

Soil N and Fert N Analysis

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Necessary libraries

Data Organisation

Read from excel

```
all_data <- read_excel("15N_N_Uptake_MaturitySummed.xlsx", sheet = 1)
str(all_data)
```

```
## tibble [84 x 10] (S3: tbl_df/tbl/data.frame)
## $ Sample.ID : chr [1:84] "107 112 Pre" "207 212 Pre" "307 312 Pre" "101 106 Pre" ...
## $ Field      : chr [1:84] "CR" "CR" "CR" "RF" ...
## $ Blk        : num [1:84] 1 2 3 1 2 3 1 2 3 1 ...
## $ Topdress   : chr [1:84] "N" "N" "N" "N" ...
## $ Stage      : chr [1:84] "PrePlant" "PrePlant" "PrePlant" "PrePlant" ...
## $ fertiliser_N: num [1:84] 0 0 0 0 0 ...
## $ soil_N     : num [1:84] 0 0 0 0 0 ...
## $ Days       : num [1:84] 0 0 0 0 0 0 47 47 47 47 ...
## $ Year       : num [1:84] 2021 2021 2021 2021 2021 ...
## $ Days_graph : num [1:84] 0 0 0 0 0 0 46 46 46 46 ...
```

Clean up variables

```
all_data <- mutate_if(all_data, is.character, as.factor)
all_data$Blk <- as.factor(all_data$Blk)
all_data$Year <- as.factor(all_data$Year)

str(all_data)
```

```
## tibble [84 x 10] (S3: tbl_df/tbl/data.frame)
## $ Sample.ID : Factor w/ 72 levels "101 106 minus H",...: 12 24 36 6 18 30 9 21 33 3 ...
## $ Field      : Factor w/ 2 levels "CR","RF": 1 1 1 2 2 2 1 1 1 2 ...
## $ Blk        : Factor w/ 6 levels "1","2","3","4",...: 1 2 3 1 2 3 1 2 3 1 ...
## $ Topdress   : Factor w/ 2 levels "N","Y": 1 1 1 1 1 1 1 1 1 1 ...
## $ Stage      : Factor w/ 4 levels "Heading","Maturity",...: 4 4 4 4 4 4 3 3 3 3 ...
## $ fertiliser_N: num [1:84] 0 0 0 0 0 ...
## $ soil_N     : num [1:84] 0 0 0 0 0 ...
## $ Days       : num [1:84] 0 0 0 0 0 0 47 47 47 47 ...
## $ Year       : Factor w/ 2 levels "2021","2022": 1 1 1 1 1 1 1 1 1 1 ...
## $ Days_graph : num [1:84] 0 0 0 0 0 0 46 46 46 46 ...
```

Sub dataset for “preplant” and “topdress”

```
preplant <- all_data %>% filter(Topdress == "N")
str(preplant)
```

```
## tibble [48 x 10] (S3: tbl_df/tbl/data.frame)
## $ Sample.ID : Factor w/ 72 levels "101 106 minus H",...: 12 24 36 6 18 30 9 21 33 3 ...
## $ Field      : Factor w/ 2 levels "CR","RF": 1 1 1 2 2 2 1 1 1 2 ...
## $ Blk        : Factor w/ 6 levels "1","2","3","4",...: 1 2 3 1 2 3 1 2 3 1 ...
## $ Topdress   : Factor w/ 2 levels "N","Y": 1 1 1 1 1 1 1 1 1 1 ...
## $ Stage      : Factor w/ 4 levels "Heading","Maturity",...: 4 4 4 4 4 4 3 3 3 3 ...
## $ fertiliser_N: num [1:48] 0 0 0 0 0 0 ...
## $ soil_N     : num [1:48] 0 0 0 0 0 0 ...
## $ Days       : num [1:48] 0 0 0 0 0 0 47 47 47 47 ...
## $ Year       : Factor w/ 2 levels "2021","2022": 1 1 1 1 1 1 1 1 1 1 ...
## $ Days_graph : num [1:48] 0 0 0 0 0 0 46 46 46 46 ...
```

```
topdress <- all_data %>% filter(Topdress == "Y")
str(topdress)
```

```
## tibble [36 x 10] (S3: tbl_df/tbl/data.frame)
## $ Sample.ID : Factor w/ 72 levels "101 106 minus H",...: 10 22 34 4 16 28 11 23 35 5 ...
## $ Field      : Factor w/ 2 levels "CR","RF": 1 1 1 2 2 2 1 1 1 2 ...
## $ Blk        : Factor w/ 6 levels "1","2","3","4",...: 1 2 3 1 2 3 1 2 3 1 ...
## $ Topdress   : Factor w/ 2 levels "N","Y": 2 2 2 2 2 2 2 2 2 2 ...
## $ Stage      : Factor w/ 4 levels "Heading","Maturity",...: 1 1 1 1 1 1 2 2 2 2 ...
## $ fertiliser_N: num [1:36] 10.99 9.79 9.19 9.3 10.05 ...
## $ soil_N     : num [1:36] 71.9 65.8 59.8 80.9 73.6 ...
## $ Days       : num [1:36] 81 81 81 81 81 81 124 124 124 124 ...
## $ Year       : Factor w/ 2 levels "2021","2022": 1 1 1 1 1 1 1 1 1 1 ...
## $ Days_graph : num [1:36] 81 81 81 81 81 81 127 127 127 127 ...
```

Initial look

Year interaction

```
soil_N_try <- lm(soil_N~Field*Year+Stage, data = preplant)
anova(soil_N_try)
```

```
## Analysis of Variance Table
##
## Response: soil_N
##          Df Sum Sq Mean Sq F value    Pr(>F)
## Field      1   1512   1511.8  20.8981 4.399e-05 ***
## Year       1      1      0.9   0.0122  0.9125
## Stage      3   71063 23687.6 327.4475 < 2.2e-16 ***
## Field:Year  1     12     11.6   0.1608  0.6905
## Residuals 41    2966    72.3
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
fert_N_try <- lm(fertiliser_N~Field*Year+Stage, data = preplant)
anova(fert_N_try)
```

