# N uptake calculations

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## Contents



## Necessary libraries

## Read and check data

```
#read data
master = read_excel('SIF_NRate_NUptake_Base_Dataframe.xlsx', sheet = 1)

master$Sample_Weight_mg <- as.numeric(master$Sample_Weight_mg)

str(master)
```

```
## tibble [336 x 12] (S3: tbl_df/tbl/data.frame)
##  $ SampleID                     : chr [1:336] "701-MG" "702-MG" "703-MG" "704-MG" ...
##  $ SIF_N_µg                     : num [1:336] 85.8 56.2 65.3 41.8 73.9 ...
##  $ Sample_Weight_mg             : num [1:336] 5.5 4.94 4.98 4.72 5.23 ...
##  $ Dry_Sample_Weight_g          : num [1:336] 5264105 9981691 7902092 8450992 5596197 ...
##  $ Area_harvested_m2            : num [1:336] 10000 10000 10000 10000 10000 10000 10000 10000 10000 1
##  $ Dry_sample_moisture_percent  : num [1:336] 14 14 14 14 14 14 14 14 14 14 ...
##  $ Microbalance_moisture_percent: num [1:336] 9.76 9.76 9.76 9.76 9.76 9.76 9.76 9.76 9.76 9.76 ...
```

```
##  $ Stage                         : chr [1:336] "Maturity_Grain" "Maturity_Grain" "Maturity_Grain" "Ma
##  $ Treatment                     : chr [1:336] "FR" "FR" "FR" "FR" ...
##  $ Blk                           : num [1:336] 7 7 7 7 7 7 7 7 7 7 ...
##  $ Topdress                      : chr [1:336] "NIL" "NIL" "NIL" "NIL" ...
##  $ Year                          : num [1:336] 2023 2023 2023 2023 2023 ...
```

```
table(master$Stage)
```

```
##
##        Heading Maturity_Grain Maturity_Straw             PI
##             48            132            132             24
```

```
table(master$Treatment)
```

```
##
## CR FR
## 36 36
```

```
table(master$Topdress)
```

```
##
##   0   1 NIL
##  96  72 168
```

```
table(master$Blk)
```

```
##
##  7  8  9
## 24 24 24
```

```
table(master$Year)
```

```
##
## 2021 2022 2023
##  132  132   72
```

```
#dataset looks good and complete
```

## N uptake calculations

N uptake for PI and 50% heading are determined from non-segregated plant parts. i.e. the whole plant was ground to a powder together and is representative of the crop's N uptake. As most of the tissue here is vegetative, we assume that ambient moisture is the same as straw (8.27%)

N uptake for maturity are determined from separated plant parts - grain and straw. This step calculates N present in grain and straw, but do not sum them yet. Moisture for is 8.27% for straw and 9.76% for grains.

Dry samples were measured after stabilizing in the oven for a period of time (>24hrs) and was measured to be 1.9%.

For 2023, we directly used yield. Grain yield was reported at 14%

For 2023, grain was harvested by combine. A sub-sample was taken to evaluate N uptake. Harvest index (HI) was quantified from this subsample and used to estimate straw weight.

