

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
```

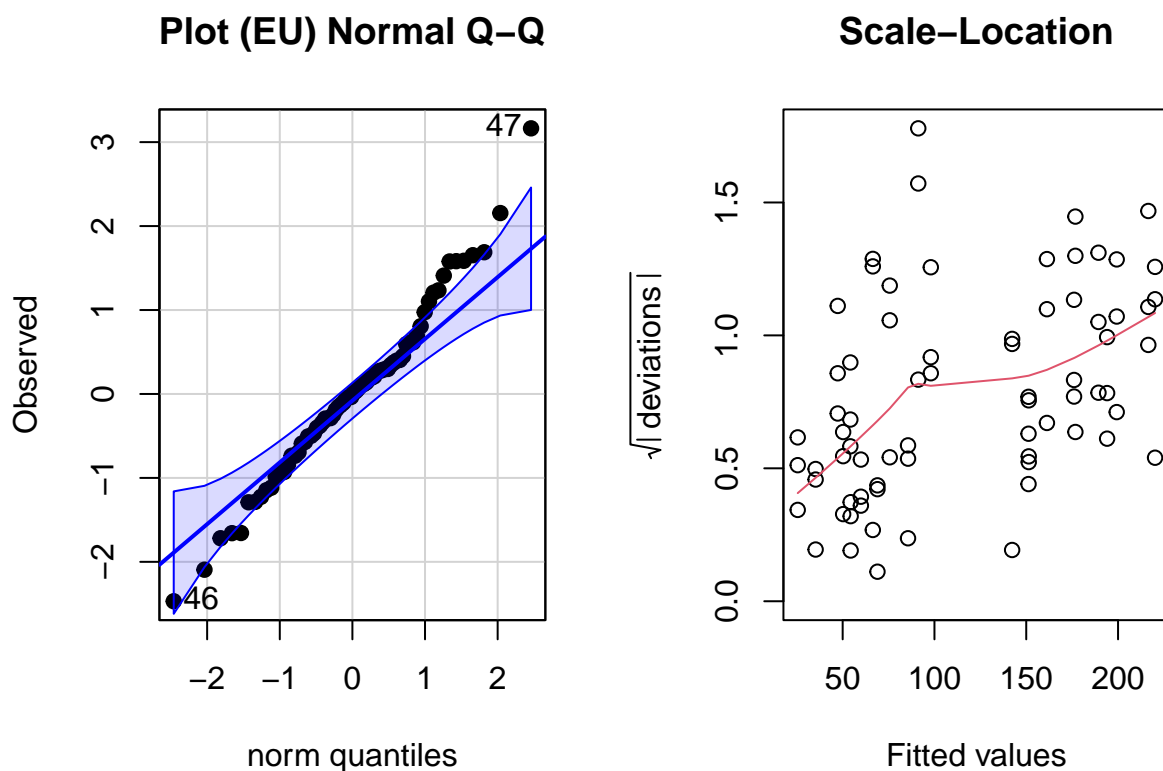
```
#dataset looks good and complete so lets have some fun huehuehue
str(master)
```

```
## 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. Potential treatment by year interaction...

```
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
```

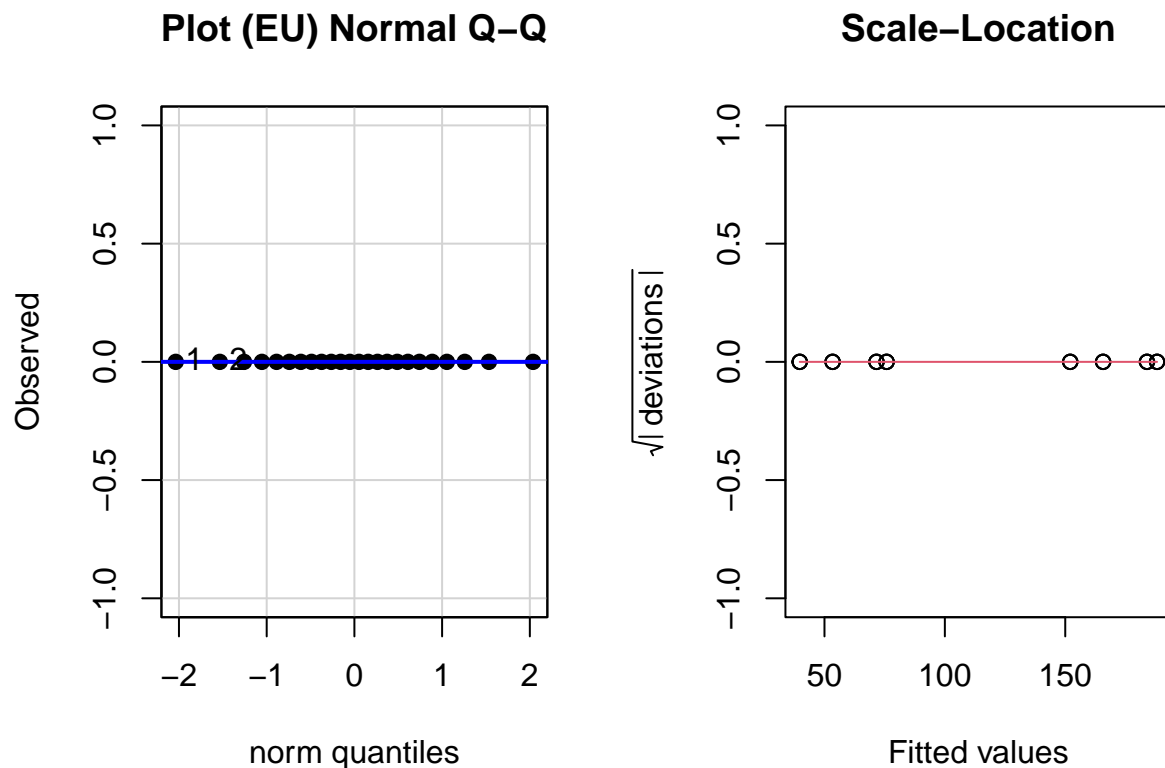
```
all_data_model_lmer <- lmer(N_total_kgha ~ Year*Treatment+Nrate_kgha_F+(1|Blk:Treatment:Nrate_kgha_F),

## 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), data = N_zero_2021)
```

