   a single row.

## Warning in geom_segment(aes(x = optimal_results %>% filter(Treatment == : All aesthetics have length
## i Please consider using ‘annotate()‘ or provide this layer with data containing
##   a single row.

## Warning in geom_segment(aes(y = optimal_results %>% filter(Treatment == : All aesthetics have length
## i Please consider using ‘annotate()‘ or provide this layer with data containing
##   a single row.

## Warning in geom_segment(aes(y = optimal_results %>% filter(Treatment == : All aesthetics have length
## i Please consider using ‘annotate()‘ or provide this layer with data containing
##   a single row.

## Warning in geom_segment(aes(x = optimal_results %>% filter(Treatment == : All aesthetics have length
## i Please consider using ‘annotate()‘ or provide this layer with data containing
##   a single row.

## Warning in geom_segment(aes(x = optimal_results %>% filter(Treatment == : All aesthetics have length
## i Please consider using ‘annotate()‘ or provide this layer with data containing
##   a single row.

## Warning in geom_segment(aes(y = optimal_results %>% filter(Treatment == : All aesthetics have length
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```
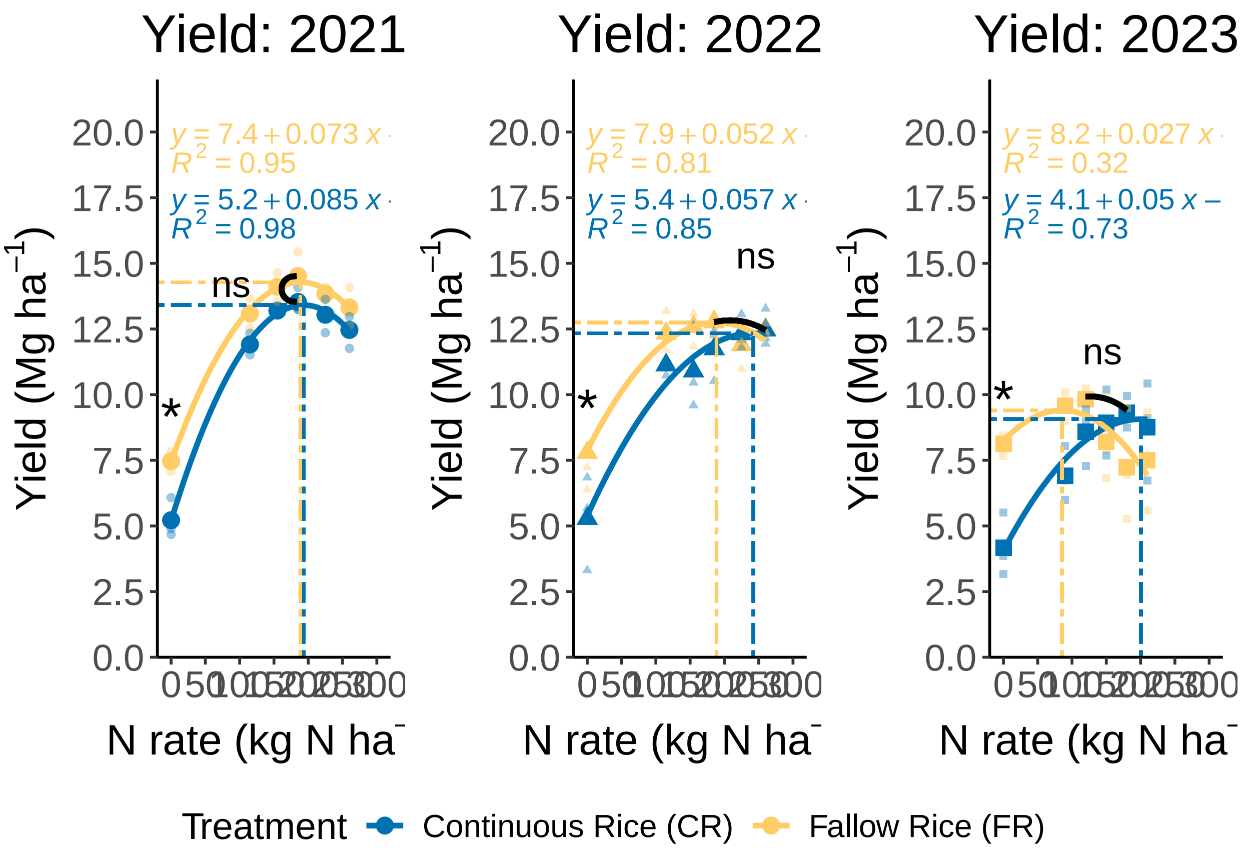

```
Yields
```



```r
ggsave(filename = "Yields_no_avg.jpg",  # Include the file extension here
       plot = Yields,              # Specify the plot
       path = "C:/Users/zhang/Documents/GitHub/FallowRice_ContinuousRice_AgronomicPerformance/Figures",
       dpi = 400,
       height = 20, width = 50, units = "cm")

ggsave(filename = "2022_NResponse.jpg",  # Include the file extension here
       plot = N_response_curve_2022,              # Specify the plot
       path = "C:/Users/zhang/Documents/GitHub/FallowRice_ContinuousRice_AgronomicPerformance/Figures",
       dpi = 400,
       height = 15, width = 15, units = "cm")
```

```
## Warning in geom_segment(aes(x = optimal_results %>% filter(Treatment == : All aesthetics have length
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```

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```

