N Uptake overtime

Zhang Zhenglin

Contents

Necessary libraries

Read and check data

```r
#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)
```
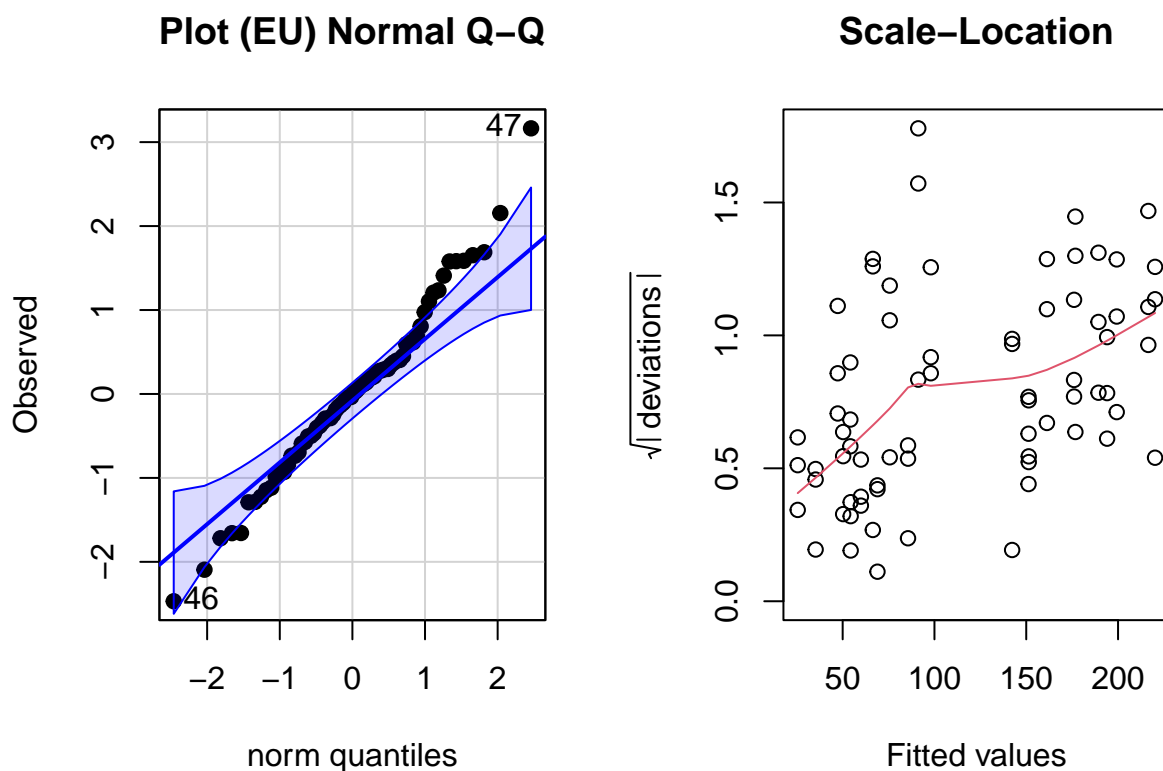
```
##
## 2021 2022
##   36   36
```

```
#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)
```

Plot (EU) Normal Q–Q

Scale–Location

Observed

norm quantiles

√|deviations|

Fitted values

47
46

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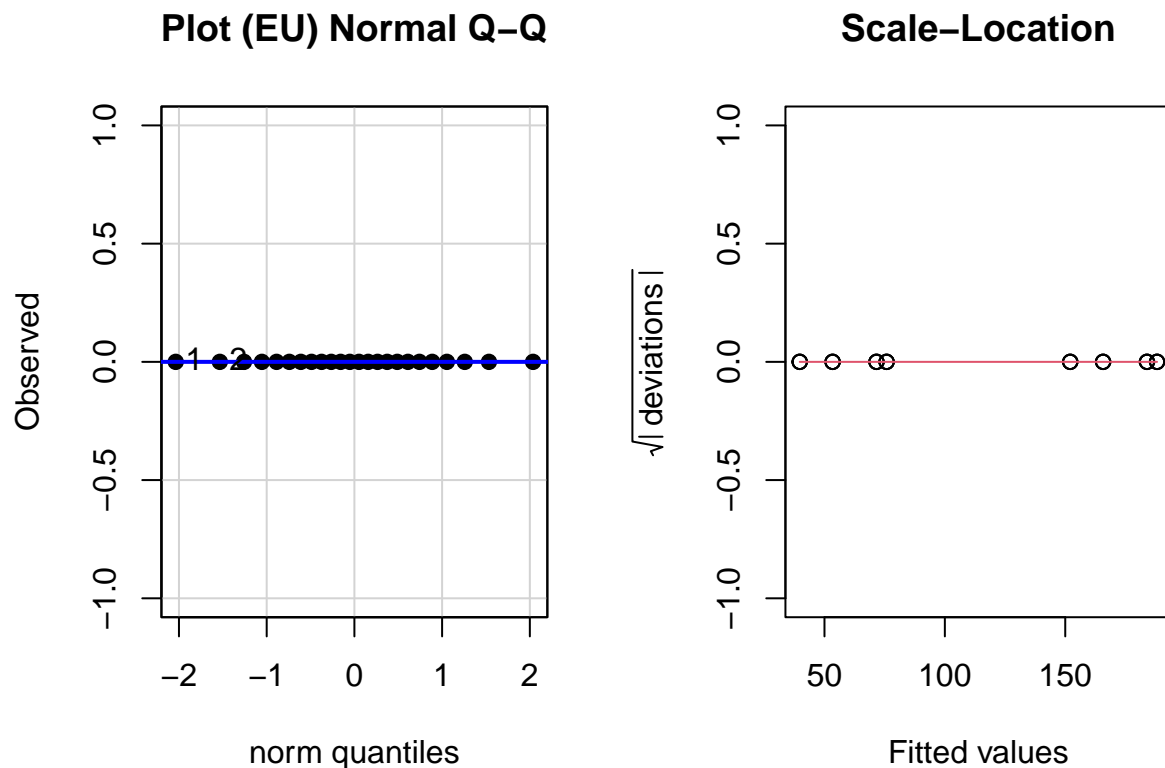
```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
## 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
```