For for information on moisture calculations: https://edis.ifas.ufl.edu/publication/AG442

```
#Getting: g N per g of microbalanced sample (g/g)

master$N_per_g_microbalanced_sample <- ((master$SIF_N_µg)/(master$Sample_Weight_mg))/1000

#Dry sample weight is at 1.9% for 2021 and 2022 samples, 14% for 2023 samples
#We need to correct the weight for ambient moisture where the samples were measured into tin capsules

master$Ambient_Sample_Weight_g <- master$Dry_Sample_Weight_g*((100-master$Dry_sample_moisture_percent)/

str(master)
```

```
## tibble [336 x 14] (S3: tbl_df/tbl/data.frame)
##  $ SampleID                     : chr [1:336] "701-MG" "702-MG" "703-MG" "704-MG" ...
##  $ SIF_N_µg                     : num [1:336] 85.8 56.2 65.3 41.8 73.9 ...
##  $ Sample_Weight_mg             : num [1:336] 5.5 4.94 4.98 4.72 5.23 ...
##  $ Dry_Sample_Weight_g          : num [1:336] 5264105 9981691 7902092 8450992 5596197 ...
##  $ Area_harvested_m2            : num [1:336] 10000 10000 10000 10000 10000 10000 10000 10000 10000 1
##  $ Dry_sample_moisture_percent  : num [1:336] 14 14 14 14 14 14 14 14 14 14 ...
##  $ Microbalance_moisture_percent: num [1:336] 9.76 9.76 9.76 9.76 9.76 9.76 9.76 9.76 9.76 9.76 ...
##  $ Stage                        : chr [1:336] "Maturity_Grain" "Maturity_Grain" "Maturity_Grain" "Ma
##  $ Treatment                    : chr [1:336] "FR" "FR" "FR" "FR" ...
##  $ Blk                          : num [1:336] 7 7 7 7 7 7 7 7 7 7 ...
##  $ Topdress                     : chr [1:336] "NIL" "NIL" "NIL" "NIL" ...
##  $ Year                         : num [1:336] 2023 2023 2023 2023 2023 ...
##  $ N_per_g_microbalanced_sample : num [1:336] 0.0156 0.01139 0.01311 0.00885 0.01412 ...
##  $ Ambient_Sample_Weight_g      : num [1:336] 5016767 9512693 7530806 8053916 5333255 ...
```

```
#Total N uptake = g N per g of microbalanced sample (g/g)*total sample weight (g)/area harvested (m2)
#then scale from g/m2 to kg/ha

master$N_total_kgha <- ((master$N_per_g_microbalanced_sample*master$Ambient_Sample_Weight_g)/1000) * (1

str(master)
```

```
## tibble [336 x 15] (S3: tbl_df/tbl/data.frame)
##  $ SampleID                     : chr [1:336] "701-MG" "702-MG" "703-MG" "704-MG" ...
##  $ SIF_N_µg                     : num [1:336] 85.8 56.2 65.3 41.8 73.9 ...
##  $ Sample_Weight_mg             : num [1:336] 5.5 4.94 4.98 4.72 5.23 ...
##  $ Dry_Sample_Weight_g          : num [1:336] 5264105 9981691 7902092 8450992 5596197 ...
##  $ Area_harvested_m2            : num [1:336] 10000 10000 10000 10000 10000 10000 10000 10000 10000 1
##  $ Dry_sample_moisture_percent  : num [1:336] 14 14 14 14 14 14 14 14 14 14 ...
##  $ Microbalance_moisture_percent: num [1:336] 9.76 9.76 9.76 9.76 9.76 9.76 9.76 9.76 9.76 9.76 ...
##  $ Stage                        : chr [1:336] "Maturity_Grain" "Maturity_Grain" "Maturity_Grain" "Ma
##  $ Treatment                    : chr [1:336] "FR" "FR" "FR" "FR" ...
##  $ Blk                          : num [1:336] 7 7 7 7 7 7 7 7 7 7 ...
##  $ Topdress                     : chr [1:336] "NIL" "NIL" "NIL" "NIL" ...
##  $ Year                         : num [1:336] 2023 2023 2023 2023 2023 ...
```

```
##  $ N_per_g_microbalanced_sample : num [1:336] 0.0156 0.01139 0.01311 0.00885 0.01412 ...
##  $ Ambient_Sample_Weight_g      : num [1:336] 5016767 9512693 7530806 8053916 5333255 ...
##  $ N_total_kgha                 : num [1:336] 78.3 108.4 98.7 71.3 75.3 ...
```

