

Cumulative_Seasonal_Emissions

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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(openxlsx)
library(zoo)
library(dplyr)
library(tidyr)
library(zoo)
```

Read Excel daily flux values(computed from gas analyses)

```
flux <- read_excel("Cable_Bateria_2023_GHG_Data_Complete_21Jan2024.xlsx", sheet = 1)
str(flux)
```

```
## tibble [48 x 6] (S3: tbl_df/tbl/data.frame)
## $ Plot          : chr [1:48] "SH1" "CB-SL1" "CB-SH1" "C1" ...
## $ CH4_flux_g_ha_day : num [1:48] 360 575 557 2767 935 ...
## $ Days_After_Seeding: chr [1:48] "35 " "35 " "35 " "35 " ...
## $ Rep           : num [1:48] 1 1 1 1 2 2 2 2 3 3 ...
## $ Trt           : chr [1:48] "SH" "CB-SL" "CB-SH" "C" ...
## $ Date          : POSIXct[1:48], format: "2023-06-27" "2023-06-27" ...
```

```
flux$Plot <- as.factor(flux$Plot)
```

```
flux %>%
  summarise(n_dates = n_distinct(Date))
```

```
## # A tibble: 1 x 1
##   n_dates
##   <int>
## 1       3
```

Linear interpolation

```
flux_2023 <- flux %>%
  filter(Date >= as.POSIXct("2023-06-26") & Date <= as.POSIXct("2023-08-14"))
```

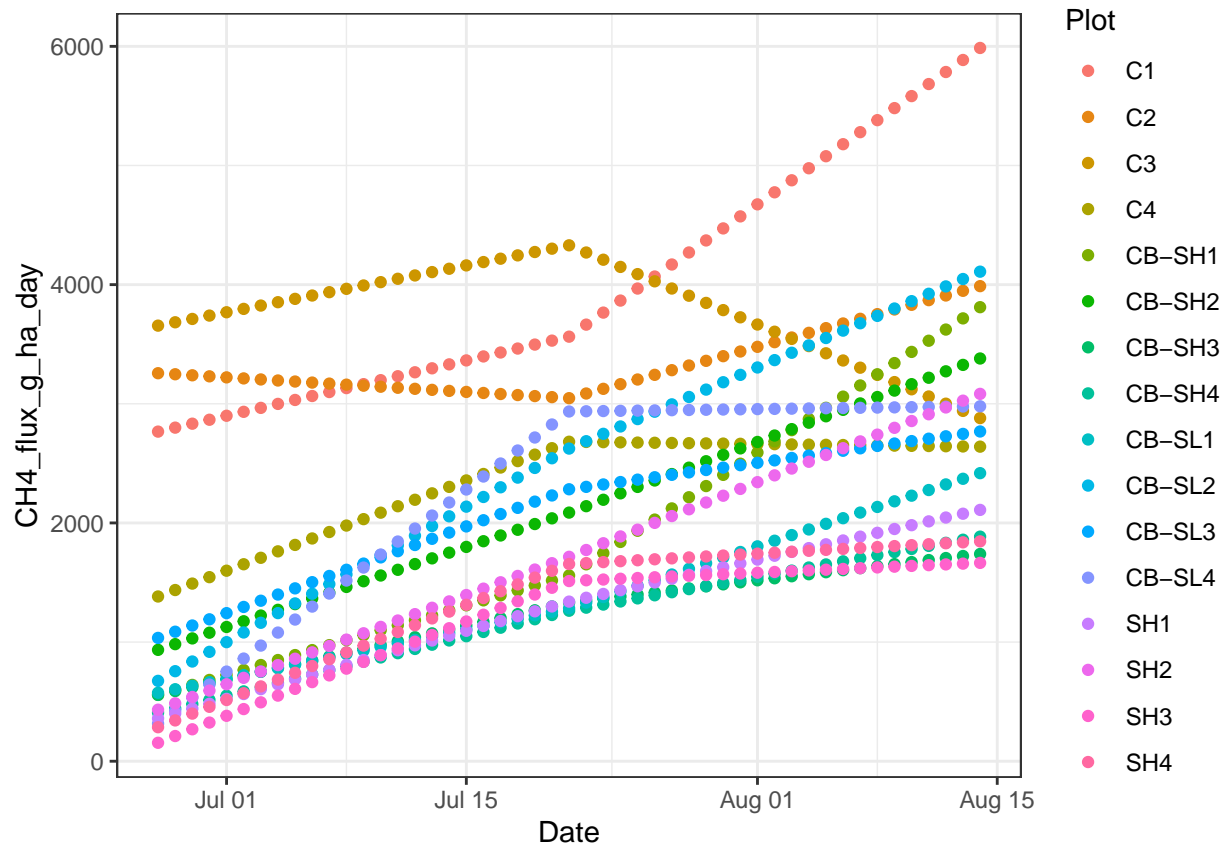
```
start_date <- as.Date("2023-06-27")
end_date <- as.Date("2023-08-14")
date_seq <- seq.Date(start_date, end_date, by = "day")
```