4

```
## 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
```

5

```
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")
```

Plot (EU) Normal Q–Q

Scale–Location
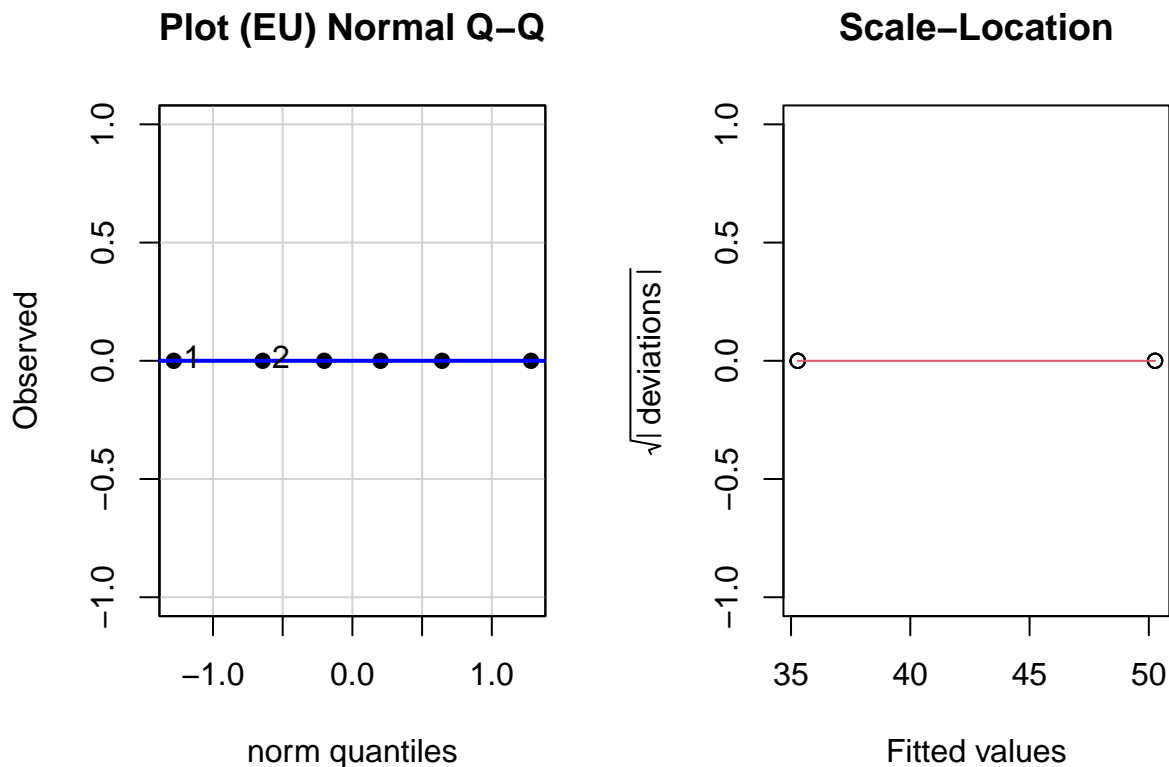

```
N_zero_means_2021 = emmeans(N_zero_model_2021,spec = 'Treatment',by = 'Stage')
N_zero_effects_2021 = contrast(N_zero_means_2021, method = 'pairwise', adjust = "tukey")
summary(N_zero_effects_2021)
```

```
## 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, 1
```

```
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
```
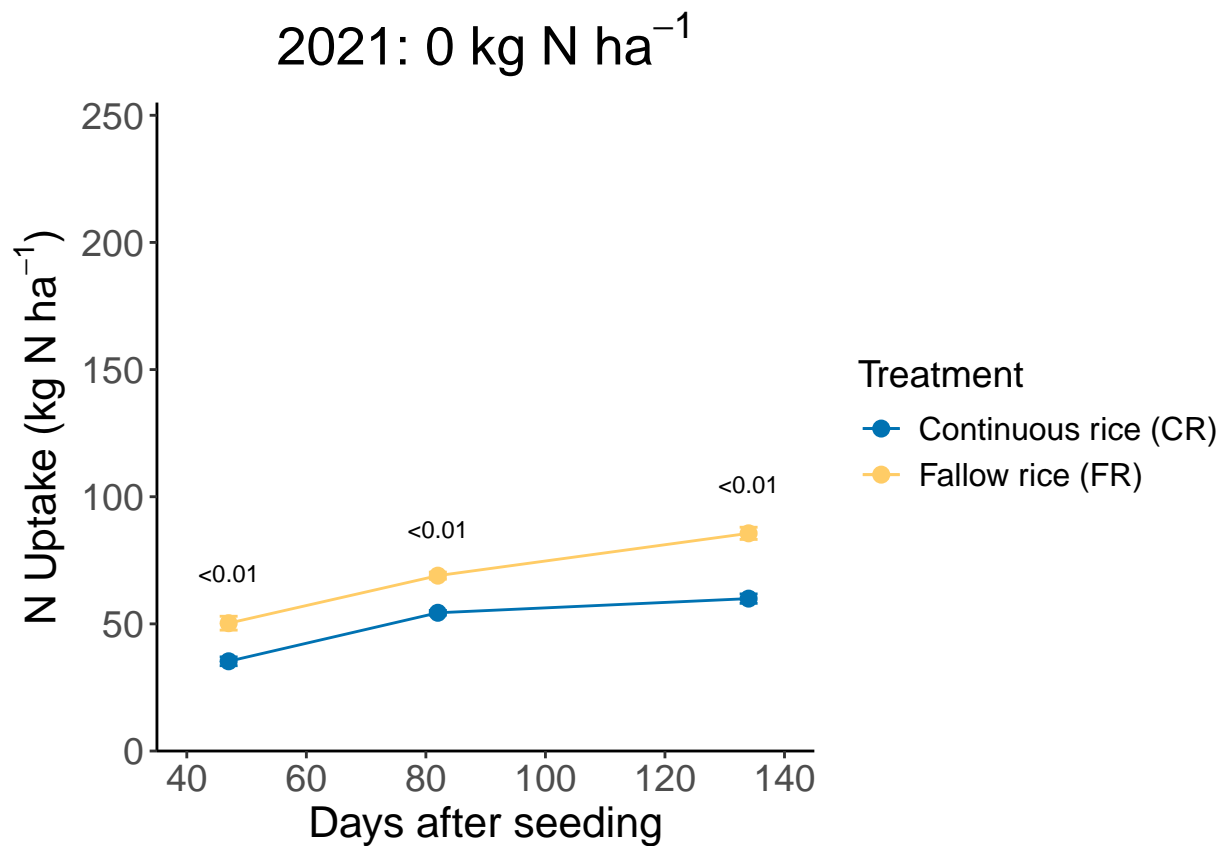

