

N Uptake overtime

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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)
```

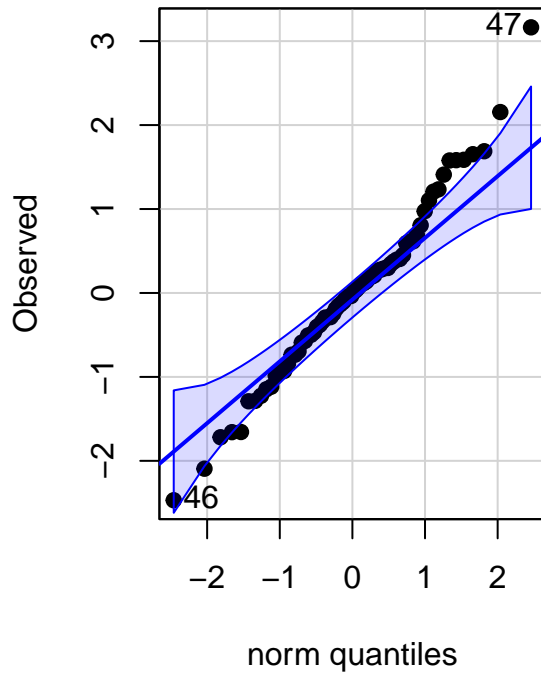
```
## tibble [72 x 11] (S3: tbl_df/tbl/data.frame)
##  $ SampleID      : Factor w/ 72 levels "403-minus-H",...: 37 49 64 46 58 70 40 52 61 43 ...
##  $ Plot           : Factor w/ 24 levels "104","105","109",...: 1 5 10 4 8 12 2 6 9 3 ...
##  $ Stage          : Factor w/ 3 levels "Heading","Maturity",...: 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 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

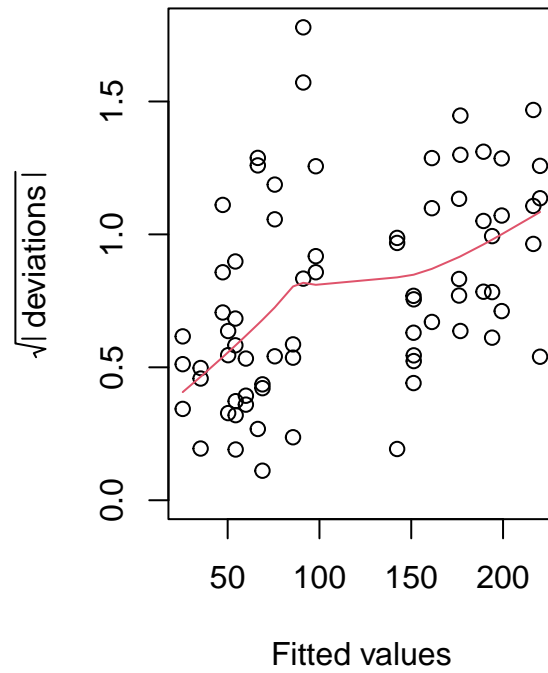
Data looks okay. Treatment effect is very evident.

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

Plot (EU) Normal Q-Q



Scale-Location



```
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),

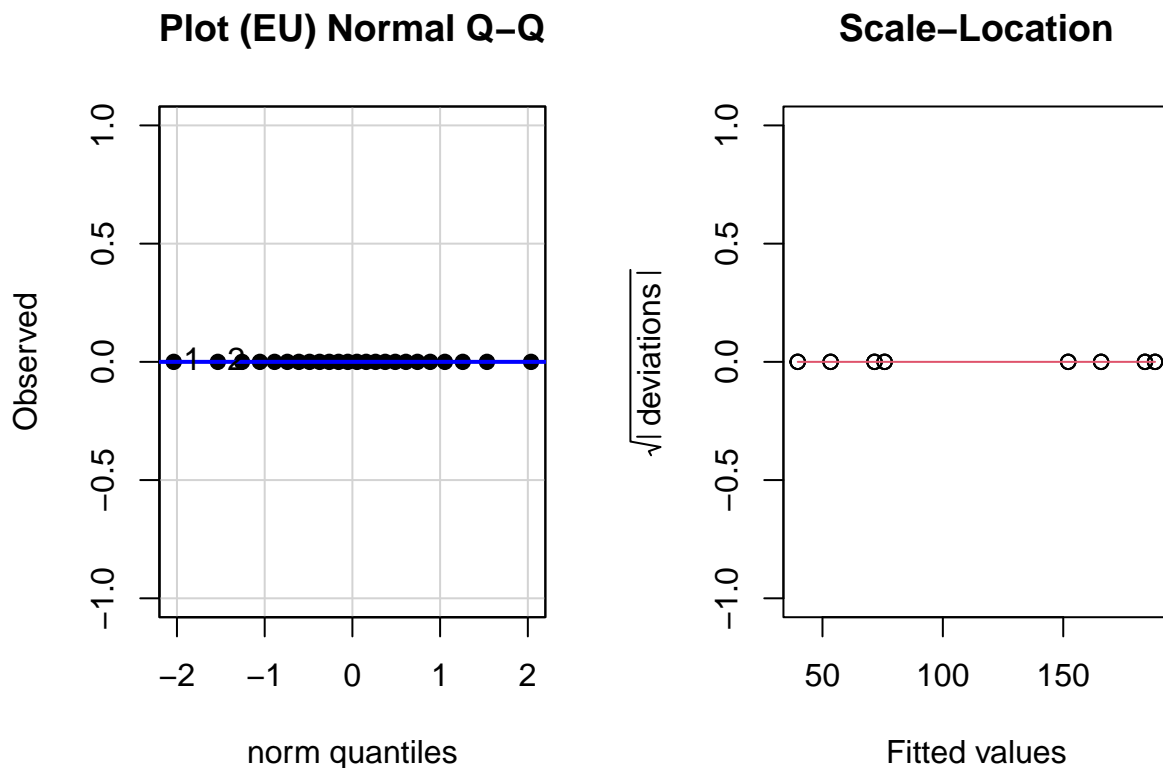
## Warning: Some predictor variables are on very different scales: consider
## rescaling

## 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
##
## Year
## Stage
## Treatment
## Nrate_kgha
## Year:Stage