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

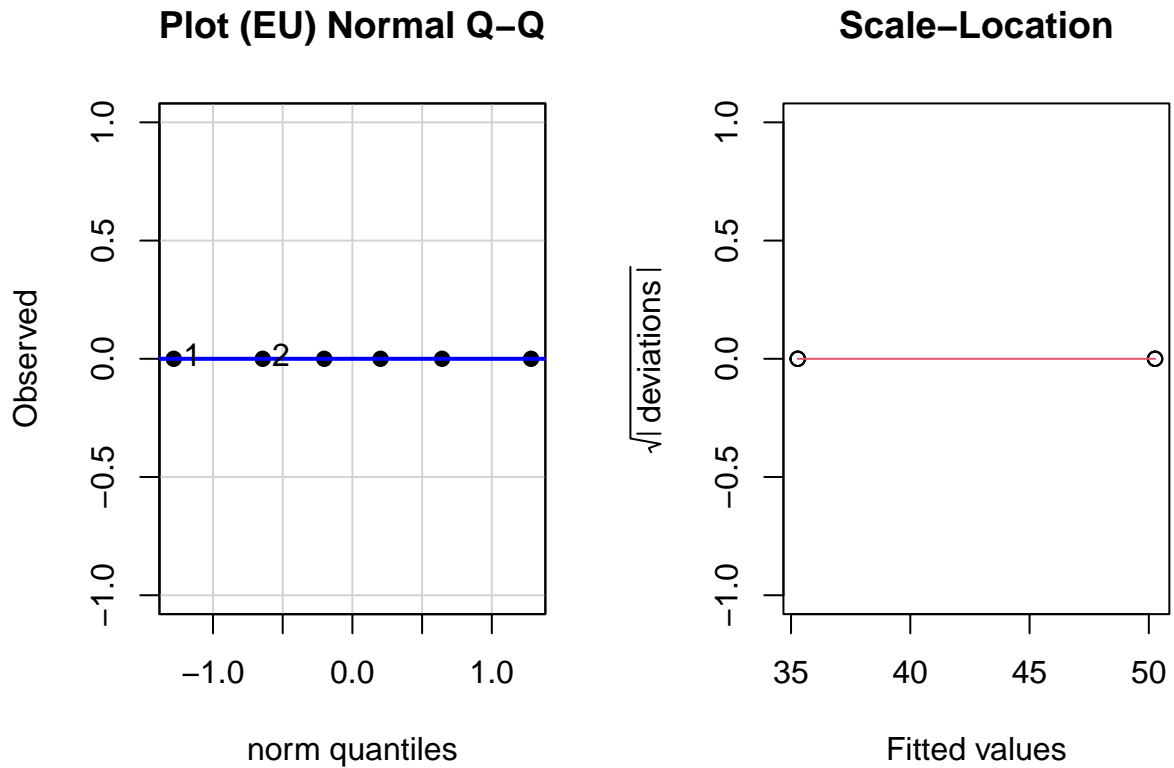
```
anova(N_zero_model_2021)
```

```
## 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)
## 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
## Residual                11.14   3.337
## Number of obs: 18, groups: Blk:Treatment, 6
##
## 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 12 -5.357 0.0002
##
## Stage = Maturity:
## contrast estimate SE df t.ratio p.value
## CR - FR -25.7 2.72 12 -9.423 <.0001
##
## Stage = PI:
## contrast estimate SE df t.ratio p.value
## CR - FR -15.0 2.72 12 -5.498 0.0001
##
## 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))

```

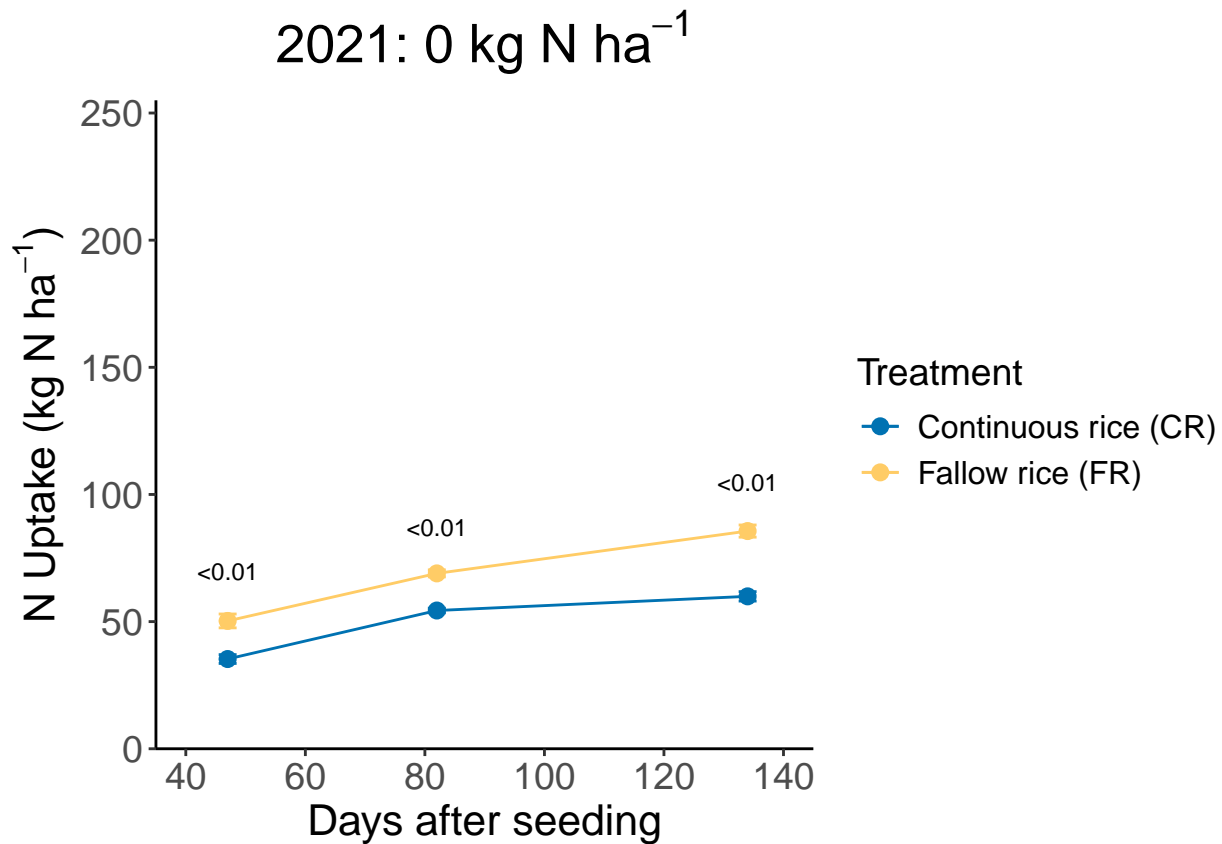


```

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

Pairwise Comparisons 2022