2022

Pairise Comparisons 2022

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

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
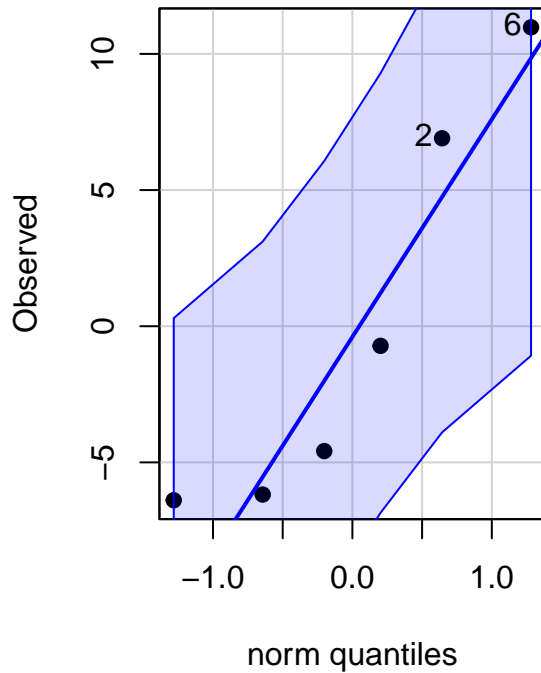
Scale–Location
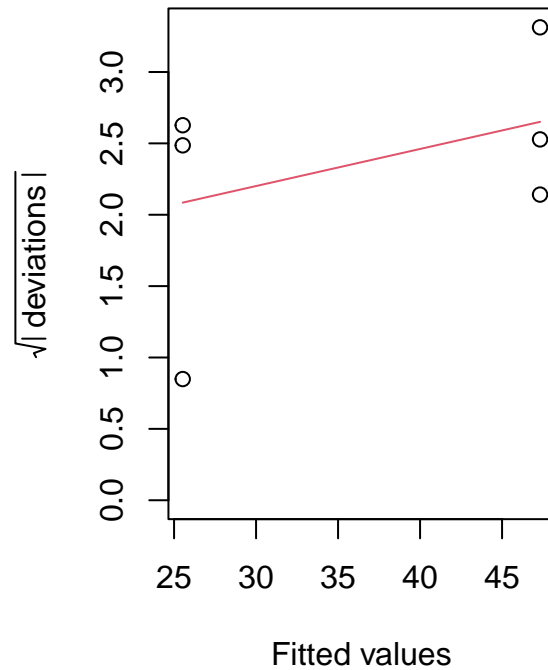

```r
N_zero_means_2022 = emmeans(N_zero_model_2022,spec = 'Treatment',by = 'Stage')
N_zero_effects_2022 = contrast(N_zero_means_2022, method = 'pairwise', adjust = "tukey")
summary(N_zero_effects_2022)
```

```
## 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
```

```r
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
```


