

# N uptake maturity

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## Necessary libraries

## Read and check data, split by year

```
#read data
master = read_excel('D:/Academics/UC Davis/School Work/Linguist Lab/Data/R stats/Agronomic paper/N uptake')

master$NrateF <- as.factor(master$Nrate_kgha)

Nrate_trial <- master %>%
  #filter(Year != 2023) %>%
  filter(Topdress!=1) %>%
  filter(Stage=="Maturity") %>%
```

```

mutate(Year= as.factor(Year))

Nrate_trial_2021 <- master %>%
  filter(Year == 2021) %>%
  filter(Topdress!=1) %>%
  filter(Stage=="Maturity") %>%
  mutate(Year= as.factor(Year))

Nrate_trial_2022 <- master %>%
  filter(Year == 2022) %>%
  filter(Topdress!=1) %>%
  filter(Stage=="Maturity") %>%
  mutate(Year= as.factor(Year))

Nrate_trial_2023 <- master %>%
  filter(Year == 2023) %>%
  filter(Topdress!=1) %>%
  filter(Stage=="Maturity") %>%
  mutate(Year= as.factor(Year))

table(Nrate_trial_2021$Nrate_kgha)

```

```

##
## 0 115 155 185 225 260
## 6 6 6 6 6 6

```

## 2021

```

model_2021 <- lmer(N_total_kgha ~ NrateF*Treatment+(1|Treatment:Blk), data=Nrate_trial_2021)

anova(model_2021)

```

```

## Type III Analysis of Variance Table with Satterthwaite's method
##              Sum Sq Mean Sq NumDF DenDF  F value    Pr(>F)
## NrateF          110725  22144.9      5     20 185.4816 4.843e-16 ***
## Treatment           629    628.6      1      4   5.2654  0.08343 .
## NrateF:Treatment    481     96.1      5     20   0.8050  0.55947
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```

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      -25.68 11.8 12.6 -2.180 0.0489
##

```

```
## NrateF = 115:
## contrast estimate SE df t.ratio p.value
## CR - FR -18.39 11.8 12.6 -1.561 0.1432
##
## NrateF = 155:
## contrast estimate SE df t.ratio p.value
## CR - FR -22.26 11.8 12.6 -1.890 0.0820
##
## NrateF = 185:
## contrast estimate SE df t.ratio p.value
## CR - FR -27.15 11.8 12.6 -2.305 0.0389
##
## NrateF = 225:
## contrast estimate SE df t.ratio p.value
## CR - FR -18.78 11.8 12.6 -1.594 0.1356
##
## NrateF = 260:
## contrast estimate SE df t.ratio p.value
## CR - FR -4.86 11.8 12.6 -0.413 0.6868
##
## Degrees-of-freedom method: kenward-roger
```

```
cld(field_means_2021)
```

```
## NrateF = 0:
## Treatment emmean SE df lower.CL upper.CL .group
## CR 59.9 8.33 12.6 41.9 78 1
## FR 85.6 8.33 12.6 67.6 104 2
##
## NrateF = 115:
## Treatment emmean SE df lower.CL upper.CL .group
## CR 148.3 8.33 12.6 130.2 166 1
## FR 166.7 8.33 12.6 148.6 185 1
##
## NrateF = 155:
## Treatment emmean SE df lower.CL upper.CL .group
## CR 167.2 8.33 12.6 149.1 185 1
## FR 189.4 8.33 12.6 171.4 207 1
##
## NrateF = 185:
## Treatment emmean SE df lower.CL upper.CL .group
## CR 189.3 8.33 12.6 171.3 207 1
## FR 216.5 8.33 12.6 198.4 235 2
##
## NrateF = 225:
## Treatment emmean SE df lower.CL upper.CL .group
## CR 209.9 8.33 12.6 191.9 228 1
## FR 228.7 8.33 12.6 210.7 247 1
##
## NrateF = 260:
## Treatment emmean SE df lower.CL upper.CL .group
## CR 243.7 8.33 12.6 225.7 262 1
## FR 248.6 8.33 12.6 230.5 267 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.
```

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

```
## Treatment NrateF emmean SE df lower.CL upper.CL .group
## CR 0 59.9 8.33 12.6 31.0 88.9 1
## FR 0 85.6 8.33 12.6 56.6 114.6 1
## CR 115 148.3 8.33 12.6 119.3 177.2 2
## FR 115 166.7 8.33 12.6 137.7 195.6 234
## CR 155 167.2 8.33 12.6 138.2 196.1 23 5
## CR 185 189.3 8.33 12.6 160.4 218.3 34567
## FR 155 189.4 8.33 12.6 160.5 218.4 23456
## CR 225 209.9 8.33 12.6 181.0 238.9 4 678
## FR 185 216.5 8.33 12.6 187.5 245.5 5678
## FR 225 228.7 8.33 12.6 199.8 257.7 78
## CR 260 243.7 8.33 12.6 214.7 272.7 8
## FR 260 248.6 8.33 12.6 219.6 277.5 8
```

```
##
## 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.
```

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

## Graph

```
Nrate_trial_2021_dataframe <- Nrate_trial_2021 %>%
  group_by(Treatment, Nrate_kgha) %>%
  mutate(N_total_kgha_se = sd(N_total_kgha)/sqrt(3)) %>%
  summarise(N_total_kgha = mean(N_total_kgha),
            N_total_kgha_se = mean(N_total_kgha_se))
```

