

Apparent Fertilizer Nitrogen Recovery Efficiency (FNRE)

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Necessary libraries

Read and check data

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

#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

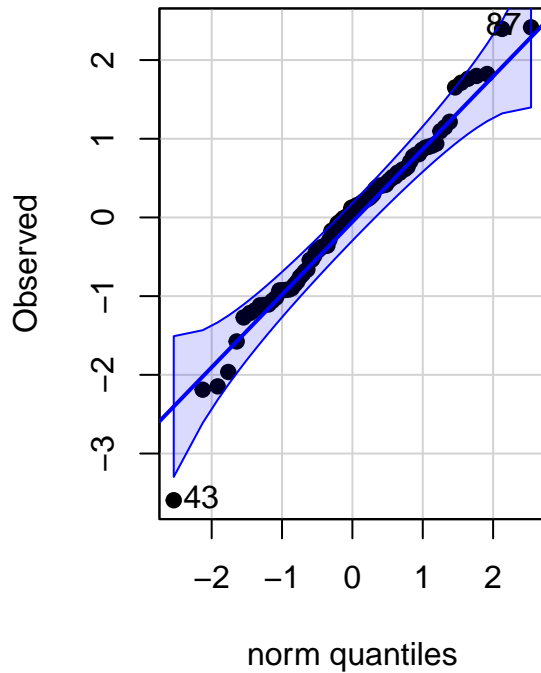
```
FNRE_all <- master_with_FNRE %>%  
  #filter(Year != 2023) %>%  
  filter(Topdress!=1) %>%  
  filter(Stage=="Maturity") %>%  
  mutate(Year= as.factor(Year))  
  
FNRE_2021 <- master_with_FNRE %>%  
  filter(Year == 2021) %>%  
  filter(Topdress!=1) %>%  
  filter(Stage=="Maturity") %>%  
  mutate(Year= 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

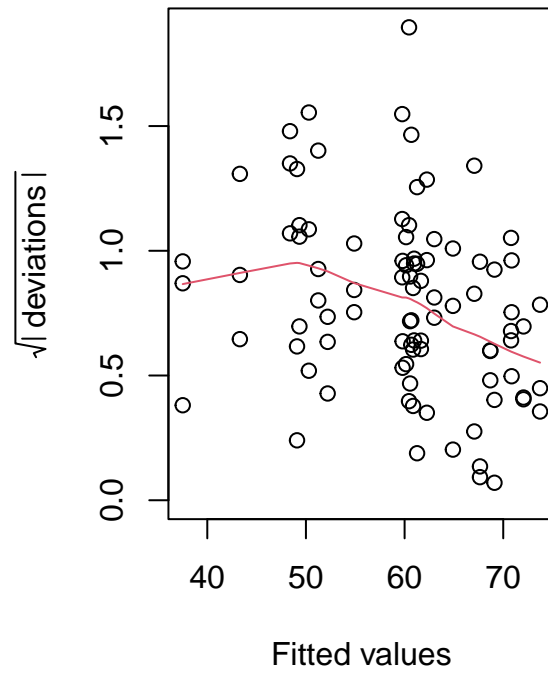
Seems that there is an effect of Nrate and Year. But no treatment effects.

```
all_factors_model <- lm(FNRE ~ Nrate_kgha*Treatment*Year, data = FNRE_all)  
  