2022: 0 kg N ha^{-1}
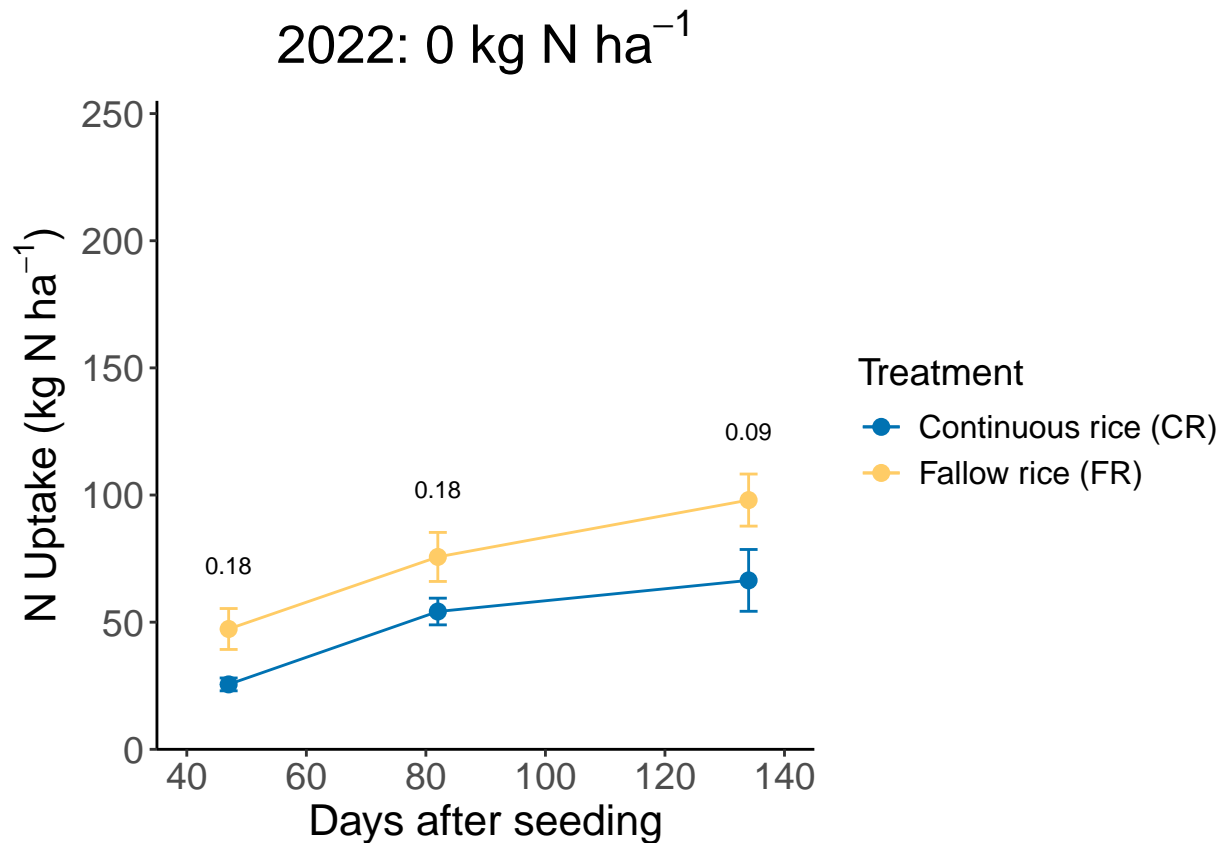
Average_zero (Figure 4)

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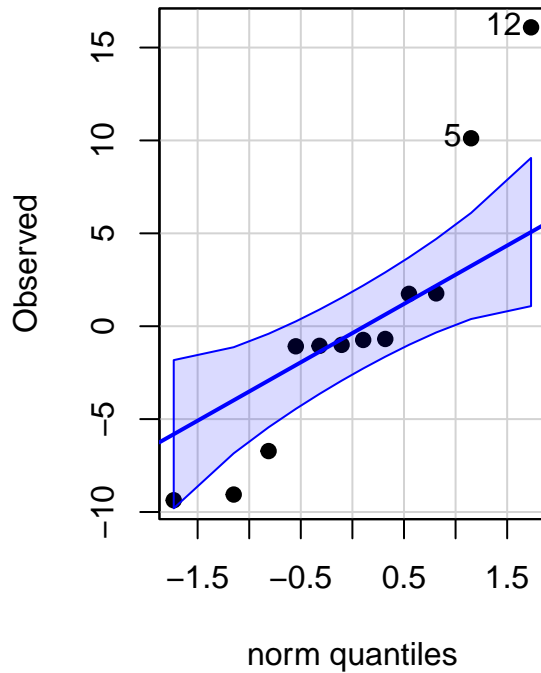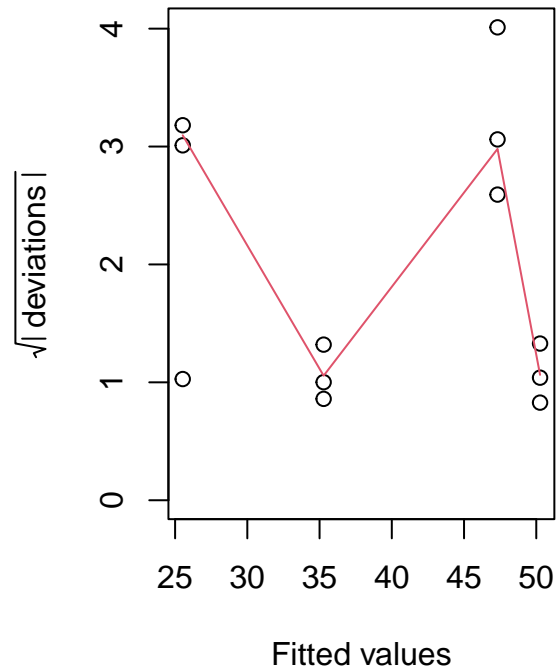
```
pls205_diagnostics(N_zero_model_average, EU="Blk:Treatment")
```