```
## Warning in geom_segment(aes(y = optimal_results %>% filter(Treatment == : All aesthetics have length
## i Please consider using ‘annotate()‘ or provide this layer with data containing
##   a single row.
```

Combine 0N yields into 1 excel file

```
all_means <- rbind(as.data.frame(field_means_2021) %>% mutate(Year = 2021),
                   as.data.frame(field_means_2022) %>% mutate(Year = 2022),
                   as.data.frame(field_means_2023) %>% mutate(Year = 2023),
                   as.data.frame(field_means_average) %>% mutate(Year = "Avg")
                  ) %>% arrange(Year) %>% filter(NrateF == "0") %>%
  mutate(yield = round(emmean, 1))

write_xlsx(all_means, "C:/Users/zhang/Documents/GitHub/FallowRice_ContinuousRice_AgronomicPerformance/Y
```

Zero N

```
zero_N <- yield_average %>% filter(Nrate == 0)

model_zero <- lmer(Yield_Mgha ~ Treatment*Year+(1|Blk), data=zero_N)

zero_means_average = emmeans(model_zero,spec = 'Treatment', by = "Year")
zero_effects_average = contrast(zero_means_average, method = 'pairwise', adjust = "Tukey")
summary(zero_effects_average)
```

```
## Year = 2021:
##  contrast estimate    SE df t.ratio p.value
##  CR - FR     -2.25 0.976  6  -2.301  0.0610
##
## Year = 2022:
##  contrast estimate    SE df t.ratio p.value
##  CR - FR     -2.52 0.976  6  -2.577  0.0419
##
## Year = 2023:
##  contrast estimate    SE df t.ratio p.value
##  CR - FR     -3.95 0.976  6  -4.047  0.0067
##
## Degrees-of-freedom method: kenward-roger
```

Graphical abstract

