N Uptake overtime

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Contents

Necessary libraries

Read and check data

```
#read data
master = read_excel('N_uptake_over_time.xlsx', sheet = 1)

master$Days <- as.numeric(master$Days)

master <- master %>% mutate_if(is.character, as.factor)
master$Nrate_kgha_F <- as.factor(master$Nrate_kgha)

table(master$Stage)
```

```
##
##  Heading Maturity       PI
##       24       24       24
```

```
table(master$Treatment)
```

```
##
## CR FR
## 36 36
```

```
table(master$Blk)
```

```
##
##  1  2  3  4  5  6
## 12 12 12 12 12 12
```

```
table(master$Year)
```

```
##
## 2021 2022
##   36   36
```

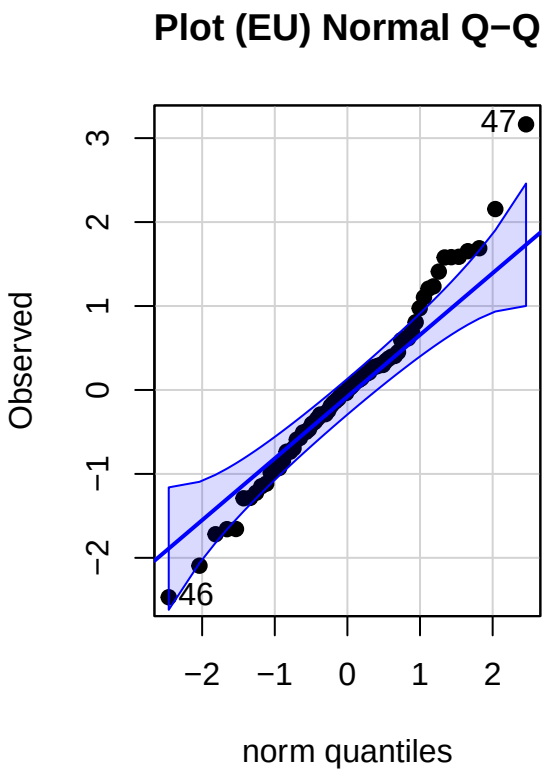
```
#dataset looks good and complete so lets have some fun huehuehue
str(master)
```

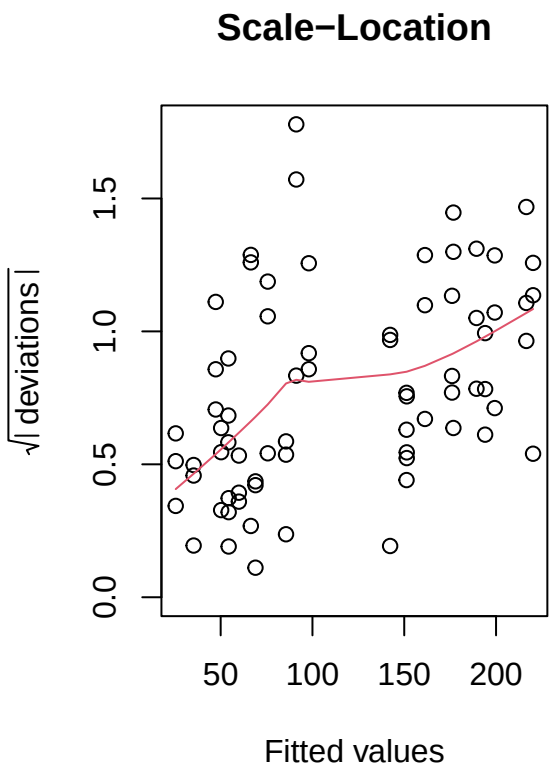
```
## tibble [72 x 11] (S3: tbl_df/tbl/data.frame)
##  $ SampleID    : Factor w/ 72 levels "403-minus-H",..: 37 49 64 46 58 70 40 52 61 43 ...
##  $ Plot        : Factor w/ 24 levels "104","105","109",..: 1 5 10 4 8 12 2 6 9 3 ...
##  $ Stage       : Factor w/ 3 levels "Heading","Maturity",..: 3 3 3 3 3 3 3 3 3 3 ...
##  $ Treatment   : Factor w/ 2 levels "CR","FR": 2 2 2 1 1 1 2 2 2 1 ...
##  $ Year        : num [1:72] 2021 2021 2021 2021 2021 ...
##  $ Topdress    : Factor w/ 1 level "0": 1 1 1 1 1 1 1 1 1 1 ...
##  $ N_total_kgha: num [1:72] 45 54.1 51.7 35.8 38 ...
##  $ Blk         : Factor w/ 6 levels "1","2","3","4",..: 1 2 3 1 2 3 1 2 3 1 ...
##  $ Days        : num [1:72] 47 47 47 47 47 47 47 47 47 47 ...
##  $ Nrate_kgha  : num [1:72] 0 0 0 0 0 0 185 185 185 185 ...
##  $ Nrate_kgha_F: Factor w/ 2 levels "0","185": 1 1 1 1 1 1 2 2 2 2 ...
```

A litmus test to see what is happening

Data looks okay. Treatment effect is very evident.

```
all_data_model <- lm(N_total_kgha ~ Year*Stage*Treatment*Nrate_kgha, data = master)
pls205_diagnostics(all_data_model)
```






```
anova(all_data_model)
```

```
## Analysis of Variance Table
##
## Response: N_total_kgha
##                                  Df Sum Sq Mean Sq  F value    Pr(>F)
## Year                              1    403     403   1.5972  0.212408
## Stage                             2  34409   17205  68.2498 9.245e-15 ***
## Treatment                         1  13267   13267  52.6314 2.995e-09 ***
## Nrate_kgha                        1 227125  227125 900.9964 < 2.2e-16 ***
## Year:Stage                        2   1161     580   2.3021  0.110997
## Year:Treatment                    1   1433    1433   5.6845  0.021116 *
## Stage:Treatment                   2    243     122   0.4828  0.620017
## Year:Nrate_kgha                   1    845     845   3.3525  0.073316 .
## Stage:Nrate_kgha                  2   2930    1465   5.8107  0.005497 **
## Treatment:Nrate_kgha              1    538     538   2.1341  0.150573
## Year:Stage:Treatment              2    285     143   0.5653  0.571926
## Year:Stage:Nrate_kgha             2     93      46   0.1842  0.832333
## Year:Treatment:Nrate_kgha         1    576     576   2.2864  0.137070
## Stage:Treatment:Nrate_kgha        2     70      35   0.1390  0.870543
## Year:Stage:Treatment:Nrate_kgha   2    268     134   0.5322  0.590716
## Residuals                        48  12100     252
## ---
## Signif. codes:  0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1 ’ ’ 1
```

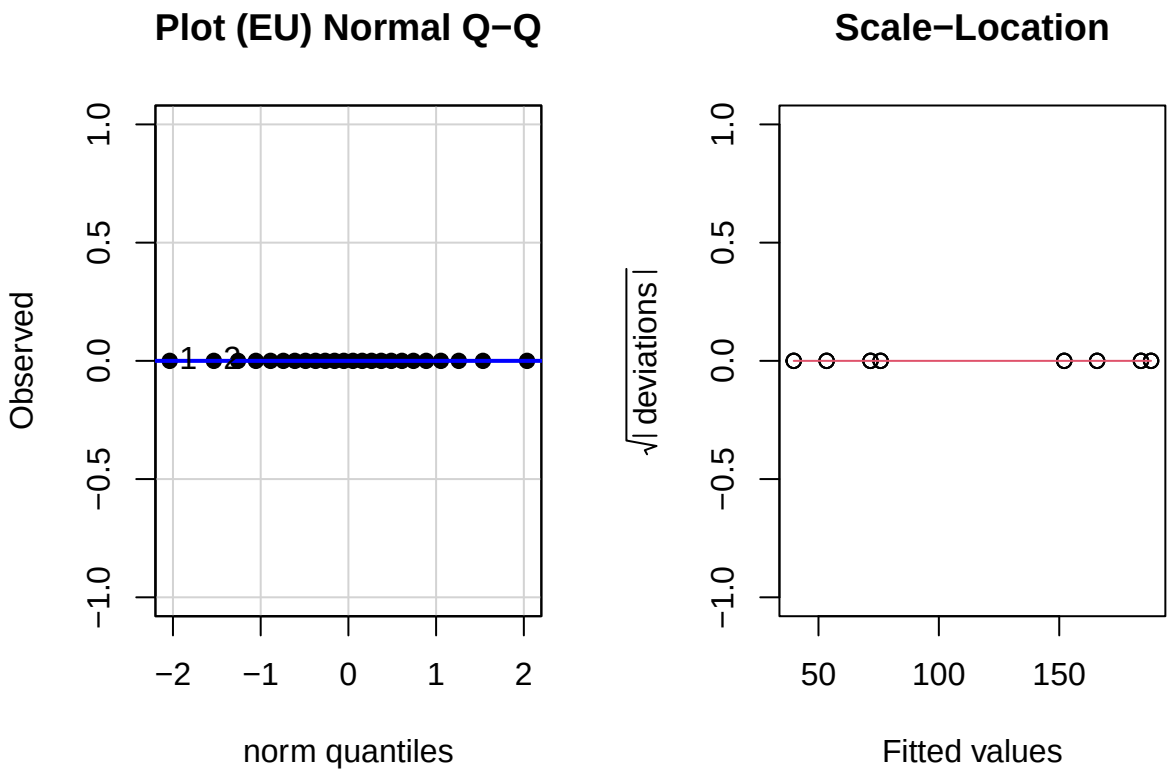
```
all_data_model_lmer <- lmer(N_total_kgha ~ Year*Treatment+Nrate_kgha_F+(1|Blk:Treatment:Nrate_kgha_F), d
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

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

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
pls205_diagnostics(all_data_model_lmer, EU ="Blk:Treatment:Nrate_kgha_F")
```




```
anova(all_data_model)
```

```
## Analysis of Variance Table
##
## Response: N_total_kgha
##                               Df Sum Sq Mean Sq  F value    Pr(>F)
## Year                           1    403     403   1.5972  0.212408
## Stage                          2  34409   17205  68.2498 9.245e-15 ***
## Treatment                      1  13267   13267  52.6314 2.995e-09 ***
## Nrate_kgha                     1 227125  227125 900.9964 < 2.2e-16 ***
## Year:Stage                     2   1161     580   2.3021  0.110997
```

```
## Year:Treatment                    1   1433    1433   5.6845  0.021116 *
## Stage:Treatment                   2    243     122   0.4828  0.620017
## Year:Nrate_kgha                   1    845     845   3.3525  0.073316 .
## Stage:Nrate_kgha                  2   2930    1465   5.8107  0.005497 **
## Treatment:Nrate_kgha              1    538     538   2.1341  0.150573
## Year:Stage:Treatment              2    285     143   0.5653  0.571926
## Year:Stage:Nrate_kgha             2     93      46   0.1842  0.832333
## Year:Treatment:Nrate_kgha         1    576     576   2.2864  0.137070
## Stage:Treatment:Nrate_kgha        2     70      35   0.1390  0.870543
## Year:Stage:Treatment:Nrate_kgha   2    268     134   0.5322  0.590716
## Residuals                        48  12100     252
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Split by Nrate