## Getting the maturity summed values: summing N uptake values of straw and grain

```
#separate into straw and grains for summing
maturity_straw <- master %>%  filter(Stage == ("Maturity_Straw"))
maturity_grain <- master %>%  filter(Stage == ("Maturity_Grain"))


#maturity_straw <-
 # maturity_straw %>%
  #filter(Year != 2021) %>%
 # mutate(Plot = substr(SampleID, 1, 3))

#maturity_grain <-
 # maturity_straw %>%
  #filter(Year != 2021) %>%
  #mutate(Plot = substr(SampleID, 1, 3))

as.numeric(maturity_straw$Plot) - as.numeric(maturity_grain$Plot)
```

```
## Warning: Unknown or uninitialised column: 'Plot'.
## Unknown or uninitialised column: 'Plot'.
```

```
## numeric(0)
```

```
#Create dataframe for maturity total N uptake
maturity_summed <- as.data.frame(rbind(master[1:36,], master[109:156,], master[241:288,]))
# just so we can keep the other columns
maturity_summed$Stage <- "Maturity"

#sum grain and straw into one maturity total N uptake dataframe
maturity_summed$N_total_kgha <- maturity_straw$N_total_kgha+maturity_grain$N_total_kgha

str(maturity_summed)
```

```
## 'data.frame':    132 obs. of  15 variables:
##  $ SampleID                    : chr  "701-MG" "702-MG" "703-MG" "704-MG" ...
##  $ SIF_N_µg                    : num  85.8 56.2 65.3 41.8 73.9 ...
##  $ Sample_Weight_mg            : num  5.5 4.94 4.98 4.72 5.23 ...
##  $ Dry_Sample_Weight_g         : num  5264105 9981691 7902092 8450992 5596197 ...
##  $ Area_harvested_m2           : num  10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 .
##  $ Dry_sample_moisture_percent : num  14 14 14 14 14 14 14 14 14 14 ...
##  $ Microbalance_moisture_percent: num  9.76 9.76 9.76 9.76 9.76 9.76 9.76 9.76 9.76 9.76 ...
##  $ Stage                       : chr  "Maturity" "Maturity" "Maturity" "Maturity" ...
##  $ Treatment                   : chr  "FR" "FR" "FR" "FR" ...
##  $ Blk                         : num  7 7 7 7 7 7 7 7 7 7 ...
```

```
##  $ Topdress                      : chr  "NIL" "NIL" "NIL" "NIL" ...
##  $ Year                          : num  2023 2023 2023 2023 2023 ...
##  $ N_per_g_microbalanced_sample : num  0.0156 0.01139 0.01311 0.00885 0.01412 ...
##  $ Ambient_Sample_Weight_g       : num  5016767 9512693 7530806 8053916 5333255 ...
##  $ N_total_kgha                  : num  163.4 165.2 175.4 95.6 151.9 ...
```

## Bind everything back again - this is such a pain in the rear end. Add in plots and Nrates

```
#Well I was a clown when I started the PhD, so I named everything for excel LOL.
#Because name formatting was different by year, I split the dataframe by year and wrangle it as needed

# extract PI and Heading N uptake values
master_maturity_summed <- rbind(master[73:108,], master[205:240,], maturity_summed)

#add in plot and treatments

master_maturity_summed_2021 <-
  master_maturity_summed %>%
  filter(Year == 2021) %>%
  mutate(Plot = substr(SampleID, 5, 7)) %>%
  mutate(Treatment = case_when(
  Plot %in% c("101", "102", "103", "104", "105", "106",
              "201", "202", "203", "204", "205", "206",
              "301", "302", "303", "304", "305", "306") ~ "FR",
  Plot %in% c("107", "108", "109", "110", "111", "112",
              "207", "208", "209", "210", "211", "212",
              "307", "308", "309", "310", "311", "312") ~ "CR",
  TRUE ~ "Other" # This line handles cases where plot is not listed
  ))

master_maturity_summed_others <-
  master_maturity_summed %>%
  filter(Year != 2021) %>%
  mutate(Plot = substr(SampleID, 1, 3)) %>%
  mutate(Treatment = case_when(
  Plot %in% c("401", "402", "403", "404", "405", "406",
              "501", "502", "503", "504", "505", "506",
              "601", "602", "603", "604", "605", "606",
              "701", "702", "703", "704", "705", "706",
              "801", "802", "803", "804", "805", "806",
              "901", "902", "903", "904", "905", "906") ~ "FR",
  Plot %in% c("407", "408", "409", "410", "411", "412",
              "507", "508", "509", "510", "511", "512",
              "607", "608", "609", "610", "611", "612",
              "707", "708", "709", "710", "711", "712",
              "807", "808", "809", "810", "811", "812",
              "907", "908", "909", "910", "911", "912") ~ "CR",
  TRUE ~ "Other" # This line handles cases where plot is not listed
  ))
```

```r
master_maturity_summed_clean <- rbind(master_maturity_summed_2021, master_maturity_summed_others)

# add in blk, days

master_maturity_summed_clean <- master_maturity_summed_clean %>%
  mutate(Blk = substr(Plot, 1, 1))%>%
  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
  ))

# read in Nrate reference file

#clean the data frame to have one plot match with one Nrate
Nrate_ref <- read_excel("D:/Academics/UC Davis/School Work/Linquist Lab/Data/R stats/Agronomic paper/Yi

# put in the Nrate for all the plots
master_maturity_summed_clean <- master_maturity_summed_clean %>%
  left_join(Nrate_ref %>% select(Plot, Nrate_kgha), by = "Plot")
```

