

# Soil N and Fert N Analysis

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## Necessary libraries

```

library(knitr)
library(ggplot2)
theme_set(theme_bw())
library(emmeans)
library(multcomp)
library(PLS205)
library(lme4)
library(lmerTest)
library(multcompView)
library(car)
library(Rmisc)
library(dplyr) #https://r4ds.had.co.nz/ (Chapter 3, Chapter 5, look at filter and select)
# https://bookdown.org/ansellbr/WEHI_tidyR_course_book/
library(stringr)
library(data.table)
library(GGally)
library(formatR)
library(readxl)
library(mgcv)
library(writexl)

```

## Data Organisation

### Read from excel

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

```
## New names:
## * ' ' -> '...10'
```

```
str(all_data)
```

```

## tibble [60 x 10] (S3: tbl_df/tbl/data.frame)
##  $ Sample.ID      : chr [1:60] "107 112 PI" "207 212 PI" "307 312 PI" "101 106 PI" ...
##  $ Field           : chr [1:60] "CR" "CR" "CR" "RF" ...
##  $ Blk             : chr [1:60] "1" "2" "3" "1" ...
##  $ Topdress        : chr [1:60] "N" "N" "N" "N" ...
##  $ Stage           : chr [1:60] "PI" "PI" "PI" "PI" ...
##  $ fertiliser_N    : num [1:60] 50.3 38.3 43.4 48.4 37.6 ...
##  $ soil_N          : num [1:60] 52.2 48.2 58.4 69.6 60.7 ...
##  $ Days            : num [1:60] 46 46 46 46 46 46 81 81 81 81 ...
##  $ Year            : num [1:60] 2021 2021 2021 2021 2021 ...
##  $ ...10           : num [1:60] 102.4 86.5 101.9 118.1 98.4 ...

```

### 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 [60 x 10] (S3: tbl_df/tbl/data.frame)
## $ Sample.ID : Factor w/ 60 levels "101 106 minus H",...: 8 18 28 3 13 23 9 19 29 4 ...
## $ 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 2 2 2 2 ...
## $ Stage : Factor w/ 3 levels "Heading","Maturity",...: 3 3 3 3 3 3 1 1 1 1 ...
## $ fertiliser_N: num [1:60] 50.3 38.3 43.4 48.4 37.6 ...
## $ soil_N : num [1:60] 52.2 48.2 58.4 69.6 60.7 ...
## $ Days : num [1:60] 46 46 46 46 46 46 81 81 81 81 ...
## $ Year : Factor w/ 2 levels "2021","2022": 1 1 1 1 1 1 1 1 1 1 ...
## $ ...10 : num [1:60] 102.4 86.5 101.9 118.1 98.4 ...

```

## Sub dataset for “preplant” and “topdress”

```

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

## tibble [36 x 10] (S3: tbl_df/tbl/data.frame)
## $ Sample.ID : Factor w/ 60 levels "101 106 minus H",...: 8 18 28 3 13 23 6 16 26 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/ 3 levels "Heading","Maturity",...: 3 3 3 3 3 3 1 1 1 1 ...
## $ fertiliser_N: num [1:36] 50.3 38.3 43.4 48.4 37.6 ...
## $ soil_N : num [1:36] 52.2 48.2 58.4 69.6 60.7 ...
## $ Days : num [1:36] 46 46 46 46 46 46 81 81 81 81 ...
## $ Year : Factor w/ 2 levels "2021","2022": 1 1 1 1 1 1 1 1 1 1 ...
## $ ...10 : num [1:36] 102.4 86.5 101.9 118.1 98.4 ...