```
N_zero <- master %>% filter(Nrate_kgha == 0)
N_zero_average <- N_zero
N_zero_2021 <- N_zero %>% filter(Year ==2021)
N_zero_2022 <- N_zero %>% filter(Year ==2022)

N_185 <-master %>% filter(Nrate_kgha == 185)
N_185_average <- N_185
N_185_2021 <- N_185 %>% filter(Year ==2021)
N_185_2022 <- N_185 %>% filter(Year ==2022)
```

0N

2021

Pairise Comparisons 2021

```
N_zero_model_2021 <- lmer(N_total_kgha~Treatment*Stage+(1|Blk:Treatment)+(1|Blk), data = N_zero_2021)
```

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

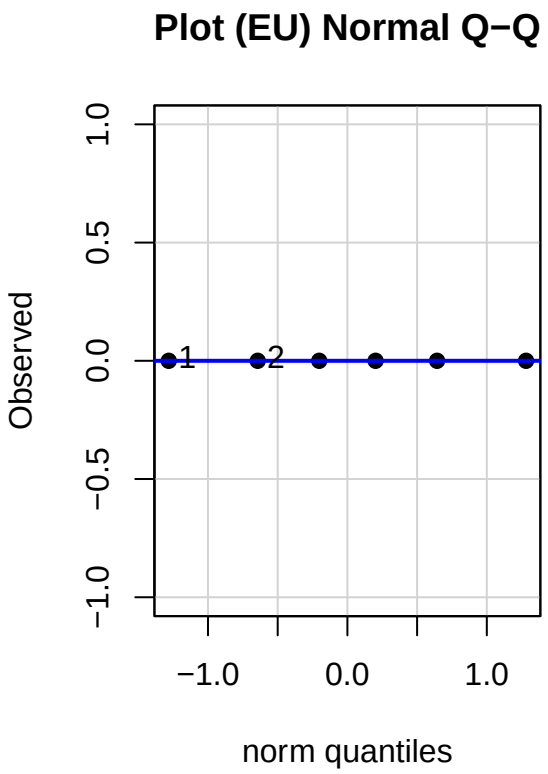
```
anova(N_zero_model_2021)
```

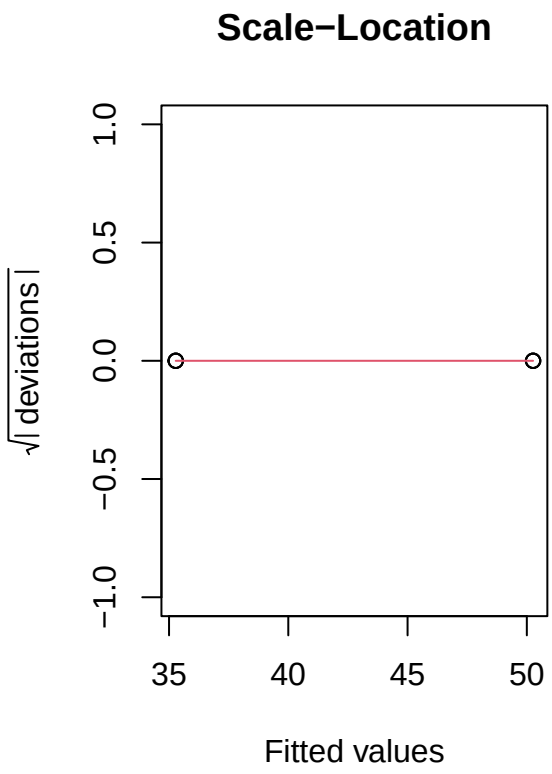
```
## Type III Analysis of Variance Table with Satterthwaite's method
##                  Sum Sq Mean Sq NumDF DenDF  F value    Pr(>F)
## Treatment       1526.59 1526.59     1    12 137.0632 6.364e-08 ***
## Stage           2759.60 1379.80     2    12 123.8837 9.718e-09 ***
## Treatment:Stage  118.66   59.33     2    12   5.3269   0.02209 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(N_zero_model_2021)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: N_total_kgha ~ Treatment * Stage + (1 | Blk:Treatment) + (1 |
##     Blk)
##    Data: N_zero_2021
##
## REML criterion at convergence: 69.6
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.57404 -0.57607 -0.04673  0.65250  1.33533
##
## Random effects:
##  Groups        Name        Variance Std.Dev.
##  Blk:Treatment (Intercept)  0.00    0.000
##  Blk           (Intercept)  0.00    0.000
##  Residual                  11.14    3.337
## Number of obs: 18, groups:  Blk:Treatment, 6; Blk, 3
##
## Fixed effects:
##                            Estimate Std. Error       df t value Pr(>|t|)
## (Intercept)                 54.3614     1.9268  12.0000  28.213 2.44e-12 ***
## TreatmentFR                 14.5980     2.7249  12.0000   5.357 0.000172 ***
## StageMaturity                5.5658     2.7249  12.0000   2.043 0.063704 .
## StagePI                    -19.0803     2.7249  12.0000  -7.002 1.43e-05 ***
## TreatmentFR:StageMaturity  11.0793     3.8536  12.0000   2.875 0.013959 *
## TreatmentFR:StagePI         0.3824     3.8536  12.0000   0.099 0.922584
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) TrtmFR StgMtr StagPI TFR:SM
## TreatmentFR -0.707
## StageMatrty -0.707  0.500
## StagePI     -0.707  0.500  0.500
## TrtmntFR:SM  0.500 -0.707 -0.707 -0.354
## TrtmnFR:SPI  0.500 -0.707 -0.354 -0.707  0.500
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')
```

```
pls205_diagnostics(N_zero_model_2021, EU="Blk:Treatment")
```






```
N_zero_means_2021 = emmeans(N_zero_model_2021,spec = 'Treatment',by = 'Stage')
N_zero_effects_2021 = contrast(N_zero_means_2021, method = 'pairwise', adjust = "tukey")
summary(N_zero_effects_2021)
```

```
## Stage = Heading:
##  contrast estimate   SE df t.ratio p.value
##  CR - FR     -14.6 2.72  9  -5.357  0.0005
##
## Stage = Maturity:
##  contrast estimate   SE df t.ratio p.value
##  CR - FR     -25.7 2.72  9  -9.423  <.0001
##
## Stage = PI:
##  contrast estimate   SE df t.ratio p.value
##  CR - FR     -15.0 2.72  9  -5.498  0.0004
##
## Degrees-of-freedom method: kenward-roger
```

```
N_zero_effects_2021_summary <-
  as.data.frame(summary(N_zero_effects_2021)) %>%
  mutate(
    p_value = case_when(
      p.value < 0.01 ~ "<0.01",           # For p-values less than 0.01
      TRUE ~ sprintf("%.2f", p.value)     # Force two decimal places for all other p-values
    )
```

```
  )%>%
  mutate(Days = case_when(
  Stage %in% c("PI") ~ "47",
  Stage %in% c("Heading") ~ "82",
  Stage %in% c("Maturity") ~ "134",
  TRUE ~ "Other" # This line handles cases where plot is not listed
  )) %>%
  mutate(Days =as.numeric(Days))

cld(N_zero_means_2021)
```

```
## Stage = Heading:
##  Treatment emmean   SE df lower.CL upper.CL .group
##  CR          54.4 1.93 12     50.2     58.6  1
##  FR          69.0 1.93 12     64.8     73.2   2
##
## Stage = Maturity:
##  Treatment emmean   SE df lower.CL upper.CL .group
##  CR          59.9 1.93 12     55.7     64.1  1
##  FR          85.6 1.93 12     81.4     89.8   2
##
## Stage = PI:
##  Treatment emmean   SE df lower.CL upper.CL .group
##  CR          35.3 1.93 12     31.1     39.5  1
##  FR          50.3 1.93 12     46.1     54.5   2
##
## 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.
```

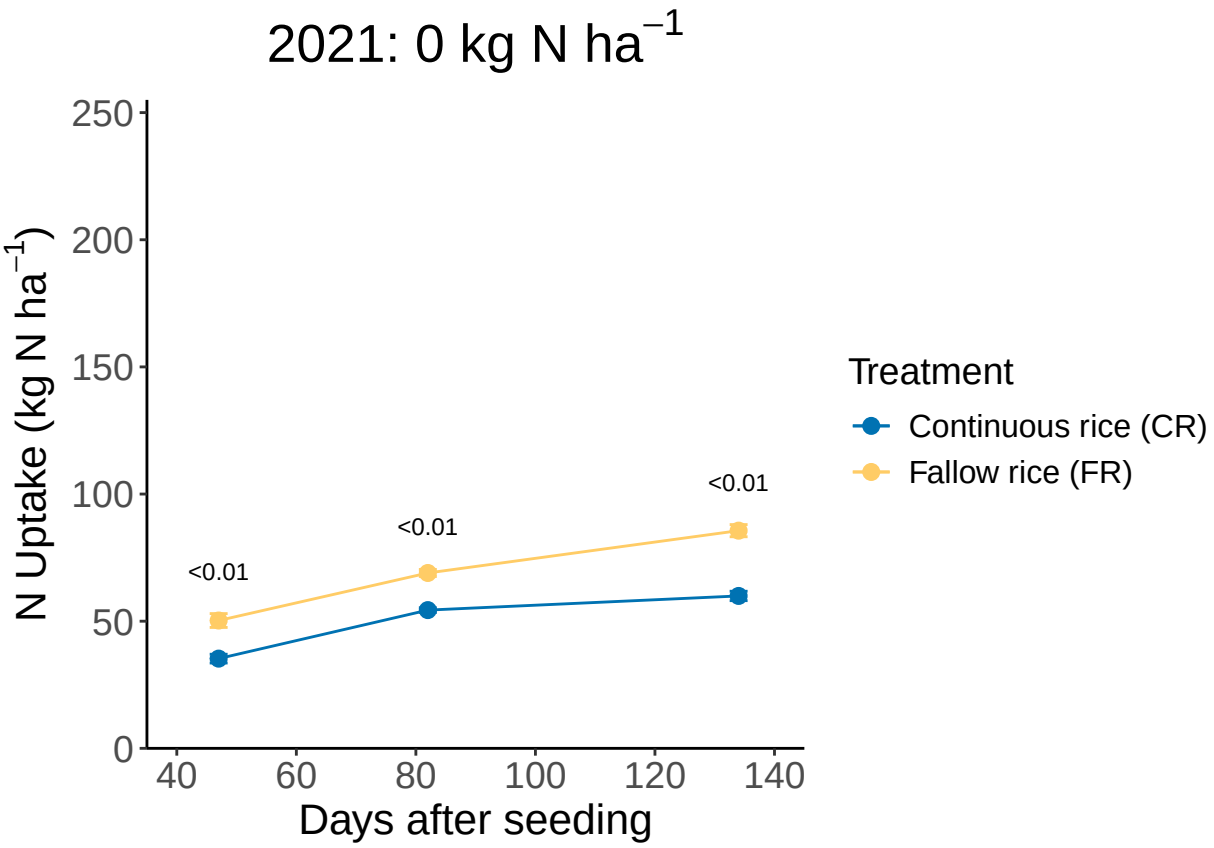
Graph_2021