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

```
Nuptake_graph_2021 <-
ggplot(Nrate_trial_2021, aes(x=Nrate_kgha, y=N_total_kgha, color=Treatment))+
  geom_point(size=1, alpha=0.4)+
  geom_point(data=Nrate_trial_2021_dataframe, size=2.5)+ #this is the mean values
  scale_shape_manual(values = c("circle"))+
```

```

geom_smooth(aes(group = Treatment),method = lm, level = 0.95)+
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), expand = c(0, 0),
  scale_y_continuous(name=expression("N uptake (kg N ha"^{-1}*")"), limits = c(0, 300), expand = c(0, 0),
#geom_errorbar(aes(ymin=N_total_kgha-N_total_kgha_se, ymax=N_total_kgha+N_total_kgha_se), width=3, pos=
#geom_vline(xintercept = c(41, 50, 78, 84, 121, 136), linetype = "dashed", color = "black") +
theme_classic()+
stat_regline_equation(aes(x=Nrate_kgha, y=N_total_kgha,color=Treatment,group = Treatment,
  label = paste(..rr.label..)),
  show.legend = FALSE,
  label.x = 200,
  label.y = c(60, 90))+
stat_regline_equation(aes(x=Nrate_kgha, y=N_total_kgha,color=Treatment,group = Treatment,
  label = paste(..eq.label..)),
  show.legend = FALSE,
  label.x = 200,
  label.y = c(70, 100))+
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("N uptake"[maturity]~": 2021"))
#annotate(
#"text",
#x = c(0),
#y = Nrate_trial_2021_dataframe %>%
#  filter(Treatment == "FR", Nrate_kgha == 0) %>%
#  mutate(N_total_kgha_plus_higher = N_total_kgha + 25) %>%
#  pull(N_total_kgha_plus_higher),
#label = "*",
#size = 7,
#vjust = 0
#)

```

Nuptake\_graph\_2021

```

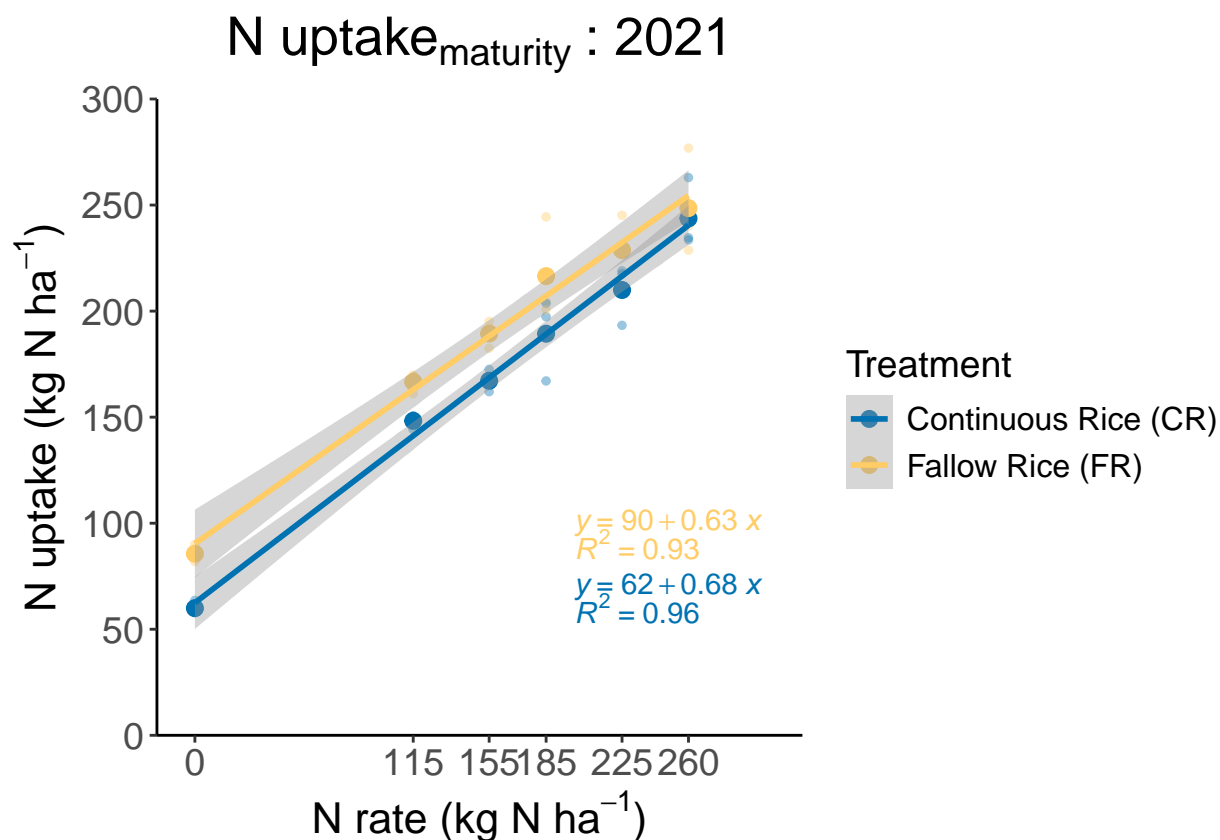
## Warning: The dot-dot notation ('..rr.label..') was deprecated in ggplot2 3.4.0.
## i Please use 'after_stat(rr.label)' instead.
## This warning is displayed once every 8 hours.
## Call 'lifecycle::last_lifecycle_warnings()' to see where this warning was
## generated.