Plot (EU) Normal Q–Q

Scale–Location


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

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

```r
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
```

```r
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+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 = 16),legend.title = element_text(size = 18))+
  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_tot
  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
```
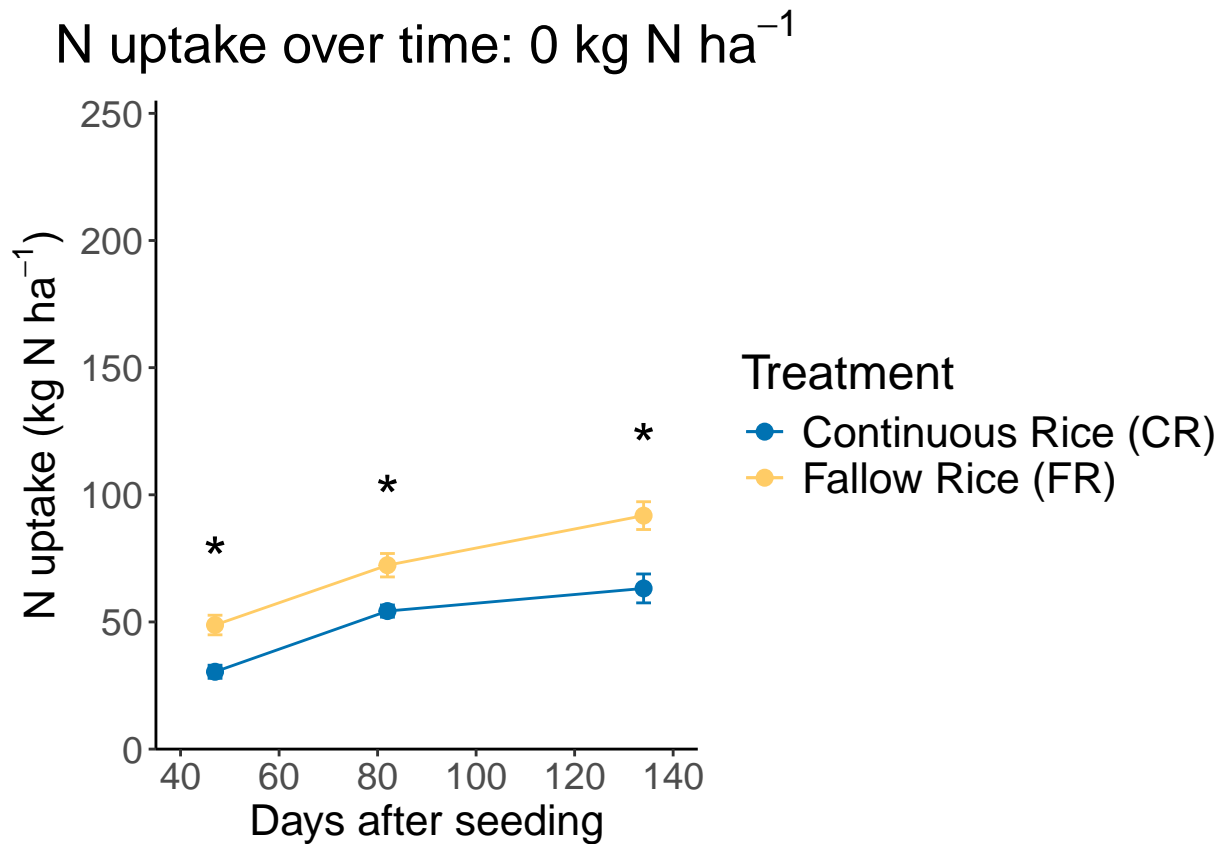
185N

