Apparent Fertilizer Nitrogen Recovery Efficiency (FNRE)

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Contents

Necessary libraries

Read and check data

```
#read data
master = read_excel('C:/Users/zhang/Documents/GitHub/FallowRice_ContinuousRice_AgronomicPerformance/N u

#making sure that the master datFNREame will be correct
master <- master %>% filter(Stage=="Maturity") %>% filter(Topdress != 1)
```

Calculate FNRE for each plot

```
# Define the FNRE calculation function
calculate_FNRE <- function(data) {

  # Ensure the datFNREame is grouped by Year, Block, and Treatment
  FNRE_df <- data %>%
    group_by(Year, Blk, Treatment) %>%

    # Nest the data within each Year, Blk, Treatment group
    do({
      # Separate ON plot (reference plot with no nitrogen application)
      zero_nitrogen_plot <- .[.$Nrate_kgha == 0,]

      # Ensure there's a ON plot to reference
      if (nrow(zero_nitrogen_plot) == 0) {
        stop("No ON plot found in one of the groups!")
      }

      # Calculate FNRE for the rest of the plots in the group
      mutate(., FNRE = (N_total_kgha - zero_nitrogen_plot$N_total_kgha) / Nrate_kgha)
    })

  # Ungroup to return a regular datFNREame
  FNRE_df <- FNRE_df %>%
    ungroup()

  return(FNRE_df)
}


master_with_FNRE <- calculate_FNRE(master) %>%
  mutate(FNRE = FNRE*100) %>%
  filter(Nrate_kgha !=0) %>%
  mutate(NrateF = as.factor(Nrate_kgha))

#write_xlsx(master_with_FNRE, "C:/Users/zhang/Desktop/master_with_FNRE.xlsx")
#manuallychecked and all looks correct
```

Split data by year

```
FNRE_all <- master_with_FNRE %>%
  #filter(Year != 2023) %>%
  filter(Topdress!=1) %>%
  filter(Stage=="Maturity") %>%
  mutate(Year= as.factor(Year))

FNRE_2021 <- master_with_FNRE %>%
  filter(Year == 2021) %>%
  filter(Topdress!=1) %>%
  filter(Stage=="Maturity") %>%
  mutate(Year= as.factor(Year))

FNRE_2022 <- master_with_FNRE %>%
  filter(Year == 2022) %>%
  filter(Topdress!=1) %>%
  filter(Stage=="Maturity") %>%
  mutate(Year= as.factor(Year))

FNRE_2023 <- master_with_FNRE %>%
  filter(Year == 2023) %>%
  filter(Topdress!=1) %>%
  filter(Stage=="Maturity") %>%
  mutate(Year= as.factor(Year))

table(FNRE_2021$Nrate_kgha)
```

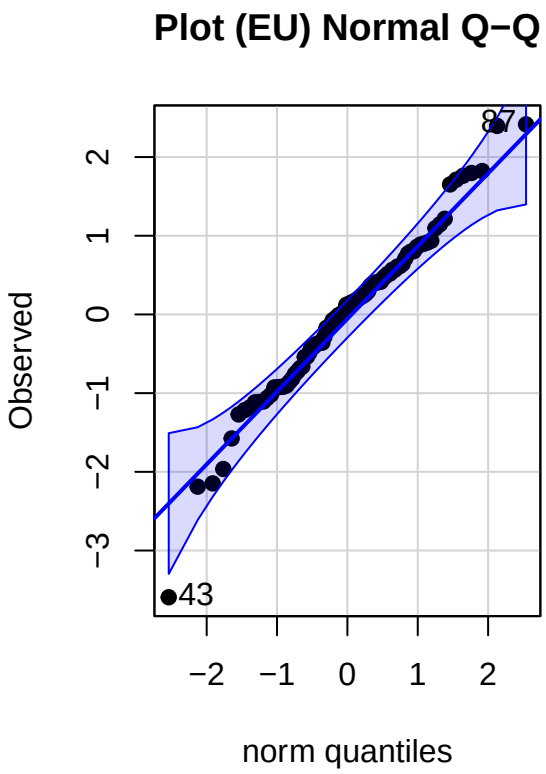
```
##
## 115 155 185 225 260
##   6   6   6   6   6
```

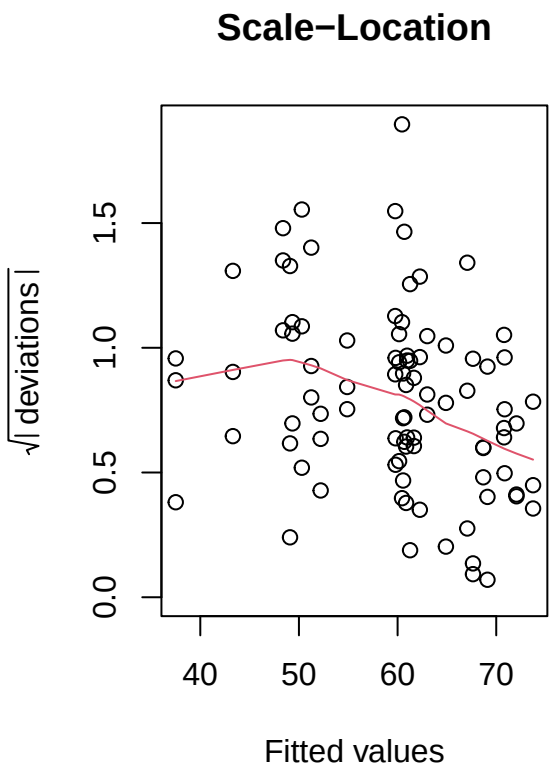
General linear model to do some exploratory analysis

Seems that there is an effect of Nrate and Year. But no treatment effects.

```
all_factors_model <- lm(FNRE ~ Nrate_kgha*Treatment*Year, data = FNRE_all)

pls205_diagnostics(all_factors_model)
```






```
anova(all_factors_model)
```