```

```

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

```



2022

```
model_2022 <- lmer(N_total_kgha ~ NrateF*Treatment+(1|Treatment:Blk), data=Nrate_trial_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          95639  19127.8      5     20  63.1071 1.477e-11 ***
## Treatment         2385   2384.9      1      4   7.8683  0.04856 *
## NrateF:Treatment   1134    226.8      5     20   0.7482  0.59698
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
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       -31.6 16.9 16.9 -1.872  0.0786
```

```
##
## NrateF = 115:
## contrast estimate SE df t.ratio p.value
## CR - FR -23.4 16.9 16.9 -1.384 0.1842
##
## NrateF = 155:
## contrast estimate SE df t.ratio p.value
## CR - FR -43.1 16.9 16.9 -2.555 0.0205
##
## NrateF = 185:
## contrast estimate SE df t.ratio p.value
## CR - FR -43.4 16.9 16.9 -2.574 0.0198
##
## NrateF = 225:
## contrast estimate SE df t.ratio p.value
## CR - FR -28.8 16.9 16.9 -1.707 0.1061
##
## NrateF = 260:
## contrast estimate SE df t.ratio p.value
## CR - FR -11.1 16.9 16.9 -0.659 0.5188
##
## Degrees-of-freedom method: kenward-roger
```

```
cld(field_means_2022)
```

```
## NrateF = 0:
## Treatment emmean SE df lower.CL upper.CL .group
## CR 66.4 11.9 16.9 41.3 91.6 1
## FR 98.0 11.9 16.9 72.8 123.2 1
##
## NrateF = 115:
## Treatment emmean SE df lower.CL upper.CL .group
## CR 142.4 11.9 16.9 117.2 167.6 1
## FR 165.8 11.9 16.9 140.6 190.9 1
##
## NrateF = 155:
## Treatment emmean SE df lower.CL upper.CL .group
## CR 148.1 11.9 16.9 122.9 173.2 1
## FR 191.2 11.9 16.9 166.0 216.3 2
##
## NrateF = 185:
## Treatment emmean SE df lower.CL upper.CL .group
## CR 176.8 11.9 16.9 151.6 201.9 1
## FR 220.2 11.9 16.9 195.0 245.3 2
##
## NrateF = 225:
## Treatment emmean SE df lower.CL upper.CL .group
## CR 205.1 11.9 16.9 180.0 230.3 1
## FR 233.9 11.9 16.9 208.7 259.1 1
##
## NrateF = 260:
## Treatment emmean SE df lower.CL upper.CL .group
## CR 235.6 11.9 16.9 210.4 260.7 1
## FR 246.7 11.9 16.9 221.5 271.8 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.
```

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

```
## Treatment NrateF emmean SE df lower.CL upper.CL .group
## CR 0 66.4 11.9 16.9 27.1 106 1
## FR 0 98.0 11.9 16.9 58.7 137 12
## CR 115 142.4 11.9 16.9 103.1 182 23
## CR 155 148.1 11.9 16.9 108.7 187 23
## FR 115 165.8 11.9 16.9 126.4 205 34
## CR 185 176.8 11.9 16.9 137.4 216 345
## FR 155 191.2 11.9 16.9 151.8 231 3456
## CR 225 205.1 11.9 16.9 165.8 244 456
## FR 185 220.2 11.9 16.9 180.8 260 456
## FR 225 233.9 11.9 16.9 194.6 273 56
## CR 260 235.6 11.9 16.9 196.2 275 6
## FR 260 246.7 11.9 16.9 207.3 286 6
```

```
##
## 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.
```

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

## Graph

```
Nrate_trial_2022_dataframe <- Nrate_trial_2022 %>%
  group_by(Treatment, Nrate_kgha) %>%
  mutate(N_total_kgha_se = sd(N_total_kgha)/sqrt(3)) %>%
  summarise(N_total_kgha = mean(N_total_kgha),
            N_total_kgha_se = mean(N_total_kgha_se))
```