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")
```
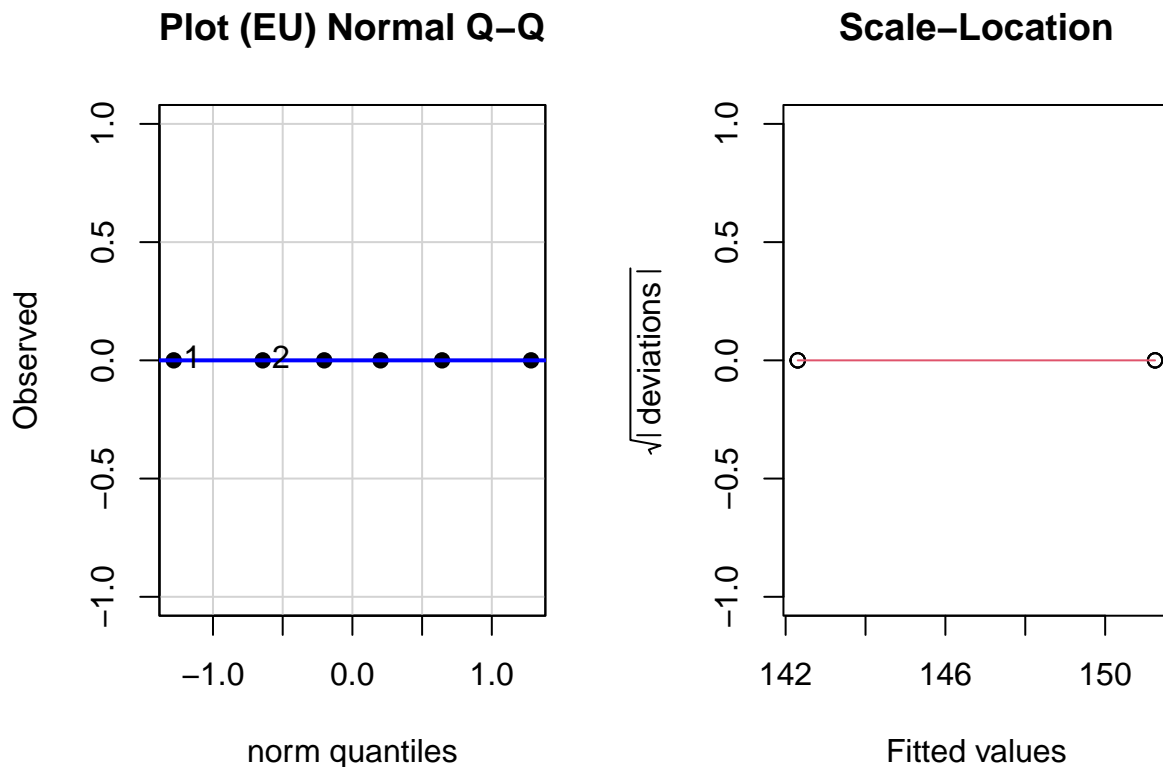


```
N_185_means_2021 = emmeans(N_185_model_2021,spec = 'Treatment',by = 'Stage')
N_185_effects_2021 = contrast(N_185_means_2021, method = 'pairwise', adjust = "tukey")
summary(N_185_effects_2021)
```

```
## 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
```

```r
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

```r
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, 1
  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_tot
  #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_k
  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
##
```

22

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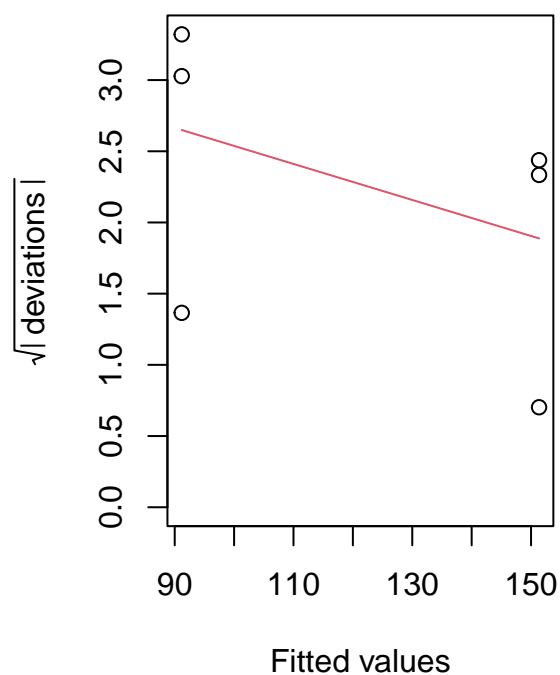
```
pls205_diagnostics(N_185_model_2022, EU="Blk:Treatment")
```

Plot (EU) Normal Q–Q
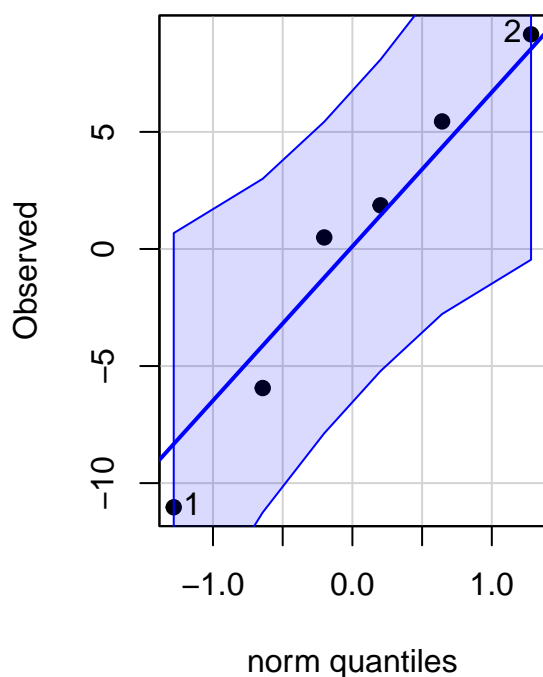
Scale–Location


```
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,
```

```r
    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_tot
    #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