```

N_zero_model_2022 <- lmer(N_total_kgha~Treatment*Stage+(1|Blk:Treatment), 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  5.0291  0.08837 .

```

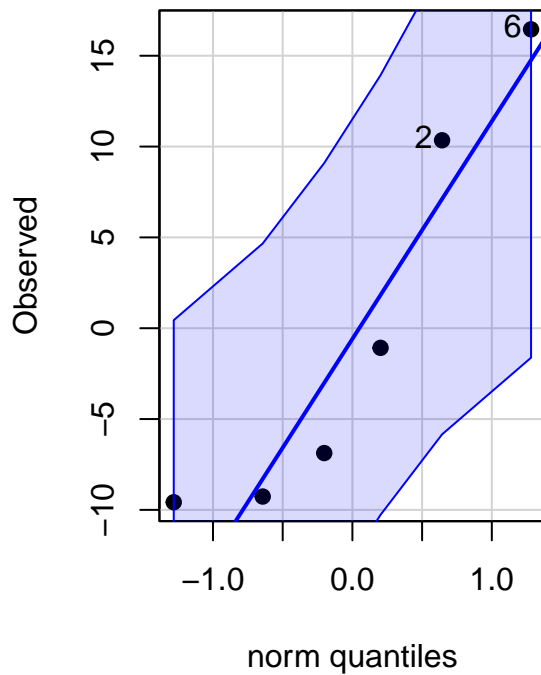
```
## Stage          6417.4  3208.7    2    8 58.6504 1.662e-05 ***
## Treatment:Stage  99.1    49.6    2    8  0.9059  0.44194
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(N_zero_model_2022)
```

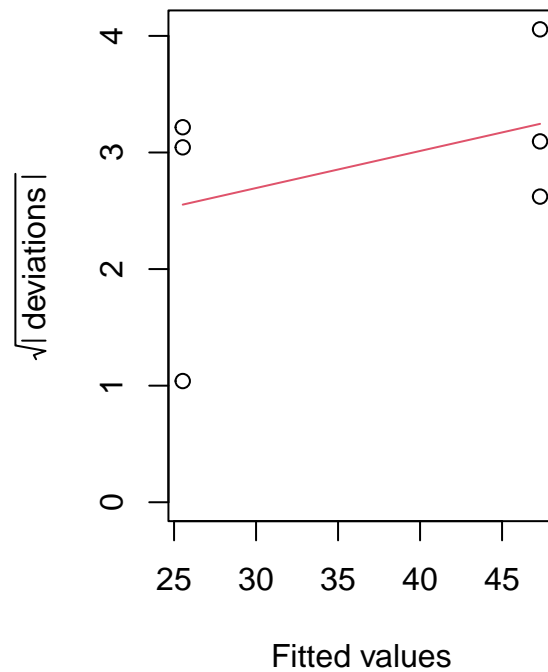
```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: N_total_kgha ~ Treatment * Stage + (1 | Blk:Treatment)
## Data: N_zero_2022
##
## REML criterion at convergence: 98
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.6538 -0.3596  0.1308  0.4196  1.3817
##
## Random effects:
## Groups          Name          Variance Std.Dev.
## Blk:Treatment (Intercept) 167.38   12.937
## Residual                54.71    7.397
## Number of obs: 18, groups: Blk:Treatment, 6
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)      54.1877    8.6040   5.6180   6.298 0.000962 ***
## TreatmentFR       21.4684   12.1679   5.6180   1.764 0.131477
## 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
```

```
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 5.62 -1.764 0.1315
##
## Stage = Maturity:
## contrast estimate SE df t.ratio p.value
## CR - FR -31.6 12.2 5.62 -2.595 0.0435
##
## Stage = PI:
## contrast estimate SE df t.ratio p.value
## CR - FR -21.8 12.2 5.62 -1.791 0.1269
##
## 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 2
##
## 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))