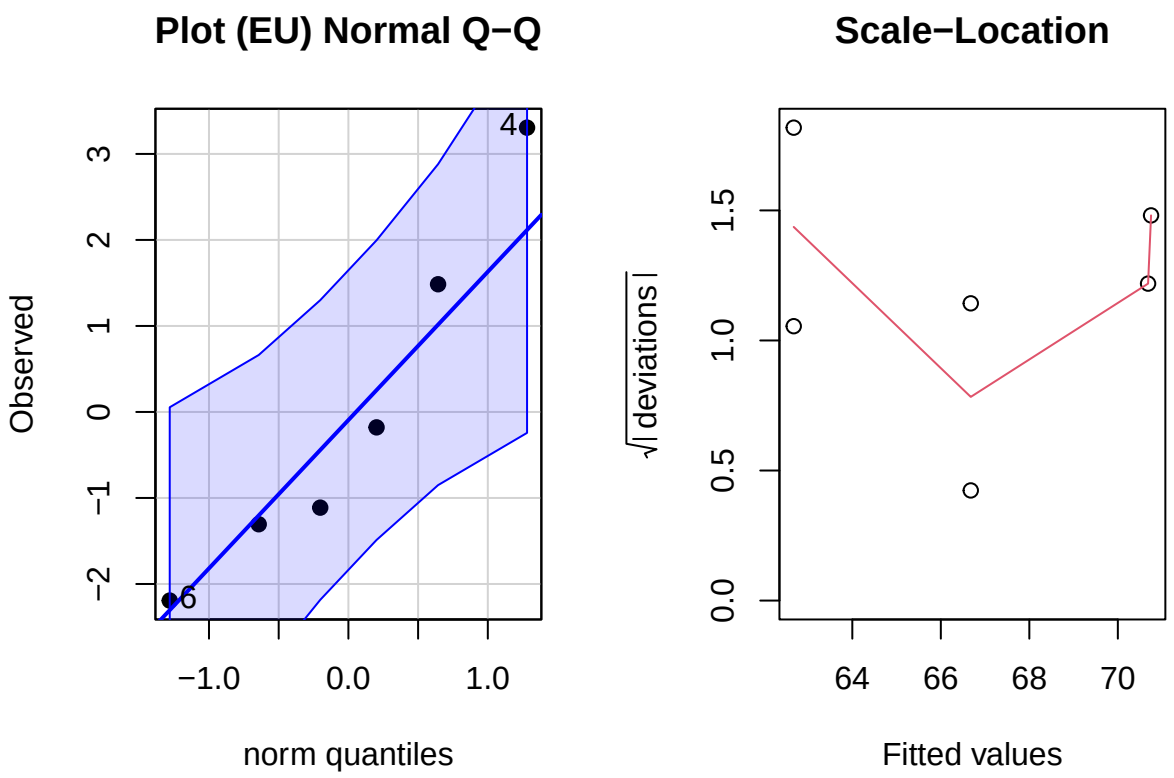
```
## Analysis of Variance Table
##
## Response: FNRE
##                            Df Sum Sq Mean Sq F value    Pr(>F)
## Nrate_kgha                  1  639.2  639.19  5.2414  0.02476 *
## Treatment                   1   23.3   23.33  0.1913  0.66302
## Year                        2 4876.7 2438.33 19.9944 9.77e-08 ***
## Nrate_kgha:Treatment        1  329.7  329.66  2.7033  0.10417
## Nrate_kgha:Year             2  528.1  264.04  2.1652  0.12158
## Treatment:Year              2   41.7   20.84  0.1709  0.84325
## Nrate_kgha:Treatment:Year   2  424.3  212.17  1.7398  0.18230
## Residuals                  78 9512.2  121.95
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

2021 (Table 2)

Statistical tests

```
model_2021 <- lmer(FNRE ~ NrateF*Treatment+(1|Blk:Treatment)+(1|Blk), data=FNRE_2021)

pls205_diagnostics(model_2021, EU="Blk:Treatment")
```




```
anova(model_2021)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##                   Sum Sq Mean Sq NumDF DenDF F value  Pr(>F)
## NrateF           266.482  66.620     4    16  2.4443 0.08889 .
## Treatment         33.214  33.214     1     2  1.2186 0.38468
## NrateF:Treatment  72.494  18.123     4    16  0.6649 0.62545
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
means_2021 = emmeans(model_2021,spec = 'Treatment',by = 'NrateF')
effects_2021 = contrast(means_2021, method = 'pairwise', adjust = "Tukey")

summary(effects_2021)
```

```
## NrateF = 115:
##  contrast estimate   SE   df t.ratio p.value
##  CR - FR     6.339 5.12 8.47   1.239  0.2485
##
```

```
## NrateF = 155:
##  contrast estimate   SE   df t.ratio p.value
##  CR - FR     2.206 5.12 8.47   0.431  0.6770
##
## NrateF = 185:
##  contrast estimate   SE   df t.ratio p.value
##  CR - FR    -0.795 5.12 8.47  -0.155  0.8801
##
## NrateF = 225:
##  contrast estimate   SE   df t.ratio p.value
##  CR - FR     3.067 5.12 8.47   0.600  0.5645
##
## NrateF = 260:
##  contrast estimate   SE   df t.ratio p.value
##  CR - FR     8.007 5.12 8.47   1.565  0.1541
##
## Degrees-of-freedom method: kenward-roger
```

```
cld(means_2021)
```

```
## NrateF = 115:
##  Treatment emmean   SE   df lower.CL upper.CL .group
##  FR          70.5 4.44 7.33     60.1     80.9  1
##  CR          76.8 4.44 7.33     66.4     87.2  1
##
## NrateF = 155:
##  Treatment emmean   SE   df lower.CL upper.CL .group
##  FR          67.0 4.44 7.33     56.6     77.4  1
##  CR          69.2 4.44 7.33     58.8     79.6  1
##
## NrateF = 185:
##  Treatment emmean   SE   df lower.CL upper.CL .group
##  CR          70.0 4.44 7.33     59.5     80.4  1
##  FR          70.8 4.44 7.33     60.3     81.2  1
##
## NrateF = 225:
##  Treatment emmean   SE   df lower.CL upper.CL .group
##  FR          63.6 4.44 7.33     53.2     74.0  1
##  CR          66.7 4.44 7.33     56.3     77.1  1
##
## NrateF = 260:
##  Treatment emmean   SE   df lower.CL upper.CL .group
##  FR          62.7 4.44 7.33     52.3     73.1  1
##  CR          70.7 4.44 7.33     60.3     81.1  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        115      76.8 4.44 7.33     66.4     87.2
##  FR        115      70.5 4.44 7.33     60.1     80.9
##  CR        155      69.2 4.44 7.33     58.8     79.6
##  FR        155      67.0 4.44 7.33     56.6     77.4
##  CR        185      70.0 4.44 7.33     59.5     80.4
##  FR        185      70.8 4.44 7.33     60.3     81.2
##  CR        225      66.7 4.44 7.33     56.3     77.1
##  FR        225      63.6 4.44 7.33     53.2     74.0
##  CR        260      70.7 4.44 7.33     60.3     81.1
##  FR        260      62.7 4.44 7.33     52.3     73.1
##
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
```

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

```
##  Treatment NrateF emmean   SE   df lower.CL upper.CL .group
##  FR        260      62.7 4.44 7.33     45.2     80.2  1
##  FR        225      63.6 4.44 7.33     46.1     81.1  1
##  CR        225      66.7 4.44 7.33     49.2     84.2  1
##  FR        155      67.0 4.44 7.33     49.5     84.5  1
##  CR        155      69.2 4.44 7.33     51.7     86.7  1
##  CR        185      70.0 4.44 7.33     52.5     87.5  1
##  FR        115      70.5 4.44 7.33     53.0     88.0  1
##  CR        260      70.7 4.44 7.33     53.2     88.2  1
##  FR        185      70.8 4.44 7.33     53.3     88.2  1
##  CR        115      76.8 4.44 7.33     59.3     94.3  1
##
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
## Conf-level adjustment: sidak method for 10 estimates
## P value adjustment: sidak method for 45 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.
```