```

	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')
```

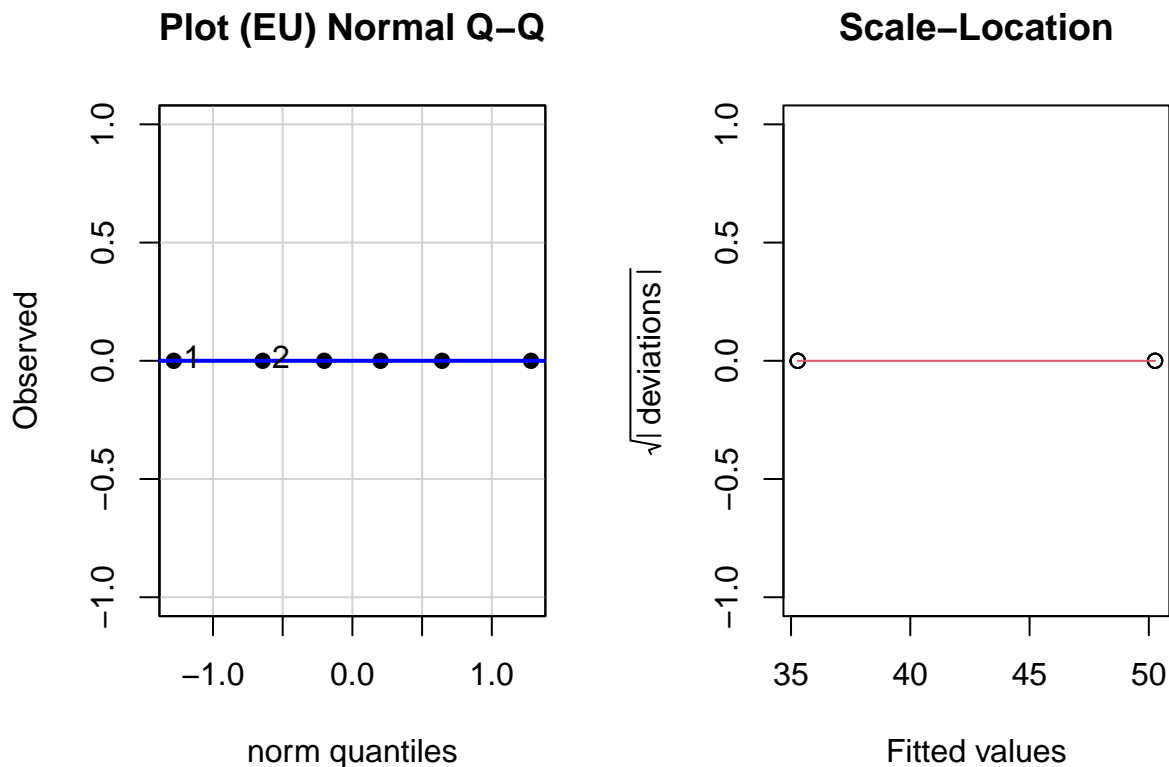
```
anova(N_zero_model_2021)
```

```
## 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, 145, 35))

```

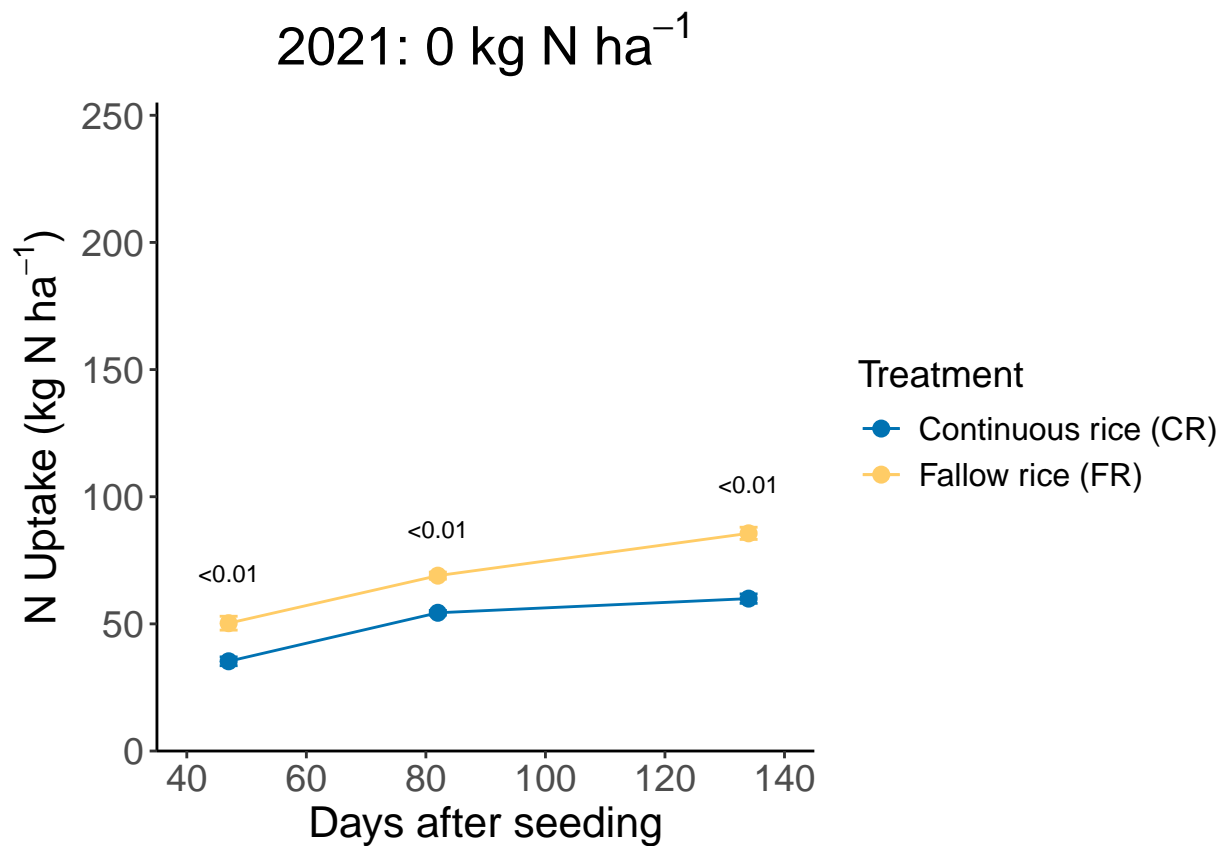