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

```
Nuptake_graph_2022 <-
ggplot(Nrate_trial_2022, aes(x=Nrate_kgha, y=N_total_kgha, color=Treatment))+
  geom_point(size=1, alpha=0.4, shape="triangle")+
  geom_point(data=Nrate_trial_2022_dataframe, size=2.5, shape="triangle")+ #this is the mean values
```



```

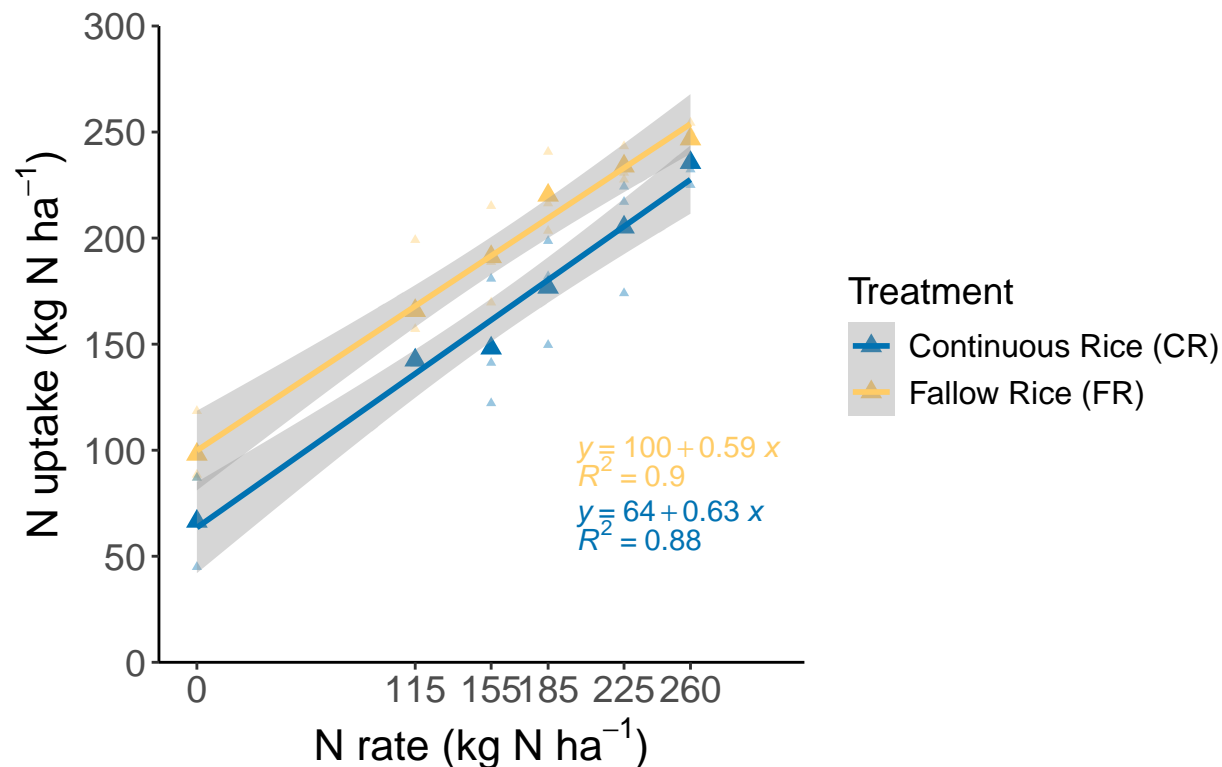
#scale_shape_manual(values = c("triangle"))+
geom_smooth(aes(group = Treatment),method = lm, level = 0.95)+
scale_color_manual(values=c("#0072B2","#FFCC66"), name = "Treatment", labels = c("Continuous Rice (CR",
  scale_x_continuous(name=expression("N rate (kg N ha"^{-1}*")"), limits = c(-20, 320), expand = c(0, 0.1),
  scale_y_continuous(name=expression("N uptake (kg N ha"^{-1}*")"), limits = c(0, 300), expand = c(0, 0.1),
#geom_errorbar(aes(ymin=N_total_kgha-N_total_kgha_se, ymax=N_total_kgha+N_total_kgha_se), width=3, pos="upper",
#geom_vline(xintercept = c(41, 50, 78, 84, 121, 136), linetype = "dashed", color = "black") +
theme_classic()+
  stat_regline_equation(aes(x=Nrate_kgha, y=N_total_kgha,color=Treatment,group = Treatment,
    label = paste(..rr.label..)),
    show.legend = FALSE,
    label.x = 200,
    label.y = c(60, 90))+
  stat_regline_equation(aes(x=Nrate_kgha, y=N_total_kgha,color=Treatment,group = Treatment,
    label = paste(..eq.label..)),
    show.legend = FALSE,
    label.x = 200,
    label.y = c(70, 100))+
  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("N uptake"[maturity]~": 2022"))