```
N_zero_graphing_2021 <- N_zero_2021 %>%
                  group_by(Treatment, Days) %>%
                  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))%
                  left_join(N_zero_effects_2021_summary %>% select(Days, p_value), by = "Days")
```

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

```
N_zero_graph_2021 <-
ggplot(N_zero_2021, aes(x=Days, y=N_total_kgha, color=Treatment))+
  geom_point(data=N_zero_graphing_2021, size=2.5)+
  geom_line(data=N_zero_graphing_2021)+
  scale_color_manual(values=c("#0072B2","#FFCC66"), labels = c("Continuous rice (CR)", "Fallow rice (FR
  scale_x_continuous(name="Days after seeding", limits = c(35, 145), expand = c(0, 0), breaks = seq(0,
```

```
  scale_y_continuous(name=expression("N Uptake (kg N ha"^{-1}*")"), limits = c(0, 255), expand = c(0, 0)
  geom_errorbar(data=N_zero_graphing_2021, aes(ymin=N_total_kgha-N_total_kgha_se, ymax=N_total_kgha+N_to
  #geom_vline(xintercept = c(41, 50, 78, 84, 121, 136), linetype = "dashed", color = "black") +
  theme_classic()+
  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"))+
  geom_text(data=N_zero_graphing_2021 %>% filter(Treatment == "FR"), aes(x=Days, y=N_total_kgha+N_total_
  label=sprintf(p_value)), size=3, vjust=-0.5, color="black")+
  ggtitle(expression("2021: 0 kg N ha"^{-1}*""))

N_zero_graph_2021
```



2022

Pairise Comparisons 2022

```
N_zero_model_2022 <- lmer(N_total_kgha~Treatment*Stage+(1|Blk:Treatment)+(1|Blk), data = N_zero_2022)
```

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

```
## Warning: Model failed to converge with 1 negative eigenvalue: -1.6e-01
```

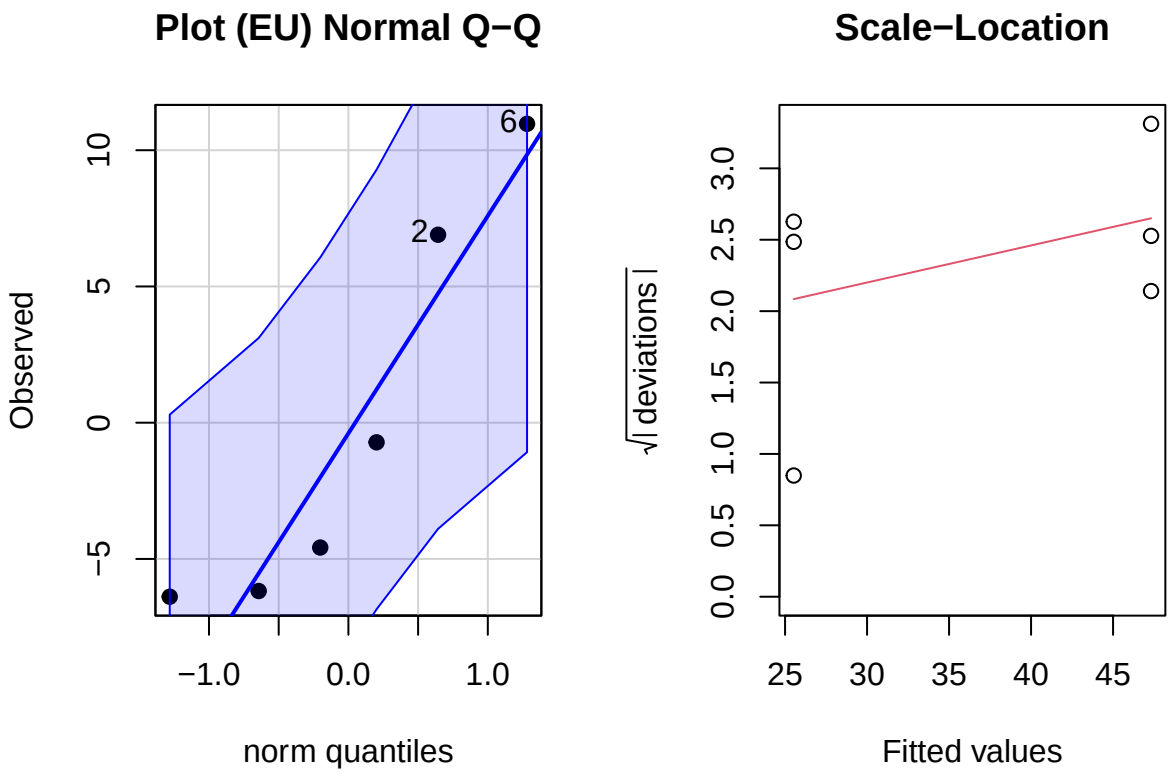
```r
anova(N_zero_model_2022)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##                 Sum Sq Mean Sq NumDF DenDF F value    Pr(>F)
## Treatment        275.1   275.1     1     4  5.0291   0.08837 .
## Stage           6417.4  3208.7     2     8 58.6504 1.662e-05 ***
## Treatment:Stage   99.1    49.6     2     8  0.9059   0.44195
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
summary(N_zero_model_2022)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: N_total_kgha ~ Treatment * Stage + (1 | Blk:Treatment) + (1 |
##     Blk)
##    Data: N_zero_2022
##
## REML criterion at convergence: 98
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.6538 -0.3596  0.1308  0.4196  1.3817
##
## Random effects:
##  Groups        Name        Variance  Std.Dev.
##  Blk:Treatment (Intercept) 1.674e+02 1.294e+01
##  Blk           (Intercept) 2.781e-08 1.668e-04
##  Residual                  5.471e+01 7.397e+00
## Number of obs: 18, groups:  Blk:Treatment, 6; Blk, 3
##
## Fixed effects:
##                            Estimate Std. Error       df t value Pr(>|t|)
## (Intercept)                 54.1877     8.6040   5.6180   6.298 0.000961 ***
## TreatmentFR                 21.4684    12.1679   5.6180   1.764 0.131476
## StageMaturity               12.2418     6.0393   8.0000   2.027 0.077212 .
## StagePI                    -28.6589     6.0393   8.0000  -4.745 0.001454 **
## TreatmentFR:StageMaturity  10.1124     8.5408   8.0000   1.184 0.270393
## TreatmentFR:StagePI         0.3207     8.5408   8.0000   0.038 0.970970
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) TrtmFR StgMtr StagPI TFR:SM
## TreatmentFR -0.707
## StageMatrty -0.351  0.248
## StagePI     -0.351  0.248  0.500
## TrtmntFR:SM  0.248 -0.351 -0.707 -0.354
## TrtmnFR:SPI  0.248 -0.351 -0.354 -0.707  0.500
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')
```

```
pls205_diagnostics(N_zero_model_2022, EU="Blk:Treatment")
```




```
N_zero_means_2022 = emmeans(N_zero_model_2022,spec = 'Treatment',by = 'Stage')
N_zero_effects_2022 = contrast(N_zero_means_2022, method = 'pairwise', adjust = "tukey")
summary(N_zero_effects_2022)
```

```
## Stage = Heading:
##  contrast estimate   SE   df t.ratio p.value
##  CR - FR     -21.5 12.2 2.84  -1.764  0.1811
##
## Stage = Maturity:
##  contrast estimate   SE   df t.ratio p.value
##  CR - FR     -31.6 12.2 2.84  -2.595  0.0855
##
## Stage = PI:
##  contrast estimate   SE   df t.ratio p.value
##  CR - FR     -21.8 12.2 2.84  -1.791  0.1766
##
## Degrees-of-freedom method: kenward-roger
```

```
N_zero_effects_2022_summary <-
  as.data.frame(summary(N_zero_effects_2022)) %>%
  mutate(
    p_value = case_when(
```

```
      p.value < 0.01 ~ "<0.01",           # For p-values less than 0.01
      TRUE ~ sprintf("%.2f", p.value)     # Force two decimal places for all other p-values
    )
  )%>%
  mutate(Days = case_when(
  Stage %in% c("PI") ~ "47",
  Stage %in% c("Heading") ~ "82",
  Stage %in% c("Maturity") ~ "134",
  TRUE ~ "Other" # This line handles cases where plot is not listed
  )) %>%
  mutate(Days =as.numeric(Days))

cld(N_zero_means_2022)
```

```
## Stage = Heading:
##  Treatment emmean  SE   df lower.CL upper.CL .group
##  CR          54.2 8.6 5.62    32.78     75.6  1
##  FR          75.7 8.6 5.62    54.25     97.1  1
##
## Stage = Maturity:
##  Treatment emmean  SE   df lower.CL upper.CL .group
##  CR          66.4 8.6 5.62    45.02     87.8  1
##  FR          98.0 8.6 5.62    76.61    119.4  1
##
## Stage = PI:
##  Treatment emmean  SE   df lower.CL upper.CL .group
##  CR          25.5 8.6 5.62     4.12     46.9  1
##  FR          47.3 8.6 5.62    25.91     68.7  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.
```

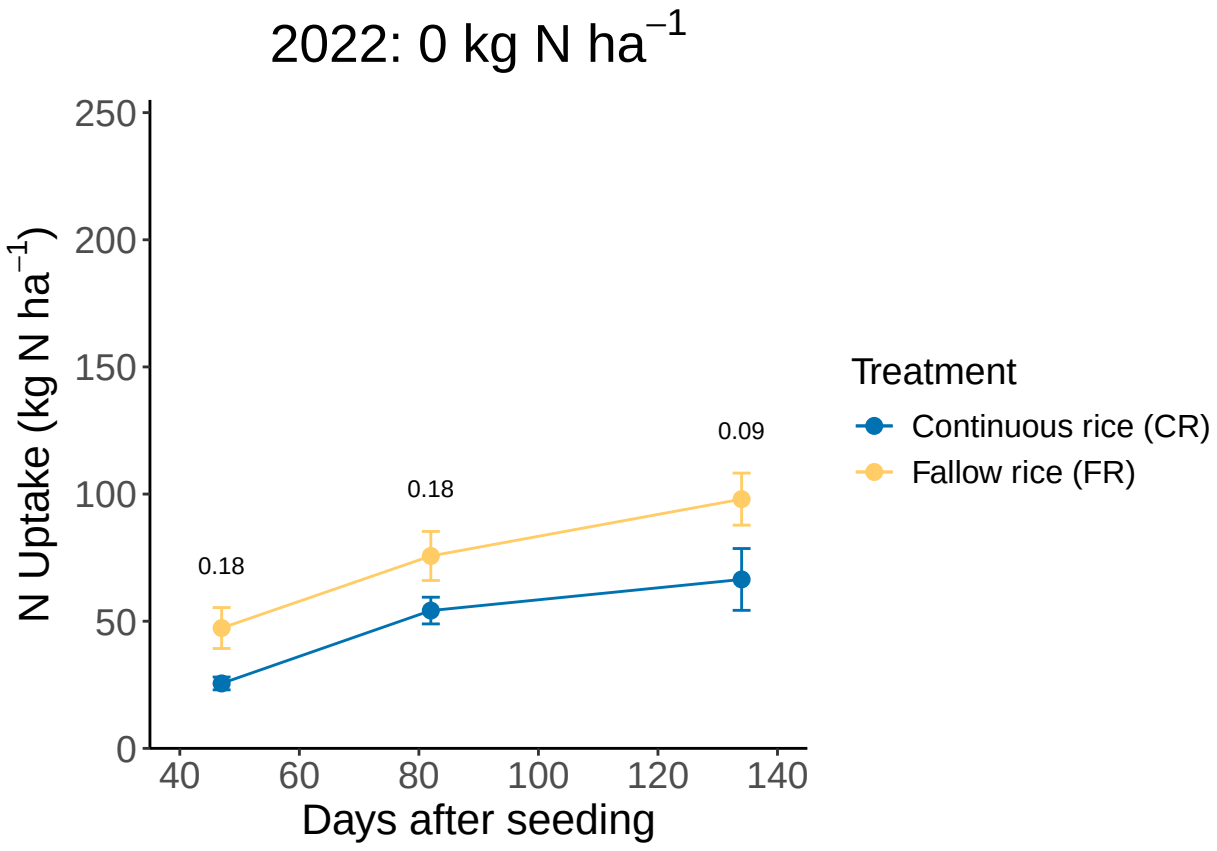
Graph_2022