```

scale_y_continuous(name=expression("N Uptake (kg N ha"^{-1}*")"), limits = c(0, 255), expand = c(0, 0.05))
geom_errorbar(data=N_zero_graphing_2021, aes(ymin=N_total_kgha-N_total_kgha_se, ymax=N_total_kgha+N_total_kgha_se),
#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_kgha_se),
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)
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)

```

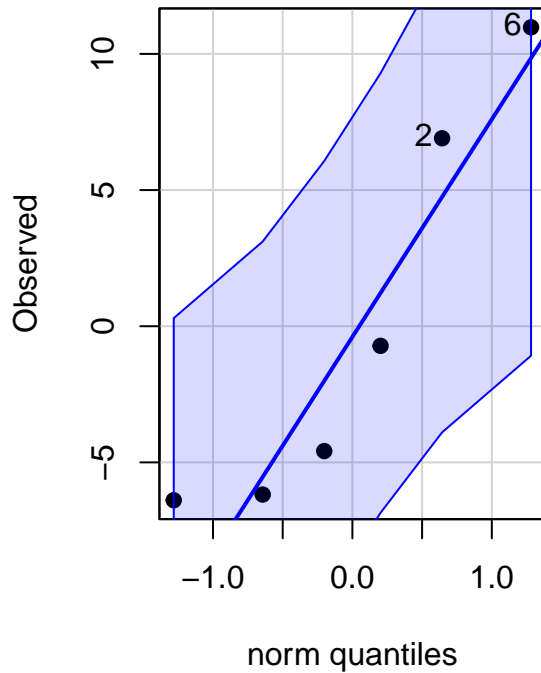
```
## Treatment      275.1   275.1      1 4.0002  5.0292  0.08836 .
## Stage          6417.4 3208.7      2 7.9999 58.6496 1.662e-05 ***
## Treatment:Stage  99.1    49.6      2 7.9999  0.9059  0.44195
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(N_zero_model_2022)
```

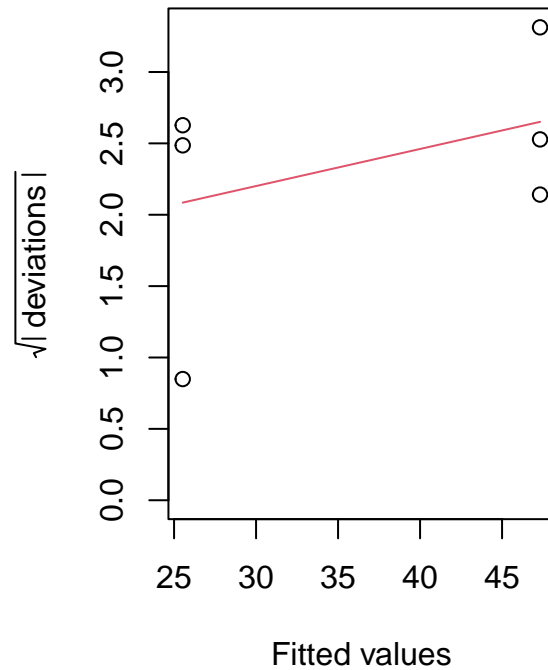
```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: N_total_kgha ~ Treatment * Stage + (1 | Blk:Treatment) + (1 |
##      Blk)
##      Data: N_zero_2022
##
## REML criterion at convergence: 98
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.6538 -0.3596  0.1308  0.4195  1.3817
##
## Random effects:
##      Groups      Name      Variance Std.Dev.
## Blk:Treatment (Intercept) 1.674e+02 12.937192
## Blk           (Intercept) 2.318e-05  0.004815
## Residual                        5.471e+01  7.396617
## Number of obs: 18, groups: Blk:Treatment, 6; Blk, 3
##
## Fixed effects:
##
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)      54.1877      8.6039    5.6183   6.298 0.000961 ***
## TreatmentFR       21.4684     12.1677    5.6183   1.764 0.131470
## StageMaturity     12.2418      6.0393    7.9999   2.027 0.077214 .
## StagePI          -28.6589      6.0393    7.9999  -4.745 0.001454 **
## TreatmentFR:StageMaturity 10.1124      8.5409    7.9999   1.184 0.270396
## TreatmentFR:StagePI      0.3207      8.5409    7.9999   0.038 0.970971
## ---
## 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
```

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

Plot (EU) Normal Q-Q



Scale-Location



```
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, 145, 35))