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

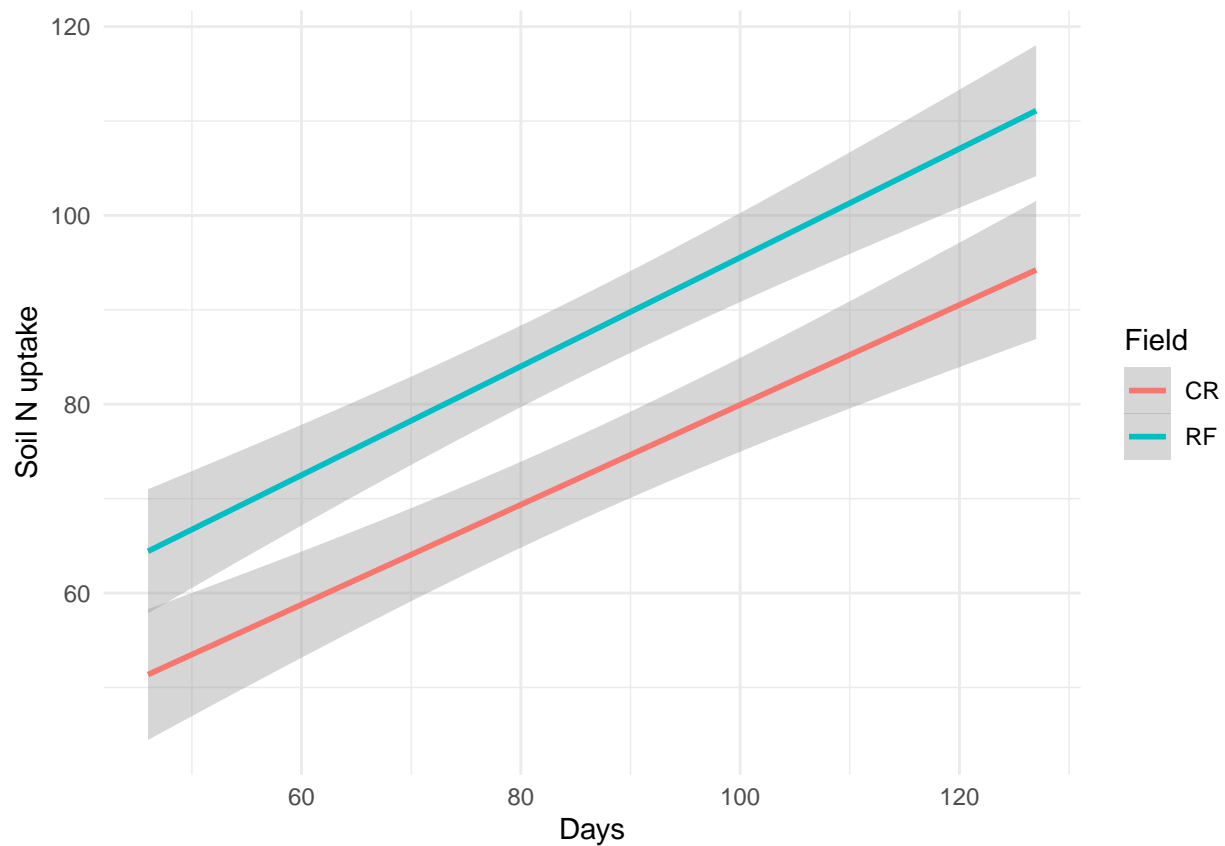
## tibble [24 x 10] (S3: tbl_df/tbl/data.frame)
## $ Sample.ID : Factor w/ 60 levels "101 106 minus H",...: 9 19 29 4 14 24 10 20 30 5 ...
## $ Field : Factor w/ 2 levels "CR","RF": 1 1 1 2 2 2 1 1 1 2 ...
## $ Blk : Factor w/ 6 levels "1","2","3","4",...: 1 2 3 1 2 3 1 2 3 1 ...
## $ Topdress : Factor w/ 2 levels "N","Y": 2 2 2 2 2 2 2 2 2 2 ...
## $ Stage : Factor w/ 3 levels "Heading","Maturity",...: 1 1 1 1 1 1 2 2 2 2 ...
## $ fertiliser_N: num [1:24] 11.41 10.16 9.53 9.65 10.43 ...
## $ soil_N : num [1:24] 71.5 65.4 59.5 80.5 73.2 ...
## $ Days : num [1:24] 81 81 81 81 81 81 127 127 127 127 ...
## $ Year : Factor w/ 2 levels "2021","2022": 1 1 1 1 1 1 1 1 1 1 ...
## $ ...10 : num [1:24] 82.9 75.6 69 90.2 83.6 ...

```

## Intial visualisation

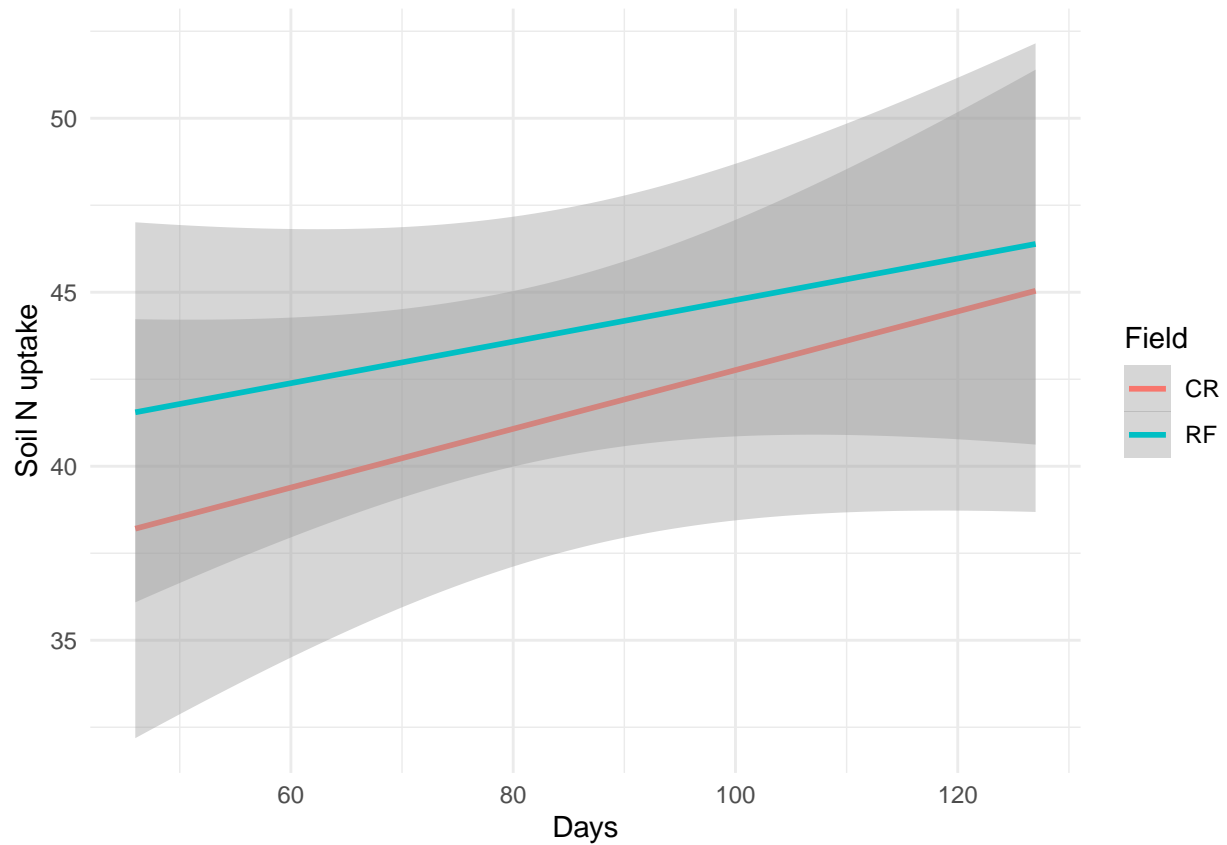
```
#preplant soil N  
ggplot(preplant, aes(x = Days, y = soil_N, color = Field)) +  