```
N_zero_graphing_2022 <- N_zero_2022 %>%
                  group_by(Treatment, Days) %>%
                  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))%
                  left_join(N_zero_effects_2022_summary %>% select(Days, p_value), by = "Days")
```

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

```
N_zero_graph_2022 <-
ggplot(N_zero_2022, aes(x=Days, y=N_total_kgha, color=Treatment))+
  geom_point(data=N_zero_graphing_2022, size=2.5)+
  geom_line(data=N_zero_graphing_2022)+
```

```
  scale_color_manual(values=c("#0072B2","#FFCC66"), labels = c("Continuous rice (CR)", "Fallow rice (FR
  scale_x_continuous(name="Days after seeding", limits = c(35, 145), expand = c(0, 0), breaks = seq(0,
  scale_y_continuous(name=expression("N Uptake (kg N ha"^{-1}*")"), limits = c(0, 255), expand = c(0, 0
  geom_errorbar(data=N_zero_graphing_2022, aes(ymin=N_total_kgha-N_total_kgha_se, ymax=N_total_kgha+N_to
  #geom_vline(xintercept = c(41, 50, 78, 84, 121, 136), linetype = "dashed", color = "black") +
  theme_classic()+
  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"))+
  geom_text(data=N_zero_graphing_2022 %>% filter(Treatment == "FR"), aes(x=Days, y=N_total_kgha+N_total_
  label=sprintf(p_value)), size=3, vjust=-0.5, color="black")+
  ggtitle(expression("2022: 0 kg N ha"^{-1}*""))

N_zero_graph_2022
```



Average_zero (Figure 4)

Pairise Comparisons average

```
N_zero_model_average <- lmer(N_total_kgha~Treatment*Stage*Year+(1|Blk:Treatment)+(1|Blk), data = N_zero_
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
anova(N_zero_model_average)
```

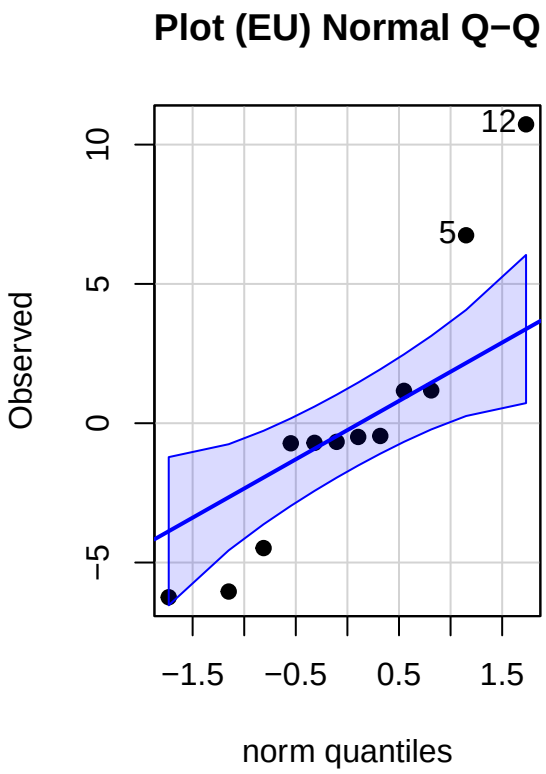
```
## Type III Analysis of Variance Table with Satterthwaite's method
##                      Sum Sq Mean Sq NumDF   DenDF F value  Pr(>F)
## Treatment             16.32  16.323     1  8.8942  0.4879 0.50272
## Stage                384.98 192.492     2 11.6444  5.7536 0.01829 *
## Year                   4.85   4.846     1  7.9885  0.1448 0.71343
## Treatment:Stage        1.62   0.811     2 14.7404  0.0242 0.97610
## Treatment:Year        11.44  11.441     1  7.9091  0.3420 0.57499
## Stage:Year           381.77 190.885     2 16.1479  5.7056 0.01335 *
## Treatment:Stage:Year   1.63   0.814     2 14.7385  0.0243 0.97601
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

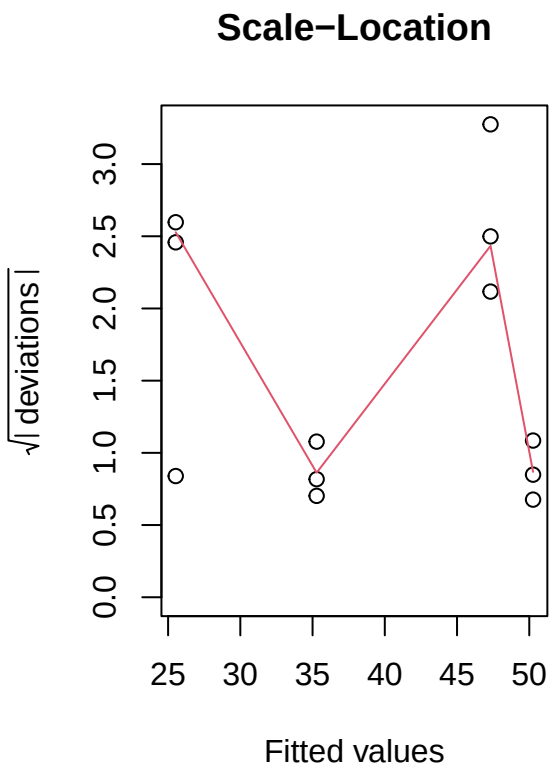
```
summary(N_zero_model_average)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: N_total_kgha ~ Treatment * Stage * Year + (1 | Blk:Treatment) +
##     (1 | Blk)
##    Data: N_zero_average
##
## REML criterion at convergence: 182.6
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.15035 -0.38160  0.02174  0.46997  1.80661
##
## Random effects:
##  Groups        Name        Variance  Std.Dev.
##  Blk:Treatment (Intercept) 8.315e+01 9.118648
##  Blk           (Intercept) 1.366e-06 0.001169
##  Residual                  3.346e+01 5.784090
## Number of obs: 36, groups:  Blk:Treatment, 12; Blk, 6
##
## Fixed effects:
##                                  Estimate Std. Error         df t value
## (Intercept)                     4.054e+02  1.782e+04  1.111e+01   0.023
## TreatmentFR                    -1.387e+04  2.521e+04  9.812e+00  -0.550
## StageMaturity                  -1.349e+04  1.350e+04  1.474e+01  -0.999
## StagePI                         1.934e+04  1.350e+04  1.485e+01   1.432
## Year                           -1.737e-01  8.817e+00  1.111e+01  -0.020
## TreatmentFR:StageMaturity       1.965e+03  1.909e+04  1.368e+01   0.103
## TreatmentFR:StagePI             1.252e+02  1.909e+04  1.403e+01   0.007
## TreatmentFR:Year                6.870e+00  1.247e+01  9.812e+00   0.551
## StageMaturity:Year              6.676e+00  6.679e+00  1.474e+01   1.000
## StagePI:Year                   -9.579e+00  6.679e+00  1.485e+01  -1.434
## TreatmentFR:StageMaturity:Year -9.669e-01  9.445e+00  1.368e+01  -0.102
## TreatmentFR:StagePI:Year       -6.178e-02  9.445e+00  1.403e+01  -0.007
```

```
##                                 Pr(>|t|)
## (Intercept)                        0.982
## TreatmentFR                        0.594
## StageMaturity                      0.334
## StagePI                            0.173
## Year                               0.985
## TreatmentFR:StageMaturity          0.920
## TreatmentFR:StagePI                0.995
## TreatmentFR:Year                   0.594
## StageMaturity:Year                 0.334
## StagePI:Year                       0.172
## TreatmentFR:StageMaturity:Year     0.920
## TreatmentFR:StagePI:Year           0.995
##
## Correlation of Fixed Effects:
##             (Intr) TrtmFR StgMtr StagPI Year   TrFR:SM TrFR:SPI TrFR:Y StgM:Y
## TreatmentFR -0.707
## StageMatrty -0.379  0.268
## StagePI     -0.379  0.268  0.500
## Year        -1.000  0.707  0.379  0.379
## TrtmntFR:SM  0.268 -0.379 -0.707 -0.354 -0.268
## TrtmnFR:SPI  0.268 -0.379 -0.354 -0.707 -0.268  0.500
## TrtmntFR:Yr  0.707 -1.000 -0.268 -0.268 -0.707  0.379   0.379
## StgMtrty:Yr  0.379 -0.268 -1.000 -0.500 -0.379  0.707   0.354    0.268
## StagePI:Yer  0.379 -0.268 -0.500 -1.000 -0.379  0.354   0.707    0.268  0.500
## TrtmFR:SM:Y -0.268  0.379  0.707  0.354  0.268 -1.000  -0.500   -0.379 -0.707
## TrtFR:SPI:Y -0.268  0.379  0.354  0.707  0.268 -0.500  -1.000   -0.379 -0.354
##             StPI:Y TFR:SM:
## TreatmentFR
## StageMatrty
## StagePI
## Year
## TrtmntFR:SM
## TrtmnFR:SPI
## TrtmntFR:Yr
## StgMtrty:Yr
## StagePI:Yer
## TrtmFR:SM:Y -0.354
## TrtFR:SPI:Y -0.707  0.500
## fit warnings:
## Some predictor variables are on very different scales: consider rescaling
```