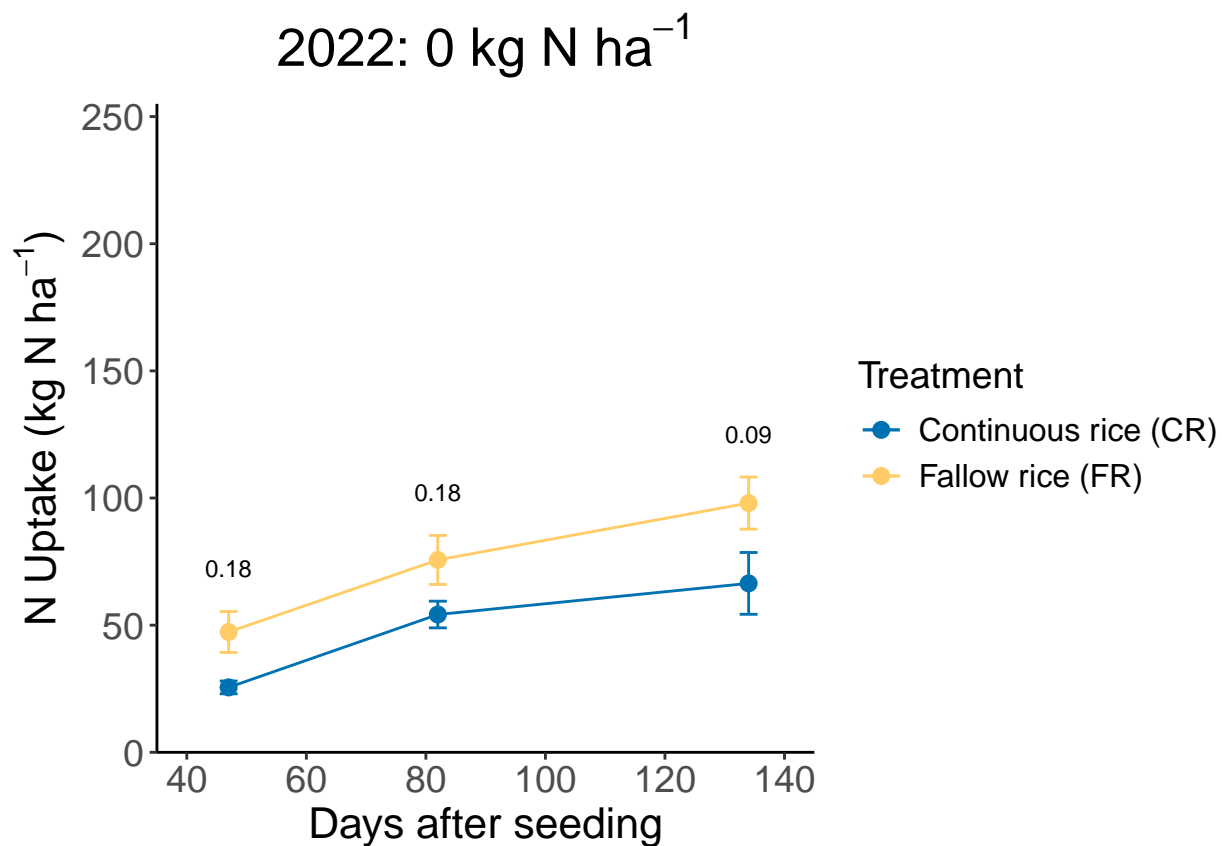
```

```

scale_y_continuous(name=expression("N Uptake (kg N ha"^{-1}*")"), limits = c(0, 255), expand = c(0, 0.05))
geom_errorbar(data=N_zero_graphing_2022, aes(ymin=N_total_kgha-N_total_kgha_se, ymax=N_total_kgha+N_total_kgha_se),
#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_kgha_se),
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

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

```

```
## 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   16.321     1   8.9804   0.4878 0.50257
## Stage        384.98  192.491     2  11.7612   5.7539 0.01809 *
## Year           4.85    4.845     1   7.9968   0.1448 0.71343
## Treatment:Stage    1.62    0.810     2  14.8449   0.0242 0.97610
## Treatment:Year     11.44   11.439     1   8.0245   0.3419 0.57478
## Stage:Year        381.77  190.885     2  16.1494   5.7059 0.01335 *
## Treatment:Stage:Year  1.63    0.814     2  14.8432   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
## -2.1504 -0.3816  0.0217  0.4700  1.8066
##
## Random effects:
##   Groups             Name             Variance Std.Dev.
## Blk:Treatment (Intercept) 83.16       9.119
## Blk              (Intercept)  0.00       0.000
## Residual                    33.45       5.784
## 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  1.192e+01   0.023
## TreatmentFR  -1.387e+04  2.521e+04  1.189e+01  -0.550
## StageMaturity -1.349e+04  1.350e+04  1.593e+01  -0.999
## StagePI       1.934e+04  1.350e+04  1.595e+01   1.432
## Year          -1.737e-01  8.817e+00  1.192e+01  -0.020
## TreatmentFR:StageMaturity  1.965e+03  1.909e+04  1.597e+01   0.103
## TreatmentFR:StagePI       1.252e+02  1.909e+04  1.598e+01   0.007
## TreatmentFR:Year          6.870e+00  1.247e+01  1.189e+01   0.551
## StageMaturity:Year        6.676e+00  6.679e+00  1.593e+01   1.000
## StagePI:Year             -9.579e+00  6.679e+00  1.595e+01  -1.434
## TreatmentFR:StageMaturity:Year -9.669e-01  9.445e+00  1.597e+01  -0.102
## TreatmentFR:StagePI:Year   -6.178e-02  9.445e+00  1.598e+01  -0.007
##              Pr(>|t|)
```

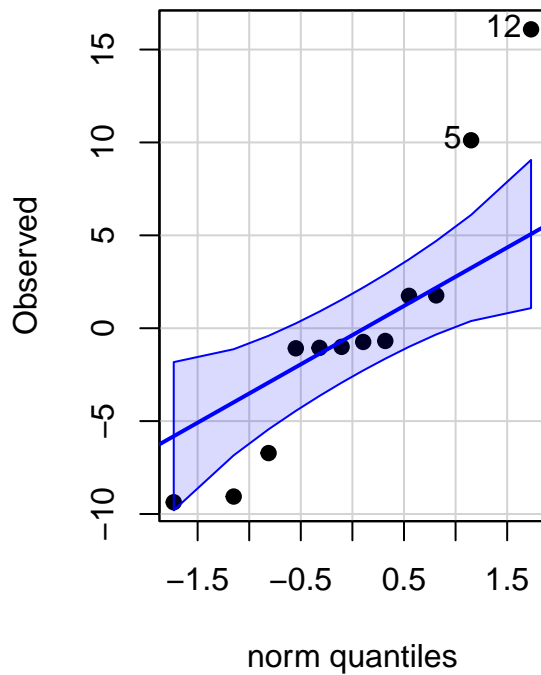
```