```

Nuptake\_graph\_2022

## 'geom\_smooth()' using formula = 'y ~ x'

## N uptake<sub>maturity</sub> : 2022



## 2023

```
model_2023 <- lmer(N_total_kgha ~ NrateF*Treatment+(1|Treatment:Blk), data=Nrate_trial_2023)
anova(model_2023)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##              Sum Sq Mean Sq NumDF DenDF F value    Pr(>F)
## NrateF          48865   9772.9      5     20 21.3442 2.157e-07 ***
## Treatment         8664   8663.5      1      4 18.9213 0.01216 *
## NrateF:Treatment   1517    303.3      5     20  0.6625 0.65603
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
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       -37.5 17.9 23.7 -2.090 0.0475
```

```
##
## NrateF = 90:
## contrast estimate SE df t.ratio p.value
## CR - FR -56.2 17.9 23.7 -3.136 0.0045
##
## NrateF = 120:
## contrast estimate SE df t.ratio p.value
## CR - FR -39.6 17.9 23.7 -2.207 0.0373
##
## NrateF = 150:
## contrast estimate SE df t.ratio p.value
## CR - FR -40.2 17.9 23.7 -2.244 0.0345
##
## NrateF = 180:
## contrast estimate SE df t.ratio p.value
## CR - FR -14.5 17.9 23.7 -0.808 0.4271
##
## NrateF = 210:
## contrast estimate SE df t.ratio p.value
## CR - FR -25.6 17.9 23.7 -1.427 0.1665
##
## Degrees-of-freedom method: kenward-roger
```

```
cld(field_means_2023)
```

```
## NrateF = 0:
## Treatment emmean SE df lower.CL upper.CL .group
## CR 56.1 12.7 23.7 29.9 82.3 1
## FR 93.6 12.7 23.7 67.4 119.7 2
##
## NrateF = 90:
## Treatment emmean SE df lower.CL upper.CL .group
## CR 84.5 12.7 23.7 58.3 110.7 1
## FR 140.7 12.7 23.7 114.5 166.9 2
##
## NrateF = 120:
## Treatment emmean SE df lower.CL upper.CL .group
## CR 113.6 12.7 23.7 87.4 139.8 1
## FR 153.1 12.7 23.7 127.0 179.3 2
##
## NrateF = 150:
## Treatment emmean SE df lower.CL upper.CL .group
## CR 136.8 12.7 23.7 110.6 163.0 1
## FR 177.0 12.7 23.7 150.9 203.2 2
##
## NrateF = 180:
## Treatment emmean SE df lower.CL upper.CL .group
## CR 156.3 12.7 23.7 130.1 182.5 1
## FR 170.8 12.7 23.7 144.6 197.0 1
##
## NrateF = 210:
## Treatment emmean SE df lower.CL upper.CL .group
## CR 175.0 12.7 23.7 148.8 201.2 1
## FR 200.6 12.7 23.7 174.4 226.7 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.
```

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

```
## Treatment NrateF emmean SE df lower.CL upper.CL .group
## CR 0 56.1 12.7 23.7 16.1 96.2 1
## CR 90 84.5 12.7 23.7 44.4 124.5 12
## FR 0 93.6 12.7 23.7 53.5 133.6 123
## CR 120 113.6 12.7 23.7 73.5 153.6 1234
## CR 150 136.8 12.7 23.7 96.8 176.9 2345
## FR 90 140.7 12.7 23.7 100.6 180.8 2345
## FR 120 153.1 12.7 23.7 113.1 193.2 2345
## CR 180 156.3 12.7 23.7 116.2 196.4 345
## FR 180 170.8 12.7 23.7 130.7 210.8 45
## CR 210 175.0 12.7 23.7 134.9 215.0 45
## FR 150 177.0 12.7 23.7 137.0 217.1 45
## FR 210 200.6 12.7 23.7 160.5 240.6 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.
```

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

## Graph

```
Nrate_trial_2023_dataframe <- Nrate_trial_2023 %>%
  group_by(Treatment, Nrate_kgha) %>%
  mutate(N_total_kgha_se = sd(N_total_kgha)/sqrt(3)) %>%
  summarise(N_total_kgha = mean(N_total_kgha),
            N_total_kgha_se = mean(N_total_kgha_se))
```