pls205_diagnostics(all_factors_model)
```

Plot (EU) Normal Q-Q



Scale-Location



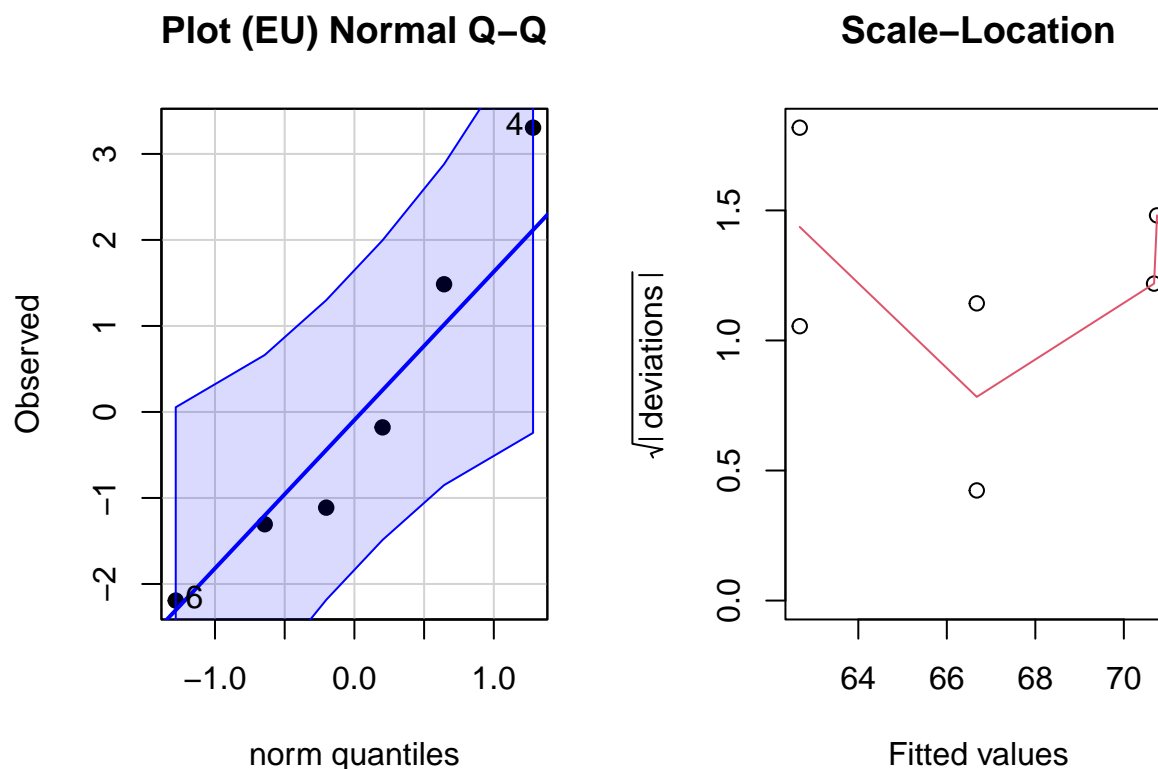
```
anova(all_factors_model)
```

```
## 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

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.numeric(NrateF))
```

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