## (Intercept)                0.982
## TreatmentFR                0.592
## StageMaturity              0.333
## StagePI                    0.171
## Year                       0.985
## TreatmentFR:StageMaturity  0.919
## TreatmentFR:StagePI       0.995
## TreatmentFR:Year           0.592
## StageMaturity:Year         0.332
## StagePI:Year               0.171
## 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
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')

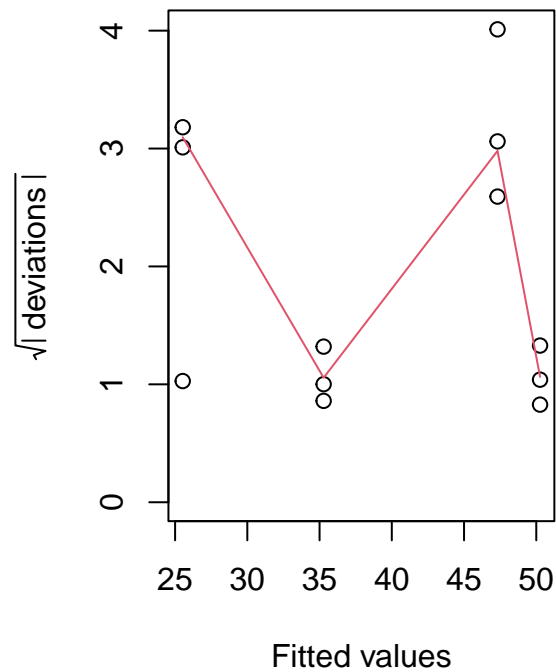
```

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

Plot (EU) Normal Q-Q



Scale-Location



```
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 -2.892 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.