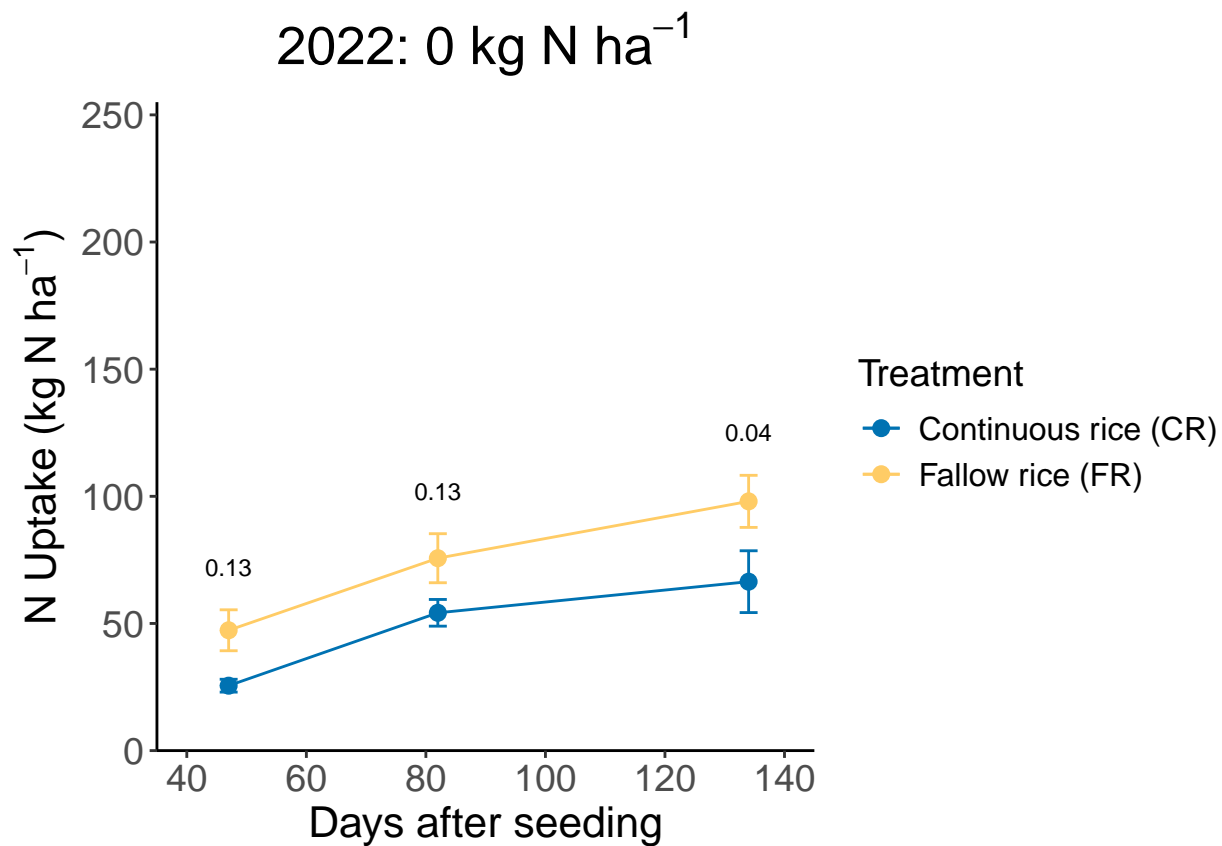
```

```

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

Pairise Comparisons average

```

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

```

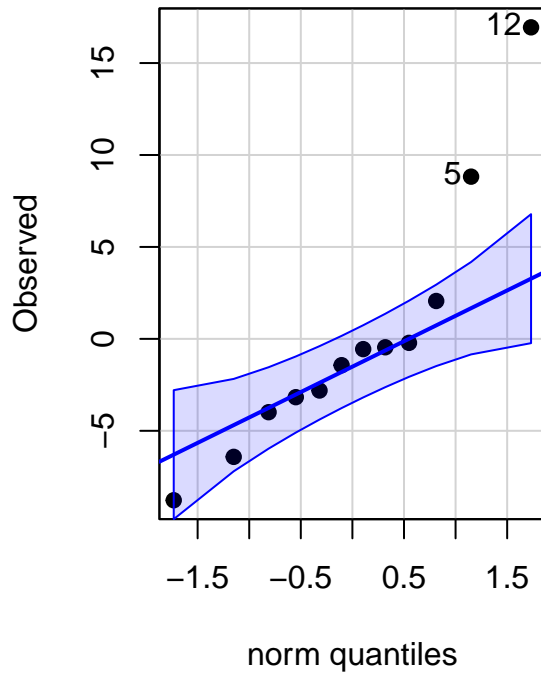
```
## Treatment      807.6   807.6    1   10 17.6309  0.001832 **
## Stage          8796.6  4398.3    2   20 96.0224 5.572e-11 ***
## Treatment:Stage 217.3   108.7    2   20  2.3725  0.118971
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(N_zero_model_average)
```

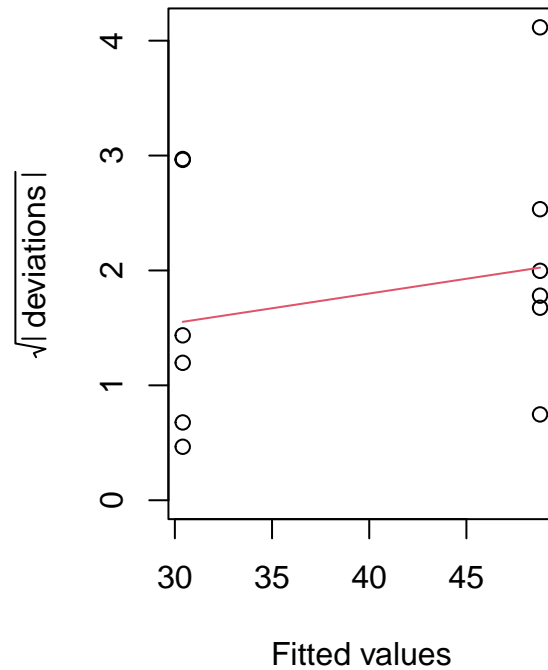
```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: N_total_kgha ~ Treatment * Stage + (1 | Blk:Treatment)
## Data: N_zero_average
##
## REML criterion at convergence: 227.2
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.5222 -0.4717 -0.1515  0.5100  2.2157
##
## Random effects:
## Groups      Name      Variance Std.Dev.
## Blk:Treatment (Intercept) 64.73    8.045
## Residual              45.81    6.768
## Number of obs: 36, groups: Blk:Treatment, 12
##
## Fixed effects:
##              Estimate Std. Error    df t value Pr(>|t|)
## (Intercept)      54.2745     4.2921 17.7954  12.645 2.51e-10 ***
## TreatmentFR       18.0332     6.0699 17.7954   2.971  0.00826 **
## StageMaturity      8.9038     3.9075 20.0000   2.279  0.03381 *
## StagePI          -23.8696     3.9075 20.0000  -6.109 5.71e-06 ***
## TreatmentFR:StageMaturity 10.5959     5.5260 20.0000   1.917  0.06958 .
## TreatmentFR:StagePI      0.3516     5.5260 20.0000   0.064  0.94991
## ---
## 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 -0.455  0.322
## StagePI      -0.455  0.322  0.500
## TrtmntFR:SM  0.322 -0.455 -0.707 -0.354
## TrtmnFR:SPI  0.322 -0.455 -0.354 -0.707  0.500
```

```
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')
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 6.07 17.8 -2.971 0.0083
##
## Stage = Maturity:
## contrast estimate SE df t.ratio p.value
## CR - FR -28.6 6.07 17.8 -4.717 0.0002
##
## Stage = PI:
## contrast estimate SE df t.ratio p.value
## CR - FR -18.4 6.07 17.8 -3.029 0.0073
##
## 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 4.29 17.8 45.2 63.3 1
## FR 72.3 4.29 17.8 63.3 81.3 2
##
## Stage = Maturity:
## Treatment emmean SE df lower.CL upper.CL .group
## CR 63.2 4.29 17.8 54.2 72.2 1
## FR 91.8 4.29 17.8 82.8 100.8 2
##
## Stage = PI:
## Treatment emmean SE df lower.CL upper.CL .group
## CR 30.4 4.29 17.8 21.4 39.4 1
## FR 48.8 4.29 17.8 39.8 57.8 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_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, 35))