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

```
Nuptake_graph_2023 <-
ggplot(Nrate_trial_2023, aes(x=Nrate_kgha, y=N_total_kgha, color=Treatment))+
  geom_point(size=1, alpha=0.4, shape="square")+
  geom_point(data=Nrate_trial_2023_dataframe, size=2.5, shape="square")+ #this is the mean values
```

```

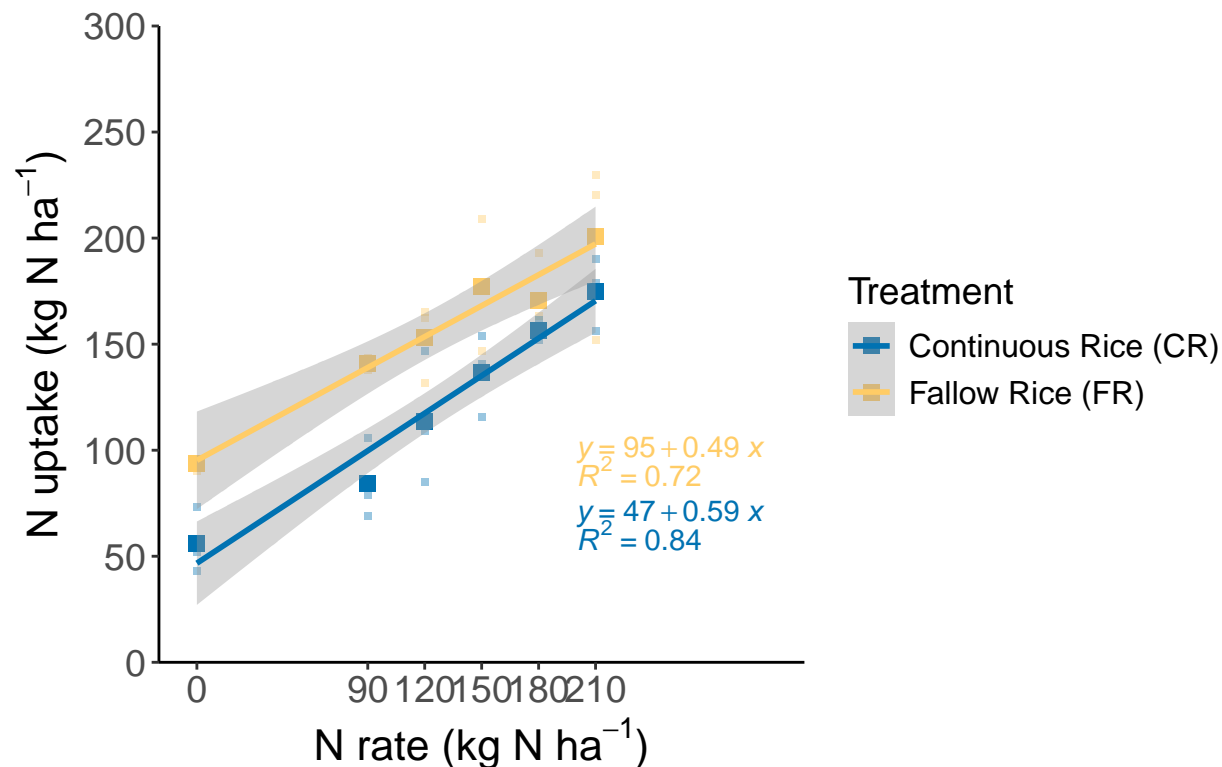
#scale_shape_manual(values = c("square"))+
geom_smooth(aes(group = Treatment),method = lm, level = 0.95)+
scale_color_manual(values=c("#0072B2","#FFCC66"), name = "Treatment", labels = c("Continuous Rice (CR",
  scale_x_continuous(name=expression("N rate (kg N ha"^{-1}*")"), limits = c(-20, 320), expand = c(0, 0),
  scale_y_continuous(name=expression("N uptake (kg N ha"^{-1}*")"), limits = c(0, 300), expand = c(0, 0),
#geom_errorbar(aes(ymin=N_total_kgha-N_total_kgha_se, ymax=N_total_kgha+N_total_kgha_se), width=3, pos="upper",
#geom_vline(xintercept = c(41, 50, 78, 84, 121, 136), linetype = "dashed", color = "black") +
theme_classic()+
  stat_regline_equation(aes(x=Nrate_kgha, y=N_total_kgha,color=Treatment,group = Treatment,
    label = paste(..rr.label..)),
    show.legend = FALSE,
    label.x = 200,
    label.y = c(60, 90))+
  stat_regline_equation(aes(x=Nrate_kgha, y=N_total_kgha,color=Treatment,group = Treatment,
    label = paste(..eq.label..)),
    show.legend = FALSE,
    label.x = 200,
    label.y = c(70, 100))+
  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("N uptake"[maturity]~": 2023"))