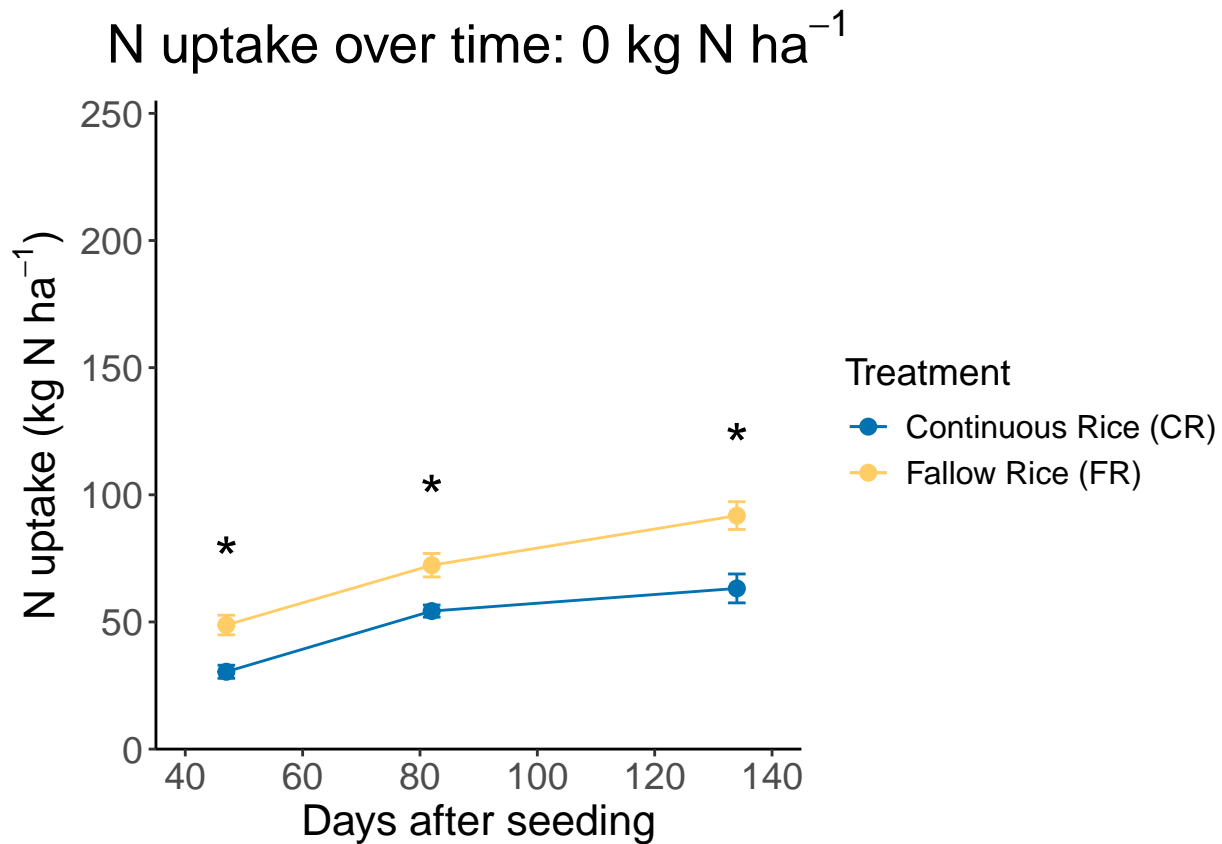
```

```

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, 145, 20))+
  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+N_total_kgha_se))+
  #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_total_kgha_se,
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)
```

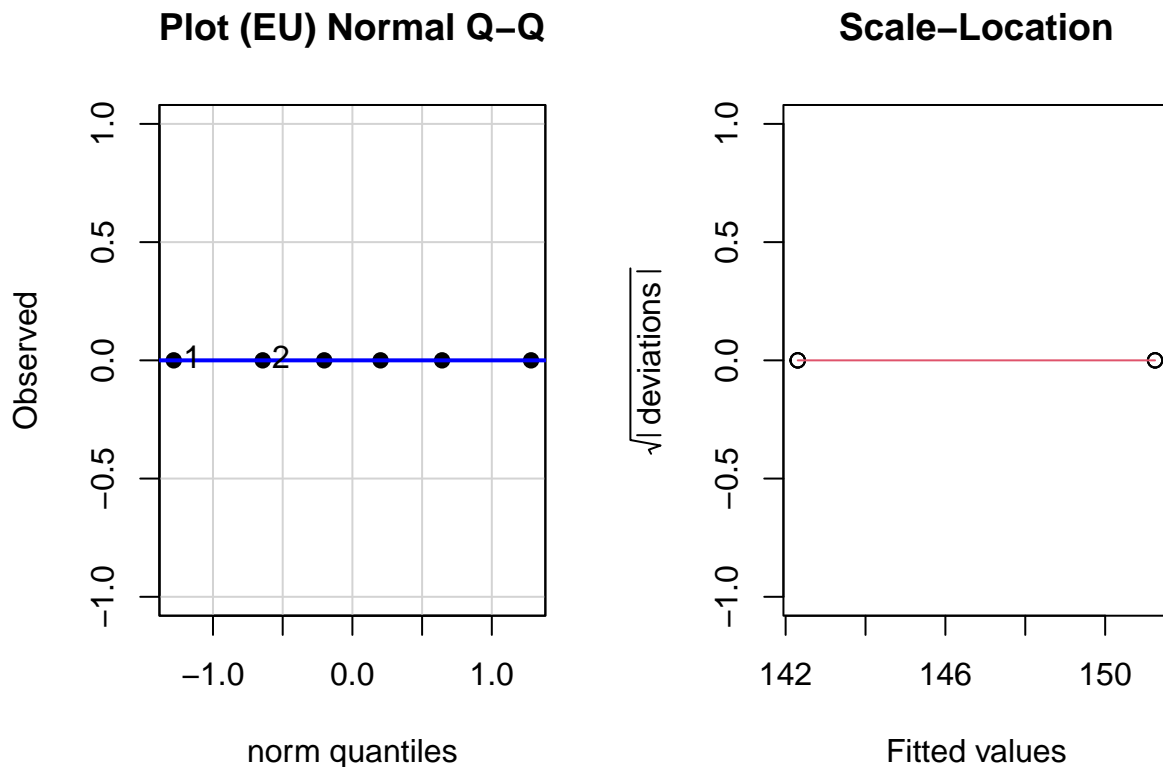
```
## Type III Analysis of Variance Table with Satterthwaite's method
##               Sum Sq Mean Sq NumDF DenDF F value    Pr(>F)
## Treatment      1463.7   1463.7     1    10  8.3816   0.01597 *
## Stage          9872.2   4936.1     2    10 28.2658 7.671e-05 ***
## Treatment:Stage  248.5    124.3     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, 145, 35)),
  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_total_kgha_se),
  #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_kgha_se,
  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
##
```

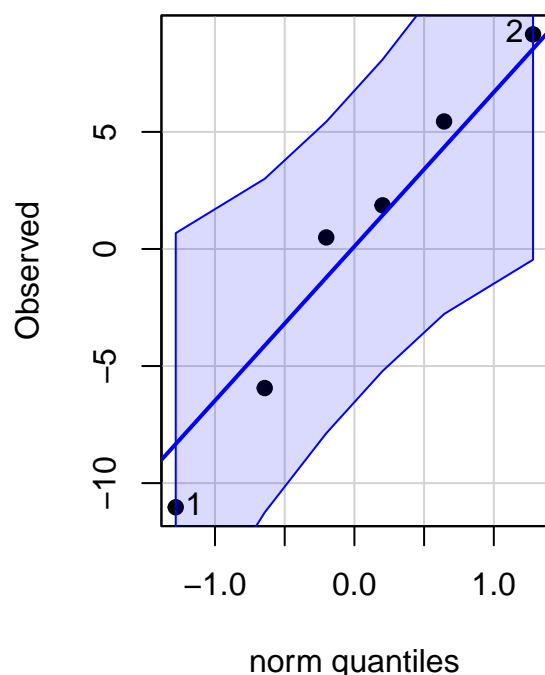
```

## 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

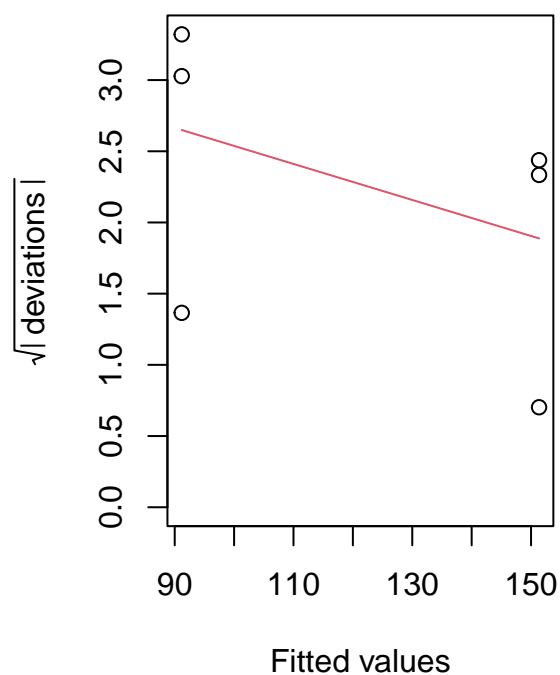
```

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

Plot (EU) Normal Q-Q



Scale-Location



```
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, 145, 35))

```

```

scale_y_continuous(name=expression("N Uptake (kg N ha"^{-1}*")"), limits = c(0, 255), expand = c(0, 0.05),
geom_errorbar(data=N_185_graphing_2022, aes(ymin=N_total_kgha-N_total_kgha_se, ymax=N_total_kgha+N_total_kgha_se),
#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_kgha_se,
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_average)

```