  geom_smooth(method = "lm") +  
  labs(x = "Days", y = "Soil N uptake", color = "Field", linetype = "Year") +  
  scale_linetype_manual(values = c("solid", "dashed")) +  
  theme_minimal()
```

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



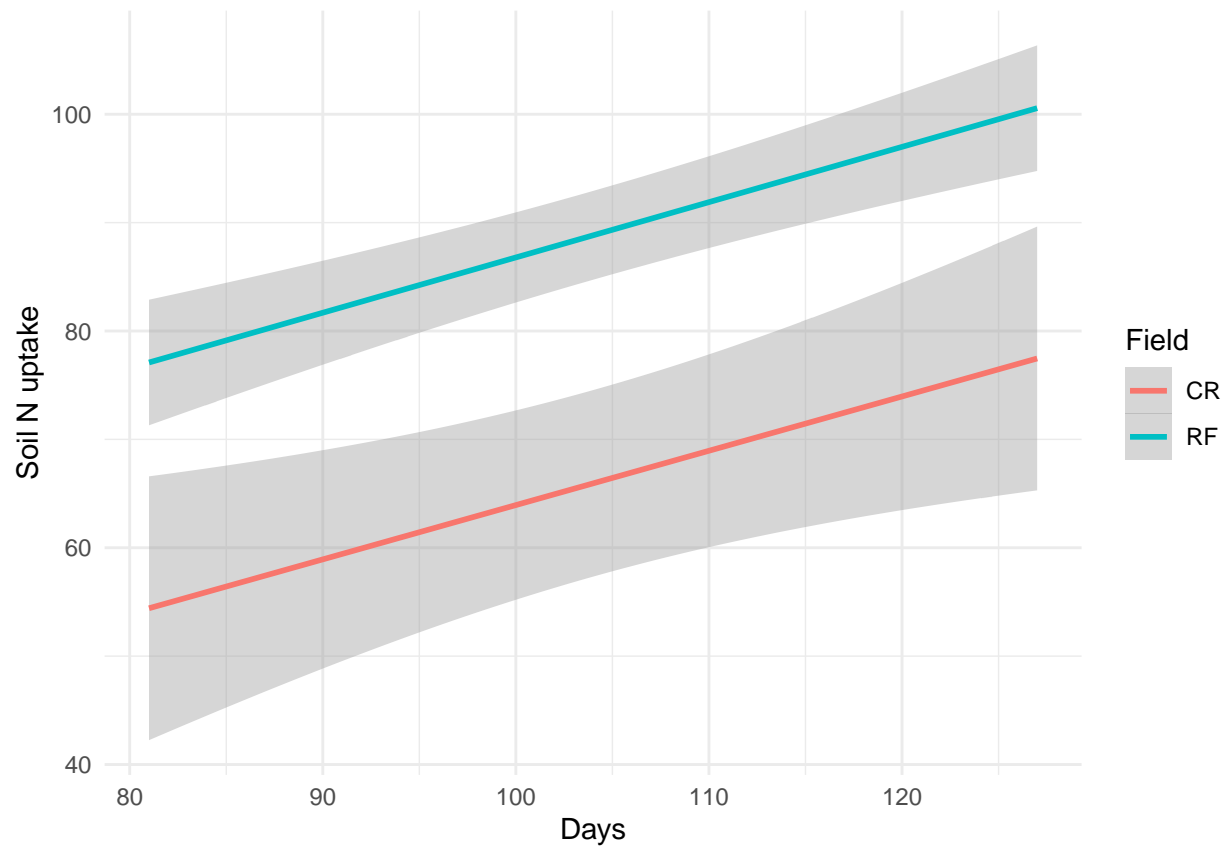
```
#preplant fert N  
ggplot(preplant, aes(x = Days, y = fertiliser_N, color = Field)) +  
  geom_smooth(method = "lm") +  
  labs(x = "Days", y = "Soil N uptake", color = "Field", linetype = "Year") +  
  scale_linetype_manual(values = c("solid", "dashed")) +  
  theme_minimal()
```

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



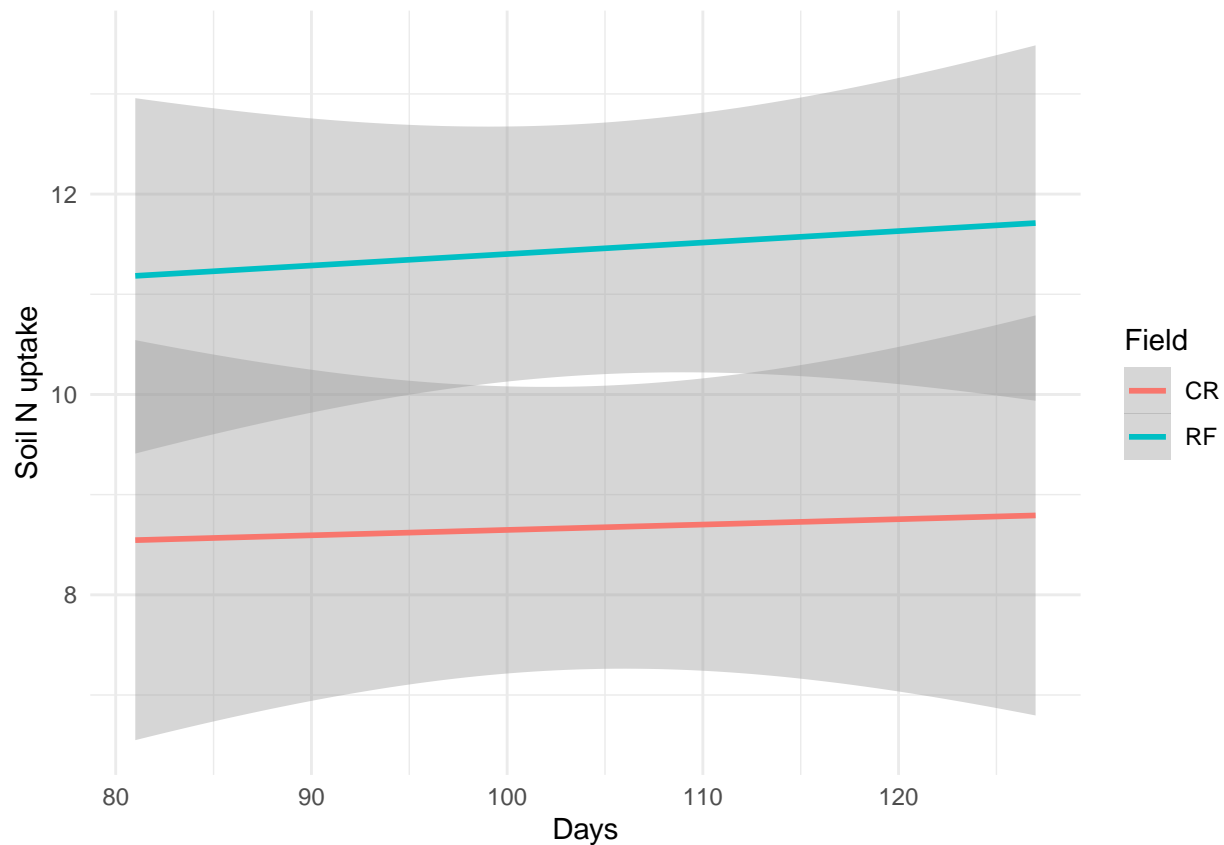
```
#topdress soil N
ggplot(topdress, aes(x = Days, y = soil_N, color = Field)) +
  geom_smooth(method = "lm") +
  labs(x = "Days", y = "Soil N uptake", color = "Field", linetype = "Year") +
  scale_linetype_manual(values = c("solid", "dashed")) +
  theme_minimal()
```

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