```

Nuptake\_graph\_2023

## 'geom\_smooth()' using formula = 'y ~ x'

## N uptake<sub>maturity</sub> : 2023



## Overall

```
model_all <- lmer(N_total_kgha ~ NrateF*Treatment+(1|Treatment:Blk), data=Nrate_trial)
anova(model_all)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##              Sum Sq Mean Sq NumDF  DenDF  F value    Pr(>F)
## NrateF          269628  26962.8     10  66.373  104.4336 < 2.2e-16 ***
## Treatment           8147    8147.3      1  16.396   31.5566 3.519e-05 ***
## NrateF:Treatment    3177     317.7     10  66.373    1.2305  0.2885
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
field_means_all = emmeans(model_all,spec = 'Treatment',by = 'NrateF')
field_effects_all = contrast(field_means_all, method = 'pairwise', adjust = "Tukey")
summary(field_effects_all)
```

```
## NrateF = 0:
## contrast estimate    SE    df t.ratio p.value
## CR - FR      -31.57  8.52  70.8  -3.704  0.0004
```

```
##
## NrateF = 90:
## contrast estimate SE df t.ratio p.value
## CR - FR -54.97 14.67 80.8 -3.747 0.0003
##
## NrateF = 115:
## contrast estimate SE df t.ratio p.value
## CR - FR -21.49 10.41 76.2 -2.065 0.0423
##
## NrateF = 120:
## contrast estimate SE df t.ratio p.value
## CR - FR -38.31 14.67 80.8 -2.612 0.0107
##
## NrateF = 150:
## contrast estimate SE df t.ratio p.value
## CR - FR -38.98 14.67 80.8 -2.658 0.0095
##
## NrateF = 155:
## contrast estimate SE df t.ratio p.value
## CR - FR -33.30 10.41 76.2 -3.200 0.0020
##
## NrateF = 180:
## contrast estimate SE df t.ratio p.value
## CR - FR -13.25 14.67 80.8 -0.903 0.3692
##
## NrateF = 185:
## contrast estimate SE df t.ratio p.value
## CR - FR -35.90 10.41 76.2 -3.450 0.0009
##
## NrateF = 210:
## contrast estimate SE df t.ratio p.value
## CR - FR -24.35 14.67 80.8 -1.660 0.1008
##
## NrateF = 225:
## contrast estimate SE df t.ratio p.value
## CR - FR -24.41 10.41 76.2 -2.345 0.0216
##
## NrateF = 260:
## contrast estimate SE df t.ratio p.value
## CR - FR -8.61 10.41 76.2 -0.827 0.4108
##
## Degrees-of-freedom method: kenward-roger
```

```
cld(field_means_all)
```

```
## NrateF = 0:
## Treatment emmean SE df lower.CL upper.CL .group
## CR 60.8 6.03 70.8 48.8 72.8 1
## FR 92.4 6.03 70.8 80.4 104.4 2
##
## NrateF = 90:
## Treatment emmean SE df lower.CL upper.CL .group
## CR 85.5 10.37 80.8 64.8 106.1 1
## FR 140.4 10.37 80.8 119.8 161.1 2
```

```

##
## NrateF = 115:
## Treatment emmean SE df lower.CL upper.CL .group
## CR 144.9 7.36 76.2 130.2 159.5 1
## FR 166.3 7.36 76.2 151.7 181.0 2
##
## NrateF = 120:
## Treatment emmean SE df lower.CL upper.CL .group
## CR 114.6 10.37 80.8 93.9 135.2 1
## FR 152.9 10.37 80.8 132.2 173.5 2
##
## NrateF = 150:
## Treatment emmean SE df lower.CL upper.CL .group
## CR 137.8 10.37 80.8 117.2 158.5 1
## FR 176.8 10.37 80.8 156.2 197.4 2
##
## NrateF = 155:
## Treatment emmean SE df lower.CL upper.CL .group
## CR 157.1 7.36 76.2 142.5 171.8 1
## FR 190.4 7.36 76.2 175.8 205.1 2
##
## NrateF = 180:
## Treatment emmean SE df lower.CL upper.CL .group
## CR 157.3 10.37 80.8 136.6 177.9 1
## FR 170.5 10.37 80.8 149.9 191.2 1
##
## NrateF = 185:
## Treatment emmean SE df lower.CL upper.CL .group
## CR 182.6 7.36 76.2 167.9 197.2 1
## FR 218.5 7.36 76.2 203.8 233.1 2
##
## NrateF = 210:
## Treatment emmean SE df lower.CL upper.CL .group
## CR 176.0 10.37 80.8 155.3 196.6 1
## FR 200.3 10.37 80.8 179.7 221.0 1
##
## NrateF = 225:
## Treatment emmean SE df lower.CL upper.CL .group
## CR 207.0 7.36 76.2 192.4 221.7 1
## FR 231.4 7.36 76.2 216.8 246.1 2
##
## NrateF = 260:
## Treatment emmean SE df lower.CL upper.CL .group
## CR 239.1 7.36 76.2 224.5 253.8 1
## FR 247.7 7.36 76.2 233.1 262.4 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.

```



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

```
## Treatment NrateF emmean SE df lower.CL upper.CL .group
## CR 0 60.8 6.03 70.8 41.8 79.9 1
## CR 90 85.5 10.37 80.8 52.9 118.1 123
## FR 0 92.4 6.03 70.8 73.4 111.4 12 4
## CR 120 114.6 10.37 80.8 82.0 147.2 2345
## CR 150 137.8 10.37 80.8 105.2 170.4 4567
## FR 90 140.4 10.37 80.8 107.8 173.1 3 567
## CR 115 144.9 7.36 76.2 121.7 168.0 56
## FR 120 152.9 10.37 80.8 120.3 185.5 5678
## CR 155 157.1 7.36 76.2 133.9 180.3 5678
## CR 180 157.3 10.37 80.8 124.7 189.9 5678
## FR 115 166.3 7.36 76.2 143.2 189.5 678
## FR 180 170.5 10.37 80.8 137.9 203.1 56789
## CR 210 176.0 10.37 80.8 143.4 208.6 6789
## FR 150 176.8 10.37 80.8 144.2 209.4 6789
## CR 185 182.6 7.36 76.2 159.4 205.7 789
## FR 155 190.4 7.36 76.2 167.2 213.6 89
## FR 210 200.3 10.37 80.8 167.7 232.9 890A
## CR 225 207.0 7.36 76.2 183.9 230.2 90
## FR 185 218.5 7.36 76.2 195.3 241.6 90A
## FR 225 231.4 7.36 76.2 208.3 254.6 0A
## CR 260 239.1 7.36 76.2 215.9 262.3 0A
## FR 260 247.7 7.36 76.2 224.6 270.9 A
##
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
## Conf-level adjustment: sidak method for 22 estimates
## P value adjustment: sidak method for 231 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_all <- cld(emmeans(model_all, ~ Treatment + NrateF),adjust = "Sidak")
```