```

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

```

```

## 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      1153.90  1153.90      1    7.1358    5.1355 0.05710 .
## Stage          2192.99  1096.49      2   12.4098    4.8800 0.02731 *
## Year           258.73   258.73      1    4.0014    1.1515 0.34364
## Treatment:Stage    669.73   334.87      2   17.6678    1.4904 0.25228
## Treatment:Year    1253.89  1253.89      1    4.0847    5.5805 0.07612 .
## Stage:Year         847.05   423.53      2   15.9844    1.8849 0.18408
## Treatment:Stage:Year 670.06   335.03      2   17.6676    1.4911 0.25213
## ---
## 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

```

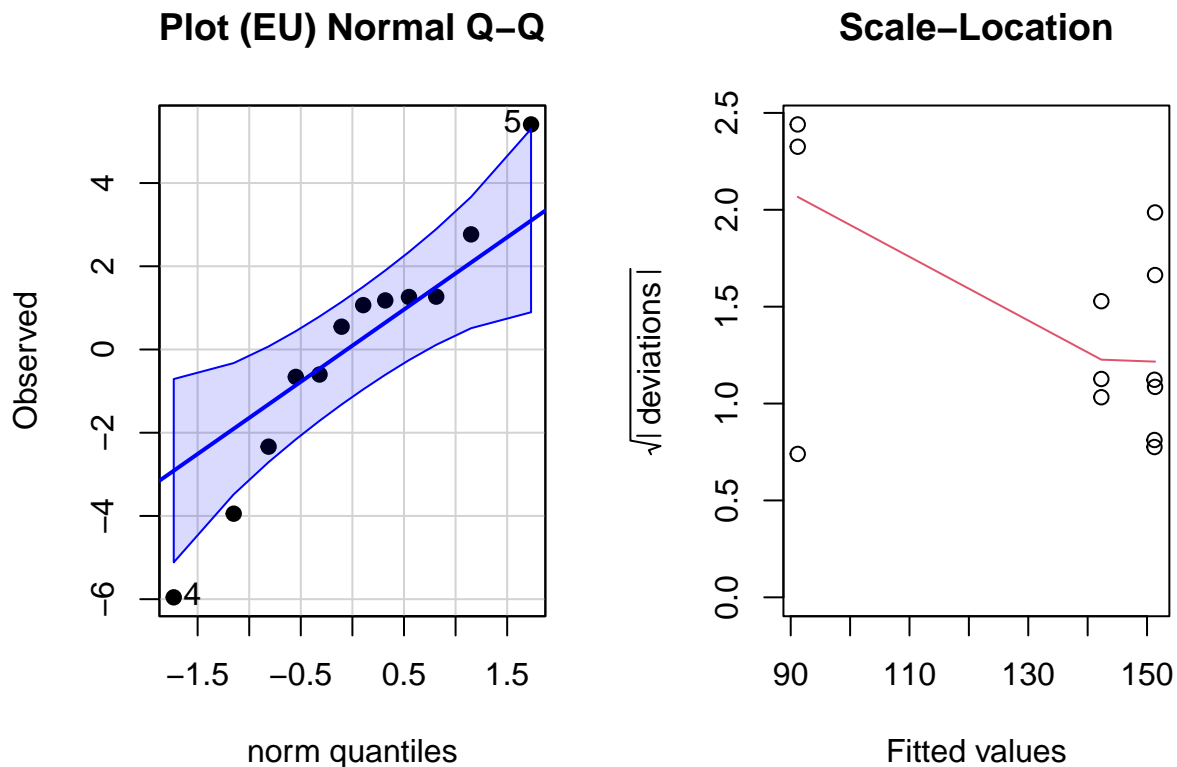
```

## -1.17772 -0.49840 0.02605 0.46417 2.14576
##
## Random effects:
## Groups Name Variance Std.Dev.
## Blk:Treatment (Intercept) 46.42 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 32493.255 14.793 0.925
## TreatmentFR -40406.266 38433.832 14.219 -1.051
## StageMaturity -4416.434 34989.275 16.097 -0.126
## StagePI 73416.715 34989.275 16.077 2.098
## Year -14.778 16.074 14.793 -0.919
## TreatmentFR:StageMaturity 7575.236 49482.306 16.120 0.153
## TreatmentFR:StagePI -63111.188 49482.307 16.131 -1.275
## TreatmentFR:Year 20.002 19.013 14.219 1.052
## StageMaturity:Year 2.192 17.309 16.097 0.127
## StagePI:Year -36.344 17.309 16.077 -2.100
## TreatmentFR:StageMaturity:Year -3.744 24.478 16.120 -0.153
## TreatmentFR:StagePI:Year 31.223 24.478 16.131 1.276
## Pr(>|t|)
## (Intercept) 0.3700
## TreatmentFR 0.3107
## StageMaturity 0.9011
## StagePI 0.0520 .
## Year 0.3726
## TreatmentFR:StageMaturity 0.8802
## TreatmentFR:StagePI 0.2202
## TreatmentFR:Year 0.3103
## StageMaturity:Year 0.9008
## StagePI:Year 0.0519 .
## TreatmentFR:StageMaturity:Year 0.8803
## TreatmentFR:StagePI:Year 0.2202
## ---
## 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
```

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



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

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