```r
N_185_model_average <- lmer(N_total_kgha~Treatment*Stage*Year+(1|Blk:Treatment)+(1|Blk), data = N_185_a
```

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

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

```r
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
```

```r
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")
```
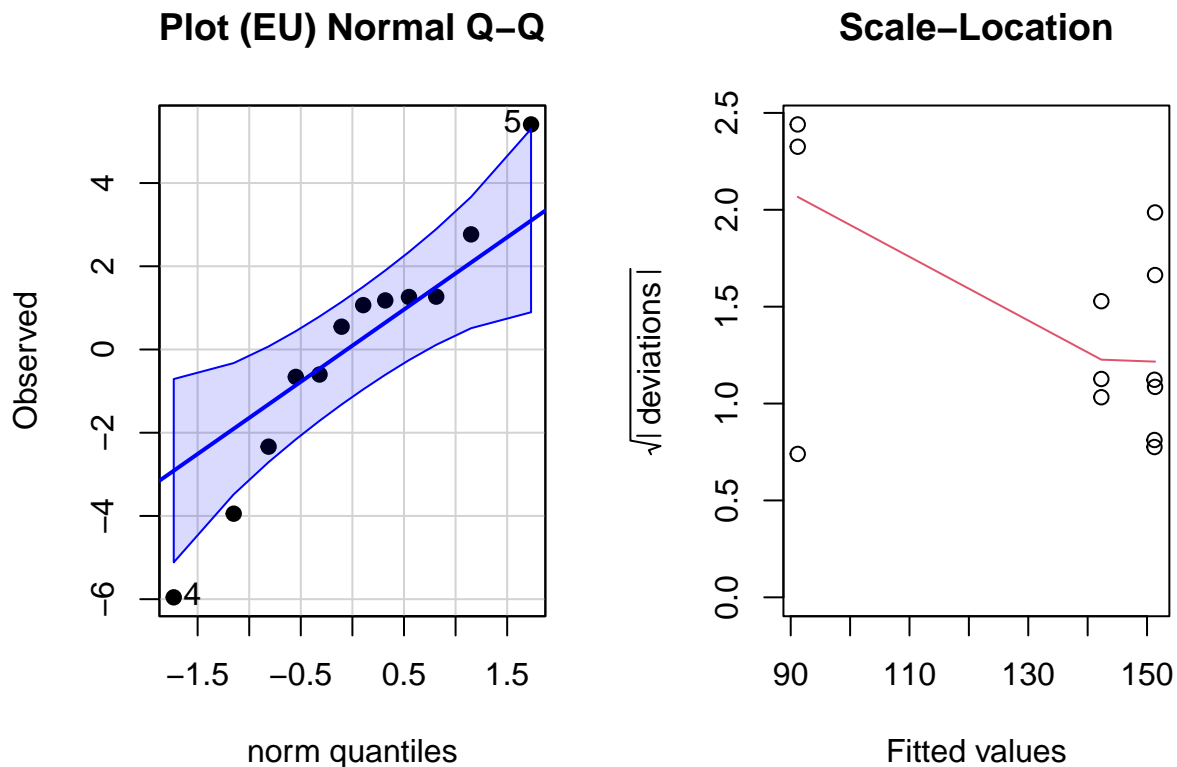


```
N_185_means_average = emmeans(N_185_model_average,spec = 'Treatment',by = 'Stage')
```

```
## 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
```

```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

```r
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.
```

```r
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 = 16),legend.title = element_text(size = 18))+
  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_tot
  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
```