```

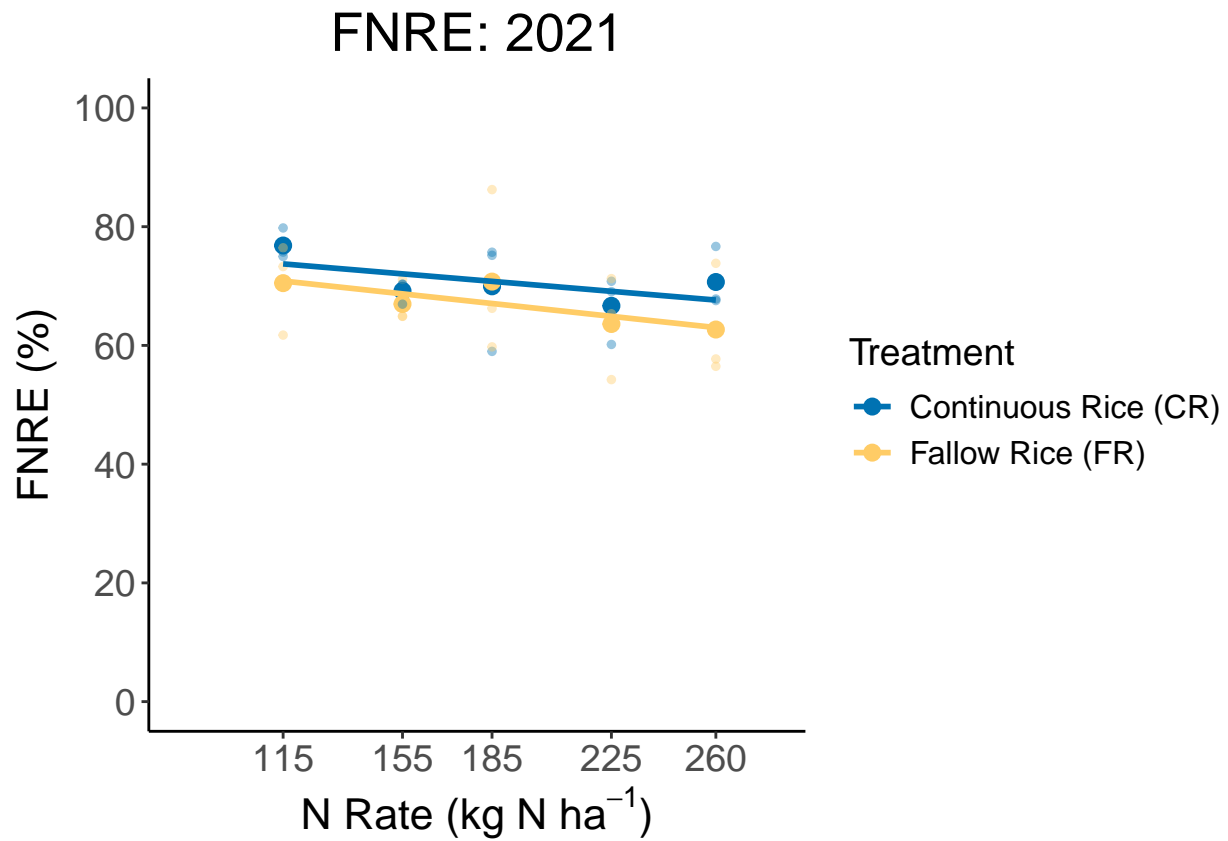
FNRE_2021_graph <-
ggplot(graphing_2021, aes(x=Nrate_kgha, y=FNRE, color=Treatment))+
  geom_point(data=graphing_2021, size=2.5)+ #this is the mean values
  geom_point(data=FNRE_2021, size=1, alpha=0.4)+ #this are the raw values
  scale_color_manual(values=c("#0072B2", "#FFCC66"), name = "Treatment", 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