```

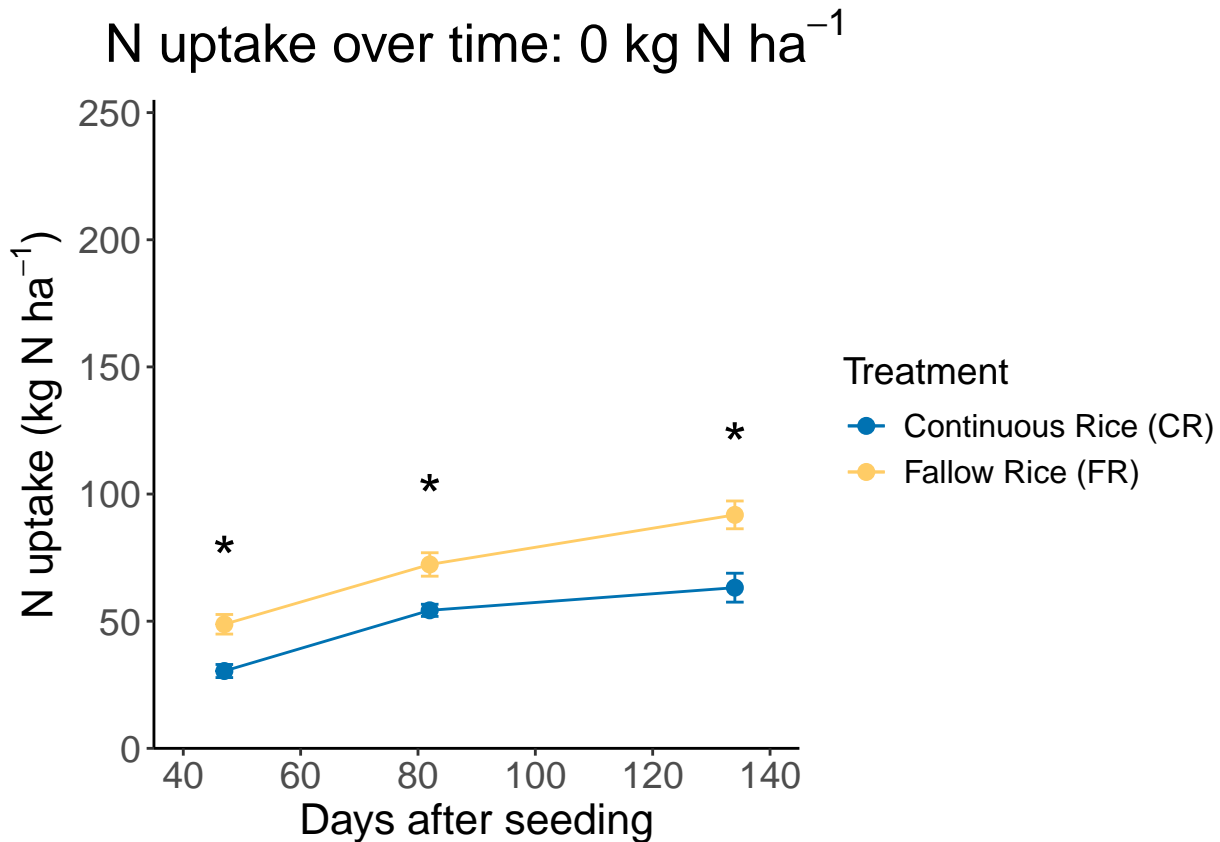


```

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_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

Pairwise Comparisons 2021

```

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

```

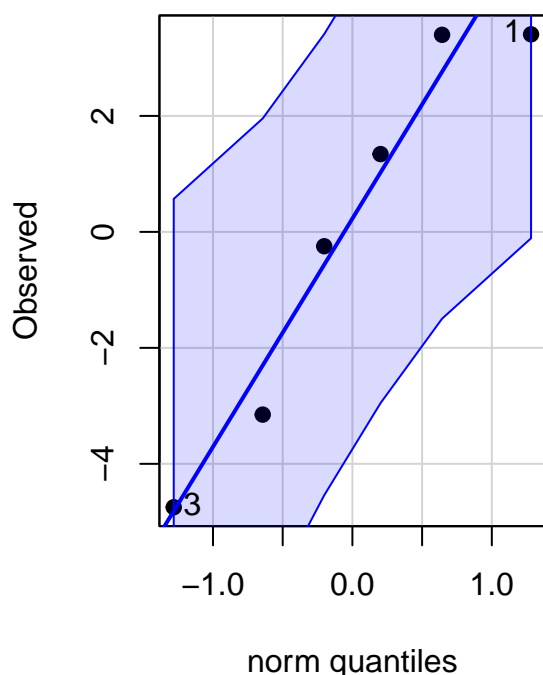
```
## Type III Analysis of Variance Table with Satterthwaite's method
##           Sum Sq Mean Sq NumDF DenDF F value    Pr(>F)
## Treatment      934.9   934.9     1     4  4.4308 0.1030749
## Stage        9872.2  4936.1     2     8 23.3944 0.0004546 ***
## Treatment:Stage  248.5   124.3     2     8  0.5889 0.5773146
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(N_185_model_2021)
```

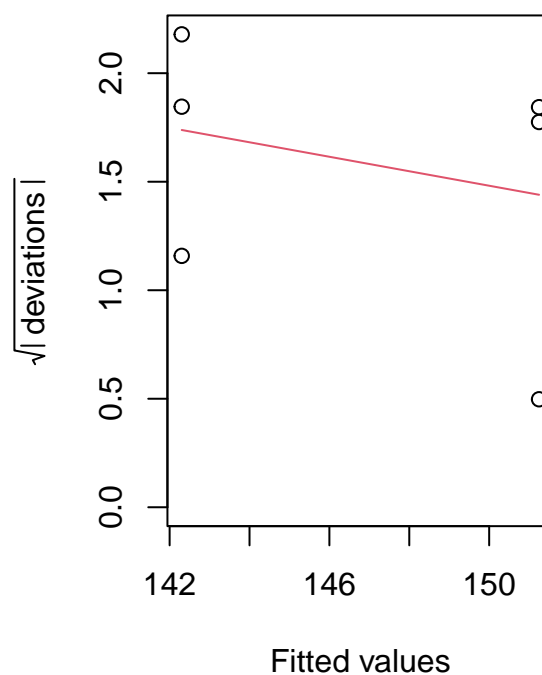
```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: N_total_kgha ~ Treatment * Stage + (1 | Blk:Treatment)
## Data: N_185_2021
##
## REML criterion at convergence: 106.7
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.2070 -0.7998  0.3039  0.3856  1.6893
##
## Random effects:
## Groups           Name          Variance Std.Dev.
## Blk:Treatment (Intercept)  39.78     6.307
## Residual                211.00    14.526
## Number of obs: 18, groups: Blk:Treatment, 6
##
## Fixed effects:
##              Estimate Std. Error    df t value Pr(>|t|)
## (Intercept)    176.043     9.143  11.425  19.255 4.58e-10 ***
## TreatmentFR      18.011    12.930  11.425   1.393  0.1901
## StageMaturity    13.301    11.860   8.000   1.122  0.2946
## StagePI        -33.740    11.860   8.000  -2.845  0.0217 *
## TreatmentFR:StageMaturity  9.138    16.773   8.000   0.545  0.6008
## TreatmentFR:StagePI    -9.065    16.773   8.000  -0.540  0.6036
## ---
## 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 -0.649  0.459
## StagePI     -0.649  0.459  0.500
## TrtmntFR:SM  0.459 -0.649 -0.707 -0.354
## TrtmnFR:SPI  0.459 -0.649 -0.354 -0.707  0.500
```

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

Plot (EU) Normal Q-Q



Scale-Location