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






```
N_zero_means_average = emmeans(N_zero_model_average,spec = 'Treatment',by = 'Stage')
```

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

```
N_zero_effects_average = contrast(N_zero_means_average, method = 'pairwise', adjust = "tukey")
summary(N_zero_effects_average)
```

```
## Stage = Heading:
##  contrast estimate   SE   df t.ratio p.value
##  CR - FR     -18.0 6.23 6.03  -2.893  0.0274
##
## Stage = Maturity:
##  contrast estimate   SE   df t.ratio p.value
##  CR - FR     -28.6 6.23 6.03  -4.592  0.0037
##
## Stage = PI:
##  contrast estimate   SE   df t.ratio p.value
##  CR - FR     -18.4 6.23 6.03  -2.949  0.0255
##
## Results are averaged over the levels of: Year
## Degrees-of-freedom method: kenward-roger
```

```
N_zero_effects_average_summary <-
  as.data.frame(summary(N_zero_effects_average)) %>%
```

```
  mutate(
    p_value = case_when(
      p.value < 0.05 ~ "*",           # For p-values less than 0.05
      TRUE ~ sprintf("%.2f", p.value)     # Force two decimal places for all other p-values
    )
  )%>%
  mutate(Days = case_when(
  Stage %in% c("PI") ~ "47",
  Stage %in% c("Heading") ~ "82",
  Stage %in% c("Maturity") ~ "134",
  TRUE ~ "Other" # This line handles cases where plot is not listed
  )) %>%
  mutate(Days =as.numeric(Days))

cld(N_zero_means_average)
```

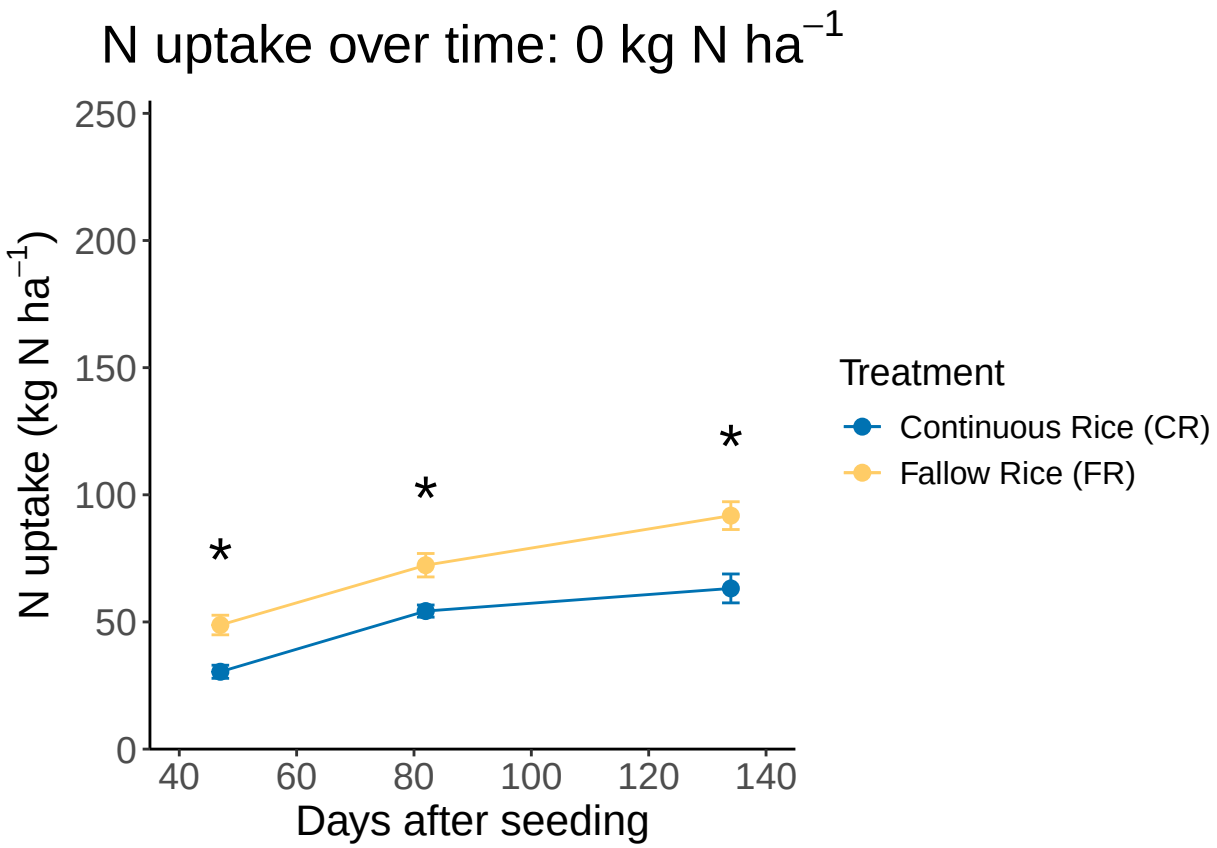
```
## Stage = Heading:
##  Treatment emmean   SE   df lower.CL upper.CL .group
##  CR          54.3 4.41 11.9     44.7     63.9  1
##  FR          72.3 4.41 11.9     62.7     81.9   2
##
## Stage = Maturity:
##  Treatment emmean   SE   df lower.CL upper.CL .group
##  CR          63.2 4.41 11.9     53.6     72.8  1
##  FR          91.8 4.41 11.9     82.2    101.4   2
##
## Stage = PI:
##  Treatment emmean   SE   df lower.CL upper.CL .group
##  CR          30.4 4.41 11.9     20.8     40.0  1
##  FR          48.8 4.41 11.9     39.2     58.4   2
##
## Results are averaged over the levels of: Year
## 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.
```

Graph_average

```
N_zero_graphing_average <- N_zero_average %>%
                  group_by(Treatment, Days) %>%
                  mutate(N_total_kgha_se = sd(N_total_kgha)/sqrt(6)) %>%
                  summarise(N_total_kgha = mean(N_total_kgha), N_total_kgha_se = mean(N_total_kgha_se))%
                  left_join(N_zero_effects_average_summary %>% select(Days, p_value), by = "Days")
```

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

```
N_zero_graph_average <-
ggplot(N_zero_average, aes(x=Days, y=N_total_kgha, color=Treatment))+
  geom_point(data=N_zero_graphing_average, size=2.5)+
  geom_line(data=N_zero_graphing_average)+
  scale_color_manual(values=c("#0072B2","#FFCC66"), labels = c("Continuous Rice (CR)", "Fallow Rice (FR
  scale_x_continuous(name="Days after seeding", limits = c(35, 145), expand = c(0, 0), breaks = seq(0,
  scale_y_continuous(name=expression("N uptake (kg N ha"^{-1}*")"), limits = c(0, 255), expand = c(0, 0
  geom_errorbar(data=N_zero_graphing_average, aes(ymin=N_total_kgha-N_total_kgha_se, ymax=N_total_kgha+
  #geom_vline(xintercept = c(41, 50, 78, 84, 121, 136), linetype = "dashed", color = "black") +
  theme_classic()+
  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"))+
  geom_text(data=N_zero_graphing_average %>% filter(Treatment == "FR"), aes(x=Days, y=N_total_kgha+N_to
  label=sprintf(p_value)), size=8, vjust=-0.5, color="black")+
  ggtitle(expression("N uptake over time: 0 kg N ha"^{-1}*""))

N_zero_graph_average
```



185N

2021

Pairise Comparisons 2021

```
N_185_model_2021 <- lmer(N_total_kgha~Treatment*Stage+(1|Blk:Treatment)+(1|Blk), data = N_185_2021)
```

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

```
anova(N_185_model_2021)
```