```
#topdress fert N
ggplot(topdress, aes(x = Days, y = fertiliser_N, color = Field)) +
  geom_smooth(method = "lm") +
  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

### Model selection and testing

```
preplant_soil_N_model <- lmer(soil_N~Field*Year*Stage+(1|Blk)+(1|Blk:Field), data = preplant)
```

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

```
anova(preplant_soil_N_model)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##
```

	Sum Sq	Mean Sq	NumDF	DenDF	F value	Pr(>F)
## Field	413.6	413.6	1	7.9999	10.1633	0.01284 *
## Year	0.0	0.0	1	7.9999	0.0006	0.98125
## Stage	12175.8	6087.9	2	16.0000	149.6038	4.407e-11 ***
## Field:Year	2.5	2.5	1	7.9999	0.0612	0.81091
## Field:Stage	22.5	11.3	2	16.0000	0.2768	0.76177
## Year:Stage	11.2	5.6	2	16.0000	0.1379	0.87223
## Field:Year:Stage	158.3	79.2	2	16.0000	1.9455	0.17526

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Strong effect of field.

```
preplant_soil_N_means = emmeans(preplant_soil_N_model, spec = 'Field', by = 'Stage')

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

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 -15.1 5.55 7.68 -2.711 0.0276
##
## Stage = Maturity:
## contrast estimate SE df t.ratio p.value
## CR - RF -16.7 5.55 7.68 -3.012 0.0176
##
## Stage = PI:
## contrast estimate SE df t.ratio p.value
## CR - RF -12.9 5.55 7.68 -2.316 0.0505
##
## Results are averaged over the levels of: Year
## Degrees-of-freedom method: kenward-roger

cld(preplant_soil_N_means)

## Stage = Heading:
## Field emmean SE df lower.CL upper.CL .group
## CR 71.8 3.93 14.8 63.4 80.1 1
## RF 86.8 3.93 14.8 78.4 95.2 2
##
## Stage = Maturity:
## Field emmean SE df lower.CL upper.CL .group
## CR 93.4 3.93 14.8 85.0 101.8 1
## RF 110.1 3.93 14.8 101.8 118.5 2
##
## Stage = PI:
## Field emmean SE df lower.CL upper.CL .group
## CR 50.3 3.93 14.8 41.9 58.7 1
## RF 63.2 3.93 14.8 54.8 71.5 1
##
## 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.
```

Preplant soil N uptake different at all 3 sampling timepoints.



## Graphing preplant soil\_N mean and SE

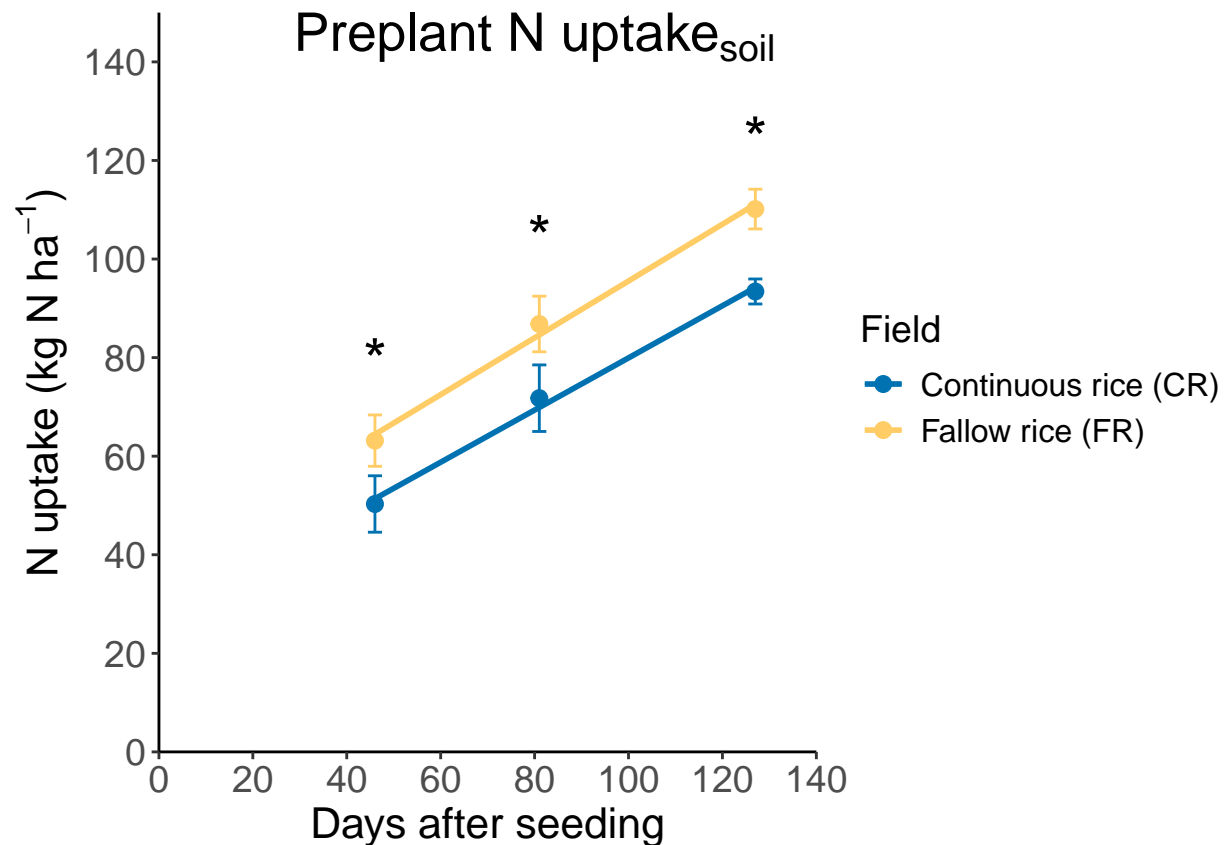
```
preplant_soilN_graphing <- preplant %>% group_by(Field, Days) %>%
  mutate(soil_N_se = sd(soil_N)/sqrt(3)) %>%
  summarise(soil_N = mean(soil_N),
            soil_N_se = mean(soil_N_se))
```