```
N_response_curve_graphical_abstract <-
ggplot(yield_2022_dataframe, aes(x=Nrate, y=Yield_Mgha, color=Treatment))+
  geom_point(data=yield_2022_dataframe %>% filter(Treatment == "FR"),
             aes(x=Nrate, y=Yield_Mgha, color="FR"), size=2.5) +
  geom_point(data=yield_2022_dataframe %>% filter(Treatment == "CR"),
             aes(x=Nrate, y=Yield_Mgha, color="CR"), size=2.5) +
  #geom_point(data=yield_2022_dataframe, size=2.5, shape ="triangle")+ #this is the mean values
  #geom_point(data=yield_2022, size=1, alpha=0.4, shape ="triangle")+ #this are the raw values
  scale_color_manual(values=c("#0072B2","#FFCC66"), name = "Treatment", labels = c('Continuous Rice (CR
  scale_x_continuous(name=expression("N rate (kg N ha"^{-1}*")"), limits = c(-20, 280), breaks = seq(0,
  scale_y_continuous(name= expression("Yield (Mg ha"^{-1}*")"), limits = c(0, 22), breaks = seq(0, 22, b
  #geom_errorbar(data=yield_2022_dataframe, aes(ymin=Yield_Mgha-Yield_Mgha_se, ymax=Yield_Mgha+Yield_Mg
  theme_classic()+
  geom_smooth(data = yield_2022, method = "lm", formula = y ~ poly(x, 2), se = FALSE)+
  #geom_vline(xintercept = c(0, 115, 155, 185, 225, 260), linetype = "twodash", color = "black") +
  theme(axis.text = element_text(size = 14), axis.title = element_text(size=16))+
  theme(legend.text = element_text(size = 12),legend.title = element_text(size = 14))+
  theme(plot.title = element_text(hjust = 0.5, size = 20, face = "bold"))+
  theme(legend.position = "bottom")+
  #ggtitle(expression("Yield: 2022"))+
  annotate(
  "text",
  x = c(0),
  y = yield_2022_dataframe %>%
       filter(Treatment == "FR", Nrate == 0) %>%
        mutate(Yield_Mgha_plus_higher = Yield_Mgha + 1) %>%
        pull(Yield_Mgha_plus_higher),
  label = "*",
  size = 7,
  vjust = 0
  )+
geom_segment(
  aes(x = optimal_results %>% filter(Treatment == "CR", Year == "2022") %>% pull(Nrate_optimal),
      xend = optimal_results %>% filter(Treatment == "CR", Year == "2022") %>% pull(Nrate_optimal),
      y = 0,  # Start exactly from 0 on y-axis
      yend = optimal_results %>% filter(Treatment == "CR", Year == "2022") %>% pull(Yield_max)),
  linetype = "twodash", color = "#0072B2", size = 0.6
) +
# Vertical line for FR
geom_segment(
  aes(x = optimal_results %>% filter(Treatment == "FR", Year == "2022") %>% pull(Nrate_optimal),
      xend = optimal_results %>% filter(Treatment == "FR", Year == "2022") %>% pull(Nrate_optimal),
      y = 0,  # Start exactly from 0 on y-axis
      yend = optimal_results %>% filter(Treatment == "FR", Year == "2022") %>% pull(Yield_max)),
  linetype = "twodash", color = "#FFCC66", size = 0.6
```

```r
) +

# Horizontal line for CR
geom_segment(
  aes(y = optimal_results %>% filter(Treatment == "CR", Year == "2022") %>% pull(Yield_max),
      yend = optimal_results %>% filter(Treatment == "CR", Year == "2022") %>% pull(Yield_max),
      x = -20,  # Start exactly from 0 on x-axis
      xend = optimal_results %>% filter(Treatment == "CR", Year == "2022") %>% pull(Nrate_optimal)),
  linetype = "twodash", color = "#0072B2", size = 0.6
) +
# Horizontal line for FR
geom_segment(
  aes(y = optimal_results %>% filter(Treatment == "FR", Year == "2022") %>% pull(Yield_max),
      yend = optimal_results %>% filter(Treatment == "FR", Year == "2022") %>% pull(Yield_max),
      x = -20,  # Start exactly from 0 on x-axis
      xend = optimal_results %>% filter(Treatment == "FR", Year == "2022") %>% pull(Nrate_optimal)),
  linetype = "twodash", color = "#FFCC66", size = 0.6
)+
    geom_curve(x = top_yields_2022 %>%
                 filter(Treatment == "FR") %>%
                 mutate(NrateF = as.numeric(paste(NrateF))) %>%
                 pull(NrateF),
                 y = top_yields_2022 %>%
                 filter(Treatment == "FR") %>%
                 pull(emmean),
               xend = top_yields_2022 %>%
                 filter(Treatment == "CR") %>%
                 mutate(NrateF = as.numeric(paste(NrateF))) %>%
                 pull(NrateF),
               yend = top_yields_2022 %>%
                 filter(Treatment == "CR") %>%
                 pull(emmean),
               color = 1, size=1,
               curvature = -0.2)+
  annotate(
  "text",
  x =   (top_yields_2022 %>%
                 filter(Treatment == "FR") %>%
                 mutate(NrateF = as.numeric(paste(NrateF))) %>%
                 pull(NrateF)+
       top_yields_2022 %>%
                 filter(Treatment == "CR") %>%
                 mutate(NrateF = as.numeric(paste(NrateF))) %>%
                 pull(NrateF))/2,
  y = mean(top_yields_2022 %>%
                 filter(Treatment == "FR") %>%
                 pull(emmean),
           top_yields_2022 %>%
                 filter(Treatment == "CR") %>%
                 pull(emmean)),
  label = "ns",
  size = 5,
  vjust = -2,
  hjust = 0.1 )+
  theme(axis.text.y=element_blank(),
        axis.ticks.y=element_blank(),
        axis.text.x=element_blank(),
        axis.ticks.x=element_blank()
        )+
theme(legend.title=element_blank())