```
cld_2021 <- cld(emmeans(model_2021, ~ Treatment + NrateF),adjust = "Sidak") %>% mutate(Nrate_kgha = as.n
```

2021 graph

Graphing dataframe

```
graphing_2021 <- FNRE_2021 %>%
    group_by(Treatment, Nrate_kgha) %>%
   mutate(FNRE_se = sd(FNRE)/sqrt(3)) %>%
  summarise(FNRE = mean(FNRE),
```

```
            FNRE_se = mean(FNRE_se)) %>%
  left_join(cld_2021 %>% select(Treatment, Nrate_kgha, group), by = c("Treatment", "Nrate_kgha"))
```

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

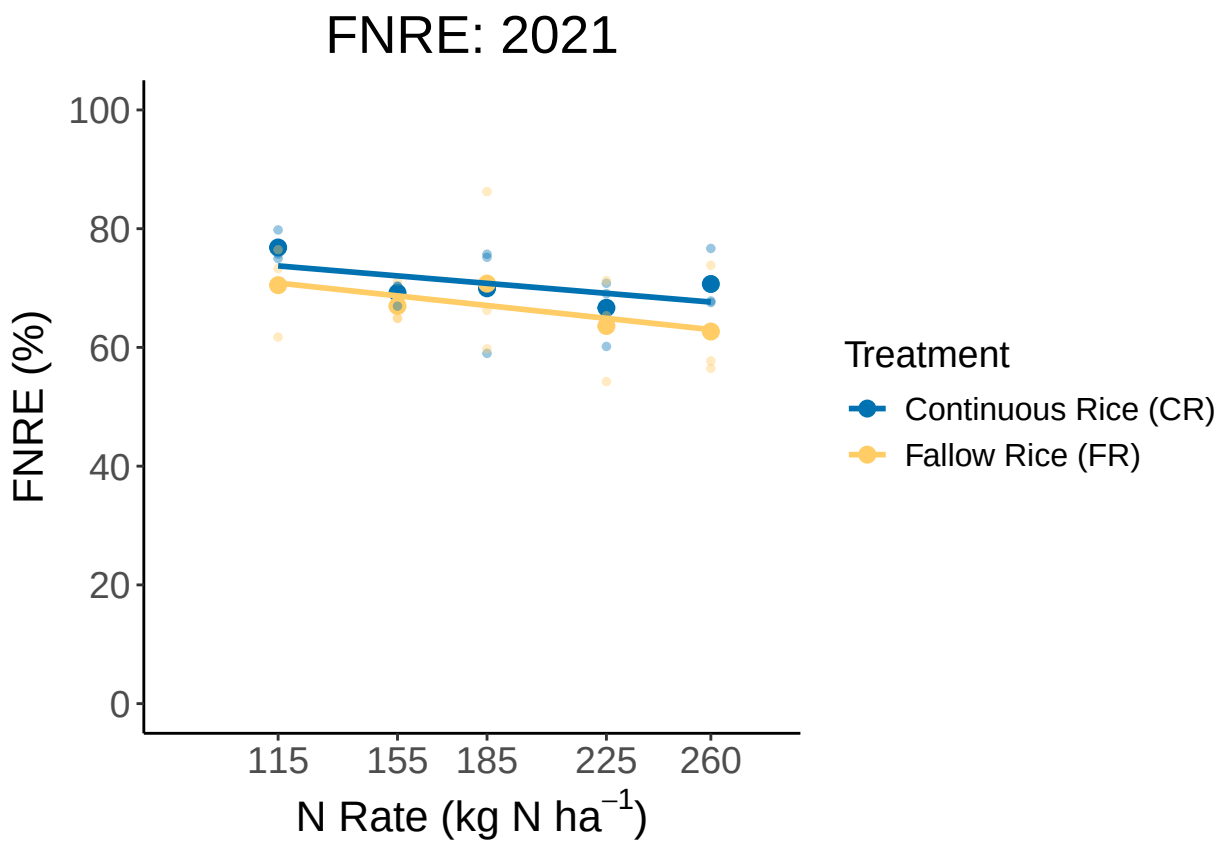
ggplot_2021

```
FNRE_2021_graph <-
ggplot(graphing_2021, aes(x=Nrate_kgha, y=FNRE, color=Treatment))+
  geom_point(data=graphing_2021, size=2.5)+ #this is the mean values
  geom_point(data=FNRE_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(80, 280), breaks = c(115,
  scale_y_continuous(name= expression("FNRE (%)"), limits = c(0, 100), breaks = seq(0, 100, by = 20))+
  theme_classic()+
  geom_smooth(data = FNRE_2021, method = "lm", se = FALSE)+

  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("FNRE: 2021"))

FNRE_2021_graph
```

```
## `geom_smooth()` using formula = 'y ~ x'
```



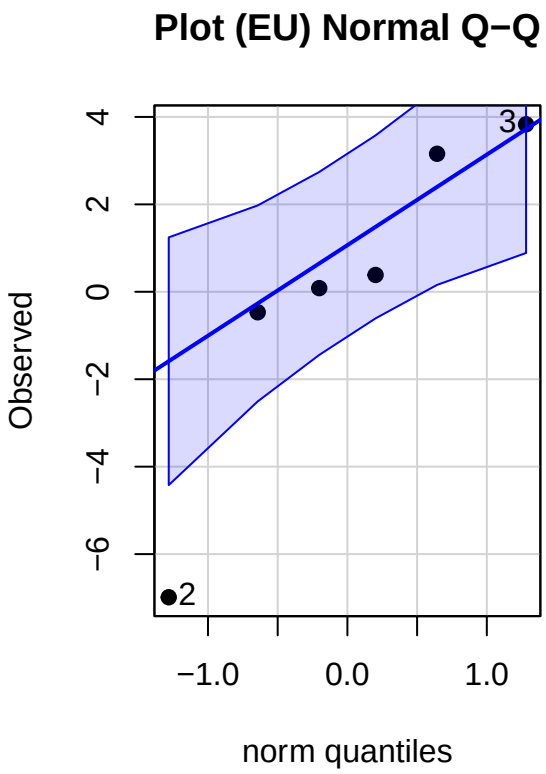
2022 (Table 2)

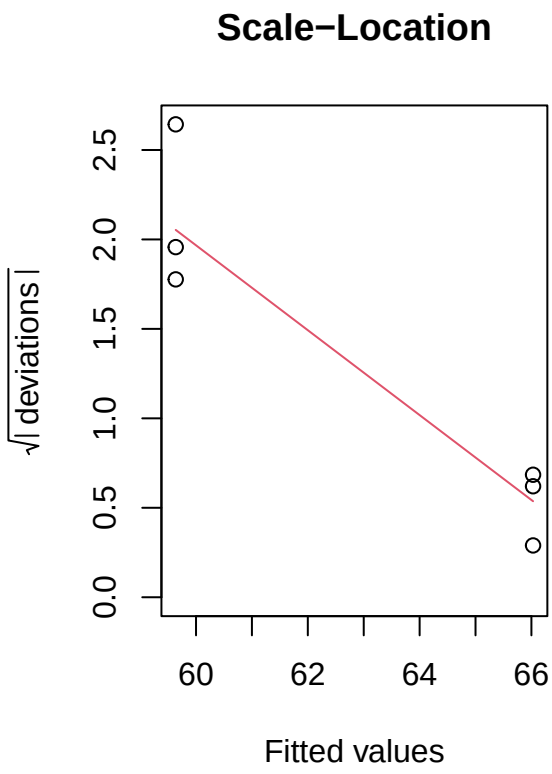
Statistical tests