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

```
preplant_soil_N_graph <-
ggplot(preplant, aes(x=Days, y=soil_N, color=Field))+
  geom_point(data=preplant_soilN_graphing, size=2.5)+
  geom_smooth(method = lm, alpha=0)+
  scale_color_manual(values=c("#0072B2", "#FFCC66"), name = "Field", labels = c("Continuous rice (CR)", "Preplant N uptake (kg N ha⁻¹)")),
  scale_x_continuous(name="Days after seeding", limits = c(0, 140), expand = c(0, 0), breaks = seq(0, 140, 20)),
  scale_y_continuous(name=expression("N uptake (kg N 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_se, ymax=soil_N+soil_N_se), 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 = 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 = 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
  )+
  annotate(
    "text",
    x = c(80),
    y = c(140),
    label = expression(paste("Preplant N uptake"[soil])),
    size = 7,
    vjust = 0
  )
preplant_soil_N_graph
```

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

```
## Warning in is.na(x): is.na() applied to non-(list or vector) of type
## 'expression'
```



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

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

```
## Warning in is.na(x): is.na() applied to non-(list or vector) of type
## 'expression'
```

## Preplant Fert N

### Model selection and testing

```
preplant_fert_N_model <- lmer(fertiliser_N~Field*Year*Stage+(1|Blk)+(1|Blk:Field), data = preplant)
```

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

```
anova(preplant_fert_N_model)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##               Sum Sq Mean Sq NumDF DenDF F value    Pr(>F)
## Field          51.427   51.427     1    20  3.6864 0.069235 .
## Year           36.703   36.703     1     4  2.6310 0.180118
```

```
## Stage          251.851 125.926      2    20  9.0266 0.001608 **
## Field:Year      172.069 172.069      1    20 12.3343 0.002193 **
## Field:Stage      46.553  23.276      2    20  1.6685 0.213724
## Year:Stage      134.753  67.377      2    20  4.8297 0.019439 *
## Field:Year:Stage 55.821  27.910      2    20  2.0007 0.161415
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Field appears not significant

```
preplant_fert_N_means = emmeans(preplant_fert_N_model, spec = 'Field', by = 'Stage')
```

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

```
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          0.511 2.16 18   0.237  0.8154
##
## Stage = Maturity:
## contrast estimate SE df t.ratio p.value
## CR - RF         -2.639 2.16 18  -1.224  0.2368
##
## Stage = PI:
## contrast estimate SE df t.ratio p.value
## CR - RF         -5.043 2.16 18  -2.339  0.0311
##
## Results are averaged over the levels of: Year
## Degrees-of-freedom method: kenward-roger
```

```
cld(preplant_fert_N_means)
```

```
## Stage = Heading:
## Field emmean SE df lower.CL upper.CL .group
## RF      40.5 2.53 7.93    34.7    46.4 1
## CR      41.1 2.53 7.93    35.2    46.9 1
##
## Stage = Maturity:
## Field emmean SE df lower.CL upper.CL .group
## CR      45.1 2.53 7.93    39.2    50.9 1
## RF      47.7 2.53 7.93    41.9    53.6 1
##
## Stage = PI:
## Field emmean SE df lower.CL upper.CL .group
## CR      38.3 2.53 7.93    32.4    44.1 1
## RF      43.3 2.53 7.93    37.5    49.2 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.
```

Preplant Fert N appears to only be different at PI.

## Graphing preplant fert\_N mean and SE

```
preplant_fertiliser_N_graphing <- preplant %>% group_by(Field, Days) %>%
  mutate(fertiliser_N_se = sd(fertiliser_N)/sqrt(3)) %>%
  summarise(fertiliser_N = mean(fertiliser_N),
            fertiliser_N_se = mean(fertiliser_N_se))
```

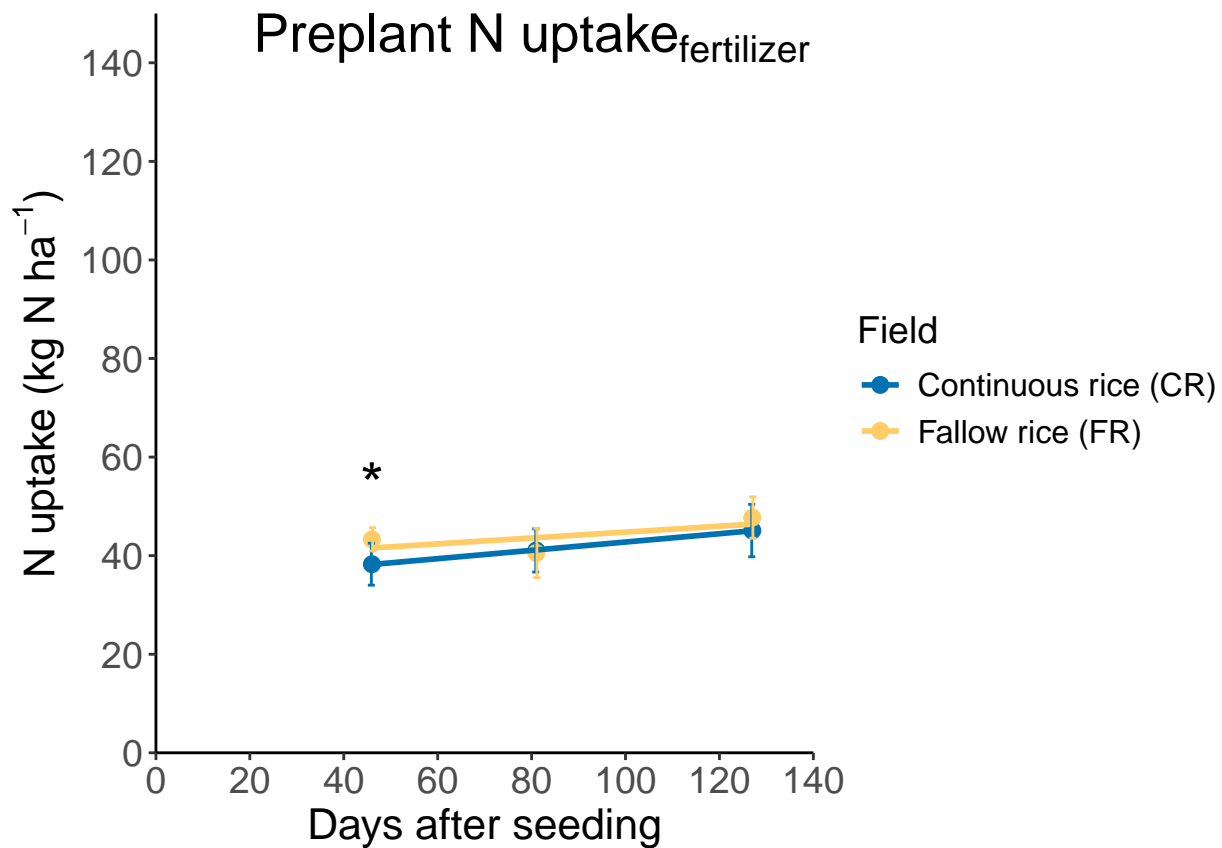
```
## 'summarise()' has grouped output by 'Field'. You can override using the
## '.groups' argument.
```