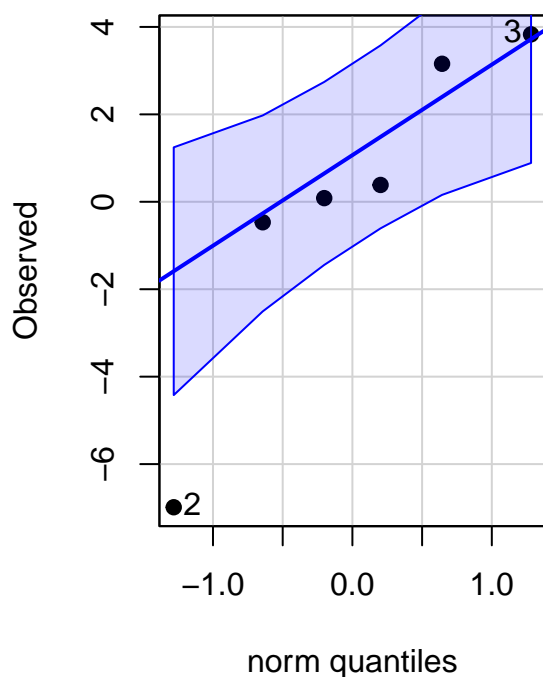
Statistical tests

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

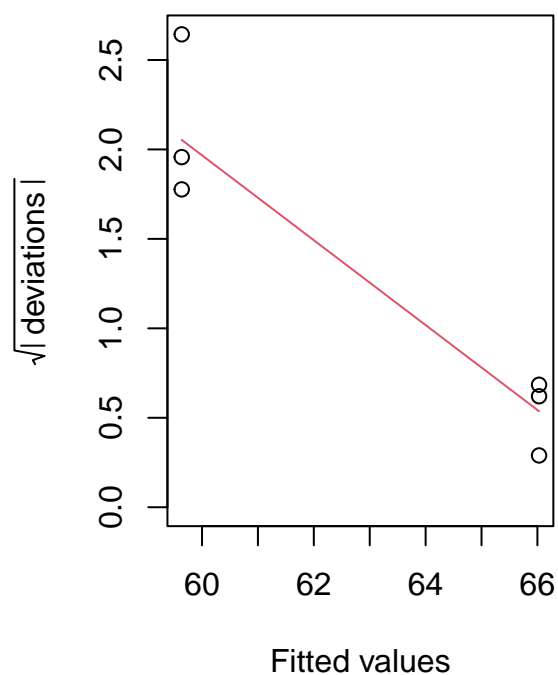
```
## boundary (singular) fit: see help('isSingular')
```

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

Plot (EU) Normal Q-Q



Scale-Location



```
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.numeric(NrateF))
```

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

```

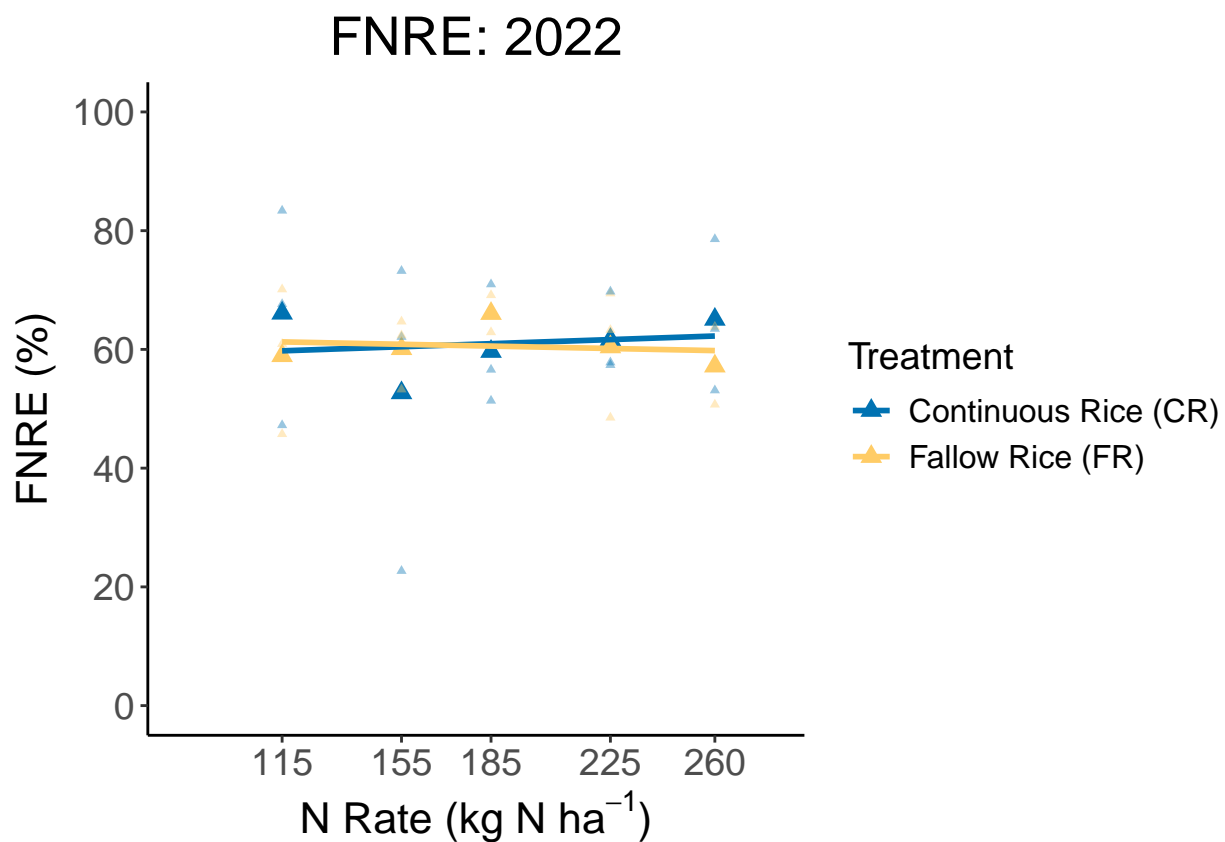
FNRE_2022_graph <-
ggplot(graphing_2022, aes(x=Nrate_kgha, y=FNRE, color=Treatment))+
  geom_point(data=graphing_2022, size=2.5, shape="triangle")+ #this is the mean values
  geom_point(data=FNRE_2022, size=1, alpha=0.4, shape="triangle")+ #this are the raw values
  scale_color_manual(values=c("#0072B2", "#FFCC66"), name = "Treatment", labels = c('Continuous Rice (CR)', 'Fallow Rice (FR)'))+
  scale_x_continuous(name=expression("N Rate (kg N ha"^{-1}*")"), limits = c(80, 280), breaks = c(115, 155, 185, 225, 260))+
  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'
```