```
model_2022 <- lmer(FNRE ~ NrateF*Treatment+(1|Blk:Treatment)+(1|Blk), data=FNRE_2022)
```

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

```
pls205_diagnostics(model_2022, EU="Blk:Treatment")
```






```
anova(model_2022)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##                    Sum Sq Mean Sq NumDF DenDF F value Pr(>F)
## NrateF            159.829  39.957     4    16  0.3540 0.8375
## Treatment           0.503   0.503     1     4  0.0045 0.9500
## NrateF:Treatment 314.409  78.602     4    16  0.6963 0.6055
```

```
means_2022 = emmeans(model_2022,spec = 'Treatment',by = 'NrateF')
effects_2022 = contrast(means_2022, method = 'pairwise', adjust = "Tukey")

summary(effects_2022)
```

```
## NrateF = 115:
##  contrast estimate   SE   df t.ratio p.value
##  CR - FR      7.16 10.7 7.79   0.671  0.5216
##
## NrateF = 155:
##  contrast estimate   SE   df t.ratio p.value
##  CR - FR     -7.43 10.7 7.79  -0.697  0.5062
##
## NrateF = 185:
##  contrast estimate   SE   df t.ratio p.value
##  CR - FR     -6.39 10.7 7.79  -0.599  0.5660
##
```

```
## NrateF = 225:
##  contrast estimate   SE   df t.ratio p.value
##  CR - FR      1.24 10.7 7.79   0.116  0.9105
##
## NrateF = 260:
##  contrast estimate   SE   df t.ratio p.value
##  CR - FR      7.87 10.7 7.79   0.738  0.4821
##
## Degrees-of-freedom method: kenward-roger
```

```
cld(means_2022)
```

```
## NrateF = 115:
##  Treatment emmean   SE   df lower.CL upper.CL .group
##  FR          58.9 7.54 13.7     42.7     75.1  1
##  CR          66.1 7.54 13.7     49.9     82.3  1
##
## NrateF = 155:
##  Treatment emmean   SE   df lower.CL upper.CL .group
##  CR          52.7 7.54 13.7     36.5     68.9  1
##  FR          60.1 7.54 13.7     43.9     76.3  1
##
## NrateF = 185:
##  Treatment emmean   SE   df lower.CL upper.CL .group
##  CR          59.6 7.54 13.7     43.4     75.8  1
##  FR          66.0 7.54 13.7     49.8     82.2  1
##
## NrateF = 225:
##  Treatment emmean   SE   df lower.CL upper.CL .group
##  FR          60.4 7.54 13.7     44.2     76.6  1
##  CR          61.6 7.54 13.7     45.4     77.8  1
##
## NrateF = 260:
##  Treatment emmean   SE   df lower.CL upper.CL .group
##  FR          57.2 7.54 13.7     41.0     73.4  1
##  CR          65.0 7.54 13.7     48.8     81.3  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        115      66.1 7.54 13.7     49.9     82.3
##  FR        115      58.9 7.54 13.7     42.7     75.1
##  CR        155      52.7 7.54 13.7     36.5     68.9
##  FR        155      60.1 7.54 13.7     43.9     76.3
##  CR        185      59.6 7.54 13.7     43.4     75.8
##  FR        185      66.0 7.54 13.7     49.8     82.2
```

```
##  CR        225      61.6 7.54 13.7     45.4     77.8
##  FR        225      60.4 7.54 13.7     44.2     76.6
##  CR        260      65.0 7.54 13.7     48.8     81.3
##  FR        260      57.2 7.54 13.7     41.0     73.4
##
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
```

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

```
##  Treatment NrateF emmean   SE   df lower.CL upper.CL .group
##  CR        155      52.7 7.54 13.7     27.6     77.8  1
##  FR        260      57.2 7.54 13.7     32.1     82.3  1
##  FR        115      58.9 7.54 13.7     33.8     84.0  1
##  CR        185      59.6 7.54 13.7     34.5     84.7  1
##  FR        155      60.1 7.54 13.7     35.0     85.2  1
##  FR        225      60.4 7.54 13.7     35.3     85.5  1
##  CR        225      61.6 7.54 13.7     36.6     86.7  1
##  CR        260      65.0 7.54 13.7     40.0     90.1  1
##  FR        185      66.0 7.54 13.7     40.9     91.1  1
##  CR        115      66.1 7.54 13.7     41.0     91.2  1
##
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
## Conf-level adjustment: sidak method for 10 estimates
## P value adjustment: sidak method for 45 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.
```

```
cld_2022 <- cld(emmeans(model_2022, ~ Treatment + NrateF),adjust = "Sidak") %>% mutate(Nrate_kgha = as.n
```

2022 graph

Graphing dataframe