## Export dataframe

```r
for_export <- master_maturity_summed_clean %>%
                          select(SampleID,
                                 Plot,
                                 Stage,
                                 Treatment,
                                 Year,
                                 Topdress,
                                 N_total_kgha,
                                 Blk,
                                 Days,
                                 Nrate_kgha)

head(master_maturity_summed_clean)
```

```
## # A tibble: 6 x 18
##   SampleID SIF_N_µg Sample_Weight_mg Dry_Sample_Weight_g Area_harvested_m2
##   <chr>       <dbl>            <dbl>               <dbl>             <dbl>
## 1 RES 104      79.3             5.39                286.                 1
## 2 RES 201      99.0             5.28                270.                 1
## 3 RES 304      74.4             5.25                341.                 1
## 4 RES 112      79.6             5.50                231.                 1
## 5 RES 212      73.3             5.02                243.                 1
## 6 RES 310      61.9             4.84                235.                 1
## # i 13 more variables: Dry_sample_moisture_percent <dbl>,
## #   Microbalance_moisture_percent <dbl>, Stage <chr>, Treatment <chr>,
## #   Blk <chr>, Topdress <chr>, Year <dbl>, N_per_g_microbalanced_sample <dbl>,
```

```
## #   Ambient_Sample_Weight_g <dbl>, N_total_kgha <dbl>, Plot <chr>, Days <chr>,
## #   Nrate_kgha <dbl>
```

```
write_xlsx(for_export, "N_uptake_Maturity_Summed_Clean.xlsx")
```

## Filtering for N uptake over time

```
N_over_time <- master_maturity_summed_clean %>%
               filter(Topdress == '0') %>%
               select(SampleID,
                                Plot,
                                Stage,
                                Treatment,
                                Year,
                                Topdress,
                                N_total_kgha,
                                Blk,
                                Days,
                                Nrate_kgha)

write_xlsx(N_over_time, "D:/Academics/UC Davis/School Work/Linquist Lab/Data/R stats/Agronomic paper/N
```

## Plot a small visualization to make sure things generally look good

```
Nrate_trial <- master_maturity_summed_clean %>%
  #filter(Year != 2023) %>%
  filter(Topdress!=1) %>%
  filter(Stage=="Maturity") %>%
  mutate(Year= as.factor(Year))
  #group_by(Treatment, Nrate_kgha, Year) %>%
  #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))


all_Nuptake_graph <-
ggplot(Nrate_trial, aes(x=Nrate_kgha, y=N_total_kgha, color=Treatment,shape = Year))+
  geom_point(size=2.5)+
  geom_smooth(aes(group = Treatment),method = lm, alpha=0.5)+
  scale_color_manual(values=c("#0072B2","#FFCC66"), name = "Treatment", labels = c("Continuous rice (CR
  scale_x_continuous(name=expression("N Rate (kg N ha"^{-1}*")"), limits = c(-20, 300), expand = c(0, 0
  scale_y_continuous(name=expression("N Uptake (kg N ha"^{-1}*")"), limits = c(0, 300), expand = c(0, 0
  #geom_errorbar(aes(ymin=N_total_kgha-N_total_kgha_se, ymax=N_total_kgha+N_total_kgha_se), width=3,pos
  #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))
```

```
ggsave(filename = "all_Nuptake_graph.png",  # Include the file extension here
       plot = all_Nuptake_graph,            # Specify the plot
       path = "D:/Academics/UC Davis/School Work/Linquist Lab/Data/R stats/Agronomic paper/Figures",
       dpi = 400,
       height = 30, width = 30, units = "cm")
```