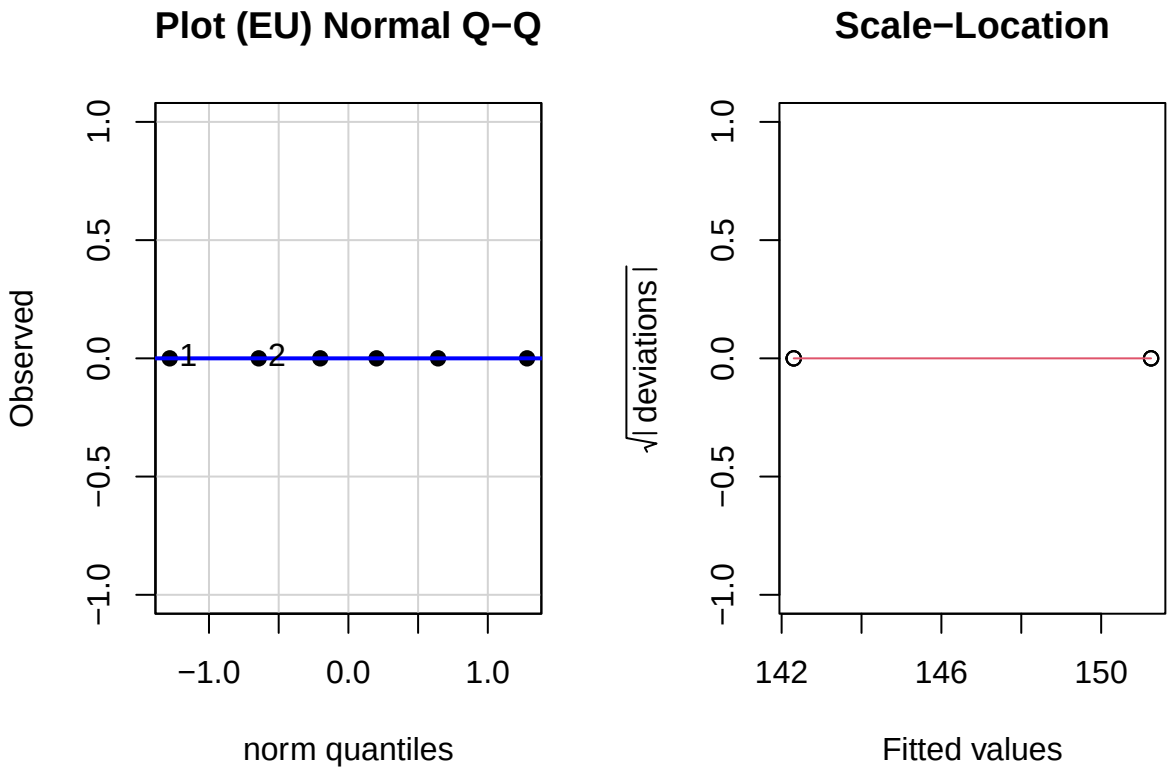
```
## Type III Analysis of Variance Table with Satterthwaite's method
##                 Sum Sq Mean Sq NumDF DenDF F value    Pr(>F)
## Treatment       1463.7  1463.7     1    10  8.3816   0.01597 *
## Stage           9872.2  4936.1     2    10 28.2658 7.671e-05 ***
## Treatment:Stage  248.5   124.3     2    10  0.7115   0.51416
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(N_185_model_2021)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: N_total_kgha ~ Treatment * Stage + (1 | Blk:Treatment) + (1 |
##     Blk)
##    Data: N_185_2021
##
## REML criterion at convergence: 105.2
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.09561 -0.64790  0.08691  0.53149  1.59846
##
## Random effects:
##  Groups        Name        Variance Std.Dev.
##  Blk:Treatment (Intercept)   0.00    0.000
##  Blk           (Intercept)  76.15    8.726
##  Residual                  174.63   13.215
## Number of obs: 18, groups:  Blk:Treatment, 6; Blk, 3
##
## Fixed effects:
##                           Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)                176.043      9.143   8.214  19.255 3.99e-08 ***
## TreatmentFR                 18.011     10.790  10.000   1.669   0.1260
## StageMaturity               13.301     10.790  10.000   1.233   0.2459
## StagePI                    -33.740     10.790  10.000  -3.127   0.0107 *
## TreatmentFR:StageMaturity    9.138     15.259  10.000   0.599   0.5626
## TreatmentFR:StagePI         -9.065     15.259  10.000  -0.594   0.5657
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) TrtmFR StgMtr StagPI TFR:SM
## TreatmentFR -0.590
## StageMatrty -0.590  0.500
## StagePI     -0.590  0.500  0.500
## TrtmntFR:SM  0.417 -0.707 -0.707 -0.354
## TrtmnFR:SPI  0.417 -0.707 -0.354 -0.707  0.500
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')
```

```
pls205_diagnostics(N_185_model_2021, EU="Blk:Treatment")
```




```
N_185_means_2021 = emmeans(N_185_model_2021,spec = 'Treatment',by = 'Stage')
N_185_effects_2021 = contrast(N_185_means_2021, method = 'pairwise', adjust = "tukey")
summary(N_185_effects_2021)
```

```
## Stage = Heading:
##  contrast estimate   SE df t.ratio p.value
##  CR - FR    -18.01 10.8  9  -1.669  0.1294
##
## Stage = Maturity:
##  contrast estimate   SE df t.ratio p.value
##  CR - FR    -27.15 10.8  9  -2.516  0.0330
```

```
##
## Stage = PI:
##  contrast estimate   SE df t.ratio p.value
##  CR - FR     -8.95 10.8  9  -0.829  0.4285
##
## Degrees-of-freedom method: kenward-roger
```

```
N_185_effects_2021_summary <-
  as.data.frame(summary(N_185_effects_2021)) %>%
   mutate(
    p_value = case_when(
      p.value < 0.01 ~ "<0.01",           # For p-values less than 0.01
      TRUE ~ sprintf("%.2f", p.value)     # Force two decimal places for all other p-values
    )
  )%>%
  mutate(Days = case_when(
  Stage %in% c("PI") ~ "47",
  Stage %in% c("Heading") ~ "82",
  Stage %in% c("Maturity") ~ "134",
  TRUE ~ "Other" # This line handles cases where plot is not listed
  )) %>%
  mutate(Days =as.numeric(Days))

cld(N_185_means_2021)
```

```
## Stage = Heading:
##  Treatment emmean   SE   df lower.CL upper.CL .group
##  CR           176 9.14 8.21      155      197  1
##  FR           194 9.14 8.21      173      215  1
##
## Stage = Maturity:
##  Treatment emmean   SE   df lower.CL upper.CL .group
##  CR           189 9.14 8.21      168      210  1
##  FR           216 9.14 8.21      196      237   2
##
## Stage = PI:
##  Treatment emmean   SE   df lower.CL upper.CL .group
##  CR           142 9.14 8.21      121      163  1
##  FR           151 9.14 8.21      130      172  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.
```

Graph_2021

```
N_185_graphing_2021 <- N_185_2021 %>%
                  group_by(Treatment, Days) %>%
                  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))%
                  left_join(N_185_effects_2021_summary %>% select(Days, p_value), by = "Days")
```

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

```
N_185_graph_2021 <-
ggplot(N_185_2021, aes(x=Days, y=N_total_kgha, color=Treatment))+
  geom_point(data=N_185_graphing_2021, size=2.5)+
  geom_line(data=N_185_graphing_2021)+
  scale_color_manual(values=c("#0072B2","#FFCC66"), labels = c("Continuous rice (CR)", "Fallow rice (FR
  scale_x_continuous(name="Days after seeding", limits = c(35, 145), expand = c(0, 0), breaks = seq(0,
  scale_y_continuous(name=expression("N Uptake (kg N ha"^{-1}*")"), limits = c(0, 255), expand = c(0, 0
  geom_errorbar(data=N_185_graphing_2021, aes(ymin=N_total_kgha-N_total_kgha_se, ymax=N_total_kgha+N_to
  #geom_vline(xintercept = c(41, 50, 78, 84, 121, 136), linetype = "dashed", color = "black") +
  theme_classic()+
  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"))+
  geom_text(data=N_185_graphing_2021 %>% filter(Treatment == "FR"), aes(x=Days, y=N_total_kgha+N_total_
  label=sprintf(p_value)), size=3, vjust=-0.5, color="black")+
  ggtitle(expression("2021: 185 kg N ha"^{-1}*""))
```

2022

Pairise Comparisons 2022

```
N_185_model_2022 <- lmer(N_total_kgha~Treatment*Stage+(1|Blk:Treatment)+(1|Blk), data = N_185_2022)

anova(N_185_model_2022)
```

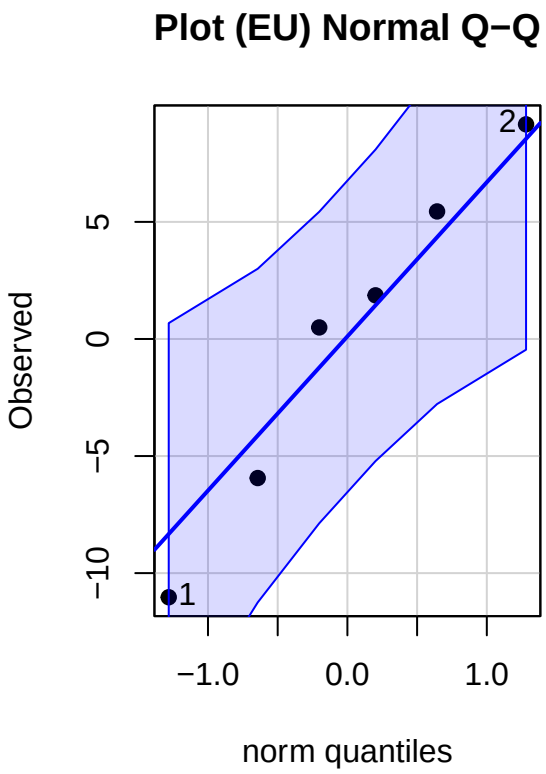
```
## Type III Analysis of Variance Table with Satterthwaite's method
##                   Sum Sq Mean Sq NumDF DenDF F value    Pr(>F)
## Treatment         3419.8  3419.8     1     2 14.3460   0.06317 .
## Stage            19542.8  9771.4     2     8 40.9907 6.248e-05 ***
## Treatment:Stage    400.6   200.3     2     8  0.8402   0.46644
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

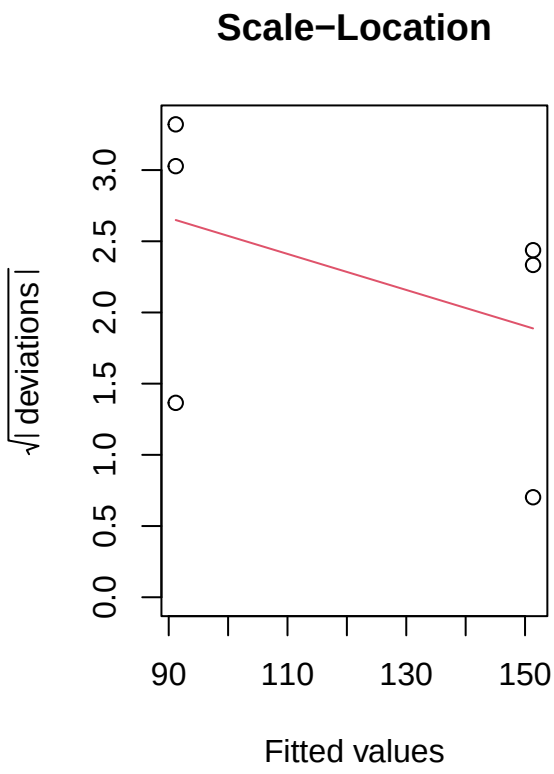
```
summary(N_185_model_2022)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: N_total_kgha ~ Treatment * Stage + (1 | Blk:Treatment) + (1 |
##     Blk)
##    Data: N_185_2022
##
## REML criterion at convergence: 112.2
##
```

```
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.1342 -0.4555 -0.1237  0.4623  1.8516
##
## Random effects:
##  Groups        Name        Variance Std.Dev.
##  Blk:Treatment (Intercept) 153.5    12.39
##  Blk           (Intercept) 132.5    11.51
##  Residual                  238.4    15.44
## Number of obs: 18, groups:  Blk:Treatment, 6; Blk, 3
##
## Fixed effects:
##                            Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)                 161.265     13.220   6.718  12.198 7.88e-06 ***
## TreatmentFR                  38.013     16.162   5.070   2.352 0.064691 .
## StageMaturity                15.493     12.606   8.000   1.229 0.253998
## StagePI                     -70.084     12.606   8.000  -5.559 0.000535 ***
## TreatmentFR:StageMaturity    5.394     17.828   8.000   0.303 0.769949
## TreatmentFR:StagePI         22.158     17.828   8.000   1.243 0.249103
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) TrtmFR StgMtr StagPI TFR:SM
## TreatmentFR -0.611
## StageMatrty -0.477  0.390
## StagePI     -0.477  0.390  0.500
## TrtmntFR:SM  0.337 -0.552 -0.707 -0.354
## TrtmnFR:SPI  0.337 -0.552 -0.354 -0.707  0.500
```

```
pls205_diagnostics(N_185_model_2022, EU="Blk:Treatment")
```






```
N_185_means_2022 = emmeans(N_185_model_2022,spec = 'Treatment',by = 'Stage')
N_185_effects_2022 = contrast(N_185_means_2022, method = 'pairwise', adjust = "tukey")
summary(N_185_effects_2022)
```

```
## Stage = Heading:
##  contrast estimate   SE   df t.ratio p.value
##  CR - FR     -38.0 16.2 5.07  -2.352  0.0647
##
## Stage = Maturity:
##  contrast estimate   SE   df t.ratio p.value
##  CR - FR     -43.4 16.2 5.07  -2.686  0.0429
##
## Stage = PI:
##  contrast estimate   SE   df t.ratio p.value
##  CR - FR     -60.2 16.2 5.07  -3.723  0.0133
##
## Degrees-of-freedom method: kenward-roger
```

```
N_185_effects_2022_summary <-
  as.data.frame(summary(N_185_effects_2022)) %>%
  mutate(
    p_value = case_when(
      p.value < 0.01 ~ "<0.01",           # For p-values less than 0.01
      TRUE ~ sprintf("%.2f", p.value)     # Force two decimal places for all other p-values
    )
```