```
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 12.9 11.4 -1.393 0.1901
##
## Stage = Maturity:
## contrast estimate SE df t.ratio p.value
## CR - FR -27.15 12.9 11.4 -2.100 0.0587
##
## Stage = PI:
## contrast estimate SE df t.ratio p.value
## CR - FR -8.95 12.9 11.4 -0.692 0.5028
##
## 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 11.4 156 196 1
## FR 194 9.14 11.4 174 214 1
##
## Stage = Maturity:
## Treatment emmean SE df lower.CL upper.CL .group
## CR 189 9.14 11.4 169 209 1
## FR 216 9.14 11.4 196 237 1
##
## Stage = PI:
## Treatment emmean SE df lower.CL upper.CL .group
## CR 142 9.14 11.4 122 162 1
## FR 151 9.14 11.4 131 171 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, 0.05),
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), 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      2179.8   2179.8      1     4  9.1442 0.03901 *
## 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)

```

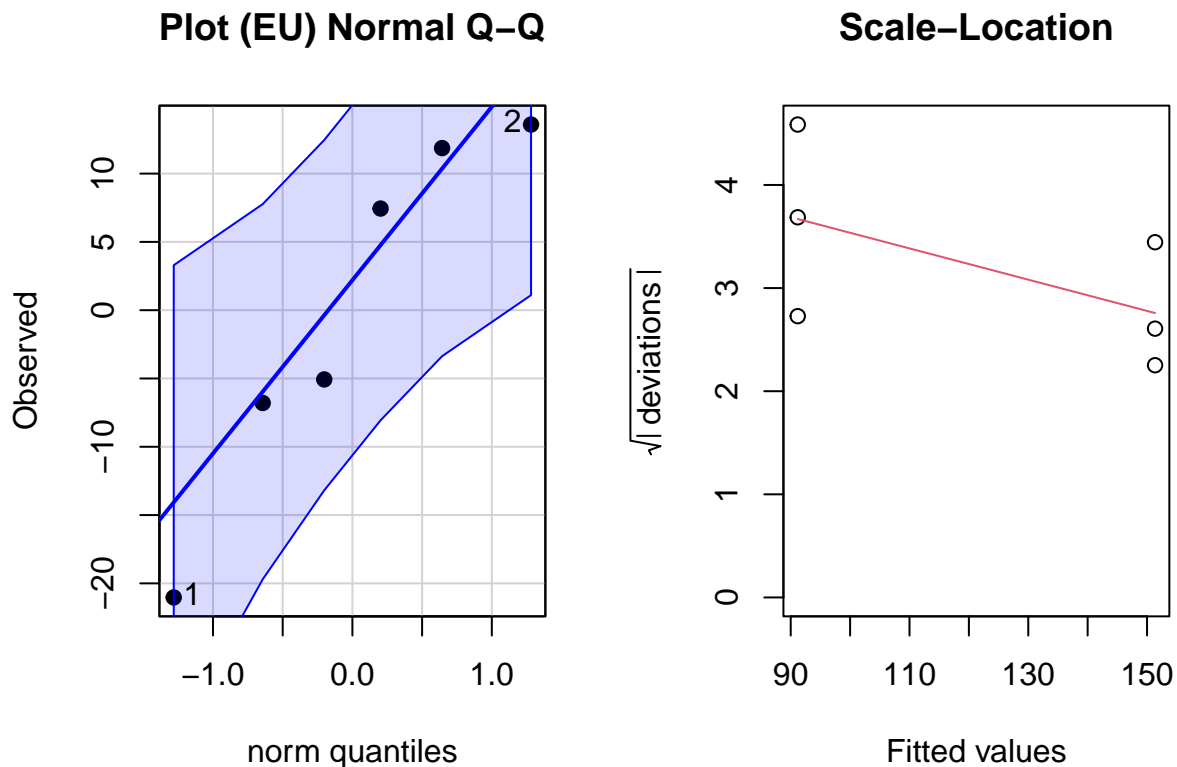
```

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: N_total_kgha ~ Treatment * Stage + (1 | Blk:Treatment)
## Data: N_185_2022
##
## REML criterion at convergence: 112.4
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.06534 -0.53463 -0.06794  0.55258  1.77649
##
## Random effects:
## Groups       Name             Variance Std.Dev.
## Blk:Treatment (Intercept) 285.9      16.91
## Residual                238.4      15.44
## Number of obs: 18, groups: Blk:Treatment, 6
##
## Fixed effects:
##              Estimate Std. Error    df t value Pr(>|t|)
## (Intercept)    161.265    13.220   7.524  12.198 3.17e-06 ***
## TreatmentFR     38.013    18.696   7.524   2.033 0.078712 .

```

```
## StageMaturity      15.493      12.606      8.000      1.229 0.253997
## StagePI            -70.084      12.606      8.000     -5.559 0.000535 ***
## TreatmentFR:StageMaturity    5.394      17.828      8.000      0.303 0.769948
## 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 -0.707
## StageMatrty -0.477  0.337
## StagePI      -0.477  0.337  0.500
## TrtmntFR:SM  0.337 -0.477 -0.707 -0.354
## TrtmnFR:SPI  0.337 -0.477 -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 18.7 7.52 -2.033 0.0787
##
```