```
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
```

```
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.
```

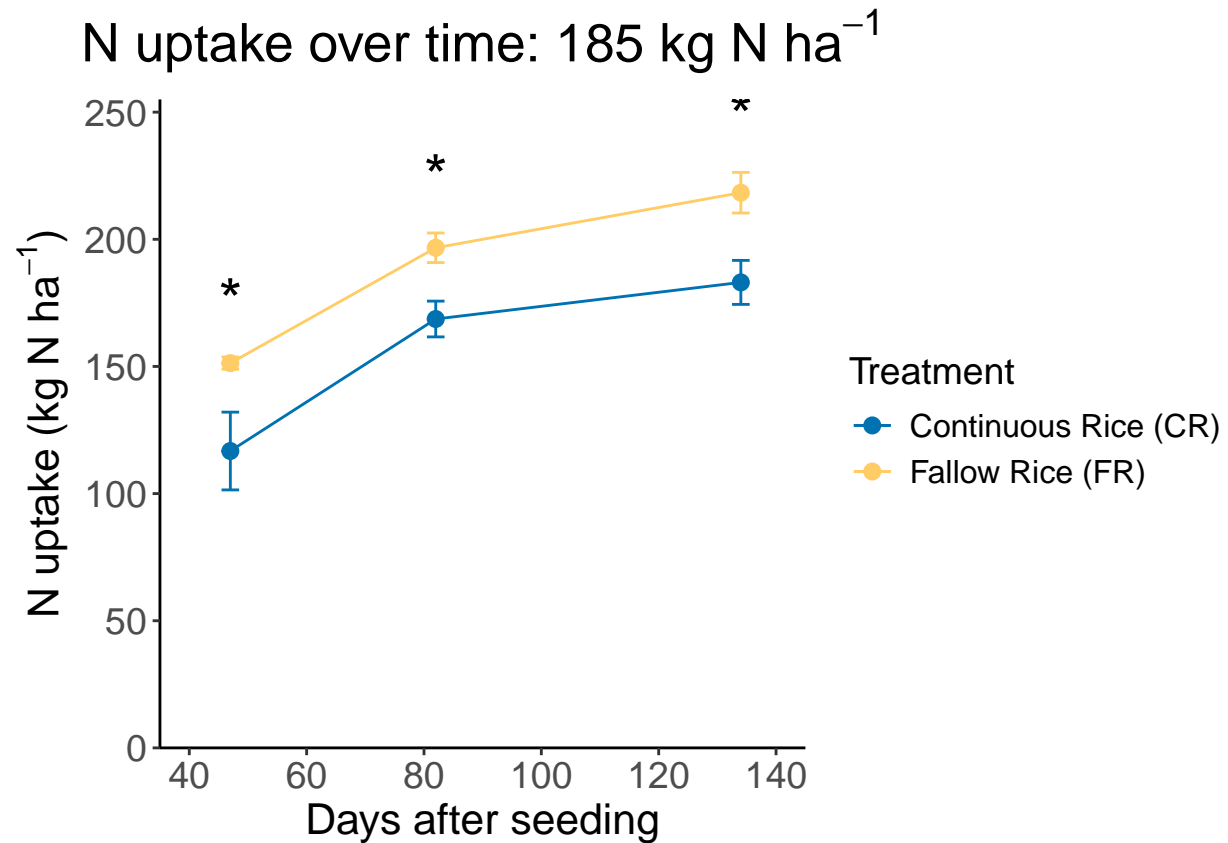
Graph_average

```
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, 145, 10)),
  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_total_kgha_se),
  #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_total_kgha_se,
  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



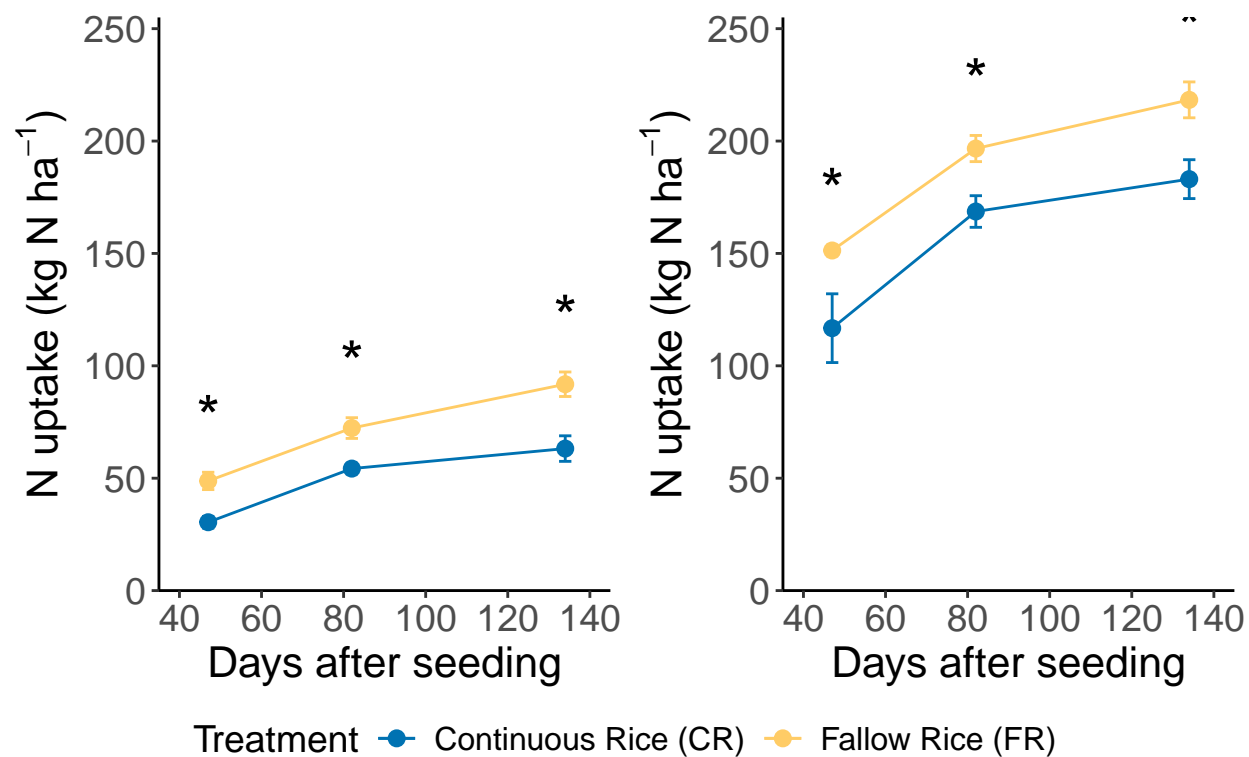
Combine graphs

```
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
```

N uptake over time: 0 kg N uptake over time: 185 kg



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