```
graphing_2022 <- FNRE_2022 %>%
    group_by(Treatment, Nrate_kgha) %>%
   mutate(FNRE_se = sd(FNRE)/sqrt(3)) %>%
  summarise(FNRE = mean(FNRE),
            FNRE_se = mean(FNRE_se)) %>%
  left_join(cld_2022 %>% select(Treatment, Nrate_kgha, group), by = c("Treatment", "Nrate_kgha"))
```

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

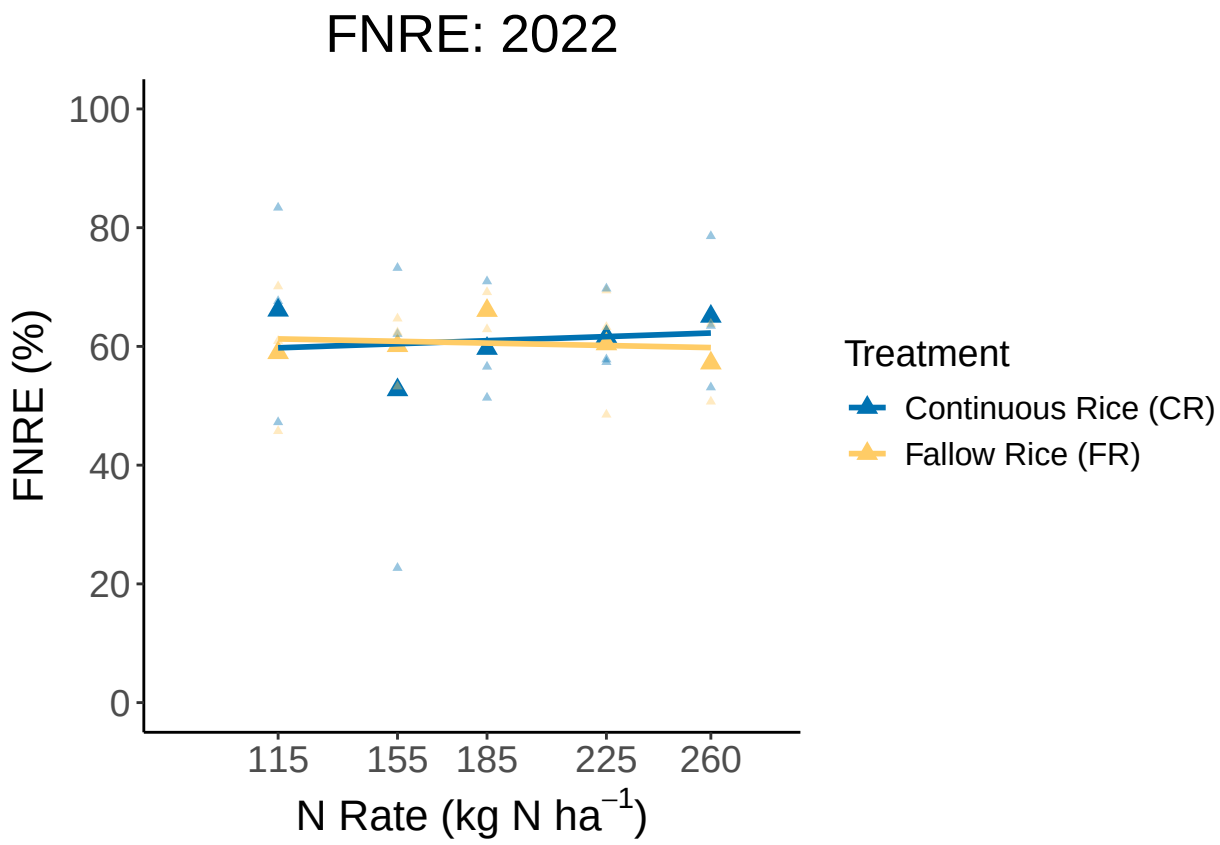
ggplot_2022

```
FNRE_2022_graph <-
ggplot(graphing_2022, aes(x=Nrate_kgha, y=FNRE, color=Treatment))+
  geom_point(data=graphing_2022, size=2.5,shape ="triangle")+ #this is the mean values
  geom_point(data=FNRE_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(80, 280), breaks = c(115,
  scale_y_continuous(name= expression("FNRE (%)"), limits = c(0, 100), breaks = seq(0, 100, by = 20))+
  theme_classic()+
  geom_smooth(data = FNRE_2022, method = "lm", se = FALSE)+

  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("FNRE: 2022"))

FNRE_2022_graph
```

```
## `geom_smooth()` using formula = 'y ~ x'
```



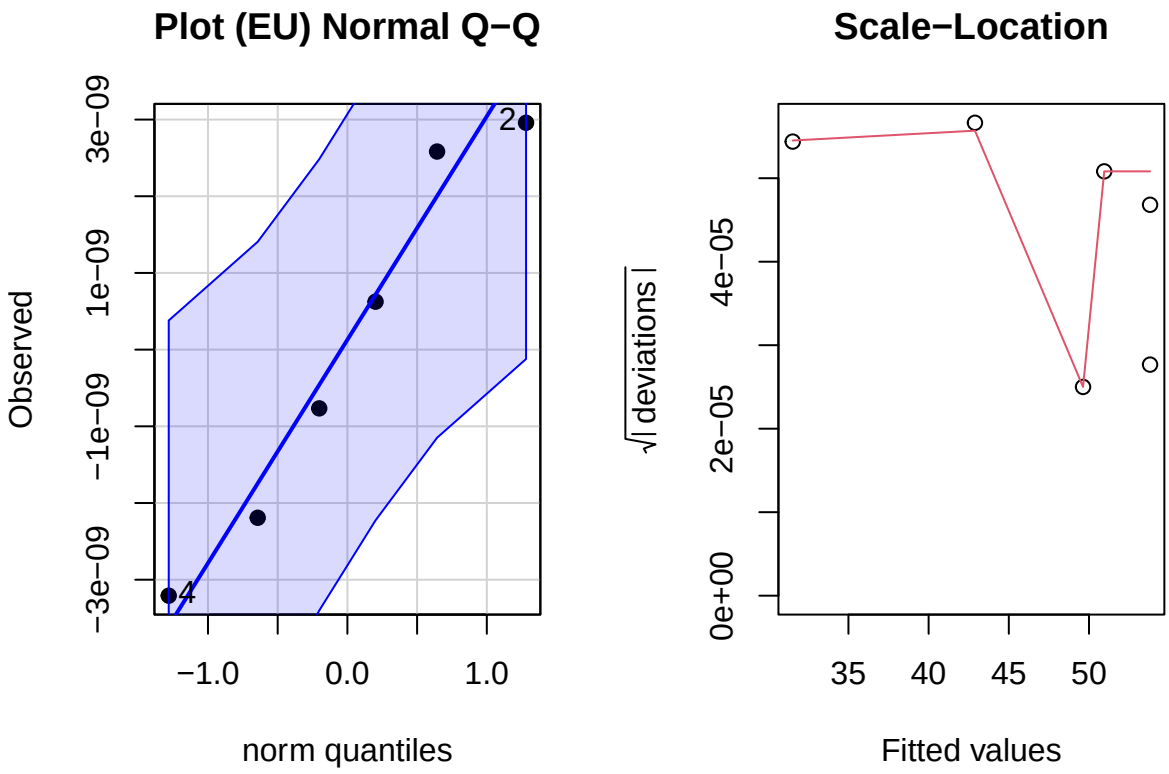
2023 (Table 2)

Statistical tests

```
model_2023 <- lmer(FNRE ~ NrateF*Treatment+(1|Blk:Treatment)+(1|Blk), data=FNRE_2023)
```

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

```
pls205_diagnostics(model_2023, EU="Blk:Treatment")
```




```
anova(model_2023)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##                  Sum Sq Mean Sq NumDF DenDF F value Pr(>F)
## NrateF           619.21 154.803     4    20  0.8204 0.5273
## Treatment         10.77  10.767     1    20  0.0571 0.8136
## NrateF:Treatment 941.83 235.458     4    20  1.2479 0.3229
```

```
means_2023 = emmeans(model_2023,spec = 'Treatment',by = 'NrateF')
effects_2023 = contrast(means_2023, method = 'pairwise', adjust = "Tukey")

summary(effects_2023)
```

```
## NrateF = 90:
##  contrast estimate   SE   df t.ratio p.value
##  CR - FR    -20.83 11.2 16.7  -1.857  0.0811
##
## NrateF = 120:
##  contrast estimate   SE   df t.ratio p.value
##  CR - FR     -1.74 11.2 16.7  -0.155  0.8784
##
## NrateF = 150:
##  contrast estimate   SE   df t.ratio p.value
##  CR - FR     -1.84 11.2 16.7  -0.164  0.8716
##
## NrateF = 180:
##  contrast estimate   SE   df t.ratio p.value
##  CR - FR     12.76 11.2 16.7   1.138  0.2712
##
## NrateF = 210:
##  contrast estimate   SE   df t.ratio p.value
##  CR - FR      5.65 11.2 16.7   0.504  0.6208
##
## Degrees-of-freedom method: kenward-roger
```