```
## Stage = Maturity:
## contrast estimate SE df t.ratio p.value
## CR - FR -43.4 18.7 7.52 -2.322 0.0508
##
## Stage = PI:
## contrast estimate SE df t.ratio p.value
## CR - FR -60.2 18.7 7.52 -3.218 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 7.52 130.4 192 1
## FR 199.3 13.2 7.52 168.5 230 1
##
## Stage = Maturity:
## Treatment emmean SE df lower.CL upper.CL .group
## CR 176.8 13.2 7.52 145.9 208 1
## FR 220.2 13.2 7.52 189.3 251 1
##
## Stage = PI:
## Treatment emmean SE df lower.CL upper.CL .group
## CR 91.2 13.2 7.52 60.4 122 1
## FR 151.4 13.2 7.52 120.5 182 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, 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_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

Pairwise Comparisons average

```
N_185_model_average <- lmer(N_total_kgha~Treatment*Stage+(1|Blk:Treatment), data = N_185_average)
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      2723.1   2723.1     1    10  10.8468  0.008103 **
## Stage          28542.0  14271.0     2    20  56.8449 5.615e-09 ***
## Treatment:Stage    96.2     48.1     2    20   0.1915  0.827192
## ---
## 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 + (1 | Blk:Treatment)
```



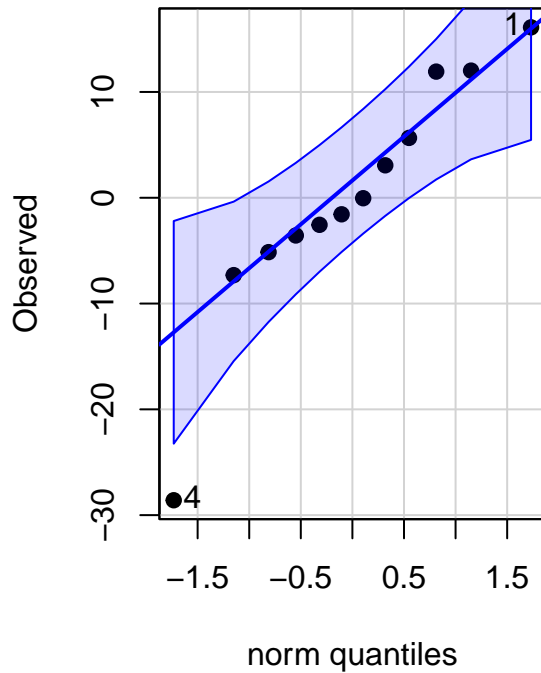
```

## Data: N_185_average
##
## REML criterion at convergence: 274.2
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.02039 -0.51441 -0.02235  0.56047  1.58564
##
## Random effects:
## Groups      Name      Variance Std.Dev.
## Blk:Treatment (Intercept) 210.5    14.51
## Residual                251.1    15.84
## Number of obs: 36, groups: Blk:Treatment, 12
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)      168.654      8.771   21.185  19.228 6.83e-15 ***
## TreatmentFR        28.012     12.404   21.185   2.258  0.0346 *
## StageMaturity       14.397      9.148   20.000   1.574  0.1312
## StagePI          -51.912      9.148   20.000  -5.675 1.49e-05 ***
## TreatmentFR:StageMaturity   7.266     12.937   20.000   0.562  0.5806
## TreatmentFR:StagePI        6.547     12.937   20.000   0.506  0.6184
## ---
## 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 -0.521  0.369
## StagePI     -0.521  0.369  0.500
## TrtmntFR:SM  0.369 -0.521 -0.707 -0.354
## TrtmnFR:SPI  0.369 -0.521 -0.354 -0.707  0.500

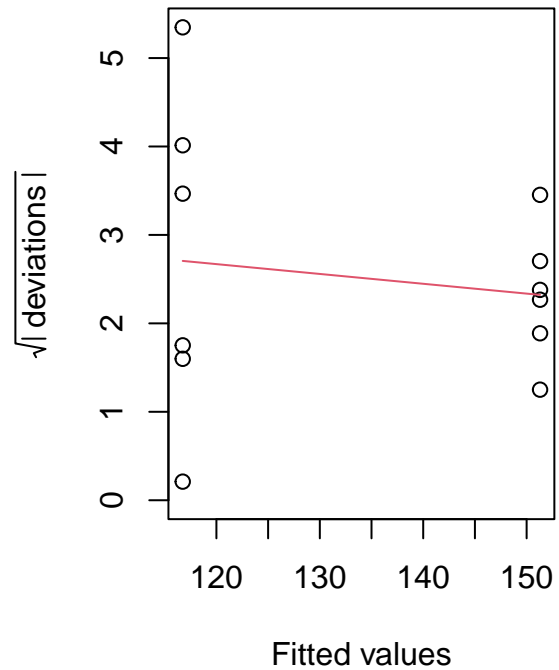
```