```
preplant_fertiliser_N_graph <-
ggplot(preplant, aes(x=Days, y=fertiliser_N, color=Field))+
  geom_point(data=preplant_fertiliser_N_graphing, size=2.5)+
  geom_smooth(method = lm, alpha=0)+
  scale_color_manual(values=c("#0072B2", "#FFCC66"), name = "Field", labels = c("Continuous rice (CR)",
                                                                              "Preplant fertilizer (PF)")),
  scale_x_continuous(name="Days after seeding", limits = c(0, 140), expand = c(0, 0), breaks = seq(0, 140, 20)),
  scale_y_continuous(name=expression("N uptake (kg N ha"^{-1}*")"), limits = c(0, 150), expand = c(0, 0)),
  geom_errorbar(data=preplant_fertiliser_N_graphing, aes(ymin=fertiliser_N-fertiliser_N_se, ymax=fertiliser_N+fertiliser_N_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 = 15))+
  annotate(
    "text",
    x = c(80),
    y = c(140),
    label = expression(paste("Preplant N uptake"[fertilizer])),
    size = 7,
    vjust = 0
  )+
  annotate("text",
    x = c(46), # X-axis positions for annotations
    y = c(50), # Y-axis positions for annotations
    label = "*",
    size = 8,
    vjust = 0 # Adjust vertical position of asterisks
  )

preplant_fertiliser_N_graph
```

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

```
## Warning in is.na(x): is.na() applied to non-(list or vector) of type
## 'expression'
```



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

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

```
## Warning in is.na(x): is.na() applied to non-(list or vector) of type
## 'expression'
```

## Topdress Soil N

### Model selection and testing

```
topdress_soil_N_model <- lmer(soil_N~Field*Year*Stage+(1|Blk)+(1|Blk:Field), data = topdress)
```

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

```
anova(topdress_soil_N_model)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##              Sum Sq Mean Sq NumDF DenDF  F value    Pr(>F)
## Field          403.3   403.3     1     8   24.3025  0.00115 **
## Year           29.2    29.2     1     8    1.7589  0.22137
## Stage         3245.9  3245.9     1     8  195.5819 6.625e-07 ***
## Field:Year      93.0    93.0     1     8    5.6036  0.04544 *
## Field:Stage      0.3     0.3     1     8    0.0160  0.90241
## Year:Stage      53.9    53.9     1     8    3.2450  0.10932
## Field:Year:Stage 22.7    22.7     1     8    1.3696  0.27557
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Field has strong effect on topdress soil N uptake.

```
topdress_soil_N_means = emmeans(topdress_soil_N_model,spec = 'Field',by = 'Stage')
```

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

```
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      -22.7 4.93 5.05 -4.598 0.0057
##
## Stage = Maturity:
## contrast estimate SE df t.ratio p.value
## CR - RF      -23.1 4.93 5.05 -4.684 0.0053
##
## Results are averaged over the levels of: Year
## Degrees-of-freedom method: kenward-roger
```

```
cld(topdress_soil_N_means)
```

```
## Stage = Heading:
## Field emmean SE df lower.CL upper.CL .group
## CR      54.4 3.49 10     46.7     62.2    1
## RF      77.1 3.49 10     69.3     84.9    2
##
## Stage = Maturity:
## Field emmean SE df lower.CL upper.CL .group
## CR      77.5 3.49 10     69.7     85.2    1
## RF     100.6 3.49 10     92.8    108.3    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.
```

## Graphing topdress soil\_N mean and SE

```
topdress_soil_N_graphing <- topdress %>% group_by(Field, Days) %>%
  mutate(soil_N_se = sd(soil_N)/sqrt(3)) %>%
  summarise(soil_N = mean(soil_N),
            soil_N_se = mean(soil_N_se))
```