```
  )%>%
  mutate(Days = case_when(
  Stage %in% c("PI") ~ "47",
  Stage %in% c("Heading") ~ "82",
  Stage %in% c("Maturity") ~ "134",
  TRUE ~ "Other" # This line handles cases where plot is not listed
  )) %>%
  mutate(Days =as.numeric(Days))

cld(N_185_means_2022)
```

```
## Stage = Heading:
##  Treatment emmean   SE   df lower.CL upper.CL .group
##  CR         161.3 13.2 6.72    129.7      193  1
##  FR         199.3 13.2 6.72    167.7      231  1
##
## Stage = Maturity:
##  Treatment emmean   SE   df lower.CL upper.CL .group
##  CR         176.8 13.2 6.72    145.2      208  1
##  FR         220.2 13.2 6.72    188.6      252   2
##
## Stage = PI:
##  Treatment emmean   SE   df lower.CL upper.CL .group
##  CR          91.2 13.2 6.72     59.7      123  1
##  FR         151.4 13.2 6.72    119.8      183   2
##
## 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.
```

Graph_2022

```
N_185_graphing_2022 <- N_185_2022 %>%
                  group_by(Treatment, Days) %>%
                  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))%
                  left_join(N_185_effects_2022_summary %>% select(Days, p_value), by = "Days")
```

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

```
N_185_graph_2022 <-
ggplot(N_185_2022, aes(x=Days, y=N_total_kgha, color=Treatment))+
  geom_point(data=N_185_graphing_2022, size=2.5)+
  geom_line(data=N_185_graphing_2022)+
  scale_color_manual(values=c("#0072B2","#FFCC66"), labels = c("Continuous rice (CR)", "Fallow rice (FR
  scale_x_continuous(name="Days after seeding", limits = c(35, 145), expand = c(0, 0), breaks = seq(0,
```

```
  scale_y_continuous(name=expression("N Uptake (kg N ha"^{-1}*")"), limits = c(0, 255), expand = c(0, 0)
  geom_errorbar(data=N_185_graphing_2022, aes(ymin=N_total_kgha-N_total_kgha_se, ymax=N_total_kgha+N_to
  #geom_vline(xintercept = c(41, 50, 78, 84, 121, 136), linetype = "dashed", color = "black") +
  theme_classic()+
  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"))+
  geom_text(data=N_185_graphing_2022 %>% filter(Treatment == "FR"), aes(x=Days, y=N_total_kgha+N_total_
  label=sprintf(p_value)), size=3, vjust=-0.5, color="black")+
  ggtitle(expression("2022: 185 kg N ha"^{-1}*""))
```

Average_185 (Figure 4)

Pairise Comparisons average

```
N_185_model_average <- lmer(N_total_kgha~Treatment*Stage*Year+(1|Blk:Treatment)+(1|Blk), data = N_185_av
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :
## unable to evaluate scaled gradient
```

```
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :
## Model failed to converge: degenerate Hessian with 1 negative eigenvalues
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
anova(N_185_model_average)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##                       Sum Sq Mean Sq NumDF   DenDF F value  Pr(>F)
## Treatment           1153.93 1153.93     1  7.1071  5.1356 0.05725 .
## Stage               2193.03 1096.52     2 12.3597  4.8801 0.02741 *
## Year                 258.75  258.75     1  3.9990  1.1516 0.34366
## Treatment:Stage      669.74  334.87     2 17.6847  1.4903 0.25226
## Treatment:Year      1253.94 1253.94     1  4.0828  5.5807 0.07615 .
## Stage:Year           847.05  423.53     2 15.9874  1.8849 0.18408
## Treatment:Stage:Year  670.06  335.03     2 17.6847  1.4911 0.25211
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

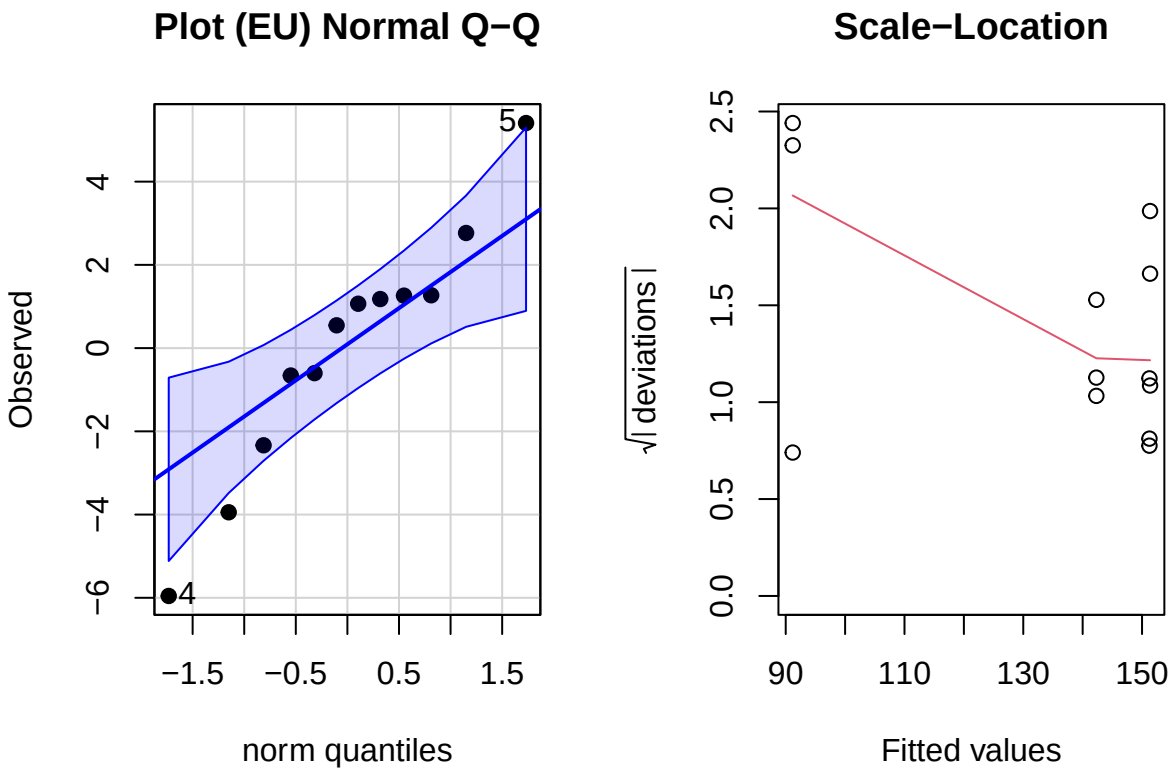
```
summary(N_185_model_average)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: N_total_kgha ~ Treatment * Stage * Year + (1 | Blk:Treatment) +
```

```
##     (1 | Blk)
##    Data: N_185_average
##
## REML criterion at convergence: 219.4
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.17771 -0.49839  0.02605  0.46417  2.14576
##
## Random effects:
##  Groups        Name        Variance Std.Dev.
##  Blk:Treatment (Intercept)  46.41    6.813
##  Blk           (Intercept) 116.44   10.791
##  Residual                  224.69   14.990
## Number of obs: 36, groups:  Blk:Treatment, 12; Blk, 6
##
## Fixed effects:
##                                  Estimate Std. Error         df t value
## (Intercept)                     30043.353  32493.039     14.788   0.925
## TreatmentFR                    -40406.265  38433.779     14.562  -1.051
## StageMaturity                   -4416.433  34989.521     15.789  -0.126
## StagePI                         73416.717  34989.521     15.749   2.098
## Year                              -14.778     16.074     14.788  -0.919
## TreatmentFR:StageMaturity        7575.235  49482.656     15.956   0.153
## TreatmentFR:StagePI            -63111.190  49482.656     15.950  -1.275
## TreatmentFR:Year                   20.002     19.013     14.562   1.052
## StageMaturity:Year                  2.192     17.309     15.789   0.127
## StagePI:Year                      -36.344     17.309     15.749  -2.100
## TreatmentFR:StageMaturity:Year     -3.744     24.478     15.956  -0.153
## TreatmentFR:StagePI:Year           31.223     24.478     15.950   1.276
##                                 Pr(>|t|)
## (Intercept)                       0.3700
## TreatmentFR                       0.3102
## StageMaturity                     0.9011
## StagePI                           0.0524 .
## Year                              0.3726
## TreatmentFR:StageMaturity         0.8802
## TreatmentFR:StagePI               0.2204
## TreatmentFR:Year                  0.3099
## StageMaturity:Year                0.9008
## StagePI:Year                      0.0522 .
## TreatmentFR:StageMaturity:Year    0.8804
## TreatmentFR:StagePI:Year          0.2204
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) TrtmFR StgMtr StagPI Year   TrFR:SM TrFR:SPI TrFR:Y StgM:Y
## TreatmentFR -0.591
## StageMatrty -0.538  0.455
## StagePI     -0.538  0.455  0.500
## Year        -1.000  0.591  0.538  0.538
## TrtmntFR:SM  0.381 -0.644 -0.707 -0.354 -0.381
## TrtmnFR:SPI  0.381 -0.644 -0.354 -0.707 -0.381  0.500
```

```
## TrtmntFR:Yr  0.591 -1.000 -0.455 -0.455 -0.591  0.644   0.644
## StgMtrty:Yr  0.538 -0.455 -1.000 -0.500 -0.538  0.707   0.354    0.455
## StagePI:Yer  0.538 -0.455 -0.500 -1.000 -0.538  0.354   0.707    0.455  0.500
## TrtmFR:SM:Y -0.381  0.644  0.707  0.354  0.381 -1.000  -0.500   -0.644 -0.707
## TrtFR:SPI:Y -0.381  0.644  0.354  0.707  0.381 -0.500  -1.000   -0.644 -0.354
##             StPI:Y TFR:SM:
## TreatmentFR
## StageMatrty
## StagePI
## Year
## TrtmntFR:SM
## TrtmnFR:SPI
## TrtmntFR:Yr
## StgMtrty:Yr
## StagePI:Yer
## TrtmFR:SM:Y -0.354
## TrtFR:SPI:Y -0.707  0.500
## fit warnings:
## Some predictor variables are on very different scales: consider rescaling
## optimizer (nloptwrap) convergence code: 0 (OK)
## unable to evaluate scaled gradient
## Model failed to converge: degenerate  Hessian with 1 negative eigenvalues
```

```
pls205_diagnostics(N_185_model_average, EU="Blk:Treatment")
```



```r
N_185_means_average = emmeans(N_185_model_average,spec = 'Treatment',by = 'Stage')
```