```
cld(means_2023)
```

```
## NrateF = 90:
##  Treatment emmean   SE df lower.CL upper.CL .group
##  CR          31.5 7.93 20     15.0     48.1  1
##  FR          52.4 7.93 20     35.8     68.9  1
##
## NrateF = 120:
##  Treatment emmean   SE df lower.CL upper.CL .group
##  CR          47.9 7.93 20     31.3     64.4  1
##  FR          49.6 7.93 20     33.1     66.2  1
##
## NrateF = 150:
##  Treatment emmean   SE df lower.CL upper.CL .group
##  CR          53.8 7.93 20     37.3     70.4  1
##  FR          55.6 7.93 20     39.1     72.2  1
##
## NrateF = 180:
##  Treatment emmean   SE df lower.CL upper.CL .group
##  FR          42.9 7.93 20     26.3     59.4  1
##  CR          55.7 7.93 20     39.1     72.2  1
##
## NrateF = 210:
##  Treatment emmean   SE df lower.CL upper.CL .group
##  FR          51.0 7.93 20     34.4     67.5  1
##  CR          56.6 7.93 20     40.1     73.1  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_2023, ~ Treatment + NrateF)
```

```
##  Treatment NrateF emmean   SE df lower.CL upper.CL
##  CR        90       31.5 7.93 20     15.0     48.1
##  FR        90       52.4 7.93 20     35.8     68.9
##  CR        120      47.9 7.93 20     31.3     64.4
##  FR        120      49.6 7.93 20     33.1     66.2
##  CR        150      53.8 7.93 20     37.3     70.4
##  FR        150      55.6 7.93 20     39.1     72.2
##  CR        180      55.7 7.93 20     39.1     72.2
##  FR        180      42.9 7.93 20     26.3     59.4
##  CR        210      56.6 7.93 20     40.1     73.1
##  FR        210      51.0 7.93 20     34.4     67.5
##
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
```

```
cld(emmeans(model_2023, ~ Treatment + NrateF),adjust = "Sidak")
```

```
##  Treatment NrateF emmean   SE df lower.CL upper.CL .group
##  CR        90       31.5 7.93 20      6.6     56.5  1
##  FR        180      42.9 7.93 20     18.0     67.8  1
##  CR        120      47.9 7.93 20     23.0     72.8  1
##  FR        120      49.6 7.93 20     24.7     74.6  1
##  FR        210      51.0 7.93 20     26.0     75.9  1
##  FR        90       52.4 7.93 20     27.4     77.3  1
##  CR        150      53.8 7.93 20     28.9     78.7  1
##  FR        150      55.6 7.93 20     30.7     80.6  1
##  CR        180      55.7 7.93 20     30.7     80.6  1
##  CR        210      56.6 7.93 20     31.7     81.5  1
##
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
## Conf-level adjustment: sidak method for 10 estimates
## P value adjustment: sidak method for 45 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.
```

```
cld_2023 <- cld(emmeans(model_2023, ~ Treatment + NrateF),adjust = "Sidak") %>% mutate(Nrate_kgha = as.n
```

2023 graph

Graphing dataframe

```
graphing_2023 <- FNRE_2023 %>%
    group_by(Treatment, Nrate_kgha) %>%
```

```
   mutate(FNRE_se = sd(FNRE)/sqrt(3)) %>%
  summarise(FNRE = mean(FNRE),
            FNRE_se = mean(FNRE_se)) %>%
  left_join(cld_2023 %>% select(Treatment, Nrate_kgha, group), by = c("Treatment", "Nrate_kgha"))
```

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

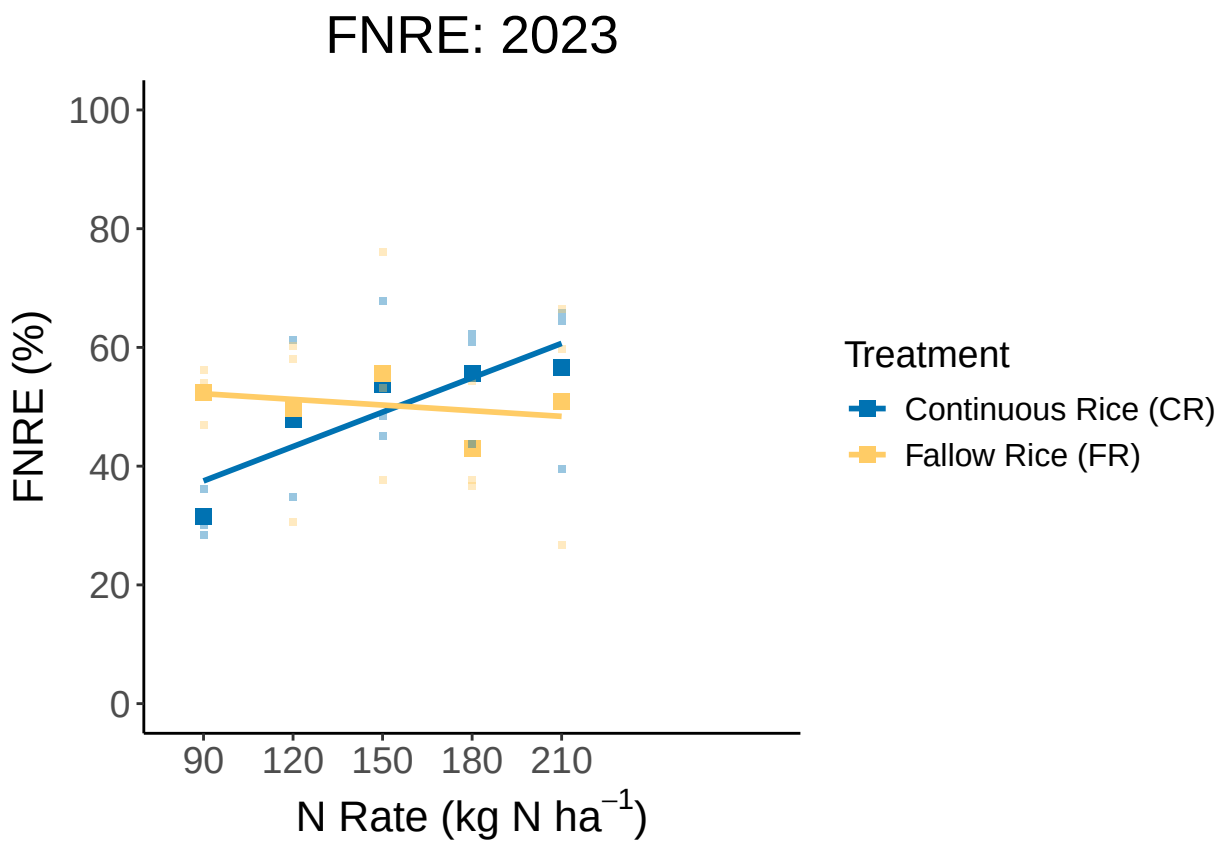
ggplot_2023