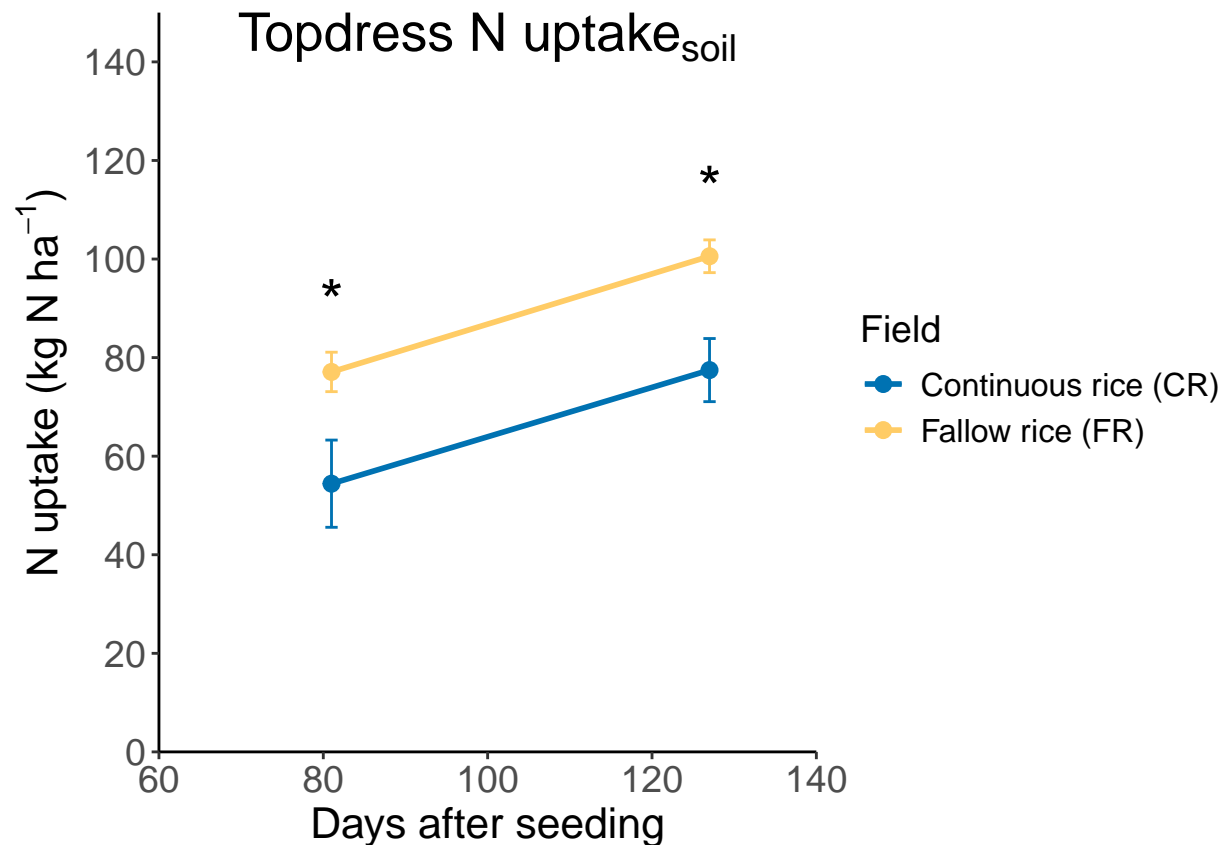
```
## 'summarise()' has grouped output by 'Field'. You can override using the
## '.groups' argument.
```

```
topdress_soil_N_graph <-
ggplot(topdress, aes(x=Days, y=soil_N, color=Field))+
  geom_point(data=topdress_soil_N_graphing, size=2.5)+
  geom_smooth(method = lm, alpha=0)+
  scale_color_manual(values=c("#0072B2", "#FFCC66"), name = "Field", labels = c("Continuous rice (CR)", "Topdress rice (TR)"),
                    breaks = seq(0, 140, 20), expand = c(0, 0))+
  scale_x_continuous(name="Days after seeding", limits = c(60, 140), expand = c(0, 0), breaks = seq(0, 140, 20),
                    labels = c("60", "80", "100", "120", "140"), expand = c(0, 0))+
  scale_y_continuous(name=expression("N uptake (kg N ha"^{-1}*")"), limits = c(0, 150), expand = c(0, 0),
                    labels = c("0", "50", "100", "150"), expand = c(0, 0))+
  geom_errorbar(data=topdress_soil_N_graphing, aes(ymin=soil_N-soil_N_se, ymax=soil_N+soil_N_se), width=0.5,
               #geom_vline(xintercept = c(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 = 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
  )+
  annotate(
    "text",
    x = c(100),
    y = c(140),
    label = expression(paste("Topdress N uptake"[soil])),
    size = 7,
    vjust = 0
  )
```

```
topdress_soil_N_graph
```

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

```
## Warning in is.na(x): is.na() applied to non-(list or vector) of type
## 'expression'
```



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

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

```
## Warning in is.na(x): is.na() applied to non-(list or vector) of type
## 'expression'
```

## Topdress Fert N

### Model selection and testing

```
topdress_fert_N_model <- lmer(fertiliser_N~Field*Year*Stage+(1|Blk)+(1|Blk:Field), data = topdress)
```

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

```
anova(topdress_fert_N_model)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##               Sum Sq Mean Sq NumDF DenDF F value    Pr(>F)
## Field          6.4224   6.4224     1     8 10.6554 0.01145 *
## Year           0.0048   0.0048     1     8  0.0080 0.93109
```



```
## Stage          0.8978  0.8978    1    8  1.4896 0.25703
## Field:Year      6.1212  6.1212    1    8 10.1557 0.01287 *
## Field:Stage     0.1181  0.1181    1    8  0.1959 0.66979
## Year:Stage      0.4537  0.4537    1    8  0.7527 0.41088
## Field:Year:Stage 1.9880  1.9880    1    8  3.2983 0.10689
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Field appears significant for preplant fert N.

```
topdress_fert_N_means = emmeans(topdress_fert_N_model, spec = 'Field', by = 'Stage')
```

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

```
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          -2.64 0.908 5.14 -2.905 0.0326
##
## Stage = Maturity:
## contrast estimate SE df t.ratio p.value
## CR - RF          -2.92 0.908 5.14 -3.213 0.0227
##
## Results are averaged over the levels of: Year
## Degrees-of-freedom method: kenward-roger
```