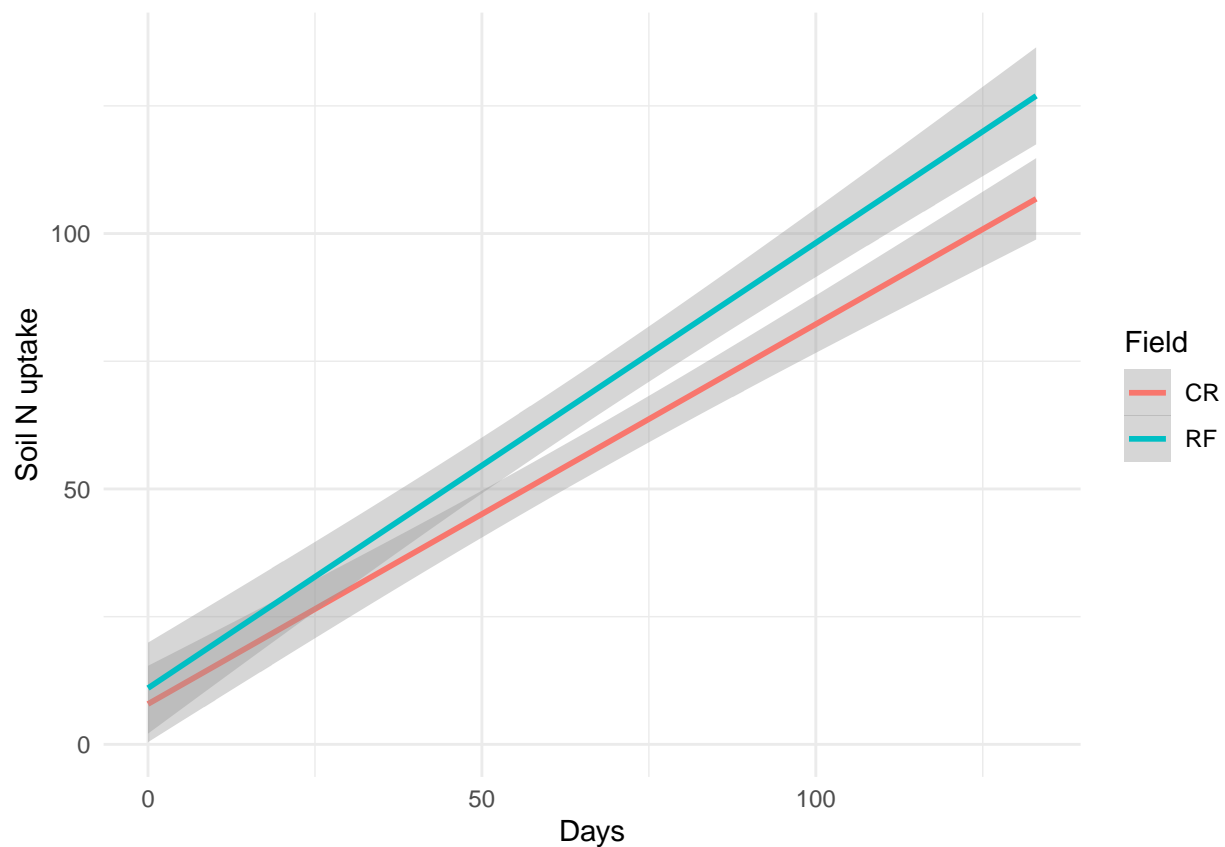
```
## Analysis of Variance Table
##
## Response: fertiliser_N
##           Df Sum Sq Mean Sq  F value    Pr(>F)
## Field      1   35.8    35.8    1.1973  0.280249
## Year       1  294.6   294.6    9.8470  0.003147 **
## Stage      3 15449.4  5149.8  172.1176 < 2.2e-16 ***
## Field:Year  1   119.9   119.9    4.0060  0.051986 .
## Residuals 41  1226.7    29.9
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Seems that only field has a very strong effect. Days expected to be very strong as N uptake will increase over time.

Visualisation

```
ggplot(preplant, aes(x = Days, y = soil_N, color = Field)) +
  geom_smooth(method = gam) +
  labs(x = "Days", y = "Soil N uptake", color = "Field", linetype = "Year") +
  scale_linetype_manual(values = c("solid", "dashed")) +
  theme_minimal()
```

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



Preplant Soil N

Remove day 0

```
preplant_no0 <-subset(preplant, Days != 0)
```

```
str(preplant_no0)
```

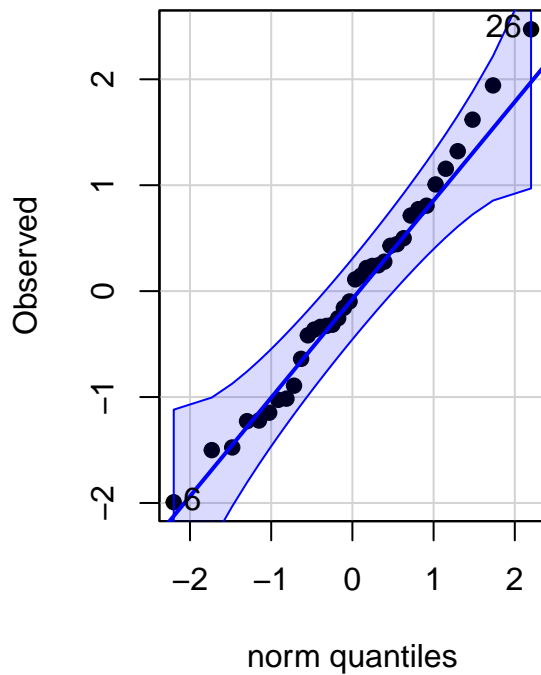
```
## tibble [36 x 10] (S3: tbl_df/tbl/data.frame)
##  $ Sample.ID    : Factor w/ 72 levels "101 106 minus H",...: 9 21 33 3 15 27 7 19 31 1 ...
##  $ Field         : Factor w/ 2 levels "CR","RF": 1 1 1 2 2 2 1 1 1 2 ...
##  $ Blk           : Factor w/ 6 levels "1","2","3","4",...: 1 2 3 1 2 3 1 2 3 1 ...
##  $ Topdress      : Factor w/ 2 levels "N","Y": 1 1 1 1 1 1 1 1 1 1 ...
##  $ Stage         : Factor w/ 4 levels "Heading","Maturity",...: 3 3 3 3 3 3 1 1 1 1 ...
##  $ fertiliser_N  : num [1:36] 48.5 37 41.9 46.7 36.2 ...
##  $ soil_N        : num [1:36] 54 49.6 60 71.4 62.1 ...
##  $ Days          : num [1:36] 47 47 47 47 47 47 81 81 81 81 ...
##  $ Year          : Factor w/ 2 levels "2021","2022": 1 1 1 1 1 1 1 1 1 1 ...
##  $ Days_graph    : num [1:36] 46 46 46 46 46 46 81 81 81 81 ...
```

Model selection and testing

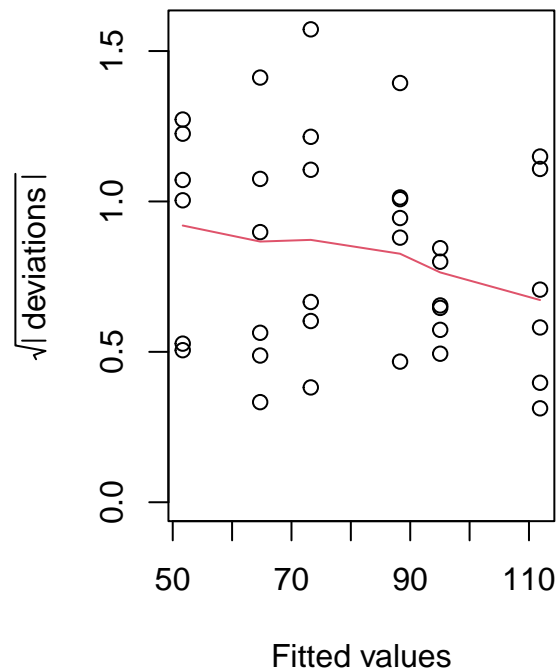
```
preplant_soil_N_model <- lm(soil_N~Field*Stage, data = preplant_no0)
```