```
FNRE_2023_graph <-
ggplot(graphing_2023, aes(x=Nrate_kgha, y=FNRE, color=Treatment))+
  geom_point(data=graphing_2023, size=2.5, shape ="square")+ #this is the mean values
  geom_point(data=FNRE_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(80, 280), breaks = c(90,12
  scale_y_continuous(name= expression("FNRE (%)"), limits = c(0, 100), breaks = seq(0, 100, by = 20))+
  theme_classic()+
  geom_smooth(data = FNRE_2023, method = "lm", se = FALSE)+

  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("FNRE: 2023"))

FNRE_2023_graph
```

```
## `geom_smooth()` using formula = 'y ~ x'
```



All together

Statistical tests

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

anova(model_average)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##                   Sum Sq Mean Sq NumDF  DenDF F value  Pr(>F)
## NrateF           2115.97 235.107     9 41.169  2.3141 0.03283 *
## Treatment           2.58   2.579     1  7.001  0.0254 0.87790
## NrateF:Treatment 1305.88 145.098     9 34.154  1.4281 0.21498
## ---
## 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 = 90:
```

```
##  contrast estimate   SE df t.ratio p.value
##  CR - FR    -20.83 8.76 47  -2.376  0.0216
##
## NrateF = 115:
##  contrast estimate   SE df t.ratio p.value
##  CR - FR      6.75 6.20 47   1.089  0.2818
##
## NrateF = 120:
##  contrast estimate   SE df t.ratio p.value
##  CR - FR     -1.74 8.76 47  -0.199  0.8433
##
## NrateF = 150:
##  contrast estimate   SE df t.ratio p.value
##  CR - FR     -1.84 8.76 47  -0.210  0.8345
##
## NrateF = 155:
##  contrast estimate   SE df t.ratio p.value
##  CR - FR     -2.61 6.20 47  -0.422  0.6753
##
## NrateF = 180:
##  contrast estimate   SE df t.ratio p.value
##  CR - FR     12.76 8.76 47   1.456  0.1520
##
## NrateF = 185:
##  contrast estimate   SE df t.ratio p.value
##  CR - FR     -3.59 6.20 47  -0.580  0.5648
##
## NrateF = 210:
##  contrast estimate   SE df t.ratio p.value
##  CR - FR      5.65 8.76 47   0.645  0.5220
##
## NrateF = 225:
##  contrast estimate   SE df t.ratio p.value
##  CR - FR      2.15 6.20 47   0.347  0.7299
##
## NrateF = 260:
##  contrast estimate   SE df t.ratio p.value
##  CR - FR      7.94 6.20 47   1.281  0.2065
##
## Degrees-of-freedom method: kenward-roger
```

```
cld(field_means_average)
```

```
## NrateF = 90:
##  Treatment emmean   SE   df lower.CL upper.CL .group
##  CR          31.5 6.75 50.5     18.0     45.1  1
##  FR          52.4 6.75 50.5     38.8     65.9   2
##
## NrateF = 115:
##  Treatment emmean   SE   df lower.CL upper.CL .group
##  FR          64.7 4.77 50.5     55.1     74.3  1
##  CR          71.5 4.77 50.5     61.9     81.0  1
##
## NrateF = 120:
```

```
##  Treatment emmean   SE   df lower.CL upper.CL .group
##  CR          47.9 6.75 50.5     34.3     61.4  1
##  FR          49.6 6.75 50.5     36.1     63.2  1
##
## NrateF = 150:
##  Treatment emmean   SE   df lower.CL upper.CL .group
##  CR          53.8 6.75 50.5     40.3     67.4  1
##  FR          55.6 6.75 50.5     42.1     69.2  1
##
## NrateF = 155:
##  Treatment emmean   SE   df lower.CL upper.CL .group
##  CR          60.9 4.77 50.5     51.3     70.5  1
##  FR          63.5 4.77 50.5     54.0     73.1  1
##
## NrateF = 180:
##  Treatment emmean   SE   df lower.CL upper.CL .group
##  FR          42.9 6.75 50.5     29.3     56.4  1
##  CR          55.7 6.75 50.5     42.1     69.2  1
##
## NrateF = 185:
##  Treatment emmean   SE   df lower.CL upper.CL .group
##  CR          64.8 4.77 50.5     55.2     74.4  1
##  FR          68.4 4.77 50.5     58.8     78.0  1
##
## NrateF = 210:
##  Treatment emmean   SE   df lower.CL upper.CL .group
##  FR          51.0 6.75 50.5     37.4     64.5  1
##  CR          56.6 6.75 50.5     43.1     70.2  1
##
## NrateF = 225:
##  Treatment emmean   SE   df lower.CL upper.CL .group
##  FR          62.0 4.77 50.5     52.4     71.6  1
##  CR          64.2 4.77 50.5     54.6     73.7  1
##
## NrateF = 260:
##  Treatment emmean   SE   df lower.CL upper.CL .group
##  FR          59.9 4.77 50.5     50.3     69.5  1
##  CR          67.9 4.77 50.5     58.3     77.4  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        90       31.5 6.75 50.5     18.0     45.1
##  FR        90       52.4 6.75 50.5     38.8     65.9
##  CR        115      71.5 4.77 50.5     61.9     81.0
##  FR        115      64.7 4.77 50.5     55.1     74.3
##  CR        120      47.9 6.75 50.5     34.3     61.4
```

```
##  FR        120      49.6 6.75 50.5     36.1     63.2
##  CR        150      53.8 6.75 50.5     40.3     67.4
##  FR        150      55.6 6.75 50.5     42.1     69.2
##  CR        155      60.9 4.77 50.5     51.3     70.5
##  FR        155      63.5 4.77 50.5     54.0     73.1
##  CR        180      55.7 6.75 50.5     42.1     69.2
##  FR        180      42.9 6.75 50.5     29.3     56.4
##  CR        185      64.8 4.77 50.5     55.2     74.4
##  FR        185      68.4 4.77 50.5     58.8     78.0
##  CR        210      56.6 6.75 50.5     43.1     70.2
##  FR        210      51.0 6.75 50.5     37.4     64.5
##  CR        225      64.2 4.77 50.5     54.6     73.7
##  FR        225      62.0 4.77 50.5     52.4     71.6
##  CR        260      67.9 4.77 50.5     58.3     77.4
##  FR        260      59.9 4.77 50.5     50.3     69.5
##
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
```