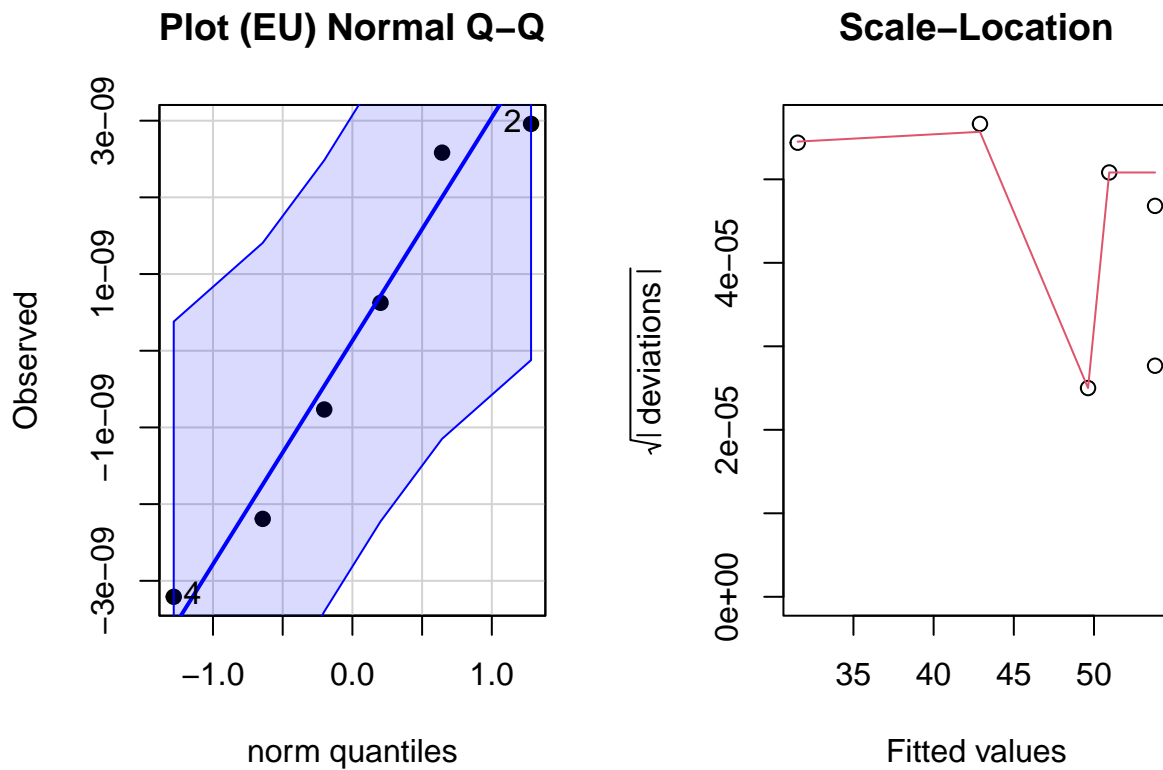
2023

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.numeric(NrateF))
```

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, 120),
  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)+

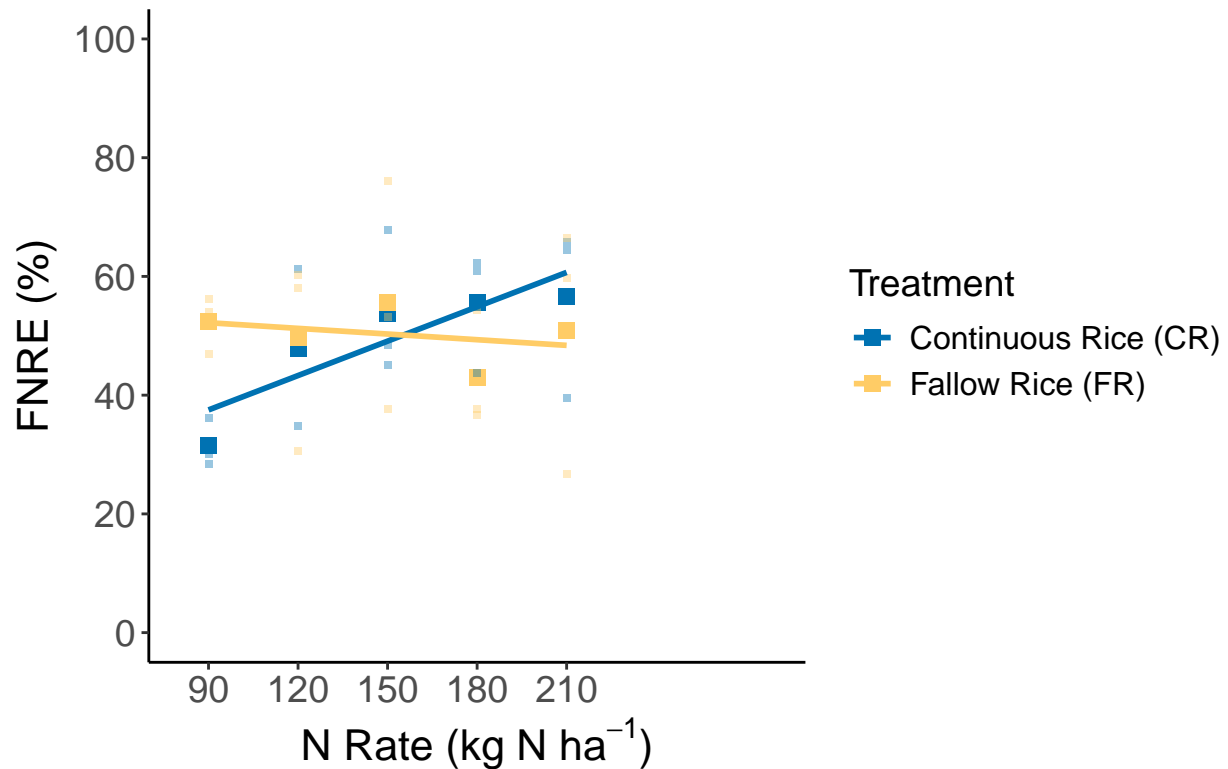
  theme(axis.text = element_text(size = 14), axis.title = element_text(size=16))+
  theme(legend.text = element_text(size = 12), legend.title = element_text(size = 14))+
  theme(plot.title = element_text(hjust = 0.5, size = 20, face = "bold"))+
  ggtitle(expression("FNRE: 2023"))