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

Plot (EU) Normal Q-Q



Scale-Location



```
N_185_means_average = emmeans(N_185_model_average,spec = 'Treatment',by = 'Stage')
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 12.4 21.2 -2.258 0.0346
##
## Stage = Maturity:
## contrast estimate SE df t.ratio p.value
## CR - FR -35.3 12.4 21.2 -2.844 0.0097
##
## Stage = PI:
## contrast estimate SE df t.ratio p.value
## CR - FR -34.6 12.4 21.2 -2.786 0.0110
##
## 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 8.77 21.2 150.4 187 1
## FR 197 8.77 21.2 178.4 215 2
##
## Stage = Maturity:
## Treatment emmean SE df lower.CL upper.CL .group
## CR 183 8.77 21.2 164.8 201 1
## FR 218 8.77 21.2 200.1 237 2
##
## Stage = PI:
## Treatment emmean SE df lower.CL upper.CL .group
## CR 117 8.77 21.2 98.5 135 1
## FR 151 8.77 21.2 133.1 170 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_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, 35))

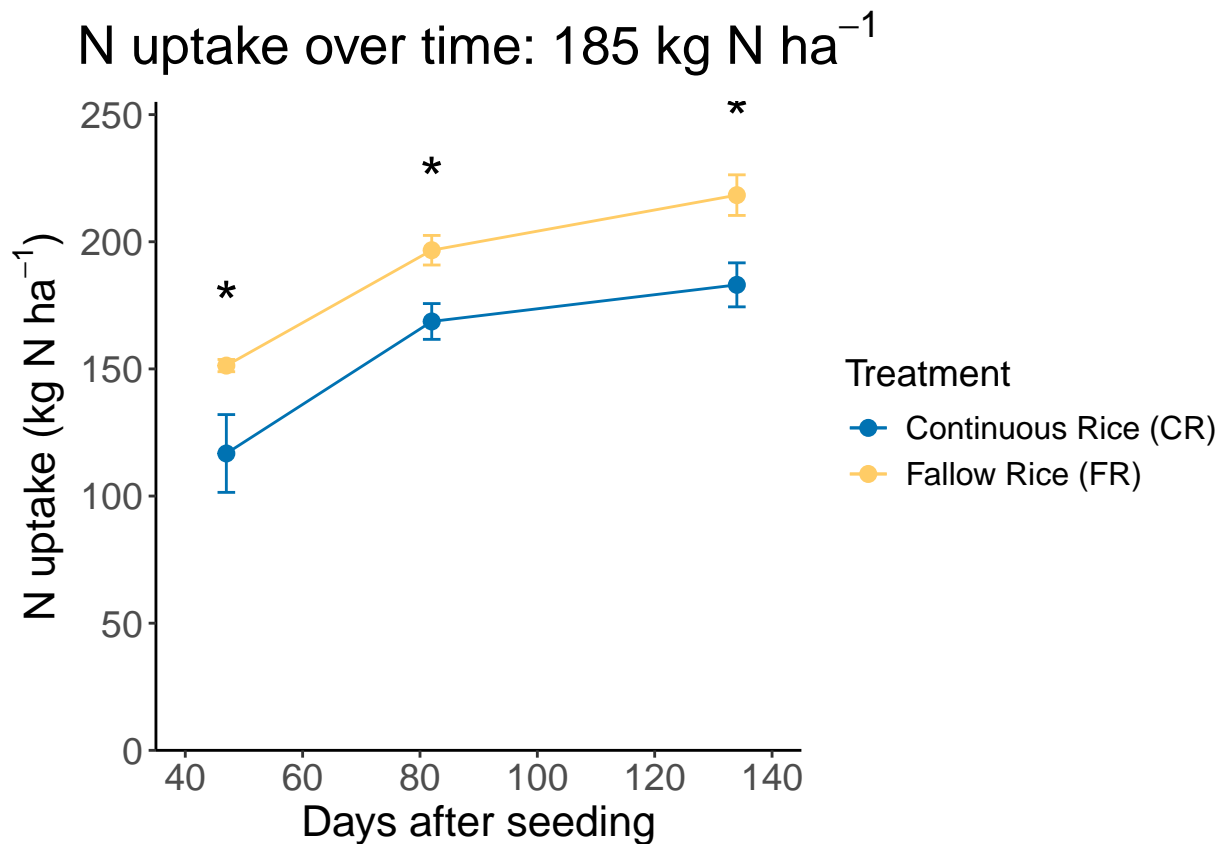
```

```

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_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

```

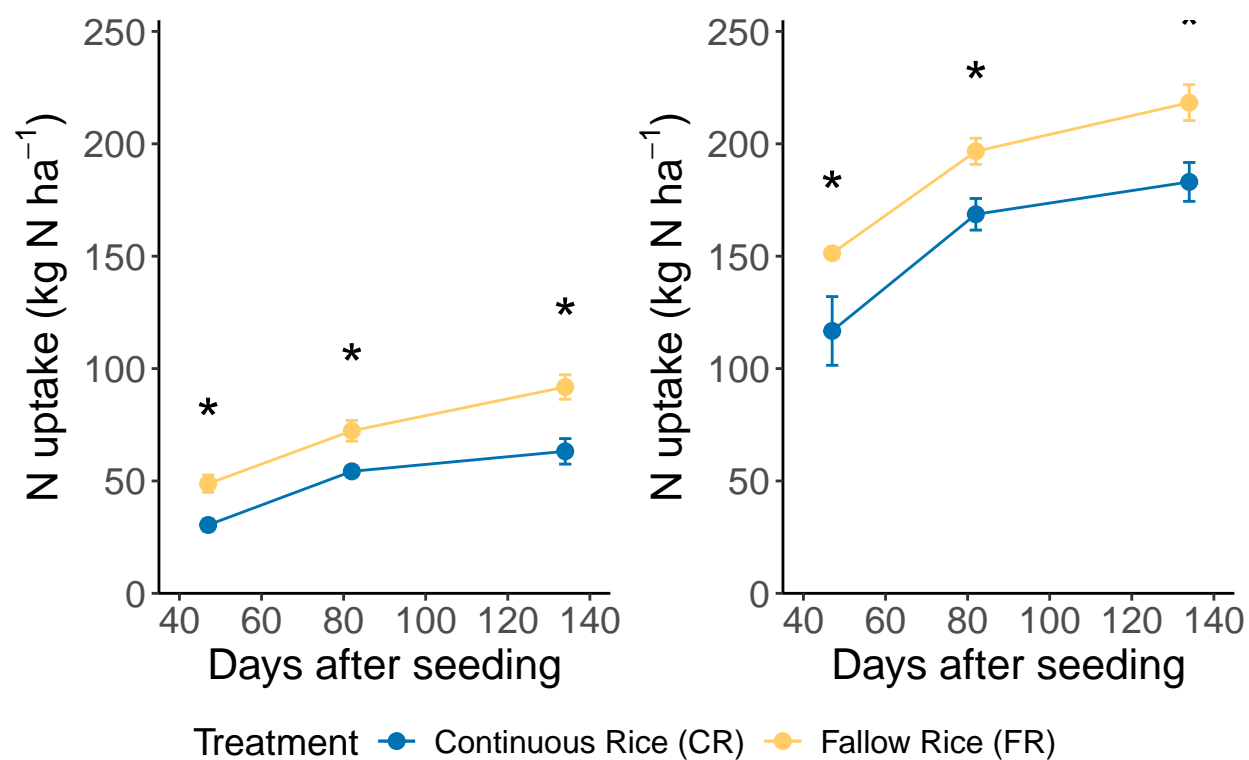
all_N_uptake_overtime <- ggarrange(#N_zero_graph_2021,
                                   #N_zero_graph_2022,
                                   N_zero_graph_average,
                                   #N_185_graph_2021,
                                   #N_185_graph_2022,
                                   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)
```