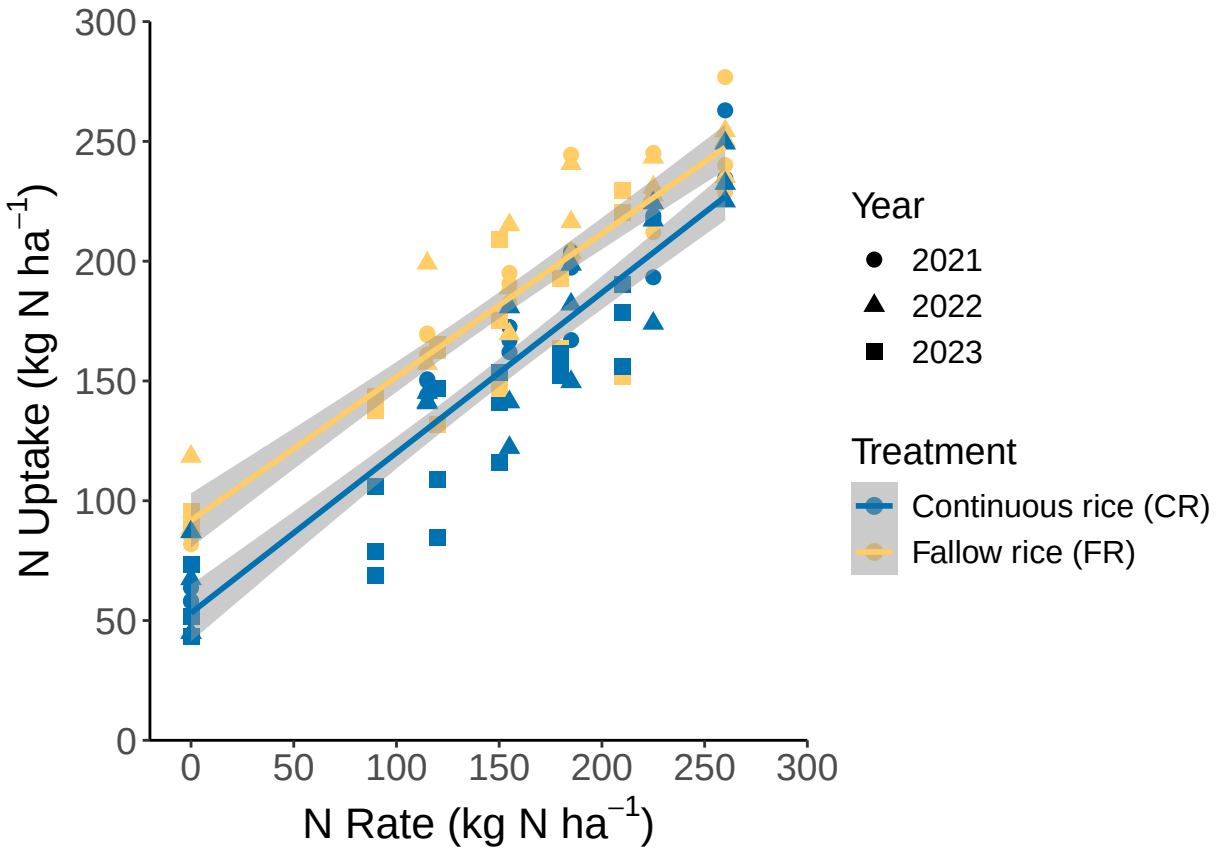
```
## `geom_smooth()` using formula = 'y ~ x'

## Warning: The following aesthetics were dropped during statistical transformation: shape.
## i This can happen when ggplot fails to infer the correct grouping structure in
##   the data.
## i Did you forget to specify a `group` aesthetic or to convert a numerical
##   variable into a factor?
```

```
all_Nuptake_graph
```

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

## Warning: The following aesthetics were dropped during statistical transformation: shape.
## i This can happen when ggplot fails to infer the correct grouping structure in
##   the data.
## i Did you forget to specify a `group` aesthetic or to convert a numerical
##   variable into a factor?
```



```
#plots seem to make sense. Lets proceed with more fun things!!!!
```