```
pls205_diagnostics(preplant_soil_N_model)
```

Plot (EU) Normal Q-Q



Scale-Location



```
preplant_soil_N_means = emmeans(preplant_soil_N_model,spec = 'Field',by = 'Stage')
preplant_soil_N_effects = contrast(preplant_soil_N_means, method = 'pairwise', adjust = "tukey")

summary(preplant_soil_N_effects)
```

```
## Stage = Heading:
## contrast estimate SE df t.ratio p.value
## CR - RF -15.0 5.22 30 -2.880 0.0073
##
## Stage = Maturity:
## contrast estimate SE df t.ratio p.value
## CR - RF -16.8 5.22 30 -3.221 0.0031
##
## Stage = PI:
## contrast estimate SE df t.ratio p.value
## CR - RF -13.0 5.22 30 -2.498 0.0182
```

```
cld(preplant_soil_N_means)
```

```
## Stage = Heading:
## Field emmean SE df lower.CL upper.CL .group
## CR 73.3 3.69 30 65.7 80.8 1
## RF 88.3 3.69 30 80.8 95.8 2
##
```

```
## Stage = Maturity:
## Field emmean SE df lower.CL upper.CL .group
## CR 95.0 3.69 30 87.5 102.6 1
## RF 111.9 3.69 30 104.3 119.4 2
##
## Stage = PI:
## Field emmean SE df lower.CL upper.CL .group
## CR 51.7 3.69 30 44.1 59.2 1
## RF 64.7 3.69 30 57.2 72.3 2
##
## 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.
```

Graphing preplant soil_N mean and SD

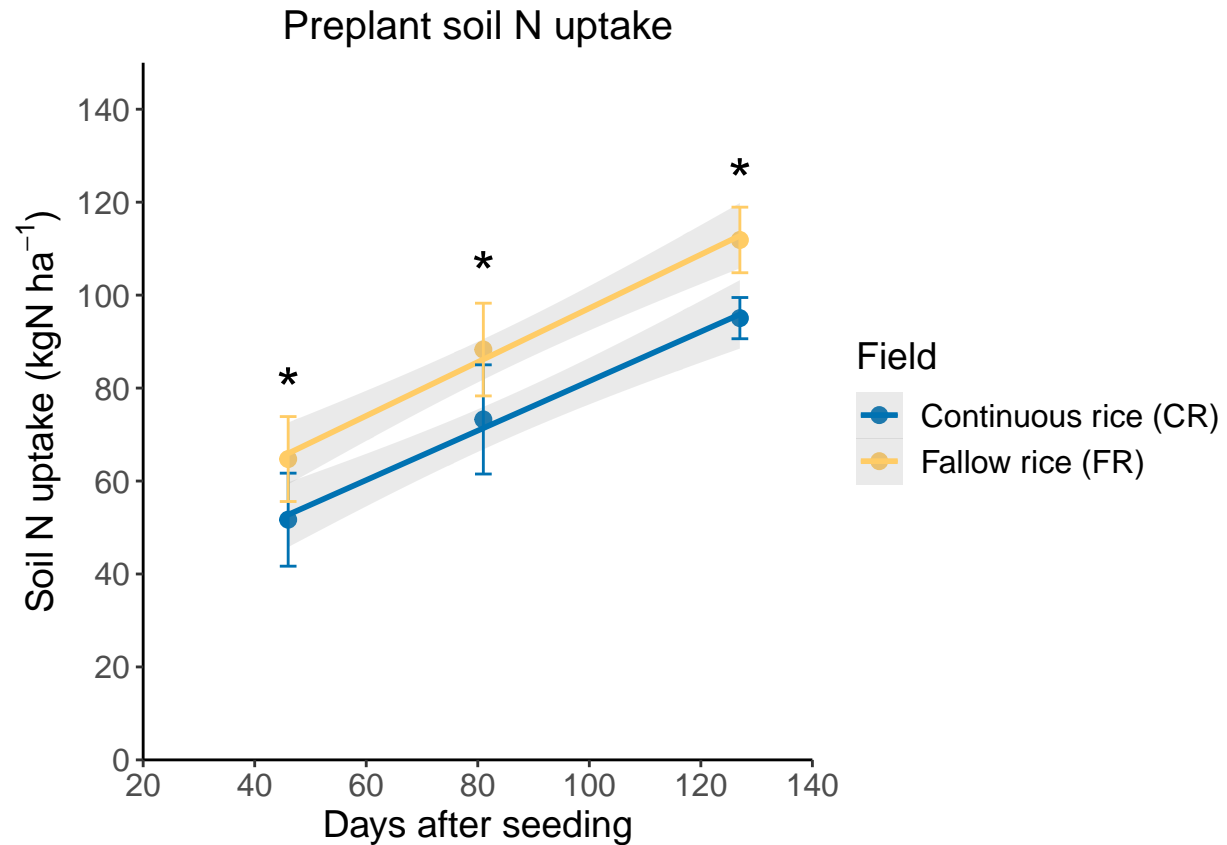
```
preplant_soilN_graphing <- preplant_no0 %>% group_by(Field, Days_graph) %>%
  mutate(soil_N_sd = sd(soil_N)) %>%
  summarise(soil_N = mean(soil_N),
            soil_N_sd = mean(soil_N_sd))
```

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