N_response_curve_graphical_abstract
```

```
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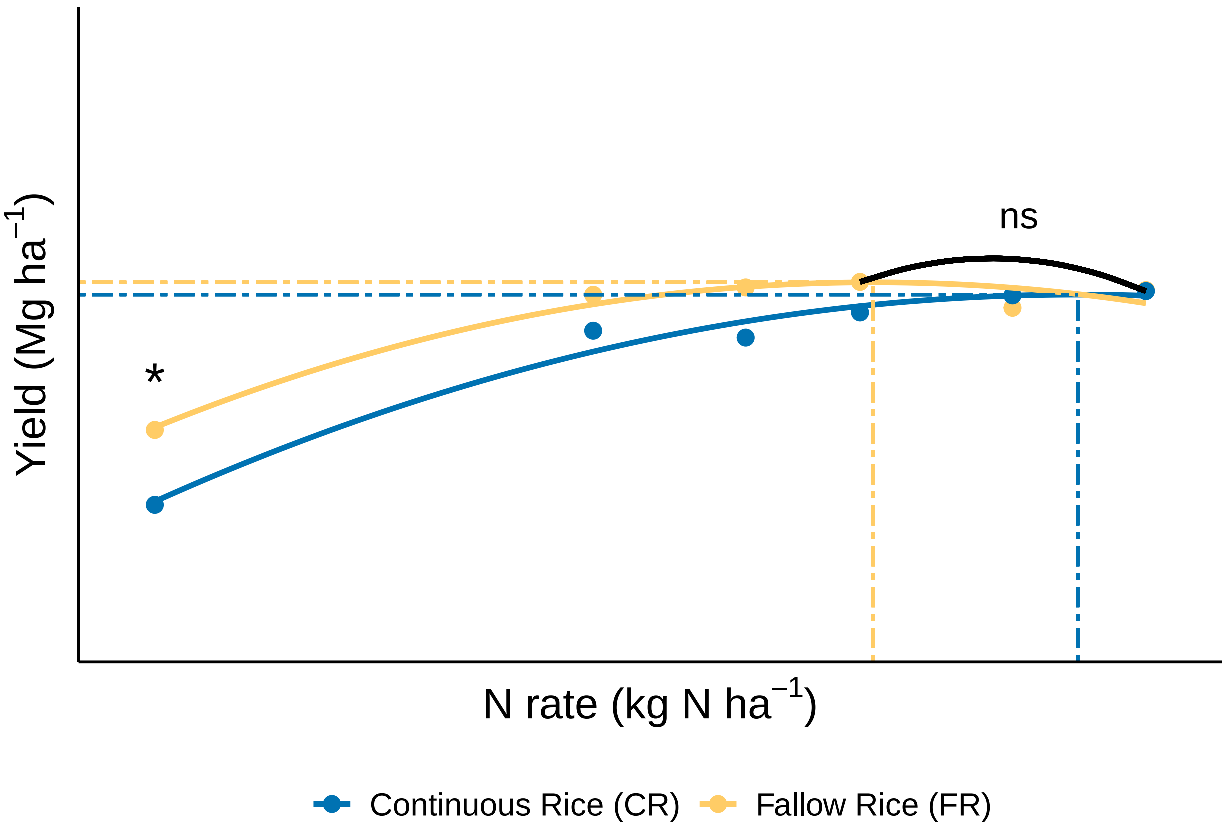
```



```
ggsave(filename = "N_response_curve_graphical_abstract.jpg",  # Include the file extension here
       plot = N_response_curve_graphical_abstract,              # Specify the plot
       path = "C:/Users/zhang/Documents/GitHub/FallowRice_ContinuousRice_AgronomicPerformance/Figures",
       dpi = 800,
       height = 10, width = 10.5, units = "cm")
```

```
## Warning in geom_segment(aes(x = optimal_results %>% filter(Treatment == : All aesthetics have length
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