```
cld(topdress_fert_N_means)
```

```
## Stage = Heading:
## Field emmean SE df lower.CL upper.CL .group
## CR      8.55 0.642 10.2 7.12 9.97 1
## RF     11.18 0.642 10.2 9.76 12.61 2
##
## Stage = Maturity:
## Field emmean SE df lower.CL upper.CL .group
## CR      8.79 0.642 10.2 7.36 10.22 1
## RF     11.71 0.642 10.2 10.28 13.14 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.
```

Preplant fert N uptake different at heading and maturity.

## Graphing topdress fert\_N mean and SE

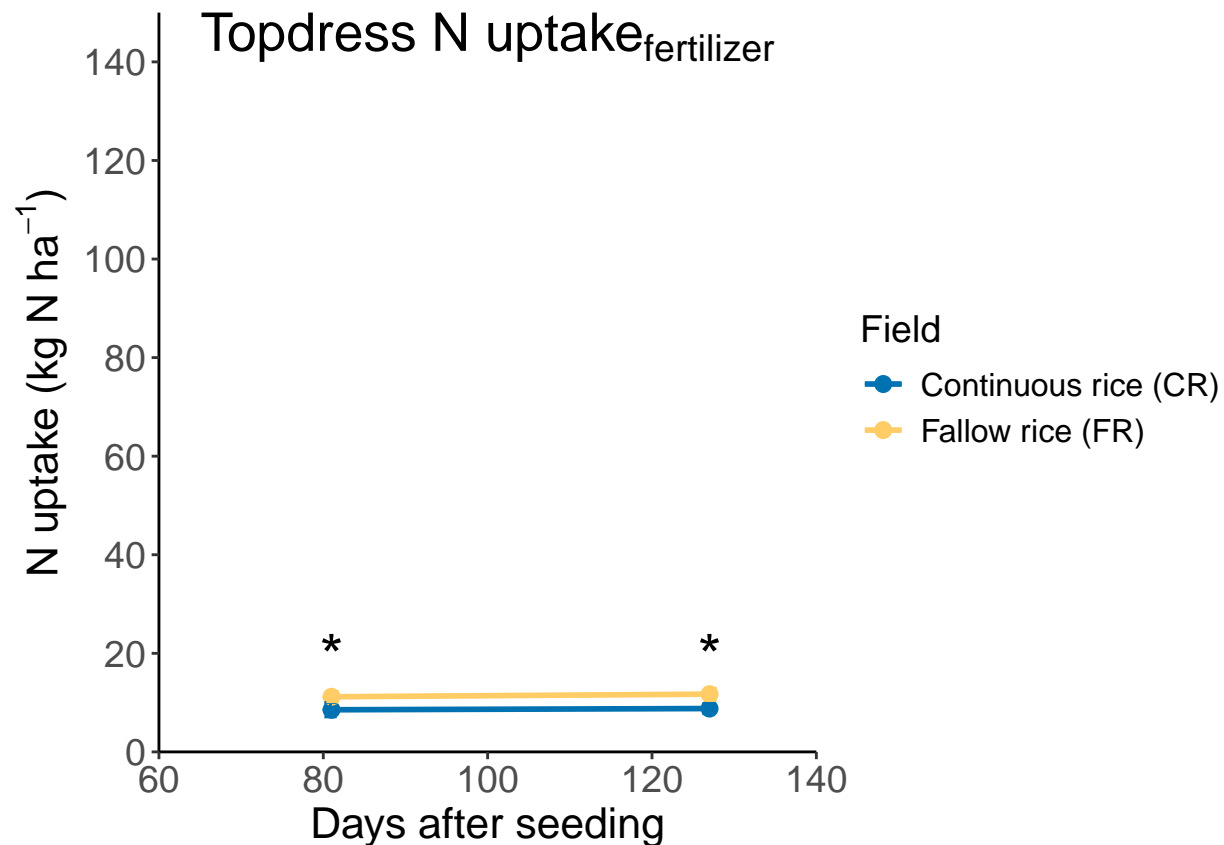
```
topdress_fertiliser_N_graphing <- topdress %>% group_by(Field, Days) %>%
  mutate(fertiliser_N_se = sd(fertiliser_N)/sqrt(3)) %>%
  summarise(fertiliser_N = mean(fertiliser_N),
            fertiliser_N_se = mean(fertiliser_N_se))
```

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

```
topdress_fertiliser_N_graph <-
ggplot(topdress, aes(x=Days, y=fertiliser_N, color=Field))+
  geom_point(data=topdress_fertiliser_N_graphing, size=2.5)+
  geom_smooth(method = lm, alpha=0)+
  scale_color_manual(values=c("#0072B2", "#FFCC66"), name = "Field", labels = c("Continuous rice (CR)", "Topdress rice (TR)"),
                    breaks = seq(0, 140, 20), expand = c(0, 0))+
  scale_x_continuous(name="Days after seeding", limits = c(60, 140), expand = c(0, 0), breaks = seq(0, 140, 20)),
  scale_y_continuous(name=expression("N uptake (kg N ha"^{-1}*")"), limits = c(0, 150), expand = c(0, 0), breaks = seq(0, 150, 20)),
  geom_errorbar(data=topdress_fertiliser_N_graphing, aes(ymin=fertiliser_N-fertiliser_N_se, ymax=fertiliser_N+fertiliser_N_se),
               #geom_vline(xintercept = c(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))+
  #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
  )+
  annotate(
    "text",
    x = c(100),
    y = c(140),
    label = expression(paste("Topdress N uptake"[fertilizer])),
    size = 7,
    vjust = 0
  )
topdress_fertiliser_N_graph
```

## 'geom\_smooth()' using formula = 'y ~ x'

## Warning in is.na(x): is.na() applied to non-(list or vector) of type  
## 'expression'



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

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

```
## Warning in is.na(x): is.na() applied to non-(list or vector) of type
## 'expression'
```

## Total N uptake

```
all_data$total_N <- all_data$fertiliser_N + all_data$soil_N
```

```
all_data %>% group_by(Topdress, Stage, Field) %>% summarise(total_N = mean(total_N))
```

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

```
## # A tibble: 10 x 4
## # Groups:   Topdress, Stage [5]
##   Topdress Stage   Field total_N
##   <fct>    <fct>   <fct>   <dbl>
## 1 N       Heading CR      113.
```

```
## 2 N      Heading RF      127.
## 3 N      Maturity CR     138.
## 4 N      Maturity RF     158.
## 5 N      PI          CR     88.6
## 6 N      PI          RF     106.
## 7 Y      Heading CR      63.0
## 8 Y      Heading RF      88.3
## 9 Y      Maturity CR      86.3
## 10 Y     Maturity RF     112.
```

```
preplant_all <- cbind(preplant_soilN_graphing,
                      preplant_fertiliser_N_graphing %>% ungroup()%>% select(-Days, -Field) %>% mutate(Topdress = 0))
topdress_all <- cbind(topdress_soil_N_graphing,
                     topdress_fertiliser_N_graphing %>% ungroup()%>% select(-Days, -Field) %>% mutate(Topdress = 1))
for_excel <- rbind(preplant_all, topdress_all)
write_xlsx(for_excel, "fert_soil_N_by_trt_and_topdress.xlsx")
```