```
preplant_soil_N_graph <-
ggplot(preplant_no0, aes(x=Days_graph, y=soil_N, color=Field))+
  geom_point(data=preplant_soilN_graphing, size=2.5)+
  geom_smooth(method = lm, alpha=0.2)+
  scale_color_manual(values=c("#0072B2", "#FFCC66"), name = "Field", labels = c("Continuous rice (CR)", "Rice fallow (RF)")),
  scale_x_continuous(name="Days after seeding", limits = c(20, 140), expand = c(0, 0), breaks = seq(0, 140, 20)),
  scale_y_continuous(name=expression("Soil N uptake (kgN ha"^-1)*"), limits = c(0, 150), expand = c(0, 0), breaks = seq(0, 150, 20)),
  geom_errorbar(data=preplant_soilN_graphing, aes(ymin=soil_N-soil_N_sd, ymax=soil_N+soil_N_sd), width=0.5),
  #geom_vline(xintercept = c(41, 50, 78, 84, 121, 136), linetype = "dashed", color = "black") +
  theme_classic()+theme(axis.text = element_text(size = 12), axis.title = element_text(size=14))+
  theme(legend.text = element_text(size = 12), legend.title = element_text(size = 14))+
  ggtitle("Preplant soil N uptake")+
  theme(plot.title = element_text(hjust = 0.5, size = 15))+
  annotate(
    "text",
    x = c(46, 81, 127), # X-axis positions for annotations
    y = c(75, 100, 120), # Y-axis positions for annotations
    label = "*",
    size = 8,
    vjust = 0 # Adjust vertical position of asterisks
  )

preplant_soil_N_graph
```

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



```
ggsave(preplant_soil_N_graph, filename = "preplant_soil_N_graph.png", height = 15, width = 20, units = "cm")
```

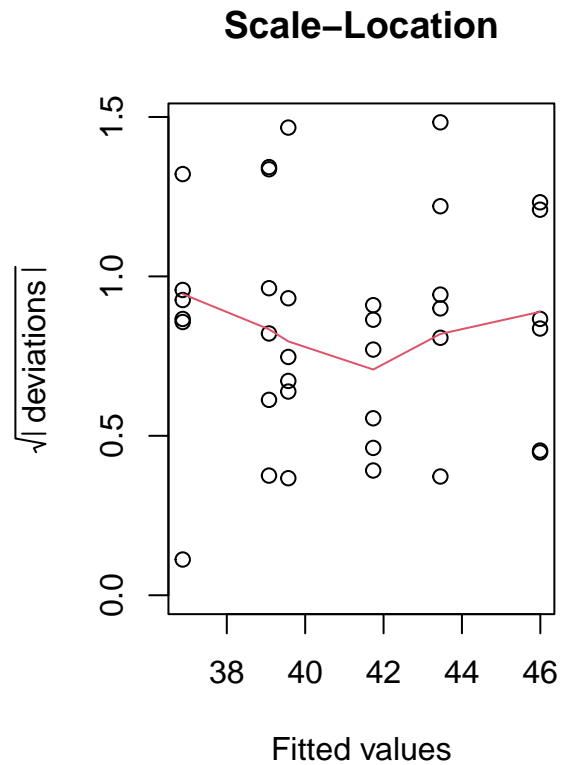
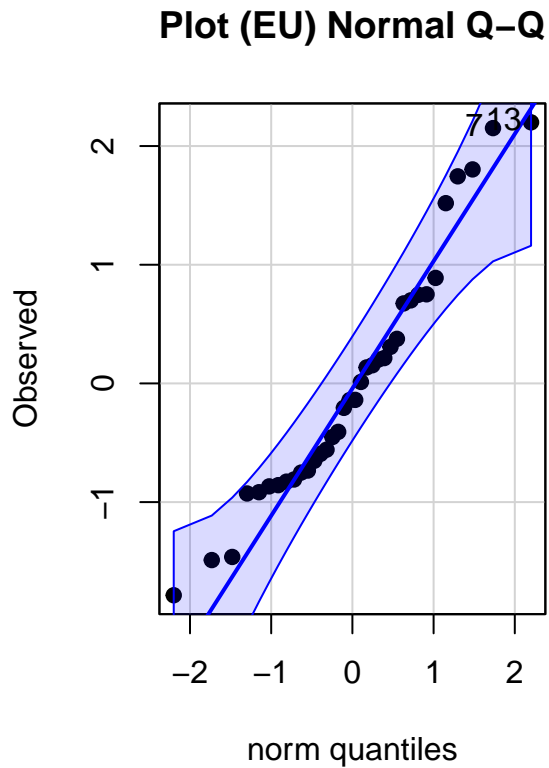
```
## 'geom_smooth()' using formula = 'y ~ x'
```

Preplant Fert N

Model selection and testing

```
preplant_fert_N_model_huehue <- lm(fertiliser_N~Field*Stage+Year, data = preplant_no0)

preplant_fert_N_model <- lm(fertiliser_N~Field*Stage, data = preplant_no0)
pls205_diagnostics(preplant_fert_N_model)
```

```
preplant_fert_N_means = emmeans(preplant_fert_N_model, spec = 'Field', by = 'Stage')
preplant_fert_N_effects = contrast(preplant_fert_N_means, method = 'pairwise', adjust = "tukey")

summary(preplant_fert_N_effects)
```

```
## Stage = Heading:
## contrast estimate SE df t.ratio p.value
## CR - RF      0.492 4.2 30   0.117  0.9074
##
## Stage = Maturity:
## contrast estimate SE df t.ratio p.value
## CR - RF     -2.543 4.2 30  -0.606  0.5492
##
## Stage = PI:
## contrast estimate SE df t.ratio p.value
## CR - RF      -4.860 4.2 30  -1.158  0.2561
```

```
cld(preplant_fert_N_means)
```

```
## Stage = Heading:
## Field emmean SE df lower.CL upper.CL .group
## RF      39.1 2.97 30    33.0    45.1    1
## CR      39.6 2.97 30    33.5    45.6    1
##
```