N uptake over time: 185 kg N ha^{-1}
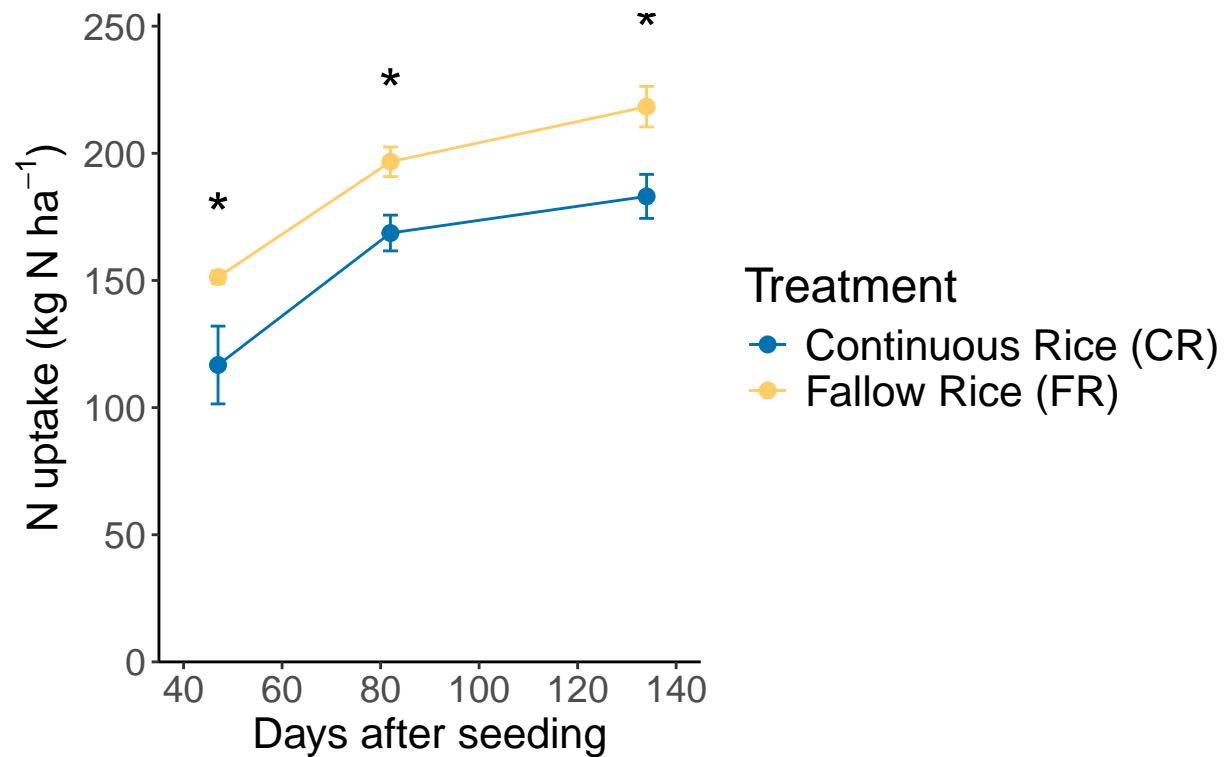
Combine graphs

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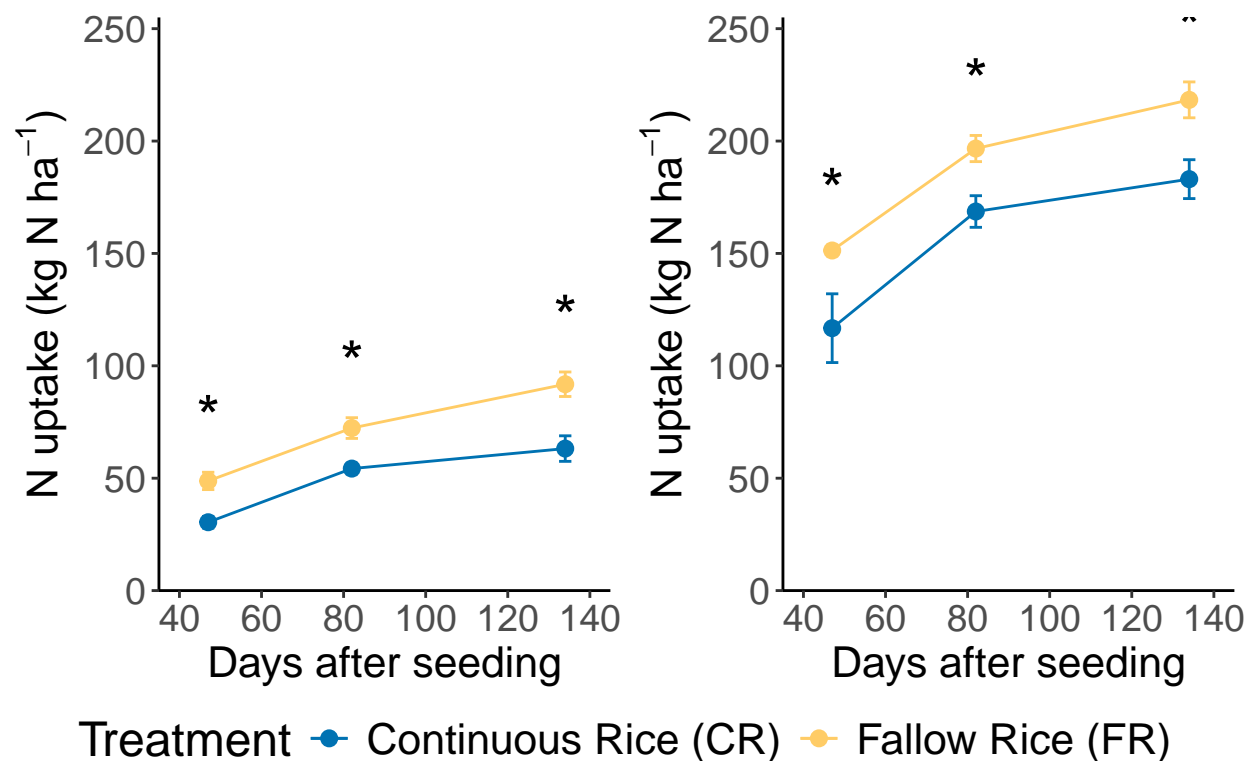
N uptake over time: 0 kg N uptake over time: 185 kg


```
ggsave(all_N_uptake_overtime,
       filename = "all_N_uptake_overtime.jpg",
       path = "C:/Users/zhang/Documents/GitHub/FallowRice_ContinuousRice_AgronomicPerformance/Figures",
       height = 20, width = 30,
       units = "cm", dpi=400)
```