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

```
##  Treatment NrateF emmean   SE   df lower.CL upper.CL .group
##  CR        90       31.5 6.75 50.5     10.1     52.9  1
##  FR        180      42.9 6.75 50.5     21.5     64.3  12
##  CR        120      47.9 6.75 50.5     26.5     69.3  12
##  FR        120      49.6 6.75 50.5     28.2     71.0  12
##  FR        210      51.0 6.75 50.5     29.5     72.4  12
##  FR        90       52.4 6.75 50.5     30.9     73.8  12
##  CR        150      53.8 6.75 50.5     32.4     75.2  12
##  FR        150      55.6 6.75 50.5     34.2     77.1  12
##  CR        180      55.7 6.75 50.5     34.2     77.1  12
##  CR        210      56.6 6.75 50.5     35.2     78.0  12
##  FR        260      59.9 4.77 50.5     44.8     75.1  12
##  CR        155      60.9 4.77 50.5     45.8     76.1  12
##  FR        225      62.0 4.77 50.5     46.9     77.2  12
##  FR        155      63.5 4.77 50.5     48.4     78.7  12
##  CR        225      64.2 4.77 50.5     49.0     79.3   2
##  FR        115      64.7 4.77 50.5     49.6     79.9   2
##  CR        185      64.8 4.77 50.5     49.7     79.9   2
##  CR        260      67.9 4.77 50.5     52.7     83.0   2
##  FR        185      68.4 4.77 50.5     53.2     83.5   2
##  CR        115      71.5 4.77 50.5     56.3     86.6   2
##
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
## Conf-level adjustment: sidak method for 20 estimates
## P value adjustment: sidak method for 190 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.
```

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

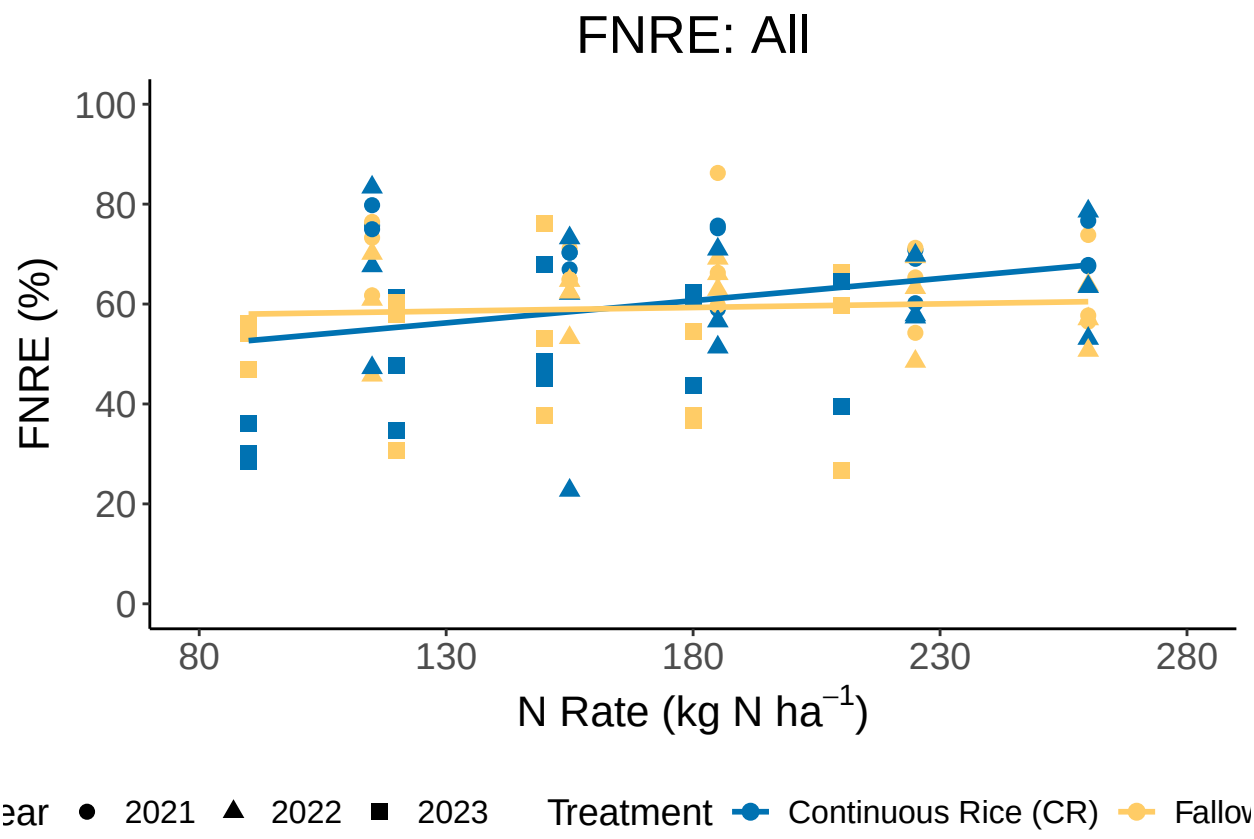
All together graph

```
FNRE_all_graph <-
ggplot(FNRE_all, aes(x=Nrate_kgha, y=FNRE, color=Treatment, shape = Year))+
  geom_point(size=2.5)+ #this is the mean values
  #geom_point(data=FNRE_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(80, 280), breaks = seq(80,
  scale_y_continuous(name= expression("FNRE (%)"), limits = c(0, 100), breaks = seq(0, 100, by = 20))+
  theme_classic()+
  geom_smooth(aes(group = Treatment), method = "lm", se = FALSE)+
  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("FNRE: All"))+
  theme(legend.position = "bottom")

FNRE_all_graph
```

```
## `geom_smooth()` using formula = 'y ~ x'
```

```
## Warning: The following aesthetics were dropped during statistical transformation: shape.
## i This can happen when ggplot fails to infer the correct grouping structure in
##   the data.
## i Did you forget to specify a `group` aesthetic or to convert a numerical
##   variable into a factor?
```



Combine into 1 graph

```
FNRE_combined <- ggarrange(FNRE_2021_graph,
                           FNRE_2022_graph,
                           FNRE_2023_graph,
                           #FNRE_all_graph,
                           nrow = 1,
                           #ncol = 2,
                           #common.legend = TRUE,
                           legend.grob = get_legend(FNRE_all_graph),
                           legend= "bottom")
```

```
## `geom_smooth()` using formula = 'y ~ x'

## Warning: The following aesthetics were dropped during statistical transformation: shape.
## i This can happen when ggplot fails to infer the correct grouping structure in
##   the data.
## i Did you forget to specify a `group` aesthetic or to convert a numerical
##   variable into a factor?

## `geom_smooth()` using formula = 'y ~ x'
## `geom_smooth()` using formula = 'y ~ x'
## `geom_smooth()` using formula = 'y ~ x'
```

```
ggsave(filename = "FNRE_combined_all_year.jpg",  # Include the file extension here
       plot = FNRE_combined,              # Specify the plot
       path = "C:/Users/zhang/Documents/GitHub/FallowRice_ContinuousRice_AgronomicPerformance/Figures",
       dpi = 400,
       height = 15, width = 40, units = "cm")
```

Combine into 1 excel file

```
all_means <- rbind(as.data.frame(means_2021) %>% mutate(Year = 2021),
                   as.data.frame(means_2022) %>% mutate(Year = 2022),
                   as.data.frame(means_2023) %>% mutate(Year = 2023)
) %>% arrange(Treatment,Year)

write_xlsx(all_means, "D:/Academics/UC Davis/School Work/Linquist Lab/Data/R stats/Agronomic paper/N up
```