```
## Stage = Maturity:
## Field emmean SE df lower.CL upper.CL .group
## CR 43.5 2.97 30 37.4 49.5 1
## RF 46.0 2.97 30 39.9 52.1 1
##
## Stage = PI:
## Field emmean SE df lower.CL upper.CL .group
## CR 36.9 2.97 30 30.8 42.9 1
## RF 41.7 2.97 30 35.7 47.8 1
##
## 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.
```

Graphing preplant fert_N mean and SD

```
preplant_fertiliser_N_graphing <- preplant_no0 %>% group_by(Field, Days_graph) %>%
  mutate(fertiliser_N_sd = sd(fertiliser_N)) %>%
  summarise(fertiliser_N = mean(fertiliser_N),
            fertiliser_N_sd = mean(fertiliser_N_sd))
```

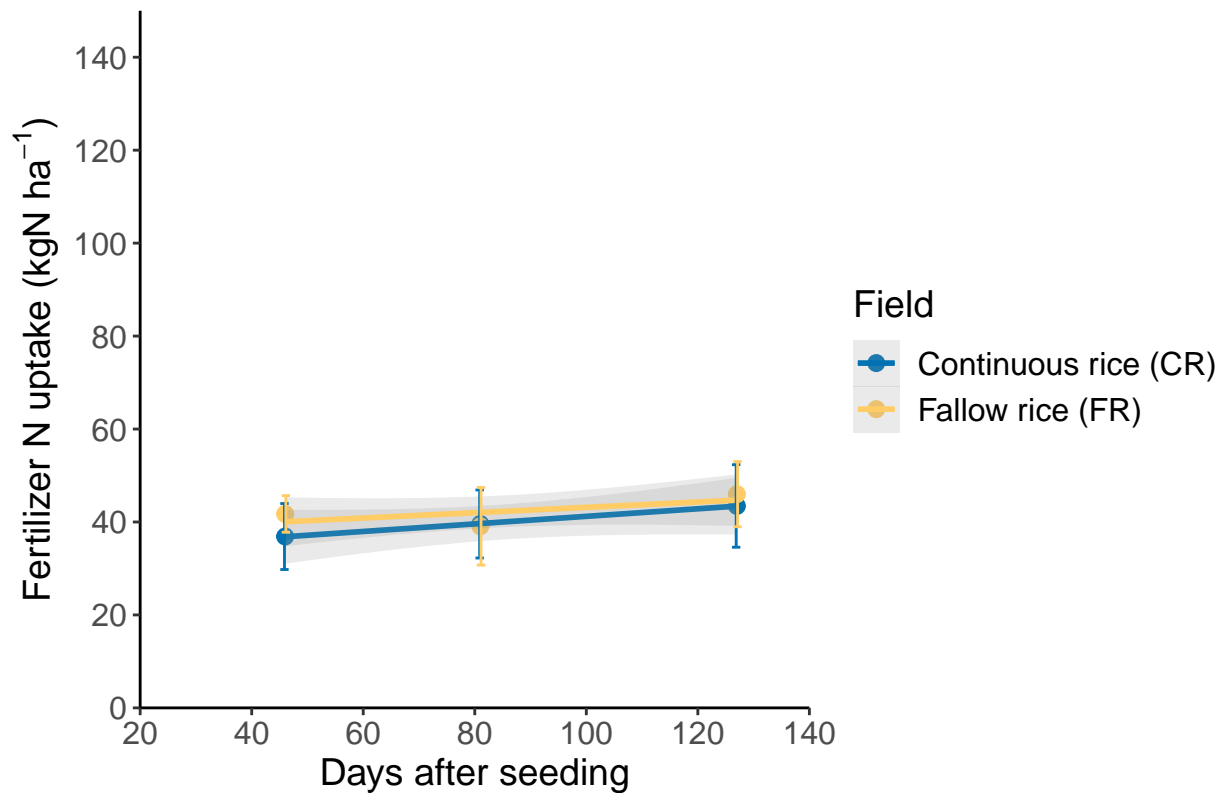
```
## 'summarise()' has grouped output by 'Field'. You can override using the
## '.groups' argument.
```

```
preplant_fertiliser_N_graph <-
ggplot(preplant_no0, aes(x=Days_graph, y=fertiliser_N, color=Field))+
  geom_point(data=preplant_fertiliser_N_graphing, size=2.5)+
  geom_smooth(method = lm, alpha=0.2)+
  scale_color_manual(values=c("#0072B2", "#FFCC66"), name = "Field", labels = c("Continuous rice (CR)", "Preplant fertilizer N uptake (kgN ha-1)*"),
  scale_x_continuous(name="Days after seeding", limits = c(20, 140), expand = c(0, 0), breaks = seq(0, 140, 20)),
  scale_y_continuous(name=expression("Fertilizer N uptake (kgN ha-1)*"), limits = c(0, 150), expand = c(0, 0)),
  geom_errorbar(data=preplant_fertiliser_N_graphing, aes(ymin=fertiliser_N-fertiliser_N_sd, ymax=fertiliser_N+fertiliser_N_sd),
  #geom_vline(xintercept = c(41, 50, 78, 84, 121, 136), linetype = "dashed", color = "black") +
  theme_classic()+
  theme(axis.text = element_text(size = 12), axis.title = element_text(size=14))+
  theme(legend.text = element_text(size = 12), legend.title = element_text(size = 14))+
  ggtitle("Preplant fertilizer N uptake")+
  theme(plot.title = element_text(hjust = 0.5, size = 15))

preplant_fertiliser_N_graph
```

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

Preplant fertilizer N uptake



```
ggsave(preplant_fertiliser_N_graph, filename = "preplant_fertiliser_N_graph.png", height = 15, width = 15)
```

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

Topdress Soil N

Remove day 0