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

```r
N_185_effects_average = contrast(N_185_means_average, method = 'pairwise', adjust = "tukey")
summary(N_185_effects_average)
```

```
## Stage = Heading:
##  contrast estimate   SE   df t.ratio p.value
##  CR - FR     -28.0 9.51 14.5  -2.947  0.0103
##
## Stage = Maturity:
##  contrast estimate   SE   df t.ratio p.value
##  CR - FR     -35.3 9.51 14.5  -3.711  0.0022
##
## Stage = PI:
##  contrast estimate   SE   df t.ratio p.value
##  CR - FR     -34.6 9.51 14.5  -3.635  0.0026
##
## Results are averaged over the levels of: Year
## Degrees-of-freedom method: kenward-roger
```

```r
N_185_effects_average_summary <-
  as.data.frame(summary(N_185_effects_average)) %>%
  mutate(
    p_value = case_when(
      p.value < 0.05 ~ "*",           # For p-values less than 0.05
      TRUE ~ sprintf("%.2f", p.value)     # Force two decimal places for all other p-values
    )
  )%>%
  mutate(Days = case_when(
  Stage %in% c("PI") ~ "47",
  Stage %in% c("Heading") ~ "82",
  Stage %in% c("Maturity") ~ "134",
  TRUE ~ "Other" # This line handles cases where plot is not listed
  )) %>%
  mutate(Days =as.numeric(Days))

cld(N_185_means_average)
```

```
## Stage = Heading:
##  Treatment emmean   SE   df lower.CL upper.CL .group
##  CR           169 8.04 14.8    151.5      186  1
##  FR           197 8.04 14.8    179.5      214   2
##
## Stage = Maturity:
##  Treatment emmean   SE   df lower.CL upper.CL .group
##  CR           183 8.04 14.8    165.9      200  1
##  FR           218 8.04 14.8    201.2      235   2
##
## Stage = PI:
##  Treatment emmean   SE   df lower.CL upper.CL .group
```

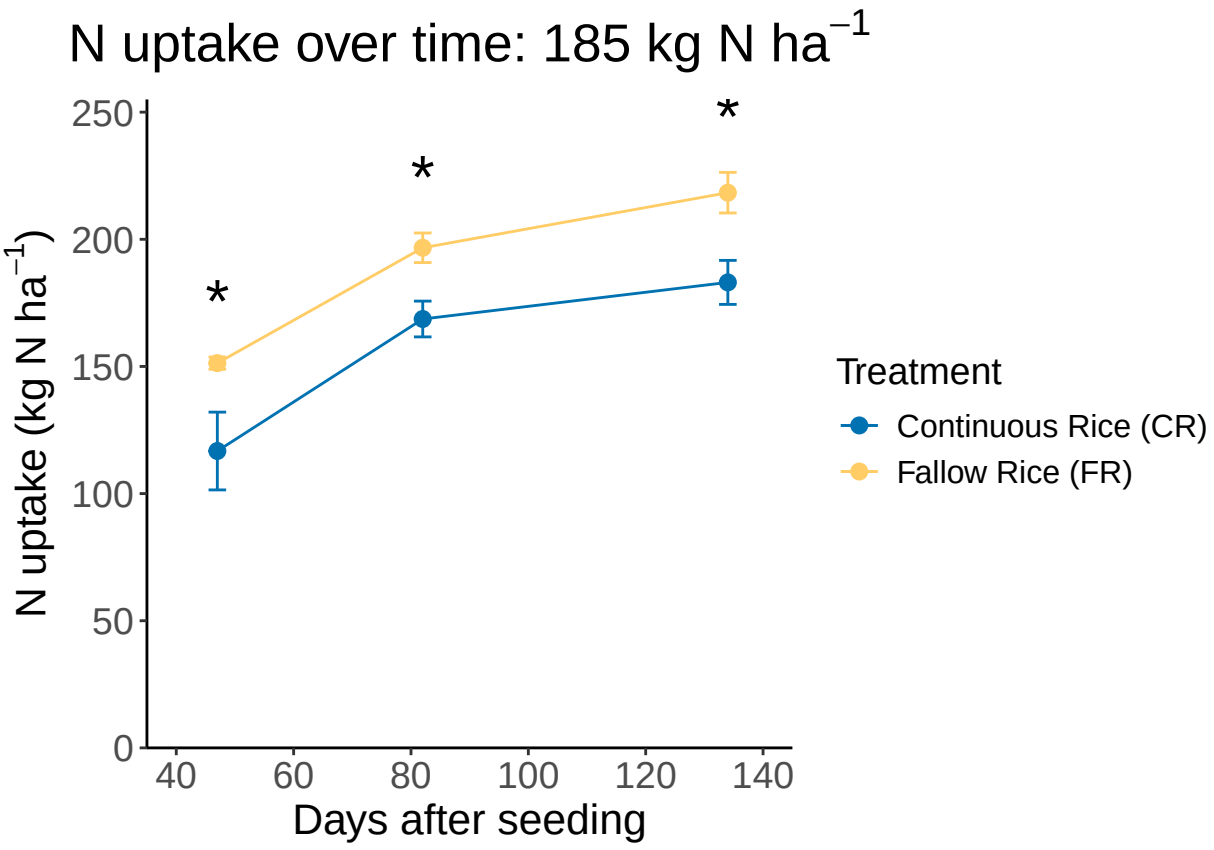
```
##  CR           117 8.04 14.8     99.6      134  1
##  FR           151 8.04 14.8    134.1      168   2
##
## Results are averaged over the levels of: Year
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
## significance level used: alpha = 0.05
## NOTE: If two or more 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.
```

Graph_average

```
N_185_graphing_average <- N_185_average %>%
                  group_by(Treatment, Days) %>%
                  mutate(N_total_kgha_se = sd(N_total_kgha)/sqrt(6)) %>%
                  summarise(N_total_kgha = mean(N_total_kgha), N_total_kgha_se = mean(N_total_kgha_se))%
                  left_join(N_185_effects_average_summary %>% select(Days, p_value), by = "Days")
```

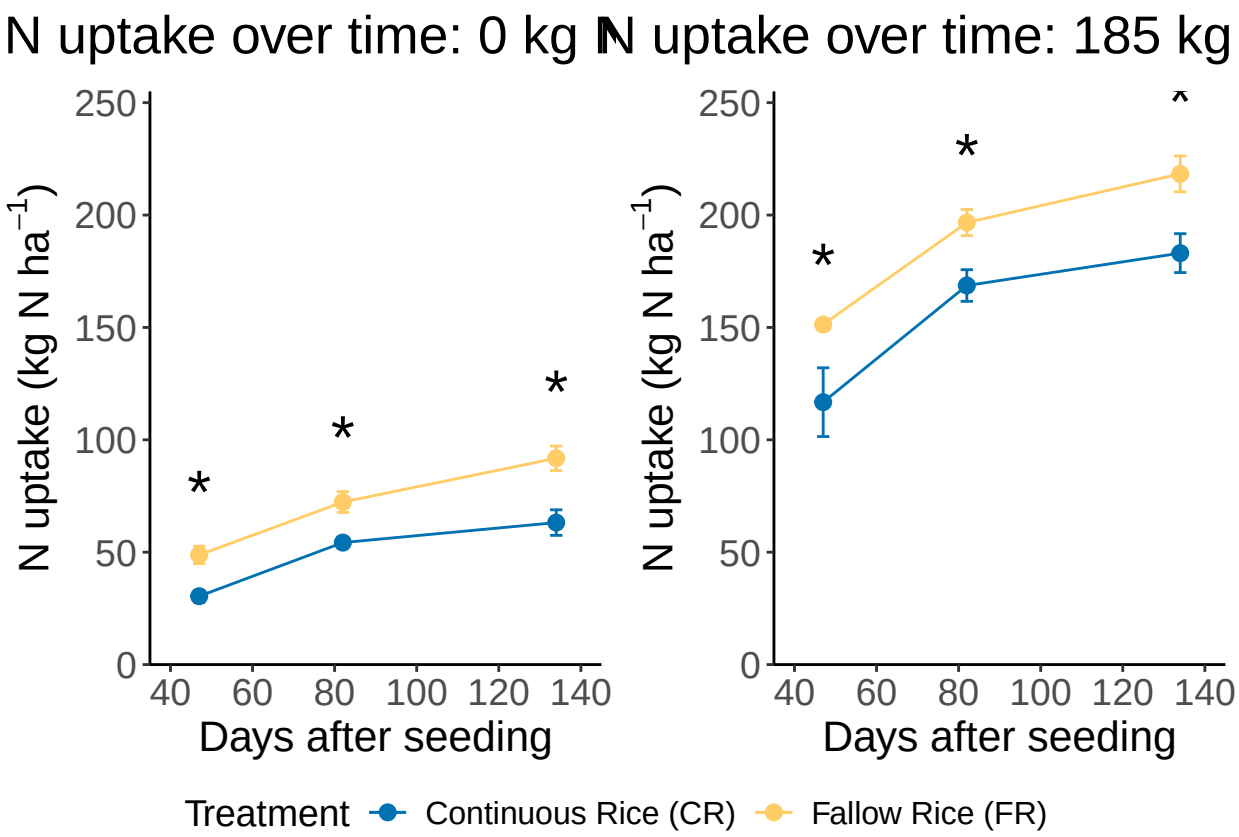
```
## `summarise()` has grouped output by 'Treatment'. You can override using the
## `.groups` argument.
```

```
N_185_graph_average <-
ggplot(N_185_average, aes(x=Days, y=N_total_kgha, color=Treatment))+
  geom_point(data=N_185_graphing_average, size=2.5)+
  geom_line(data=N_185_graphing_average)+
  scale_color_manual(values=c("#0072B2","#FFCC66"), labels = c("Continuous Rice (CR)", "Fallow Rice (FR)
  scale_x_continuous(name="Days after seeding", limits = c(35, 145), expand = c(0, 0), breaks = seq(0,
  scale_y_continuous(name=expression("N uptake (kg N ha"^{-1}*")"), limits = c(0, 255), expand = c(0, 0)
  geom_errorbar(data=N_185_graphing_average, aes(ymin=N_total_kgha-N_total_kgha_se, ymax=N_total_kgha+N_
  #geom_vline(xintercept = c(41, 50, 78, 84, 121, 136), linetype = "dashed", color = "black") +
  theme_classic()+
  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"))+
  geom_text(data=N_185_graphing_average %>% filter(Treatment == "FR"), aes(x=Days, y=N_total_kgha+N_tota
  label=sprintf(p_value)), size=8, vjust=-0.5, color="black")+
  ggtitle(expression("N uptake over time: 185 kg N ha"^{-1}*""))

N_185_graph_average
```



Combine graphs

```
all_N_uptake_overtime <- ggarrange(#N_zero_graph_2021,
                                   #N_zero_graph_2022,
                                   N_zero_graph_average,
                                   #N_185_graph_2021,
                                   #N_185_graph_2022,
                                   N_185_graph_average,
                  nrow = 1,
                  ncol = 2,
                  common.legend = TRUE,
                  legend= "bottom")

all_N_uptake_overtime
```




```
ggsave(all_N_uptake_overtime,
       filename = "all_N_uptake_overtime.jpg",
       path = "D:/Academics/UC Davis/School Work/Linquist Lab/Data/R stats/Agronomic paper/Figures",
       height = 20, width = 30,
       units = "cm", dpi=400)
```