## Graph

```
all_Nuptake_graph <-
ggplot(Nrate_trial, aes(x=Nrate_kgha, y=N_total_kgha, color=Treatment, shape=Year))+
  geom_point(size=2.5)+
  geom_smooth(aes(group = Treatment),method = lm, level = 0.95)+
  scale_color_manual(values=c("#0072B2", "#FFCC66"), name = "Treatment", labels = c("Continuous rice (CR)", "Fallow (FR)"))+
  scale_x_continuous(name=expression("N rate (kg N ha"^-1*"")"), limits = c(-20, 320), expand = c(0, 0.05))
  scale_y_continuous(name=expression("N uptake (kg N ha"^-1*"")"), limits = c(0, 300), expand = c(0, 0.05))
  #geom_errorbar(aes(ymin=N_total_kgha-N_total_kgha_se, ymax=N_total_kgha+N_total_kgha_se), width=3, position="dodge")
  #geom_vline(xintercept = c(41, 50, 78, 84, 121, 136), linetype = "dashed", color = "black") +
  theme_classic()+
  stat_regline_equation(aes(x=Nrate_kgha, y=N_total_kgha,color=Treatment,group = Treatment,
  label = paste(..rr.label..)),
```

```

    show.legend = FALSE,
    label.x = 200,
    label.y = c(60, 90))+
stat_regline_equation(aes(x=Nrate_kgha, y=N_total_kgha,color=Treatment,group = Treatment,
    label = paste(..eq.label..)),
    show.legend = FALSE,
    label.x = 200,
    label.y = c(70, 100))+
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("Total N uptake: All"))+
theme(legend.position = "bottom")

all_Nuptake_graph

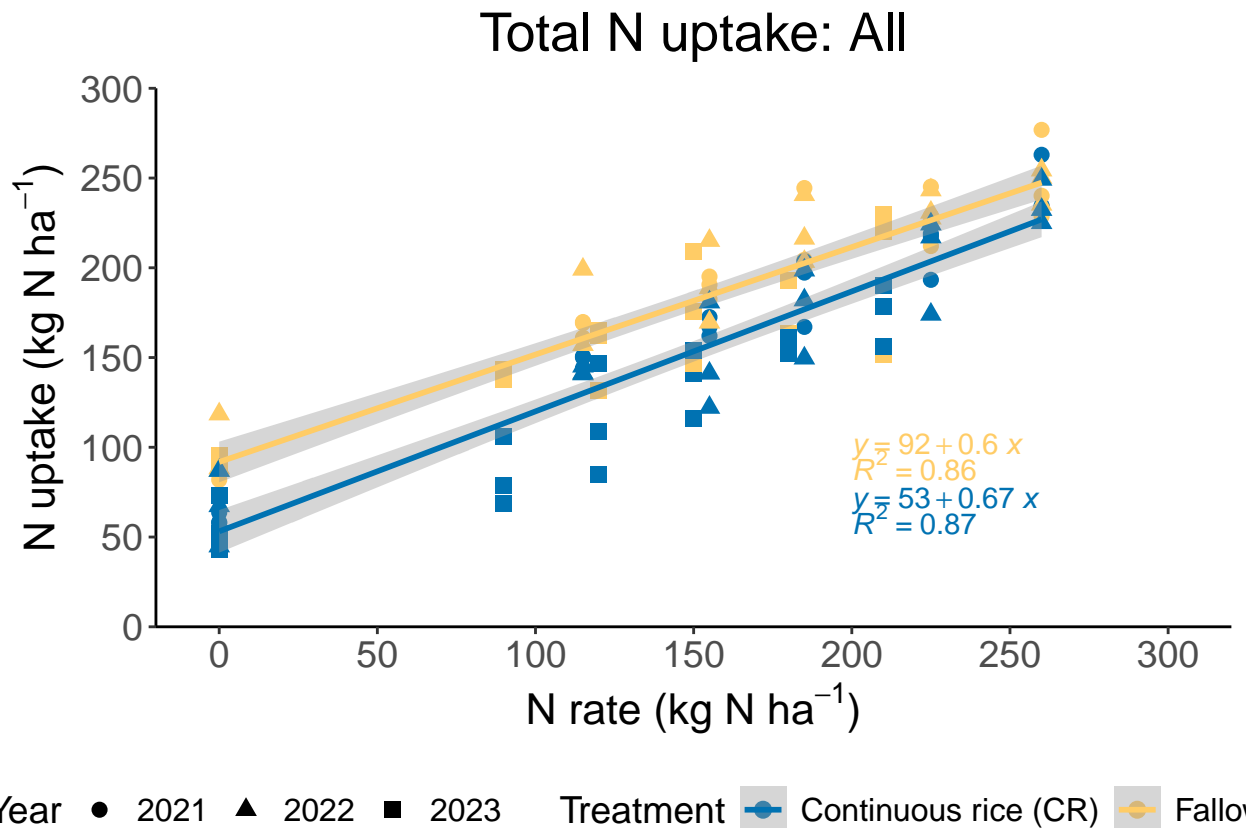
```

```
## '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?
## 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?
## 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

```

N_uptake_maturity <- ggarrange(Nuptake_graph_2021 + theme(legend.position = "none"),
  Nuptake_graph_2022 + theme(legend.position = "none"),
  Nuptake_graph_2023 + theme(legend.position = "none"),
  #all_Nuptake_graph,
  nrow = 1,
  ncol = 3,
  common.legend = TRUE,
  #legend.grob = get_legend(all_Nuptake_graph),
  legend = "bottom")

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

ggsave(filename = "N_uptake_maturity.jpg", # Include the file extension here
  plot = N_uptake_maturity, # Specify the plot
  path = "D:/Academics/UC Davis/School Work/Linguist Lab/Data/R stats/Agronomic paper/Figures",
  dpi = 400,
  height = 20, width = 50, units = "cm")
  
```

## Combine 0N into one table

```
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_all) %>% mutate(Year = "Avg")
                  ) %>% arrange(Year) %>% filter(NrateF == "0") %>%
  mutate(Nuptake = round(emmean, 1))

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