```
topdress_no0 <-subset(topdress, Days != 0)
```

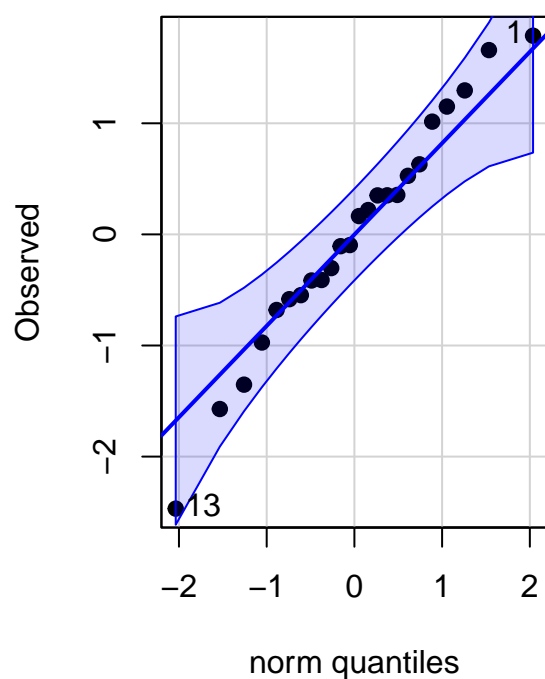
```
str(topdress_no0)
```

```
## tibble [24 x 10] (S3: tbl_df/tbl/data.frame)
##  $ Sample.ID      : Factor w/ 72 levels "101 106 minus H",...: 10 22 34 4 16 28 11 23 35 5 ...
##  $ Field           : Factor w/ 2 levels "CR","RF": 1 1 1 2 2 2 1 1 1 2 ...
##  $ Blk             : Factor w/ 6 levels "1","2","3","4",...: 1 2 3 1 2 3 1 2 3 1 ...
##  $ Topdress        : Factor w/ 2 levels "N","Y": 2 2 2 2 2 2 2 2 2 2 ...
##  $ Stage           : Factor w/ 4 levels "Heading","Maturity",...: 1 1 1 1 1 1 2 2 2 2 ...
##  $ fertiliser_N    : num [1:24] 10.99 9.79 9.19 9.3 10.05 ...
##  $ soil_N          : num [1:24] 71.9 65.8 59.8 80.9 73.6 ...
##  $ Days            : num [1:24] 81 81 81 81 81 81 124 124 124 124 ...
##  $ Year            : Factor w/ 2 levels "2021","2022": 1 1 1 1 1 1 1 1 1 1 ...
##  $ Days_graph      : num [1:24] 81 81 81 81 81 81 127 127 127 127 ...
```

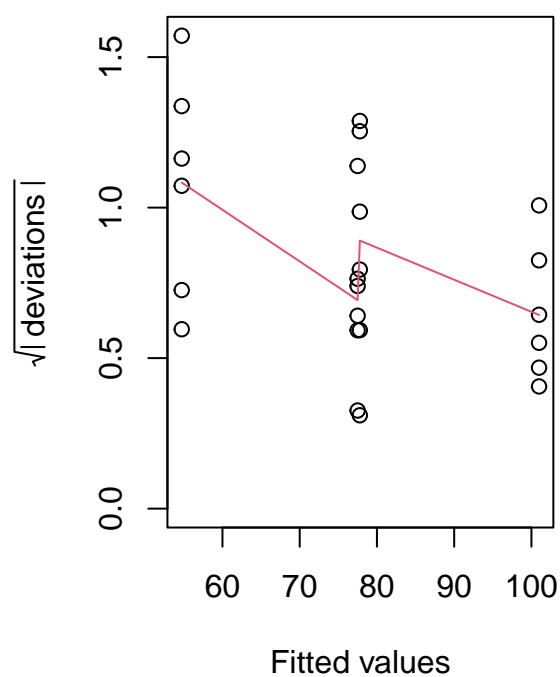
Model selection and testing

```
topdress_soil_N_model <- lm(soil_N~Field*Stage, data = topdress_no0)
pls205_diagnostics(topdress_soil_N_model)
```

Plot (EU) Normal Q-Q



Scale-Location



```
topdress_soil_N_means = emmeans(topdress_soil_N_model, spec = 'Field', by = 'Stage')
topdress_soil_N_effects = contrast(topdress_soil_N_means, method = 'pairwise', adjust = "tukey")
summary(topdress_soil_N_effects)
```

```
## Stage = Heading:
## contrast estimate SE df t.ratio p.value
## CR - RF -22.8 6.08 20 -3.743 0.0013
##
## Stage = Maturity:
## contrast estimate SE df t.ratio p.value
## CR - RF -23.2 6.08 20 -3.814 0.0011
```

```
cld(topdress_soil_N_means)
```

```
## Stage = Heading:
## Field emmean SE df lower.CL upper.CL .group
```

```
## CR      54.7 4.3 20      45.8      63.7 1
## RF      77.5 4.3 20      68.5      86.5 2
##
## Stage = Maturity:
## Field emmean SE df lower.CL upper.CL .group
## CR      77.8 4.3 20      68.8      86.8 1
## RF     101.0 4.3 20      92.0     110.0 2
##
## 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.
```

Graphing topdress soil_N mean and SD

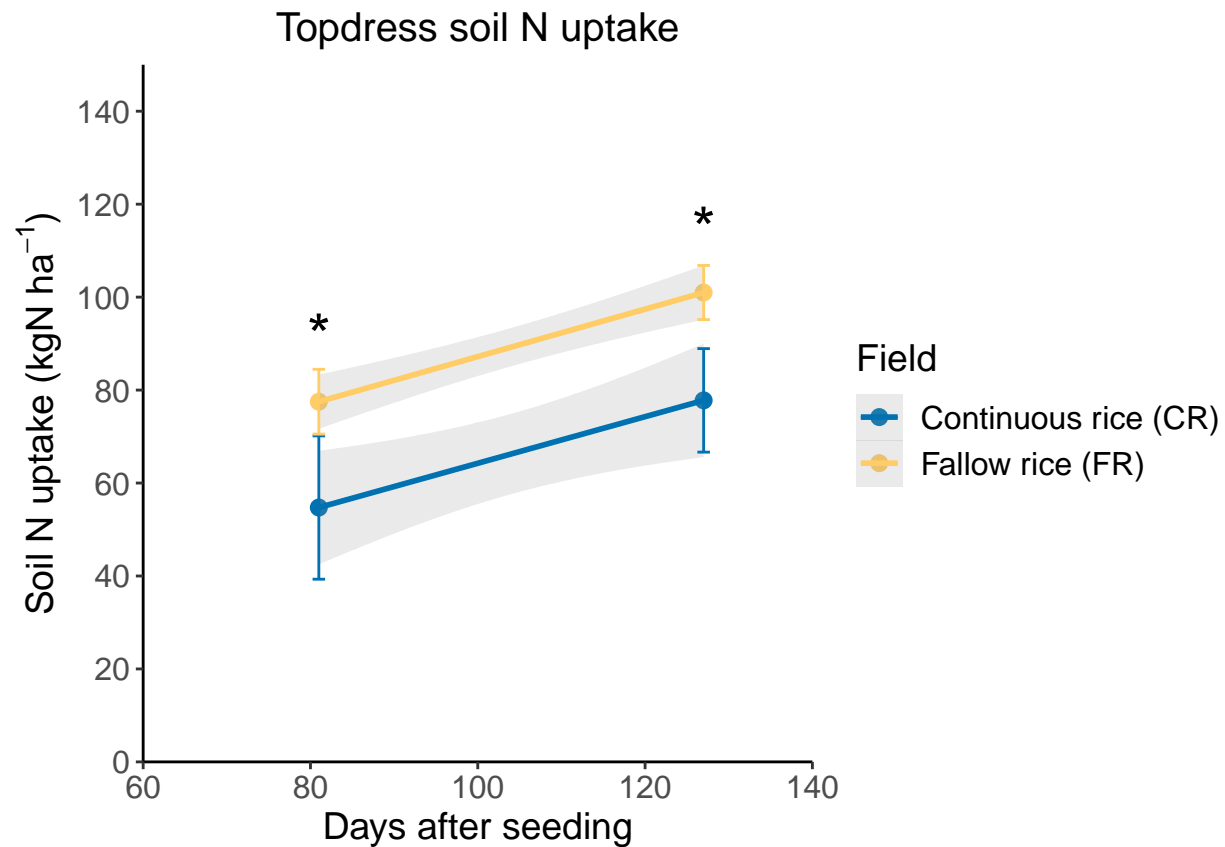
```
topdress_soil_N_graphing <- topdress_no0 %>% group_by(Field, Days_graph) %>%
  mutate(soil_N_sd = sd(soil_N)) %>%
  summarise(soil_N = mean(soil_N),
            soil_N_sd = mean(soil_N_sd))
```

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