```
interpolated <- flux_2023 %>%
  group_by(Plot) %>%
  complete(Date = date_seq) %>%
  #mutate(Trt = Trt)
  ungroup()
```

```
interpolated <- interpolated %>%
  group_by(Plot) %>%
  mutate(CH4_flux_g_ha_day = na.approx(CH4_flux_g_ha_day, rule = 2)) %>%
  ungroup()
```

```
rice_seasonal_emissions <- interpolated %>%
  group_by(Plot) %>%
  summarize(total_CH4_emissions = sum(CH4_flux_g_ha_day, na.rm = TRUE)) %>%
  mutate(total_CH4_emissions_kg_ha = total_CH4_emissions/1000) %>%
  mutate(Treatment = str_sub(Plot, 1, -2))
```

```
ggplot(interpolated, aes(y=CH4_flux_g_ha_day, x=Date, color = Plot)) + geom_point()
```



```
#ggplot(flux_2025_rice_interpolated, aes(y=N2O_g_ha_day, x=Date, color = Plot)) + geom_point()
```

Statistical analysis

```
model <- lm(total_CH4_emissions_kg_ha~Treatment, data=rice_seasonal_emissions)
anova(model)
```

```
## Analysis of Variance Table
##
## Response: total_CH4_emissions_kg_ha
##           Df Sum Sq Mean Sq F value    Pr(>F)
## Treatment  3 22361.4   7453.8   11.997 0.0006353 ***
## Residuals 12  7455.9    621.3
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Treatment_means = emmeans(model, spec = 'Treatment')
Treatment_effects = contrast(Treatment_means, method = 'pairwise', adjust = "Tukey")
summary(Treatment_effects)
```

```
## contrast      estimate    SE df t.ratio p.value
## C - (CB-SH)      85.8 17.6 12   4.868  0.0019
## C - (CB-SL)      63.5 17.6 12   3.602  0.0166
## C - SH           96.3 17.6 12   5.466  0.0007
## (CB-SH) - (CB-SL) -22.3 17.6 12  -1.266  0.5996
## (CB-SH) - SH      10.5 17.6 12   0.597  0.9309
## (CB-SL) - SH      32.8 17.6 12   1.864  0.2930
##
## P value adjustment: tukey method for comparing a family of 4 estimates
```

```
cld(Treatment_means) #note that the cumulative emission here is in kgCH4/ha-1
```

```
## Treatment emmean    SE df lower.CL upper.CL .group
## SH          68.4 12.5 12    41.2    95.5    1
## CB-SH       78.9 12.5 12    51.8   106.1    1
## CB-SL      101.2 12.5 12    74.1   128.4    1
## C          164.7 12.5 12   137.6   191.9    2
##
## Confidence level used: 0.95
## P value adjustment: tukey method for comparing a family of 4 estimates
## 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.
```

Percentage decreases

```
reduction <- as.data.frame(Treatment_means) %>%
  mutate(C_value = emmean[Treatment == "C"],
         pct_reduction = (C_value - emmean) / C_value * 100) %>%
  select(Treatment, emmean, pct_reduction)

reduction #note that the cumulative emission (emmean) here is in kgCH4/ha-1
```

```
## Treatment    emmean pct_reduction
## 1          C 164.71726      0.00000
## 2        CB-SH  78.91170     52.09263
## 3        CB-SL 101.23188     38.54203
## 4          SH  68.38287     58.48469
```