```

FNRE_2023_graph

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

FNRE: 2023



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")
```

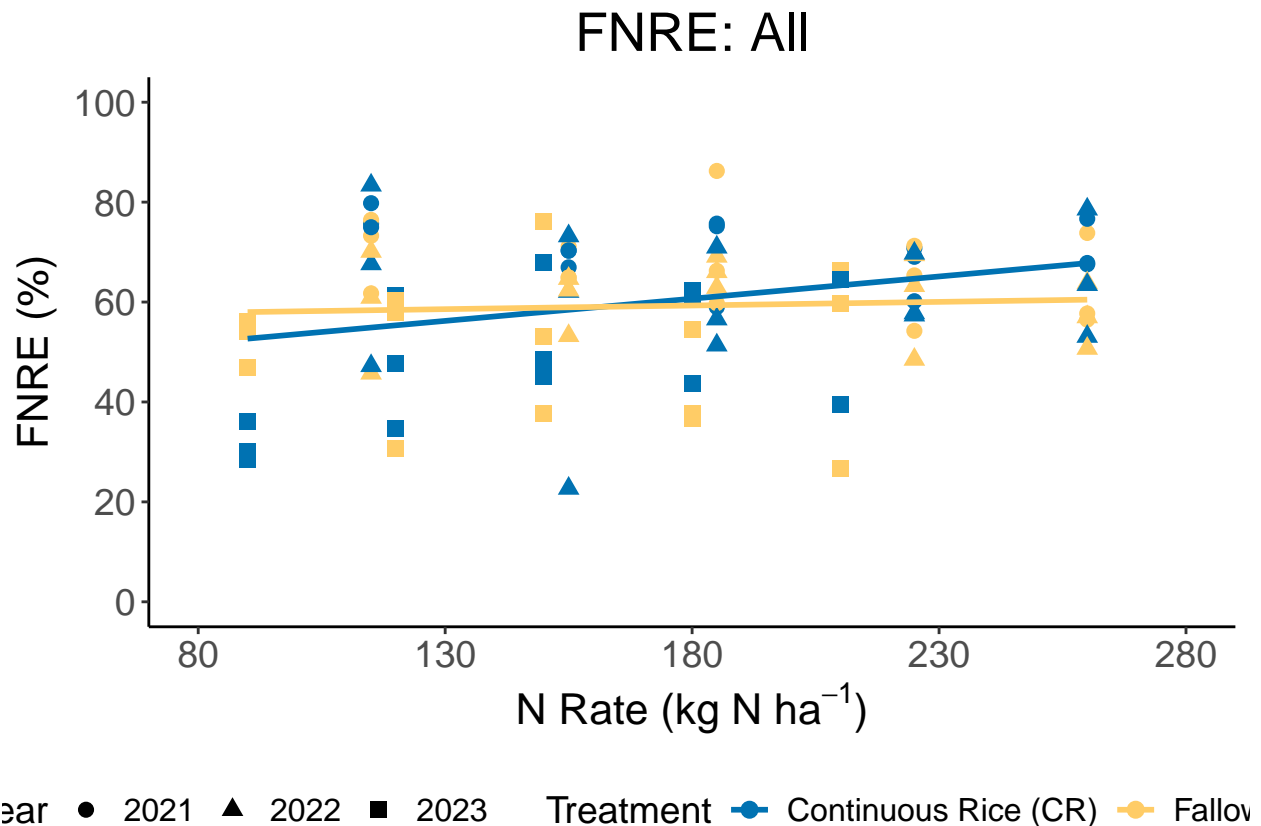
All together graph

```
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/Linguist Lab/Data/R stats/Agronomic paper/N up
```