```
topdress_soil_N_graph <-
ggplot(topdress_no0, aes(x=Days_graph, y=soil_N, color=Field))+
  geom_point(data=topdress_soil_N_graphing, size=2.5)+
  geom_smooth(method = lm, alpha=0.2)+
  scale_color_manual(values=c("#0072B2", "#FFCC66"), name = "Field", labels = c("Continuous rice (CR)", "Topdress rice (RF)")),
  scale_x_continuous(name="Days after seeding", limits = c(60, 140), expand = c(0, 0), breaks = seq(60, 140, 20)),
  scale_y_continuous(name=expression("Soil N uptake (kgN ha"^-1)*"), limits = c(0, 150), expand = c(0, 0), breaks = seq(0, 150, 20)),
  geom_errorbar(data=topdress_soil_N_graphing, aes(ymin=soil_N-soil_N_sd, ymax=soil_N+soil_N_sd), width=0.5),
  #geom_vline(xintercept = c(78, 84, 121, 136), linetype = "dashed", color = "black") +
  theme_classic()+
  theme(axis.text = element_text(size = 12), axis.title = element_text(size=14))+
  theme(legend.text = element_text(size = 12), legend.title = element_text(size = 14))+
  ggtitle("Topdress soil N uptake")+
  theme(plot.title = element_text(hjust = 0.5, size = 15))+
  annotate(
    "text",
    x = c(81, 127), # X-axis positions for annotations
    y = c(87, 110), # Y-axis positions for annotations
    label = "*",
    size = 8,
    vjust = 0 # Adjust vertical position of asterisks
  )
```

```
topdress_soil_N_graph
```

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



```
ggsave(topdress_soil_N_graph, filename = "topdress_soil_N_graph.png", height = 15, width = 20, units = "in")
```

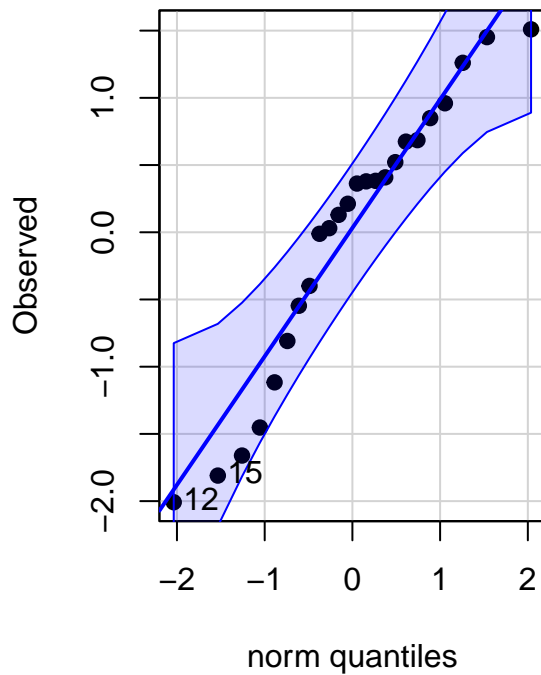
```
## 'geom_smooth()' using formula = 'y ~ x'
```

Topdress Fert N

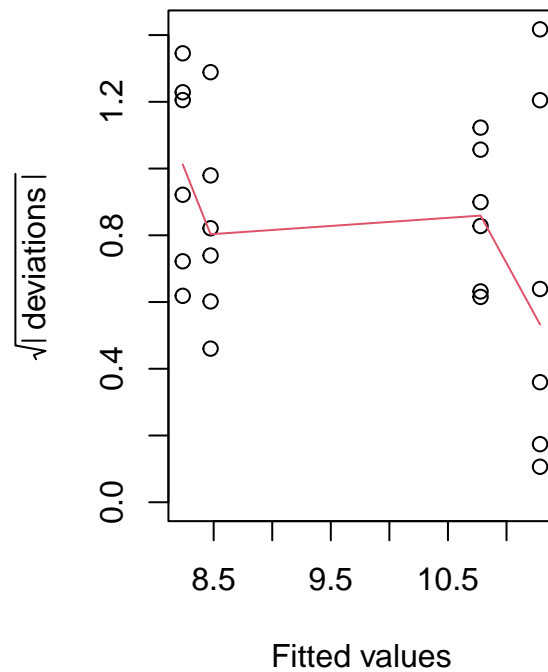
Model selection and testing

```
topdress_fert_N_model <- lm(fertiliser_N~Field*Stage, data = topdress_no0)
pls205_diagnostics(topdress_fert_N_model)
```

Plot (EU) Normal Q-Q



Scale-Location



```
topdress_fert_N_means = emmeans(topdress_fert_N_model,spec = 'Field',by = 'Stage')
topdress_fert_N_effects = contrast(topdress_fert_N_means, method = 'pairwise', adjust = "tukey")

summary(topdress_fert_N_effects)
```

```
## Stage = Heading:
## contrast estimate SE df t.ratio p.value
## CR - RF -2.54 1.16 20 -2.201 0.0397
##
## Stage = Maturity:
## contrast estimate SE df t.ratio p.value
## CR - RF -2.81 1.16 20 -2.435 0.0244
```

```
cld(topdress_fert_N_means)
```

```
## Stage = Heading:
## Field emmean SE df lower.CL upper.CL .group
## CR 8.24 0.817 20 6.53 9.94 1
## RF 10.78 0.817 20 9.07 12.48 2
##
## Stage = Maturity:
## Field emmean SE df lower.CL upper.CL .group
## CR 8.47 0.817 20 6.77 10.18 1
## RF 11.29 0.817 20 9.58 12.99 2
```

```
##
## 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.
```

Graphing topdress fert_N mean and SD

```
topdress_fertiliser_N_graphing <- topdress_no0 %>% group_by(Field, Days_graph) %>%
  mutate(fertiliser_N_sd = sd(fertiliser_N)) %>%
  summarise(fertiliser_N = mean(fertiliser_N),
            fertiliser_N_sd = mean(fertiliser_N_sd))
```

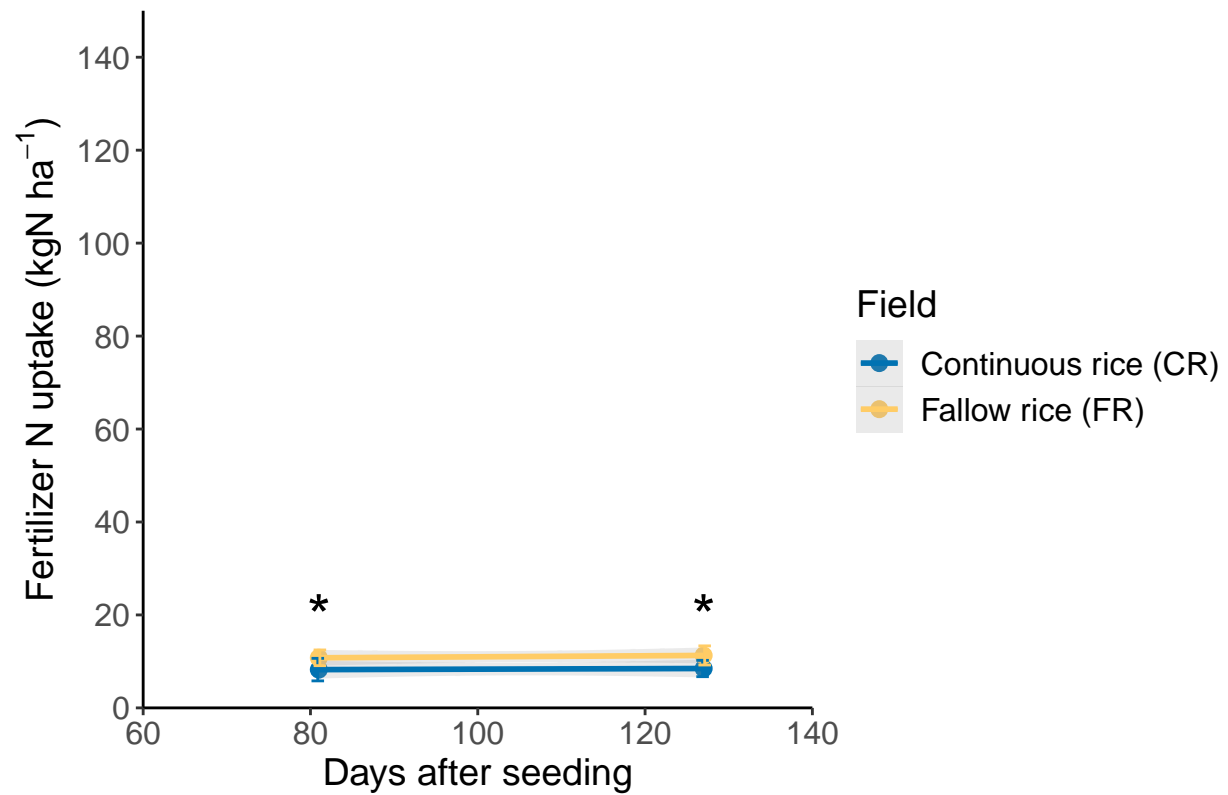
```
## 'summarise()' has grouped output by 'Field'. You can override using the
## '.groups' argument.
```

```
topdress_fertiliser_N_graph <-
ggplot(topdress_no0, aes(x=Days_graph, y=fertiliser_N, color=Field))+
  geom_point(data=topdress_fertiliser_N_graphing, size=2.5)+
  geom_smooth(method = lm, alpha=0.2)+
  scale_color_manual(values=c("#0072B2", "#FFCC66"), name = "Field", labels = c("Continuous rice (CR)",
  scale_x_continuous(name="Days after seeding", limits = c(60, 140), expand = c(0, 0), breaks = seq(0,
  scale_y_continuous(name=expression("Fertilizer N uptake (kgN ha"^-1)*"), limits = c(0, 150), expand
  geom_errorbar(data=topdress_fertiliser_N_graphing, aes(ymin=fertiliser_N-fertiliser_N_sd, ymax=fertil
  #geom_vline(xintercept = c(78, 84, 121, 136), linetype = "dashed", color = "black") +
  theme_classic()+
  theme(axis.text = element_text(size = 12), axis.title = element_text(size=14))+
  theme(legend.text = element_text(size = 12), legend.title = element_text(size = 14))+
  ggtitle("Topdress fertilizer N uptake")+
  theme(plot.title = element_text(hjust = 0.5, size = 15))+
  annotate(
    "text",
    x = c(81, 127), # X-axis positions for annotations
    y = c(15, 15), # Y-axis positions for annotations
    label = "*",
    size = 8,
    vjust = 0 # Adjust vertical position of asterisks
  )

topdress_fertiliser_N_graph
```

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


Topdress fertilizer N uptake



```
ggsave(topdress_fertiliser_N_graph, filename = "topdress_fertiliser_N_graph.png", height = 15, width = 15)
```

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